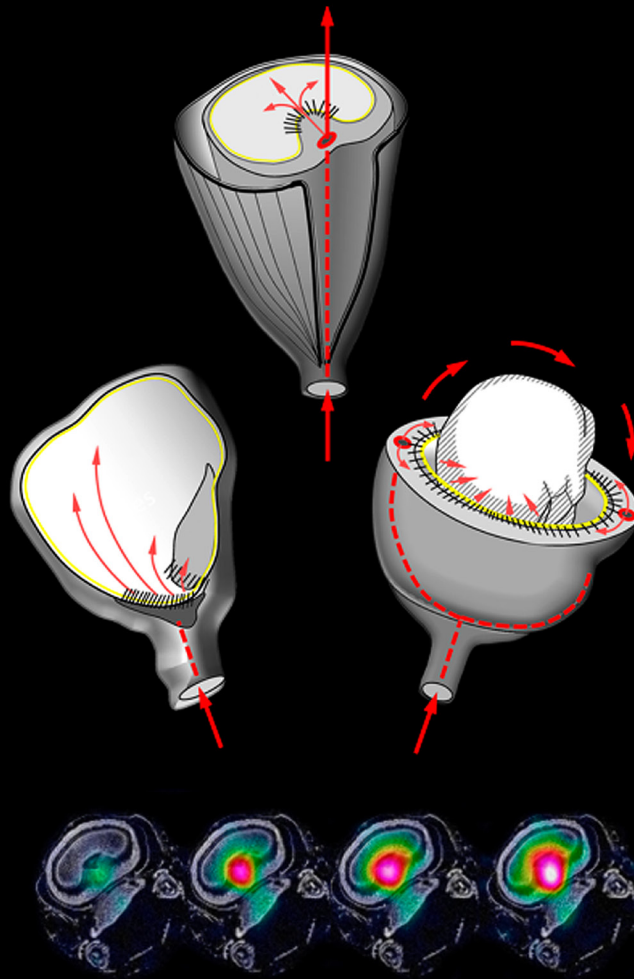


ADVANCES IN SEED BIOLOGY

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ADVANCES IN SEED BIOLOGY

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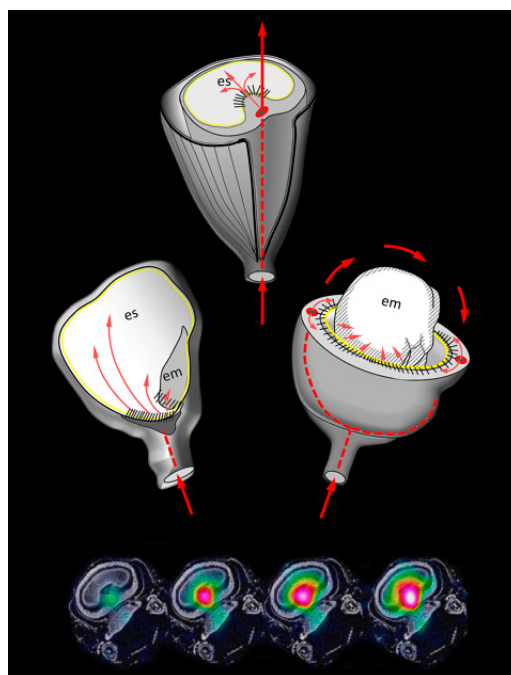


Image shows various routes of assimilate delivery (red arrows) via seed coat to the developing embryo and endosperm (from left: maize, barley and pea). For details, see Radchuk and Borisjuk (2014), <http://dx.doi.org/10.3389/fpls.2014.00510>.

The seed plays a fundamental role in plant reproduction as well as a key source of energy, nutrients and raw materials for developing and sustaining humanity. With an expanding and generally more affluent world population projected to reach nine billion by mid-century, coupled to diminishing availability of inputs, agriculture is facing increasing challenges to ensure sufficient grain production. A deeper understanding of seed development, evolution and physiology will undoubtedly provide a fundamental basis to improve plant breeding practices and ultimately crop yields.

Recent advances in genetic, biochemical, molecular and physiological research, mostly brought about by the deployment of novel high-throughput and high-sensitivity technologies, have begun to uncover and connect the molecular networks that control and integrate different aspects of seed development and help determine the economic value of grain crops with unprecedented details.

The objective of this e-book is to provide a compilation of original research articles, reviews, hypotheses and perspectives that have recently been published in *Frontiers in Plant Science*, *Plant Evolution and Development* as part of the Research Topic entitled “Advances in Seed Biology”.

Editing this Research Topic has been an extremely interesting, educational and rewarding experience, and we sincerely thank all authors who contributed their expertise and in-depth knowledge of the different topics discussed. We hope that the information presented here will help to establish the state of the art of this field and will convey how exciting and important studying seeds is and hopefully will stimulate a new crop of scientists devoted to investigating the biology of seeds.

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New insights into how seeds are made

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Keywords: seed development, seed metabolism, seed genetics, seed epigenetics, seed evolution, seed physiology, seed genomics, seed germination

It is difficult to overstate the importance of seeds for the evolutionary success of the spermatophytes and the development of human cultures and their survival. For hundreds of millions of years since their appearance in the Devonian period, seed plants have colonized many environments, thanks in part to several adaptations, including seed formation. Seeds can spread over large areas over long time spans, while also protecting the embryo from pathogens and adverse environmental conditions. Seeds vary greatly in shape and structure, but they typically possess three major components: the sporophyte (*i.e.*, the embryo), a storage metabolite compartment (*i.e.*, cotyledons, endosperm or perisperm) enabling the early growth of the seedling before it is autotrophic, and a protective coat. Since agriculture began around 10,000 years ago, certain seed plants have been domesticated and methodically bred to provide food and raw materials. Today, vast swaths of land are planted to a few grain crops that have proven highly nutritious and productive. In view of the exploding (and generally more affluent) human population, which is projected to reach nine billion by mid-century, crop genetic erosion, constrained fossil fuel availability, and global climate change put enormous pressure on agriculture. The continuous genetic improvement of seed plants has played a key role in sustaining the human population for thousand of years, but additional improvements are necessary in the future. A clear understanding of the biological processes controlling seed development, quality, and yield is required to meet the challenges facing agriculture.

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Our comprehension of seed development has progressed considerably, thanks to model plant systems, development of high through-put techniques, and increased understanding of genetic and biochemical pathways. The goal of this Research Topic on Advances in Seed Biology is to update key aspects of seed development, evolution and physiology.

The first step in seed formation is a double fertilization event, which involves the egg cell and central cell in the female gametophyte each fusing with a sperm cell. This process is tightly regulated, and Bleckmann et al. (2014) describe the complex signaling pathways that control pollen tube growth, communication with female flower structures, and gametes interaction. The fertilized egg and central cell go on to form the embryo and the endosperm, respectively, by multiplying and expanding through several variant cell cycles, such as mitotic cell proliferation, acytokinetic mitosis, and endoreduplication. Dante et al. (2014) and Sabelli et al. (2014) describe core cell cycle factors that play important roles in the regulation of the cell division cycle during seed development and its coordination with cell differentiation and maturation.

Seed development and the success of sexual plant reproduction are affected by the ploidies of the parental gametes and by epigenetic mechanisms causing parent-of-origin-dependent gene expression (*i.e.*, genomic imprinting). These phenomena are commonly interpreted according to the parental-conflict hypothesis, but a reassessment may be in order. In his perspective on maize, Birchler (2014) focuses on crosses between parents with abnormal genome ratios, which generally result in endosperm failure and seed abortion.

He proposes this interploidy barrier can be explained primarily by genome dosage interaction between the female gametophyte and the triploid primary endosperm nucleus. Furthermore, based on information derived from large transcriptomic studies, Bai and Settles (2015) observe that genomic imprinting, although widespread among angiosperms, is neither highly conserved with respect to the nature and patterns of genes or genome fractions involved, nor does it appear to be necessary. Thus, these authors propose imprinting may represent an evolutionary strategy that, through specific epigenetic regulation early in seed development, allows rapid evolution and neofunctionalization of new alleles without necessarily compromising fitness of the adult sporophyte.

Becker et al. (2014) present an overview of transcriptome-based analyses for unraveling gene networks and pathways controlling seed development, which are especially valuable when coupled with the ability to isolate relatively homogeneous cell populations.

Li and Li (2014) review regulation of protein degradation by the 26S proteasome as an emerging critical mechanism by which seed size and organ growth are controlled. Burton and Fincher (2014) take an evolutionary perspective to compare composition of cell walls in cereal grains, which are particularly rich in (1,3;1,4)- β -glucans, to those of other monocots and dicots.

A number of articles focus on seed metabolism. Galili et al. (2014) discuss how seed metabolism and energy status are impacted by low levels of oxygen, photosynthetic activity, and effects on the Asp-family of amino acids. Wu and Messing (2014) discuss how different proteins and sulfur are dynamically balanced in developing maize seeds and describe the outcomes of experiments aimed at shifting the seed proteome to increase seed nutritional value. Herman (2014) analyses the interplay between

protein content and composition in the soybean proteome and the critical roles played both by genetic and physiological factors. Arcalis et al. (2014) review pathways affecting protein trafficking and storage organelle development in cereal seeds and discuss their significance with regard to our ability to produce recombinant proteins through transgenic approaches. Mainieri et al. (2014) show accumulation of the maize 27-kD γ -zein in protein bodies depends on several cysteine residues in its N-terminal domain, which results in insoluble endoplasmic reticulum (ER)-localized prolamin accretions. Holding (2014) provides an update on cereal storage protein accumulation, particularly in maize, and on past and present strategies to study their function in developing endosperm.

Ravel et al. (2014) present a detailed analysis of promoter regions in wheat seed storage protein alleles and identify conserved and unique motifs. Burrieza et al. (2014) draw several important analogies between quinoa and grass seed structures, suggesting these species underwent convergent evolution with regard to seed structure and the function of specific compartments. Domínguez and Cejudo (2014) discuss the regulation of programmed cell death and how it affects different tissues during cereal seed development and germination. Radchuk and Borisjuk (2014) assess roles of the seed coat in protection, transducing environmental signals to inner seed compartments and influencing seed size. Smýkal et al. (2014) provide a detailed discussion of the role of the testa in controlling legume seed germination through its physical and chemical properties. And last but not least, Nonogaki (2014) provides a critical and stimulating review of the mechanisms involved in seed dormancy and germination, highlighting the emergence of new paradigms integrating genetics, the action of hormones and epigenetic modifications of chromatin conformation and gene activity.

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The beginning of a seed: regulatory mechanisms of double fertilization

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The launch of seed development in flowering plants (angiosperms) is initiated by the process of double fertilization: two male gametes (sperm cells) fuse with two female gametes (egg and central cell) to form the precursor cells of the two major seed components, the embryo and endosperm, respectively. The immobile sperm cells are delivered by the pollen tube toward the ovule harboring the female gametophyte by species-specific pollen tube guidance and attraction mechanisms. After pollen tube burst inside the female gametophyte, the two sperm cells fuse with the egg and central cell initiating seed development. The fertilized central cell forms the endosperm while the fertilized egg cell, the zygote, will form the actual embryo and suspensor. The latter structure connects the embryo with the sporophytic maternal tissues of the developing seed. The underlying mechanisms of double fertilization are tightly regulated to ensure delivery of functional sperm cells and the formation of both, a functional zygote and endosperm. In this review we will discuss the current state of knowledge about the processes of directed pollen tube growth and its communication with the synergid cells resulting in pollen tube burst, the interaction of the four gametes leading to cell fusion and finally discuss mechanisms how flowering plants prevent multiple sperm cell entry (polyspermy) to maximize their reproductive success.

Keywords: pollen tube, ovule, gamete interaction, cell fusion, signaling, fertilization, polyspermy

INTRODUCTION

High crop yield strongly depends on efficient formation of numerous ovules, which after successful fertilization, develop into seeds comprising seed coat, embryo, and endosperm. In angiosperms, the haploid gametophytic generations produce the male and female gametes required to execute double fertilization. Both gametophytes are reduced to only a few cells. The female gametophyte is deeply embedded and thus protected by the maternal sporophytic tissues of the pistil (**Figure 1**). It harbors the female gametes (egg and central cell) and is surrounded by the nucellus tissue as well as the inner and outer integuments. After fertilization these different tissues form the seed coat. The female gametophyte arises from a megaspore mother cell through processes known as megasporogenesis and megagametogenesis (for review see Evans and Grossniklaus, 2009; Drews and Koltunow, 2011). In ~70% of all angiosperm species including *Arabidopsis* and maize the embryo sac develops according to the Polygonum type (Drews et al., 1998). The functional megaspore undergoes three mitotic divisions resulting in a syncytium containing eight nuclei. After nuclei migration and cellularization seven cells are differentiated: the haploid egg cell and its two adjoining synergid cells are located at the micropylar pole forming the egg apparatus. The homodiploid central cell containing two fused or attached nuclei is located more centrally, whereas three antipodal cells are found at the chalazal pole of the ovule opposite to the egg apparatus. While synergid cells are essential for

pollen tube attraction, burst and sperm cell release (see below), the function of antipodal cells is so far unknown. During female gametophyte maturation antipodal cells are degenerating in the ovule of the eudicot model plant *Arabidopsis* (Mansfield et al., 1991), whereas they proliferate in other species including grasses and form a cluster of about 20–40 cells (Diboll and Larson, 1966).

The haploid male gametophyte (pollen grain) is formed during the processes of microsporogenesis and microgametogenesis from the microspore mother cell by meiosis and two successive mitotic divisions resulting in the formation of a tricellular pollen grain. The vegetative cell encases the two sperm cells, which are connected with the vegetative cell nucleus by the generative cell plasma membrane, forming the male germ unit (MGU). MGU formation ensures the simultaneous delivery of both gametes to the ovule (for review see McCue et al., 2011). The major task of the vegetative cell is to deliver the sperm cells through the maternal tissues of the style and ovary to an unfertilized ovule. After pollen germination, the vegetative cell forms a tube and grows by tip-based-growth mechanism along papillae cells of the stigma into the style toward the transmitting tract. Inside the transmitting tract, pollen tubes are guided toward the ovules by mechanical and chemotactic cues involving numerous interactions with the sporophytic style tissues. In many eudicots pollen tubes exit the transmitting tract and grow along the septum, the funiculus and the outer integument

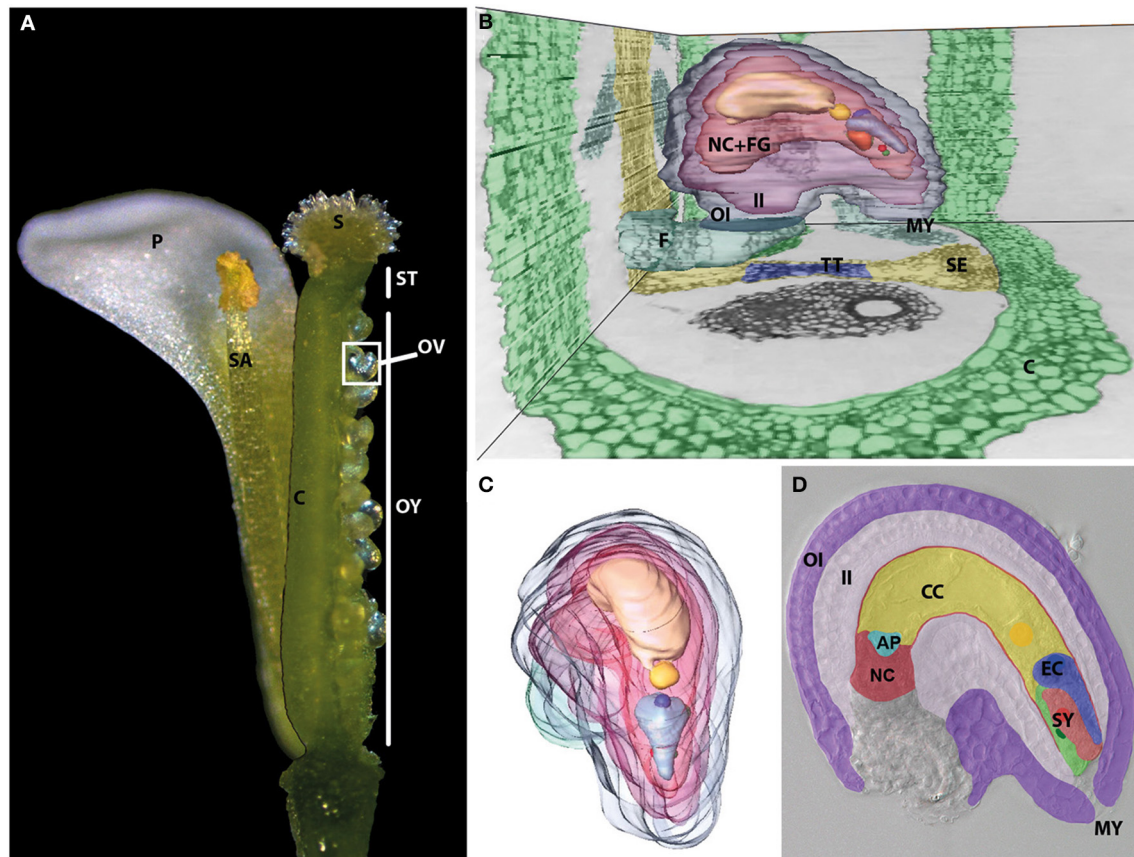


FIGURE 1 | The female gametophyte is deeply imbedded inside the female flower organs. (A) Dissected and reconstructed *Arabidopsis* flower. One of four petals (P) and one of six stamens (SA) are shown. They surround the pistil, which represents the female flower organ. It can be dissected into three parts. The upper part contains the papilla cells and forms the stigma (S), which is connected to the ovary (OY) by the style (ST). The ovary is formed by two fused carpels (C), which harbor two rows of ovules (OV). A side view (B) and front view (C) of a 3D-remodeled ovule reconstructed from toluidine blue stained single, successive ultra-thin sections of a dissected pistil. See Supplemental Movie 1 for whole series of sections. The ovule is connected to the septum (SE, yellow) containing the transmitting tract (TT, blue) by the funiculus (F, petrol) and surrounded by the carpel tissue (C) (green). A 3D-model of a dissected ovule shown from various angles is shown in Supplemental Movie 2. The mature female gametophyte cells (FG) and the nucellus tissue (NC) are surrounded

by the outer (OI) and inner integuments (II) (OI, blue; II, purple). The vacuole and nucleus of the different female gametophyte cells showed highest contrast and are therefore shown individually. Near to the micropyle (MY), the two nuclei of the two synergid cells (SY) are shown in red and green. The egg cell, indicated by EC in (D), has a comparably large vacuole (light blue) and its nucleus (blue) is located at its chalazal pole. The center of the female gametophyte is filled by the vacuole (light yellow) of the central cell, indicated by CC in (D), and its homo-diploid nucleus (yellow). The three degenerating antipodal cells, indicated by AP in turquoise color in (D) at the chalazal pole are not highlighted. (D) DIC microscopical image of a mature female gametophyte surrounded by the maternal sporophytic tissues of the ovule. The cell types and tissues are artificially colored as shown in (B,C). At full maturity the nucellus cell (NC) layer surrounding the developing embryo sac is flattened between inner integument (II) and female gametophyte cells.

toward the micropyle of unfertilized ovules. In grasses the ovary contains a single ovule and the pollen tube is directly guided toward its surface after leaving the blind ending transmitting tract. The pollen tube continues to grow along its surface toward the micropylar region (for review see Lausser and Dresselhaus, 2010). Finally, the pollen tube enters the micropyle, an opening between the inner and outer integuments, and grows toward the two synergid cells. The pollen tube bursts and sperm cells are released. This process is associated with the degeneration of the receptive synergid cell due to programmed cell death. Subsequently, both sperm cells arrive at the gamete fusion site and fertilize the egg and central cell (Hamamura et al., 2011). From the moment of germination until sperm discharge the pollen

grain/tube communicates with at least five different sporophytic and three different gametophytic cell types to successfully accomplish fertilization (Palanivelu and Tsukamoto, 2012). Its extended growth inside the female flower tissue is regulated by many different guidance, attraction and support mechanisms. After sperm cell release all gametes are activated, followed by fusion of their membranes and nuclei by processes known as plasma- and karyogamy, respectively. After successful double fertilization further signaling events are activated to prevent polyspermy. In this review we will summarize and discuss the cell-cell communication processes, which are essential to successfully accomplish double fertilization and to initiate seed development in angiosperms.

POLLEN TUBE GROWTH AND ATTRACTION

POLLEN REJECTION

Pollen tube growth and guidance toward the female gametes are controlled at various stages by chemotactic signals and growth support molecules derived from the sporophytic and gametophytic tissues of the female flower organs. Pollen grains placed on the stigma (**Figure 1A**) by contact, wind or different pollinators stick to the papilla cells and start to hydrate followed by their germination. The efficient adhesion of the pollen grain to the papilla cell is regulated by interaction events between these cells and may activate thereby inter- and intra-species barriers to prevent unsuccessful pollination and fertilization events already at this early time point during reproduction. Angiosperms possess different strategies to recognize self from alien pollen and evolved independent self-incompatibility (SI) mechanisms to prevent self-fertilization. Early SI mechanisms are based on cell-cell communication events between the papilla cells and the pollen grains, whereas later SI mechanisms occur while the growing pollen tube interacts with the cells of the transmitting tract. Species of the *Solanaceae*, for example, use a pistil-expressed S-RNase, which penetrates the pollen tube (McClure et al., 1989; Luu et al., 2000). A compatible pollen tube expresses the S-locus F-box protein (SLF), which leads to the degradation of the S-RNase (Hua and Kao, 2006; Kubo et al., 2010), while in incompatible interactions intact S-RNase degrades RNAs resulting, for example, in the disruption of the actin cytoskeleton and other cellular processes (Liu et al., 2007; Roldán et al., 2012). In *Papaveraceae* SI depends on the small pistil secreted protein *Papaver rhoeas* style S (PrsS), which binds to the S-locus pollen tube membrane protein *P. r.* pollen S (PrpS) and activates a Ca^{2+} -dependent signaling cascade resulting in pollen inhibition and programmed cell death (Wheeler et al., 2009; Wu et al., 2011). SI is best understood in *Brassicaceae*, which use a surface-localized S-locus receptor kinase (SRK) in papilla cells (Takasaki et al., 2000) and a pollen coat localized cysteine-rich protein (SP11/SCR) (Schopfer, 1999; Shiba et al., 2001) to distinguish self from alien pollen. Their successful interaction leads to proteasome dependent degradation of Exo70A1, an essential component of the exocyst complex. It is thought to be involved in secretion of essential pollen germination factors necessary for pollen hydration (Synek et al., 2006; Samuel et al., 2009). Rejection of pollen in *Brassicaceae* thus occurs already during pollen hydration and germination at the surface of papilla cells. Little is known about SI in the economically important grasses (reviewed in Dresselhaus et al., 2011). Pollen hydration and germination appear not to be affected, although only grass pollen tubes are capable of penetrating the style and reach the transmitting tract. This indicates that SI in the grasses depends on successful interaction of the pollen tube with the sporophytic cells of the style and transmitting tract. The signaling events involved in this recognition process still await their discovery. More details about SI mechanisms can be found in Iwano and Takayama (2012), Watanabe et al. (2012) and Dresselhaus and Franklin-Tong (2013).

POLLEN TUBE GUIDANCE TOWARD AND THROUGH THE TRANSMITTING TRACT

After adhesion and hydration, compatible pollen germinates, penetrates the style and grows through the extracellular space of

stylar cells toward the transmitting tract (**Figure 1B**). The growth direction of the pollen tube is regulated by the formation of different gradients including water, γ -amino butyric acid (GABA), calcium and other small molecules such as D-serine. The water flow during hydration forms an external gradient specifying the site of pollen tube outgrowth and was shown to be controlled by triacylglyceride (Lush et al., 1998; Wolters-Arts et al., 1998). Ca^{2+} influx into the pollen tube tip region is known to be essential for germination and tube growth (Brewbaker and Kwack, 1963; for a review see Steinhorst and Kudla, 2013a) and leads to the generation of an oscillating apex-based cytoplasmic Ca^{2+} ($\text{Ca}_{\text{cyto}}^{2+}$) gradient (Miller et al., 1992; Calder et al., 1997). Initially, papilla cells export $\text{Ca}_{\text{cyto}}^{2+}$ by the auto-inhibited Ca^{2+} -ATPase13 (ACA13) at the pollen grain adhesion site (Iwano et al., 2004, 2014). Extracellular Ca^{2+} is then imported into the pollen tube by glutamate receptor-like channels (GLRs), which can be stimulated by D-serine (Michard et al., 2011). In animal systems it was shown that GLRs are non-selective cation channels catalyzing Na^{+} and/or Ca^{2+} influx into cells. Binding of the agonist D-serine to GLRs should thus lead to channel opening resulting in a $\text{Ca}_{\text{cyto}}^{2+}$ increase (Gilliam et al., 2006). D-serine is produced by Serine-Racemase1 (SR1), which shows an expression peak in the style indicating D-serine availability. The induced changes in $\text{Ca}_{\text{cyto}}^{2+}$ concentration in the pollen tube might thereafter regulate and coordinate many different signaling events like actin polymerization and thus influence pollen tube growth behavior and growth direction. $\text{Ca}_{\text{cyto}}^{2+}$ -sensors, belonging to the protein families of calmodulin (CaM), calmodulin-like proteins (CMLs), calcium-dependent protein kinases (CDPKs), and calcineurin B-like proteins (CBLs) are expressed in the pollen tube and are thought to control different cell-cell communication events indicated by their localization and overexpression phenotypes. The presence of these different $\text{Ca}_{\text{cyto}}^{2+}$ receptors around the sperm cells and at the pollen tube tip indicate an essential role of Ca^{2+} signals both during pollen tube growth and double fertilization (Zhou et al., 2009; Steinhorst and Kudla, 2013b).

During pollen tube growth the tip needs to modulate the surrounding cell wall of stylar cells enabling its penetration through the extra-cellular space, most likely by interaction with extensin-like proteins and arabinogalactan proteins as well as the secretion of cell wall softening enzymes and inhibitors such as polygalacturonases and pectin methylesterase inhibitors (Cosgrove et al., 1997; Grobe et al., 1999; Stratford et al., 2001; Ogawa et al., 2009; Nguema-Ona et al., 2012; Woriedh et al., 2013). The transmitting tract is composed of small cylindrical cells that are surrounded by an extracellular matrix (ECM), which contains a mixture of glycoproteins, glycolipids, and polysaccharides (Lennon et al., 1998). The ECM provides essential nutrients as well as components for an accelerated, extended and guided pollen tube growth (Palanivelu and Preuss, 2006). Without an intact transmitting tract like in the *NO TRANSMITTING TRACT* (NTT) mutant or its target *HALF FILLED* (HAF), pollen tube growth is severely affected and either slowed down or prematurely terminated. NTT encodes a C2H2/C2HC zinc finger transcription factor involved in ECM production and is essential for programmed cell death in the transmitting tract upon pollination (Crawford et al., 2007). HAF encodes a bHLH transcription factor and is involved in NTT dependent transmitting tract regulation (Crawford and Yanofsky,

2011). The transmitting tract-specific arabinogalactan glycoproteins TTS1 and TTS2 have a positive effect on *in vitro* grown tobacco pollen and show a gradient of increased glycosylation correlating with pollen tube growth direction inside the transmitting tract (Cheung et al., 1995; Wu et al., 1995). Another factor which has a positive effect on pollen tube growth and guidance is chemocyanin, a small secreted peptide in the style of lily (Kim et al., 2003). The different sporophyte-derived signals do not only guide or increase pollen tube growth rate, but rather lead to a change in the pollen transcriptome and thereby activate the pollen for female gametophyte-derived attraction signals (Higashiyama et al., 1998; Palanivelu and Preuss, 2006). Recently, *de novo* expression of closely related MYB transcription factors and other genes were reported to be induced during pollen tube growth through the style regulating themselves a number of downstream genes. Hence pollen tubes mature during their growth through the sporophytic tissue and thereby become competent for fertilization (Leydon et al., 2013, 2014).

OVULAR POLLEN TUBE GUIDANCE

The signaling events that control pollen tube exit from the transmitting tract and guidance toward the ovule are not known. In *Arabidopsis* this process was shown to be tightly regulated and usually only a single pollen tube exits the transmitting tract in proximity of an unfertilized ovule. The pollen tube grows on the septum surface toward the funiculus, the tissue connecting the ovule with the septum (Figures 1B–D; Supplemental Movies 1, 2). At the funiculus the pollen tube is directed through the micropyle inside the ovule by a mechanism known as micropylar guidance (Shimizu and Okada, 2000). In *Arabidopsis* a gradient of GABA was reported in front of the ovule. The transaminase POLLEN ON PISTIL2 (POP2) forms this gradient through GABA degradation. At moderate concentrations GABA stimulates pollen tube growth and thus likely supports growth toward the ovule (Palanivelu et al., 2003). Another candidate involved in micropylar guidance is D-serine, which was already described above. Its synthesizing enzyme gene *SR1* is also expressed in the ovule indicating the presence of D-serine (Michard et al., 2011). Semi-*in vitro* fertilization experiments revealed an oscillation of $\text{Ca}_{\text{cyto}}^{2+}$ levels in growing pollen tubes depending on their distance from an unfertilized ovule and especially from the synergid cells (Shi et al., 2009; Iwano et al., 2012). The connection between $\text{Ca}_{\text{cyto}}^{2+}$ and D-serine by GLR channels in growing pollen tubes was already described above. The observed changes in the $\text{Ca}_{\text{cyto}}^{2+}$ level depending on its distance from the synergid cells might again result from this interplay.

Recently, two pollen-expressed mitogen-activated protein kinases (MAPKs), MPK3 and MPK6, were identified in *Arabidopsis*, which are part of the ovular guidance network. *In vivo* pollination assays revealed that *mpk3/6* double mutant pollen tubes were not capable of growing along the funiculus after transmitting tract exit but micropylar guidance (see below) was not effected in the double mutants (Guan et al., 2014). MPK3/6 are two cytoplasmic protein kinases, which seem to be part of the signaling cascade mediating extracellular stimuli to changes in pollen tube growth direction.

In summary, our current understanding of ovular pollen tube guidance is very limited, but a whole orchestra of small molecules derived from the ovule seem to be involved in pollen tube growth support and attraction, and multiple signaling networks are required in pollen tubes to respond to the diverse set of signals and to direct their growth behavior.

MICROPYLAR POLLEN TUBE GUIDANCE

After arrival at the surface of the ovule, the pollen tube reaches the last phase of its journey, which is known as micropylar pollen tube guidance. It enters the micropyle, an opening between the two integuments, and directly grows toward the egg apparatus in species such as *Arabidopsis* (Figure 2A). In grasses the pollen tube first has to overcome a few layers of nucellus cells (Márton et al., 2005) before it also gets in contact with the filiform apparatus of the synergid cells, a thickened and elaborated cell wall at their micropylar pole, where the cell surface is extensively invaginated (Willemse and van Went, 1984; Huang and Russell, 1992). It was believed for a long time that the pollen tube grows through the filiform apparatus to enter one synergid cell, leading to pollen tube burst and cell death of the receptive synergid cell. Recently, it was shown that the pollen tube is repelled by the filiform apparatus and instead grows along the cell wall of the synergid cells until it reaches a certain point after the filiform apparatus where its growth is arrested and burst occurs explosively (Leshem et al., 2013). Pollen tube burst results in the discharge of its cytoplasmic contents including the two sperm cells. The synergid cells represent the main source for chemo-attractants required for micropylar pollen tube guidance. Moreover, laser ablation experiments in *Torenia fournieri* have demonstrated that a single synergid cell is sufficient and necessary to attract pollen tubes (Higashiyama et al., 2001). The major function of the filiform apparatus may thus be to considerably increase the micropylar surface of the synergid cells, which represent glandular cells of the egg apparatus. Many known components required for pollen tube growth and guidance are membrane-associated and accumulate at the filiform apparatus, which gives it the additional role of a signaling platform. It contains, for example, a high Ca^{2+} concentration, which is known to play a key role during the regulation of pollen tube growth (Brewbaker and Kwack, 1963; Chaubal and Reger, 1990; Iwano et al., 2004; Michard et al., 2011) and also seems to trigger pollen tube burst afterwards (see below). In *Arabidopsis* the formation of the filiform apparatus as well as the expression of different attractants in the synergid cells depend on the activity of the R2R3-type Myb transcription factor MYB98 (Kasahara et al., 2005; Punwani et al., 2007). Among other genes, MYB98 regulates the expression of genes encoding cysteine-rich proteins (CRPs), including those representing a subgroup of defensin-like (DEFL) polypeptides (Punwani et al., 2008; Takeuchi and Higashiyama, 2012).

In *Torenia* it was shown that a DEFL subgroup of CRPs called LUREs are secreted from the synergid cells and accumulate at the filiform apparatus (Okuda et al., 2009; Kanaoka et al., 2011). LUREs attract pollen tubes in a species-preferential manner from a distance of about 100–150 μm and were recently shown to bind to the tip region of pollen tubes (Okuda et al., 2009, 2013). Due to their rapid molecular evolution it was difficult to

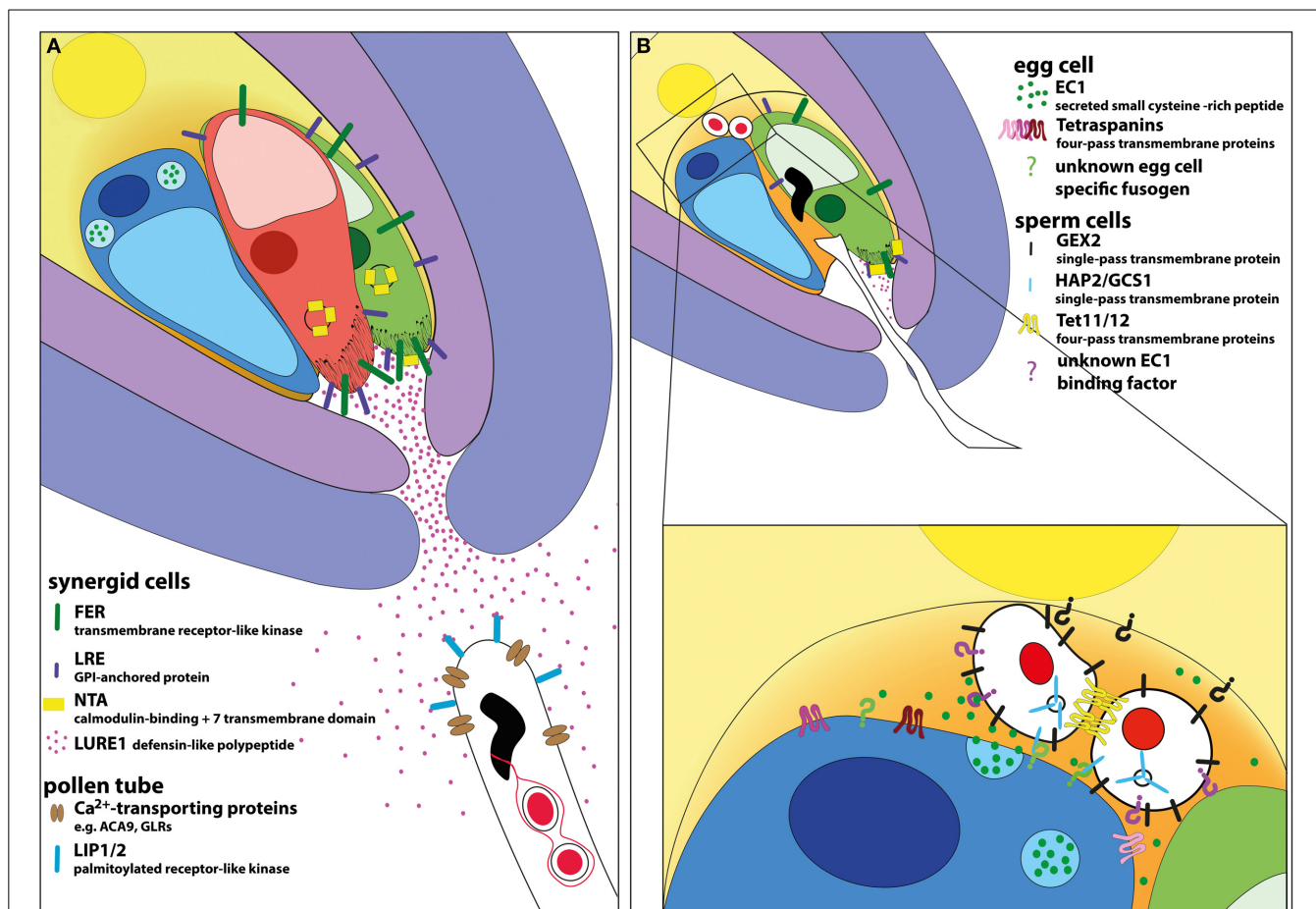


FIGURE 2 | Model of signaling events during micropylar pollen tube attraction and double fertilization in *Arabidopsis*. (A) The micropylar opening of the ovule is formed by the inner and outer integuments. The female gametophyte is “naked” at its micropylar pole containing one egg (colored in blue) and two synergid cells (colored in green and red) representing the egg apparatus. The central cell surrounds the egg apparatus. The synergid cells are the main sources of pollen tube attractants. Among other components, they secrete LURE peptides, which bind to pollen expressed LIP1/2 receptors thus directing pollen tube growth. Calcium transporters are involved in pollen tube growth control. The plasma membranes of synergid cells harbor a high concentration of receptors like FER and LRE, especially in the region of the filiform apparatus. Upon pollen tube perception NTA is relocated to the plasma membrane by FER activity likely regulated by Ca²⁺ oscillations inside the synergid cells. (B) The pollen

tube bursts when it reaches a certain point beyond the filiform apparatus and releases its cytoplasmic contents including the two sperm cells. Pollen tube burst depends on the presence and activation of FER-, LER-, NTA-, and VDD-dependent signaling cascades culminating in the death of the receptive synergid cell (indicated by diffusing red color). Released sperm cells are located at the gamete fusion side, between the two female gametes. The two sperm cells are connected to each other, likely involving tetraspanins. The male gametes adhere to female gametes by GEX2 located at their surface. After activation, the egg cell secretes EC1 leading to sperm cell activation and HAP2/GCS1 localization to the plasma membrane. HAP2/GCS1 and tetraspanins at the surface of gametes may be involved in mediating membrane fusion. Unknown egg and central cell-specific fusogenic proteins as well as EC1 receptor are indicated by question marks in green, black, and purple, respectively.

identify orthologs in other plant species, but finally the DEFL subgroup CRP810/AtLURE1 of *Arabidopsis* was discovered to be involved in micropylar pollen tube guidance (Takeuchi and Higashiyama, 2012). In *Zea mays*, EGG APPARATUS1 (ZmEA1), a small hydrophobic precursor protein of 94 aa was reported as an egg apparatus-specific protein required for micropylar pollen tube guidance (Márton et al., 2005, 2012). ZmEA1 was shown to bind in a species-specific manner to the apical region of the pollen tube, where it is quickly internalized and degraded, likely keeping the pollen tube susceptible to pollen tube attractants while growing through the micropylar nucellus cell layers (Márton et al., 2012; Uebler et al., 2013).

More puzzling is the role of the central cell in micropylar guidance of the pollen tube. For example *magatama* (*maa*) mutants show defects in central cell maturation; both haploid nuclei are smaller and often fail to fuse. Pollen tubes grow in the direction of an unfertilized *maa* ovule but lose their way just before entering the micropyle. Moreover, mutant female gametophytes attracted two pollen tubes at a high frequency (Shimizu and Okada, 2000). MAA3 was recently shown to encode a helixase required for general RNA metabolism, which could explain the central cell maturation defect but not the defect in pollen tube guidance (Shimizu et al., 2008). Another example of central cell-dependent defects in micropylar pollen tube guidance is the

transcriptional regulator CENTRAL CELL GUIDANCE (CCG), which is expressed exclusively in the central cell of the female gametophyte (Chen et al., 2007). These guidance defects may be indirect and caused by non-functional or immature central cells influencing maturation of egg apparatus cells and thus the generation of guidance components in these cells. It might also be possible that molecules generated by the MAA3 and CCG pathways directly regulate the generation of guidance molecules in the neighboring cells. Also the egg cell seems to be involved in micropylar guidance. GAMETE EXPRESSED 3 (GEX3) is a plasma membrane-localized protein, which is expressed in the unfertilized egg cell. Down-regulation of *GEX3* by antisense RNA in the egg cell leads to defects in micropylar guidance by an unknown mechanism (Alandete-Saez et al., 2008).

Until recently, male factors and signaling pathways reacting to attractants secreted from the egg apparatus were unknown. The receptor-like kinases (RLKs) LOST IN POLLEN TUBE GUIDANCE1 (LIP1) and 2 (LIP2) have been identified, which are preferentially expressed in the pollen tube. Both proteins show membrane localization due to a palmitoylation site and are involved in the AtLURE1-dependent guidance mechanism. *lip1/2* double mutant pollen reach the funiculus but fail to grow through the micropyle inside the ovule, and the pollen tube shows a reduced attraction toward AtLURE1 (Liu et al., 2013). However, it is unclear whether LIP1/2 are directly involved in LURE perception.

POLLEN TUBE BURST AND SPERM CELL DISCHARGE

Pollen tube burst seems to be regulated by RLKs located at surfaces of both male and female interaction partners (Figures 2A,B). The RLK FERONIA/SIRENE (FER/SRN) is expressed in most tissues including the synergid cells, where it localizes predominately at their surface in the filiform apparatus region. Loss-of-function mutants display a pollen tube-overgrowth phenotype. Pollen tube growth arrest and sperm cell discharge fail in *fer* ovules (Huck et al., 2003; Rotman et al., 2003; Escobar-Restrepo et al., 2007). *FER* acts as a cell surface regulator for RAC/ROP GTPases. Recently it was shown that FER binds to the small secreted peptide Rapid Alkalinization Factor (RALF), which leads to the inhibition of a plasma membrane H^+ -ATPase resulting in the suppression of cell elongation in the primary root (Haruta et al., 2014). Besides changes in the pH, RALF also induces the increase of Ca_{cyto}^{2+} (Pearce et al., 2001; Haruta and Constabel, 2003; Haruta et al., 2008) and thus may influence pollen tube growth arrest and eventually its burst. The *Arabidopsis* genome contains around 30 RALF-like genes indicating the possibility that a pollen secreted RALF-like peptide may indeed be involved in FER-dependent pollen tube perception (Olsen et al., 2002). Other proteins were identified whose loss-of-function resemble the *fer* phenotype such as the glycosylphosphatidylinositol (GPI)-anchored protein LORELEI (LRE) and the Mildew Resistance Locus O (MLO) family protein NORTIA (NTA). Both genes are expressed in synergid cells and show a similar pollen tube overgrowth phenotype (Capron et al., 2008; Kessler et al., 2010). *NTA* encodes a protein with multiple potential transmembrane domains as well as a calmodulin-binding site. The frequency of unfertilized ovules in *lre/lre* and *nta/nta* is less

pronounced compared to *fer/fer* pistils. This finding indicates that FER activity is essential for pollen tube perception, while other, yet unknown factors act redundantly with LRE and NTA. These factors are all present at the synergid plasma membrane during pollen tube contact. However, while FER accumulates at the filiform apparatus already prior to pollen tube arrival, NTA relocates to the plasma membrane of the synergid cells at the filiform apparatus region upon pollen tube contact. In a transient expression system NTA is directly targeted to the plasma membrane. However, in *Arabidopsis* ovules under control of its endogenous promoter, NTA localizes to uncharacterized compartments within the cell, and becomes relocated to the plasma membrane upon pollen tube arrival, indicating the presence of an active retention mechanism. This relocation is FER-dependent and therefore connects FER to NTA in the same signaling network (Kessler et al., 2010). The presence of a calmodulin-binding domain in NTA supports the idea of a Ca^{2+} -dependent signaling network, which is activated upon pollen tube arrival. Due to its predicted signal peptide and GPI anchor, LRE is expected to localize to the extracellular side of the plasma membrane after passage through the secretory pathway. But so far plasma membrane localization could only be shown in a transient expression system and not in synergid cells themselves (Capron et al., 2008). Whether LRE localization also changes during the process of fertilization needs to be elucidated. Another factor required for successful pollen tube/synergid cell communication is VERDANDI (VDD), a member of the plant-specific B3 superfamily of transcription factors. *Vdd* mutants show defects in antipodal and synergid cell identity and result in the lack of pollen tube burst after reaching the synergid cells. In contrast to *fer*, *nta*, or *lre* mutants, an overgrowth phenotype was not reported indicating that VDD may act downstream of cell surface signaling components (Matias-Hernandez et al., 2010). Little is known about male factors involved in pollen tube/synergid cell communication. Two closely related homologs of FER, ANXUR1 (ANX1), and ANX2 were reported to be involved in the timing of pollen tube burst or more precisely in the inhibition of pollen tube burst. In an *in vitro* pollen tube growth assay, pollen of double mutants show spontaneous discharge already after pollen bulge formation, whereas *in vivo*-grown pollen tubes germinate normally on a stigma but rupture in the style before arriving at the egg apparatus. Both receptors localize mainly to the apical tip of the pollen tube as well as in small vesicles (Boisson-Dernier et al., 2009; Miyazaki et al., 2009). Their over-expression inhibits growth by over-acting exocytosis and over-accumulation of secreted cell wall material (Boisson-Dernier et al., 2013) suggesting that the main function is associated with coordination of growth through the style rather than sperm cell discharge. Other male factors, which are involved in pollen tube growth and reception, are the pollen-expressed transcription factors MYB97, MYB101 and MYB120. *myb97/101/120* triple mutants exhibited uncontrolled growth and failed to discharge their sperm cells after entering the embryo sac (Liang et al., 2013). It is thought that these factors are required to enable pollen tube to communicate with the pistil tissues and the female gametophyte (Leydon et al., 2014). As already mentioned, the level of Ca_{cyto}^{2+} alters during pollen tube elongation. Upon pollen tube arrival Ca_{cyto}^{2+} level starts to oscillate in the

synergid cells, triggered by the contact of the pollen tube tip with the synergid cell. This oscillation can be observed until pollen tube burst, which leads to the degeneration of one synergid cell (Sandaklie-Nikolova et al., 2007; Iwano et al., 2012; Denninger et al., 2014; Ngo et al., 2014). These changes in $\text{Ca}_{\text{cyto}}^{2+}$ level are essential for sperm delivery and are depending on FER and LRE activity, respectively. Downstream of FER, NTA localization to the synergid cell surface and its activity likely depend on sufficient $\text{Ca}_{\text{cyto}}^{2+}$ level in the synergid cells (Ngo et al., 2014). The synergid cell, which is in contact with the pollen tube follows a regulated cell death program that is somehow associated and controlled by pollen tube burst and linked to oscillation of $\text{Ca}_{\text{cyto}}^{2+}$ level (Higashiyama et al., 2000; Sandaklie-Nikolova et al., 2007; Denninger et al., 2014; Ngo et al., 2014). It cannot be explained by mechanical breakdown due to an invading pollen tube. In *fer* mutant, for example, pollen tube growth continues around the synergid cells, which must be associated with mechanical stress but does not induce synergid cell death (Escobar-Restrepo et al., 2007). However, the signaling events, which are responsible for programmed cell death in the synergid cell, are not understood yet. In maize pollen tube arrival is associated with the secretion of defensin-like ZmES proteins, inducing pollen tube burst by activating the K^{+} -channel *Zea mays* 1 (KZM1) in the pollen tube membrane (Amien et al., 2010). Whether these “toxin”-like molecules are also capable of inducing synergid cell burst remains to be shown.

GAMETE INTERACTION AND PREVENTION OF POLYSPERMY SPERM CELL DELIVERY, ACTIVATION, AND GAMETIC MEMBRANE INTERACTIONS

Once released, the two sperm cells are delivered to the so-called gamete fusion site between egg and central cell (**Figure 2B**). It is controversial whether this requires active transport or is solely based on cytoplasmic flow associated with burst of both pollen tube and receptive synergid cell and/or the architecture of the egg apparatus. Most flowering plants, like *Arabidopsis*, generate isomorphic sperm cells and therefore fusion of sperm cell appears to be random, either with the egg or the central cell (Berger et al., 2008; Ingouff et al., 2009; Liu et al., 2010). Some reports suggest that fertilization of the egg cell is preferred, which was demonstrated, for example, in mutants of *CYCLIN DEPENDENT KINASE A1* (*CDKA1*), which generate only one sperm-like germ cell (Iwakawa et al., 2006; Nowack et al., 2006). Experiments with photo-labeled sperm cells have demonstrated that there is no preference for either female gamete (Hamamura et al., 2011). The differentiation into two equal sperm cells depends on the activity of the MYB transcription factor DUO POLLEN 1 (*DUO1*), which is required for correct male germ cell differentiation by regulating key genes essential for fertilization such as *GAMETE EXPRESSED 2* (*GEX2*) and *GENERATIVE CELL SPECIFIC 1* (*GCS1*), also known as *HAPLESS 2* (*HAP2*) (Brownfield et al., 2009). *GEX2* encodes a single-pass transmembrane protein with filamin repeats exposed to the extracellular space. *GEX2* localizes to the sperm cell plasma membrane and contains extracellular immunoglobulin-like domains, similar to gamete interaction factors reported in algae and mammals (Misamore et al., 2003; Inoue et al., 2005). In the presence of *GEX2* the two gametes

adhere to the egg and central cell. *gex2* mutant sperm cells show reduced adhesion to female gametes, likely causing cell fusion failure (Mori et al., 2014). *GCS1/HAP2* is another factor required for gamete interaction in *Arabidopsis*. After pollen tube burst, both sperm cells of *gcs1/hap2* loss of function mutants remain at the fusion site and fail to fuse with female gametes, leading to the attraction of additional pollen tubes (polytubey). It was further shown that in the absence of the potential fusogen *GCS1/HAP2*, attachment of male to the female gamete occurs but no membrane fusion is visible, implying that the protein mediates membrane fusion as a component of signaling events, or more likely that it is directly involved in the fusion event (Wong and Johnson, 2010; Mori et al., 2014). *GCS1/HAP2* is a conserved protein and has been identified in genomes of all major eukaryotic taxa except fungi. *Gcs1/hap2* mutants in protozoan and algal gametes result in fusion failure, suggesting that this protein is required for a common mechanism of membrane fusion in eukaryotes (Mori et al., 2006; Hirai et al., 2008; Liu et al., 2008; Steele and Dana, 2009; Wong and Johnson, 2010). Upon sperm cell arrival at the gamete fusion site (**Figure 2B**) the egg cell starts to secrete small cysteine-rich proteins of the EGG CELL 1 (*EC1*) family. *EC1* leads to the relocalization of *HAP2/GCS1* from the endomembrane system to the sperm cell plasma membrane and thus activates sperm cells enabling them to fuse with the female gametes (Sprunck et al., 2012). The egg cell appears to require activation itself and calcium may play a key role in this process; this is indicated by a single strong $\text{Ca}_{\text{cyto}}^{2+}$ transient in the egg cell associated with pollen tube burst and sperm delivery (Denninger et al., 2014), which thus precedes *EC1* secretion.

The relocalization of a transmembrane fusogen was also described for the mammalian-specific fusogen *IZUMO1* (Inoue et al., 2005). Female components, which are directly involved in gamete fusion are so far unknown in higher plants. In mammals, *CD9*-like membrane spanning proteins of the tetraspanin family are located at the plasma membrane of eggs and were shown to be required for gamete fusion (Kaji et al., 2000; Le Naour et al., 2000; Miyado et al., 2000). In *Arabidopsis* the conserved tetraspanin family consists of 17 members. While *TET11* and especially *TET12* are located at the surface of sperm cells and reach high concentrations in the membrane region connecting both sperm cells, *TET9* appears at the surface of female gametophyte cells including the egg and central cell (Boavida et al., 2013). *Arabidopsis* tetraspanins were shown to form homo- and heterodimers, but so far functional studies are missing. However, their presence at the surface of plant gametes and structural homology to mammalian *CD9*-like proteins suggest that they may possess a similar role during gamete interaction.

DEGRADATION OF FUSOGENS AND PREVENTION OF POLYSPERMY

In general polyspermy blocks prevent multiple fertilization events that would otherwise lead to abnormal development or even embryo lethality, and thus reproductive failure. In *Chlamydomonas* *FUS1*, a single-pass transmembrane protein with a high similarity to prokaryotic invasion and adhesion molecules, mediates membrane fusion (Ferris et al., 1996; Misamore et al., 2003). In *Chlamydomonas* both *GCS1/HAP2* and *FUS1* are rapidly degraded after cell fusion, resulting in a fast membrane

block to prevent polygamy (Misamore et al., 2003; Liu et al., 2010). In mammals, it was recently shown that IZUMO1 is recognized by the GPI-anchored protein JUNO on the egg cell surface. Rapid degradation of JUNO after fertilization suggests an additional mechanism for membrane block to prevent polyspermy (Bianchi et al., 2014).

In *Arabidopsis* it was shown that the polyspermy block only functions in the egg cell and not in the central cell, which is capable of fusing with more than one sperm cell, as demonstrated in the *tetraspore* (*tes*) mutant. This mutant produces more than one sperm pair, which is released simultaneously at the gamete fusion site. After fertilization, polyploidy resulting from multiple fertilization events was observed in the developing endosperm, but not in the embryo (Scott et al., 2008). The cause of the egg cell-specific fast block to polyspermy is unclear. *In vitro* fertilization experiments with maize egg and sperm cells have shown that cell wall material is detectable already within 30 sec after fusion (Kranz et al., 1995) and thus may prevent further gametic membrane interactions. Additionally, a quick block to polyspermy may also depend on the degradation of fusogens as described above. Calcium may play a role in immediate signaling of successful plasmogamy and release of cell wall material as an extended $\text{Ca}_{\text{cyto}}^{2+}$ transient is observed in the egg cell associated with successful gamete fusion (Denninger et al., 2014). However, the precise cellular function of calcium signaling during gamete interaction is currently unclear and will require further experimentation.

Another way to prevent polyspermy is the deactivation of pollen tube guidance and the activation of repelling mechanisms. In *Arabidopsis* usually only a single pollen tube is guided inside the ovule to execute double fertilization. After unsuccessful fertilization events, for example by failure of cell-cell fusion in *gcs1/hap2*, *duo1*, *duo3*, *gex2*, *cdka;1*, or *ec1-RNAi* gametes (Beale et al., 2012; Kasahara et al., 2012; Sprunck et al., 2012; Maruyama et al., 2013; Mori et al., 2014), secondary pollen tubes are attracted by the remaining synergid cell by a process named as polytubey. This process is delayed by a couple of hours (Kasahara et al., 2012), suggesting that pollen tube repellents are released upon sperm cell discharge and require degradation until additional pollen tubes can be attracted by the remaining synergid cell. After successful fertilization this cell quickly disintegrates, but remains viable for significantly longer times upon fertilization failure (Beale et al., 2012). A recent report showed that both female gametes independently control successful fertilization thus maximizing reproductive success (Maruyama et al., 2013). The key to prevent polytubey is the quick degeneration of the 2nd synergid cell. In order to investigate its death, it was recently reported that an Ethylene-Insensitive (EIN3-EIN2)/Ethylene-Insensitive3-like2 (EIL2)-dependent, ethylene-response cascade is activated after fertilization. Its artificial activation results in premature synergid cell disintegration and thus a block to pollen tube attraction (Völz et al., 2013). The degeneration of the 2nd synergid cell thus leads to the stop of attractant secretion and ultimately prevents polyspermy.

ACTIVATION OF SEED DEVELOPMENT

Both female gametes need to be fertilized to produce viable progeny. Although equipped with the genetic repertoire to

generate every cell type (in the case of the fertilized egg cell) or a number of highly specialized cell types (in the case of the fertilized central cell), both female gametes appear in an arrested state until activated through fertilization. In contrast, parthenogenetic egg cells do not arrest and initiate cell division without fertilization. The central cell, however, requires fertilization in most plant species, even in those containing parthenogenetic egg cells. Its activation is closely related to seed development as both parthenogenetic embryogenesis and seed development arrest at an early stage without central cell fertilization (Koltunow and Grossniklaus, 2003; Barcaccia and Albertini, 2013). Recent reports in *Arabidopsis* confirm intensive cross-talk between endosperm and embryo as well as between endosperm and seed coat shortly after fertilization (Costa et al., 2014; Figueiredo and Köhler, 2014). It was further shown that the zygotic genome is activated shortly after fertilization in this species and both maternal and paternal genomes contribute equally to the transcriptome of the early embryo (Nodine and Bartel, 2012). Research in the last two decades has discovered many differences in epigenetic modification between male and female genomes, which lead to variations in expression profiles between their genes before and after fertilization. Polycomb group genes and RNA silencing mechanisms play a major role in these processes, but will not be considered here in more detail as excellent reviews can be found elsewhere (e.g., Van Ex et al., 2011; Gehring, 2013).

It is well conceivable that sperm cells deliver factors, which activate female gametes after fusion. A transcript encoding the Interleukin-1 Receptor-Associated Kinase (IRAK)/Pelle-like kinase gene *SHORT SUSPENSOR* (*SSP*), which was shown to be delivered by sperm cells, becomes translated in the zygote and acts in the YODA (YDA) MAPK pathway during zygote elongation (Bayer et al., 2009). In the zygote, the regulatory network activated by SSP-YDA is yet unknown. Activation of the cell cycle might also represent a key mechanism for the activation and progression of seed development. However, *cdka;1* mutant single sperm-like germ cells, defective in a master cell cycle regulator are capable of fertilizing egg cells and activating the embryonic program (Iwakawa et al., 2006; Nowack et al., 2006). Although the mutant *cdka;1* central cell showed mitotic divisions upon egg cell fertilization, it appeared mostly unfertilized, and endosperm proliferation and thereby seed development stopped after a certain time point. This finding suggested a positive proliferation signal from the zygote leading to cell cycle activation in the central cell. However, occasionally two *cdka;1* sperm cells are delivered to the gamete fusion site leading to cell-cell fusion of both female gametes with one *cdka;1* mutant sperm cell each. It was further reported that fusion between nuclei of sperm and central cell fails. The failure of karyogamy in the central cell prevents incorporation of the paternal genome, impairs endosperm development and causes seed abortion. This and the above findings using parthenogenetic species imply that the paternal genome plays an essential role during early seed development and that sperm cell factors are also required to activate central cell development (Aw et al., 2010). In summary, very little is known about the molecular mechanisms activating both female gametes that lead to the initiation of seed development.

CONCLUSIONS

Efficient and successful fertilization of all developed ovules is a key to reproductive success and essential for high crop yield. Using the model plant *Arabidopsis* tremendous progress has been made in the past couple of years to understand the underlying cellular and molecular mechanisms that regulate pollen tube growth and guidance, sperm delivery and gamete interaction resulting in blocks to polytubey and polyspermy. Little is known about the activation of gametes and thus seed development immediately after fertilization. Many of the processes described above involve conserved mechanisms and proteins. Some of these proteins are highly polymorphic and species-specific, allowing female flower organs to discriminate self from alien pollen grains/pollen tubes to avoid reproductive failure after pollination and fertilization with incompatible gametophytes and gametes, respectively. In summary, we have learned that species-specific or even ecotype-specific molecules and plant family-specific mechanisms are required during compatible interactions. These are used by papilla cells to control pollen germination, by transmitting tract cells during pollen tube growth and by the ovule and female gametophyte cells during the last steps of pollen tube journey. Moreover, even sperm cell discharge is regulated in a species-preferential manner. Whether gamete interactions depend on species-specific molecules remains to be shown. Up to now the final processes of fertilization seem to involve partly conserved proteins even from lower to higher eukaryotes. The knowledge generated can now be used to investigate, for example, speciation mechanisms or can be applied to overcome hybridization barriers between species. Initial attempts enabling ovules to attract pollen tubes from unrelated plant families have been successful (Márton et al., 2012). However, as outlined above double fertilization mechanisms are very complex and regulated at multiple levels, and it will be a challenge to overcome all steps simultaneously allowing wide hybridization between plant species that presently cannot be crossed. A major challenge for the near future is to understand fertilization mechanisms also in crop plants, especially in the grasses, which represent the most economically important plant family. Maize was suggested as a grass and crop model to investigate these processes (Dresselhaus et al., 2011), but transformation difficulties, the low number of available insertion mutants, the requirement of sufficient greenhouse space and especially technical problems to visualize the fertilization process *in vivo* still limit its utilization for reproduction biologists. Concerted efforts are now required to understand the molecular mechanisms of double fertilization in crop plants, which significantly differ from *Arabidopsis* in both reproductive structures and genetic repertoire.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <http://www.frontiersin.org/journal/10.3389/fpls.2014.00452/abstract>

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Cell cycle control and seed development

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Seed development is a complex process that requires coordinated integration of many genetic, metabolic, and physiological pathways and environmental cues. Different cell cycle types, such as asymmetric cell division, acytokinetic mitosis, mitotic cell division, and endoreduplication, frequently occur in sequential yet overlapping manner during the development of the embryo and the endosperm, seed structures that are both products of double fertilization. Asymmetric cell divisions in the embryo generate polarized daughter cells with different cell fates. While nuclear and cell division cycles play a key role in determining final seed cell numbers, endoreduplication is often associated with processes such as cell enlargement and accumulation of storage metabolites that underlie cell differentiation and growth of the different seed compartments. This review focuses on recent advances in our understanding of different cell cycle mechanisms operating during seed development and their impact on the growth, development, and function of seed tissues. Particularly, the roles of core cell cycle regulators, such as cyclin-dependent-kinases and their inhibitors, the Retinoblastoma-Related/E2F pathway and the proteasome-ubiquitin system, are discussed in the contexts of different cell cycle types that characterize seed development. The contributions of nuclear and cellular proliferative cycles and endoreduplication to cereal endosperm development are also discussed.

Keywords: cell division, cotyledon, cyclin-dependent kinase, embryo, endoreduplication, endosperm, retinoblastoma-related, seed coat

INTRODUCTION

SEED DEVELOPMENT PHASES

Angiosperms reproduce sexually via the production of seeds, which are typically derived from the fertilization of ovules, or asexually via apomixis. Mature seeds characteristically contain three major structures: a sporophyte (the embryo), nutrient storage tissues or organs (the endosperm and/or the embryonic cotyledons), which support embryogenesis and early post-embryonic sporophyte development, and a protective structure (the seed coat or testa). A prominent triploid endosperm is typically present in mature monocot seeds, while most of its cells are consumed during dicot seed development. The seed coat is a maternal structure derived from the ovule integuments that functions in seed protection, dormancy, germination, and, in some dicot species like legumes (Fabaceae or Leguminosae family), transiently in nutrient storage. In the monocot Poaceae family (grasses), the seed coat is fused to the pericarp (the fruit coat). The maternal plant makes significant contributions to seed production by providing nutrients, conveying hormonal and environmental cues and imposing mechanical constraints on the floral structures within which seeds develop. Consequently, seed production is influenced by a range of zygotic, sporophytic, and environmental factors (Egli, 2006).

The size of a multicellular organism, its organs and tissues depend on the number and size of constituent cells. Cell number, in turn, depends on the rate of cell division, the number of dividing

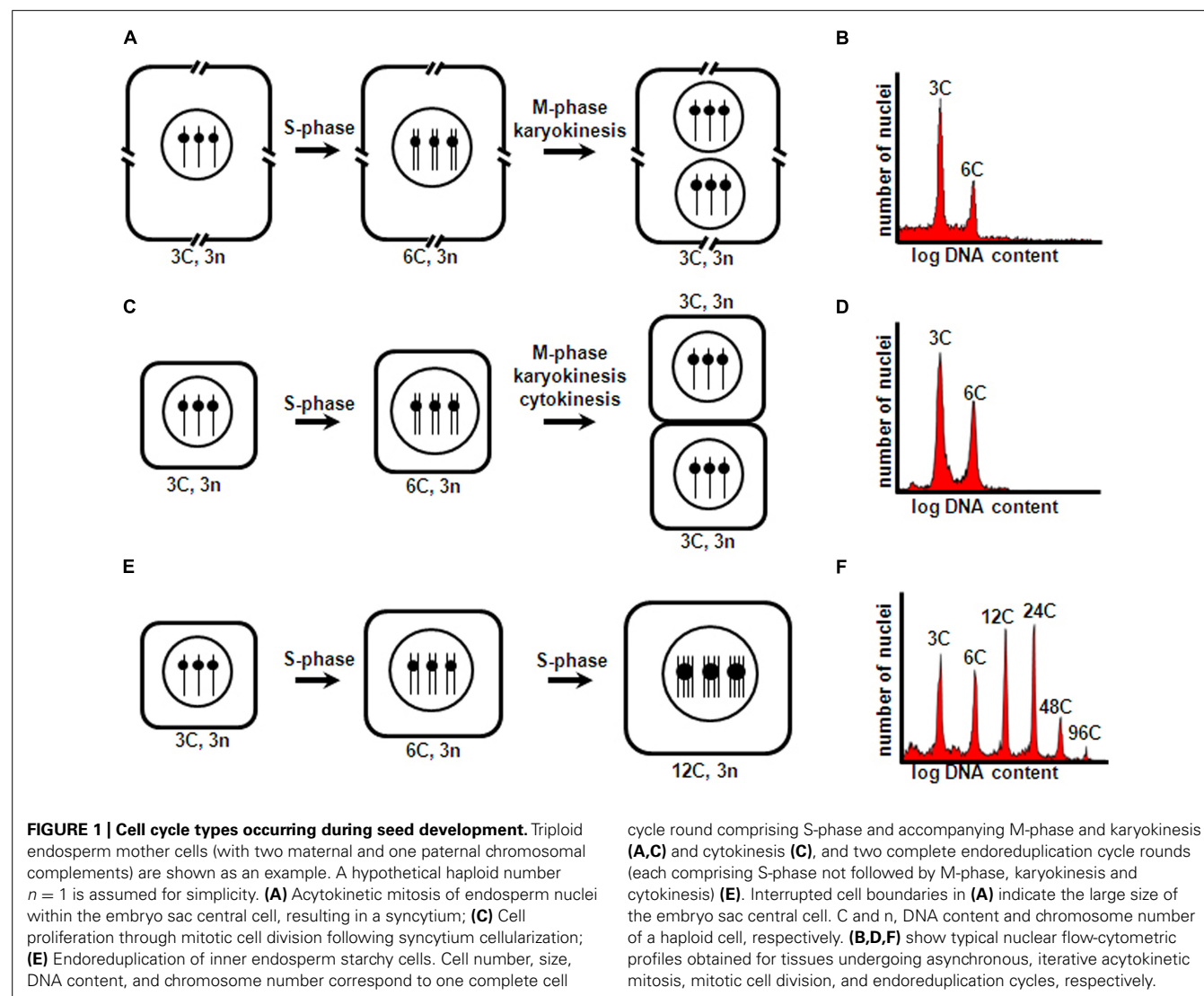
cells, and the duration of the cell proliferation phase during development, while the size of non-dividing cells is influenced by cell growth and cell expansion (defined as increases in cell macromolecular mass and cell volume, respectively; Sugimoto-Shirasu and Roberts, 2003). In plants, cell number generally seems to make a larger contribution than cell size to the size of comparable organs (reviewed by Mizukami, 2001). However, seed size and weight are highly influenced by cell size via the growth and expansion brought about by massive accumulation of storage compounds (proteins, lipids, and/or carbohydrates) and water intake by cotyledon or endosperm cells. In cereal and legume crops, seed growth and development typically comprise three partially overlapping phases: an initial lag phase initiated at fertilization and characterized by cell proliferation and minimal dry weight gain (phase I); seed filling, a linear phase of large dry weight gain associated with cell enlargement and accumulation of storage compounds (phase II); and a final phase of reduced dry weight gain associated with desiccation and dormancy (phase III; Egli, 2006). In phase I, various seed tissues and domains are specified and established, including the vital transfer cells, a filial conduit with the mother plant vascular tissue that nourishes the developing seed. Phase I is also characterized by uptake of sucrose, which is rapidly converted to hexoses via cell wall-bound invertase activity. Even though phase I is critical for seed development and grain yield, its contribution is indirect, as the cells generated in this phase are very small and contribute little to seed biomass. However,

during phase II most of the endosperm or cotyledon cells generated in phase I accumulate storage compounds. Thus, phase II is characterized by cell enlargement due to cell growth and cell expansion, and a peak in seed water content (Egli, 2006). In storage cells of the cereal endosperm and legume cotyledons, phase II is also characterized by endoreduplication (also known as endopolyploidization, endocycling, or endoreplication), a type of cell cycle that leads to polyploidy. During phase III, water concentration decreases dramatically and physiological maturity is reached.

CELL CYCLE TYPES OCCURRING DURING SEED DEVELOPMENT

Briefly, the prototypical mitotic cycle consists of a DNA replication phase (S-phase), and a chromosome condensation and sister chromatid segregation phase (M-phase), which are preceded by G1 and G2 gap phases, respectively. Typically, this cell cycle is associated with cell division, and M-phase is generally coupled to karyokinesis and cytokinesis, which generate daughter cells with chromosome number and nuclear DNA content identical to those

of their mother cell. However, in several plant tissues, cell types, and developmental stages, alternative cell cycle types can occur. In the context of seed development, frequently these are acytokinetic mitosis and endoreduplication (Figure 1). In acytokinetic mitosis, the mitotic cell cycle is coupled to karyokinesis in the absence of cytokinesis, thus producing a syncytium or multinucleate cell. Endoreduplication is characterized by recurrent and alternating gap and S-phase, without intervening sister chromatid segregation, karyokinesis and cytokinesis, thus resulting in polyploid cells with an unaltered number of chromosomes, but with each chromosome containing multiple chromatids (reviewed by Edgar et al., 2014). All these different cell cycle types influence the growth and development of seed structures. Early in development, asymmetric cell divisions in the embryo generate polarized daughter cells that take on diverse differentiation paths, and rapid nuclear proliferation and cellularization in the endosperm establish the initial cell populations that occupy the embryo sac. Subsequent intense cell proliferation, coupled to cell differentiation, essentially produces all the embryo and endosperm cell types and tissues.



Finally, endoreduplication occurs, which is inherently associated with cell enlargement and accumulation of storage compounds in specialized cotyledon or endosperm cells.

Seed biology aspects such as comparative development and anatomy of seed structures and their underlying signaling networks were reviewed in-depth recently (Sabelli and Larkins, 2009b; Nowack et al., 2010; Lau et al., 2012; Sabelli, 2012b). Likewise, the role of cell cycle regulation in plant growth and development has also been reviewed thoroughly elsewhere (De Veylder et al., 2011; Heyman and De Veylder, 2012; Edgar et al., 2014; Sabelli, 2014). Hence, we focus on recent findings that clarify the role of core cell cycle regulators and different cell cycle types in the development, growth, and function of seed structures.

CELL CYCLE CONTROL AND CORE REGULATORS IN PLANTS: AN OVERVIEW

CYCLIN-DEPENDENT KINASES AND CYCLINS

In eukaryotes, cell cycle progression is controlled by the periodic activity of various heterodimeric threonine/serine protein kinases composed of catalytic and regulatory subunits, a cyclin-dependent kinase (CDK) and a cyclin, respectively. Plants possess relatively large sets of genes encoding different CDKs and cyclins, which can interact to form a potentially large number of combinations (Van Leene et al., 2011). Plants contain eight types of CDK-like proteins (reviewed by Dudits et al., 2007). Among the major CDKs involved with cell cycle regulation are members of the A-type, which characteristically contain in their cyclin-interacting α -helix a hallmark PSTAIRE amino acid motif; these function during S-phase and at the G1/S and G2/M transitions. In the plant-specific B-type CDKs, which function primarily at the G2/M transition, the PSTAIRE motif is replaced by PPTALRE (B1-subtype) or PPTTLRE (B2-subtype). D- and F-type CDKs, also known as CDK-activating kinases (CAKs), regulate A- and B-type CDKs through phosphorylation of specific residues (reviewed by Inzé and De Veylder, 2006). Angiosperm genomes possess a cyclin complement of ~50–60 genes organized into ~10 types (Wang et al., 2004; La et al., 2006; Hu et al., 2010; Ma et al., 2013). The majority of D-type cyclins are involved in the control of the G1/S transition; A-type cyclins, S-phase, and the G2/M transition; and B-type cyclins, G2/M, and intra-mitotic transitions (Inzé and De Veylder, 2006). CDK/cyclin complexes are subjected to different levels of regulation, including binding by non-catalytic CDK-specific inhibitors (CKIs), activating or inhibitory phosphorylation of CDK subunits, and cell cycle phase-specific cyclin synthesis and proteolysis, the latter of which is mediated by the ubiquitin-proteasome system (UPS; Inzé and De Veylder, 2006). A simplified diagram depicting some major molecular mechanisms of the plant cell cycle is shown in **Figure 2**.

THE RETINOBLASTOMA-RELATED PATHWAY

In higher eukaryotes, proteins of the retinoblastoma-related (RBR) family are known as repressors of the G1/S transition for their inhibitory effect on heterodimeric E2F/DP transcription factors. These, in turn, control the expression of multiple genes required for this cell cycle transition and S-phase progression, such as those encoding the subunits of the helicase MINICHROMOSOME

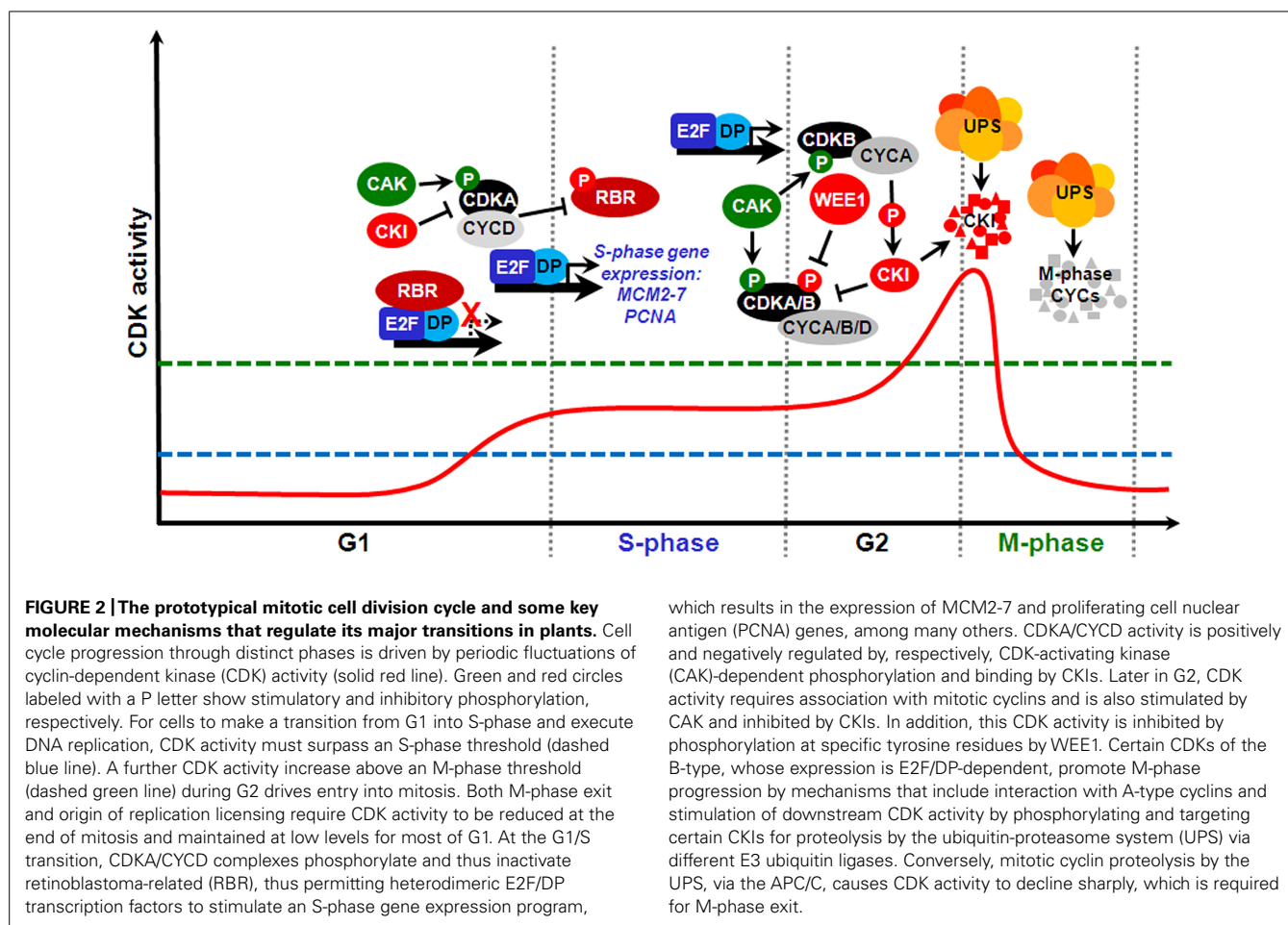
MAINTENANCE2-7 (MCM2-7) and the replication processivity factor proliferating cell nuclear antigen (PCNA) complexes (reviewed by Sabelli and Larkins, 2009c). RBR proteins are sequentially phosphorylated and inhibited by different CDK complexes, which relieves the block on E2F/DP-dependent gene expression and results in the transition into S-phase. In plants, CDK complexes containing D- and A-type cyclins seem to phosphorylate and thus inhibit RBR proteins. Grasses possess a more numerous and functionally diverse set of RBR proteins than most dicots, including *Arabidopsis thaliana* (Sabelli and Larkins, 2006, 2009c). The maize (*Zea mays*) genome contains at least four RBR genes that are grouped into two distinct types of duplicated genes, exemplified by *RBR1* and *RBR3* (Sabelli et al., 2005; Sabelli and Larkins, 2006). While *RBR1* functions as a repressor of cell cycle progression (Sabelli et al., 2013), *RBR3* stimulates the expression of genes encoding MCM2–7 proteins and DNA replication (Sabelli et al., 2009). *RBR3* is itself an E2F/DP target whose expression is negatively regulated by *RBR1* (Sabelli et al., 2005).

DNA REPLICATION INITIATION FACTORS

Regulation of DNA replication in plants is generally believed to follow conserved eukaryotic patterns (reviewed by Costas et al., 2011). Initiation of S-phase requires priming of chromatin via the assembly, at origins of replication, of the pre-replication complex consisting of ORIGIN OF REPLICATION COMPLEX (ORC1-6), CDC6, CDT1, and MCM2-7 proteins. ORC1-6 associate with origins of replication throughout the cell cycle but become sequentially bound by different proteins. Interaction of CDC6 and CDT1 with ORCs during G1 promotes the loading of MCM2-7, effectively licensing the origins for DNA replication (reviewed by Tuteja et al., 2011). These replication origin complexes are activated by CDKs at the G1/S transition, which leads to the recruitment of the replication machinery, the unwinding of DNA through MCM-dependent helicase activity, and DNA synthesis with the formation of replication forks. MCM protein complexes are displaced from replication origins as replication forks advance along the DNA, which prevents re-licensing of origins until S-phase and M-phase are completed. In endoreduplication cycles, DNA replication is initiated independently of M-phase, resulting in repeated rounds of DNA synthesis in the absence of mitosis. However, endoreduplication results from specific cell cycle modifications rather than merely uncontrolled activation of replication origins, which would cause over- and incomplete DNA replication (Costas et al., 2011; De Veylder et al., 2011; Sabelli, 2012a).

UBIQUITIN-DEPENDENT PROTEOLYSIS

Ubiquitin-Proteasome System-mediated proteolysis promotes the controlled destruction of several cell cycle regulators, which is critical for cell cycle phase transitions. Cyclins, CKIs, and other cell cycle regulators are targeted to the proteasome via their selective modification by various ubiquitin-protein ligases. Among the multimeric E3 ubiquitin-protein ligases functioning in plant cell cycle control are the anaphase promoting complex/cyclosome (APC/C), the Skp1/Cullin/F-box complex, and the Cullin-RING Ubiquitin Ligases (Heyman and De Veylder, 2012; Genschik et al., 2013). During late mitosis and most of G1, CDK activity is typically reduced via the targeting of A- and B-type cyclins



to the proteasome by the APC/C. In addition to its roles in the cell division cycle, E3 ligases control endoreduplication cell cycles, those occurring in trichome and root nodule cells being perhaps the best characterized such examples (Cebolla et al., 1999; Roodbarkelari et al., 2010; Heyman and De Veylder, 2012; Genschik et al., 2013).

CDK-SPECIFIC INHIBITORS

Non-catalytic inhibitors of CDK/cyclin complex activity, generally termed CKIs, have been identified as chief cell cycle regulators in all eukaryotes, and act by obstructing substrate interaction and ATP binding. Two types of CKIs have been identified and characterized in plants: INHIBITOR OF CDC2 KINASE/KIP-RELATED (ICK/KRP) and SIAMESE/SIAMESE-RELATED (Yi et al., 2014). ICK/KRPs typically bind to complexes containing A-type CDKs and D-type cyclins (Wang et al., 2008), although interaction with B-type CDKs was also reported (Nakai et al., 2006). Plant CKIs are targeted by several E3 ligases for degradation (Zhou et al., 2003; Weinl et al., 2005; Jakoby et al., 2006; Ren et al., 2008; Roodbarkelari et al., 2010). In mitotic cell cycles, ICKs/KRPs are phosphorylated by B1-type CDKs and targeted for UPS-mediated degradation, with consequent stimulation of A-type CDK activity and M-phase (Verkest et al., 2005).

The core molecular factors controlling the cell cycle in plants conform, to a large extent, to those identified in other higher eukaryotes. However, plant genomes are often characterized by a larger complement of key cell cycle genes as well as by uniquely possessing certain types of CDKs, E2Fs, and CKIs. The resulting complexity in cell cycle regulatory mechanisms, which appears to have considerable redundancy, may have evolved largely to fine-tune the cell cycle for the requirements of the sessile life style of plants.

ROLES OF DIFFERENT CELL CYCLES AND REGULATORS IN SEED DEVELOPMENT

EMBRYO

Cell proliferation, patterning, and morphogenesis during embryo development

From the first zygotic division through the early globular (8–16 cells) stages, many aspects of embryo development in monocots and dicots are conserved (Lau et al., 2012; Sabelli, 2012b). The zygote divides asymmetrically and generates an apical cell with dense cytoplasm and a large vacuolated basal cell at the chalazal and micropylar ends of the embryo sac, respectively, establishing early embryo polarity and patterning. The apical and basal cells produce, respectively, the proembryo and the suspensor, which has an embryo proper-nourishing function. Afterwards, cell

proliferation and differentiation occur coordinately to produce all embryo cell types and tissues, including the cotyledon(s), which in dicots accumulate storage compounds and typically occupy a large fraction of the mature seed volume. In dicots, periclinal divisions of the octant cells result in the globular embryo. Subsequently, the heart stage is reached with the characteristic emergence of two cotyledon primordia as opposite lateral extensions of the apical end. Next, cell proliferation and differentiation of the basal cell tier lead to the torpedo stage. As growth proceeds under mechanical constraints imposed by the ovule, the embryo increasingly assumes its typical curved shape. During development, monocot and dicot embryos display increasingly different morphologies. Patterns of cell division and cell lineages usually become less organized in monocot embryos and while two prominent cotyledons emerge in dicots, the origin of the single monocot cotyledon, the scutellum, is spatially more variable. In dicots, cotyledon cells undergo endoreduplication (Dhillon and Miksche, 1983; Lemontey et al., 2000; Rewers and Sliwinski, 2012).

The importance of cell cycle control during embryogenesis extends beyond its most recognizable aspects related to cell division and endoreduplication cycles. In *Arabidopsis thaliana* and *Nicotiana tabacum*, disruption of proper developmental patterns through lengthening or impairment of cell division by interfering with CDKA;1 (Hemerly et al., 2000), DNA polymerase ϵ (Jenik et al., 2005), and A3-type cyclin (Yu et al., 2003) indicates the dependence of embryo patterning and morphogenesis on the correct execution of cell divisions. Also, loss-of-function of *HOBBIT* (*HBT*), which encodes a homolog of the APC/C subunit CDC27 (Blilou et al., 2002), causes defects in hypophyseal cell specification and basal embryo cell division, perturbing root meristem formation (Willemssen et al., 1998). Recent investigation on *Arabidopsis* post-embryonic development indicates that moderate and high levels of CDKA;1 activity determine whether cells divide symmetrically or asymmetrically, respectively, and that CDKA;1 activity is conveyed via RBR1 and its control over cell cycle- and differentiation-related genes (Weimer et al., 2012). Similar mechanisms connecting CDKs and RBR1 appear to operate during embryogenesis (Nowack et al., 2012), and several studies have shed light on the roles of the RBR/E2F pathway, CDKs, D-type cyclins, CKIs, as well as additional APC/C components, in developing *Arabidopsis* seeds, underscoring the importance of precise cell cycle control for embryonic patterning, cell proliferation, and endoreduplication.

The role of D-type cyclins in embryogenesis

Collins et al. (2012) carried out a comprehensive investigation of D-type cyclin expression and function in developing *Arabidopsis* seeds. Various D-type cyclin genes show distinct and overlapping tissue-specific expression patterns during seed development. Developmental progression characterized in loss-of-function mutants revealed that embryo development is slower in the triple D3-type cyclin mutant, but not in single and double mutant combinations, indicating that this cyclin subtype is necessary for normal development, with individual, partly redundant components. Ectopic CYCD3;1 expression delays progression of embryonic development and causes atypical divisions in the

hypophysis and suspensor. In contrast to CYCD3;1, ectopic expression of CYCD7;1, a previously uncharacterized cyclin that is not expressed in wild-type seeds, induces cell proliferation and cell enlargement in the embryo (and endosperm), causing excessive growth and higher seed lethality. These results suggest that adequate control of spatiotemporal patterns of cell division, through the regulation of specific D-type cyclins and thus possibly their CDK complexes, is important for embryo patterning and growth.

Roles of CDKs, the RBR pathway, and CKIs in embryogenesis

A combinatorial analysis of mutants recently allowed functional dissection of five members of the ICK/KRP-type of CKIs during *Arabidopsis* seed development and revealed a link between ICK/KRPs, the RBR/E2F pathway and cell proliferation (Cheng et al., 2013). CDK activity gradually increased as individual ICK/KRP T-DNA insertion mutants were combined, indicating that ICK/KRPs act at least partially as dosage-dependent CDK inhibitors. Although single-gene mutants and most multiple-gene mutants have wild-type morphological phenotypes, the quadruple *ick1ick2ick6ick7*, and the quintuple *ick1ick2ick5ick6ick7* mutants have a slightly altered leaf shape, suggesting some degree of redundancy among individual genes. The quintuple mutant has larger cotyledons, leaves, petals, and seeds than wild type. The ICK/KRP mutants generally have more numerous but smaller cells in all organs examined, and this phenotype is enhanced as the number of combined mutant genes is increased. The quintuple mutant displays extensive up-regulation of the E2F pathway via increased phosphorylation of RBR1, consistent with reduced inhibition of CDK complexes.

An additional connection between CDKs and RBR1 was provided by combinatorial analyses of their corresponding mutants (Nowack et al., 2012). Delayed development and drastically altered cell numbers and sizes are observed during embryogenesis in null *cdka;1* mutants (indicating that embryogenesis can adjust to variations of cell number and size), while loss of function of both CDKA;1 and B1-type CDKs leads to embryogenesis arrest. Because post-embryonic defects in *cdka;1* mutants can be restored by *rbr1* mutations (Nowack et al., 2012), CDKA;1 most likely acts via the RBR/E2F pathway to control embryogenic cell proliferation. *Arabidopsis* *DEL1* encodes an E2F-DP-like DNA binding protein that was previously shown to be mostly expressed in dividing cells and to inhibit endoreduplication (Vlieghe et al., 2005). A loss-of-function *del1* mutant exhibits a small (~11%) but significant increase in seed size (Van Daele et al., 2012), although it was not determined whether this phenotype is due to stimulated endoreduplication. Collectively, these results suggest complex interactions among plant ICK/KRPs, which can function redundantly, but also in a dosage-dependent manner, to control the activity of CDK complexes, the RBR1/E2F pathway and cell proliferation.

The influence of the APC/C in embryogenesis

Functional characterization of genes encoding APC/C subunits and activators during embryogenesis revealed roles in cell-type specification and morphogenesis, in addition to cell division and endoreduplication. Mutations in both APC4 (Wang et al., 2012)

and APC1 subunits (Wang et al., 2013) cause defective gametogenesis and developmental arrest during embryogenesis, which seem to be associated with accumulation of B-type cyclin and altered auxin distribution. *SAMBA* encodes a conserved plant-specific protein that binds to and potentially regulates the APC/C (Eloy et al., 2012). *SAMBA* expression is high during embryogenesis and, to a lesser extent, early post-embryonic development. Loss-of-function *samba* mutants have defective male gametogenesis and enlarged shoot and root apical meristems that result in the production of larger seeds, embryos, leaves, and roots. Increased organ size in *samba* mutants could be attributed to a larger number of more highly endoreduplicated cells, rather than to larger cells. *SAMBA* binds an A2-type cyclin, which is stabilized in *samba* mutants during early development. Thus, *SAMBA* negatively regulates cell proliferation at least partially by targeting A2-type cyclins for proteolysis via the APC/C.

In conclusion, precise cell cycle regulation, both spatially and temporally, is critical for embryogenesis and plant reproduction. The core cell cycle regulators CDKs, cyclins, RBR1, ICK/KRPs, and the APC/C seem to play concerted roles and thus affect asymmetrical cell divisions, cell proliferation and endoreduplication during embryogenesis.

ENDOSPERM

Patterns of endosperm development

The endosperm functions in nourishing the sporophyte during embryogenesis and controlling germination and, mostly limited to monocots, also during early post-embryonic development. However, it also plays important roles in other aspects of seed development, including epigenetic regulation, coordination of cell patterning and proliferation, signaling among the major seed structures and control of seed size (Berger et al., 2006; Sabelli and Larkins, 2009b; Nowack et al., 2010; Fiume and Fletcher, 2012; Costa et al., 2014). The different cell cycle types occurring during the development of the persistent endosperm in grasses have mostly been investigated in traditional biological models and valued crop species, such as maize and rice (*Oryza sativa*).

The nuclear type of endosperm development is the most frequently encountered pattern among Angiosperms, and with regard to its early stages up to cellularization, is highly conserved in monocots and dicots (Olsen, 2004; Sabelli and Larkins, 2009b; Becraft and Gutierrez-Marcos, 2012). In this developmental type, the primary endosperm nucleus and its derivatives undergo acytokinetic mitosis iteratively, resulting in a syncytium that can comprise up to thousands of nuclei that are initially distributed around the central vacuole of the central cell (Olsen, 2004). Anticlinal cell wall deposition, forming alveoli encasing individual nuclei, creates the first endosperm cell layer, and reiteration of anticlinal cell wall deposition, alveolation, periclinal cell wall formation and periclinal cell division results in centripetal generation of additional cell layers, gradually replacing the space occupied by the central vacuole with cells. Cellularization is typically completed within three to six days after pollination (DAP) in cereals and by the torpedo stage in *Arabidopsis*. In the following developmental stage, mitotic divisions coupled to cytokinesis result in cell proliferation, thus producing most of the endosperm cells. Past

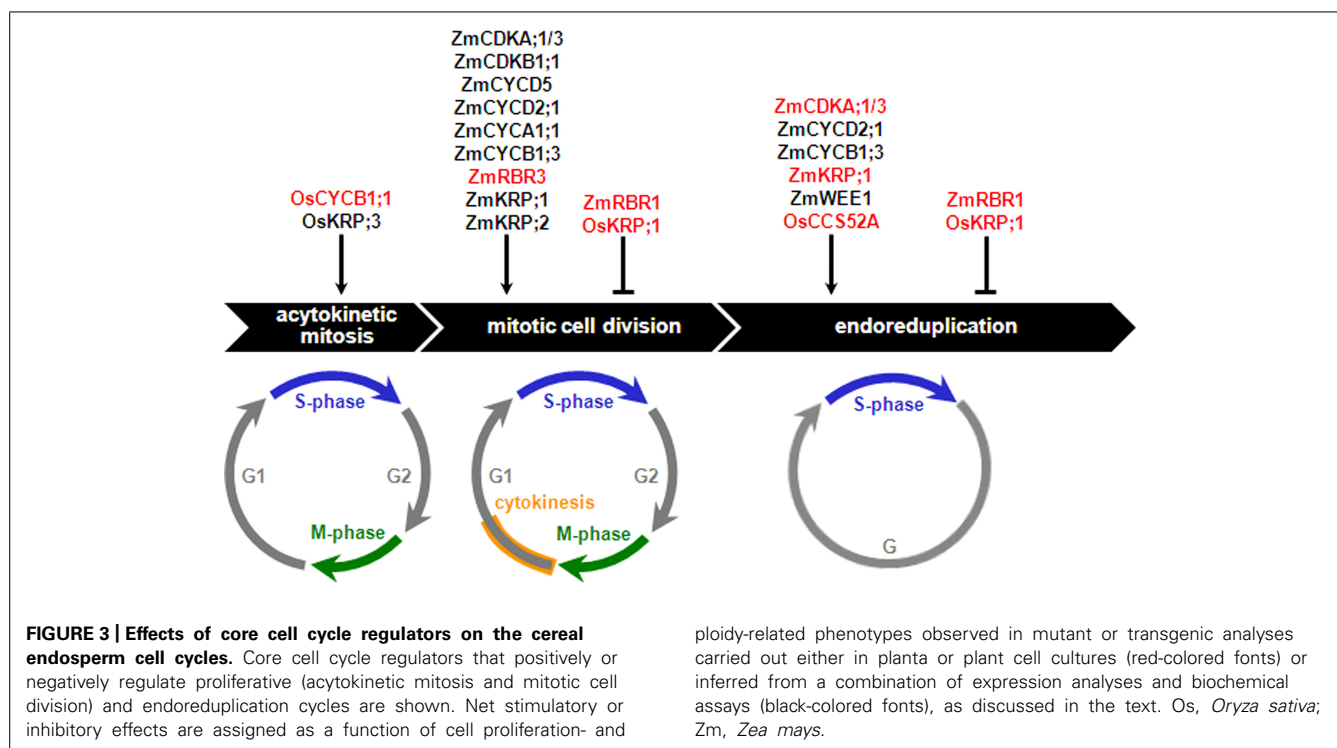
the cell proliferation stage, in nonendospermic species, such as *Arabidopsis*, the endosperm is absorbed by the rapidly developing embryo and is limited to a single or few cell layers at seed maturity. In contrast, in endospermic species, the endosperm is persistent and its development progresses through relatively conserved stages, comprising a period of cell enlargement typically associated with endoreduplication, followed by maturation involving programmed cell death (PCD) of specific cell types, dehydration, and dormancy. The roles played by core cell cycle regulators in the different cell cycles of cereal endosperm development are discussed in the following sections and summarized in Figure 3.

Maize endosperm development: an overview

Endosperm development in maize (and related cereals) follows the general monocot developmental pattern described earlier (Sabelli and Larkins, 2009b). Starting around three DAP, as the syncytium is cellularized, endosperm growth is mostly attained by an increase in cell number through mitotic cell divisions, which peak at eight to 10 DAP (Kiesselbach, 1949; Kowles and Phillips, 1985; Lur and Setter, 1993). Initiating in the endosperm central regions, also around eight to 10 DAP and then extending centrifugally, cells gradually and asynchronously cease mitotic cell divisions and switch to endoreduplication. As a result, the nuclei of many central endosperm cells reach high DNA content levels (some in excess of 200C; C = DNA content of haploid nuclei) and contain multiple, apparently uniform, copies of chromosomes (Bauer and Birchler, 2006). In agreement with the high correlation between ploidy level and cell size observed in numerous cell types and organisms, the spatiotemporal pattern of mitosis-to-endoreduplication switch in the maize endosperm creates a gradient of nuclear ploidy and cell size. Small non- or under-endoreduplicated cells are located mostly at the peripheral aleurone and sub-aleurone layers, as opposed to the increasingly large and endoreduplicated inner starchy endosperm cells. By 16 DAP, the expanded endoreduplicated cells account for most of the endosperm volume (Vilhar et al., 2002) and as many as 75% of its cells can become endoreduplicated at later developmental stages (Dilkes et al., 2002). Starchy endosperm cells typically display concomitant accumulation of starch and proteins with endoreduplication, which has long suggested a causal relationship between these processes (Larkins et al., 2001; Kowles, 2009; Sabelli and Larkins, 2009a,b; Sabelli, 2012b). Starchy endosperm cells subsequently undergo PCD (reviewed by Young and Gallie, 2000; Sabelli, 2012a), and the peripheral aleurone layer persists as the only living tissue past seed desiccation.

The contrasting endosperm development in *Brachypodium distachyon* and other model cereals

In comparison with maize, rice, and other major cereals, initial analyses of seed development in the emerging grass model, *Brachypodium distachyon*, have revealed important differences with respect to cell cycle control and its possible relationship with storage compound accumulation (Guillon et al., 2012; Trafford et al., 2013). In contrast to its related species, barley (*Hordeum vulgare*), *Brachypodium* endosperm displays reduced cell proliferation and enlargement. Also, the expression of a B1-type CDK and



an A3-type cyclin is reduced, in agreement with a withdrawal from a mitotic cell cycle program, but >6C nuclei are absent, indicating no occurrence of endoreduplication. Along with these differences, *Brachypodium* endosperm cells exhibits limited starch deposition and thickened cell walls, the cell wall polysaccharide, β -glucan, representing the main seed storage carbohydrate. Accordingly, the expression of genes involved with starch biosynthesis is reduced. Thus, an interpretation of the contrasting endosperm developmental patterns in *Brachypodium* and other cereals is that starch accumulation drives endosperm cell enlargement (Trafford et al., 2013) and, consequently, high nuclear ploidy levels are correlated with large cell sizes.

The importance of early nuclear and cell proliferation activities for endosperm development

Regulation of the syncytium-to-cellularization transition seems to be key for endosperm development and seed growth. Rice *THOUSAND-GRAIN WEIGHT 6* (*TGW6*), which encodes an indole-3-acetic acid (IAA)-glucose hydrolase, appears to stimulate, by elevating IAA levels, the expression of *CYCB2;2* and *E2F1* during the first three days after fertilization; it also stimulates premature cellularization of the syncytium and reduces endosperm final cell number, grain length, and weight (Ishimaru et al., 2013). In addition, suppressing the expression of rice *CYCB1;1* results in delayed endosperm cellularization and seeds containing only an enlarged embryo at maturity (Guo et al., 2010). Heat stress affects rice endosperm cellularization by interfering with the expression of the epigenetic regulator *FERTILIZATION-INDEPENDENT ENDOSPERM 1* of the Polycomb Repressive Complex 2 (PRC2), thus reducing seed size (Folsom et al., 2014). In *Arabidopsis*, over-expression

of *SHORT HYPOCOTYL UNDER BLUE 1* (*SHB1*) promotes early endosperm nuclear proliferation, a delay in cellularization, enlarged chalazal endosperm, and enhanced proliferation and expansion of embryo cells, leading consequently to increased seed size (Zhou et al., 2009). It is possible that these effects are mediated by members of the *HAIKU* pathway, which function downstream of *SHB1* to promote syncytial endosperm and seed growth via epigenetic control of cytokinin signaling (Li et al., 2013).

The rate and duration of proliferative cell cycles seem to also play an important role in maize seed size. Recently, Sekhon et al. (2014) examined transcriptional and developmental changes during seed development of maize populations that were selected for large and small seed sizes (termed KLS30 and KSS30, respectively). KLS30 seeds are more than fourfold heavier and twofold larger than KSS30 seeds and contain proportionally larger endosperms. Metabolite and genome-wide expression analyses indicated that, compared to KLS30 seeds, the linear phase of the grain filling (phase II) in KSS30 seeds initiates earlier, but it also occurs at slower rates and terminates earlier. Notably, KLS30 endosperms, relative to their KSS30 counterparts, display up-regulated sucrose metabolism and expression of the cell wall invertase *INCW2* (encoded by the *MINIATURE 1* gene), which is required for normal endosperm cell proliferation and expansion (Vilhar et al., 2002; Chourey et al., 2006). KLS30 endosperms also exhibit higher expression at 12–18 DAP of several genes encoding D- and B-type cyclins and APC/C subunits. Although cell number, size, and nuclear ploidy were not determined in KLS30 and KSS30 endosperms, these gene expression profiles suggest higher mitotic activity in the former. The balance between cell proliferation and endoreduplication activities as a factor influencing

endosperm and seed sizes is also supported by the analyses of multiple small-seeded popcorn inbred lines in comparison to typically large-seeded dent inbred lines (Dilkes et al., 2002; Coelho et al., 2007). Popcorn lines revealed higher endosperm ploidy levels from as early as 13 DAP in comparison to dent inbred lines. This difference could be attributed to an earlier transition between the cell division to endoreduplication stages, and/or higher rates of endoreduplication in popcorn lines. The importance of correct timing for cessation of cell proliferation and commencement of cell enlargement as an underlying factor for growth has been documented (reviewed by Powell and Lenhard, 2012). Collectively, these studies suggest a causal relationship between increased periods and/or rates of cell proliferation with larger endosperms (and, consequently, larger seeds), by establishing a stronger-sink tissue, one possessing more numerous cells that subsequently enlarge and accumulate larger amounts of storage compounds.

SEED COAT DEVELOPMENT, CELL CYCLE CONTROL, AND EPIGENETIC CONTROL OF SEED DEVELOPMENT

In most Angiosperms, the two ovule integuments that enclose the nucellus differentiate into the seed coat following fertilization, and develop through stages of cell division, cell elongation, differentiation, and PCD in coordination with embryo and endosperm development (Haughn and Chaudhury, 2005). Investigation of *Arabidopsis* seed coat development revealed the existence of complex communication and interaction between these seed structures and that their underlying cell proliferation and enlargement are major determinants of seed size (reviewed by Nowack et al., 2010). Impairing the elongation of integument cells via the *transparent testa glabra 2 (ttg2)* mutation reduces endosperm and seed growth (Garcia et al., 2005). *megaintegumental/auxin-response factor 2 (mnt/arf2)* mutants exhibit more numerous integument cells and enlarged seeds and embryos compared to wild type (Schruff et al., 2006). Premature syncytium cellularization reduces endosperm growth and integument cell elongation in *haiku (iku)* mutants (Garcia et al., 2005), whereas delayed cellularization and extended endosperm cell proliferation is associated with integument cell elongation in the enlarged seeds of *apetala 2 (ap2)* mutants (Ohto et al., 2009). The enhanced cell proliferation in *mnt/arf2* and *ap2* mutants seems to be associated with increased expression of D3- and B1-type cyclins (Schruff et al., 2006; Ohto et al., 2009), indicating that the corresponding transcription factors repress cell divisions through a pathway that involves down-regulation of these core cell cycle regulators.

Epigenetic mechanisms are particularly important for integrating growth and development of the seed coat, embryo, and endosperm. Particularly among core cell cycle regulators, RBR1 is involved in gametophyte cell differentiation and endosperm nuclear proliferation along with epigenetic regulators such as PRC2 and DNA METHYLTRANSFERASE 1 (Ebel et al., 2004; Ingouff et al., 2006; Johnston et al., 2008; Jullien et al., 2008). *rbr1* mutants display fertilization-independent endosperm development, reduced cell proliferation in the ovule integuments prior to fertilization and impaired differentiation of the seed coat (Ebel et al., 2004; Ingouff et al., 2006).

In conclusion, there appears to be extensive crosstalk and coordination, in which epigenetic control and RBR1 play significant roles, between cell cycle activity in the developing seed coat and inner seed structures, such as the embryo and endosperm. These mechanisms could modify both signaling and mechanical constraints imposed by maternal tissues on developing seed structures, and consequently could control seed size (Haughn and Chaudhury, 2005).

THE ROLE OF CORE CELL CYCLE REGULATORS IN THE CEREAL ENDOSPERM: THE MAIZE PROTOTYPE AND RELATED EXAMPLES

CONTROL OF ENDOREDUPLICATION IN ENDOSPERM

The mechanisms that control the transition from the mitotic cell cycle into endoreduplication and its progression in various cell types and species have been recently reviewed in detail (Edgar et al., 2014; Sabelli, 2014). Among plant core cell cycle regulators, certain CDK/cyclin complexes, CKIs, APC/C activators and the RBR/E2F pathway have been functionally linked to the onset and/or rates of endoreduplication cycles. Although these cell cycle regulators are widely conserved across higher eukaryotes and appear to be recurrently deployed to produce cell cycle modifications that result in endoreduplication, their individual contributions may be species- and cell-type-specific (Roodbarkelari et al., 2010; Edgar et al., 2014). In maize endosperm, induced S-phase CDK activity and inhibited M-phase CDK activity were proposed to cause endoreduplication cycles (Grafi and Larkins, 1995). In support of this model, endoreduplication is inhibited and stimulated, respectively, by over-expression of a catalytically inactive, dominant-negative form of CDKA;1 (Leiva-Neto et al., 2004) and by decreased RBR1 activity and consequent up-regulation of E2F/DP-dependent gene expression (Sabelli et al., 2013). In addition, developing maize endosperm exhibits the contrasting expression of different CKIs (Coelho et al., 2005) and functionally distinct RBR homologs of the RBR1 and RBR3 types (Grafi et al., 1996; Sabelli et al., 2005, 2009, 2013). Endosperm endoreduplication particularly correlates with the potential inhibitory phosphorylation of CDK subunits by a WEE1 homolog (Sun et al., 1999a), differential cyclin expression (Sun et al., 1999b; Dante et al., 2014) and apparent down-regulation of UPS-mediated proteolysis of members of various cyclin types, including potential mitotic cyclins (Dante et al., 2014).

CKIs

ICK/KRP-type CKIs appear to have variable roles in different cell cycle types during cereal endosperm development. KRP;1 is expressed at nearly constant levels in 7–21 DAP endosperm, while KRP;2 protein levels decline during this period, suggesting a more positive role in endoreduplicating cells for KRP;1 than KRP;2, which in contrast could be preferentially involved with regulation of the mitotic cell cycle or its transition into the endoreduplication cycle (Coelho et al., 2005). Biochemical assays showed KRP;1 activity corresponds partly to a CDK inhibitory activity existing in endoreduplicating endosperm (Grafi and Larkins, 1995). KRP;1 and KRP;2 are able to partially inhibit

the complex CDK fraction that binds p13^{suc1}, and they specifically inhibit the CDK activity associated with A1- and D5-type cyclins, but not that associated with CYCB1;3 (Coelho et al., 2005). Overexpression of KRP;1 along with the wheat dwarf virus RepA protein, which antagonizes RBR1 (Graf et al., 1996; Xie et al., 1996; Gordon-Kamm et al., 2002; Sabelli et al., 2005, 2009), causes ectopic endoreduplication in cultured, proliferating maize cells, indicating that coupling the stimulation of G1/S transition to the inhibition of certain CDK complexes is sufficient for endoreduplication onset in otherwise dividing cells (Coelho et al., 2005).

Expression and functional analyses *in planta* revealed that KRPs impact rice endosperm development. KRP;1 RNA is preferentially expressed at the mitosis-to-endoreduplication transition in wild-type rice plants, and its over-expression results in decreased kernel weight and filling rate, in addition to perturbed production and lower ploidy levels of endosperm cells (Barrôco et al., 2006). In contrast, KRP;3 RNA is most highly expressed in the syncytial endosperm, but its level declines subsequently in the cellularized endosperm, suggesting a specific function in the syncytial cell cycle or during the transition to cellularization (Mizutani et al., 2010).

THE CDK AND RBR PATHWAYS

Recently, Sabelli et al. (2013) showed that RBR1 controls multiple molecular and cellular aspects of maize endosperm development. *RBR1* down-regulation via RNAi in endosperm cells results in enhanced expression of *RBR3*-type, *MCM2–7*, and *PCNA* genes. Mitotic and endoreduplication cell cycles are both stimulated by the alleviated inhibition of RBR1 on the G1/S transition, which causes *RBR1*-RNAi endosperm to have 58% more cells and ~70% more DNA than its wild type counterpart by 19 DAP. However, this creates a surprising reduction in cell and nuclear sizes, in spite of increased endoreduplication, thus ruling out a causal and direct relationship between these processes, at least in the specific context of *RBR1* down-regulation. Larger cell numbers and higher ploidy levels together cause a 43% increase in DNA content in mature endosperm upon *RBR1* down-regulation, although no measurably altered storage protein content or kernel weight (a proxy for starch accumulation) were observed. Genetic interaction analysis of *RBR1* and *CDKA;1* (Leiva-Neto et al., 2004), down-regulated individually or in combination, indicated that *CDKA;1* requires *RBR1* for controlling endoreduplication, but conversely *RBR1* represses downstream target genes independently from *CDKA;1*. These observations suggest distinct *RBR1* activities at controlling endoreduplication, in which *CDKA;1* probably participates via its inhibitory phosphorylation of *RBR1*, and at repressing E2F-dependent gene expression in a *CDKA;1*-independent manner. *RBR1* down-regulated endosperm exhibits levels of p13^{suc1}-adsorbed CDK activity similar to those of wild-type endosperm even in the presence of dominant-negative *CDKA;1*, indicating that various CDK complexes and *RBR1* are negatively and reciprocally regulated, and implying that CDKs other than *CDKA;1* participate in cell cycle stimulation upon *RBR1* down-regulation (Leiva-Neto et al., 2004; Sabelli et al., 2013; Dante et al., 2014). Thus, perturbing *RBR1* function revealed its key roles in integrating various processes in maize endosperm, but this did not translate in altered seed size

and weight, suggesting the presence of a higher order, homeostatic regulation of endosperm development (discussed in next section).

The stimulation of CDK activity in down-regulated *RBR1* maize endosperm prompts the question of the identity of CDKs, besides *CKDA;1*, controlling cell division and endoreduplication cycles (Sabelli et al., 2013). The identification and expression of different CDKs expressed in maize endosperm were reported recently (Dante et al., 2014). Previously uncharacterized CDKs of the A-type and B1-types, termed, respectively, *CDKA;3* and *CDKB1;1*, were found to be expressed in endosperm. Protein levels of A-type CDKs are nearly constant throughout endosperm development, whereas expression of *CDKB1;1* becomes markedly reduced during the transition into the endoreduplication stage and is stimulated upon *RBR1* down-regulation. These observations are in agreement with the role of A-type CDKs in both mitotic and endoreduplication cell cycles and that of B1-type CDKs specifically in the mitotic cell cycle established in other species. Similar expression patterns, cyclin binding properties, and maintenance of nearly wild-type levels of CDK activity upon combined down-regulation of *RBR1* and *CDKA;1* collectively indicate that *CDKA;1* and *CDKA;3* are partially redundant or function coordinately (Sabelli et al., 2013; Dante et al., 2014). *RBR1* down-regulated endosperm possesses more numerous cells and also exhibits higher ploidy levels, indicating that both cell division and endoreduplication are stimulated in distinct spatiotemporal patterns (Sabelli et al., 2013). These results suggest some redundancy among A-type CDKs and a specialized role for *CDKB1;1* in positively regulating cell division during maize endosperm development (Leiva-Neto et al., 2004; Sabelli et al., 2013; Dante et al., 2014). Consistent with this interpretation, *Arabidopsis* possesses a single A-type CDK, and its B1-type CDKs can drive progression through cell division, but not endoreduplication cycles, in the absence of *CDKA;1* and *RBR1* (Nowack et al., 2012).

CYCLIN/CDK COMPLEXES

The spatiotemporal expression of A-, B-, and D-type cyclins and their associated kinase activities in developing maize endosperm were recently investigated (Dante et al., 2014). Two main transcript expression patterns are apparent, one characterized by rapidly declining RNA levels with the onset of endoreduplication (A- and B-type cyclins), and the other with nearly constant RNA levels throughout endosperm development (D-type cyclins). However, these patterns are not consistent with those at the protein level, as shown by a discrepancy between declining *CYCB1;3* RNA in endoreduplicating endosperm but sustained levels of the encoded protein. While *CYCB1;3* and *CYCD2;1* proteins are localized to both the cytoplasm and nucleus of cells throughout the endosperm, *CYCD5* protein is localized solely in the cytoplasm of peripheral cell layers. CDK activity associated with *CYCA1* is tightly associated with cell division, while *CYCB1;3*-, *CYCD2;1*-, and *CYCD5*-associated CDK activities are highest at the transition from cell division to endoreduplication. These patterns together suggest roles for *CYCA1* and *CYCD5* in the cell division cycle, while *CYCB1;3* and *CYCD2;1* could participate in both cell division and endoreduplication. In particular, the switch to an endoreduplication program is marked

by a drastic reduction in kinase activity associated with CYCA1. A-, B-, and D-type cyclins are more resistant to proteasome-dependent degradation in endoreduplicating compared to mitotic endosperm, which potentially contributes to the sustained levels of proteins, particularly CYCB1;3, in endoreduplicating cells. Consequently, the mitosis-to-endoreduplication transition and the accompanying cell enlargement typical of starchy endosperm cells are possibly associated with cell cycle modifications created by reduced proteasome-dependent proteolysis of several types of cyclins and, potentially, that of additional core cell cycle regulators (Dante et al., 2014).

UPS-MEDIATED PROTEOLYSIS

Functional and expression analyses in rice revealed roles for APC/C activators that seem in part distinct from those of their homologs in dicots. Reduced expression of CELL CYCLE SWITCH 52A (*OsCCS52A*), a homolog of the APC/C activating subunit, results in smaller seeds and, despite reduced nuclear and cell size of endosperm cells, only modest reduction in their ploidy levels (Su'udi et al., 2012b). Also, reduced expression of the related *OsCCS52B* protein negatively impacts seed and cell sizes, but has no impact on endoreduplication (Su'udi et al., 2012a). Thus, collectively, *OsCCS52A* and *B* seem to play rather minor roles in rice endosperm endoreduplication, but have important roles in controlling cell and seed sizes. Although plant *CCS52* homologs are known to promote proteolysis of A- and B-type cyclins and endoreduplication (reviewed by Heyman and De Veylder, 2012), the targets and mechanisms by which *OsCCS52A* and *B* control cell and seed sizes remain unknown. Some unidentified cyclins are presumably targeted by *OsCCS52A* and *B*, but the apparent down-regulation of UPS-mediated cyclin degradation and its contribution to sustained CYCB1;3 expression in endoreduplicating maize endosperm cells (Dante et al., 2014) further suggests that *CCS52* homologs have a more significant role in cyclin proteolysis in mitotic as opposed to endoreduplicating endosperm. Also, these observations are consistent with others made in dicot model species, underscoring that various plant cell cycle regulators are targeted to UPS-mediated degradation by E3 ubiquitin ligases in cell-type- and cell cycle-type-dependent manners (Roodbarkelari et al., 2010; Heyman and De Veylder, 2012). Thus, dissecting the specific roles of E3 ubiquitin ligases and the UPS at large in governing various aspects of endosperm development, including cell cycle control, merits further investigation.

Besides the apparently reduced UPS activity in endoreduplicating compared to mitotic endosperm, translational regulation may also be responsible, at least in part, for sustained CYCB1;3 protein levels despite drastically reduced amounts of its RNA, as cyclin expression is known to be regulated at this level. In addition, many levels of gene expression regulation operate extensively during seed development, as a comparative analysis of the developing maize seed transcriptome and proteome revealed large discrepancies between cognate RNA and protein levels (Walley et al., 2013). Possible underlying mechanisms include differential stability of RNA and protein pairs, transport of proteins between tissues and out-of-phase circadian accumulation

of corresponding RNAs and proteins (Walley et al., 2013). Thus, the expression of CYCB1;3 and other core cell cycle regulators in different seed structures may be subject to complex regulation.

WHAT IS THE ROLE OF ENDOREDUPLICATION? EVIDENCE FROM THE MAIZE ENDOSPERM

Proliferative cell cycles are ultimately responsible for establishing the number of cells in a tissue, organ or body and, together with cell enlargement, determine their overall size. Although increased tissue/organ/body size resulting from stimulated cell proliferation has been documented in plants, typically the proliferation and enlargement of cells are inversely correlated, as more numerous cells are compensated for at the tissue/organ level by reduced cell size, essentially resulting in no overall differences (reviewed by John and Qi, 2008; Powell and Lenhard, 2012; Sabelli, 2014). A long-standing debate persists that opposes the “cell-based” or “cellular theory” (whereby cell proliferation and enlargement drive tissue/organ/body growth in a cell-autonomous manner) and the “organismal theory” (cell proliferation and enlargement follow a higher-order, supra-cellular program; Beemster et al., 2006; John and Qi, 2008; Sabelli, 2014).

While the impact of cell proliferation on tissue/organ/body size can be easily appreciated, that of endoreduplication is more controversial. Endoreduplication displays remarkable coincidence with cell enlargement in numerous cell types associated with different specialized functions. In an emerging and unifying view, endoreduplication facilitates cell expansion, growth, and accompanies differentiation in multiple cell types in which the occurrence of cell division could impair their function (Edgar et al., 2014). Among plant cells, the cellular functional specializations and attributes commonly associated with cell enlargement and endoreduplication include ability for rapid cell elongation (e.g., hypocotyl cells), branched cell morphology (e.g., trichomes), nutrient storage (e.g., cotyledons and endosperm of seeds and pericarp of fleshy fruits), hosting endosymbiotic bacteria (e.g., nodule giant cells) and interaction with pathogens and parasites (e.g., giant cells in galls and feeding sites). Some functions of endoreduplication in plant cells are only beginning to be elucidated (reviewed by John and Qi, 2008; Chevalier et al., 2011, 2013; De Veylder et al., 2011; Edgar et al., 2014; Sabelli, 2014). Recently, the contribution of endoreduplication to cell morphogenesis and cell identity maintenance (Bramsiepe et al., 2010), as well as regulation of gene expression and karyoplasmic homeostasis (Bourdon et al., 2012) were investigated. Bramsiepe et al. (2010) reported that, upon targeted reduction of endoreduplication levels by modification of core cell cycle gene expression, *Arabidopsis* trichome number is reduced due to dedifferentiation and resumption of mitosis by these cells. Conversely, promoting endoreduplication causes restoration of trichome cell identity, which revealed a role for endoreduplication in determining trichome cell fate. In endoreduplicated cells of the tomato pericarp, the nuclear surface has extensive grooves that are filled with mitochondria, thus allowing fairly constant nuclear surface/volume ratios, suggesting the existence of high ATP demand by nuclear processes

(Bourdon et al., 2012). Accordingly, rRNA and mRNA transcription in individual nuclei is positively correlated with ploidy levels.

In the terminally differentiated starchy cells of maize endosperm, endoreduplication can be viewed as a mechanism that supports increased gene expression and the enhanced metabolic activity associated with cell enlargement and massive accumulation of starch and storage protein (Larkins et al., 2001; Sabelli and Larkins, 2009a; Sabelli, 2014). However, modification of endosperm endoreduplication, by perturbing the function of core cell cycle regulators, has challenged some aspects of this paradigm (Leiva-Neto et al., 2004; Sabelli et al., 2013). Similar to maize kernels in which the expression of a dominant-negative CDKA;1 reduces endoreduplication (Leiva-Neto et al., 2004), the size, weight, and morphology of RBR1 down-regulated kernels are essentially identical to their wild-type counterparts (Sabelli et al., 2013). Thus, evidence from modification of maize endosperm endoreduplication suggests this cell cycle does not contribute to metabolic and growth processes, at least at a whole-tissue level.

Surprisingly, RBR1 down-regulation in endosperm also results in coordinated reduction in cell and nuclear sizes (Sabelli et al., 2013). This indicates a role for RBR1 in coupling DNA content to nuclear and cell sizes. Importantly, these results invoke the existence of a causal relationship between nuclear and cell sizes in endosperm cells, which is not affected by perturbing RBR1 function, in support of the general karyoplasmic ratio theory. In addition, the observation of a larger number of smaller cells in RBR1 down-regulated endosperm seems to agree with the organismal theory of development. Consequently, one interpretation of the effects of RBR1 down-regulation in maize endosperm is that suppression of RBR1 function leads to enhanced cell proliferation, which results in a larger number of cells that, nonetheless, undergo less pronounced enlargement imposed by supra-cellular control of tissue size. Nuclear sizes are adjusted to the sizes of respective cells, regardless of their higher ploidy levels, which are achieved via enhanced endoreduplication. In RBR1 down-regulated endosperm, both the uncoupling of ploidy levels from cell and nuclear size and the reduced storage protein gene expression per unit of nuclear DNA possibly arise from increased DNA methylation and chromatin condensation (Sabelli et al., 2013), in a fashion similar to *Arabidopsis* cotyledon cells (van Zanten et al., 2011). Importantly, additional chromatin produced by enhanced endoreduplication in RBR1 down-regulated endosperm seems to be less transcriptionally active (Sabelli et al., 2013), providing latent transcriptional capacity in case cell enlargement is resumed or continued. Consequently, at the individual cell level, endoreduplication in the endosperm could function in the adjustment of nuclear size to cell size (thus preserving the karyoplasmic ratio) through a process influencing chromatin condensation states and transcription. This view seems to be supported by evidence from other model systems (Wu et al., 2010; Bourdon et al., 2012).

A deeper understanding of the role endoreduplication plays in endosperm development may require genetic analyses of this cell cycle by perturbing individual genes other than those

encoding core cell cycle regulators, whose possible functions at coupling endoreduplication to cellular outputs may produce confounding results. The existence of compensatory mechanisms mediating tissue homeostasis may also require approaches based on a suite of technologies such as transmission electron and fluorescence microscopy, immunohistochemistry, DNA and RNA *in situ* hybridization, *in vitro* tissue culture and flow cytometry/fluorescence-activated nuclear sorting to unmask cell-autonomous effects (Gruis et al., 2006; Bourdon et al., 2012).

CONCLUDING REMARKS

Acytokinetic mitosis, symmetric and asymmetric cell division, and cell enlargement greatly impact seed growth and development. During embryogenesis, correct execution of cell division is required for patterning and morphogenesis. Both the rates of proliferative and endoreduplication cell cycles (the latter of which being typically integral to cell enlargement and differentiation in storage compartments) and the timing of the developmental transitions between these cell cycles influence the final size of seed structures and ultimately that of the whole seed. In *Arabidopsis*, a pivotal role of its only RBR member, RBR1, in asymmetric cell divisions, gametogenesis and embryogenesis has been revealed, while in the developing cereal endosperm the RBR1 homolog is central to the control of cell proliferation and endoreduplication cycles and nuclear and cell sizes, underscoring the importance of this family of core cell cycle regulators for plant reproduction and development. Differential expansion of families of key cell cycle genes in various plant species seems to allow the establishment of both functional redundancy and specialization, creating complex cell cycle regulatory networks. Genome-wide analyses and functional gene characterization studies have recently begun to reveal potentially important differences in cell cycle control between dicots and monocots. These differences are evident from genetic analyses of members of the RBR family, whose increased complexity in grass species can allow functional diversification, as exemplified by RBR1 and RBR3. The APC/C and cyclin proteolysis appear to play less prominent roles in the control of cereal endosperm endoreduplication than in dicot root nodules, trichomes, and pericarp. More investigation is needed to unravel the functions of different cell cycle types and their underlying regulatory pathways in endosperm growth, development, and function.

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Expression, regulation and activity of a B2-type cyclin in mitotic and endoreduplicating maize endosperm

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Cyclin-dependent kinases, the master regulators of the eukaryotic cell cycle, are complexes comprised of a catalytic serine/threonine protein kinase and an essential regulatory cyclin. The maize genome encodes over 50 cyclins grouped in different types, but they have been little investigated. We characterized a type B2 cyclin (CYCB2;2) during maize endosperm development, which comprises a cell proliferation phase based on the standard mitotic cell cycle, followed by an endoreduplication phase in which DNA replication is reiterated in the absence of mitosis or cytokinesis. *CYCB2;2* RNA was present throughout the period of endosperm development studied, but its level declined as the endosperm transitioned from a mitotic to an endoreduplication cell cycle. However, the level of CYCB2;2 protein remained relatively constant during both stages of endosperm development. CYCB2;2 was recalcitrant to degradation by the 26S proteasome in endoreduplicating endosperm extracts, which could explain its sustained accumulation during endosperm development. In addition, although CYCB2;2 was generally localized to the nucleus of endosperm cells, a lower molecular weight form of the protein accumulated specifically in the cytosol of endoreduplicating endosperm cells. In dividing cells, CYCB2;2 appeared to be localized to the phragmoplast and may be involved in cytokinesis and cell wall formation. Kinase activity was associated with CYCB2;2 in mitotic endosperm, but was absent or greatly reduced in immature ear and endoreduplicating endosperm. CYCB2;2-associated kinase phosphorylated maize E2F1 and the “pocket” domains of RBR1 and RBR3. CYCB2;2 interacted with both maize CDKA;1 and CDKA;3 in insect cells. These results suggest CYCB2;2 functions primarily during the mitotic cell cycle, and they are discussed in the context of the roles of cyclins, CDKs and proteasome activity in the regulation of the cell cycle during endosperm development.

Keywords: cell cycle, cyclin, cyclin-dependent kinase, endoreduplication, endosperm, maize, proteasome

INTRODUCTION

The eukaryotic cell division cycle is driven by the activity of complexes between a serine/threonine cyclin-dependent kinase (CDK) and a regulatory cyclin (CYC) protein. Periodic activation of different CDK/CYC complexes ensures the typically unidirectional execution of cell cycle steps, such as DNA replication and chromosome segregation (mitosis), and progress through their intervening transitions. A number of mechanisms are known to regulate CDK/CYC activity, including gene transcription, phosphorylation, and dephosphorylation of key amino acids, proteolysis by the 26S proteasome, and binding by specific inhibitors (De Veylder et al., 2007; Harashima et al., 2013). Compared to yeast and mammals, plant genomes encode a larger number of these two components of CDK complexes, and it has been challenging to dissect their function, especially because of the genetic redundancy within the two protein families. Understanding the mechanisms governing the cell cycle, coupled with the ability to manipulate it, offer the potential to enhance crop performance and yield, and several important examples are known in which alteration of cell cycle control

has significantly impacted crop evolution and breeding (Sabelli, 2014). Although the cell cycle is relatively well characterized in the model species *Arabidopsis thaliana*, our understanding of cell cycle control in economically important crops, and particularly in major grasses such as maize, rice and wheat, is still in its infancy, and there is a pressing need to unravel the roles of key cell cycle-controlling genes in these crops. Because yield in maize and related cereals is in part determined by grain size and weight, it is important to understand how different cell cycle genes are regulated and how they function during seed development.

The most economically important seed tissue is the endosperm, which originates at fertilization by the fusion of one sperm cell nucleus with two polar nuclei within the central cell of the female gametophyte (reviewed in Becraft et al., 2001; Olsen, 2004; Sabelli and Larkins, 2009c). In maize, the primary triploid endosperm nucleus goes on to proliferate by acytokinetic mitoses to generate a syncytium. Deposition of cell wall material between nuclear domains followed by cell proliferation through mitotic cell division give rise to virtually all the endosperm cells by approximately

12 days after pollination (DAP). However, starting from around 8–10 DAP, inner cells of the endosperm switch to an endoreduplication type of cell cycle, which is characterized by reiterated rounds of DNA synthesis in the absence of mitosis or cell division; typically, this results in large, polyploid nuclei and cells. Endoreduplication proceeds toward the periphery of the endosperm and is roughly coincident with the massive accumulation of storage compounds, such as starch and zein proteins. From around 16 DAP, central endosperm cells begin to undergo programmed cell death, and this continues so that at seed maturity all endosperm cells are dead, except for the peripheral aleurone layer. Because the mitotic phase of endosperm development produces virtually all the cells involved in storage compound accumulation and because the endoreduplication phase is associated with rapid cell growth and endosperm expansion and filling, it is important to understand how the cell cycle is regulated during these two phases (Sabelli and Larkins, 2009b). In this context, three maize CDKs: CDKA;1, CDKA;3, and CDKB1;1; several cyclins belonging to the A1, B1, D2, and D5 types (Graf and Larkins, 1995; Sun et al., 1999b; Leiva-Neto et al., 2004; Dante et al., 2014); two CDK inhibitors (Coelho et al., 2005); a Wee1 homolog (Sun et al., 1999a); and members of the retinoblastoma-related (RBR) protein family (Graf et al., 1996; Sabelli et al., 2005, 2013) have been studied in some detail.

Recent genome-wide analyses revealed the cyclin family in maize comprises over 50 members (Hu et al., 2010), and for the most part these genes have not been investigated. B-type cyclins are believed to be primarily involved in the regulation of M-phase and appear to play important roles in plant growth and seed development. CYCBs are known to stimulate cell division and tissue growth in ectopic or over-expression studies (Doerner et al., 1996; Lee et al., 2003). Knockdown of CYCB1;1 in rice caused aborted seed endosperm due to abnormal cellularization of the syncytium (Guo et al., 2010) and resulted in large, triploid embryo cells (Guo et al., 2014). In addition, CYCB2;2 was implicated in the timing of rice endosperm cellularization, cell number, and grain size and yield (Ishimaru et al., 2013). Here we describe CYCB2;2 from maize with respect to its spatiotemporal expression patterns, interaction with CDKs, associated kinase activity, and proteolysis patterns during endosperm development. These data suggest this cyclin likely functions during cell division and cell wall formation in mitotic cells and becomes stabilized in endoreduplicating cells with the accumulation of a lower molecular weight form in the cytoplasm.

MATERIALS AND METHODS

PLANT MATERIALS

Maize (*Zea mays* L.) B73 plants were grown in the field or a greenhouse and hand-pollinated. Endosperms were dissected from kernels harvested at different stages of development and processed for molecular and immunohistochemical analyses as described in previous publications (Leiva-Neto et al., 2004; Sabelli et al., 2005, 2013; Dante et al., 2014).

DATABASE SEARCHES AND SEQUENCE ANALYSES

A nucleotide sequence encoding CYCB2;2 was initially obtained by querying Pioneer Hi-Bred's maize EST database. Additional

searches were made in the Maize Genome Sequencing Project¹, MaizeGDB² (Lawrence et al., 2004), Phytozome v10³, Rice Genome Annotation Project v7⁴ (Kawahara et al., 2013), Gramene v42⁵ (Ware et al., 2002), and Pfam v27⁶ (Finn et al., 2014) databases and the Maize eFP Browser⁷ (Sekhon et al., 2011). Functional motifs were predicted with the Eukaryotic Linear Motif Resource⁸ (Dinkel et al., 2014). Subcellular localization was predicted using LocTree 3⁹ (Goldberg et al., 2012), Plant-mPLoc¹⁰ (Chou and Shen, 2010), and BaCelLo¹¹ software. Multiple sequence alignments were carried out with M-Coffee¹² (Di Tommaso et al., 2011) or MUSCLE (Edgar, 2004). An un-rooted Neighbor-Joining tree of a set of 35 plant B-type cyclin amino acid sequences, spanning the conserved Cyc_N and Cyc_C domains (Nugent et al., 1991), was constructed using MEGA6 software package (Tamura et al., 2013). Amino acid sequences were selected based on previous analyses (La et al., 2006; Guo et al., 2007; Hu et al., 2010; Jia et al., 2014) and novel database searches. Only one amino acid sequence per locus was selected in the case of multiple predicted transcripts. Several shorter amino acid sequences (GRMZM2G025200_P01, Loc_Os02g41720, AT1G34460, Sb07g003015, Potri.006G035200.2) were not included in the analysis. The evolutionary distances were computed using the Poisson correction method. All positions containing gaps and missing data were eliminated. There were a total of 235 positions in the final dataset.

ANALYSES OF ENDOSPERM RNA AND PROTEINS

Detailed procedures for purification of endosperm RNA and protein and their analyses by RT-PCR and immunoblotting, respectively, are given in previous publications (Sabelli et al., 2005, 2013; Dante et al., 2014). The following RT-PCR primers were used for CYCB2;2: CYCB2;2F (GAAAATGAGGCTAAGAGTTGTG-TAAG) and CYCB2;2R (GAGCTCCAGCATGAAAATGACGCT) and actin: ACT1-F (ATTTCAGGTGATGGTGTGAGCCACAC) and ACT1-R (GCCACCGATCCAGACACTGTACTTCC). Each developmental stage comprised a pool of 5–13 endosperm RNA samples. Two analysis replicates were carried out and the RNA levels averaged, normalized to those of actin control, and displayed relative to those at 7-DAP.

Analysis of CYCB2;2 RNA accumulation patterns in 14 different tissues/developmental stages was carried out by compiling Nimblegen-derived RNA expression data from Sekhon et al. (2011), available at the Maize eFP Browser⁷.

¹<http://www.maizesequence.org>

²<http://www.maizegdb.org/>

³<http://phytozome.jgi.doe.gov>

⁴<http://rice.plantbiology.msu.edu/>

⁵<http://www.gramene.org/>

⁶<http://pfam.xfam.org/>

⁷http://bar.utoronto.ca/efp_maize/cgi-bin/efpWeb.cgi?dataSource=Sekhon_et_al

⁸<http://elm.eu.org/>

⁹<https://roslab.org/services/loctree3/>

¹⁰<http://www.csbio.sjtu.edu.cn/bioinf/plant-multi/>

¹¹<http://gpcr.biocomp.unibo.it/bacello/>

¹²<http://tcoffee.crg.cat/apps/tcoffee/index.html>

Immunohistochemical localization assays were carried out essentially as described by Dante et al. (2014), except for a monoclonal anti-tubulin antibody (YOL 1/34, Accurate Chemical and Scientific Corp., Westbury, NY, USA), which was used to stain microtubules. Antibodies were utilized at a concentration of 0.5–1 µg/ml. Immunoprecipitation and kinase activity assays were carried out as described previously (Dante et al., 2014).

PROTEIN EXPRESSION IN HETEROLOGOUS SYSTEMS AND ANTIBODIES

Sequences encoding selected domains of maize cyclins (amino acid residues 1–243 of CYCA1;1, 1–206 of CYCB1;3, and 4–143 of CYCB2;2) were expressed as GST fusions in *Escherichia coli* and purified according to procedures described previously (Dante et al., 2014). For CYCB2;2, a cDNA fragment encoding a 139-aa long, N-terminal domain was amplified with primers B2;2 4–143F (ATCGCGGATCCGCGCGGCGGATGAAACCGCAGACC) and B2;2 1–62R (CCGCTCGAGTCAGAGCAATTCATCTTCGTTTCATAATGTCC), and cloned at the *Bam*HI and *Xho*I sites of the pGEX4T-3 vector (GE Healthcare, Life Sciences). Antibodies were generated in rabbits (anti-cyclin) and affinity purified or purchased (anti-actin) as previously reported (Dante et al., 2014).

For expression in *Drosophila* S2 cells, CYCB2;2 was PCR-amplified with primers E2-KpnI (ATCCGCGGTACCAAACATGGCGGCGGGCGGCTGACGAGAAC) and E2HAS2 (ATCGCGAATTCCTATTAGGCGTAATCGGGCACATCGTAGGGGTAGTTTGCACCTGAAGGAGGCGG), cloned into the *Kpn*I and *Eco*RI sites of the pHSKMCS vector (kindly provided by Dr. Thomas Bunch, University of Arizona), expressed in *Drosophila* S2 cells either alone or co-expressed with maize CDKA;1 or CDKA;3, and analyzed essentially as described previously for other cyclins (Dante et al., 2014). CYCB2;2 was immunoprecipitated from cell lysates and assayed for interaction with co-expressed maize CDKs using an anti-PSTAIR (Sigma, catalog No. P7962) antibody (Dante et al., 2014). Immunoprecipitates were also tested for kinase activity on histone H1 substrate in *in vitro*-assays as described (Dante et al., 2014).

PROTEIN STABILITY ASSAYS

³⁵S-radiolabeled CYCB2;2, and a T417A mutant (CYCB2;2T/A) polypeptides were synthesized *in vitro* using TNT T7 Quick for PCR DNA kit (Promega, Madison, WI, USA) as described (Dante et al., 2014). These proteins were incubated with cell extracts obtained from prevalently mitotic (i.e., 7-DAP) or endoreduplicating (i.e., 15-DAP) endosperm for 90 min before being subjected to SDS-PAGE and autoradiography. The 26S proteasome-specific inhibitor, carboben-zoxyl-leuciny-leuciny-leucinal (MG-132, Sigma), was utilized to determine whether protein degradation was proteasome-dependent. Procedures for these assays were as previously reported (Dante et al., 2014).

RESULTS

IDENTIFICATION OF CYCB2;2 FROM MAIZE

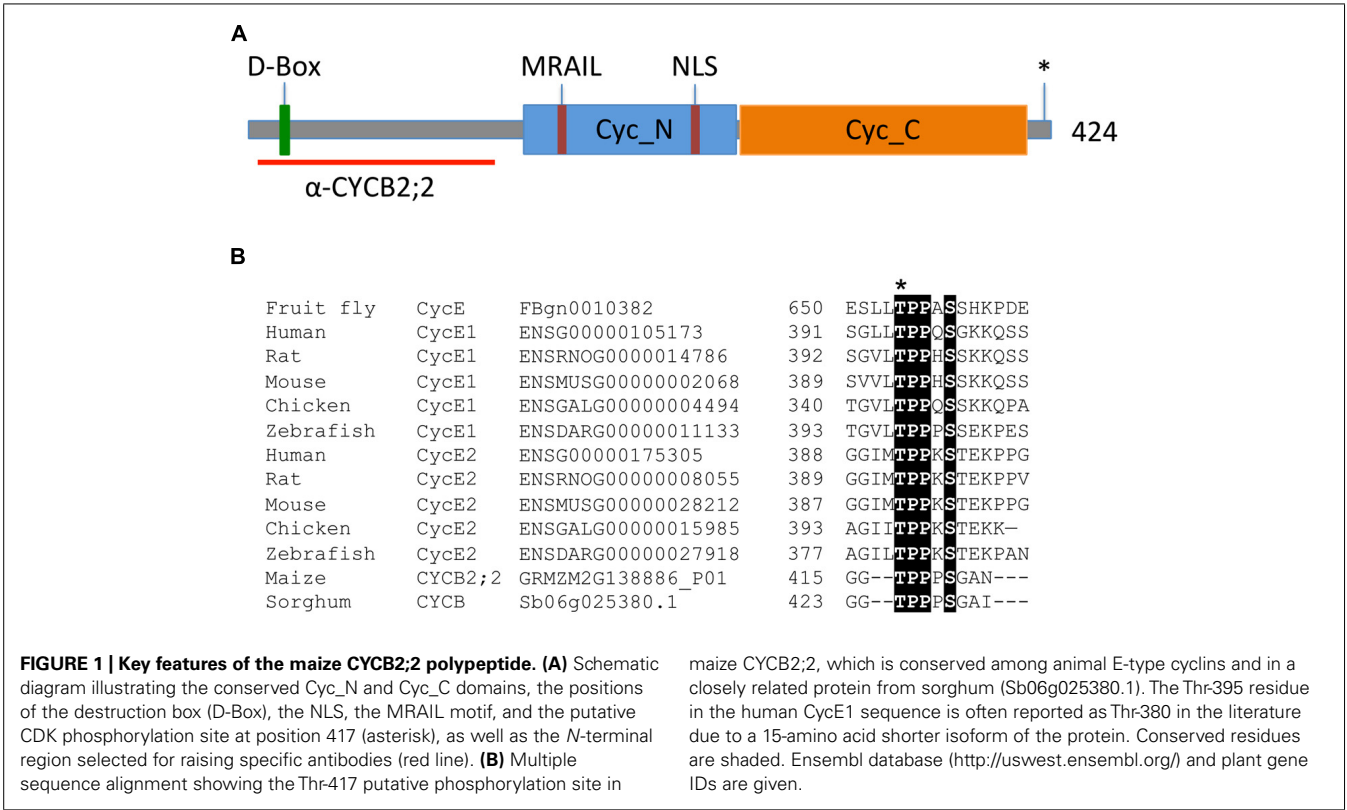
An EST encoding a B-type cyclin from maize, hereafter termed CYCB2;2, was identified by searching Pioneer Hi-Bred Inc.'s database. Subsequently, a corresponding genomic sequence located on chromosome 2, with accession number

GRMZM2G138886, was also identified. The deduced CYCB2;2 protein sequence is 424 amino acids long, with a calculated molecular weight of 47.5 kDa. It possesses two all-alpha fold domains embedded in the so-called and highly conserved “cyclin core,” which are characteristic of cyclin proteins: Cyc_N (or cyclin box), which contains the CDK-binding site and is located between residues 163 and 289, and Cyc_C, which however, is less conserved among cyclins, and is located between residues 291 and 407 (Nugent et al., 1991; **Figure 1A**). A potential PRKK nuclear localization signal (NLS) is located between residues 231–234. A protein destruction box (SRRALTDIK, D-Box), targeted by the anaphase-promoting complex/cylosome (APC/C) and which is required for anaphase-specific proteolysis, is predicted at residues 26–34. A MRail motif, which is involved in cyclin binding to substrates containing the RxL motif, such as CDK-specific inhibitors and RBRs (Schulman et al., 1998), is located between residues 192–196.

Thr-417 represents a potential CDK phosphorylation site, which is conserved with similar phosphorylation sites in animal CycE proteins (**Figures 1A,B**). Phosphorylation of this site contributes to CycE proteolysis via the SCF-Fbw7 ubiquitin ligase pathway (Welker et al., 2003; Hwang and Clurman, 2005; Hao et al., 2007). Through database searches, a closely related cyclin from sorghum (Sb06g025380.1) was identified that also possesses this putative phosphorylation site (**Figures 1B** and **2**), though it does not appear that this motif is conserved in other plant cyclins.

Phylogenetic analyses indicated that the maize CYCB2;2 cyclin described in this study clusters with other B2-type cyclins from monocots (maize, sorghum, and rice) and dicots (*Arabidopsis* and poplar). These results are in general agreement with previous analyses (Hu et al., 2010). During the course of this study, a gene was identified on chromosome 10 (GRMZM2G061287) that encodes a closely related and previously un-reported maize cyclin, which was termed CYCB2;3. The closest cyclins from rice (CYCB2;1) and sorghum (Sb06g025380.1; **Figure 2**) also lack functional characterization to date, which makes it difficult to predict a precise function for maize CYCB2;2 based on sequence similarity.

An N-terminal region of CYCB2;2 (amino acid residues 4–143) that has little or no sequence identity with other maize cyclins identified so far (~39% identity with the corresponding regions in CYCB2;1, the closest maize homolog) was selected to raise specific antibodies (**Figure 1A**). This region of the protein lies outside the Cyc_N domain, and thus these antibodies were not likely to interfere with the catalytic or CDK-binding activity of CYCB2;2. The corresponding CYCB2;2 cDNA sequence was expressed in *E. coli* as a GST fusion and polyclonal antibodies were raised in rabbits against the purified protein, and were affinity purified. These antibodies were tested against the recombinant CYCB2;2 antigen and comparable N-terminal regions of maize CYCA1;1 and CYCB1;3, which were also expressed as GST-fusions in *E. coli* as described previously (Dante et al., 2014; **Figure 3**). While these antibodies effectively recognized the CYCB2;2 N-terminal polypeptide, no cross-reactivity was observed with either CYCA1;1 or CYCB1;3.



EXPRESSION OF CYCB2;2 DURING ENDOSPERM DEVELOPMENT

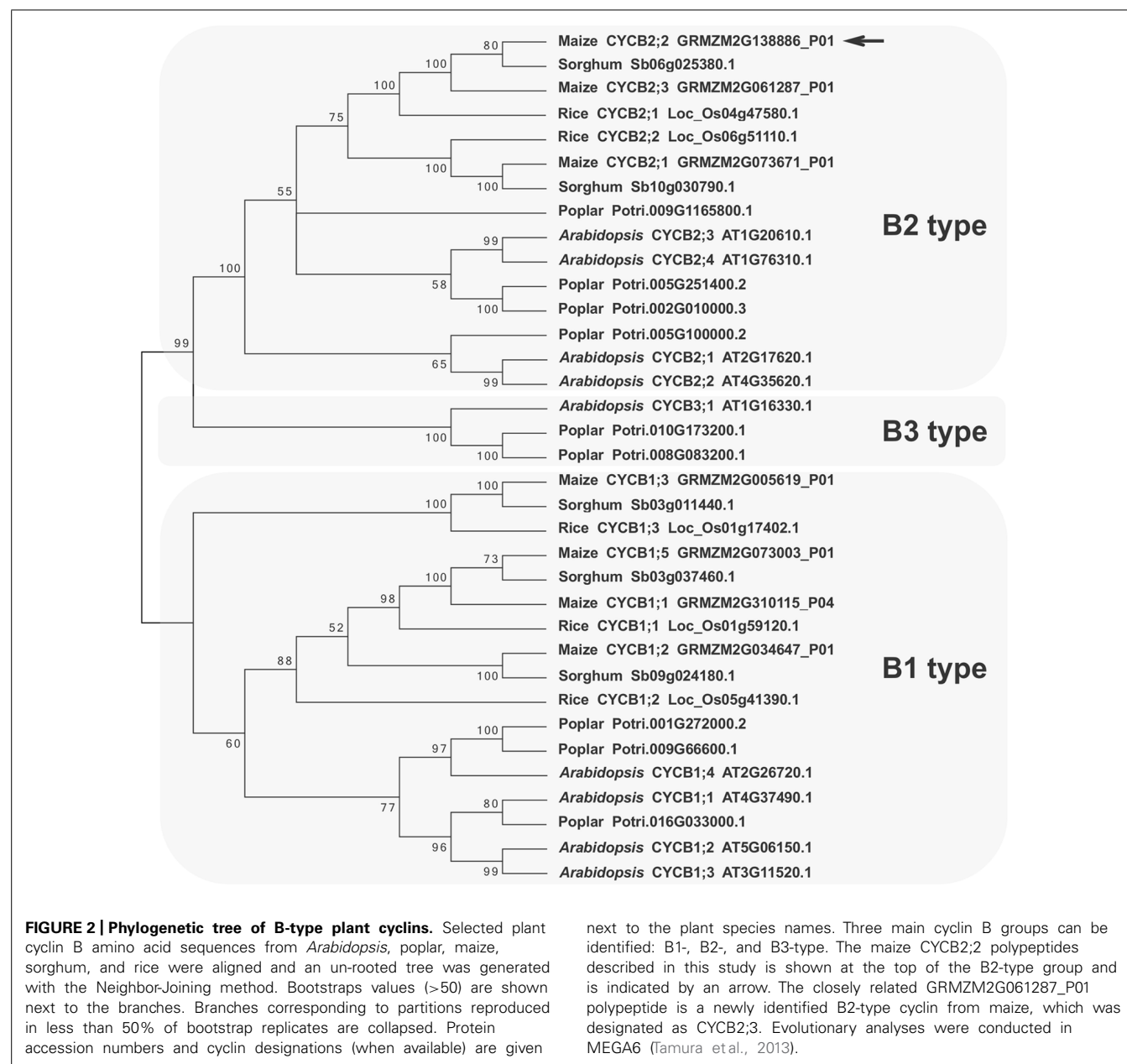
The expression patterns of CYCB2;2 RNA and protein during endosperm development were analyzed by RT-PCR and western blotting, respectively (Figure 4). These experiments showed that CYCB2;2 RNA levels are relatively high in 7-DAP endosperm and decline steadily thereafter, reaching by 13-DAP a minimum of less than 20% the 7-DAP reference levels, and remaining low up to 21-DAP (Figures 4A,B). This result is in agreement with the expression pattern of CYCB2;2 RNA obtained through global transcriptome analyses of developing maize endosperm (12–24 DAP) and available through the Maize eFP Browser (Sekhon et al., 2011; Figure 4C). Additionally, the data shown in Figure 4C indicate that CYCB2;2 RNA is widely expressed in maize tissues, and particularly at high levels in those known to contain an elevated proportion of mitotic cells, such as the primary root, shoot tip, leaf base, immature ear, embryo, and young endosperm.

The anti-CYCB2;2 antibody recognized a polypeptide of the expected molecular weight in endosperm extracts (Figure 4D). However, longer autoradiograph exposure times revealed the presence of an additional band of slightly lower molecular weight, which tended to accumulate specifically during the endoreduplication phase of endosperm development and was detectable from around 13–15 DAP (Figure 4E). This low-molecular-weight (LMW) CYCB2;2-related polypeptide was never detected in 7- or 9-DAP extracts; its accumulation appeared to be associated with the endoreduplication phase of endosperm development, which suggests it may play a specific role in this specialized type of cell cycle.

Comparison of the CYCB2;2 RNA and protein accumulation patterns revealed a discrepancy between the marked decline of RNA levels and the relatively constant protein levels observed between 7 and 21 DAP. This observation raises the possibility that CYCB2;2 protein may be subject to different turnover regulation in early (i.e., 7-DAP) versus more advanced (i.e., 13–21 DAP) endosperm developmental stages, which primarily comprise cells that are mitotic or endoreduplicating, respectively. Specifically, CYCB2;2 may not be as efficiently degraded in endoreduplicating endosperm as in mitotic endosperm.

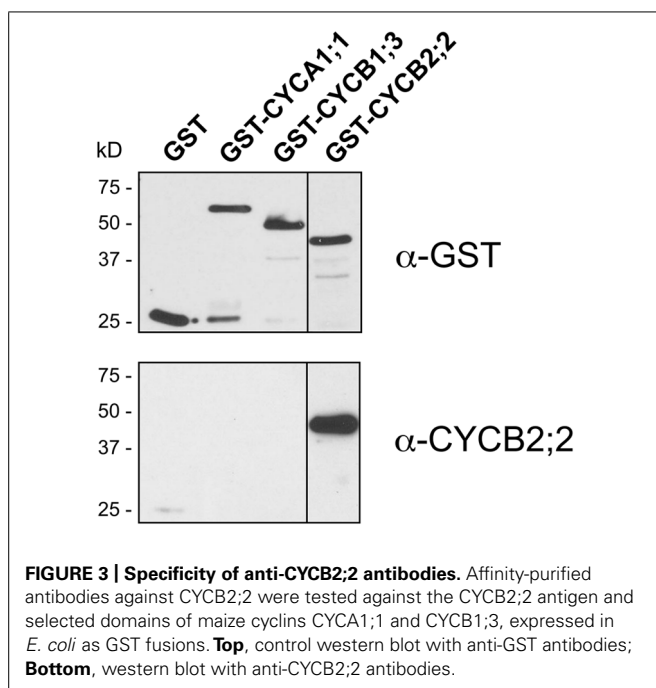
SUBCELLULAR LOCALIZATION OF CYCB2;2 PROTEIN

Sequence analyses by subcellular localization prediction software and the presence of a putative NLS in the CYCB2;2 amino acid sequence suggested this protein could be targeted to the nucleus. We investigated the localization pattern of CYCB2;2 in endosperm, embryo, and root tip cells by immunofluorescence using anti-CYCB2;2 antibody (Figure 5). DNA and tubulin were stained as markers for nuclei and the microtubule cytoskeleton, respectively, in the same tissue sections. In 7-DAP endosperm, CYCB2;2 was clearly localized to the nucleus, though a weak signal was also detected in the cytoplasm (Figures 5A–D). Although most endosperm nuclei stained positively for CYCB2;2, the signal among nuclei differed notably, with a rather diffused CYCB2;2 accumulation pattern in some nuclei and a sharply punctuate one in others. These differences in localization patterns within a population of cells that are asynchronously engaged in the cell cycle are typical of cell cycle-regulated proteins. In 13-DAP endosperm cells, CYCB2;2 was



clearly localized to the nucleus but it also showed extensive and diffuse localization in the cytoplasm, which was clearly more pronounced than in 7-DAP endosperm cells (**Figures 5E–H**). However, peripheral cells gave a relatively stronger CYCB2;2 signal than inner endosperm cells in both 7- (**Figures 5A,D**) and 13-DAP (**Figures 5E,H**) sections, but it is not clear whether this might be due to physiological differences between the two cell types or to the highly dense cytoplasm of peripheral cells at both developmental stages. Analysis of 7-DAP endosperm (**Figure 5A**, arrow indicates a telophase cell), embryo (**Figures 5I–L**, arrow indicates a late-phragmoplast cell in which the residual phragmoplast is being eroded beginning from its central zone) and meristematic root tip cells (**Figure 5M**), which typically proliferate through the mitotic cell cycle and do

not undergo endoreduplication, revealed CYCB2;2 was localized to the phragmoplast between two daughter nuclei, suggesting a potential role for CYCB2;2 in late mitosis-early cytokinesis and the deposition of the new cell wall separating daughter cells. In root tip cells (**Figure 5M**), CYCB2;2 was localized to the cytoplasm but also to the mitotic spindle's mid-zone in anaphase (center arrow), the phragmoplast mid-zone in telophase (right arrow) and at the site of cell wall formation at cytokinesis (left arrow). Both in mitotic and endoreduplicating cells, the nuclear fraction of CYCB2;2 did not appear to coincide with the DNA, and thus it appeared to be generally excluded from chromatin, similarly to CYCB2;1 (Mews et al., 1997), but there was some overlap with the microtubule cytoskeleton.



We compared the subcellular distribution patterns of CYCB2;2 between 9-DAP endosperm cells, which are mostly mitotic, and 15-DAP cells, which are primarily endoreduplicating. Subcellular fractions enriched for nuclear and cytosolic proteins were prepared from these two endosperm developmental stages and assayed for CYCB2;2 accumulation by western blotting (Figure 6). CYCB2;2 appeared prevalently localized to the nuclear fraction in 9-DAP endosperm, but a lower molecular weight polypeptide, corresponding to the additional LMW band shown in Figures 4D,E, accumulated specifically in the cytosolic fraction in 15-DAP endosperm. The presence of intact actin protein as well as tubulin and other cyclins as recently reported (Dante et al., 2014) indicates that the LMW, CYCB2;2-related band was not due to general protein degradation in the extract. These results are in agreement with the immunohistochemistry data shown in Figure 5, which does not discriminate signal based on molecular weight differences. In prevalently mitotic endosperm (i.e., 7–9 DAP), CYCB2;2 is mostly nuclear with relatively little signal from the cytoplasm. In endoreduplicating cells (i.e., 13–15 DAP), however, CYCB2;2 becomes more extensively localized to the cytoplasm, and the cell fractionation analysis suggests that this shift in localization is due to the specific accumulation of an extra-nuclear, LMW form of the protein (Figure 6). The presence of similar amounts of full-length CYCB2;2 in mitotic and endoreduplicating endosperm cells suggests this protein maybe involved in regulating cell cycle processes that are common to these two cell types, such as DNA synthesis. Alternatively, partial CYCB2;2 proteolysis and exclusion from the nucleus may be associated with the endocycle and may underscore a role for the intact protein in mitosis and/or cytokinesis. Thus, in contrast to mitotic cells, endoreduplicating endosperm cells are characterized by specific nuclear-to-cytosol redistributions of CYCB2;2, specifically suggesting that accumulation of the

LMW component in the cytoplasm may be critical for the transition from the mitotic to endoreduplication phase of endosperm development.

CYCB2;2-ASSOCIATED KINASE ACTIVITY

We investigated whether CYCB2;2 is part of active kinase complexes, is capable of phosphorylating various substrates, and its activity varies between immature ear and endosperm at different stages of development. CYCB2;2 was immunoprecipitated from extracts prepared with either immature ear and 9-DAP endosperm, two tissues comprising prevalently mitotic cells, and tested for phosphorylation of histone H1 substrate by *in vitro* assays (Figure 7A). Whereas virtually no CYCB2;2-associated kinase activity was detected in extracts from immature ear, a strong signal was obtained from 9-DAP endosperm extracts. These patterns were similar to those of CYCB1;3, and antithetic to those of CYCD2;1 or CYCD5, which displayed much strong associated kinase activities in immature ear relative to endosperm. These experiments indicate there are specific differences with regard to the kinase activity associated with CYCB2;2 between immature ears and 9-DAP endosperm, as well as those associated with other types of cyclins. Although both tissues are known to exhibit high mitotic activity, these data underscore the presence of potentially important differences in the regulation of the cell cycle between these two tissues, and suggest a more prominent role in endosperm for B-type cyclins. We next asked whether CYCB2;2-associated kinase activity from 9-DAP endosperm could phosphorylate different recombinant polypeptides expressed as GST fusions (Figure 7B). The pocket domain of RBR3 was effectively phosphorylated, although RBR1 pocket was only weakly phosphorylated in this assay. Neither N-terminal domain of these proteins was phosphorylated, consistent with the typical predominance of conserved CDK targets specifically within the pocket domain of RBR proteins from many organisms (Sabelli et al., 2005; Sabelli and Larkins, 2009a; Burke et al., 2012). The E2F1 substrate was also phosphorylated by CYCB2;2-associated kinase activity, similarly to recent results for CYCB1;3-associated kinase activity (Dante et al., 2014). By 9-DAP, some endosperm cells could have already initiated the transition to endoreduplication, particularly those located in the center of the tissue, and thus analyses of kinase activity at this stage may not exclusively reflect mitotic cells. We thus measured CYCB2;2-associated kinase activity in 7-DAP endosperm extracts, a stage characterized exclusively by mitotic cells as shown by flow-cytometric profiles (Dante et al., 2014), in 15-DAP extracts, a stage in which cells are actively endoreduplicating and mitotic figures are rare, as well as at 11-DAP, which represents a transition stage with high rates of mitotic and endoreduplication cell cycle activities (Dante et al., 2014). As shown in Figure 7C, while CYCB2;2-associated kinase activity was high and virtually at the same levels in 7- and 11-DAP endosperm, it declined dramatically in 15-DAP endosperm. Collectively, these results indicate that CYCB2;2/CDK complexes are more active in mitotic than in endoreduplicating endosperm cells.

We next investigated whether CYCB2;2 can form complexes with A-type CDKs when co-expressed in a heterologous cell system, and whether such complexes are active (Figure 8).

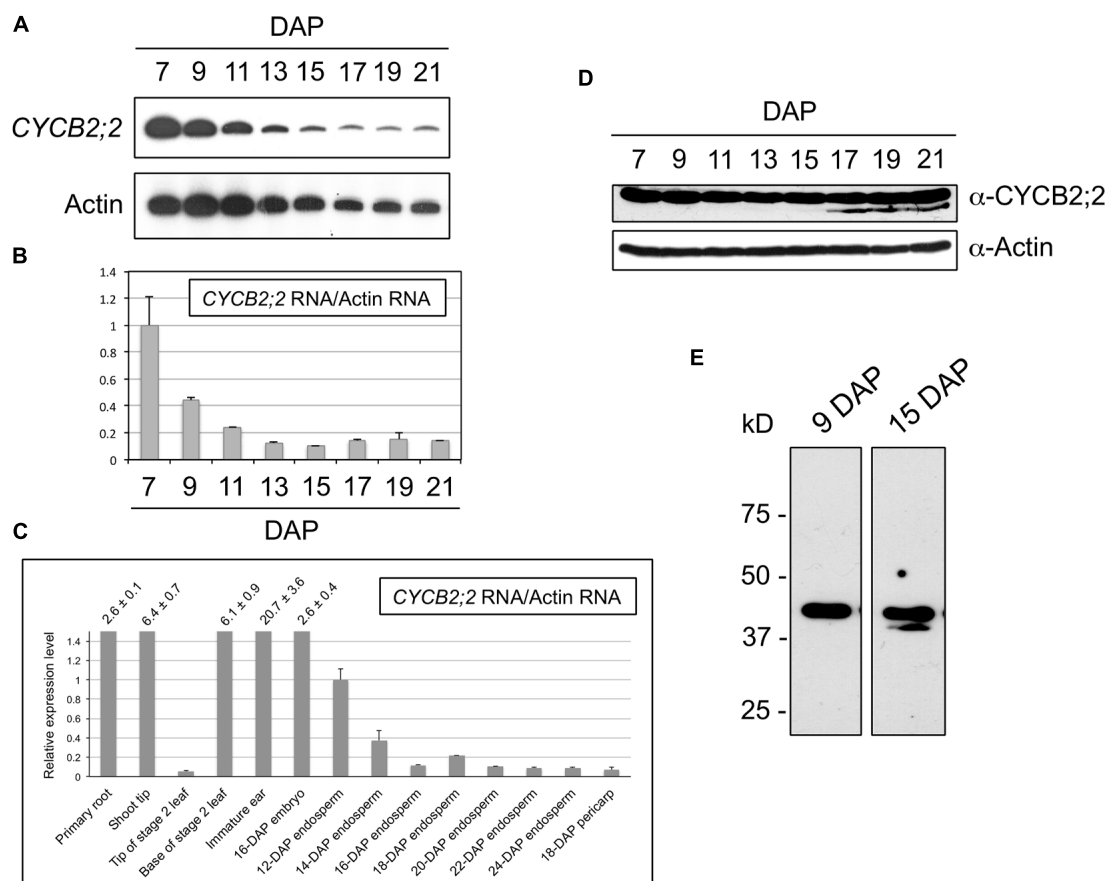


FIGURE 4 | CYCB2;2 expression patterns during maize endosperm development. (A–C) Analyses of RNA accumulations patterns. **(A,B)** Analysis of CYCB2;2 RNA accumulation pattern during endosperm development from 7 to 21 DAP by RT-PCR. Actin RNA was used as a control. Error bars indicate standard deviations. **(C)** Analysis of CYCB2;2 RNA accumulation, relative to that of actin, in 14 maize tissues and developmental stages. Error bars indicate standard deviations. This analysis was based on data from a previous

study by Sekhon et al. (2011). **(D,E)** Western blots. Actin expression pattern was used as a control. Accumulation of CYCB2;2 protein is roughly constant, despite decreasing levels of RNA. A lower molecular weight CYCB2;2-related polypeptide accumulated specifically in endoreduplicating (e.g., 15-DAP) endosperm cell extracts **(E)**. The actin blot was part of a set of common experiments carried out during a larger study and was published previously (Sabelli et al., 2005).

CYCB2;2 was co-expressed with either maize CDKA;1 or CDKA;3 in *Drosophila* S2 cells. Protein extracts were immunoprecipitated with anti-CYCB2;2 antibody and tested for the presence of either CDKA using anti-PSTAIR antibodies. In both cases, a clear interaction between CYCB2;2 and CDKA;1 or CDKA;3 was detected. However, these CDKA/CYCB2;2 complexes did not phosphorylate histone H1 substrate (**Figure 8B**), suggesting either that the CYCB2;2-associated kinase activity in endosperm extracts is due to a CDK other than CDKA;1 or CDKA;3 or that the expression system utilized for this assay was deficient for some other necessary factors, such as, for example, specific CDK-activating kinases typically acting upstream of CDKs (Umeda et al., 2000; Shimotohno et al., 2004).

PROTEASOME-DEPENDENT DEGRADATION OF CYCB2;2 IN ENDOSPERM

The sustained accumulation of CYCB2;2 protein during endosperm development, in spite of rapidly declining levels of

its RNA, suggested that perhaps CYCB2;2 was becoming resistant to degradation by the 26S proteasome during the endoreduplication phase. Indeed, we recently showed that endoreduplicating endosperm can be differentiated from mitotic endosperm by virtue of sustained expression of certain A-, B-, and D-type cyclins associated with their reduced ubiquitin-mediated proteolysis (Dante et al., 2014). A similar outcome was obtained for CYCB2;2 in the present investigation (**Figure 9**). *In vitro*-synthesized CYCB2;2 was almost entirely degraded by a 90-min incubation with mitotic (i.e., 7-DAP) endosperm extracts, whereas it was unaffected by endoreduplicating (i.e., 15-DAP) extracts (**Figure 9A**). Degradation by mitotic extracts at 7-DAP was primarily due to the 26S proteasome, as it could largely be prevented by the addition of the proteasome-specific inhibitor, MG-132 (**Figure 9B**). In addition, we tested whether Thr-417 is required for CYCB2;2 proteolysis. This residue, in fact, is a potential CDK phosphorylation site that is conserved in animal CycE proteins and is necessary for protein degradation via the ubiquitin-dependent pathway (Welker et al., 2003; Hwang and

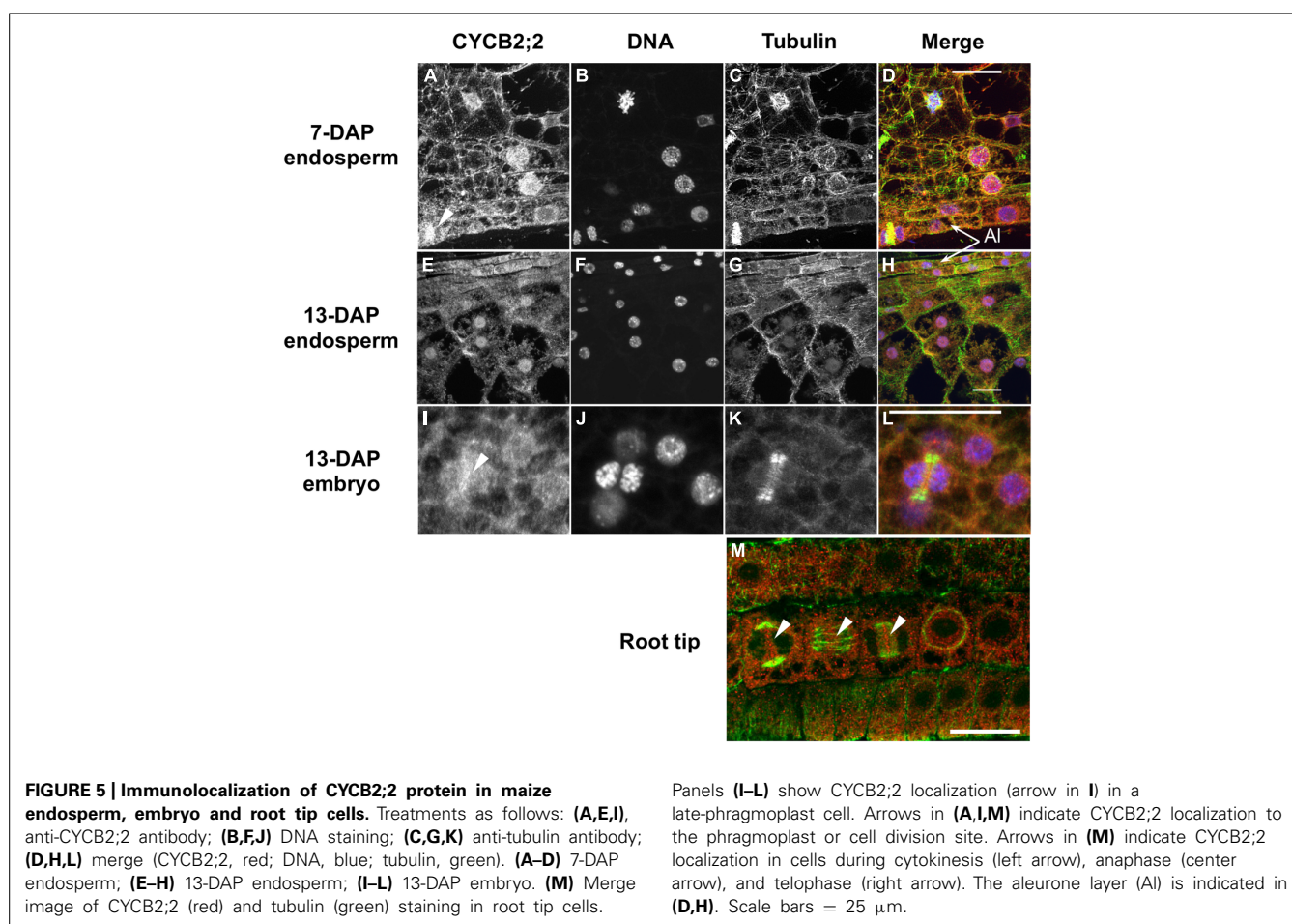


FIGURE 5 | Immunolocalization of CYCB2;2 protein in maize endosperm, embryo and root tip cells. Treatments as follows: (A,E,I), anti-CYCB2;2 antibody; (B,F,J) DNA staining; (C,G,K) anti-tubulin antibody; (D,H,L) merge (CYCB2;2, red; DNA, blue; tubulin, green). (A–D) 7-DAP endosperm; (E–H) 13-DAP endosperm; (I–L) 13-DAP embryo. (M) Merge image of CYCB2;2 (red) and tubulin (green) staining in root tip cells.

Panels (I–L) show CYCB2;2 localization (arrow in I) in a late-phragmoplast cell. Arrows in (A,I,M) indicate CYCB2;2 localization to the phragmoplast or cell division site. Arrows in (M) indicate CYCB2;2 localization in cells during cytokinesis (left arrow), anaphase (center arrow), and telophase (right arrow). The aleurone layer (Al) is indicated in (D,H). Scale bars = 25 μ m.

Clurman, 2005; Hao et al., 2007). Thr-417 was mutagenized to Ala-417 (Figure 9C), which would destroy the putative phosphorylation site in CYCB2;2, but the mutant CYCB2;2T/A protein was degraded by incubation with mitotic extracts just as effectively as the wild-type protein (Figure 9A), suggesting that Thr-417, at least *in vitro*, is not required for CYCB2;2 proteolysis.

DISCUSSION

Cyclin proteins of the A-, B, and D-type are essential components of CDK complexes that drive the plant cell cycle. Specifically, they contribute to the regulation of the rhythmic activation of CDK activity during the cell cycle and help determine substrate specificity. Here we report the characterization of a B2;2-type cyclin from maize during the development of the seed endosperm, which, similarly to other cereals, typically comprises two successive phases characterized by cell proliferation through the mitotic cell cycle and endoreduplication, which is associated with cell expansion and the growth of the whole tissue.

The temporal expression pattern of CYCB2;2 is characterized by relatively high RNA levels during the mitotic phase of endosperm development (i.e., 7–9 DAP) and a dramatic decline during the endoreduplication phase (i.e., 13–21 DAP). By 13-DAP, the CYCB2;2 RNA level is less than 20% that of the 7-DAP level, and remains below this figure throughout the period of

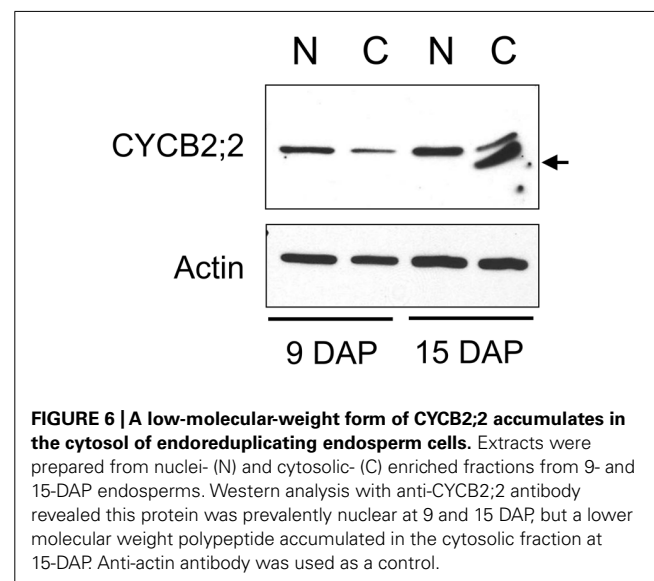


FIGURE 6 | A low-molecular-weight form of CYCB2;2 accumulates in the cytosol of endoreduplicating endosperm cells. Extracts were prepared from nuclei- (N) and cytosolic- (C) enriched fractions from 9- and 15-DAP endosperms. Western analysis with anti-CYCB2;2 antibody revealed this protein was prevalently nuclear at 9 and 15 DAP, but a lower molecular weight polypeptide accumulated in the cytosolic fraction at 15-DAP. Anti-actin antibody was used as a control.

endosperm development studied up to 21-DAP. This pattern is similar to those of CYCA1;1, CYCA1;2, and CYCB1;3 and clearly distinct from those of D-type cyclins, which display less marked differences in RNA levels between mitotic and endoreduplicating

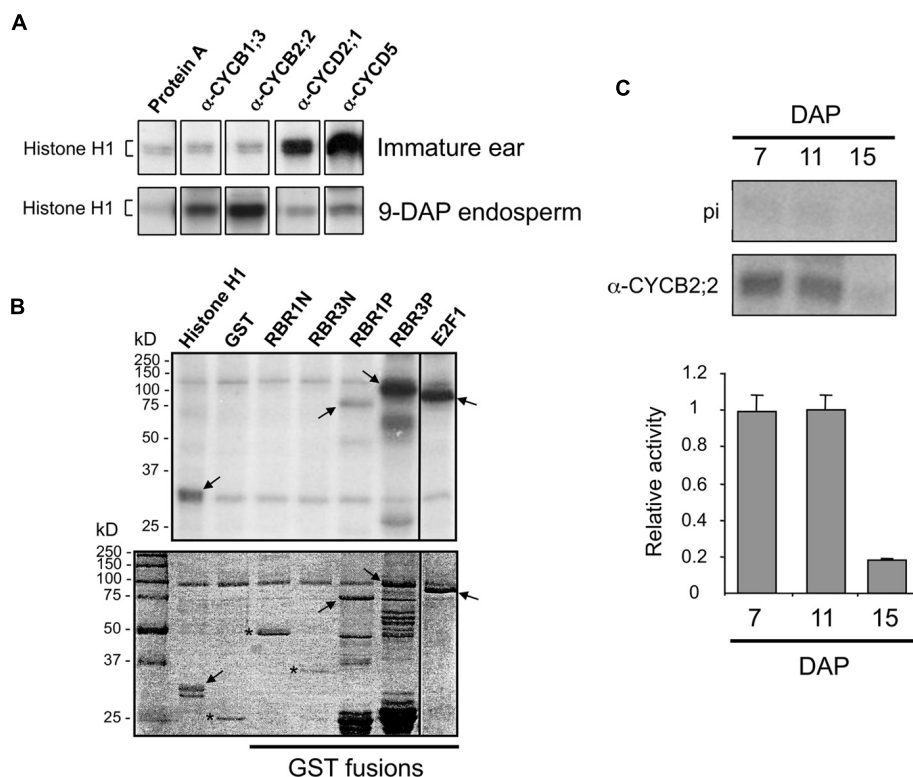
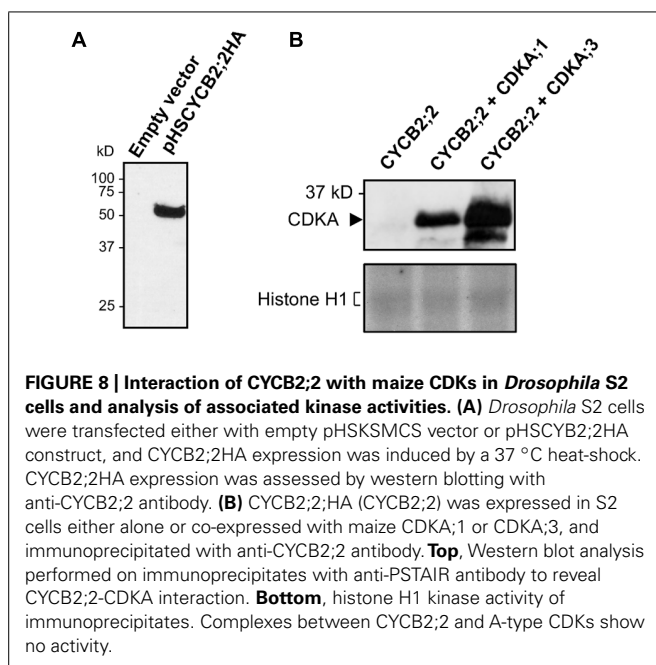


FIGURE 7 | Analysis of CYCB2;2-associated kinase activity.

(A) Phosphorylation of histone H1 substrate by kinase activities immunoprecipitated from immature ear and 9-DAP endosperm with antibodies against CYCB2;2, and various other cyclins as indicated. Protein A indicates a control reaction carried out without antibody showing background signal due to agarose-Protein A beads. **(B)** Phosphorylation of various recombinant substrates by CYCB2;2-associated kinase activity immunoprecipitated from 9-DAP endosperm (top). Substrates include histone H1, GST, as well as GST fusions of the N-terminal domains of RBR1 (RBR1N) and RBR3 (RBR3N), the pocket domains of RBR1 (RBR1P) and RBR3 (RBR3P), and full-length E2F1 (shown in the stained gel, bottom). Arrows indicate specific phosphorylation of substrates. Asterisks indicate substrates that were not phosphorylated (bottom panel). **(C)** Phosphorylation of histone H1 by CYCB2;2-associated kinase immunoprecipitated from 7-, 11-, and 15-DAP endosperm. Top: Autoradiographic detection. Control assays with IgG from pre-immune serum are shown (pi). Bottom: quantitation of kinase activities. Values are averages of two independent experiments, from which background phosphorylation with pre-immune IgG was subtracted. Relative values were normalized by the highest values in each experiment. Error bars represent standard deviations.

endosperm (Dante et al., 2014). This observation suggests that the primary endosperm role of CYCB2;2 may be in the mitotic cell cycle, which is also supported by the high levels of its RNA observed specifically in mitotic tissues in the Sekhon et al. (2011) dataset. However, when the pattern of accumulation of the encoded protein was analyzed using specific antibodies, it was found the protein is present at roughly constant levels in 7- through 21-DAP endosperm. This pattern is reminiscent of that recently described for CYCB1;3 (Dante et al., 2014), and suggests that the activity of these B-type cyclins is sustained in endoreduplicating cells. Interestingly, a CYCB2;2 immunologically related polypeptide of slightly lower molecular weight accumulated specifically in endoreduplicating but not mitotic endosperm cells, suggesting it may have a specific function during endoreduplication. It is not known whether this LMW protein represents an incomplete form of CYCB2;2 due, for example, to alternative RNA splicing (though there is no evidence of such an occurrence in genomics datasets), the specific presence/absence of phosphate groups, or partial proteolysis, although the latter is unlikely since we found no evidence of CYCB2;2 degradation

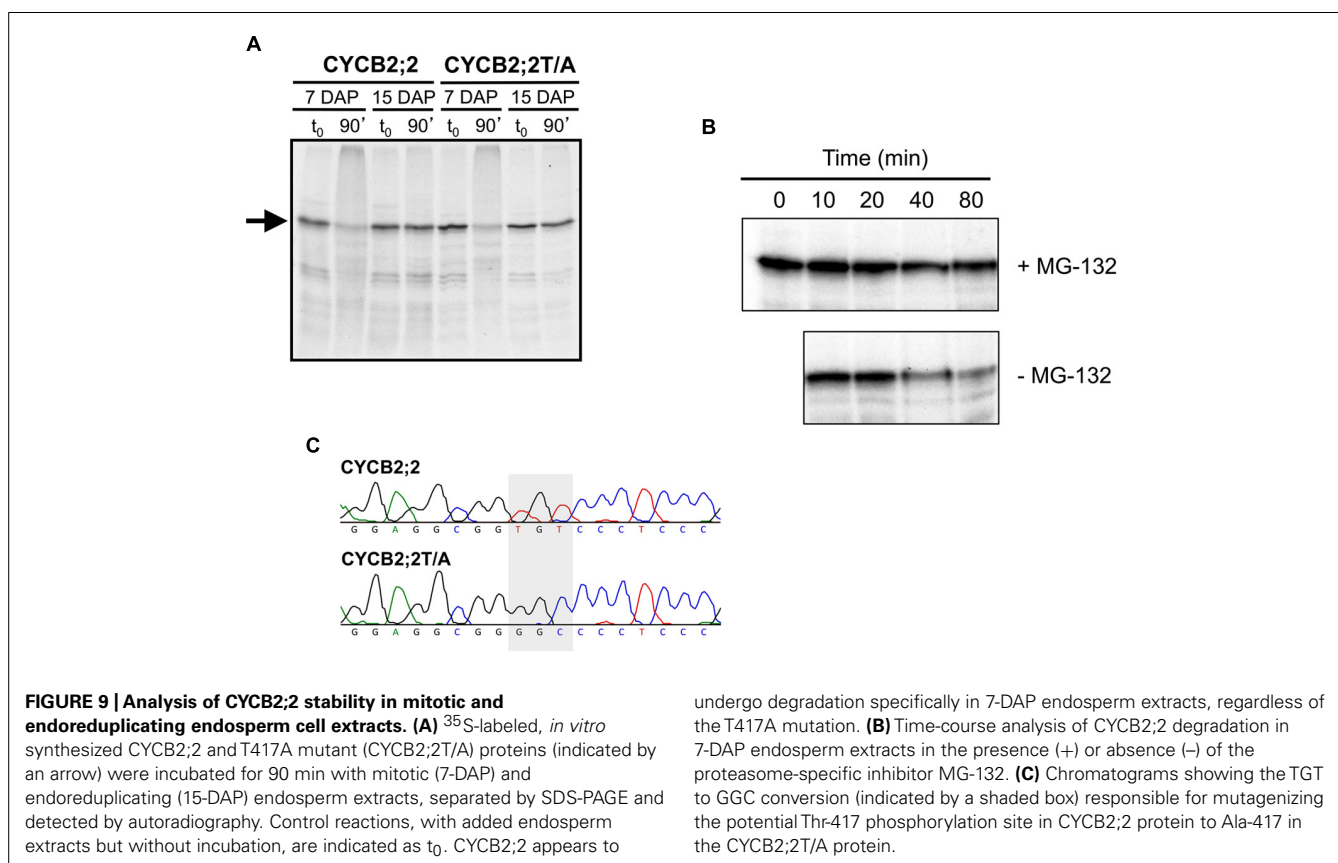
in endoreduplicating endosperm extracts. An alternative possibility is that this LMW polypeptide reflects the accumulation of another immunologically cross-reactive cyclin. The anti-CYCB2;2 antibodies used in this study do not cross-react with CYCB1;3 or CYCA1;1. The two most closely related maize proteins to CYCB2;2 are CYCB2;1 and the CYCB2;3 polypeptide identified in this study. CYCB2;1 has a calculated MW of 50 kDa, which is larger than that of CYCB2;2 and shares only 39% sequence identity with CYCB2;2 over the N-terminal region selected to raise antibodies. The N-terminal region of CYCB2;3, on the other hand, is 78% identical to that of CYCB2;2, which suggests potential antibody cross-reactivity between these two cyclins, but CYCB2;3 is slightly larger than CYCB2;2 (426 amino acid-long with a calculated MW of 47.7 kDa). Thus, the above features of CYCB2;1 and CYCB2;3 make it unlikely for either of them, at least as a full-length protein, to account for the CYCB2;2 LMW polypeptide detected in endoreduplicating extracts. Additionally, data on RNA levels available at the Maize eFP Browser (Sekhon et al., 2011) indicate that CYCB2;1 and the newly identified GRMZM2G061287_T01 (encoding CYCB2;3) transcripts



decrease dramatically in the endosperm after 12-DAP, which does not support the idea they could encode the LMW CYCB2;2 band. Thus, unraveling the identity of this LMW CYCB2;2 polypeptide will require further investigation.

Analysis of sub-cellular fractions revealed CYCB2;2 is primarily a nuclear protein in both mitotic and endoreduplicating endosperm. The LMW polypeptide, however, accumulated specifically in endoreduplicating endosperm extracts, confirming data from whole cell extracts, but was solely detected in the cytosolic fraction. Clearly, whatever the identity of this protein, its accumulation pattern suggests it may play a role in determining whether endosperm cells engage in the mitotic or endoreduplication cycle. However, a possible role for this polypeptide in other cytoplasm-associated aspects of endosperm development linked to endoreduplication, such as cell expansion, storage compound deposition and grain filling, cannot be ruled out.

Based on immunohistochemical analyses, CYCB2;2 appears to be localized primarily to the nucleus of mitotic endosperm cells, whereas by 13-DAP it is also distributed extensively throughout the cytoplasm. These data are in agreement with the results from the subcellular fractionation analysis, and presumably a large proportion of the extra-nuclear signal in cells of endoreduplicating endosperm sections is due to the accumulation of the LMW form of the protein. Considerable overlap between CYCB2;2 localization and the microtubule cytoskeleton was consistently observed, which suggests that this cyclin is involved in regulating aspects of cytoskeleton structure and organization, in agreement with previous observations (Mews et al., 1997; John et al., 2001; Weingartner et al., 2004). In dividing cells, whether in the endosperm, embryo or the root tip, CYCB2;2 appeared to accumulate preferentially at



the intervening domains between daughter chromatin and nuclei, and it was closely associated with the phragmoplast and with the sites of deposition of the cell plate and nascent cell walls. CYCB2;2 is clearly localized to the residual phragmoplast as it is gradually eroded at cytokinesis (**Figures 5I–L**), further suggesting a role in cell wall formation and cell division. These patterns resemble those of KNOLLE (a cytokinesis-specific syntaxin required for cell plate formation) and NACK1 (a kinesin-like protein involved in the vesicular traffic required for phragmoplast outgrowth; Weingartner et al., 2004), although a large number of proteins are also known to be associated with the phragmoplast and/or the cell plate (McMichael and Bednarek, 2013).

These observations suggest a role for CYCB2;2 in cytokinesis and cell wall formation. Previous data on the expression patterns and accumulation of plant B-type cyclins indicate a mitotic role, but they are contrasting with regard to an involvement in cytokinesis. Typically, the expression profiles of B-type cyclins display a peak in early mitosis, due to transcriptional up-regulation at the G2/M-phase transition coupled to proteolysis during anaphase, and their destruction in late M-phase is essential for proper microtubule cytoskeleton re-organization in late mitosis and cell cycle progression. Over- or ectopic expression of at least some B1- and B2-type cyclins stimulate M-phase entry and cell division (Doerner et al., 1996; Schnittger et al., 2002; Lee et al., 2003; Weingartner, 2003). CYCB1;1 from tobacco and CYCB2;2 from rice associate with metaphase chromosomes and are degraded thereafter (Criqui et al., 2000; Lee et al., 2003; Weingartner, 2003). Tobacco CYCB2;2 is also degraded after prophase (Weingartner, 2003). In maize, CYCB1;1 is prevalently nuclear prior to mitosis, whereas CYCB1;2 is associated with the pre-prophase band, condensed chromosomes and the mitotic spindle and is degraded at anaphase, while CYCB2;1 is predominantly nuclear and becomes associated with the spindle and the phragmoplast at telophase (Mews et al., 1997). The persistence of maize CYCB2;2 (and CYCB2;1 – Mews et al., 1997; John et al., 2001) at the phragmoplast and the site of cell plate formation during telophase clearly contrasts with the typical degradation of most B-type cyclins after metaphase (Bulankova et al., 2013). These differences highlight likely functional specialization among different members within the cyclin B family and its subfamilies (John et al., 2001), as recently confirmed by a large study in *Arabidopsis* (Bulankova et al., 2013). Indeed, we found that maize CYCB2;2 possesses a D-Box and undergoes proteasome-dependent degradation in mitotic endosperm extracts, suggesting it may be destroyed, like other related cyclins, late in mitosis. However, our immunolocalization results indicate that the protein remains present during anaphase and telophase, suggesting that the observed proteasome-dependent degradation is part of the normal turnover regimen for this protein and may not be related to M-phase exit. Interestingly, the apparent ability of maize CYCB2;2 to elude degradation by the proteasome in endoreduplicating endosperm is reminiscent of the outcome of expressing a non-degradable form of tobacco CYCB1;1 (with a non-functional D-Box), which resulted in microtubule disorganization, inhibited phragmoplast formation and caused endomitosis and increased DNA content (Weingartner et al., 2004). It is tempting to postulate that partial proteolysis

of CYCB2;2 is responsible for its exclusion from the nucleus in endoreduplicating endosperm cells, which thus would be unable to divide, resulting in an accumulation of the LMW form of the protein in endoreduplicating endosperm. This interpretation is in agreement with the phosphorylation-dependent redistribution of mammalian CycD1 to the cytoplasm (Diehl et al., 1998) and is consistent with the localization of CYCB2;2 to the phragmoplast in mitotic embryo, 7-DAP endosperm, and root tip cells, which is suggestive of a role in cytokinesis. However, redistribution of D1 cyclin to the cytoplasm is coupled with its degradation (Diehl et al., 1998), whereas we did not observe any evidence for proteolysis of CYCB2;2 in endoreduplicating cells. On the contrary, it appears that, like other cyclins, CYCB2;2 is specifically stabilized in endocycling cells (Dante et al., 2014). However, although our analyses of proteolytic activities revealed a clear difference between mitotic and endoreduplicating endosperm in carrying out CYCB2;2 degradation, they are based on a substrate synthesized *in vitro*, which could lack some co- or post-translational modification essential for targeting the protein for proteolysis in a physiological context.

CYCB2;2-associated kinase activity is relatively high in 9-DAP endosperm but only slightly above background levels in immature ear, which is similar to the situation for another maize B-type cyclin, CYCB1;3. In contrast, the kinase activities associated with CYCD2;1 and CYCD5 are high in immature ear and relatively low, though appreciably higher than background, in endosperm. Although both tissues are known to be prevalently mitotic, these differences point to some additional developmental roles specific for D-type cyclins in immature ear and for B-type cyclins in the endosperm. In particular, the kinase activity associated with CYCB2;2 in 9-DAP endosperm can phosphorylate *in vitro* substrates, such as RBR1, RBR3 and E2F1, which are part of the CDK–RBR–E2F pathway controlling the G1/S-phase transition and DNA replication (Sabelli et al., 2013). The presence of a MRAIL motif in the CYCB2;2 sequence is consistent with the observed phosphorylation of RBRs by CYCB2;2/CDK complexes. However, it is not currently known whether these substrates are actual targets of CYCB2;2-associated kinase *in vivo*. Such a kinase activity is sustained at relatively high levels between 7 and 11 DAP, and drops dramatically by 15-DAP, a stage at which starchy endosperm cells are almost exclusively endoreduplicated. The much lower kinase activity at 15-DAP suggests that CYCB2;2/CDK complexes do not significantly participate in the regulation of endoreduplication cycles. In contrast, CYCB1;3-associated activity is very low at 7-DAP, reaches a peak at 11-DAP, and drops only marginally by 15-DAP (Dante et al., 2014). Clearly the kinase activities associated with CYCB1;3 and CYCB2;2 have distinct patterns during endosperm development, suggesting that CYCB1;3, but not CYCB2;2, may also play a role in the endocycle. In insect cells, CYCB2;2 forms complexes, albeit inactive, with CDKA;1 and CDKA;3. CDKA;1 protein has not been found associated with the phragmoplast or the cell plate in maize root tip cells (Colasanti et al., 1993), and thus it is unlikely that it forms active complexes with CYCB2;2 to regulate microtubule dynamics during late mitosis and cytokinesis. Interaction between CYCB2;2 and a B-type CDK (CDKBs

specifically regulate the G2/M-phase transition and suppress the endocycle in mitotic *Arabidopsis* cells – Boudolf et al., 2004, 2009), and formation of active kinase were indeed shown in rice (Lee et al., 2003). It remains to be seen whether these interactions occur in a physiological context in maize (i.e., endosperm cells) and whether they result in phosphorylation of downstream targets. However, it is tempting to speculate that inactivation of CYCB2;2/CDK complexes could contribute to down-regulating M-phase-specific kinase activity, thereby licensing endosperm cells for endoreduplication.

Together, these results suggest that CYCB2;2 may possess some specific function particularly associated with mitotic endosperm. However, it is intriguing that this protein and the closely related LMW polypeptide accumulate during the endoreduplication phase of endosperm development, although they apparently possess little, if any, associated kinase activity at this developmental phase. Evidence for a general decrease in proteasome-dependent proteolysis of cyclins that contributes to their stabilization during endosperm development has recently been obtained (Dante et al., 2014). Furthermore, comprehensive analyses have shown there is generally a weak correlation between RNA and proteins levels in maize seeds, and that proteins can disproportionately accumulate in relation to low RNA levels (Walley et al., 2013). The above paradigms seem to hold true also for CYCB2;2, and whether this protein has any role in post-mitotic endosperm development remains to be established.

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Conflict of Interest Statement: A patent application has been filed on the maize CYCB2;2 nucleotide and protein sequences.

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Interploidy hybridization barrier of endosperm as a dosage interaction

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Crosses between plants at different ploidy levels will often result in failure of endosperm development. The basis of this phenomenon has been attributed to parental gene imprinting of genes involved with endosperm development but a review of the data from maize indicates a dosage interaction between the contributions of the female gametophyte and the primary endosperm nucleus to early endosperm development. However, it is noted that parental imprinting is a non-mutational means that can alter dosage sensitive factors and therefore can contribute to this effect. Operationally, the genes determining ploidy hybridization barrier would qualify for Dobzhansky-Muller incompatibilities that prevent gene flow between species.

Keywords: endosperm, dosage, imprinting, gene balance hypothesis, Dobzhansky-Muller incompatibility, small kernel effect, ploidy hybridization barrier, polyploidy

The endosperm is a nutritive tissue in angiosperms that results from the fusion of one of the two sperm involved in double fertilization with the central cell of the megagametophyte (Birchler, 1993). In many species it is consumed before seed maturation but is persistent in the grains and hence its value for human nutrition. It has long been recognized that interploidy crosses would result in failure of endosperm development and hence seed abortion (Figure 1A). The basis of this phenomenon has been a matter of debate but operationally it serves as a hybridization barrier between any polyploid and its diploid progenitor(s), at least in many plants.

One idea to explain the evolution of interploidy hybridization barrier involves parental conflict with regard to resource allocation to the progeny (Haig and Westoby, 1989). The concept is that select genes involved with resource development will be imprinted from one parent or the other in such a manner that a maternal parent will optimize resources to all progeny but any one paternal parent, when there are different ones, will optimize the resources for his own progeny over other potential fathers.

The phenomenon of imprinting of individual genes was discovered by Kermicle in his analysis of the maize anthocyanin gene, *r1* (Kermicle, 1970). It exhibits full color when transmitted through the female but a mottled expression across cells when transmitted through the male parent regardless of dose. Imprinting has also been attributed to endosperm size factors that are found when chromosomal segments are missing from the sperm (Lin, 1982); however, we revisit this interpretation below.

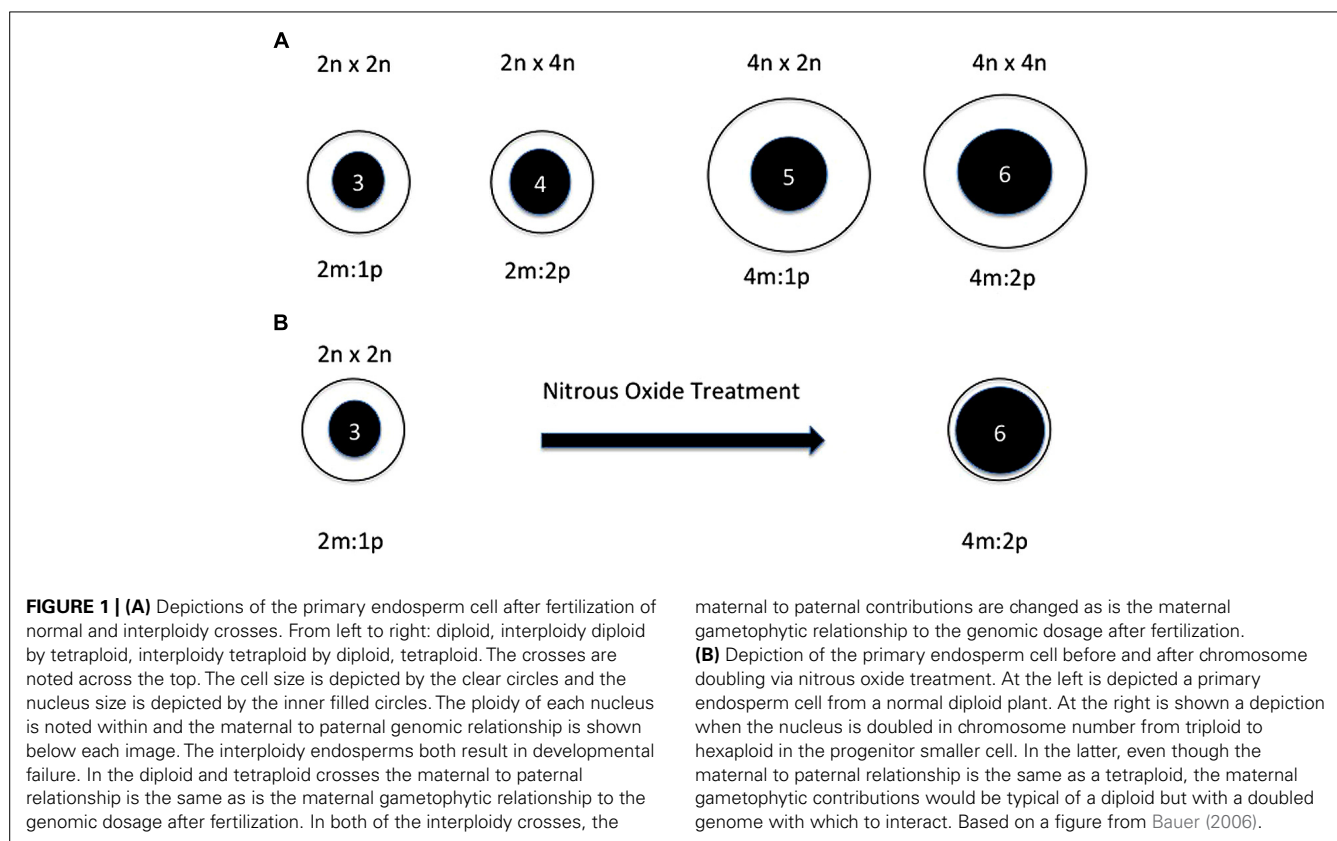
Endosperm size factors refer to the situation that occurs with some translocations between the supernumerary B chromosome and normal A chromosomal segments in maize (Birchler and Hart, 1987). The B chromosome is basically inert and is neither required nor detrimental to plants possessing them unless their numbers exceed about 15 copies. It is maintained in populations by an accumulation mechanism that consists of

nondisjunction at the second pollen mitosis, which makes the two sperm, and then preferential fertilization of the egg by the sperm that has the two B chromosomes. Thus, translocations between the B chromosome and the A chromosomes will have nondisjunction of the chromosomal segment attached to the B centromere. When some B-A translocations are used as a male parent, the progeny missing a paternal contribution to the endosperm are smaller than normal siblings (Roman, 1947; Lin, 1982; Birchler and Hart, 1987).

Several regions of the genome will produce this effect to a greater or lesser degree including 1S, 1L, 4S, 5S, 7L, and 10L being the most prominent in most backgrounds (Birchler and Hart, 1987). At least for the effect of 1L and 10L, there is evidence that the effect is cumulative from several regions that contribute to the whole arm impact (Lin, 1982; Birchler and Hart, 1987).

The argument that this small kernel effect is a reflection of imprinting was that for 10L, introduction of extra copies through the female parent was not observed to have any effect nor could it rescue the absence of the paternal copy (Lin, 1982). While this is the case for 10L in some backgrounds, extra copies of other chromosome arms introduced through the female parent does not rescue but enhances the paternal small kernel effect (Birchler and Hart, 1987). Indeed, the specific region of 10L that itself is responsible for a small kernel effect will enhance the analogous effect of 1S when transmitted in extra dosage through the female parent. This observation suggests that these genes function when passed through the female (including in the zygote) or at least in the female gametophyte.

Moreover, by crossing B-A translocations among themselves, it was realized that the same arms that produce the paternal effect would enhance that response of other arms when present in extra copy through the female parent (Birchler and Hart, 1987). Indeed, in the author's materials, self pollination of the 10L translocations produce an additional class of further reduced



sized kernels compared with crossing the translocation to normal females—just as occurs with all other regions of the genome that produce the small kernel effect. This result suggests that the responsible loci are in fact expressed when transmitted through the female parent and that they are involved in the same developmental process. The reason why this experience differs from Lin's results is unknown but would seem to reflect background effects. Furthermore, the enhancement results indicate that these factors operate in a dosage sensitive manner and also that the stoichiometry of one region relative to others would magnify the effect. It was postulated that the developmental program established in the female gametophyte has a quantitative component that interacts with the dosage of the primary endosperm nucleus following fertilization (Birchler and Hart, 1987; Figure 1A).

Indeed, if one postulates that the small kernel effects are due to the absence of a gene that is normally expressed from only the paternal allele, then no such hypothetical gene could be vital because no known region of the maize genome is lethal to the endosperm when missing in the sperm. The maternal enhancement seems unlikely to result from imprinting because it does not involve an all or none contribution from the female parent but rather the number of copies transmitted. Moreover, there is no apparent impact on endosperm growth unless the same or other regions of the genome are paternally absent. Also, it is important to note that there are many mutations that when homozygous recessive are highly defective to the endosperm but no paternal absence in the genome has any such effect suggesting that none of

these genes are expressed exclusively from the paternally derived allele. These considerations point to a quantitative explanation for the small kernel effects.

Many years later, studies of tetraploid formation suggested a related explanation of the interploidy disruption of endosperm development. Kato and Birchler (2006) produced tetraploid derivatives of several inbred lines of maize by treating self-pollinated diploid plants with nitrous oxide gas, which causes chromosome doubling, at about the time of the first mitotic divisions after fertilizations. Interestingly, the kernels on the ears of such treated plants have many defective endosperms. If the endosperms were doubled in ploidy, there would be no change in maternal/paternal genomic relationship but rather a change of the quantitative relationship of the maternal gametophytic gene products to the copy number of genomes in the now doubled primary endosperm nucleus (Figure 1B).

Bauer (2006) examined this phenomenon in more detail. Treatment of pollinated diploid plants near the timing of the first endosperm mitosis produced numerous defective endosperms. Cytological analysis indicated doubling of chromosome numbers to 60 chromosomes in the defective kernel class although some defective kernels were doubled twice or three times to yield ~120 or ~240 chromosomes, respectively. A time course of nitrous oxide treatment revealed very little effect at 12–17 hours after pollination (HAP), which immediately precedes the first division in the endosperm. The percentage of defective endosperms with elevated ploidy increased progressively with treatments at 14–19

HAP, 16–21 HAP and 20–15 HAP and then sharply decreased with treatment at 24–29 HAP. The latter result is not due to a failure of the action of nitrous oxide because at this timepoint, there is a sharp increase in the number of normal-sized hexaploid endosperms at the expense of normal-sized triploid endosperms. The results are consistent with the interpretation that genome doubling to produce defective endosperms has an early developmental window.

It should be noted that interploidy crosses have multiple variables that complicate their interpretation. They vary the maternal to paternal genomic ratios within the endosperm itself but they also vary the contribution of female gametophyte contributions to the number of genomic targets after fertilization. The chromosome doubling experiment separates these variables. The maternal to paternal ratio within the endosperm is maintained but the relationship of the maternal gametophytic contributions to the genomic targets is altered suggesting this possibility as the basis of the endosperm failure.

The timing of this relationship can be further deduced based on the behavior of B-A translocations after fertilization (Birchler, 1980). At a low frequency, B-A chromosomes are lost during development of the endosperm. If they carry an anthocyanin pigment marker, such loss can be readily recognized as a mosaic kernel. For the regions of the genome that produce the small kernel effect when there is no paternal contribution to the endosperm at all, there is no detectable effect in these mosaic kernels even for those with loss at early divisions (Birchler, 1980). These observations indicate that the maternal/primary endosperm relationship is critical at the initiation of endosperm development but not shortly thereafter. This nonautonomy could potentially be a reflection of the syncytial nature of early endosperm development but this consideration does not rule out the noted critical relationship. It should be noted that the syncytial nature of early endosperm development does not obscure the mosaic pattern of the anthocyanin marker or other mosaicism that results from transposable element action or chemical or irradiation mutagenesis of pollen.

Given that the interploidy endosperm failure can be mimicked by changing the maternal/zygotic dosage without changing the maternal/paternal relationship and the small kernel effect of paternal absence of regions of the genome is enhanced by maternal increase might suggest that segmental or genomic relative dosage might be responsible. These effects might not necessarily be the result of parental imprinting. However, some factors involved with early endosperm development, which have been identified in *Arabidopsis*, are in fact expressed only from alleles originating from one parent but not the other (Dilkes and Comai, 2004; Kradošfer et al., 2013). But imprinting results in a type of dosage effect and so an entanglement of interpretations is potentially possible. Dilkes and Comai (2004) have discussed development of the endosperm and how differential resource allocation among different paternal parents seems unlikely. It is potentially the case then that imprinting is a non-mutational process of manipulating the dosage of genes (Beaudet and Jiang, 2002) involved with endosperm development (Kradošfer et al., 2013). Those that exhibit imprinting that are involved with endosperm development are likely a subset of the whole group of genes

that affect this process. Clearly, genes can be imprinted in the endosperm that have no impact on kernel size (e.g., the *r1* locus), which fact might also be taken to suggest that imprinting and resource allocation are not necessarily connected. Indeed, endosperm size is basically determined maternally; there is no perceptible difference in size when pollen parents from lines with very different endosperm sizes are used onto a common female line. Thus, there is no evidence in maize to suggest that the paternal parent has any influence on endosperm resource allocation.

What then is the driving evolutionary force for ploidy hybridization barrier in the endosperm? There may be none: it might simply be a neutral reflection of developmental and gene regulatory processes that have dosage components. However, operationally, it might serve to prevent the widespread occurrence of triploids in populations if allotetraploids and the diploid progenitors were to hybridize. While such hybridization in itself would not be productive, the widespread occurrence of any resulting triploids that would hybridize with both tetraploids and diploids to produce many aneuploid progeny would likely disrupt the population fitness to a much greater degree. Individuals with an inability to produce triploids would have a higher reproductive fitness. Mechanisms that prevent triploid production would potentially be selected and were apparently established early in angiosperm evolution but, as noted, this might be a neutral reflection of developmental mechanism.

There is considerable evidence from many experimental avenues that genomic balance when upset can have detrimental effects on the phenotype (Birchler and Veitia, 2010, 2012). As described above, the small kernel effect and the endosperm doubling results are consistent with this type of stoichiometric relationship. Thus, the endosperm interploidy hybridization barrier is likely an extension of the genomic balance phenomena. Indeed, all other tissues show impacts of aneuploidy so it would be unusual if the endosperm did not: the small kernel effects are the likely manifestation.

It is known from work primarily in potato that the genes for interploidy barrier are multigenic and can be overcome with manipulation of genome dosage (Johnston et al., 1980; Johnston and Hanneman, 1982). With divergence of the quantitative expression of these genes, a hybridization barrier occurs without a change in ploidy. These cases might qualify as classical Muller-Dobzhansky species incompatibility genes (Dobzhansky, 1937; Muller, 1942) that are compatible within species but not between species (Kradošfer et al., 2013). Consequently, while the responsible genes might diverge in a neutral fashion, they serve de facto as an isolating mechanism between polyploids and related diploids.

Based on the evidence described above, we argue that the ploidy hybridization barrier and the small kernel effect from segmental paternal absence represent a type of dosage interaction between the maternal contributions from the female gametophyte and the genome or segmental dosage in the primary endosperm nucleus. Because this interaction has a stoichiometric character to its behavior, it is likely related to the basis of standard aneuploidy syndromes (Birchler and Veitia, 2012).

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Imprinting in plants as a mechanism to generate seed phenotypic diversity

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Normal plant development requires epigenetic regulation to enforce changes in developmental fate. Genomic imprinting is a type of epigenetic regulation in which identical alleles of genes are expressed in a parent-of-origin dependent manner. Deep sequencing of transcriptomes has identified hundreds of imprinted genes with scarce evidence for the developmental importance of individual imprinted loci. Imprinting is regulated through global DNA demethylation in the central cell prior to fertilization and directed repression of individual loci with the Polycomb Repressive Complex 2 (PRC2). There is significant evidence for transposable elements and repeat sequences near genes acting as cis-elements to determine imprinting status of a gene, implying that imprinted gene expression patterns may evolve randomly and at high frequency. Detailed genetic analysis of a few imprinted loci suggests an imprinted pattern of gene expression is often dispensable for seed development. Few genes show conserved imprinted expression within or between plant species. These data are not fully explained by current models for the evolution of imprinting in plant seeds. We suggest that imprinting may have evolved to provide a mechanism for rapid neofunctionalization of genes during seed development to increase phenotypic diversity of seeds.

Keywords: epigenetics, DNA methylation, histone modification, imprinting, genomics, seed development, maize endosperm, *Arabidopsis* endosperm

OVERVIEW OF ANGIOSPERM SEED DEVELOPMENT

In this review, we focus on the developmental role of epigenetic regulation, specifically genomic imprinting, in maize and *Arabidopsis* seeds. Imprinting, or parent-of-origin specific gene expression, has evolved convergently in mammals and angiosperms (Pires and Grossniklaus, 2014). Imprinted gene expression in angiosperms is found in developing seeds. Angiosperm seeds initiate with double fertilization of the megagametophyte (Peris et al., 2010). The pollen tube delivers two haploid sperm cells to the embryo sac. One sperm cell fuses with the haploid egg to generate a diploid embryo, and the other sperm cell fuses with the diploid central cell to form the triploid endosperm. The resulting embryo and endosperm are genetically identical except for their ploidy level with the endosperm having two maternal doses of the genome and one paternal dose. Although the endosperm and embryo have essentially the same genotype, they have markedly different developmental programs (Figure 1; Kiesselbach, 1949; Brown et al., 1999; Chandler et al., 2008; Peris et al., 2010).

The endosperm starts development by dividing nuclei without completing cytokinesis (reviewed in Olsen, 2004; Sabelli and Larkins, 2009b). This syncytial development transitions to cellularization in which the nuclei become enclosed in cell walls (Figure 1). As the endosperm cellularizes, the cells begin to take on differentiated fates with internal endosperm cells accumulating nutrient storage reserves (Kiesselbach, 1949; Brown et al., 1994, 1996, 1999; Stangeland et al., 2003). In many eudicots, like *Arabidopsis*, the embryo consumes the endosperm reserves

as it develops resulting in most of the endosperm degenerating by seed maturity. By contrast, the internal storage cells in the maize endosperm persist through seed development and the storage reserves are used during seedling growth (Kiesselbach, 1949). Epidermal endosperm cells take on different fates from the internal storage cell types. In *Arabidopsis*, there are distinct endosperm cell morphologies at the micropylar and chalazal ends of the embryo sac (Brown et al., 1999). In maize, epidermal endosperm cells differentiate into basal transfer cells, embryo surrounding region, and aleurone (Kiesselbach, 1949). All maize endosperm cells, except the aleurone, undergo programmed cell death prior to seed maturation (Figure 1; Young et al., 1997; Young and Gallie, 2000).

Embryo development starts with asymmetric cell division of the zygote to form an apical-basal axis (Chandler et al., 2008; Peris et al., 2010). Basal cells divide to develop the suspensor and contribute to the root meristem. Apical cells initially develop a globular embryo, which transitions to form the shoot and root apical meristems along with cotyledons in *Arabidopsis* or a scutellum, coleoptile, and embryonic leaves in maize (i.e., transition stage). The genetic programs controlling meristem specification and lateral organ initiation have been extensively reviewed (Chandler et al., 2008; De Smet et al., 2010; Wendrich and Weijers, 2013).

Imprinted genes primarily show parent-of-origin expression patterns in the endosperm although there are imprinted genes also in the developing embryo (Jahnke and Scholten, 2009; Raissig et al., 2013). Endosperm growth has a significant impact

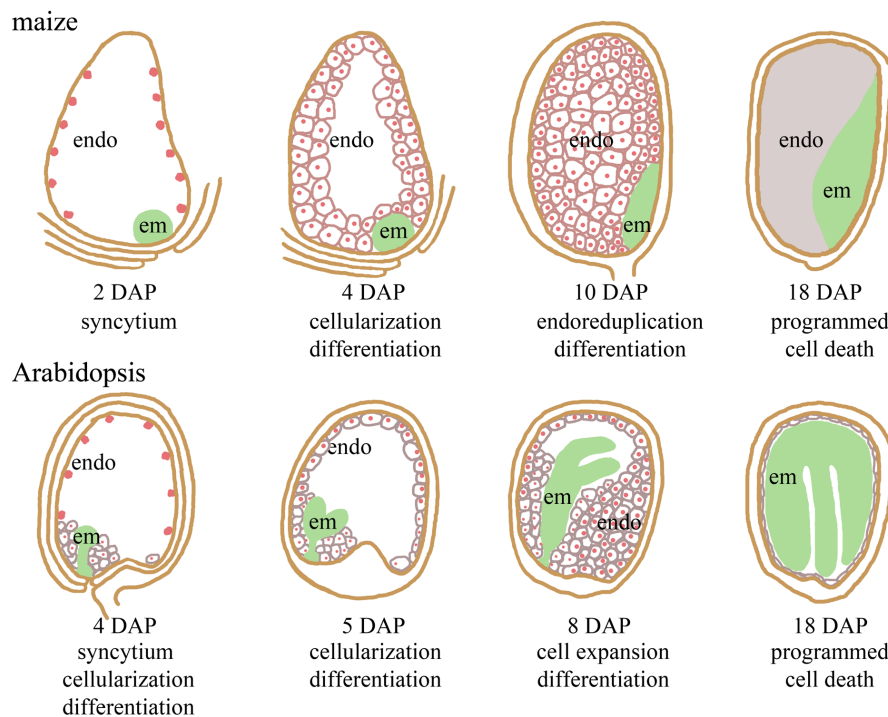


FIGURE 1 | Comparison of seed development in maize and *Arabidopsis thaliana*. The endosperm proliferates initially as a multi-nucleate syncytium, while the globular embryo develops. Endosperm cellularization precedes embryo transition. Endosperm cells expand and accumulate storage molecules once cellularization

is complete. In maize, the endosperm is persistent and undergoes programmed cell death starting around 18 days after pollination (DAP). The *Arabidopsis* embryo consumes most of the endosperm prior to seed maturation. Endosperm (endo) nuclei are indicated in red. The embryo (em) is in green.

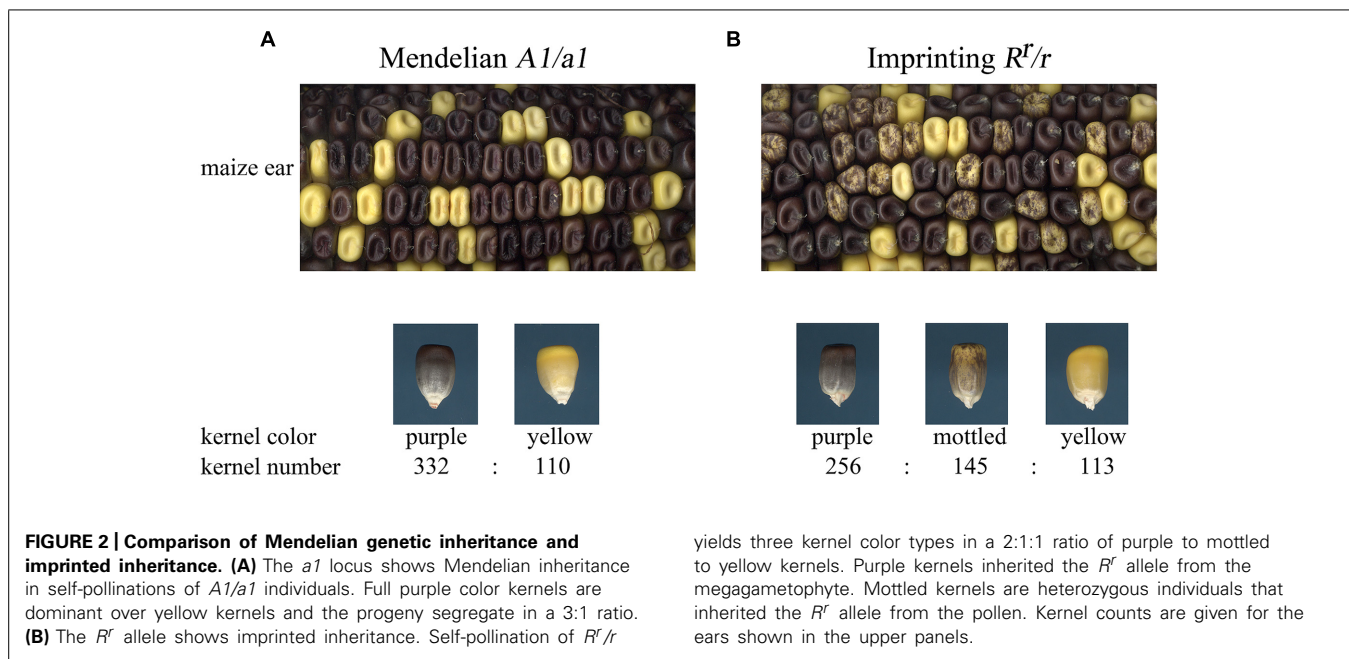
on final seed size, and imprinting has been hypothesized to regulate seed size (Arnaud and Feil, 2006; Xiao et al., 2006; Li and Berger, 2012; Fatihi et al., 2013). However, there is significant data arguing that the endosperm has developmental functions beyond providing nutrition for the developing embryo. Embryo transition occurs soon after endosperm cell differentiation, and recent evidence indicates differentiated endosperm is important for embryo developmental programs. For example, the embryo surrounding endosperm in *Arabidopsis* secretes the ESF1 signaling peptide to promote normal basal embryo development (Costa et al., 2014). Failure to differentiate the embryo surrounding endosperm in maize causes an embryo developmental block at the transition stage suggesting a similar function for this cell type in maize (Fouquet et al., 2011). Later in *Arabidopsis* seed development, the ZHOUP1 basic-helix-loop-helix transcription factor is expressed exclusively in the embryo surrounding region and activates a signaling pathway required for normal epidermal differentiation in the embryo (Yang et al., 2008; Xing et al., 2013). These data show that the endosperm plays an active role in promoting embryo development and argue that epigenetic regulation of endosperm gene expression could have consequences for seed size as well as embryo developmental programs.

WHAT IS IMPRINTING?

Genomic imprinting in plants is an epigenetic phenomenon by which genetically identical alleles are differentially expressed in

a parent-of-origin dependent manner. Imprinted gene expression primarily occurs in the endosperm and there is strong data for imprinted genes controlling early endosperm cell divisions as well as regulating the transfer of nutrients to the seed (Gutierrez-Marcos et al., 2004; Day et al., 2008; Sabelli and Larkins, 2009a; Tiwari et al., 2010; Shirzadi et al., 2011; Costa et al., 2012). Imprinting is an exception from Mendel's Laws on the expression and inheritance of the two parental alleles in which dominant alleles express phenotypes over recessive alleles irrespective of the parental source of the allele. Instead, imprinted genes will express either the maternal or paternal allele even though the primary sequences of these alleles may be identical.

It is easiest to understand imprinted inheritance through an example. The *A1* locus of maize encodes a structural gene for anthocyanin biosynthesis (O'Reilly et al., 1985), while the *R* locus encodes a transcription factor that induces anthocyanin biosynthesis (Ludwig et al., 1989; Perrot and Cone, 1989). The *A1* locus shows Mendelian inheritance, while certain haplotypes of the *R* locus are imprinted (Kermicle, 1969). Indeed, *R* was the first imprinted locus described in plants. The *R'* allele shows altered expression when *R'* is inherited from pollen. The expression pattern of paternally inherited *R'* can be seen by contrasting self-pollinations of heterozygous individuals for *A1/a1* or *R'/r* (Figure 2). When a plant heterozygous for *A1/a1* is self-pollinated, the seeds segregate in a 3:1 ratio for full color to yellow kernels (Figure 2). Self-pollination of *R'/r* yields three kernel color types



in a 2:1:1 ratio of purple to yellow to mottled purple kernels. These mottled purple kernels have an endosperm genotype of $r\ r/R^r$ where the dominant allele inherited from the male is repressed in a stochastic pattern in the seed. The same paternal R^r allele is not affected in the embryo and plants from mottled kernels will yield full color kernels if crossed as female to an r/r plant and mottled kernels if crossed as a male to the r/r genotype.

One interpretation of the mottled $r\ r/R^r$ kernel phenotype is that it is due to an insufficient dosage as a consequence of the endosperm fusing a diploid maternal central cell with a haploid paternal sperm cell. However, introducing multiple copies of R^r with translocation and trisomic stocks does not alter the anthocyanin phenotypes. When more than two doses are inherited maternally, the kernel is always full color, and when multiple R^r alleles are inherited paternally, the mottled phenotype always results (Kermicle, 1970). These and more recent data indicate that imprinting is an independent phenomenon from dosage effects.

The r locus is an example of maternal bias of gene expression. Imprinted genes can show bias for either the maternal or paternal allele and consequently are classified into maternally expressed genes (MEGs) and paternally expressed genes (PEGs). MEGs and PEGs can be identified molecularly by examining allele-specific expression in reciprocal crosses. Single nucleotide polymorphisms and small insertion-deletions within transcripts from diverse parents are used to identify the expression level of both the maternal and paternal allele. By carrying out the same gene expression analysis on reciprocal crosses, it is possible to identify genes that express only the maternal or only the paternal allele irrespective of the polymorphisms found within the alleles of the genes. A variety of molecular strategies have been employed to identify individual imprinted genes such as *Maternally expressed gene1* (*Meg1*) and *Maternally expressed in embryo1* (*Mee1*) in maize (Gutierrez-Marcos et al., 2004; Jahnke and Scholten, 2009).

RNA-seq transcriptomics allows global analysis of imprinted gene expression at a much larger scale. Maize is particularly well suited for allele identification in RNA-seq experiments, because maize inbred lines show high levels of polymorphism allowing for a large number of genes to be assayed for imprinting in a single experiment (Chia et al., 2012; Jiao et al., 2012). Initial experiments in maize examined reciprocal crosses between the reference genome inbred line, B73, and Mo17 (Waters et al., 2011; Zhang et al., 2011). These studies identified hundreds of MEGs and PEGs with relatively little overlap between them. By examining additional time-points during seed development and additional inbred crosses more than 500 genes show statistically significant bias for gene expression based on the parent of origin (Waters et al., 2013; Zhang et al., 2014). Many imprinted genes only show parent-of-origin bias transiently. For example, *Meg1* is maternally expressed early during seed development and is biallelic, expressed from both maternal and paternal alleles, by mid-seed development (Gutierrez-Marcos et al., 2004). Attempts to apply transcriptomics to early stages of developing maize seeds did not effectively isolate endosperm or embryo tissue from maternal tissue, so most identified maize MEGs and PEGs show imprinted expression patterns after embryo transition (Xin et al., 2013). The overlap of imprinted genes between all data sets is low. For example, Waters et al. (2013) found that only 5–10% of the imprinted genes in a survey of four inbred lines showed imprinting in all genotype combinations. These results have raised questions about whether sequencing depth, statistical approaches, allele-specific effects, or environmental factors have significant impact on the genes detected as imprinted.

Similar transcriptomic approaches have been applied to identify imprinted genes in *Arabidopsis*. Endosperm and embryo transcripts from reciprocal crosses between *Col-0* and *Ler* accessions identified over 200 imprinted genes (Gehring et al., 2011; Hsieh et al., 2011). Expanding these studies to additional accessions

found that, like in maize, only a small number of genes consistently show imprinting in all accessions (Wolff et al., 2011; Pignatta et al., 2014). For example, Pignatta et al. (2014) found about 10% of MEGs and 5% of PEGs are shared between the three accessions they surveyed. It seems surprising that both maize and *Arabidopsis* transcriptome surveys have found only a few conserved imprinted genes within each species. Considering both the maize and *Arabidopsis* observations, the data suggest that relatively few loci are stably selected for imprinted gene expression.

Transcriptomic studies have also identified allele-specific imprinting in both maize and *Arabidopsis* (Waters et al., 2013; Pignatta et al., 2014). Allele-specific imprinted genes have MEG or PEG expression for a single allele from a single accession or inbred line, much like the *R^r* allele of maize. Using kernel phenotypes, allele-specific imprinting has been observed in other maize loci including the *dzr1^{Mol17}* and *B-Boliva* alleles that control zein and anthocyanin accumulation, respectively (Chaudhuri and Messing, 1994; Selinger and Chandler, 2001). These older examples indicate that allele-specific imprinting can have significant effects on kernel phenotypes. However, phenotypes have not been associated with the more recently discovered allele-specific imprints.

With hundreds of imprinted genes identified, annotation of these genes suggests that imprinted loci do function in processes proximate to developmental programs. Imprinted genes include proteins involved in chromatin modification, transcription factors, hormone signaling, ubiquitin-targeted protein degradation, and RNA processing (Gehring et al., 2011; Hsieh et al., 2011; Wolff et al., 2011; Zhang et al., 2011; Xin et al., 2013; Pignatta et al., 2014). MEGs show some enrichment for transcription factors, such as MYB family genes (Hsieh et al., 2011; Pignatta et al., 2014), while PEGs show enrichment for chromatin and transcriptional modifiers (Waters et al., 2013; Pignatta et al., 2014). However, only two genes show conserved imprinted expression between *Arabidopsis*, rice, and maize (Waters et al., 2013). A loss of function allele of one of these PEGs, *ZmYuc1*, is tightly linked to the recessive *defective endosperm18* locus of maize, suggesting that residual maternal expression is sufficient to confer normal seed development (Bernardi et al., 2012). Both allele-specific imprinting and the low conservation of imprinted gene expression across angiosperms suggest that deeply conserved developmental circuits have not been selected for this type of epigenetic regulation in angiosperms. Based on these and additional arguments below, we suggest that imprinting is primarily a form of regulation to enable rapid diversifying selection of seed phenotypes.

MOLECULAR MECHANISMS OF IMPRINTING

Altering the expression state of an allele depending upon the parent-of-origin requires epigenetic modification of the alleles inherited by the male and female gametes. The mechanisms by which MEGs and PEGs are identified and programmed have been extensively reviewed (Köhler et al., 2012; Gehring, 2013; Zhang et al., 2013). As a brief overview, both histone modification and DNA methylation have essential roles in setting imprinted patterns of gene expression. The *Arabidopsis* model for establishing contrasting epigenetic states in the male and female gametes starts

with differential demethylation of the genome. The DNA glycosylase gene, *DEMETER* (*DME*), is expressed in the central cell of the megagametophyte but not the sperm cells of the pollen (Choi et al., 2002; Schoft et al., 2011). *DME* activity removes 5-methylcytosine predominantly from transposable element and repeat sequences leading to most repetitive sequences having reduced methylation in the developing endosperm (Gehring et al., 2009; Hsieh et al., 2009). Surprisingly, maize does not show these global patterns of DNA hypomethylation in the endosperm (Zhang et al., 2011, 2014). Instead, allele-specific bisulfite sequencing of endosperm DNA revealed a pattern of DNA hypomethylation at maternal alleles with corresponding hypermethylation at paternal alleles for specific sites within the genome (Zhang et al., 2014). These maize results are consistent with DNA demethylation specifically occurring in the central cell.

The differential loss of DNA methylation sets-up contrasting chromatin marks in *Arabidopsis* repeat sequences near the paternal and maternal alleles. Methylation marks can then be interpreted by the genome with a variety of molecular mechanisms. For example, methylation of the paternal allele can lead to a transcriptionally silent state, while the demethylated maternal allele would become transcriptionally active (Kinoshita et al., 2004; Jullien et al., 2006a; Hermon et al., 2007; Tiwari et al., 2008). There are also a few examples where RNA-directed DNA methylation (RdDM) is critical in the male parent to ensure silencing of the paternal allele at MEG loci, suggesting that small RNAs can have a significant role in setting MEG expression patterns (Bratzel et al., 2012; Vu et al., 2013). Although these models can explain MEG patterns of expression, PEGs can also be hypermethylated at the paternal allele and hypomethylated at the maternal allele (Gehring et al., 2009; Hsieh et al., 2009; Zhang et al., 2014). This maternal hypomethylation is essential for silencing of the maternal allele for many PEGs (Hsieh et al., 2011; Wolff et al., 2011).

How can the same epigenetic mark of reduced DNA methylation in the maternal allele result in opposite MEG and PEG expression patterns? Trimethylation of lysine 27 on histone H3 (H3K27me3) is another chromatin mark that is required for imprinted gene expression (Schuettengruber and Cavalli, 2009; Köhler et al., 2012). H3K27me3 marks are catalyzed by the Polycomb Repressive Complex2 (PRC2). In the *Arabidopsis* endosperm, the PRC2 complex is referred to as the FERTILIZATION INDEPENDENT SEED (FIS) complex and is composed of four core subunits: the MEDEA (MEA) Enhancer of zeste homolog, the FERTILIZATION INDEPENDENT SEED2 (FIS2) Suppressor of zeste homolog, the FERTILIZATION INDEPENDENT ENDOSPERM (FIE) Extra sex combs homolog, and the MULTICOPY SUPPRESSOR OF IRA1 (MSI1), which is a WD-40 repeat protein that is homologous to Drosophila p55 (Grossniklaus et al., 1998; Kiyosue et al., 1999; Luo et al., 1999; Köhler et al., 2003). The H3K27me3 post-translational modification is a repressive chromatin mark, and FIS-PRC2 is known to be required to repress paternal alleles of MEGs as well as maternal alleles of PEGs (Köhler et al., 2003, 2005; Baroux et al., 2006; Makarevich et al., 2006; Fitz Gerald et al., 2009; Weinhofer et al., 2010).

It is not inherently obvious how PRC2 would differentially target hypo- or hypermethylated DNA. PRC2 is recruited to cis-elements at repressed loci. These PRC2 recruitment elements have

been identified in multiple organisms and can include repeat sequences (Kinoshita et al., 2007; Makarevich et al., 2008), small segments of CG-rich sequence (Jermann et al., 2014), or transcription factor binding sites (Berger et al., 2011; Liu et al., 2011; Lodha et al., 2013). In addition, non-coding RNA has been shown to interact with PRC2 and target it to specific loci in plants (Heo and Sung, 2011). DNA methylation interferes with PRC2 function and prevents H3K27me3 modification (Weinhofer et al., 2010; Deleris et al., 2012; Jermann et al., 2014). Thus, hypermethylation of paternal alleles can interfere with PRC2 recruitment sites allowing expression of the paternal allele, while PRC2 activity at the maternal, hypomethylated allele would result in transcriptional silencing to give a PEG pattern of expression. Global analysis of H3K27me3 sites in maize supports this model (Makarevich et al., 2013). Indeed, Zhang et al. (2014) found that PEGs showed enrichment for maternal H3K27me3 marks concomitant with hypomethylation at the maternal allele and hypermethylation at the paternal allele.

PRC2 is also required to repress the paternal allele of some MEGs (Baroux et al., 2006; Gehring et al., 2006; Jullien et al., 2006b). However, there is no molecular mechanism proposed for how PRC2 would preferentially target the hypermethylated, paternal allele at a MEG locus. Maternal specific expression is also observed for the *Arabidopsis* ZIX locus, but the MEG pattern of expression does not depend upon DME or FIS-PRC2 (Ngo et al., 2012). Moreover, imprinted gene expression is documented within the embryo of both maize and *Arabidopsis* (Jahnke and Scholten, 2009; Raissig et al., 2013). The DME DNA glycosylase is not expressed significantly in the *Arabidopsis* egg cell (Choi et al., 2002), and there is no evidence for global DNA demethylation in the embryo (Hsieh et al., 2009). The FIS-PRC2 complex is required for some embryo imprinted gene expression suggesting that H3K27me3 does have a functional role in setting-up MEG and PEG expression in the embryo (Raissig et al., 2013). These observations indicate that we are far from completely understanding the molecular mechanisms guiding imprinted expression patterns during seed development.

IS IMPRINTING NECESSARY FOR SEED DEVELOPMENT?

Genetic analysis of imprinted genes suggests a similar spectrum of developmental functions as for biallelic-expressed genes. As mentioned earlier, imprinting in maize can affect non-essential genes regulating anthocyanin biosynthesis or storage protein accumulation. There are also numerous imprinted genes that have been shown to have critical roles in seed development. Superficially, it is simple to conclude that imprinted expression patterns are therefore critical to seed development. However, we argue that most of these examples fail to provide conclusive evidence that the imprinted pattern is indispensable as opposed to a minimum expression level of the gene being critical.

The *MEA*, *FIE*, and *FIS2* genes encode subunits of PRC2 and are MEGs in *Arabidopsis* (Luo et al., 2000). Loss-of-function mutations in these genes have profound effects on seed development with 50% seed abortion, delays in endosperm and embryo development, and increased cell proliferation in the developmentally delayed endosperm and embryo (Ohad et al., 1996; Chaudhury et al., 1997; Grossniklaus et al., 1998; Kiyosue et al.,

1999). Moreover, these mutants can begin central cell divisions even when the ovule is not fertilized. The FIS-PRC2 phenotypes have been interpreted as imprinted expression of PRC2 being a key repressor of seed growth. However, very similar phenotypes are observed in mutants of the non-imprinted subunit of the FIS-PRC2 complex, *MSI1*, suggesting that imprinted gene expression is not directly responsible for the seed phenotypes (Köhler et al., 2003; Guitton and Berger, 2005; Leroy et al., 2007). This conclusion is further supported by the maize *MEA/Enhancer of zeste* (*Mez1*) gene, which is an endosperm MEG (Haun et al., 2007). A transposon insertion in the promoter region of the locus causes biallelic expression of *Mez1* but no change in seed phenotype (Haun et al., 2009). These data show that FIS-PRC2 function needs to be expressed at sufficient levels in both the female gametophyte and developing seed. However, direct evidence is lacking to support the hypothesis that imprinted expression of the PRC2 subunits is required.

The *PHERES1* (*PHE1*) gene is consistently up-regulated in *Arabidopsis* *mea*, *fie*, and *fis2* mutants (Köhler et al., 2003). The *PHE1* locus was the first PEG to be identified and encodes the AGAMOUS-LIKE37 (AGL37) MADS-domain protein that is a predicted transcription factor (Köhler et al., 2003, 2005). Knocking-down expression of *PHE1* in a *mea* mutant can partially rescue *mea* defective seed phenotypes suggesting that part of the FIS-PRC2 mutant phenotypes are due to increased *PHE1* expression (Köhler et al., 2003). However, insertion mutants in the 3' regulatory region of *PHE1* can cause a loss of imprinting, switching to a biallelic pattern, with no effect on seed phenotype reported (Makarevich et al., 2008). *PHE1* is one of several AGL genes, including *AGL28*, *AGL36*, *AGL40*, *AGL62*, and *AGL90*, which are up-regulated when endosperm cellularization is delayed either by PRC2 mutants or genome dosage imbalances (Kradolfer et al., 2013a). Although *AGL28* and *AGL36* are MEGs (Shirzadi et al., 2011; Wolff et al., 2011), the other AGL genes are expressed from both parental alleles. Mutations in *AGL62* cause recessive seed defects illustrating that FIS-PRC2 complex influences biallelic genes as well as imprinted genes (Kang et al., 2008). Total expression levels of the AGL co-expression network correlates well with the timing of endosperm cellularization and embryo development (Walia et al., 2009; Tiwari et al., 2010; Kradolfer et al., 2013a). The divergent mechanisms of epigenetic control for these AGL genes and the lack of a requirement for paternal expression of *PHE1* suggest that imprinting *per se* is not likely the primary regulator of this developmental node.

An additional *Arabidopsis* PEG, *ADMETOS* (*ADM*), has been implicated in regulating the AGL gene node (Kradolfer et al., 2013b). *ADM* encodes a recently evolved J-domain protein that is only found in a few genera of the *Brassicaceae*. Consistent with its PEG expression, the *adm* locus was identified as a paternal-specific suppressor of seed abortion due to paternal genome excess (Kradolfer et al., 2013b). When mutated, *adm* reduces the over-expression of *PHE1* and other AGL genes toward normal both in interploidy crosses and in *mea* mutants. Although *ADM* is a PEG in multiple *Arabidopsis* accessions (Hsieh et al., 2011; Wolff et al., 2011), natural variation reducing *ADM* expression level in the *Ler* accession is correlated with improved seed development and viability in paternal genome excess crosses (Kradolfer

et al., 2013b). When *adm* is mutant in both maternal and paternal gametes, *adm* more effectively reduces *AGL* expression as well as more effectively suppresses seed abortion due to either paternal genome excess or *mea*, suggesting the maternal allele expresses at a developmentally significant level (Kradolfer et al., 2013b). Interestingly, homozygous *adm/adm* plants, overexpression of *ADM*, and biallelic expression of *ADM* have no seed phenotype in diploid crosses, suggesting that imprinting of this gene is not necessary for normal diploid seed development. The wild-type function of *ADM* is primarily to block interploidy and interspecific hybridizations.

The *Arabidopsis* *FORMIN HOMOLOGUE5* (*AtFH5*) gene is a MEG in which the paternal allele is repressed by PRC2 (Fitz Gerald et al., 2009). *ATFH5* is an actin nucleator and is critical for cell plate formation and endosperm cellularization (Ingouff et al., 2005). Ectopic expression of the paternal allele of *AtFH5* does not impact *mea* mutant phenotypes (Fitz Gerald et al., 2009), suggesting paternal silencing of *AtFH5* may not be required for normal endosperm development. Moreover, double mutants of *mea* and *atfh5* show additive endosperm cellularization and morphogenic defects (Fitz Gerald et al., 2009). These genetic results typically would be interpreted as indicating *mea* and *atfh5* act in different genetic pathways. Although *AtFH5* is clearly an imprinted gene with a critical endosperm development function, it is unclear whether the imprinted gene expression pattern has a significant role in endosperm development.

The role of imprinting for the *Arabidopsis* *MATERNALLY EXPRESSED PAB C-TERMINAL* (*MPC*) gene is even less clear than for *AtFH5*. *MPC* encodes the C-terminal domain of poly(A) binding proteins (PABP) and is hypothesized to have a role in regulating translation of mRNA (Tiwari et al., 2008). The *MPC* gene is a MEG, and homozygous *mpc* RNAi lines show abnormal embryo and endosperm development. However, the role of imprinted gene expression for *MPC* function is difficult to address, since the gene body sequence is necessary to confer maternal specific expression (Tiwari et al., 2008).

In maize, only one imprinted gene has been functionally characterized in seed development. The *meg1* locus encodes a small, secreted peptide that is expressed specifically in the basal endosperm transfer cell layer of the developing endosperm (Gutierrez-Marcos et al., 2004). *Meg1* is initially expressed from the maternal allele and becomes biallelic around 12 days after pollination. RNAi of *meg1* results in reduced transfer cell differentiation and smaller seeds than non-transgenic controls (Costa et al., 2012). Ectopic expression of *Meg1* results in patchy, ectopic transfer cell differentiation throughout the epidermal endosperm, indicating that MEG1 protein is a positive regulator of transfer cell fate.

Meg1 is part of a gene family with six members expressing at significant levels in transfer cells during seed development (Xiong et al., 2014). Only *Meg1* shows imprinted expression with all other *Meg* family members expressing similarly when inherited through either parent. The developmental function of these other *Meg* family members has not yet been experimentally tested. However, the expression patterns of these genes are very similar to *Meg1* in both developmental timing and location, suggesting that these genes are also likely to be regulators of transfer cell differentiation

(Xiong et al., 2014). To directly test the role of imprinting on *Meg1* function, Costa et al. (2012) developed a non-imprinted, synthetic *Meg1* gene with two different transfer cell specific promoters. These transgenics show a dosage-sensitive increase both in the number of transfer cells and in seed size suggesting that imprinting of *Meg1* serves to limit nutrient uptake and seed size. Thus, among more than a dozen seed developmental genes studied in detail, only *Meg1* has strong evidence indicating that imprinted gene expression has a significant impact on development and growth of the seed.

WHY DOES IMPRINTING EXIST IN ANGIOSPERMS?

Parent-of-origin specific gene expression is a fascinating pattern of molecular regulation of the genome, and its evolution has been the subject of extensive theoretical debate (Patten et al., 2014). The most accredited explanation for imprinting in plants is provided by the parental-conflict hypothesis, also known as the kinship theory of selection (Haig and Westoby, 1989; Haig and Westoby, 1991; Haig, 2013). This hypothesis argues that imprinting evolves when the maternal parent provides resources during offspring development. In angiosperms, seeds require nutrition from the maternal parent from fertilization until seed maturation. The parental-conflict hypothesis states that the paternal genome expression is selected to increase support for individual progeny, while the maternal genome expression is selected to limit resources to maximize seed set.

The parental-conflict hypothesis predicts that MEGs should reduce seed size and potentially reduce seed set in unfavorable conditions. Conversely, PEGs would increase seed size and promote seed set. Loss-of-function phenotypes of the FIS-PRC2 mutants *mea*, *fis2*, *fie*, and *msi1* have been interpreted to support parental-conflict theory, because these mutants extend cell proliferation in the endosperm and embryo at the cost of failing to complete development (Grossniklaus et al., 1998; Kiyosue et al., 1999; Guitton and Berger, 2005; Ingouff et al., 2005). However, parental-conflict predicts stable networks of imprinted genes with MEGs and PEGs balancing each other for normal seed development (Patten et al., 2014). As discussed above, most imprinted genes, except for *Meg1*, that have been studied in detail can lose imprinted gene expression without significant consequence to seed development, suggesting MEG or PEG expression does not undergo significant selection pressure. The case of the *Meg1* gene also argues against the parental-conflict hypothesis. *Meg1* is normally maternally expressed, and a non-imprinted *Meg1* transgene shows a positive dosage effect for increasing seed size (Costa et al., 2012). The parental-conflict hypothesis would predict that a maternally expressed peptide like MEG1 should be a repressor of transfer cell development or that *Meg1* should be a PEG.

An alternate hypothesis to explain imprinting is the maternal-offspring coadaptation model of gene expression, in which maternal alleles may be selected for imprinted expression to provide the greatest combined fitness for the mother and offspring (Wolf and Hager, 2006). This model is meant primarily to explain the larger number of MEGs over PEGs that have been identified in both mammals and angiosperms. For *Meg1*, the model correctly predicts maternal specific expression, but maternal-offspring coadaptation does not explain the relatively extensive number of

PEGs or the apparent mutability of most angiosperm imprinted genes to switch between biallelic and imprinted states (Patten et al., 2014).

More in-depth evolutionary analysis of the identified imprinted genes in *Arabidopsis* suggests that imprinting correlates with rapid evolution of gene duplicates. More than two-thirds of *Arabidopsis* imprinted genes derive from recent gene duplication events (Qiu et al., 2014). *Arabidopsis* imprinted genes also show reduced domains of expression and increased evolutionary rates over non-imprinted paralogs. This analysis argues strongly that imprinted genes are undergoing neofunctionalization. Neither the parental-conflict nor the coadaptation models predict that recent gene duplication events would be favored for imprinted expression, although the bias toward gene duplicates does not specifically argue against these evolutionary models (Patten et al., 2014).

The current understanding of cis-elements targeting genes for imprinting further suggests that imprinting is primarily a rapid form of evolution. Transposons and short repeats appear to be the targets of differential demethylation in the central cell versus sperm cells (Gehring et al., 2009; Hsieh et al., 2009). Transposon movement allows random conversion of genes to an imprinted pattern of expression. For example, differences in transposon insertions near genes are associated with allele-specific imprinting in *Arabidopsis* (Pignatta et al., 2014). Transposon and other insertions can also convert imprinted genes to biallelic expression patterns, providing a fast mechanism to revert alleles into Mendelian, diploid expression (Haun et al., 2009). Importantly, transposition is known to increase in plants exposed to abiotic and biotic stress, suggesting imprinted gene expression is expected to change more rapidly when plants are poorly adapted to an environment (reviewed in Chénais et al., 2012). Although transposon insertions are generally thought to reduce gene expression, genome-wide analysis of gene expression and DNA methylation of 140 *Arabidopsis* accessions suggests transposon insertion within genes is associated with increased expression levels specifically during seed and pollen development (Schmitz et al., 2013). This more permissive epigenetic state allows genes silenced in other tissues to be expressed during seed development.

Based on the recent genome-wide analyses of imprinting and epigenetic regulation, we suggest that imprinting is a form of epigenetic regulation that allows more rapid selection on recent gene duplicates. Imprinting uncovers individual alleles by converting genes into a pseudohaploid mode of expression during seed development. There is no evidence for prolonged, imprinted expression of genes after germination, and many imprinted genes are expressed later in plant development (Pignatta et al., 2014). Thus, imprinting of one copy of a gene duplicate enables the imprinted gene to accumulate mutations without compromising whole plant fitness. Monoallelic expression in the seed exposes an imprinted allele to more rapid selection acting primarily upon the seed phenotype. Imprinting of recessive, advantageous alleles can confer greater fitness if only expressed from one parent. By contrast, selection against deleterious imprinted alleles is not as strong as in true haploid inheritance. Deleterious imprinted alleles would only be selected against when inherited from the parent conferring expression. For example, a deleterious PEG would be

neutral when inherited from the mother. If a deleterious PEG is linked to an advantageous MEG allele, it could be maintained in a population for a significant period, potentially allowing time for additional compensatory mutations. Thus, imprinted expression may allow plant genomes to explore a larger space of allelic and phenotypic variation in the seed while avoiding deleterious plant phenotypes. The mature seed phenotype is expected to be a major driver of species fitness, and we suggest imprinting is a form of gene expression that allows for more efficient diversifying selection on the seed phenotype.

An important consequence of hypothesizing imprinting as a form of diversifying selection is that most imprinted expression patterns would be expected to have neutral effects on the fitness of the seed. Gene networks that appear to fit parental-conflict or coadaptation models are expected to evolve under diversifying selection. However, the prediction is that the bulk of imprinted expression patterns could revert to biallelic expression with no consequence on seed phenotype. Similarly, allele specific imprinting and novel imprinted loci would be expected to evolve at high frequency. Additional functional data of imprinted genes in outcrossing species such as maize, would help resolve whether parental-conflict or other types of selection is the primary driving force for the evolution of imprinted genes.

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Genomic dissection of the seed

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Seeds play an integral role in the global food supply and account for more than 70% of the calories that we consume on a daily basis. To meet the demands of an increasing population, scientists are turning to seed genomics research to find new and innovative ways to increase food production. Seed genomics is evolving rapidly, and the information produced from seed genomics research has exploded over the past two decades. Advances in modern sequencing strategies that profile every molecule in every cell, tissue, and organ and the emergence of new model systems have provided the tools necessary to unravel many of the biological processes underlying seed development. Despite these advances, the analyses and mining of existing seed genomics data remain a monumental task for plant biologists. This review summarizes seed region and subregion genomic data that are currently available for existing and emerging oilseed models. We provide insight into the development of tools on how to analyze large-scale datasets.

Keywords: *Arabidopsis*, next generation sequencing, oilseed, RNA seq, seed, soybean, transcriptome

INTRODUCTION

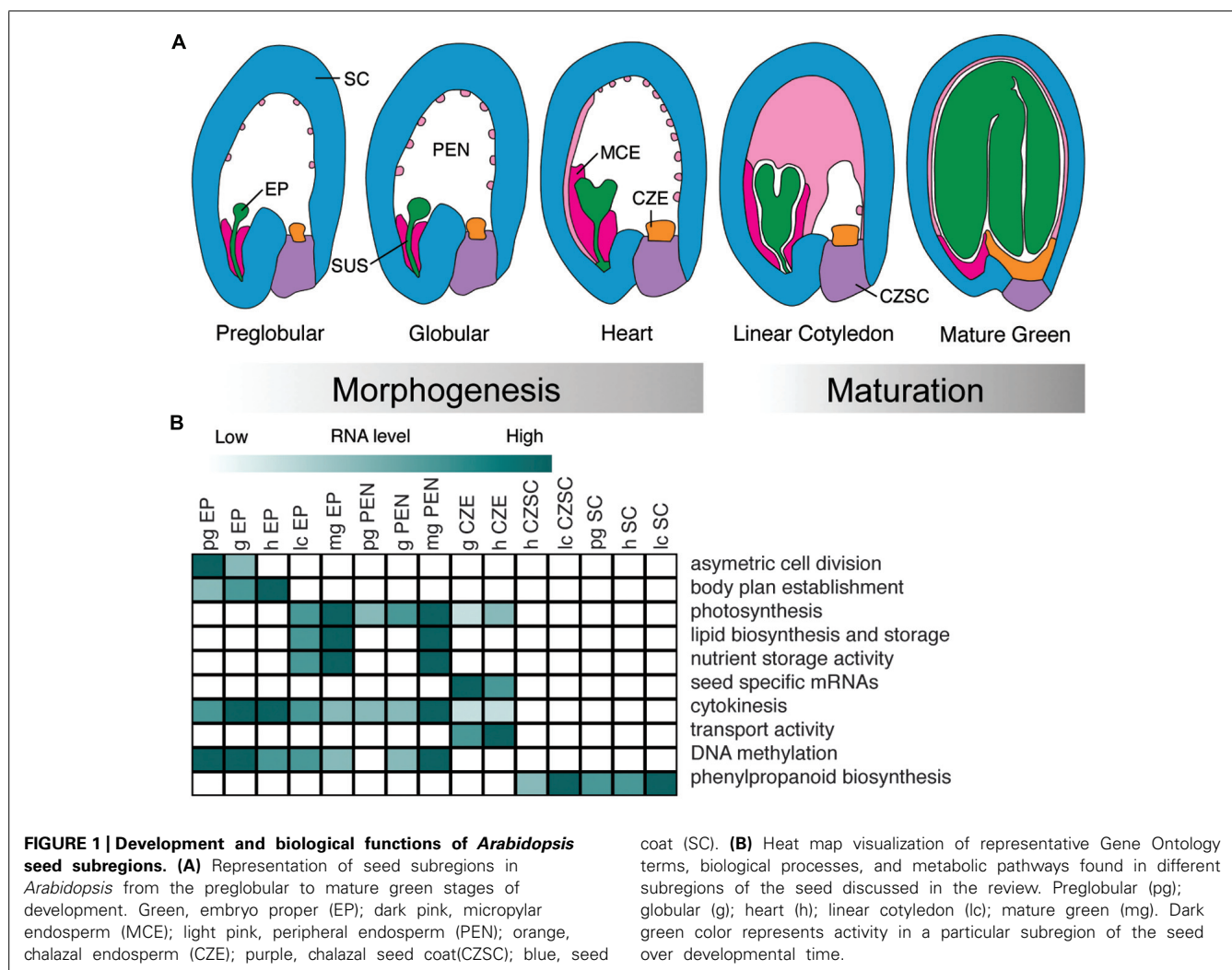
With the world population expected to reach over 9 billion by the middle of the 21st century, one of the biggest challenges facing humanity will be the production of sustainable food supplies (Godfray et al., 2010; Cleland, 2013). To accommodate world food demands, it is estimated that crop production will need to double without increasing current agricultural land use (Foley et al., 2011; Tilman et al., 2011; Ray et al., 2013). Since the direct consumption of seeds and their use as animal feed account for more than 70% of the human diet (Sreenivasulu and Wobus, 2013), recent discussions on food security have turned to enhancing crop production through seed genomics. Seed genomics is the study of genomes and the expression of genes that are required to make a seed. This includes the spatial and temporal expression and regulation of all genes active during seed development. While classical breeding strategies have proven to be effective in producing more robust and productive plant cultivars, they can be complemented and greatly improved through the utilization of genomics-based knowledge (Tester and Langridge, 2010; Feuillet et al., 2011; Langridge and Fleury, 2011).

A seed is formed upon fertilization of the female gametophyte and early stages of development involve the deterioration of maternal gametophytic structures and the establishment of the sporophyte. Seed development is initiated by a double fertilization event that results in a seed that can be divided into three distinct regions: the embryo, the endosperm, and the seed coat (SC; Ohad et al., 1999; Le et al., 2007). In the first fertilization event, a sperm, and egg cell nucleus fuse, resulting in a zygotic embryo. The embryo is part of the next sporophytic plant generation. The endosperm results from the second fertilization event between the sperm and central cell, and it will serve to support the embryo during the early stages of seed development and/or

seedling growth. Finally, the seed coat (SC) is of maternal origin and is derived from the integuments that form during ovule development. The SC transfers assimilates from the maternal plant and serves to protect the embryo throughout seed development. Further, the developmental programs that underlie seed development can be divided into two distinct phases. First, during morphogenesis, the body plan of the embryo is established and the nuclei of the endosperm proliferate. Second, during the maturation phase, large shifts in gene activity are observed across all three regions of the seed, initiating the accumulation of storage materials that help to protect the embryo in preparation for desiccation.

We can further dissect seed regions into subregions. In numerous plants including *Arabidopsis*, the zygote differentiates into the embryo proper, which will become cotyledonous and eventually form the vegetative plant, and the suspensor, which acts to facilitate communication between the embryo proper and surrounding seed regions. The endosperm develops into three distinct subregions: the micropylar endosperm (MCE, proximal to the embryo), the peripheral endosperm (PEN), and the chalazal endosperm (CZE, distal to the embryo; Brown et al., 2003). The maternally derived SC can be divided into two subregions, the chalazal seed coat (CZSC), and distal SC (Figure 1A). Depending on the model seed, these subregions can further be divided into tissue and cell types.

This review focuses on the genomic analysis of seed regions and subregions using established and emerging plant models. We discuss how genomics has been used successfully to study the development of the embryo, endosperm, and SC regions of the seed, and how new cutting-edge tools can be used to further dissect every cell and tissue of the seed into subregions for further interrogation. Finally, we present tools on how to analyze large-scale transcriptome datasets.



CHARACTERIZING THE SEED TRANSCRIPTOME

In the current genomics era we have uncovered a number of developmental and regulatory pathways responsible for making a seed. However, we still have yet to fully understand all of the mechanisms responsible for the coordination of gene activity underlying the sophisticated development of all seed regions and subregions. Many regulatory mechanisms surrounding primary and secondary metabolism, hormone regulation, gene imprinting, transcriptional-, translational-, and post-translational regulation all operate in concert to mediate the complex processes occurring during seed development. These processes are under the regulation of 100s and 1000s of genes that are often obscured by genetic redundancy and thus difficult to identify using traditional forward genetics screens (Curtin et al., 2011). Arguably, the best way to investigate coordinated events such as cell fate specification, differentiation, and morphogenesis of the developing seed is by monitoring the expression of large gene sets with high throughput genomics-focused microarray and sequencing strategies. Bioinformatic analyses can then be used to identify transcriptional networks and key regulators of seed development.

As Next Generation Sequencing experiments such as deep genomic sequencing, RNA-, small RNA-, and DNA methylome-sequencing become commonplace in the laboratory and as sequencing technologies continue to evolve, the challenge faced by the scientific community is no longer the acquisition of data, but rather compiling and analyzing the data. Publicly available databases like NCBI (The National Center for Biotechnological Information¹), GEO (Gene Expression Omnibus²), and SRA (Sequence Reads Archive³) contain large amounts of DNA microarray and nucleic acid sequence data that can be queried and mined to provide answers to challenging biological questions about the seed.

USING DNA MICROARRAYS TO PROFILE THE SEED

The Affymetrix ATH1 GeneChip microarray was one of the most widely used tools to profile the *Arabidopsis* transcriptome, and it was used to investigate numerous processes underlying

¹<http://www.ncbi.nlm.nih.gov>

²<http://www.ncbi.nlm.nih.gov/geo>

³<http://www.ncbi.nlm.nih.gov/sra>

the seed including gibberellin response (Ogawa et al., 2003), response to abscisic acid (Nishimura et al., 2007), seed dormancy (Finch-Savage et al., 2007), seed imbibition (Nakabayashi et al., 2005; Preston et al., 2009), seed germination (Dean Rider et al., 2003; Penfield et al., 2006; Dekkers et al., 2013), and development (Day et al., 2008; Le et al., 2010; Dean et al., 2011; Belmonte et al., 2013; Khan et al., 2014).

Le et al. (2010) published the *Arabidopsis* seed transcriptome at seven stages of development from ovule to seedling and identified putative regulators of seed development. At each stage of development, between 8,779 and 13,722 distinct mRNAs were detected at the level of the GeneChip with 15,563 unique transcripts detected over all stages of seed development. Of these, only 2% (289) of the transcripts were considered seed-specific with the vast majority being specific to a given stage of development (e.g., globular-cotyledon). Of these seed-specific genes, 17% coded for transcription factors (TFs) and contained known regulators of seed development, such as *LEAFY COTYLEDON1 (LEC1)*, *LEAFY COTYLEDON2 (LEC2)*, *FUSCA3 (FUS3)*, and *MEDEA* (Le et al., 2010).

Similar analyses were conducted for developing soybean seed from five developmental time points ranging from mid-maturation through seed desiccation (Jones et al., 2010). This study noted an increase in TF activity late in seed development. TFs accumulating late in development included those involved in ethylene and auxin responses, as well as genes that were largely uncharacterized in soybean. Orthologous genes in *Arabidopsis* and rice suggest these genes are involved in processes such as abscisic acid and gibberellic acid signaling, sugar and nitrogen metabolism, and germination.

PROFILING THE SEED USING LASER MICRODISSECTION COUPLED WITH MICROARRAYS

Traditional studies that isolated seed regions like the embryo, endosperm, and SC for seed genomics used forceps or fine needles. The lack of precision of these manual techniques makes it nearly impossible to isolate individual regions without contamination from neighboring cells or tissues. These challenges limit the resolution of genomics research and dilute low abundant transcripts that may otherwise be detected using more sophisticated dissection methods. Regardless of the dissection tool used, the advancement of genomics-based seed research relies on contamination-free isolation of the cells and tissues of interest.

Currently, the most successful way to dissect regions and subregions of the seed for genomics studies without contamination of other cells types is through laser microdissection (LMD) technologies (Khan et al., 2014). Whole-seed mRNA profiling experiments provided some of the most informative seed genomic data across developmental time for *Arabidopsis* and soybean, but the application of LMD to these seeds provided higher resolution and more sensitive profiles of gene activity in developing seed. For example, Casson et al. (2005) dissected the *Arabidopsis* embryo to study mechanisms associated with apical / basal polarity. This study detected expression of ~65% of the 22,810 probe sets on the ATH1 array during the early

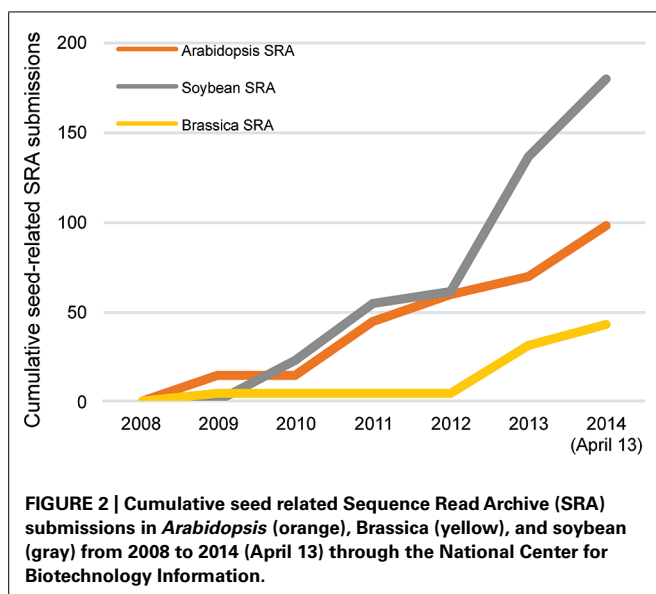
stages of embryo development. Characterization of the spatial and temporal expression of 220 genes known to cause defects in embryo development when mutated, including *PASTIC-CINO1*, *PINOID*, *PIN-FORMED3*, and *PIN-FORMED4* during embryo development provided insight into their control. Further, several of these genes are being used as markers for the embryo.

The endosperm has been a difficult seed region to study using transcriptome analysis given that the endosperm subregions are not easily isolated. LMD has proven to be an effective and contamination-free technique to isolate the individual subregions of the endosperm for transcriptional profiling (Day et al., 2008). An initial study identified 800 genes, 27 encoding TFs that are preferentially expressed during early endosperm development. Biological processes associated with the progression and control of the cell cycle, DNA processing, chromatin assembly, protein synthesis, cytoskeleton- and microtubule-related processes, and cell/organelle biogenesis were all predicted to characterize endosperm proliferation and cellularization.

The most comprehensive developmental series of any seed was recently published by Belmonte et al. (2013) with the goal of identifying all of the genes and defining the gene regulatory networks responsible for guiding seed development. Thirty-six seed subregions across five developmental stages revealed complex dominant patterns of gene activity in both space and time in *Arabidopsis* (Belmonte et al., 2013; data available at seedgenenetwork.net). The combination of LMD and the ATH1 GeneChip identified at least 17,594 distinct mRNAs that are detectable during seed development and 1,316 of those mRNAs are specifically expressed in the *Arabidopsis* seed compared to vegetative and reproductive tissues. Similar data describing mRNA profiles at high spatial resolution are also available for soybean from experiments that used the Affymetrix soybean GeneChip to analyze 40 subregions across four developmental stages (Le et al., 2007; data available at seedgenenetwork.net). The reader is referred to Nelson et al. (2006) and Day et al. (2007) for reviews on methods and protocols used for LMD of plant tissues (Figure 1B).

USING NEXT GENERATION SEQUENCING TO PROFILE THE SEED

There are a number of advantages to NGS sequencing technology when compared to DNA microarrays: (i) the ability to detect low abundance transcripts, (ii) the identification of novel alternatively spliced isoforms of mRNAs, (iii) little requirement for *a priori* knowledge of the organism, (iv) increased sensitivity in the detection of differentially expressed genes, (v) more reproducible results, and (vi) the ability to compare expression profiles between distantly related organisms. For example, RNA sequencing facilitated the study of oil accumulation in four non-model oilseeds (or “emerging models”): castor (*Ricinus communis*), rapeseed (*Brassica napus*), burning bush (*Euonymus alatus*), and nasturtium (*Tropaeolum majus*; Troncoso-Ponce et al., 2011). These species differ in their location for oil deposition, triacylglycerol composition and content. Analysis of the data revealed a core set of well-conserved enzymes involved in triacylglycerol production that exhibit similar temporal expression



patterns in all species, suggesting a conserved evolutionary relationship in the production of seed oil. Putative regulators and mediators of oil production in *Arabidopsis* were identified and an online resource, “ARALIP⁴,” was established to facilitate utilization of these data. It is important to note that while NGS has several advantages over microarray technology, the detection of low abundant transcripts as well the detection of alternative splice sites is largely dependent on the depth of sequencing and should be carefully considered during the design of the experiment.

Many other RNA sequencing studies of seed genomics have focused on soybean, largely because of its global economic importance. An indication of this emphasis is that seed-related submissions of soybean RNA sequencing data to the SRA and NCBI databases nearly double those of *Arabidopsis* (Figure 2). This has produced several large datasets for soybean seed development. Two particular studies stand out, one that profiled the whole soybean seed at seven time points between 10 and 42 days after fertilization (Severin et al., 2010), and an independent study focusing on whole soybean seeds at 15–65 days after fertilization (Chen et al., 2012). These studies showed that 49,151 transcripts are detected during seed development, ~12,000 mRNAs more than the 37,500 transcripts represented on the current soybean Affymetrix array. Furthermore, 9,930–14,058 (Severin et al., 2010) and 11,592–16,255 (Chen et al., 2012) transcripts are differentially expressed compared to the earliest stage of seed development. Both of these studies provide examples of how RNA sequencing data can be mined using a range of bioinformatics approaches including gene ontology term enrichment and co-expression analyses.

Next Generation Sequencing also provides an effective method for the characterization of small RNA (sRNA) populations within the developing seed. Two classes of sRNAs highly expressed within seed tissues are microRNAs (miRNAs) and small interfering RNAs

(siRNAs). miRNAs are ~21 nucleotide, single-stranded, non-coding RNAs that mediate the degradation or translational inhibition of target mRNAs with complementary nucleotide sequences (Chen, 2012). siRNAs, derived from double-stranded RNA, cause the degradation of target mRNAs and carry out *de novo* deposition of repressive chromatin marks and will be discussed later in this review.

Much of the recent work profiling sRNAs during seed development focus on economically important emerging models. Two independent studies examined sRNA populations in soybean, focusing on the identification of miRNAs active during development and their putative targets (Song et al., 2011; Shamimuzzaman and Vodkin, 2012). Of the miRNA targets identified, 50% (Song et al., 2011) and 82% (Shamimuzzaman and Vodkin, 2012) were TFs, including auxin response factors and growth regulating factors. Eleven annotations were found in both datasets including Argonaute Protein, Auxin Response Factor, Growth Regulating Factor, HD-ZIP TF, No Apical Meristem protein, TCP Family TF, and Nuclear Factor YA. These studies also report an increase in mRNA target diversity late in development, suggesting miRNAs have a role in the shift into maturation, which agrees with data from earlier work done with *Arabidopsis* (Tang et al., 2012).

Huang et al. (2013) characterized *B. napus* sRNA populations in whole seeds at nine time points in development and in dissected endosperm, embryo, and SC at three of those stages. Similar to *Arabidopsis* and soybean, the authors suggest that miRNAs have a role in controlling seed maturation. In addition, 279 miRNAs were identified that had been previously reported, including 182 in *Arabidopsis* and 56 in soybean. Also in *B. napus*, Zhao et al. (2012) characterized miRNA populations in high- and low-oil content seeds, and they identified putative miRNA regulators of oil metabolism.

Several databases for miRNAs and their mRNA targets are available to the researcher. Currently 427, 573, and 92 mature miRNA sequences for *Arabidopsis*, soybean, and canola, respectively, have been deposited in miRBase, an online database for published miRNA sequences (⁵Kozomara and Griffiths-Jones, 2014). Another database, MiRTarBase (⁶Hsu et al., 2014) contains experimentally confirmed miRNA-target interactions (Hsu et al., 2014). In addition, MiRFANs (⁷Liu et al., 2012) stores miRNA functional annotations specifically for *Arabidopsis*, and it includes an analysis toolbox.

The production of data from Next Generation Sequencing studies is providing the scientific community with vast amounts of genomic data that can be mined to answer many important biological questions about the seed. Dramatic improvements to seed transcriptome experiments, including enhanced sequencing chemistries and better bioinformatics tools should provide the necessary tools and data required to answer these questions. With Next Generation Sequencing, subtle changes to the transcriptome can now be detected with high confidence and exploited to identify most of the genes and gene products responsible for seed development.

⁵<http://www.mirbase.org>

⁶<http://mirtarbase.mbc.nctu.edu.tw>

⁷www.cassava-genome.cn/mirfans

⁴<http://aralip.plantbiology.msu.edu/>

GENOMICS OF EMBRYO DEVELOPMENT

Embryogenesis is the developmental period during which the zygote differentiates into the mature embryo. Embryo development can be divided temporally into two phases, morphogenesis and maturation (Goldberg et al., 1994). During the morphogenesis phase, the diploid zygote derived from fertilization of the egg cell by a sperm cell undergoes an asymmetric cell division, producing the apical and basal cells (Lau et al., 2012). In many plants, the apical cell gives rise to most of the embryo proper. The basal cell develops largely into the suspensor, although the uppermost suspensor cell divides to form the hypophysis that will become the quiescent center of the root apical meristem and the central root cap cells of the embryo proper. Development of the embryo proceeds along two primary axes. Along the apical-basal axis, the embryo becomes sequentially partitioned into specific pattern elements that become the cotyledons, shoot apical meristem, hypocotyl, root, and root apical meristem. The embryo proper also becomes compartmentalized along its radial axis to generate the embryonic tissue systems: procambium, ground tissue, and protoderm. The suspensor is an ephemeral structure of the embryo that serves a structural role by pushing the embryo proper into the nutrient-rich endosperm and a physiological role by transferring nutrients and growth factors to the embryo proper at early developmental stages (Kawashima and Goldberg, 2010).

As the embryo transitions from the morphogenesis to the maturation phase, morphogenetic processes, including cell division, become largely repressed (Harada, 1997; Vicente-Carbajosa and Carbonero, 2005). During the maturation phase, the embryo acquires the ability to withstand stresses imposed by desiccation that occur late in seed development and accumulates storage proteins, lipids, and/or carbohydrates to massive amounts, causing the embryo to grow as a result of cell expansion. The storage macromolecules serve as a nutrient source for the developing seedling during post-germinative development. By the end of the maturation phase, the embryo is quiescent metabolically and arrested developmentally, and it remains in this state until conditions appropriate for germination and post-germinative development are perceived.

CONTRIBUTIONS OF THE MATERNAL AND PATERNAL GENOMES TO EARLY EMBRYO DEVELOPMENT

The zygote represents the first stage of the morphogenesis phase, and two studies have addressed the question of when the zygotic genome becomes active transcriptionally following fertilization of the egg cell. In animals, early embryonic development is regulated by maternal mRNAs deposited in the egg prior to fertilization, and the zygotic genome becomes transcriptionally active several cell cycles after fertilization (Tadros and Lipshitz, 2009). The maternal-to-zygotic transition was analyzed in *Arabidopsis* by sequencing RNAs from early stage embryos derived from crosses between plants of different ecotypes and using single nucleotide polymorphisms to distinguish mRNAs derived from maternal and paternal alleles. Autran et al. (2011) reported that the majority of mRNAs in an *Arabidopsis* embryo at the two to four cell embryo proper stage are from the maternal genome,

although approximately 10% of mRNAs are encoded by paternal alleles at this early stage. The paternal contribution to the mRNA population increased to 36% by the globular stage, which was interpreted to represent a gradual activation of the paternal genome. Paternal genome activity is maternally regulated through epigenetic mechanisms involving RNA-dependent DNA methylation, KRYPTONITE-mediated histone methylation, and CAF-1 complex-induced histone exchange (Autran et al., 2011). By contrast, a separate study of the maternal-to-zygotic transition reported that maternal and paternal genomes contribute almost equally to the transcriptomes of *Arabidopsis* embryos at the earliest stages of embryogenesis (Nodine and Bartel, 2012). Many mRNAs that are undetectable in the egg and sperm constitute the top 50% most abundant mRNAs in one or two-cell embryos, suggesting that the zygotic genome is activated immediately after fertilization and plays a major regulatory role during early embryogenesis. Discrepancies between the findings of these two studies may have resulted from the use of different *Arabidopsis* ecotypes by the two laboratories (Baroux et al., 2013). Alternatively, the high proportion of maternally derived mRNAs may have resulted from contamination of embryo samples by mRNAs from the SC that is entirely of maternal origin (Nodine and Bartel, 2012). Nevertheless, both studies demonstrated that the maternal-to-zygotic transition occurs at the earliest stage of embryo development in *Arabidopsis*.

ROLE OF microRNAs IN THE TRANSITION FROM THE MORPHOGENESIS TO MATURATION PHASE

The transition from the morphogenesis to the maturation phase represents a major shift in the developmental programs that occur during embryogenesis (Harada, 1997; Vicente-Carbajosa and Carbonero, 2005). The transcriptomes of *Arabidopsis* embryos that were isolated from the seed by LMD or hand dissection were profiled at several stages of development (Xiang et al., 2011; Belmonte et al., 2013), and these studies demonstrated that gene expression changes dramatically as embryos transition into the maturation phase. For example, the vast majority of mRNAs that accumulate in the embryo proper at a specific stage of development do so at the maturation phase. This gene set is enriched for those involved in maturation processes, including mRNAs encoding storage proteins, oilbody proteins, and proteins involved in lipid storage.

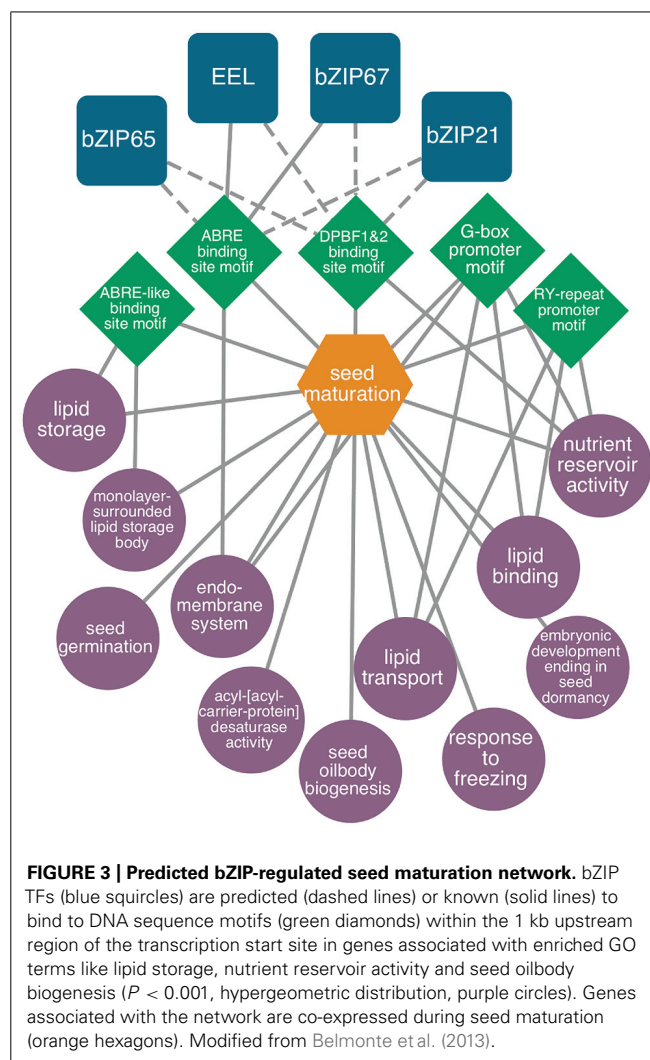
microRNAs play a critical role in controlling the transition from the morphogenesis to the maturation phase (Nodine and Bartel, 2010; Willmann et al., 2011). The role of miRNAs in controlling the transition from morphogenesis to maturation phase was revealed by studies of mutations affecting *DICER-LIKE1* (*DCL1*), which encodes an enzyme required for miRNA biosynthesis. Early in embryo development, loss-of-function *dcl1* mutants display abnormal cell division patterns in the hypophysis, a cell that will become incorporated into the root apical meristem, and in subprotodermal regions of the embryo. These findings were interpreted to suggest that miRNAs are required for embryo patterning events that occur during the morphogenesis phase (Nodine and Bartel, 2010; Willmann et al., 2011). Transcriptome analyses showed that mRNAs that normally accumulate specifically during the maturation phase, including those

encoding storage proteins, oil body proteins, lipid biosynthesis enzymes, and several transcriptional regulators of the maturation phase, accumulate prematurely in *dcl1* mutant embryos. By contrast, two TFs, ASIL1, and HDA6/SIL1, that normally repress maturation genes after germination were downregulated in *dcl1* mutants (Willmann et al., 2011). These results, along with the finding that chloroplast maturation occurs earlier in *dcl1* mutant than wild-type embryos, were interpreted to indicate that miRNAs are required to repress maturation processes during the morphogenesis phase and that the precocious onset of the maturation phase in *dcl1* mutants causes defects in pattern formation. In particular, one set of miRNAs and their target mRNAs were implicated to mediate temporal control of the maturation phase. In *dcl1* mutants, disruption of *miR156* accumulation causes the premature upregulation of two differentiation promoting TFs, SPL10, and SPL11, and experiments analyzing the effects of altering *SPL10* and *SPL11* expression suggested that they are at least partially responsible for repressing the maturation processes early in embryogenesis. A different miRNA, *miR166*, has been shown to repress genes expressed specifically during the maturation phase in vegetatively growing plants (Tang et al., 2012). Together, these observations suggest miRNAs play critical roles in controlling embryonic processes.

MATURATION GENE REGULATORY NETWORKS

Several studies have focused on understanding the gene regulatory networks that operate during the maturation phase of seed development (reviewed by Santos Mendoza et al., 2005; Gutierrez et al., 2007; Braybrook and Harada, 2008; Holdsworth et al., 2008; Suzuki and McCarty, 2008; Junker et al., 2010). To gain insight into embryo maturation gene regulatory networks, Belmonte et al. (2013) identified DNA sequence motifs that are overrepresented in the 5' flanking regions of a set of genes that are expressed in embryos specifically during the maturation phase. TFs that are known or predicted to bind these overrepresented DNA sequence motifs were also identified, permitting a putative gene regulatory network to be created. The network included a number of *cis*-acting DNA elements that have been shown previously to regulate genes expressed during the maturation phase, including the *ABRE*, *ABRE-like*, *DPBF1*, *DPBF2*, and *RY* motifs. Identified among the TFs known to bind these motifs were EEL and bZIP67, which are known to regulate genes during the maturation phase. An example of a maturation gene regulatory network is presented in Figure 3 and a description of the construction of gene regulatory networks is presented in "Identifying regulatory networks required to program the *Arabidopsis* seed" below.

Studies to characterize regulators of the maturation phase have focused on the *Arabidopsis* LEC1, LEC2, FUS3, and ABI3 TFs (Koornneef et al., 1984; Meinke, 1992; Keith et al., 1994; Meinke et al., 1994; West et al., 1994). LEC1 is a HAP3 (a.k.a. NF-YB) subunit of the CCAAT-binding (NF-Y) TF (Lotan et al., 1998), whereas LEC2, FUS3, and ABI3 are B3-domain TFs (Giraudat et al., 1992; Luerssen et al., 1998; Stone et al., 2001). The central roles of these maturation TFs in controlling embryo and seed development was established initially through investigations of mutations in these genes. Loss-of-function mutations



in these maturation TF genes cause embryo lethality or the ablation of embryo parts, because mutant embryos are intolerant of desiccation and storage protein and lipid accumulation is defective. Ectopic expression of these maturation TF genes induces somatic embryo development, fatty acid biosynthesis, oil body accumulation and storage protein biosynthesis in vegetative cells (Parcy et al., 1994; Lotan et al., 1998; Kagaya et al., 2005a; Santos Mendoza et al., 2005; Mu et al., 2008; Stone et al., 2008; Feeney et al., 2013).

The maturation TFs LEC1, LEC2, FUS3, and ABI3 are involved in complex and redundant regulatory interactions during embryo development (reviewed by Braybrook and Harada, 2008; Junker et al., 2010). Genetic and molecular experiments have shown that LEC1 functions upstream of LEC2, FUS3, and ABI3 and, therefore, is likely to act at or near the top of the regulatory hierarchy controlling maturation (Kagaya et al., 2005b; To et al., 2006). Redundancy is observed in interactions among the other maturation TFs that is dependent on their spatial location in the embryo (To et al., 2006). For example, the *FUS3* gene is regulated by LEC1, LEC2, and ABI3 in cotyledons, by LEC2 and ABI3 in the embryonic axis, and by LEC2 and FUS3 in the root tip. Together, the results

suggest that these maturation TFs play key but complex roles in the regulatory network controlling the maturation phase of seed development.

In recent years, initial dissection of the maturation gene regulatory network has occurred through the genome-wide identification of target genes that are directly regulated by the maturation TFs. Direct target genes are generally defined as those that are bound by a TF, as determined by chromatin immunoprecipitation experiments, and that are regulated by that TF. Genes that are up- and downregulated by a TF are often identified by comparing their mRNA levels in embryos with a mutation in the TF gene versus wild type. Alternatively, regulated genes are identified by using inducible forms of the TF. Imposing a gene expression constraint on the identification of direct target genes is important, because fewer than 10% of genes that are bound by a TF are regulated by that TF (Farnham, 2009). Genome-wide analysis identified 98 genes that are both bound by ABI3 and regulated following the induction of ABI3 activity, including genes encoding 2S seed albumins, 12S seed storage globulins, oleosins, and desiccation-related LEA proteins (Monke et al., 2012). Most of these target genes are generally expressed during the maturation phase, and they require abscisic acid for their activation, consistent with the observation that mutations in *ABI3* confers insensitivity to ABA (Koornneef et al., 1984). Analysis of the *ABI3* target genes identified two DNA sequence motifs that are both overrepresented in the first 250 bp upstream of the transcription start site: a RY element that is known to be bound by ABI3 and a G-box motif. The G-box is part of a well-characterized ABA-responsive element (e.g., *ABRE*) motif that interacts with bZIP TFs. These findings are consistent with previous studies showing that ABI3 interacts with a bZIP TF to regulate the transcription of genes involved in maturation processes (Nakamura et al., 2001; Lara et al., 2003).

Target genes for another B3-domain maturation TF, FUS3, were identified from embryonic culture tissue overexpressing the *AGL15* gene that expresses *FUS3* constitutively (Wang and Perry, 2013). *FUS3* target genes were enriched for maturation processes, and showed a 17% overlap with *ABI3* target genes. The 5' flanking regions of the *FUS3* target genes were enriched for RY and G-box motifs. These studies confirmed on a genome-wide scale that there is at least partial redundancy in the functions of *FUS3* and *ABI3*. *FUS3* also directly regulates another B3-domain TF, *VAL1*, which along with *VAL2* and *VAL3*, acts as repressors of the maturation network during seedling development (Suzuki and McCarty, 2008). *FUS3* was also shown to regulate miRNA genes, including *miR156*, *miR160*, *miR166*, *miR169*, *miR369*, and *miR390*. Thus, *FUS3* may be involved in controlling the shift from the morphogenesis to maturation phase given the proposed role of *miR156* in this transition.

Genetic and molecular studies place *LEC1* at or near the top of the regulatory hierarchy controlling the maturation phase (Kagaya et al., 2005a; To et al., 2006). Analysis of genes that are bound and regulated by *LEC1* identified two genes, *LEC1-LIKE* and *FATTY ACID BIOSYNTHESIS2*, which suggested a potential role for *LEC1* in lipid biosynthesis and other maturation processes (Junker et al., 2010). Other direct target genes regulated by *LEC1* are involved in auxin and brassinosteroid biosynthesis and signaling, light

responses and transcription regulation. The studies also demonstrated an interaction between *LEC1* and ABA signaling. For example, although *LEC1* can bind to the 5' flanking sequences of the *YUC10* gene that encodes an auxin biosynthetic enzyme in the absence of ABA, *LEC1*-induced *YUC10* expression is ABA dependent. Together, these results suggest that *LEC1* plays an integrative role during plant development.

GENOMICS OF ENDOSPERM DEVELOPMENT

Endosperm development is initiated with the fertilization of the central cell of the female gametophyte by a sperm cell and proceeds through three distinct stages in most angiosperms: syncytial, cellularization, and cellular (Olsen, 2004; Li and Berger, 2012). During the syncytial stage, the endosperm undergoes nuclear divisions without corresponding cell divisions, generating a syncytium of nuclei that each associates with a cytoplasmic region to form nuclear-cytoplasmic domains (Brown et al., 1999). This period of syncytial development is followed by cellularization in which cell walls form around nuclear cytoplasmic domains, beginning after the eighth nuclear divisions in *Arabidopsis*. Cellularization proceeds in a wave-like manner from the micropylar to the chalazal ends of the endosperm (Figure 1A). During the cellular stage, additional endosperm cells are formed through cytokinesis primarily at the periphery of the endosperm. Complex patterning of the endosperm is perhaps best exemplified by the *Brassicaceae*, including *Arabidopsis* and canola, in which three distinct endosperm subregions form corresponding to their positions within the seed: micropylar, peripheral, and chalazal (Figure 1A). These spatial domains are specified at the earliest stage of endosperm development in that their nuclear, cytoskeletal, and cytoplasmic characteristics and positions within the endosperm are distinguished by the fourth mitotic division (Brown et al., 2003). Depending upon the species, the endosperm remains largely intact throughout seed development as occurs in cereal grains, or it degrades as in *Arabidopsis*, canola, and soybean seeds.

ENDOSPERM DOMAINS HAVE DISTINCT AND OVERLAPPING FUNCTIONS

Transcriptome analyses of the *Arabidopsis* endosperm have provided novel insights into the relationship between the micropylar, peripheral, and CZE subregions. Previous work using LMD to profile endosperm mRNA populations provided the first characterization of gene expression genome-wide in the micropylar, peripheral, and chalazal subregions (Belmonte et al., 2013). These studies showed that a small subset is expressed specifically in each endosperm subregion at virtually all stages of development, suggesting strongly that each subregion fulfills a unique function within the seed. In particular, the CZE has the largest number of genes that are expressed specifically in a single subregion of the seed and the most seed-specific genes among all subregions. Analyses of these CZE-specific genes showed that they encoded rate-limiting enzymes involved in the biosynthesis of the hormones gibberellic acid, abscisic acid, and cytokinin (Day et al., 2008; Belmonte et al., 2013), confirming the work of others who localized these enzymes to the CZE (Miyawaki et al., 2004; Lefebvre et al., 2006; Hu et al., 2008). Chalazal endosperm-derived abscisic

acid, cytokinin, and gibberellic acid, respectively, are involved in controlling seed dormancy, endosperm cellularization, and growth of maternal tissues. Thus, the CZE may serve as a hub that supplies hormones to regulate developmental processes in developing seeds.

Analyses of the transcriptome datasets uncovered dominant patterns of gene activity for mRNAs that are involved in processes critical for seed development and that occur in all three endosperm domains and in the embryo. Clustering analyses identified a number of different gene sets that are expressed at early stages of seed development in the embryo and micropylar and PEN, but their expression in the CZE is delayed until the late developmental stages (Belmonte et al., 2013). One set encodes proteins involved in cytokinesis, consistent with the observation that embryo cells undergo cytokinesis concurrently with mitosis, whereas endosperm cellularization proceeds from the micropylar to the chalazal ends of the endosperm. Another set is involved in photosynthesis and carbon metabolism, a surprising result given that these processes were known to occur in the embryo but much less was known about their role in the endosperm. Additional analyses provided strong evidence that maturation processes occur not only in the embryo but also in all endosperm subregions. Together, these results emphasize a strong degree of overlap in gene expression programs between the embryo and endosperm regions of the seed.

GENOMIC IMPRINTING AND THE CONTROL OF SEED SIZE

The endosperm has a profound influence on seed size. It has been shown or hypothesized that the size of the endosperm early in seed development, the timing of cellularization of endosperm cells, the provisioning of maternally derived nutrients from the endosperm to the embryo, and the influence of the endosperm on the proliferation and elongation of SC cells are major determinants in specifying seed size (Scott et al., 1998; Garcia et al., 2003, 2005; Melkus et al., 2009; Ohto et al., 2009). The endosperm influences seed size through parent-of-origin effects. Parent-of-origin effects are exemplified by genetic crosses between plants of different ploidy levels. Progeny from interploidy crosses that have an excess of maternal genomes (e.g., tetraploid female crossed with diploid male) produce seeds that are smaller than self-fertilized diploid plants, whereas plants with an excess of paternal genomes (e.g., diploid female by tetraploid male) produce larger seeds (Scott et al., 1998). The parental conflict theory has been proposed to explain the antagonistic influences of the mother and father. It is hypothesized that in polygamous organisms, the father will attempt to enhance the allocation of maternally derived resources specifically to his offspring to maximize their growth, whereas the mother will try to distribute resources equally to all offspring to equalize their growth (Haig and Westoby, 1989).

Parental influences on seed size are thought to be mediated by genomic imprinting. Imprinted genes are expressed following fertilization predominately from either the maternal or paternal alleles unlike the vast majority of genes that are expressed nearly equally from both alleles. Imprinted genes are thought to control resource allocation to the embryo and therefore support its growth. Consistent with this hypothesis, an imprinted gene has

been shown to be involved in controlling maternal nutrient uptake and seed biomass (Costa et al., 2012). Imprinted genes have been identified using RNA sequencing experiments in which *Arabidopsis* plants of different ecotypes were crossed, and mRNAs from maternal and paternal alleles in the progeny were distinguished based on single nucleotide polymorphisms (Gehring et al., 2011; Hsieh et al., 2011; Wolff et al., 2011). These studies identified between 60 and 208 imprinted genes and showed that maternally expressed imprinted genes (MEGs) are more prevalent than paternally expressed imprinted genes (PEGs). Although these studies rarely identified any genes as being imprinted in the embryo, a recent study by Raissig et al. (2013) identified 11 MEGs and one PEG in the *Arabidopsis* embryo.

Genomic imprinting is regulated through epigenetic mechanisms involving DNA methylation and the Polycomb Repressive Complex 2 (PRC2). 5'-Methylcytosine in DNA is an epigenetic mark that is often associated with transcriptionally silenced genes, and PRC2 mediates gene silencing through the trimethylation of lysine 27 of histone H3 (H3K27me3, Kohler et al., 2012). To dissect the mechanisms regulating imprinted genes, Hsieh et al. (2011) and Wolff et al. (2011) analyzed the effects of mutations that cause defects in DNA methylation, DNA demethylation, and the PRC2 complex on gene imprinting. Collectively, their results showed that the DNA methylation status of MEGs correlated strongly with their imprinting. During female gametophyte development, the genome of the central cell, that is the maternal precursor of the endosperm, becomes hypomethylated globally due to the activity of DME, a DNA glycosylase that removes methylcytosine residues from DNA (Gehring et al., 2009; Hsieh et al., 2009). Hypomethylation of MEGs in the central cell results in the expression of maternal alleles of MEGs in the endosperm, whereas the paternal alleles retain their DNA methylation marks and remain silenced. The paternal alleles of some MEGs have also been shown to be silenced through the PRC2 pathway. By contrast, the paternal alleles of PEGs are active, but the maternal alleles are silenced predominately through the PRC2 pathway. These studies support the idea that demethylation of the maternal allele of some PEGs is required to permit the gene to be silenced by the PRC2 (Weinhofer et al., 2010). Thus, a complex set of epigenetic regulatory mechanisms underlies genomic imprinting.

A potential causal link between parent-of-origin effects and endosperm size came from studies of 24 nucleotide p4 siRNAs in developing endosperm (Lu et al., 2012). p4 siRNAs, which in endosperm are derived specifically from the maternal genome, function in RNA-dependent DNA methylation to target specific loci for methylation (Mosher et al., 2009; Law and Jacobsen, 2010). p4 siRNAs primarily target transposable elements for DNA methylation. However, a significant fraction of genes are closely associated with transposons, and methylation of some of these transposons influences the expression of the linked gene. Genome-wide profiling of siRNAs in interploidy crosses of *Arabidopsis* showed that 24 nt siRNAs corresponding to specific genomic loci were strongly overrepresented in endosperm of seeds with a maternal genome excess relative to seeds with a paternal genome excess. Several of these loci corresponded to genes encoding AGL TFs, one of which has been shown to inhibit endosperm cellularization

(Kang et al., 2008). These findings were interpreted to indicate that p4 siRNAs targeting AGL TFs are overrepresented in endosperm with a maternal genome excess, causing premature repression of the expression of AGL genes and precocious cellularization, resulting in a smaller seed. Together, these findings indicate a critical role for the endosperm in several aspects of seed development.

GENOMICS OF SEED COAT DEVELOPMENT

Compared to the embryo and endosperm, the SC has received little attention at the genomics level. The maternally derived SC is responsible, in part, for the evolutionary success of the seed, and it plays an integral role in filling (Verdier et al., 2013), protection, and dispersal of seeds (Haughn and Chaudhury, 2005). The SC region, like the embryo and endosperm, can further be divided into subregions based on morphological and anatomical features. For example, in *Arabidopsis* and canola, the distal SC comprised the inner and outer integuments, undergoes dramatic anatomical transformations including cell expansion, changes in cell wall deposition, and anthocyanin and mucilage accumulation followed by programmed cell death, all in preparation for seed dormancy. Conversely, the CZSC, located proximal to the funiculus, is found at the junction with the maternal plant. In seeds of legumes, like soybean, a total of six subregions have been identified: (i) endothelium, (ii) hour glass, (iii) palisades, (iv) parenchyma, (v) epidermis, and (vi) hilum. The hilum in soybean is considered to be similar in function to the CZSC in *Arabidopsis* and presents the first point of entry of material destined for filial seed compartments.

While the development and anatomy of the SC in oilseeds, such as *Arabidopsis*, soybean, and canola, have been extensively studied (Beeckman et al., 2000; Western et al., 2000; Windsor et al., 2000; Macquet et al., 2007; Young et al., 2008; Dean et al., 2011) there is remarkably little information about the genes and gene regulatory networks underlying this multicellular structure. Even less information is available about the genomics of SC development in emerging model crop systems. Of the few studies that have examined the SC at the genomics level (Jiang and Deyholos, 2010; Dean et al., 2011; Belmonte et al., 2013; Khan et al., 2014), data suggest the SC is more similar to maternal tissues than to the embryo or the endosperm. Despite the vast amount of data currently being generated and the different technologies being employed to study the SC, it is still unclear how many genes are active in each subregion and how those numbers change between species.

TRANSCRIPTIONAL REGULATION IN THE SEED COAT

When comparing the SC to other seed regions, *Arabidopsis* is the best plant model studied to date. Hierarchical clustering of GeneChip data showed differences between each subregion of the SC. It is clear that global similarities and differences exist in the SC region compared to the embryo and endosperm and have likely evolved over time to protect the embryo and to adapt to environmental conditions (Debeaujon et al., 2000). Quantitative differences in gene activity within subregions of the SC provided insight into the biological processes underlying its development. Dominant patterns of gene expression were identified from comprehensive RNA profiling of *Arabidopsis* seed subregions. This

analysis identified sets of genes that show spatial (between different subregions) and temporal (across seed development) differences in expression (Belmonte et al., 2013; Khan et al., 2014). Co-expressed gene sets were shown to represent biological processes associated with the development of SC color (Zhang et al., 2013), anthocyanin deposition (Debeaujon et al., 2003), and mucilage accumulation (Western et al., 2001), which have been extensively studied using forward genetic analyses. These studies revealed essential processes associated with the SC that are controlled by individual genes or small sets of genes, yet it was still unclear how all of these processes may be coordinated over the lifecycle of the seed.

Cellular processes that occur in the SC have been independently shown to be controlled by TFs belonging to MYB (Nesi et al., 2001; Penfield et al., 2001), HD-Zip (Johnson et al., 2002; Ishida et al., 2007), and MADS-Box (Nesi et al., 2002; Huang et al., 2011) families. Our comprehensive SC transcriptome analysis identified all of these TF mRNAs in a single analysis (Khan et al., 2014). Not only were all of these known regulators identified in our experiment, we also identified a number of possible gene targets responsible for cell fate specification, the accumulation of mucilage, the deposition of anthocyanin, flavonoid biosynthesis, and SC color.

TRANSCRIPTIONAL REGULATION OF SEED COAT COLOR

Seed coat color is an agroeconomically important trait and is determined by the presence or absence of flavonoids, more specifically, proanthocyanidins. Flavonoids are secondary metabolites produced in plants derived from the phenylpropanoid pathway and are thought to have a number of functional roles, including photoprotection (Agati et al., 2013) and cellular signaling (Pourcel et al., 2013). Proanthocyanidins accumulate exclusively in the SC. When cells in the SC die, the proanthocyanidins oxidize and polymerize to form brown pigments that darken the seed. Mutants that have defects in proanthocyanidin production form a lighter colored or transparent SC (yellow/green). The yellow/green SC coloration is often associated with other desired agroeconomic traits such as thinner SCs, decreased fiber, and higher protein and oil contents (Simbaya et al., 1995; Lipsa et al., 2011; Jiang et al., 2013b). Proanthocyanidin deficient mutants do not appear to have any major physiological disturbances other than SC color; however, some evidence suggests the mutants may have diminished responses to abiotic/biotic stress (Pourcel et al., 2013), longevity, and germination (Dean et al., 2011; Jiang et al., 2013a).

Seminal work in the genetics and biochemistry of SC color in *Arabidopsis* revealed complex networks of genes and gene products responsible for this trait (Yu, 2013). In canola and soybean, genes that contribute to SC color are more difficult to identify genetically due to redundancies within the genome. RNA sequencing of brown- and yellow-coated *B. juncea* revealed three dihydroflavonol reductase genes and three anthocyanin reductase genes that were highly expressed in the brown-seeded variety with almost no detectable expression in the yellow-seeded variety (Liu et al., 2013a). The expression of three phenylpropanoid biosynthetic genes, ten flavonoid biosynthetic genes and four regulatory genes were studied using qRT-PCR at seven

developmental stages in yellow- and brown-seeded *B. napus*. Two propanoid biosynthetic genes (*PHENYLALANINE AMMONIA LYASE*, *TRANS-CINNAMATE 4-MONOOXYGENASE*), two flavonoid biosynthetic genes (*TRANSPARENT TESTA4*, 6), five anthocyanidin/proanthocyanidin biosynthetic genes (3,4-*DICHLOROPHENOL GLYCOSYLTRANSFERASE 2*, *TRANSPARENT TESTA3*, 10, 12, 18), and three TFs (*TRANSPARENT TESTA8*, *TRANSPARENT TESTA GLABRA1*, 2) had different expression patterns in yellow seeds (Qu et al., 2013). Further, eleven quantitative trait loci mediating SC color and fiber content were identified using high-density SNP arrays in canola (Liu et al., 2013a). Together genomics studies of SC color provide new targets for improving desirable traits, such as seed oil quality, and highlight the genetic complexity of SC color (Liu et al., 2013b). The analysis and identification of new QTLs combined with RNA sequence data should provide the information needed to design improved breeding strategies.

TRANSCRIPTIONAL REGULATION IN THE CHALAZAL SEED COAT

While the distal SC has been the primary focus of numerous functional studies, the CZSC has not been studied in the same detail. Bioinformatic analysis of CZSC mRNA populations uncovered a number of transport processes that showed dynamic programs of activity across development. These processes had not been described previously because of the inaccessibility of the CZSC within the seed for experimental analysis. For example, genes associated with phloem unloading including *SUCROSE-PROTON SYMPORTER 2* (*SUC2*) and a complement of *SWEET* genes encoding sucrose efflux transporters, amino acid transport genes including *BIDIRECTIONAL AMINO ACID TRANSPORTER 1* (*BAT1*), *AMINO ACID PERMEASE 2* (*AAP2*), water transport genes encoding tonoplast intrinsic proteins (*TIP1*;1), and plasma membrane intrinsic protein are all expressed in the CZSC. These findings support the hypothesis that transport processes are enriched in the CZSC. Co-expression networks generated from transcriptome data provided insight into the regulation of these transport processes. A putative G-box regulated network controlling water and sugar transport in the developing seed through bZIP TFs, including bZIP25, bZIP28, and LRL1 (Khan et al., 2014). Functional characterization of these transcriptional regulators predicted to be associated with CZSC function presents a new avenue of targeted seed improvement through modification of maternally derived subregions.

IDENTIFYING REGULATORY NETWORKS REQUIRED TO PROGRAM THE *Arabidopsis* SEED

To better understand the underlying transcriptional mechanisms required to program the seed, an integrative systems biology approach should be applied that incorporates molecular and computational biology. First, large-scale datasets are required for such an approach, and excellent sources of seed genomic data are available at databases such as GEO and NCBI as discussed previously. However, mining this data effectively requires the development of more advanced and user-friendly tools that are available to a broader scientific audience through online

databases. Tools from the BioArrayResource⁸, Genevestigator⁹, and The *Arabidopsis* Information Resource¹⁰ are all excellent resources for genomics-based data including but not limited to whole seed, seed region, and seed subregion datasets. In addition, the seedgenenetwork.net database houses whole seed, seed region, and seed subregion transcriptome, sRNA, and DNA methylome datasets from *Arabidopsis* and soybean. Although usability of online tools continues to improve, it remains difficult to identify genes with key roles in seed development with these online tools.

Using high-resolution seed datasets from *Arabidopsis* (Le et al., 2010; Belmonte et al., 2013; Khan et al., 2014), we developed a user-friendly bioinformatics program to identify transcriptional circuits from large-scale datasets at every stage of the seed life-cycle¹¹. We identified genes, focusing our attention on TFs that are predicted to control biological processes across developmental time or that are specific to a seed subregion, including the embryo proper, micropylar endosperm, CZE, or the distal and CZSCs. The transcriptional module analysis is based on the association of a specific set of co-expressed genes with their enriched Gene Ontology terms, known DNA sequence motifs, metabolic processes, and TF families and presents the user with possible gene targets regulating biological processes within the seed.

For example, we identified a transcriptional module consisting of genes expressed specifically in the micropylar endosperm and that are enriched for the WRKY DNA sequence motif in their 5' flanking regions. Our model predicts *MINISEED3* to control processes associated with the endomembrane system in the early stages of seed development. While *MINISEED3* has previously been shown to localize to the micropylar endosperm (Luo et al., 2005), the model allows us to predict gene targets of this TF which were previously unknown (Figure 4A). We also studied a putative transcriptional network underlying the CZE. Up until recently, genetic information about this understudied subregion was lacking. However, through our integrative bioinformatics approach we identified a putative *CIRCADIAN CLOCK ASSOCIATED1*-regulated transcriptional circuit controlling ubiquitin-dependent protein catabolic processes (Figure 4B). Within the SC, we identified a number of regulators that have been previously associated with SC development, allowing a high degree of confidence in our predictive transcriptional modules (Figure 4C). The *TRANSPARENT TESTA GLABRA* complex is implicated in the regulation of flavonoid biosynthesis, and several MYB TFs (including MYB5) are implicated in the regulation of mucilage biosynthesis and the differentiation of the outer integuments (Khan et al., 2014).

While this type of data analyses has been used successfully to identify existing transcriptional circuits, the real power of this approach lies in the identification of unknown interactions and prediction of the biological processes controlled by a TF. One of the caveats to this method is that a well-annotated genome must

⁸www.bar.utoronto.ca

⁹www.genevestigator.com

¹⁰www.arabidopsis.org

¹¹http://seedgenenetwork.net/presentation#software

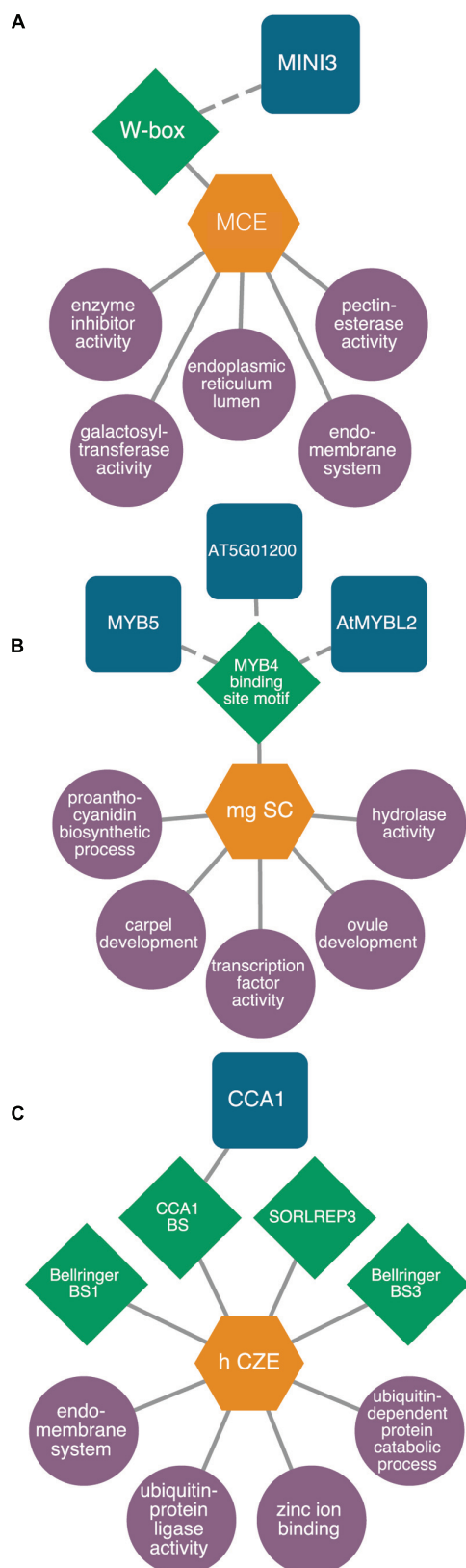


FIGURE 4 | Continued

FIGURE 4 | Continued**Predictive transcriptional circuits in subregions of the *Arabidopsis* seed.**

(A) *MINI3* (*MINI3*)-W-box transcriptional circuit in the micropylar endosperm (MCE) regulating processes like the endomembrane system. (B) A *CIRCADIAN CLOCK ASSOCIATED 1* (*CCA1*) module in the chalazal endosperm (CZE) of heart-stage seeds. (C) A *MYB* transcriptional module in the mature green (mg) seed coat (SC) predicted to control processes like proanthocyanidin metabolism and ovule and carpel development. TFs (blue squares) are predicted (dashed lines) or known (solid lines) to bind to DNA sequence motifs (green diamonds) within the 1 kb upstream region of the transcription start site in genes associated with enriched ($P < 0.001$, hypergeometric distribution) GO terms (purple circles) within patterns of co-expressed gene sets (orange hexagons). All networks are modified from Belmonte et al. (2013).

be available as a reference. Thus, one of the challenges in emerging crop systems will be the annotation of genomes for which genomics research is still in its early stages. While we are beginning to understand some of the molecular mechanisms underlying the development and properties of different seed subregions and regions, the interconnectedness of these transcriptional circuits will remain a priority in the effort to elucidate the complex regulatory pathways responsible for seed development. The spectacular increase in genomic resources applicable to the seed will enable a more comparative approach to uncover and study both conserved and unique transcriptional circuits among related seed species such as the *Brassicaceae* or the *Leguminosae*. Current efforts are directed at implementing and developing computational programs to identify gene regulatory networks for important crop species like canola and soybean. The ability to predict transcriptional circuits in cell and tissue types previously thought to be inaccessible within the seed provides unprecedented insight into the regulation of biological processes over developmental time.

IDENTIFICATION OF TFs ESSENTIAL FOR SEED DEVELOPMENT

Analysis of putative gene regulatory networks is an excellent way to identify possible regulators of seed development. However, experimental validation and functional characterization of the TFs are required to validate the network. Identification of essential seed genes is a cumbersome task yet remains a priority for those interested in studying seed biology and genomics. While research has focused on essential seed genes that when mutated cause a seed lethal phenotype, other mutant phenotypes may result in defects in metabolic pathways or biochemical processes, cellular development, morphology, or other more subtle molecular phenotypes. Through our work, we have identified a number of region- and subregion-specific TFs; however, the vast majority of mutant alleles of these regulators failed to show a seed lethal phenotype (Le et al., 2010; Belmonte et al., 2013). Thus, the function of most subregion-specific TF mRNAs discovered in our work remains unknown.

Much has been learned about the seed through the use of forward genetics. Forward genetics involves generation of random mutations within an organism through radiation-, chemical-, or insertion-induced mutagenesis followed by screening for an aberrant phenotype. Systems for phenotyping mutants are

becoming increasingly automated (Fiorani and Schurr, 2013), and NGS strategies are being used to map the mutation site in what is being referred to as “fast-forward” genetics (Schneeberger and Weigel, 2011). Through forward genetics, an extensive collection of *Arabidopsis* T-DNA mutants is available through the SALK Institute (Alonso et al., 2003), and a database of essential seed genes has been established at seedgenes.org (Meinke et al., 2008) and the *Arabidopsis* Biological Resource Center.

As we continue to characterize the seed genome, forward genetics becomes increasingly ineffective as the likelihood of discovering previously uncharacterized mutants decreases. Molecular tools such as RNA interference and over-expression lines have provided researchers with important information about their genes of interest. However, new genome editing techniques utilizing the CLUSTERED REGULARLY INTERSPACED SHORT PALINDROMIC REPEATS (CRISPR)/CRISPR-Associated System (CAS; Xie and Yang, 2013), Transcription Activator-Like Effector Nucleases (TALENs; Christian et al., 2013), and Zinc Finger Nucleases (ZFNs; Zhang et al., 2010; de Pater et al., 2013), are becoming popular alternatives to classical mutagenesis. Unlike the previous approaches that relied solely on chance, emerging technologies provide an efficient means to achieve targeted mutagenesis and target multiple alleles simultaneously (Curtin et al., 2011). In addition, there is the potential for targeting non-coding regions of the genome to elucidate regulatory functions of nucleic acid sequences (Gaj et al., 2013). Of these systems, the most recent to emerge is the CRISPR/CAS system. Unlike ZFNs and TALENs that rely on complicated protein–DNA interactions, the CRISPR/CAS system uses guiding RNAs and simple base pairing between the RNA construct and target site. In addition, this technology has the ability to perform multiple genome edits by targeting more than one location simultaneously (Cong et al., 2013). This technology is also proving to have several additional practical applications, such as the modification of gene expression *in vivo* through gene fusion to transcriptional activation or repression domains (Bikard et al., 2013) or for the labeling of individual chromosomal loci (Chen et al., 2013). Taken together, the ability to manipulate transcriptional networks and fine-tune gene expression would prove valuable tools for the molecular dissection and engineering of seeds.

FUTURE DIRECTIONS

It is an exciting time to study the underlying mechanisms of seed development through genomics. The complex morphological and metabolic transformations of the seed lend themselves to intensive genomic interrogation. While seminal work dissecting cells, tissues, and organs of both *Arabidopsis* and soybean seeds has revealed an incredible abundance of information, there are still pressing questions when it comes to the coordination and regulation of seed development at the cellular and tissue levels. To answer these questions seed biologists are using modern sequencing strategies. The incredible amount of information produced by these technologies is overwhelming, and the information extracted from these analyses will only continue to improve as we perfect the chemistries and foster new collaborations with mathematics, statistics and computer science. These

in-depth analyses yield significant information about the transcriptional circuitry underlying complex tissue systems responsible for the development of the seed. Moreover, identification of transcriptional regulators from large-scale datasets will provide the necessary starting point for research focusing on improving seeds.

To achieve these goals, plant biologists are coupling cutting-edge technologies that are capable of dissecting or isolating individual cells and tissues of the seed with sequencing platforms. In addition to mRNA profiling, LMD has been coupled to genomics strategies such as bisulfite sequencing to study global changes in DNA methylation marks, degradome sequencing to study miRNA cleavage sites, and ChIP sequencing to identify protein/TF DNA interactions during seed development. DNA sequencing, bisulfite sequencing, RNA and small-RNA sequencing, degradome sequencing, ChIP sequencing, and CLIP sequencing (protein–RNA interactions) each provide a piece to the developmental puzzle, and sophisticated integrative computational analyses will be required to put all of the pieces together. Thus, the development of integrative computational tools to analyze complex and possibly disparate datasets in all plants will remain a major challenge for the scientific community.

Despite the tremendous advances in genomics-focused research including NGS platforms and the continuing reduction in the cost and production of high-resolution datasets, functional characterization of genes responsible for seed development, especially in emerging model systems, remains a challenge. Functional testing and characterization of the biological information derived from the billions of data points that sample the dynamic biological processes underlying seed development will take decades using current molecular biology tools. Thus, high-throughput functional characterization of genes and gene products remains a top priority for plant biologists. There are four areas of seed genomics and its application that we suggest need to be targeted to further improve our understanding of the seed: (i) update and curate small- and large-scale genomics data in publicly available databases; (ii) implement user-friendly data analysis pipelines and educate scientists on how to use them effectively; (iii) profile and characterize the genomes of emerging models important for global crop production and development; (iv) functionally characterize every gene responsible for plant traits relevant to sustainable agriculture.

CONCLUSION

Current advancements in seed genomics are illuminating the genetic forces driving seed development. It is now possible to identify most of the genes responsible for guiding seed development in every cell, tissue, and organ throughout the seed lifecycle. Together, modern breeding strategies that include information derived from genomics-based research will provide the necessary tools to improve seeds: seeds with improved nutritional value, that can endure adverse environmental conditions, or one that can withstand biological attack. Our dependence on seeds for food, fuel, and other resources means seed improvement research through genomics will continue to have a significant impact on global biosustainability.

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Ubiquitin-mediated control of seed size in plants

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Seed size in higher plants is an important agronomic trait, and is also crucial for evolutionary fitness. In flowering plants, the seed comprises three major anatomical components, the embryo, the endosperm and the seed coat, each with different genetic compositions. Therefore, seed size is coordinately determined by the growth of the embryo, endosperm and maternal tissue. Recent studies have revealed multiple pathways that influence seed size in plants. Several factors involved in ubiquitin-related activities have been recently known to determine seed size in *Arabidopsis* and rice. In this review, we summarize current knowledge of ubiquitin-mediated control of seed size and discuss the role of the ubiquitin pathway in seed size control.

Keywords: seed size, seed development, ubiquitin, ubiquitin receptor, E3 ubiquitin ligase

INTRODUCTION

In angiosperms, seed development is an important process in the life cycle. The seed contains the basic architecture of the plant and accumulates nutrients for germination and early seedling growth. The size of seeds is important for evolutionary fitness and stress responses. In addition, seed size is one of the most important components of seed yield. Crop plants have undergone selection for large seed size during domestication (Sundaresan, 2005; Song et al., 2007; Shomura et al., 2008; Fan et al., 2009).

Seed development begins with double fertilization in which one sperm cell fuses with the egg cell to form the diploid embryo, and the other sperm cell fuses with the central cell to give rise to the triploid endosperm (Chaudhury et al., 2001; Sundaresan, 2005). In monocots, the endosperm constitutes the major part of the mature seed. In most dicots, the endosperm grows rapidly in the beginning and is eventually consumed, and the embryo occupies most of the mature seed. Maternal integuments surrounding the developing embryo and endosperm develop into seed coat after fertilization (Chaudhury and Berger, 2001; Chaudhury et al., 2001). Therefore, the size of a seed is determined by the coordinated growth of the diploid embryo, the triploid endosperm and the maternal sporophytic integuments. However, it is only in recent decades that we have begun to identify some genes involved in seed size control (reviewed in Kesavan et al., 2013).

The ubiquitin pathway has been recently known to play an important part in plant seed size determination (Song et al., 2007; Li et al., 2008; Xia et al., 2013; Du et al., 2014). Ubiquitin is a conserved 76-amino-acid protein that is covalently attached to target proteins through the sequential action of three enzymes (Hershko and Ciechanover, 1998; Moon et al., 2004). Firstly, the ubiquitin activating enzyme (E1) forms a thioester bond with the C-terminal glycine of ubiquitin in an ATP-dependent manner and transfers the activated ubiquitin to a cysteinyl residue on the ubiquitin conjugating enzyme (E2). The E2 can either bind with the ubiquitin protein ligase (E3) to transfer ubiquitin directly to substrate proteins, or transfer ubiquitin to E3 in

the case of HECT (homology to E6-AP C terminus) E3s, which then transfers it to the substrates (Pickart, 2001). In both cases, E3 defines the substrate specificity. Conjugation of a single ubiquitin to a substrate protein can modify its activity (Mukhopadhyay and Riezman, 2007); however, the ubiquitination process can repeat several times to attach new ubiquitin to the lysine residue of the conjugated ubiquitin on the substrate to form a polyubiquitin chain. The number and the location of ubiquitin molecules that are attached define the fates of the target. One of the famous forms of ubiquitylation with Lys-48 linked polyubiquitin chains often leads the substrate protein to the 26S proteasome for degradation (Vierstra, 2009).

The 26S proteasome is a multi-subunit protease that consists of a cylindrical 20S core particle (CP), capped on each end by a 19S regulatory particle (RP) (Finley, 2009). The 19S RP contains lid and base components, which recognize the ubiquitinated substrates, remove and recycle the ubiquitin moieties, unfold the target proteins and transport them into the central chamber of CP. The CP is a core protease in which proteolysis takes place and unfolded proteins are broken into peptides (Vierstra, 2009). During the degradation of polyubiquitinated proteins, ubiquitin chains linked to the substrates can be cleaved and recycled by deubiquitinating enzymes (DUBs) (Sadanandom et al., 2012). DUBs also generate free ubiquitin moieties from their initial translation products, or reverse the effects of ubiquitination by removing ubiquitin from the targets (Smalle and Vierstra, 2004). Thus, the ubiquitylation process in the cell is dynamic and highly controlled (Sadanandom et al., 2012).

Genomic analysis revealed that more than 1400 genes in *Arabidopsis thaliana* encode components of ubiquitin-26S proteasome pathway (Smalle and Vierstra, 2004). Ubiquitin-mediated signaling is involved in diverse aspects of plant life cycle, such as hormone signaling, circadian rhythm, pathogen responses, and abiotic stress responses (Sadanandom et al., 2012). Recently, several components of the ubiquitin pathway have been found to play critical roles in the regulation of seed and organ size

(Table 1). In this review, we aim to summarize current knowledge on ubiquitin-mediated control of seed size and discuss the role of the ubiquitin pathway in seed growth.

REGULATION OF SEED SIZE BY THE UBIQUITIN RECEPTORS DA1 AND DAR1

The *Arabidopsis da1-1* (DA means “large” in Chinese) mutant was isolated from a genetic screen for mutations that increase seed and organ size (Li et al., 2008). The *da1-1* mutant produced larger and heavier seeds than the wild type (Li et al., 2008). The increased seed size in *da1-1* was a result of enlargement of sporophytic integuments. In addition, *da1-1* plants formed large flowers, siliques, leaves and increased biomass compared with wild-type plants. DA1 controls seed and organ growth by restricting cell proliferation. The *da1-1* mutation causes an arginine-to -lysine mutation in the position 358 of the DA1 protein (DA1^{R358K}). In *Arabidopsis*, seven DA1-related (DAR) proteins share extensive amino acid similarity with DA1. DA1 homologs were also found in other plant species but not in animals, indicating a plant-specific mechanism to control seed and organ growth. Interestingly, the disruption of DA1 or its closest family member DAR1 with T-DNA insertions did not cause obvious seed and organ size phenotypes, while the simultaneous disruption of both DA1 and DAR1 resulted in large seeds and organs, indicating that DA1 and DAR1 act redundantly to restrict seed and organ growth. This genetic analysis also suggests that the mutant protein encoded by *da1-1* may have negative effects on DA1 and DAR1. Consistent with this notion, overexpression of a *da1-1* cDNA dramatically increased seed and organ size of wild-type plants.

DA1 encodes a ubiquitin receptor containing two ubiquitin interacting motifs (UIMs) and a single zinc-binding LIM domain defined by its conservation with the canonical Lin-11, Isl-1, and Mec-3 domains (Li et al., 2008). UIM-containing proteins are characterized by coupled ubiquitin binding and ubiquitylation, which generally bring about monoubiquitylation of the ubiquitin receptor proteins. This, in turn, promotes the conformation change of the receptors, regulates their activity or binding

capacity with other proteins, and initiates a signal cascade (Hicke et al., 2005). Considering that UIM domains of DA1 have the ubiquitin-binding activity, DA1 may be involved in ubiquitin-mediated signaling processes by coupled ubiquitin binding and ubiquitylation. On the other hand, ubiquitin receptors could bind polyubiquitinated proteins and mediate their degradation by the 26S proteasome (Verma et al., 2004). Thus, it is also possible that DA1 may interact with its polyubiquitinated substrates via UIM domains and facilitate their degradation.

REGULATION OF SEED SIZE BY THE E3 UBIQUITIN LIGASES BB/EOD1, DA2, AND GW2

There are two E1s, at least 37 E2s and more than 1300 E3s in *Arabidopsis* (Smalle and Vierstra, 2004). E3s function at the last step of the ubiquitylation cascade and recognize the specific substrates. E3s fall into two groups according to their conserved domains: HECT or RING (Really Interesting New Gene)/U-box type. The RING-type E3 ubiquitin ligases can act independently or as components of multi-subunit E3 complexes including SCF (SKP1-CULLIN-F-box), CUL3 (CULLIN 3)- BTB/POZ (Bric a brac, Tramtrack and Broad complex/Pox virus and Zinc finger), CUL4-DDB1 (UV-Damaged DNA Binding Protein 1) and APC (Anaphase Promoting Complex) (Mazzucotelli et al., 2006). Currently, several RING-type E3 ubiquitin ligases have been identified as key factors of seed size control in dicot and monocot plants.

Two RING-type E3 ubiquitin ligases, DA2 and Big Brother (BB)/Enhancer of DA1 (EOD1), were identified as negative regulators of seed size in *Arabidopsis* (Li et al., 2008; Xia et al., 2013). Loss-of-function *da2-1* and *eod1/bb* mutants shared similar phenotypes, such as large organs and increased biomass. Overexpression of either DA2 or BB/EOD1 resulted in a reduction in organ size (Disch et al., 2006; Xia et al., 2013). In addition, both EOD1 and DA2 act maternally to regulate seed size by restricting cell proliferation in the integuments of ovules and developing seeds (Li et al., 2008; Xia et al., 2013), suggesting that these two E3 ubiquitin ligases may share similar mechanisms in seed size control. Importantly, both the *eod1* and *da2-1* mutations

Table 1 | List of ubiquitin-related proteins involved in seed size control.

Categories	Protein name	Species	Accession number	Reference(s)
Ubiquitin receptors	DA1	<i>Arabidopsis</i>	AT1G19270	Li et al., 2008
	DAR1	<i>Arabidopsis</i>	AT4G36860	Li et al., 2008
E3 ligases	DA2	<i>Arabidopsis</i>	AT1G78420	Xia et al., 2013
	EOD1/BB	<i>Arabidopsis</i>	AT3G63530	Disch et al., 2006; Li et al., 2008
	DA2L	<i>Arabidopsis</i>	AT1G17145	Xia et al., 2013
	GW2	Rice	EF447275	Song et al., 2007
	TaGW2	Wheat	JN896622, JN896623	Su et al., 2011; Bednarek et al., 2012; Yang et al., 2012
	ZmGW2	Maize	EU968771, FJ573211, EU962093	Li et al., 2010
Other regulators	UBP15	<i>Arabidopsis</i>	AT1G17110	Liu et al., 2008; Du et al., 2014
	Rpt2a	<i>Arabidopsis</i>	AT4G29040	Kurepa et al., 2009
	SAMBA	<i>Arabidopsis</i>	AT1G32310	Eloy et al., 2012
	GW5	Rice	AB433345	Shomura et al., 2008; Weng et al., 2008

synergistically enhance the seed size and weight phenotypes of *dal1-1*, suggesting that both EOD1 and DA2 may function with DA1 to control seed size by modulating the activity of common downstream targets. However, genetic analyses show that DA2 and EOD1 function independently to control seed size (Figure 1) (Xia et al., 2013), suggesting that DA2 and EOD1 may target distinct growth stimulators for degradation, with common regulation via DA1. The synergistic effects could result from the simultaneous disruption of two components of a protein complex (Perez-Perez et al., 2009; Lanctot et al., 2013). It has been demonstrated that the ubiquitin receptor DA1 interacts with the E3 ligase DA2 through its C-terminal region (Xia et al., 2013), and the UIM domains of DA1 can bind ubiquitin (Li et al., 2008). Thus, it is likely that the interaction between DA1 and DA2 helps DA1 to bind the ubiquitinated substrates of DA2 and facilitate their degradation by the proteasome.

In rice (*Oryza sativa*), a quantitative trait locus (QTL) for GRAIN WIDTH AND WEIGHT2 (GW2) encodes a RING-type E3 ubiquitin ligase (Song et al., 2007). Loss-of-function GW2 allele caused wide spikelet hulls and accelerated grain milk-filling rates, resulting in increased grain width, weight and yield. The naturally occurring WY3 allele of GW2 encoding a truncated version of the protein with a 310-amino acid deletion produced wide and heavy grains due to increased cell proliferation in spikelet hulls. In contrast, transgenic rice plants overexpressing GW2 formed smaller and lighter grains than wild-type plants. Thus, GW2 might negatively affect the level or the activity of factors promoting cell proliferation. Interestingly, GW2 shares significant

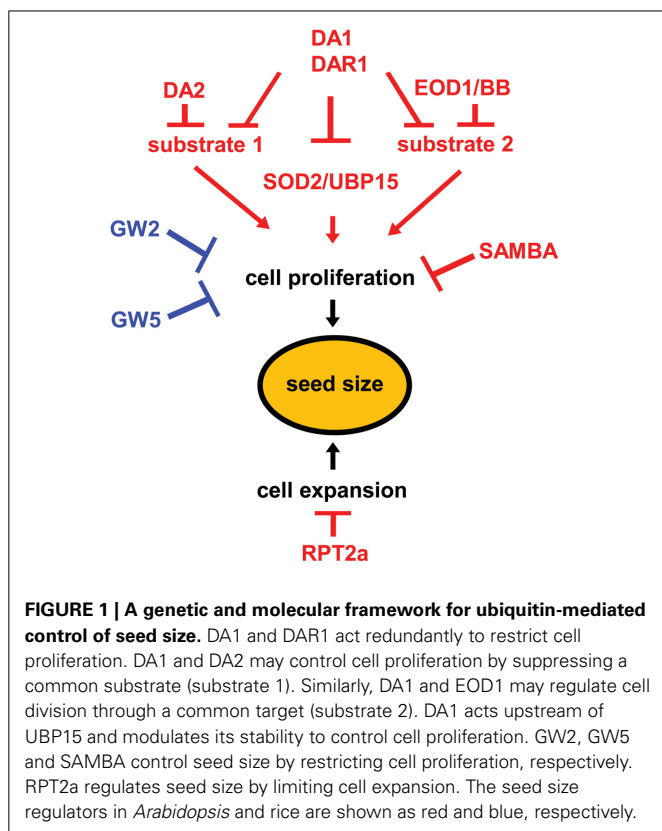
similarity with *Arabidopsis* DA2 and DA2-like protein (DA2L) (Xia et al., 2013). Overexpression of GW2 in *Arabidopsis* resulted in small seeds and organs, as it has been observed in 35S:DA2 and 35S:DAL2 transgenic plants (Xia et al., 2013), indicating a possible conserved function in *Arabidopsis* and rice. The RING domain of GW2 is characterized by a Cys at metal ligand position 5 and a His at metal ligand position 6 (C5HC2) (Song et al., 2007). This feature is shared by the RING domain of maize, wheat, yeast and fungal homologs. Although the spacing of the Cys residues in the RING domain of DA2 is similar to that in the RING domain of GW2, the RING domain of DA2 or its dicot homologs lacks a conserved His residue that is replaced by Asn (Asn-91) (Xia et al., 2013). Biochemical and genetic analyses showed that this amino acid (Asn-91) is not required for DA2 E3 ligase activity and the roles of DA2 in seed size control, suggesting that the RING domain of DA2 might be a variant of that found in GW2.

In wheat (*Triticum aestivum*), there are three GW2 homologs (originating from A, B, and D genomes, respectively) (Su et al., 2011). Analysis of modern varieties showed that *TaGW2-6A* Hap-6A-A is a superior allele for grain size. Varieties with *TaGW2-6A* Hap-6A-A allele had higher mean grain width than those with Hap-6A-G. This effect was due to the higher expression level of *TaGW2* in the varieties with Hap-6A-G allele, indicating that the expression level of *TaGW2* was negatively correlated with grain width. Meanwhile, a single base (T) insertion in the eighth exon of *TaGW2-6A* was detected in a large-kernel wheat variety, Lankaodali. This mutation produced a truncated protein, indicating that *TaGW2-6A* has a negative effect on grain size. In contrast, another report showed that overall down-regulation of *TaGW2* by RNA interference resulted in decreased grain size and weight, suggesting that *TaGW2* may positively regulate grain size (Bednarek et al., 2012). Further studies are needed to elucidate the role of *TaGW2* in grain size control.

ZmGW2-CHR4 and *ZmGW2-CHR5*, two homologs of the rice GW2, have been found in maize (*Zea mays*) (Li et al., 2010). These two loci were located on duplicated maize chromosomal regions that have co-orthologous relationships with the rice region containing GW2. Single nucleotide polymorphism (SNP) in the promoter region of *ZmGW2-CHR4* was significantly associated with kernel width and one-hundred kernel weight, and the expression level of *ZmGW2-CHR4* was negatively correlated with kernel width. Similarly, *ZmGW2-CHR5* also affected kernel width (Li et al., 2010).

REGULATION OF SEED SIZE BY THE UBIQUITIN-SPECIFIC PROTEASE UBP15

SUPPRESSOR2 OF DA1 (SOD2) encodes UBIQUITIN-SPECIFIC PROTEASE15 (UBP15), which is a deubiquitinating enzyme (Liu et al., 2008; Du et al., 2014). UBP15 contains a ubiquitin-specific protease (UBP) domain that is required for deubiquitination activity, and a signature MYND-type zinc finger domain (Zf-MYND) that is supposed to function in protein-protein interaction. *sod2/ubp15* mutants were identified as suppressors of *dal1-1*. *sod2/ubp15* plants produced small leaves, flowers and seeds, whereas plants overexpressing *UBP15* formed large seeds and organs, indicating that UBP15 is a positive regulator of seed and organ growth. UBP15 functions to regulate



seed size by promoting cell proliferation in maternal integuments of ovules and developing seeds. Genetic analyses show that *ubp15* is epistatic to *da1-1* with respect to seed size, suggesting that UBP15 acts downstream of DA1 to promote seed growth (Figure 1). UBP15 protein is stabilized by adding proteasome inhibitor MG132, suggesting that UBP15 is degraded by the 26S proteasome. Furthermore, DA1 physically interacts with UBP15 and modulates its stability. It is likely that the ubiquitin receptor DA1 targets UBP15 and mediates its degradation by the proteasome. However, UBP15 acts independently of the E3 ubiquitin ligases BB/EOD1 and DA2 to control seed size (Figure 1), indicating that UBP15 is not the substrate of the E3 ubiquitin ligases DA2 or EOD1, and also suggesting that other E3 ligase(s) might be involved in proteasome-dependent degradation of UBP15.

The *Arabidopsis* genome encodes 27 UBPs, which were clustered into 14 subfamilies (Yan et al., 2000). The *UBP15* subfamily contains five genes (*UBP15-19*). Although loss of function in the *UBP16* gene had no obvious growth defects, the *ubp16* mutation enhanced the organ growth phenotypes of *ubp15*, indicating that UBP15 and UBP16 function redundantly to control organ size (Liu et al., 2008). It would be interesting to investigate whether UBP16 is involved in seed size control. It is also a worthwhile challenge to know if DA1 could interact genetically and physically with UBP16 and target it for degradation.

REGULATION OF SEED SIZE BY RPT2a, A SUBUNIT OF THE 26S PROTEASOME

The RP of the 26S proteasome is composed of a lid containing non-ATPase subunits (RPN3, 5–9, and 11–12) and a base consisting of six related AAA-ATPases (RPT1–6) and three non-ATPase subunits (RPN1, 2, and 10) (Smalle and Vierstra, 2004). One of the base subunits, the regulatory particle RPT2, has been found to affect seed size (Kurepa et al., 2009). There are two RPT2 homologs (RPT2a and RPT2b) in *Arabidopsis*, which share 98.8% identity in amino acid sequences. Loss-of-function of RPT2a caused a weak defect in 26S proteasome activity and led to enlargement of most organs including seeds. The size of cells in *rpt2a* mutants was increased compared with that in the wild type, while the number of cells in *rpt2a* mutants was reduced, suggesting a possible compensation mechanism between cell proliferation and cell expansion. It is plausible that the RP of 26S is required for the degradation of the positive regulators of cell expansion, thereby influencing seed size.

REGULATION OF SEED SIZE BY SAMBA, A PLANT-SPECIFIC APC/C REGULATOR

Plant organ growth is coordinated by cell division and cell expansion. Cell cycle progression is controlled by the degradation of essential cell cycle regulators such as securin or cyclins (De Veylder et al., 2003). In plants, A- and B-type cyclins are specifically recognized by a multi-subunit E3 ubiquitin ligase complex called anaphase-promoting complex/cyclosome (APC/C) (Heyman and De Veylder, 2012). The cyclins are then subjected to proteolysis by the 26S proteasome, and this promotes the mitotic progression. The activities of plant APC/C are regulated by different activating proteins or inhibitors including CELL

DIVISION CYCLE 20 (CDC20), CDC20 HOMOLOG1/CELL CYCLE SWITCH 52 (CDH1/CCS52), ULTRAVIOLENT-B-INSENSITIVE4 (UVI4), UVI4-like/OMISSION OF SECOND DIVISION1/GIGAS CELL1 (UVI4/OSD1/GIG1), and SAMBA. SAMBA is a plant-specific APC/C regulator that plays a role in seed size control (Eloy et al., 2012). In *Arabidopsis thaliana*, SAMBA is expressed in developing seeds and during early plant development stages. Loss of function of SAMBA stabilizes the A-type cyclin CYCA2;3 and promotes cell proliferation and endoreduplication, resulting in large seeds and organs. The yeast two-hybrid assay showed that SAMBA specifically interacts with A-type cyclins. These results indicate that SAMBA targets A-type cyclins for APC/C-mediated degradation and acts as a negative regulator of seed growth.

REGULATION OF SEED SIZE BY GW5

Rice GW5 is a major QTL that controls rice grain width and weight (Shomura et al., 2008; Wan et al., 2008; Weng et al., 2008). Fine mapping of this locus uncovered that a 1212-bp deletion including the GW5 gene is correlated with increased grain width (Shomura et al., 2008; Weng et al., 2008). Genotyping analysis of rice cultivars revealed that an intact GW5 was detected in the slender-grain rice, whereas the 1212-bp deletion was observed in the wide-grain lines, suggesting a strong artificial selection during breeding (Shomura et al., 2008). GW5 encodes a nucleus-localized protein of 144 amino acids with a predicted nuclear localization signal and an arginine-rich domain. GW5 interacted with polyubiquitin in a yeast two-hybrid assay (Weng et al., 2008), suggesting that GW5 might be involved in the ubiquitin-proteasome pathway to regulate cell division during seed development. As the E3 ubiquitin ligase GW2 also controls glume cell division and grain width, it has been hypothesized that GW5 and GW2 might act in the same pathway. However, genetic analyses showed that plants pyramiding *gw2* and *gw5* exhibited an enhanced phenotype of grain width compared with those carrying one of the two major QTLs (Ying et al., 2012), suggesting that they may act in different pathways or function in a same complex to regulate rice grain size.

CHALLENGES AND FUTURE PERSPECTIVES

During the past decade, several factors involved in ubiquitin-related activities have been identified to influence seed size in plants, indicating that the ubiquitin pathway plays an important role in seed size control. Interestingly, most of these factors affect not only seed size but also organ growth. For example, *da1* mutant showed large seeds, leaves, and flowers (Li et al., 2008), whereas *sod2* mutants produced small seeds and organs (Du et al., 2014), suggesting a possible link between seed size control and organ growth. By contrast, several other mutants with large organs formed normal-sized seeds (Horiguchi et al., 2005; White, 2006; Xu and Li, 2011), implying that seed and organ size is not always positively related. These results suggest that seeds and organs may possess both common and distinct pathways to regulate their respective size.

Our current knowledge of ubiquitin-mediated control of seed size is rather fragmented, relying on several seemingly independent pathways full of gaps (Figure 1). One of the major challenges

in the future is to define the molecular function of the known factors in seed size control. For example, what are the specific targets of the ubiquitin receptors and the E3 ubiquitin ligases? How are the activities of these receptors and E3 ligases regulated? Thus, identification of their interacting proteins and downstream targets by biochemical and genetic approaches will help fill up the major gaps in each pathway and understand the molecular mechanisms of these factors in seed size control. To identify novel ubiquitin-related factors in seed size control, both forward and reverse genetic approaches could be used. Genetic screens for modifiers of the known genes will help identify downstream targets of the ubiquitin receptors or the E3 ligases. The use of the newly developed genome editing technology (reviewed in Gaj et al., 2013) will greatly facilitate the functional characterization of candidate ubiquitin-related genes involved in seed size regulation. On the other hand, systems biology approaches, such as transcriptomic, proteomic, and metabolomics analysis, should yield novel insights into the molecular networks of ubiquitin-mediated control of seed size.

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Evolution and development of cell walls in cereal grains

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The composition of cell walls in cereal grains and other grass species differs markedly from walls in seeds of other plants. In the maternal tissues that surround the embryo and endosperm of the grain, walls contain higher levels of cellulose and in many cases are heavily lignified. This may be contrasted with walls of the endosperm, where the amount of cellulose is relatively low, and the walls are generally not lignified. The low cellulose and lignin contents are possible because the walls of the endosperm perform no load-bearing function in the mature grain and indeed the low levels of these relatively intractable wall components are necessary because they allow rapid degradation of the walls following germination of the grain. The major non-cellulosic components of endosperm walls are usually heteroxylans and (1,3;1,4)- β -glucans, with lower levels of xyloglucans, glucomannans, and pectic polysaccharides. Pectic polysaccharides and xyloglucans are the major non-cellulosic wall constituents in most dicot species, in which (1,3;1,4)- β -glucans are usually absent and heteroxylans are found at relatively low levels. Thus, the “core” non-cellulosic wall polysaccharides in grain of the cereals and other grasses are the heteroxylans and, more specifically, arabinoxylans. The (1,3;1,4)- β -glucans appear in the endosperm of some grass species but are essentially absent from others; they may constitute from zero to more than 45% of the cell walls of the endosperm, depending on the species. It is clear that in some cases these (1,3;1,4)- β -glucans function as a major store of metabolizable glucose in the grain. Cereal grains and their constituent cell wall polysaccharides are centrally important as a source of dietary fiber in human societies and breeders have started to select for high levels of non-cellulosic wall polysaccharides in grain. To meet end-user requirements, it is important that we understand cell wall biology in the grain both during development and following germination.

Keywords: arabinoxylans, biosynthesis, cellulose, evolution, (1,3;1,4)- β -glucan, non-cellulosic polysaccharides

INTRODUCTION

Two major differences distinguish the cell walls of cereal grains from those found in seeds of other higher plant species. Firstly, the cell walls of the Poaceae family, which includes the grasses as well as the economically important cereals, are fundamentally different in composition, compared with walls in dicotyledons and in most other monocotyledons. Secondly, walls in the grain of the Poaceae are usually quite different than those found in vegetative tissues. Here we will examine emerging evolutionary evidence and potential selection pressures that might account for these two levels of differences in wall composition in cereal grains.

Studies on the evolution and development of cell walls in cereal grains have been greatly accelerated through emerging technologies and genetic resources. In examining cell wall composition during grain development, it is clear that walls vary greatly in various parts of the grain and even between adjacent cells (Burton et al., 2010). It is therefore crucial to deploy new, high resolution *in situ* methods to define the heterogeneity of wall composition in plant material that contains different cell types. Thus, sophisticated methods for determining polysaccharides present in walls during grain development are under development. For example, there has been a recent surge in the availability of reliable antibodies and carbohydrate binding modules that detect specific epitopes on wall polysaccharides (Verhertbruggen et al., 2009;

Pattathil et al., 2010) and can therefore be used to distinguish different wall compositions in immunocytochemical labeling at both the light and electron microscopy levels (Wilson et al., 2012). In addition, there are new imaging methods with improved resolution, such as Fourier-transform infra-red (FT-IR), Raman and nuclear magnetic resonance (NMR) spectroscopy, and matrix-assisted laser desorption/ionization mass spectrometry imaging (MALDI-MSI). The use of these spectroscopic and immunocytochemical methods have confirmed that there is no such thing as a “standard” homogeneous cell wall in any tissue and this is no less true in the various cell types of cereal grains.

Evolutionary studies on cell wall polysaccharides have been greatly assisted by the identification of genes that encode polysaccharide synthases that are responsible for wall synthesis (Pear et al., 1996; Dhugga et al., 2004; Burton et al., 2006; Sterling et al., 2006; Doblin et al., 2009) and the recognition that the synthases are encoded by families of genes (Richmond and Somerville, 2000; Hazen et al., 2002). Our knowledge of the genes that mediate wall polysaccharide biosynthesis is increasingly assisted by the availability of genome sequences of important cereal and grass species, high throughput transcript profiling, and by the availability of rapidly expanding genetic resources for cereal species, including mutant libraries. Further exploration of non-crop grass species and the increasing use of grain development mutants, coupled

with the emerging imaging and transcript analysis capabilities, will surely throw up more surprises and help us unravel the complex process of grain development. Here, we briefly review the current knowledge of wall composition in cereal grain and consider the evolutionary origins of diverse grain compositions.

MORPHOLOGY OF WALLS IN THE GRAIN

Large variations are observed in cell wall compositions between different species of grasses. Until recently most attention was focused on walls of the cereals, including wheat (Mares and Stone, 1973), barley (Fincher, 1975), and rice (Shibuya and Iwasaki, 1985). More recently, information has been published on endosperm walls from the grass *Brachypodium distachyon* (Guillon et al., 2011). Significant differences are observed in the polysaccharide compositions of the walls in these species and in the morphology of the endosperm although only a relatively narrow range of forms have been described. Indeed, Terrell (1971) surveyed 169 grass genera and found that a significant proportion of these had persistent liquid, soft, or semi-solid endosperm, the investigation of which surely has implications for grain quality and for the field of cell wall biology in general. The values in **Table 1** illustrate the differences in wall compositions between grains of selected grass species and between vegetative tissues and fruit of grass and dicotyledonous species.

The starchy endosperms of most economically important cereals display a range of morphological forms (**Figure 1A**) and a range of cell shapes and sizes across the grain. In barley there are wings of irregularly shaped starchy endosperm cells that flank a central core of prismatic cells overlying the transfer cells (TC; Becraft and Asuncion-Crabb, 2000). The outer endosperm cells in wheat are prismatic whilst the inner cells are rounded (Toole et al., 2007). In rice grain the endosperm cells are radially symmetrical and so appear to be tube-like (Srinivas, 1975). In sorghum, hard or translucent endosperm tissue surrounds a softer, opaque core (Waniska, 2000). In the former there are no air spaces and the starch granules are packed in tightly. In the softer core region there are large intergranular air spaces that affect both the properties of the tissue and the way that it reflects light. Maize kernels possess the same features (**Figure 1B**) and sorghum and maize grain can

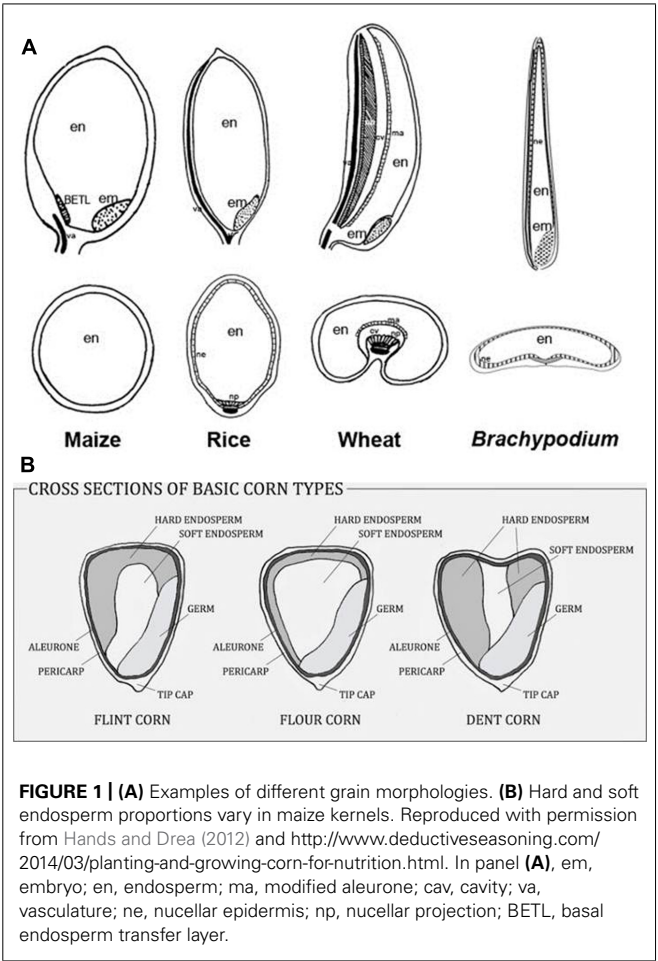


FIGURE 1 | (A) Examples of different grain morphologies. **(B)** Hard and soft endosperm proportions vary in maize kernels. Reproduced with permission from Hands and Drea (2012) and <http://www.deductiveseasoning.com/2014/03/planting-and-growing-corn-for-nutrition.html>. In panel **(A)**, em, embryo; en, endosperm; ma, modified aleurone; cav, cavity; va, vasculature; ne, nucellar epidermis; np, nucellar projection; BETL, basal endosperm transfer layer.

be dominated by one particular type of endosperm and thus can be predominantly soft or hard (Evers and Millar, 2002). In the same way, barley varieties can be described as mealy or steely (Ferrari et al., 2010). Grain hardness and strength, for example in sorghum and maize, is related to the packing of the starch granules within their protein matrix, rather than to the cell walls (Chandrashekar and Mazhar, 1999).

Table 1 | Selected comparisons of polysaccharide compositions in walls of vegetative tissues, fruit, and grains/seeds (% w/w).

Tissue	Hetero-xylan	(1,3;1,4)-β-Glucan	Cellulose	Hetero-mannan	Pectin	Xyloglucan	Reference
Barley coleoptiles (4 days)	32	10	35	nr	12	10	Gibeaut et al. (2005)
Barley aleurone	71	26	2	2	nd	nd	Bacic and Stone (1981)
Barley starchy endosperm	20	70	3	2	nd	nd	Fincher (1975)
Maize internodes	46	3	35	2	trace	6	Zhang et al. (2014)
<i>Brachypodium</i> whole grain	4.7	42.4	6	trace	nr	nr	Guillon et al. (2011)
Rice endosperm	32	nr	36.3	nr	7.3	nr	Shibuya and Iwasaki (1978)
<i>Arabidopsis</i> leaves	4	0	14	nr	42	20	Zabackis et al. (1995)
Grape berries (114 DPA)	7	0	31	3	45	8	Nunan et al. (1998)

nd, not detected; nr, not reported.

WALL COMPOSITION IN GRAIN DIFFERS FROM THAT IN VEGETATIVE TISSUES

In most dividing cells of vegetative tissues of higher plants, a callosic cell plate forms between the newly separated nuclei (Waterkeyn, 1967; Morrison and O'Brien, 1976). The cell plate acts as a scaffold on which the new wall is built. Cellulosic and non-cellulosic polysaccharides are deposited on both sides of the cell plate until the nascent wall eventually separates the daughter cells. The cell plate is compressed to a thin middle lamella layer that lies between walls of the two daughter cells. Wall deposition continues as the cells expand, but at this stage the wall remains relatively thin to allow this expansion to occur and is usually referred to as the primary wall. As cell expansion ceases, wall deposition continues in many cells to form a much thicker and stronger secondary wall, which can be further strengthened by the deposition of lignin and through lamination of parallel sheets of cellulose microfibrils that are oriented in different directions.

As noted above, the first distinguishing feature of walls in grasses compared with other plant species is related to their composition. Although pectic polysaccharides are amongst the earliest wall components to be deposited in both dicotyledons and monocotyledons, the levels of pectic polysaccharides in the walls of grasses decline during wall development to low levels relative to those observed in dicot walls. Other non-cellulosic polysaccharides are deposited during primary wall formation, including xyloglucans, heteromannans, and heteroxylans. In primary walls of the grasses, pectic polysaccharides and xyloglucans are found at relatively low levels, while the heteroxylans appear to form the core non-cellulosic polysaccharides of most walls (Burton and Fincher, 2009). An additional wall polysaccharide is often deposited, namely the (1,3;1,4)- β -glucans. This polysaccharide is not widely distributed outside the Poaceae and the genes that mediate its biosynthesis are believed to have evolved relatively recently. The wall composition of the grasses can be contrasted with the walls of *Arabidopsis*, where xyloglucans appear to be the core non-cellulosic polysaccharides, pectic polysaccharides remain relatively high, and the levels of heteroxylans are low (Zabackis et al., 1995).

The differences are exemplified in developing coleoptiles of barley (Gibeau et al., 2005), where pectic polysaccharides decrease from about 30% w/w to just a few percent of walls over 6 days. Heteroxylan levels remain at about 30% w/w throughout coleoptile development, while xyloglucan levels are generally 10% w/w or less (Figure 2; Gibeau et al., 2005). Similar results were reported for the composition of walls in elongating maize internodes, which can also be viewed as a useful system for monitoring developmental changes in wall composition in vegetative tissues of the Poaceae (Zhang et al., 2014).

The second distinguishing feature of wall composition in the Poaceae is seen in comparisons between vegetative tissues and grain and, more particularly, the starchy endosperm. Botanically, grains are one-seeded fruits, or caryopses (Esau, 1977). Formation of cell walls in the developing endosperm proceeds via a completely different developmental program from other tissues. Fusion of a sperm cell with two haploid central cell nuclei gives

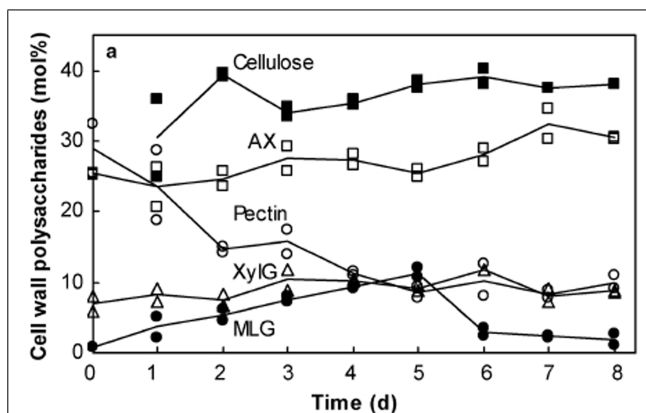
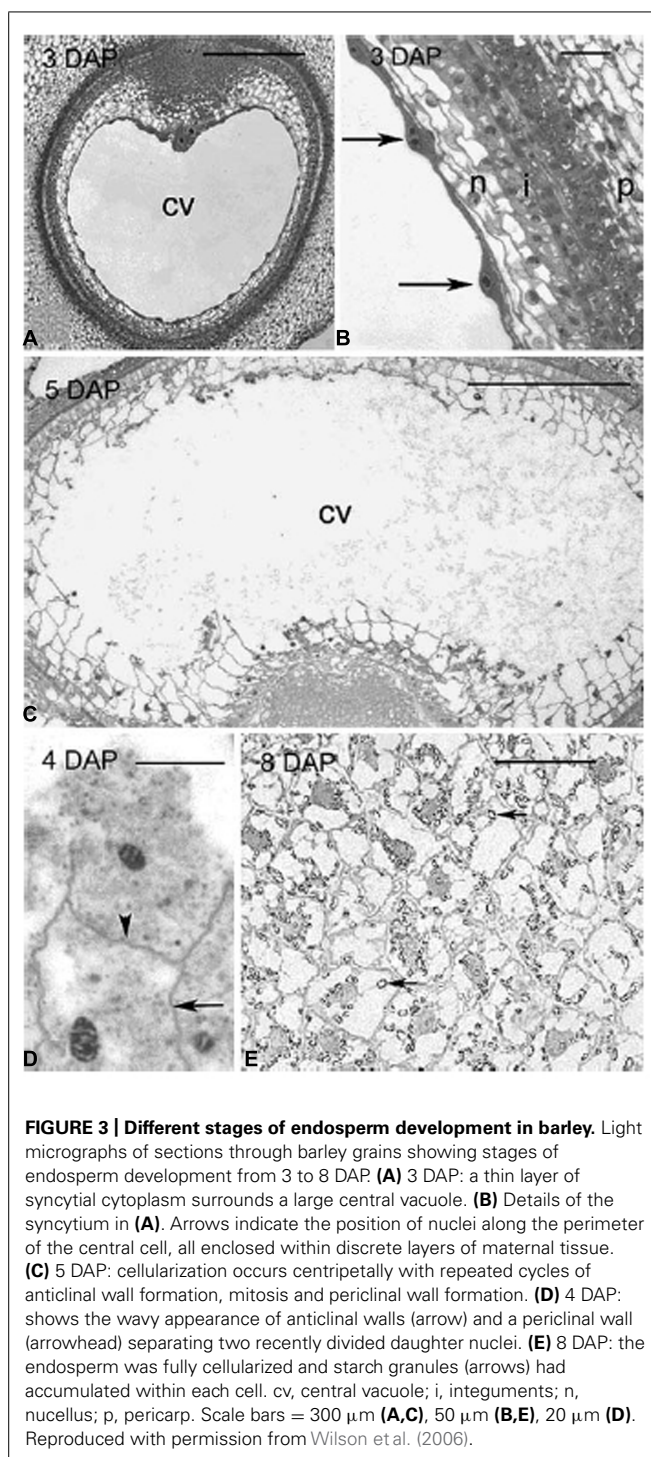


FIGURE 2 | Changes in cell wall composition during the development of barley coleoptiles. Compositions were deduced from data obtained by alditol acetate, methylation and acetic-nitric acid analyses. Changes in cellulose (filled square), arabinoxylan (AX, open square), pectic polysaccharides (pectin, open circle), xyloglucan (XylG, triangle), and (1,3;1,4)- β -glucan (MLG, filled circle) are shown. Reproduced with permission from Gibeau et al. (2005).

rise to a triploid endosperm nucleus. Repeated nuclear division produces many nuclei in a syncytium, which is essentially a cavity in the caryopsis. In most cases, cellularization follows, where callosic cell walls are laid down from the outside in, simultaneously separating the nuclei and apportioning them evenly into cells until the newly formed endosperm walls eventually meet at a central point to fill the coenocyte, as exemplified by rice (Brown et al., 1994), sorghum (Paulson, 1969), and barley (Wilson et al., 2006; Figure 3). In both cellularizing barley and rice endosperm callose is believed to be the major component of the cell walls that grow around the nuclei in the syncytium. In barley callose is found along the central cell wall at 3 days after pollination (DAP); it is present in the first and subsequent anticlinal walls from 4 DAP, in the periclinal walls at 5 DAP and disappears at 6 DAP, except in the vicinity of plasmodesmata (Wilson et al., 2006).

Callose often re-appears much later during barley and wheat grain development (Fulcher et al., 1977; Bacic and Stone, 1981). At 28 DAP, newly deposited patches of callose are detected at irregular spacings along the aleurone-subaleurone interface of barley grain (Wilson et al., 2012). The function of these deposits is unclear but they may represent a wound response to the osmotic stresses imposed by desiccation of the maturing grain or by periods of water stress during grain maturation (Fincher, 1989).

Despite the different cellular developmental patterns in the grain, the walls of the mature grain are still composed of the polysaccharides observed in vegetative walls. However, in the endosperm of many grass species, the amount of cellulose is reduced to just a few percent on a weight basis, which can be contrasted with cellulose contents of 30% (w/w) or more of primary walls in vegetative tissues (Fincher, 2009). The low cellulose content in the endosperm is consistent with the fact that these cells have no load-bearing function, as distinct from walls in barley coleoptiles or maize stalk internodes, and because it is



important for walls of endosperm cells to be quickly degraded in the germinated grain. High levels of cellulose in these walls would almost certainly slow their rate of degradation following germination. However, it must be noted that walls in the starchy endosperm of grain do have to withstand pressures exerted by grain expansion and later by dehydration as the grain matures, and such stresses may trigger changes in the matrix polysaccharides of the wall.

WALL COMPOSITION IN DIFFERENT TISSUES OF THE GRAIN

Most of the discussion above has been focused on the development of cell walls in the starchy endosperm of grains of the Poaceae. However, as the grain develops several other specific cell types can be distinguished. These include, in addition to the starchy endosperm cells, which are the main repository for starch and storage protein, TC, which are clustered around the vascular network that feeds the growing grain, aleurone cells, which envelop the starchy endosperm and are rich in oil and protein bodies, sub-aleurone cells that arise through periclinal division of the aleurone cells, and finally the embryo itself, which is comprised of many organ-specific vegetative tissues. Information on the cell walls of these tissues is not extensive, but some interesting data are emerging.

ALEURONE LAYER

Aleurone cells form a layer around the starchy endosperm that varies from one to three or four cells in thickness, depending on the species, and are indeed components of the endosperm as a whole. Aleurone cells are typically cuboid in shape with much thicker cell walls, usually at least twice the thickness of those in the central starchy endosperm. Aleurone cells contain a dense granular cytoplasm comprised of aleurone grains and small vacuoles containing inclusion bodies (Olsen, 2004). They are rich in proteins and oil but contain no starch and, unlike the cells of the starchy endosperm which undergo programmed cell death (Young and Gallie, 2000), they remain living in the mature grain. This is essential if they are to perform their key role in grain germination, where they synthesize and release a range of hydrolyzing enzymes that are responsible for mobilizing the storage polymers of the starchy endosperm. Aleurone cells usually remain triploid, unlike the starchy endosperm cells, which undergo endoreduplication and become polyploidy in nature (Olsen, 2001).

The walls of aleurone cells in mature barley and wheat grain have two quite distinct layers (Taiz and Jones, 1973; Basic and Stone, 1981). The inner layer is thinner and may have higher concentrations of (1,3;1,4)- β -glucans (Wood et al., 1983). The thicker outer layer of the aleurone wall may be enriched in arabinoxylans, although ferulic acid residues were believed to be evenly distributed across the two wall layers (Fincher, 1989). The two layered structure of aleurone walls might be important during grain germination, when the thick outer layer is rapidly dissolved, while the thin, inner layer remains intact. The outer layer might be removed to facilitate the secretion of newly synthesized hydrolytic enzymes into the starchy endosperm (Van der Eb and Nieuwdorp, 1967; Gubler et al., 1987), while the retention of the thin inner layer might be necessary to maintain the physical integrity of the aleurone cells until their role in enzyme secretion is complete (Fincher, 1989). Walls of the scutellar epithelium layer, which is important in the secretion of hydrolytic enzymes into the starchy endosperm early after germination (McFadden et al., 1988), have morphological features that are similar to those of the aleurone and it is likely that the walls of the scutellar epithelium have a similar composition to those of the aleurone layer (Fincher, 1989).

The developmental cues for aleurone cells are complex and not yet fully understood. In wheat, they have a specific molecular

signature by 6 days post anthesis, conferred by their position in the “surface layer” (Gillies et al., 2012). However, aleurone cell fate remains plastic up to the last cell division and specific signals are necessary to maintain cell identity (Becraft and Yi, 2011). In barley grain, aleurone cells are present at 10 DAP and their walls continue to thicken until 22 DAP when grain maturation begins (Wilson et al., 2012). Many cereals also have a zone of cells that separate the true aleurone from the starchy endosperm cells. These subaleurone layers arise from periclinal division of the aleurone cells (Becraft and Asuncion-Crabb, 2000) and in barley they are present by 14 DAP (Wilson et al., 2012). Sub-aleurone cells are larger than aleurone cells but smaller than starchy endosperm cells, and contain small starch granules and protein bodies.

The developmental signals that dictate the number of cell layers and hence the thickness of the aleurone layer overall are gradually being unraveled (Sabelli and Larkins, 2009). Aleurone layer thickness, the number of cell layers therein and the regularity of thickness has been examined in a range of cereals by Hands et al. (2012). Barley was found to be the only grain to consistently possess a layer more than one cell in thickness. The non-cultivated species *B. distachyon* and *Festuca pratensis* have markedly more disorganized and irregular aleurone layers, which may imply that there is a correlation between regularity of shape and domestication, since this trait may have been selected to meet certain grain quality parameters, such as speed of germination and endosperm mobilization (Hands et al., 2012). However, our knowledge of grain ultrastructure in non-crop species of the Poaceae is generally poor but increasing the number of cell layers in aleurone layers could be beneficial. Approximately half the volume of cereal bran is comprised of aleurone tissue and since this is the most dietary beneficial part of the bran, rich in proteins, oils, and other phytonutrients, increasing the amount further is desirable in human health and animal nutrition (Okarter and Liu, 2010). However, there are also milling considerations, since aleurone cell walls are so thick the cells may remain intact and their contents unobtainable (Minifie and Stone, 1988).

The core polysaccharides found in aleurone cell walls are also arabinoxylans, although relatively high levels of (1,3;1,4)- β -glucan are found in wheat and barley grain. Early work in which aleurone cells were isolated and analyzed showed that aleurone walls from wheat and barley contained about 65% arabinoxylan and about 28% (1,3;1,4)- β -glucan; cellulose and glucomannan levels were again very low (Bacic and Stone, 1981). Several groups have used immunolabeling, Raman spectroscopy, and IR microspectroscopy to monitor changes in aleurone cell walls, *in situ*, during the development of wheat grain. Aleurone walls are more heterogeneous early in grain development compared with those at maturity (Jamme et al., 2008). Antibody labeling indicated the presence of the pectic polysaccharide epitopes RGI, (1,5)- α -arabinan and (1,4)- β -galactan in the aleurone, particularly on the inner surface of the cell wall, and in the pericarp in mature grain (Jamme et al., 2008; Chateigner-Boutin et al., 2014).

Strong autofluorescence has long been known in aleurone and is attributable to high levels of the phenolic acids, ferulic acid, and *p*-coumaric acid in mature aleurone walls in wheat (Fulcher et al., 1972; Bacic and Stone, 1981; Robert et al., 2011) and other

cereals. These phenolic compounds have been examined more closely by Jaaskelainen et al. (2013) using *in situ* optical and Raman microscopy. In the aleurone cells of both barley and wheat, the anticlinal walls contain high amounts of phenolic acids compounds, with much less in the inner periclinal walls. In barley, phenolic compounds were particularly strong in the outer periclinal walls. Ferulic acid, and indeed arabinoxylan, were first detected in the newly differentiated aleurone walls in barley grain at 12 DAP (Wilson et al., 2012). Jaaskelainen et al. (2013) confirmed that there is no (1,3;1,4)- β -glucan in the middle lamella of aleurone walls but that arabinoxylan is enriched here and in the outer cell wall layers.

TRANSFER CELLS

Transfer cells provide the major route for nutrient acquisition by the developing endosperm and they are therefore a key determinant of grain filling. TCs are present in a range of tissues in many plant species and they can be classified into two types, namely reticulate and flange-like. Through the deposition of secondary cell wall material, both types develop a massively expanded surface area to facilitate the transfer of nutrients. Wang et al. (1994) estimated that the plasma membrane surface area increases up to 22-fold. Reticulate types are exemplified by TCs found in *Vicia faba* cotyledons whereas flange-like types are typically found in cereals (McCurdy et al., 2008; **Figure 4**). Reticulate TCs arise from re-differentiation of epidermal cells (Offler et al., 1997), which is a very different pathway from the direct differentiation of flange-like TCs from endosperm cells in developing cereal grains. The latter occurs opposite the nucellar projection as early as 5 DAP in barley, when the first wall ingrowths appear in the syncytium (Thiel et al., 2012b). By 7 DAP the TC walls are enlarged with net-like and branched strands on the inner wall and TCs represent 6.7% of the total endosperm volume; they increase in area ninefold between 5 and 10 DAP. By 10 DAP the walls are thicker with rib-shaped projections and cells are flattened in parallel with the long axis of the grain; by 12 DAP the wall thickenings are asymmetric and irregularly spaced and the flanges have fused; and by 14 DAP TCs represent a much lower proportion of the total endosperm volume at just 0.9% (Thiel et al., 2012b). Wheat TCs develop in a similar fashion to those in barley (Zheng and Wang, 2011), whilst maize TCs present a dense network of flanges and are found in the basal endosperm (Zheng and Wang, 2010), and rice TCs are found in the aleurone layers in the dorsal region of the grain adjacent to the major vascular bundle in the pericarp. Development of TCs in rice is uneven but they also show wall in-growths (Hoshikawa and Wang, 1990).

The deposition of layers of material onto the original wall in TCs has been defined as secondary wall thickening. This occurs widely in many vegetative parts of the plant as cell expansion ceases and wall deposition continues to form a much thicker and stronger secondary wall, which can be further strengthened through the deposition of lignin and *via* lamination. We know that the major polysaccharides laid down through secondary thickening are cellulose and heteroxylans, with the deposition of lignins to further strengthen and, in some cases, to waterproof the wall. Although we know much less about the composition of TC walls, it would

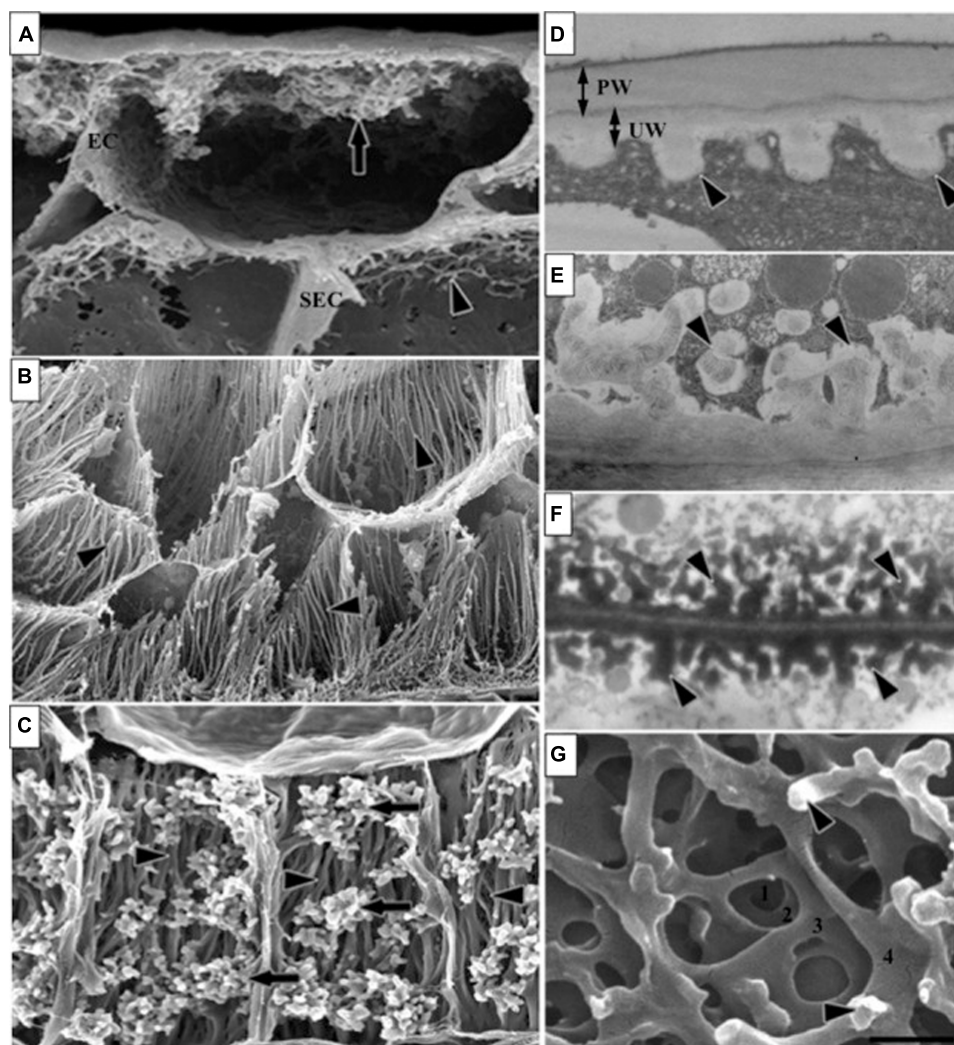


FIGURE 4 | Different types of transfer cells (TC) in cereals and other seeds. These images of TC of developing seeds illustrate various ingrowth wall morphologies. **(A)** Epidermal transfer cells (ETC) of a *Vicia faba* cotyledon with an extensive reticulate ingrowth wall labyrinth including clumps of ingrowth material (arrow) and smaller wall ingrowths in the subepidermal cells (SEC; arrowhead). **(B)** Basal endosperm TC of *Zea mays* exhibiting flange wall ingrowth morphology; arrowheads indicate small lateral protrusions from the linear ribs (modified after Talbot et al., 2002). **(C)** Thin-walled parenchyma TC located at the inner surface of the inner seed coat of *Gossypium hirsutum* with wall ingrowth flanges (darts) extending the length of each cell on which are deposited groups of reticulate wall ingrowths (arrows; modified after Pugh et al., 2010). **(D–F)** Transmission electron microscope images of portions of transverse sections of TC: **(D)** the outer periclinal wall of an adaxial epidermal cell of a *V. faba* cotyledon

induced to trans-differentiate to a transfer cell morphology displaying primary wall (PW) and uniform walls (UW). **(E)** Small papillate ingrowths (darts) of a seed coat transfer cell of *V. faba* exhibiting reticulate architecture. **(F)** Antler-shaped reticulate wall ingrowths (darts) of a nucellar projection transfer cell of a developing *Triticum turgidum* var. durum seed (modified after Wang et al., 1994). **(G)** Field emission scanning electron microscope image of the cytoplasmic face of the reticulate ingrowth wall labyrinth of an abaxial epidermal transfer cell of a *V. faba* cotyledon following removal of the cytoplasm and dry cleaving (for method see Talbot et al. (2001), image modified after Talbot et al. (2001)) where the darts indicate ingrowth papillae on the most recently deposited wall layer. Single scale bar for **(A,B)** = 2.5 μm ; for **(C)** = 5 μm ; for **(D,E)** = 1 μm ; for **(F)** = 0.25 μm ; for **(G)** = 0.5 μm . Figure legend and images reproduced with permission from Andriunas et al. (2013).

seem likely that they do not resemble a typical secondary wall. Significantly, lignin is absent and in wheat, arabinoxylan is the predominant component from 5 to 23 DAP (Robert et al., 2011), and is more highly substituted than the arabinoxylan in the walls of the aleurone layer. After 23 DAP, the TC walls become enriched in (1,3;1,4)- β -glucan, which also occurs in the aleurone, and again this is not typical of secondary cell walls in other parts of the plant.

Recently, laser-microdissection methods have been used successfully to define tissue-specific transcripts and allow metabolite profiling of TCs in barley (Thiel et al., 2012a; Thiel, 2014).

MINOR WALL POLYSACCHARIDES IN THE GRAIN

The core non-cellulosic wall polysaccharides of the grain are the heteroxylans and, in some cases, (1,3;1,4)- β -glucans, while cellulose contents are usually low, as noted above (Fincher and Stone,

2004). However, there is one notable variant when it comes to wall composition in the starchy endosperm of grasses. The endosperm walls of mature rice grain are comprised of significant amounts of cellulose, up to 30% as reported by Shibuya and Nakane (1984). Cellulose is also present at higher levels during the very early stages of barley grain development (Wilson et al., 2006).

Although arabinoxylan and (1,3;1,4)- β -glucan predominate in cereal grain cell walls, we are starting to discover the presence of other polysaccharides which, although only minor components of the walls, may represent key determinants of wall plasticity and other properties. Thus, levels of pectic polysaccharides, heteromannans, and xyloglucans are low in many grains, including wheat and barley (Mares and Stone, 1973; Fincher, 1975). Again an exception here appears to be rice, which contains relatively high levels of pectin (Shibuya and Nakane, 1984) and xyloglucan (Shibuya and Misaki, 1978). Xyloglucan can also be detected in barley grain during early grain development, but appears to be transitory in nature. It first appears at 3 DAP in the central cell wall but is undetectable by 6 DAP (Wilson et al., 2012). Mannans first appear in barley endosperm walls at 5–6 DAP, after cellularization is complete and, based on the accumulation of mannose, mannans, or glucomannans continue to be deposited at low levels up to 20 DAP (Wilson et al., 2012); the final levels of mannans or glucomannans in mature wheat and barley grain are about 2–3% w/w (Mares and Stone, 1973; Fincher, 1975).

Small but significant pectic deposits have recently been reported in wheat grain (Chateigner-Boutin et al., 2014). Pectins have previously been reported in rice endosperm cell walls (Shibuya and Nakane, 1984) and in *B. distachyon* (Guillon et al., 2011) but little is known about their presence or otherwise in the majority of cereal grains. Pectins are complex, multi-domain polysaccharides that bear many different epitopes (Caffall and Mohnen, 2009). Chateigner-Boutin et al. (2014) used antibodies that recognize specific pectic epitopes on sections of developing and mature wheat grains. The inclusion of pre-labeling enzymatic digests with lichenase and xylanase to remove a portion of the major polysaccharides (1,3;1,4)- β -glucan and arabinoxylan proved to be a key step in rendering the pectic epitopes accessible. In the developing grain LM20, which recognizes methyl-esterified homogalacturonan (HG; Verhertbruggen et al., 2009), labeled the pericarp and early endosperm walls, where elasticity would be required. In older grain, large bodies containing unesterified HG, as detected by LM19, were found located in the subcuticle layer, and the reason for their presence here is currently unclear (Chateigner-Boutin et al., 2014).

EVOLUTIONARY DIFFERENCES IN HETEROXYLANS IN THE GRAIN

Consistent with the low cellulose content of endosperm walls, the levels of the core wall polysaccharide in the Poaceae, the heteroxylans, are relatively higher in the starchy endosperm, while the levels of the core polysaccharides of dicotyledonous plants, pectic polysaccharides, and xyloglucans, are generally much lower. Indeed, heteroxylans are found in all walls of the grasses and are the major non-cellulosic polysaccharide in most walls. However, there is evidence of evolutionary forces at work on the heteroxylans

of the Poaceae. In dicotyledonous plants, glucuronoarabinoxylans are abundant and in some cases glucuronyl residues predominate. In the grasses, two types of heteroxylans can be distinguished. Glucuronoarabinoxylans are relatively abundant in the outer, pericarp-testa layers of the grain and in bran, while arabinoxylans are the major non-cellulosic polysaccharides of the aleurone and starchy endosperm cell walls (Fincher and Stone, 2004).

The species best characterized for arabinoxylan is wheat, where isolated endosperm walls comprise about 70% of this polysaccharide (Mares and Stone, 1973). The (1,4)- β -xylan backbone of the polysaccharide displays both structural and spatial heterogeneity with regard to its degree of substitution and this heterogeneity varies throughout endosperm development, as assessed by enzyme mapping, FT-IR, and Raman microscopy and NMR spectroscopy (Toole et al., 2007, 2009, 2010, 2012). Early in endosperm development more of the backbone (1,4)- β -linked xylosyl residues are di-substituted with arabinofuranosyl residues at the O-2 and O-3 positions, but as the grain matures, a higher degree of mono-substitution at the O-3 position is observed, possibly to allow more inter-chain interactions to occur to withstand mechanical stresses as the grain dries out. Ferulic acid and to a lesser extent *p*-coumaric acid residues are ester-linked at O-5 of some of the O-3 mono-substituted arabinosyl groups and it has been reported that these can form covalent cross-links between arabinoxylan chains through oxidative dimerization (Iiyama et al., 1990). There is a gradient of arabinoxylan substitution patterns across the grain as prismatic cells give way to round cells (Toole et al., 2010). Barley endosperm cell walls also contain about 20% arabinoxylan (Fincher, 1975) and show subtle inter-species variation in the types and amounts of backbone substitutions (Izydorczyk, 2014). This is also evident in rye grain, which has a much higher ratio of mono- to di-substitutions than wheat (Rantanen et al., 2007).

The substitution of the extended (1,4)- β -xylan backbone with arabinofuranosyl residues sterically hinders the aggregation of the (1,4)- β -xylan chains into insoluble microfibrils and results in the formation of a long, asymmetrical polysaccharide that is partly soluble in water and can form gel-like structures in the cell wall matrix (Fincher and Stone, 2004). As expected, the degree of substitution of the (1,4)- β -xylan backbone will affect the physical properties of the polysaccharide and, in particular, its solubility. Highly substituted, soluble arabinoxylans, which have a characteristically high arabinose:xylose ratio, are found in the endosperm cells of the grain, while arabinoxylans with lower degrees of substitution are less soluble and are located in the outer layers of the grain (Fincher and Stone, 2004; Izydorczyk, 2014).

EVOLUTION OF (1,3;1,4)- β -GLUCANS IN THE GRASSES

Another key difference in walls of cereal grains compared with other seeds is the presence of (1,3;1,4)- β -glucan. This polysaccharide has an interesting distribution in the plant kingdom (Harris and Fincher, 2009). It is found in many species of the Poaceae but is also occasionally found in other Poales, and in lower plants such as the *Equisetum* spp. horsetail ferns (Trethewey et al., 2005; Fry et al., 2008; Sørensen et al., 2008), bryophytes (Popper and Fry, 2003), some fungi (Pettolino et al., 2009), brown, green and red algae (Lechat et al., 2000; Eder et al., 2008; Popper and Tuohy, 2010),

and lichens (Stone and Clarke, 1992). This distribution pattern of (1,3;1,4)- β -glucans in higher and lower plants is suggestive of convergent evolution. The (1,3;1,4)- β -glucans seem to have been widely adopted only in the Poaceae, where one might conclude there is positive selection pressure to retain the polysaccharide in the walls.

The (1,3;1,4)- β -glucans of the grasses are comprised of an unsubstituted chain of glucosyl residues linked either through (1,4)- β - or (1,3)- β -linkages. About 90% of the polysaccharide chain is comprised of cellotriosyl (DP3) and cellotetraosyl (DP4) units that are linked through (1,3)- β -linkages; adjacent β -linkages are rare or absent (Buliga et al., 1986). Approximately 10% of the polysaccharide is comprised of longer chains of adjacent (1,4)- β -linkages (Woodward et al., 1983). The DP3 and DP4 units are arranged randomly along the chain (Staudte et al., 1983). The combination of the single (1,3)- β -linkages and the random arrangement of the cellotriosyl (DP3) and cellotetraosyl (DP4) units, and hence the (1,3)- β -linkages, result in an extended polysaccharide chain that has a limited capacity to align with other (1,3;1,4)- β -glucan chains. The (1,3;1,4)- β -glucans from many cereal grains are therefore at least partly soluble in water; they adopt an asymmetrical conformation and can form gel-like structures that are believed to be functionally advantageous for non-cellulosic cell wall polysaccharides in the matrix phase of the wall (Fincher and Stone, 2004).

The ratio of the DP3:DP4 units can be used to predict the solubility of the molecule and its rheological behavior (Papageorgiou et al., 2005). High and low ratios indicate a predominance of cellotriosyl and cellotetraosyl residues, respectively, and in both cases the conformation of the polysaccharide becomes more uniform and hence more capable of aligning into insoluble aggregates (Burton et al., 2010). High and low ratios are characteristic of the insoluble (1,3;1,4)- β -glucans from lower plants such as horsetail ferns and fungi (Burton et al., 2010). The DP3:DP4 ratio in (1,3;1,4)- β -glucans from the Poaceae have intermediate values, usually around 2–3:1 (Trafford and Fincher, 2014). It would appear that (1,3;1,4)- β -glucans with these structures and physical properties have evolved and are retained by the grasses for functional reasons. Nevertheless, the ratios vary considerably across cereal species (Table 1; Burton and Fincher, 2012) and grains in which (1,3;1,4)- β -glucans are particularly abundant often have a lower DP3:DP4 ratio and are more soluble (Trafford and Fincher,

2014). The exception here is the relatively insoluble (1,3;1,4)- β -glucan in the grain of *B. distachyon*, where this polysaccharide has a ratio of 5.8:1 and clearly has evolved to perform a storage function (Guillon et al., 2011).

Although the chemical structures of the arabinoxylans and the (1,3;1,4)- β -glucans are quite different (Figure 5), their physical properties are similar and well adapted to a structural role in cell walls. This is therefore an example of convergent evolution to the extant state. Arabinoxylans are extended asymmetrical molecules by virtue of their linear (1,4)- β -xylan backbone and are partly soluble because of the steric hindrance of intermolecular aggregation afforded by their arabinofuranosyl substituents. Solubility is further influenced by acetylation and feruloylation which participate in cross-link formation between arabinoxylan and other wall components. This is exemplified in wheat endosperm walls where the degree of acetylation declines affecting solubility as the grain matures (Veličković et al., 2014) and where arabinoxylan in older walls is rendered less soluble by significant ferulate cross-linking (Saulnier et al., 2009). In contrast, the (1,3;1,4)- β -glucans are extended asymmetrical molecules by virtue of the predominance of “cellulosic” (1,4)- β -glucosyl linkages along their linear backbone and are partly soluble because of the steric hindrance of aggregation caused by the random disposition of (1,3)- β -glucosyl residues that result in randomly distributed molecular kinks in the macromolecule. Just as the solubility of arabinoxylans can be predicted from the degree of substitution and cross-linking, so too can the physical properties of (1,3;1,4)- β -glucans be predicted from their DP3:DP4 ratio. Different chemical strategies have evolved to produce the same physicochemical properties in heteroxylans and (1,3;1,4)- β -glucans.

(1,3;1,4)- β -Glucan is the predominant polysaccharide in the starchy endosperm cell walls of barley and oats and comprises about 15% of starchy endosperm cell walls in wheat grain (Mares and Stone, 1973). Recently, Veličković et al. (2014) used MALDI-MS to examine the spatial distribution of both (1,3;1,4)- β -glucan and arabinoxylan across the wheat grain. They reported higher amounts of (1,3;1,4)- β -glucan and arabinoxylan in outer endosperm regions of young grain and showed that this distribution became more even in mature grain, although cells close to the embryo had walls rich in (1,3;1,4)- β -glucan at all stages of grain development (Saulnier et al., 2009). In barley,

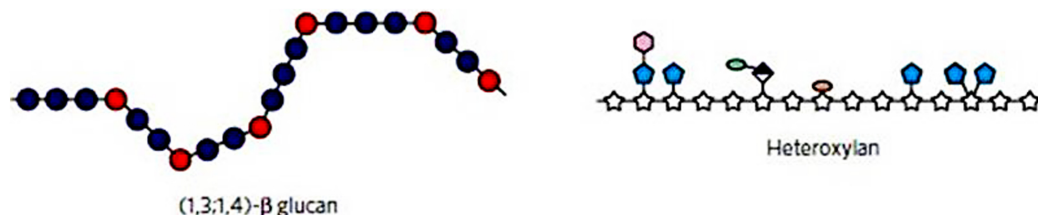


FIGURE 5 | Diagrammatical representations of the major non-cellulosic wall polysaccharides from cereal grains. The (1,3;1,4)- β -glucan (left) has relatively extended regions of adjacent (1,4)- β -glucosyl residues (blue) with irregularly spaced, single (1,3)- β -glucosyl residues. The latter residues form molecular “kinks” in the polysaccharide chain and limit intermolecular

alignment and microfibril formation. In the heteroxylan (right), intermolecular alignment of the xylan backbone (stars) and microfibril formation is limited by steric hindrance afforded by the substituents (blue, pink, etc.). Reproduced with permission from Burton et al. (2010).

the (1,3;1,4)- β -glucan is reported to be evenly distributed in endosperm walls by 10 DAP (Wilson et al., 2012), but little (1,3;1,4)- β -glucan was detected between 12 and 16 DAP in the peripheral starchy endosperm cells closest to the differentiating aleurone. This has also been noted in wheat (Philippe et al., 2006) but while this situation persists in wheat, in barley by 16 DAP (1,3;1,4)- β -glucan deposition has occurred in the peripheral starchy endosperm. There are clearly microdomains present across the endosperm where cell wall composition varies but the requirement for these subtle variations is presently unclear. There is also currently little information on spatial differences in the DP3:DP4 ratio of (1,3;1,4)- β -glucans across developing grain of any species, which is undoubtedly related to the lack of high resolution detection methods. However, the MALDI-MS method shows promise for these kinds of analyses. Veličković et al. (2014) were able to quantify oligosaccharides released by *in situ* digestion of (1,3;1,4)- β -glucans with lichenase and reported that the DP3:DP4 ratio was elevated to 7:1 in younger endosperm, compared with around 4:1 in mature tissue.

EVOLUTION OF POLYSACCHARIDE SYNTHASE GENES

Many of the enzymes that catalyze the polymerization of the backbone chains of wall polysaccharides are encoded by genes that belong to the “cellulose synthase gene superfamily.” This gene family has close to 50 members in most higher plants (Richmond and Somerville, 2000; Hazen et al., 2002) and it has proved difficult to unequivocally assign functions to individual genes and some clades. The *CesA* clade encodes cellulose synthases (Pear et al., 1996; Arioli et al., 1998), but it is clear that several *CesA* enzymes and a number of other enzymes and/or proteins are required for an active cellulose synthesis complex (Doblin et al., 2002; Burton and Fincher, 2014). Several of the cellulose synthase-like (*Csl*) clades of the gene superfamily have been implicated in the synthesis of different wall polysaccharides. The *CslA* group of genes is likely to encode mannan and glucomannan synthases (Dhugga et al., 2004; Liepman et al., 2005). Cocuron et al. (2007) have presented evidence for a role of the *CslC* group of genes in the synthesis of the (1,4)- β -glucan backbone of xyloglucans and the genes in the *CslD* clade may be involved in cellulose synthesis, particular in cells that exhibit tip growth (Doblin et al., 2001; Favery et al., 2001; Wang et al., 2001).

A good deal of effort has been focused on the identification of genes that mediate the synthesis of the cereal grain arabinoxylans and (1,3;1,4)- β -glucans. In the case of the arabinoxylan enzymes, much of the initial work on the identification of genes involved was focused on analyses of *Arabidopsis* mutant lines and transcript profiling. These studies implicated genes from the *GT8*, *GT43*, *GT47*, and *GT61* families (Brown et al., 2007, 2009; Mitchell et al., 2007; Pena et al., 2007; Persson et al., 2007; Oikawa et al., 2010). However, these approaches are plagued with interpretative difficulties imposed by the large gene families, compensation, and pleiotropic effects in transgenic lines during proof-of-function tests, and the difficulties associated with developing reliable biochemical assays for expressed enzymes. Mitchell et al. (2007) and Pellny et al. (2012) used comparative bioinformatics analyses to predict the functions of candidate genes and concluded that genes in the *GT43* and *GT47* families might encode backbone (1,4)- β -xylan synthases

in wheat, genes in the *GT61* family might encode xylan (1,2)- α - or (1,3)- α -L-arabinosyl transferases, and that *BAHD* genes encode feruloyl-arabinoxylan transferases. This group recently provided additional and compelling evidence for wheat *GT61* genes, which they designated *TaXAT* for wheat, as xylan (1,3)- α -L-arabinosyl transferases (Anders et al., 2012), whilst another member of the *GT61* family in rice, called *XAX1*, was shown to be responsible for adding the xylose residues in Xylp-(1 \rightarrow 2)- α -Araf-(1 \rightarrow 3) substitutions (Chiniquy et al., 2012). Zeng et al. (2010) used *GT43*-specific antibodies to co-immunoprecipitate a complex from wheat microsomes that contained *GT43*, *GT47*, and *GT75* proteins, and Lovegrove et al. (2013) used RNA interference suppression of *GT43* and *GT47* genes to reduce the total amount of arabinoxylan in wheat endosperm walls by 40–50%. Analysis of the glucuronoarabinoxylan polymer synthesized by the complex suggested a regular structure containing Xyl, Ara, and GluA in a ratio of 45:12:1. The authors suggested that this may represent a core complex in the biosynthetic process of xylans but to date we have no definitive evidence for the involvement of specific genes or proteins in the synthesis of the backbone or in the addition of certain substituents. Mortimer et al. (2010) reported that the products of two *GT8* genes mediate the addition of α -GluA and α -4-*O*-methylglucuronic acid residues to the heteroxylan of *Arabidopsis*, and Rennie et al. (2012) later established that the *GT8* gene *GUX1* performs substitution of the xylan backbone with GlcA. α -Galacturonosyl transferases that are involved in HG synthesis are also members of the *GT8* family (Yin et al., 2009). Double mutant plants for these genes (*gux1gux2*) contain xylan that is almost completely unsubstituted, but still contain wild-type amounts of the xylan backbone. This indicates that the synthesis of the backbone and its substitution can be uncoupled; a somewhat surprising observation when the behavior of such an unsubstituted and hence possibly insoluble polysaccharide in an aqueous environment is considered, although potential insolubility may be ameliorated by extensive acetylation. The domain of unknown function protein, DUF579, which was reported by Jensen et al. (2011) to be involved in xylan biosynthesis, has since been shown to encode a glucuronoxylan 4-*O*-methyl transferase that catalyzes the methyl etherification of C(O)4 of glucuronyl residues in heteroxylans of *Arabidopsis* (Urbanowicz et al., 2012).

The genes involved in the biosynthesis of (1,3;1,4)- β -glucans are reasonably well defined and include members of the *CslF* and *CslH* clades of the cellulose synthase gene superfamily. These genes are found only in the Poaceae (Hazen et al., 2002) and when transformed into *Arabidopsis thaliana* mediate the biosynthesis of (1,3;1,4)- β -glucans in the walls of transgenic plants (Burton et al., 2006; Doblin et al., 2009). As a dicotyledon, *Arabidopsis* does not normally have (1,3;1,4)- β -glucans in its walls and does not have *CslF* or *CslH* genes. These genes are members of smaller gene sub-families that contain about 10 *CslF* genes and just a few *CslH* genes (Burton and Fincher, 2012). It has not yet been demonstrated that all genes in these two clades encode (1,3;1,4)- β -glucan synthases. Additional evidence for the involvement of these genes in (1,3;1,4)- β -glucan synthesis was obtained through over-expression in barley of the *CslF6* gene driven by an endosperm-specific promoter. This resulted in increases of more

than 80% in (1,3;1,4)- β -glucan content in the transgenic barley grain (Burton et al., 2010). Similarly, a mutant barley line in which there is a lesion in the *CslF6* gene has no (1,3;1,4)- β -glucan in its grain (Taketa et al., 2012). It is worth noting that the *CslF6* gene might act in concert with other proteins or enzymes during (1,3;1,4)- β -glucan synthesis and to investigate this possibility genome-wide association mapping has been used in attempts to identify other genes that might contribute to the biosynthesis or regulation of (1,3;1,4)- β -glucan synthesis (Rasmussen and Shu, 2014).

Given that the Poaceae evolved relatively recently (Feuillet et al., 2008) and that (1,3;1,4)- β -glucans are largely restricted to the Poaceae in higher plants (Harris and Fincher, 2009), it seems likely that the *CslF* and *CslH* clades evolved from other clades in the cellulose synthase gene superfamily. The *CslF* and *CslH* clades are not particularly close on the phylogenetic tree (Farrokhi et al., 2006) and this suggests that genes involved in (1,3;1,4)- β -glucan synthesis might have evolved independently on at least two occasions (Fincher, 2009). Whether these evolutionary events were based on duplication and ensuing steady changes in other *Csl* genes or whether recombination caused domain swapping in enzymes that resulted in genes encoding the (1,3;1,4)- β -glucan synthases is not known. However, it is clear that some competitive advantage must be associated with the presence of (1,3;1,4)- β -glucans in walls of the Poaceae and that selection pressure has retained the capacity of enzymes encoded by *CslF* and *CslH* genes to synthesize (1,3;1,4)- β -glucans. Detailed phylogenetic analyses indicate that the *CslF* genes shared a common ancestor with *CslD* genes and are now under a stationary selection barrier (Yin et al., 2009). A stationary selection barrier would suggest that the evolution of (1,3;1,4)- β -glucans has provided functional advantages for the Poaceae.

The recent availability of the three-dimensional structure of a bacterial cellulose synthase (Morgan et al., 2013) and a molecular model of a cellulose synthase from cotton (Sethaphong et al., 2013), provide new opportunities to link evolution at the gene level with the evolution of a new enzyme with the capacity for (1,3;1,4)- β -glucan synthesis. For example, the nascent (1,3;1,4)- β -glucan synthase enzymes might have evolved by virtue of subtle changes in the three-dimensional dispositions of active site residues or through changes in surface amino acid residues that are involved in protein–protein interactions. We are now in a position to test these possibilities.

HAVE CELL WALL POLYSACCHARIDES EVOLVED A STORAGE FUNCTION?

A striking feature of some cereal grains is the highly variable amounts of (1,3;1,4)- β -glucan that they contain; this can vary from close to zero in rice to 45% w/w in the starchy endosperm of *B. distachyon* Bd21 (Guillon et al., 2011). The starchy endosperm walls of *B. distachyon* are enormously thick compared with other cereals (Figure 6). In the Bd21 line there is a concomitant drop in grain starch content from values of 60–65% that are typical for grains of the Triticeae to 6% w/w (Guillon et al., 2011). Trafford et al. (2013) specifically compared grains of *B. distachyon* Bd21 and barley in terms of cell division, cell expansion, and endoreduplication during grain development. All of these processes were

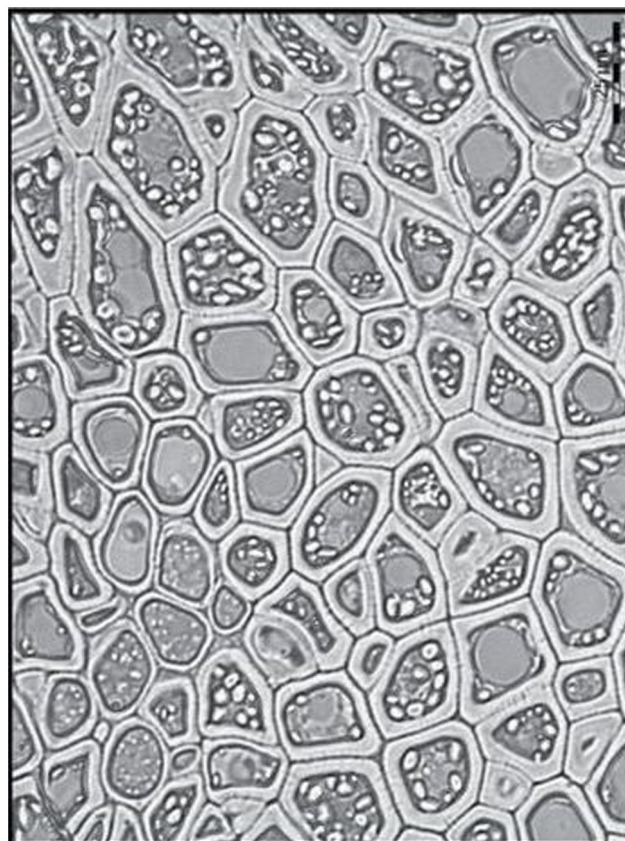


FIGURE 6 | Thick endosperm cell walls in *Brachypodium distachyon* grain. Reproduced with permission from Trafford et al. (2013).

markedly reduced in Bd21, as were transcript levels of certain cell-cycle and starch biosynthesis genes. However, transcript levels of the (1,3;1,4)- β -glucan synthase genes, notably *BdCslF6*, were not affected. This led to the hypothesis that the thick walls in *B. distachyon* grain are the result of continued accretion of (1,3;1,4)- β -glucan onto walls of cells that are not expanding (Trafford et al., 2013). Even though the endosperm walls of Bd21 are thicker, they contain a similar amount of (1,3;1,4)- β -glucan on a weight percentage of walls basis; the values are 80% w/w for Bd21 and about 70% w/w for barley endosperm walls. Trafford et al. (2013) suggested that if starch accumulation is a driver for cell expansion, as may occur in cereals such as wheat and barley, then the much lower level of starch synthesis in Bd21 may be primarily responsible for the reduced cell size and the concomitant re-direction of carbon into cell wall (1,3;1,4)- β -glucans.

The reasons for the variability of (1,3;1,4)- β -glucan content in cereal grains is not known, but it has been suggested that this polysaccharide acts as a secondary store of metabolizable glucose and that this function might be the key to the adoption of (1,3;1,4)- β -glucans during the evolution of the grasses (Burton and Fincher, 2012). It is clear that (1,3;1,4)- β -glucans are not essential structural components of cell walls in the Poaceae, because their levels are very low in some species and in many tissues of species that have high levels in their grain. It is equally clear that *B. distachyon*

uses (1,3;1,4)- β -glucans as a storage polysaccharide in its grain, where small amounts of starch are present (Guillon et al., 2011). There is also indirect evidence that (1,3;1,4)- β -glucans are used as an alternative source of metabolizable energy in the leaves of barley seedlings (Roulin et al., 2002). During daylight hours, the (1,3;1,4)- β -glucan content of the leaves is about 10% w/w, but this rapidly decreases to close to zero when the plants are placed in the dark. Levels of the degradative enzymes, (1,3;1,4)- β -glucan endohydrolase isoenzyme EI and a broad-specificity β -glucan exohydrolase, increase when the plants are placed in the dark. When the lights are turned on again, the (1,3;1,4)- β -glucans rise to initial levels (Roulin et al., 2002). It has been argued that (1,3;1,4)- β -glucans would be a better short term form of stored glucose than starch, because they require a relatively simple enzyme system for both synthesis and subsequent depolymerization, and they can be deposited in the wall without the complexities of plastidial starch granule synthesis (Burton and Fincher, 2012). Might this be the reason that (1,3;1,4)- β -glucans are concentrated near the vasculature of young barley leaves (Figure 7)?

In the majority of cereal grains that have been examined, starch is the major storage carbohydrate. In *B. distachyon* storage metabolism seems to have shifted to (1,3;1,4)- β -glucan for unknown reasons, although disadvantageous mutations in starch synthase and cell cycle genes are possible explanations (Trafford et al., 2013). Grain anatomy, morphology, and development of *B. distachyon* has been well described (Guillon et al., 2011; Opanowicz et al., 2011; Hands and Drea, 2012; Hands et al., 2012) and grain characteristics have been compared with other domesticated cereals and non-crop species (Hands et al., 2012; Trafford et al., 2013). It is clear that the use of cell wall polysaccharides as a major source of storage carbohydrate in grains and seeds is not confined to *B. distachyon*. Of the grasses, species

of *Bromus*, notably *Bromus mollis* (Hands and Drea, 2012), also possess thickened endosperm walls and a reduced starch content, suggesting that such a shift from starch to cell wall polysaccharides occurs elsewhere in the grasses but in general terms is unusual. However, a significant number of dicotyledonous seeds use cell wall polysaccharides rather than starch as the main storage medium in the endosperm (Buckeridge, 2010). These include mannans in coffee, lettuce, and tomato, glucomannan in orchids and galactomannans in legumes such as guar, fenu-greek, and carob (Campbell and Reid, 1982; McCleary et al., 1985). In other examples, cell wall arabinogalactans are found as storage reserves in lupins, and xyloglucans are found in tamarind (Kumar and Bhattacharya, 2008) and nasturtium cotyledons (Edwards et al., 1985). Again, the shift from starch to wall polysaccharides is not widespread, but is seen in isolated species or genera.

Where an alternative storage carbohydrate is found in storage tissues, one would expect to see a battery of corresponding hydrolytic enzymes expressed in the germinated grain or seed, to catalyze the efficient breakdown of the polysaccharide into component sugars for use by the growing embryo and young seedling. There is little information available on germination processes in *B. distachyon* grain but it would be interesting to see if the balance of hydrolytic enzymes has also adjusted to the paucity of starch and the dominance of (1,3;1,4)- β -glucan.

CONCLUDING REMARKS

The distinguishing features of cell walls in the grasses include the adoption of heteroxylans as the “core” non-cellulosic polysaccharide and the corresponding lower levels of xyloglucans and pectic polysaccharides. The widespread adoption of (1,3;1,4)- β -glucans in the Poaceae family also distinguishes the grasses from other monocotyledonous and dicotyledonous plants, although it is intriguing that (1,3;1,4)- β -glucans do not appear to be an essential structural component of walls in these species. One might question whether these distinguishing characteristics of cell walls of the grasses and their grain might in any way contribute to the obvious evolutionary success of the Poaceae family. It has been estimated that the grasses, which have appeared relatively recently in evolutionary history (Feuillet et al., 2008), now dominate plant ecosystems of about 20% of terrestrial land on the planet (Gaut, 2002). Does cell wall composition contribute to the ecological dominance of the grasses? Is the widespread adoption of (1,3;1,4)- β -glucans in walls of grass species and their possible function as a secondary source of metabolizable glucose important for the evolutionary success of grasses? It is clear that the (1,3;1,4)- β -glucans have appeared in other plant species, including in the walls of primitive dicots and in fungi, but they are widespread only in the Poaceae.

The non-cellulosic wall polysaccharides of plants are important components of dietary fiber and increased intake of dietary fiber has been advocated to reduce the risk of contracting serious human diseases, including colorectal cancer, type II diabetes, and cardiovascular disease (Collins et al., 2010; Burton and Fincher, 2014). Over-expression of the *HvCslF6* gene in barley led to more than 50% increases in dietary fiber in the transgenic grain (Burton et al., 2011). Given that cereal species are probably the

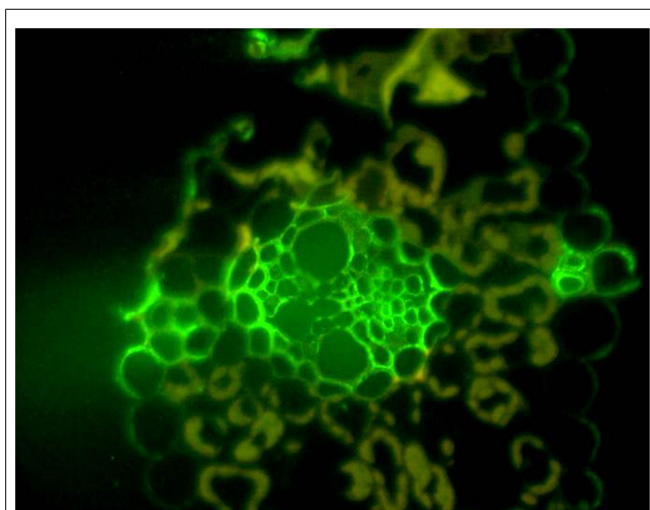


FIGURE 7 | Thin section of a young barley leaf probed with the BG1 monoclonal antibody. The high concentration of (1,3;1,4)- β -glucans can be seen around the vasculature and the polysaccharide appears to be associated with secondary cell walls of the vasculature and other cells. Reproduced with permission from Burton et al. (2011).

most important source of caloric intake on Earth, one can predict that the non-cellulosic polysaccharides of cereal grains will play an important future role in human health. Conversely, the non-cellulosic wall polysaccharides present a number of technical problems in the malting and brewing industries and in animal feedstock formulations. It is therefore likely that the genetics, cell biology, and biochemistry of these polysaccharides and the enzymes that are responsible for their synthesis will remain the subjects of research interest in the immediate future. It can also be anticipated that advances in high-throughput genomics technologies, the increasing availability of complete genome sequences, and the continuing development of *in situ* methods will greatly facilitate that research.

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The role of photosynthesis and amino acid metabolism in the energy status during seed development

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Seeds are the major organs responsible for the evolutionary upkeep of angiosperm plants. Seeds accumulate significant amounts of storage compounds used as nutrients and energy reserves during the initial stages of seed germination. The accumulation of storage compounds requires significant amounts of energy, the generation of which can be limited due to reduced penetration of oxygen and light particularly into the inner parts of seeds. In this review, we discuss the adjustment of seed metabolism to limited energy production resulting from the suboptimal penetration of oxygen into the seed tissues. We also discuss the role of photosynthesis during seed development and its contribution to the energy status of developing seeds. Finally, we describe the contribution of amino acid metabolism to the seed energy status, focusing on the Asp-family pathway that leads to the synthesis and catabolism of Lys, Thr, Met, and Ile.

Keywords: seed development, metabolism and bioenergetics, photosynthesis, branched chain amino acids, TCA cycle

INTRODUCTION

Seeds are the major organ responsible for the evolutionary upkeep of the plant lineage. They store the genetic material of the plant within the embryo, thus guaranteeing continuation of the plant's life cycle in the next generation. Seed development is highly regulated, with distinct transcript, protein and metabolite switches occurring in a concerted manner throughout its progression (Fait et al., 2006; Sreenivasulu et al., 2008; Xu et al., 2008; Angelovici et al., 2010). Seeds produce a great variety of storage compounds, among them a myriad of carbohydrates (especially starch), storage proteins, and storage lipids. These provide – both directly in the form of food and indirectly in the form of feed ~70% of the world's human caloric intake (Sreenivasulu and Wobus, 2013). Storage metabolites are subsequently used as nutrient and energy sources to support early stages of seed germination, while the seedling is still heterotrophic. Production of storage compounds whose generation by respiration becomes limiting due to a limitation of oxygen penetration into the dense seed tissues requires a considerable amount of energy. The requirement for oxygen and hence energy production becomes particularly critical during reserve metabolites accumulation and seed desiccation, in which the dense seed tissues limit the oxygen penetration and thus limit mitochondrial energy production (Weber et al., 2005; Angelovici et al., 2010). Photosynthesis in green seeds, and other energy conservation mechanisms, such as a decrease of overall respiration rates during embryo development, somewhat relieve the major drop in energy demand, but do not sufficiently compensate for the energy requirement (Weber et al., 2005; Angelovici et al., 2010). In seeds of the model plant *Arabidopsis thaliana*, amino acid metabolism is modulated so that many amino acids are synthesized and accumulated during seed desiccation (Fait et al., 2006). In recent years, several lines of evidence have implied

that amino acids are not only used for the synthesis of storage proteins, but also, upon energy demand, can be catabolized and their catabolic products fed into the TCA cycle to generate energy (Zhu and Galili, 2004; Angelovici et al., 2010; Galili, 2011). This was also shown for plants exposed to extended darkness, another condition characterized by energy deprivation (Ishizaki et al., 2005, 2006; Araujo et al., 2010). In this mini-review, we describe lines of evidence demonstrating the contribution of photosynthesis and amino acid metabolism to the energy production in developing seeds and the contribution of amino acid catabolism to the energy status of seedlings exposed to extended darkness.

DEVELOPING SEEDS FACE AN EXTREME SHORTAGE OF ENERGY DUE TO LIMITED PENETRATION OF OXYGEN, PARTICULARLY INTO THE INNER SEED PARTS

Since developing seeds are quite dense, they suffer from limited penetration of oxygen, particularly into the inner seed tissues. The shortage of oxygen extensively limits energy-requiring metabolic processes crucial for seed development and embryo maturation (Vigeolas et al., 2003, 2011; van Dongen et al., 2004). In developing seeds of dicotyledonous (dicot) plant species, photosynthesis in the developing embryo contributes a considerable amount of oxygen to the seed tissue, which further fuels energy-generating biochemical pathways, such as glycolysis and respiration (Rolletschek et al., 2003; Ruuska et al., 2004; Borisjuk et al., 2005; Tschiersch et al., 2011, 2012). This is in contrast to developing non-green seeds of monocotyledonous (monocot) plants that do not generate energy via photosynthesis, and hence must depend on alternative energy-generating metabolic processes in addition to glycolysis and respiration in order to fuel seed development. The chemical donors for energy-generation are hypothetically

produced in the vegetative parts of the plant, using particularly energy derived from photosynthesis, and are transported to the developing seeds (van Dongen et al., 2004). A number of different metabolites produced in the vegetative tissues are transported to the seeds; however, at a quantitative level, the amino acid Asn, which accumulates to relatively high levels during senescence, is particularly notable as a major energy source (Credali et al., 2013). Its role as an energy donor occurs via the conversion of Asn into Asp, the direct precursor of the branched Asp-family pathway (Figure 1). The Asp-family pathway synthesizes the amino acids Lys, Thr, Met, and Ile, which, under conditions of energy shortage, are further catabolized by the TCA cycle to generate energy (Galili, 2011). An energy shortage does not occur only in seeds, but also in vegetative tissues that lack photosynthesis, and upon exposure of plants to extended darkness. Under these energy shortage conditions, Lys is directly catabolized into the TCA cycle, while Thr and Met are converted into Ile, which is then directly catabolized into the TCA cycle (Joshi et al., 2006; Araujo et al., 2010). We focus in this review on the catabolism of Lys and Ile in respect to the contribution of amino acid catabolism to the energy status either during seed development or upon exposure to extended darkness.

CONTRIBUTION OF SEED PHOTOSYNTHESIS TO OXYGEN AVAILABILITY IN DEVELOPING SEEDS

A significant amount of information on the role of seed photosynthesis for the synthesis of seed reserve compounds has been gathered at the IPK Institute for Plant Genetics in Gatersleben Germany (<http://www.ipk-gatersleben.de/en/>), where they analyzed developing soybean seeds, which possess active seed photosynthesis (Rolletschek et al., 2003; Ruuska et al., 2004; Borisjuk et al., 2005; Tschiersch et al., 2011, 2012). Light intensity and oxygen level progressively decrease with a progressive increase in seed depth (Vigeolas et al., 2003). Oxygen level is highest in light illuminated seeds, progressively lower in seeds that are not illuminated and lowest in seeds exposed to darkness. The ATP/ADP ratio is markedly higher in developing seeds exposed to light, indicating that photosynthesis in illuminated seeds contributes to the production of energy (Borisjuk et al., 2005). These results indicate that photosynthesis, which produces oxygen, significantly contributes to the energy status of developing seeds. Interestingly, in an independent study, overexpression of hemoglobin 2 in *Arabidopsis* seeds improved the energy status of seeds under low oxygen conditions and led to an increase in the fatty acid content of developing and mature seeds, further emphasizing the importance of oxygen availability during seeds development (Vigeolas et al., 2011). Photosynthesis could also be important in relatively large seeds, such as soybean seeds, whose inner cell layers receive significantly lower oxygen levels than the outer seed tissues. Borisjuk et al. (2005) demonstrated that developing dicot seeds with green embryos display a reduction in photosynthetic activity during development, starting from the interior of the embryo. This indicates the contribution of this photosynthetic activity to seed energy status.

Photosynthesis encompasses two different reactions, namely: (i) the light reactions that lead to reduction of NADP to NADPH and create a proton gradient across the chloroplast membrane

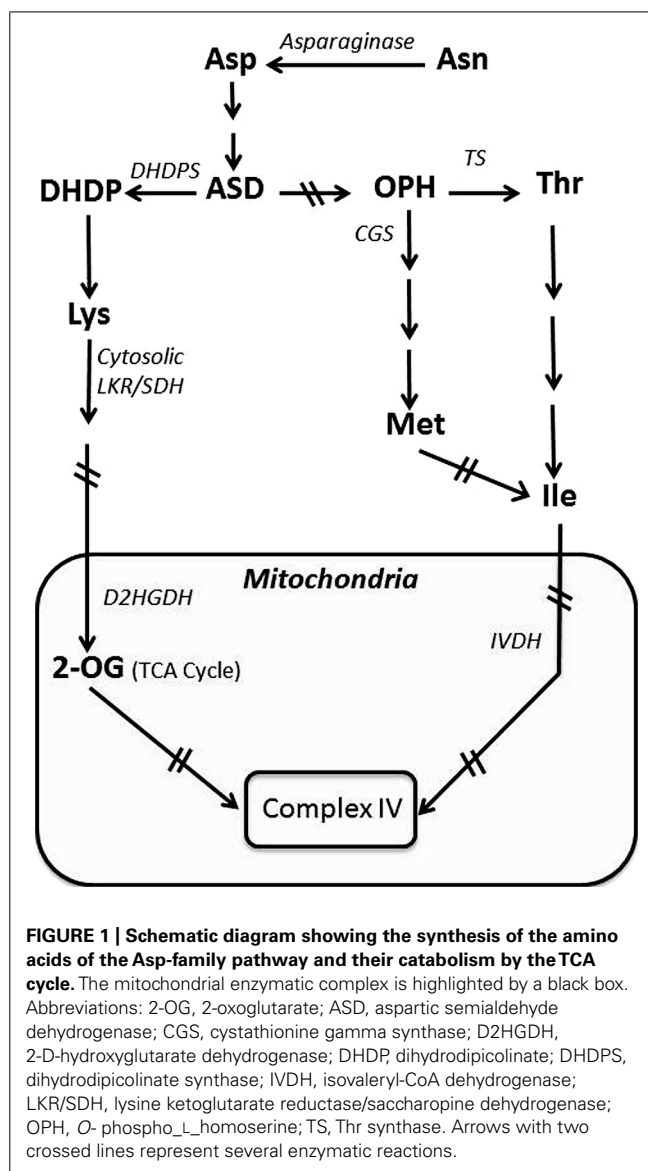


FIGURE 1 | Schematic diagram showing the synthesis of the amino acids of the Asp-family pathway and their catabolism by the TCA cycle. The mitochondrial enzymatic complex is highlighted by a black box. Abbreviations: 2-OG, 2-oxoglutarate; ASD, aspartic semialdehyde dehydrogenase; CGS, cystathionine gamma synthase; D2HGDH, 2-D-hydroxyglutarate dehydrogenase; DHDP, dihydrodipicolinate; DHPS, dihydrodipicolinate synthase; IVDH, isovaleryl-CoA dehydrogenase; LKR/SDH, lysine ketoglutarate reductase/saccharopine dehydrogenase; OPH, O-phospho-L-homoserine; TS, Thr synthase. Arrows with two crossed lines represent several enzymatic reactions.

that is used for ATP synthesis; and (ii) the light-independent reactions in which RuBisCO fixes CO₂ from the atmosphere in a NADPH-requiring process, and the Calvin–Benson cycle produces sugars (Buchanan et al., 2000). Interestingly, developing oilseed rape (*Brassica napus* L) embryos possess active photosynthesis, and RuBisCO acts in a special metabolic context without the Calvin–Benson cycle in order to improve the efficiency of carbon utilization during the synthesis of oil storage (Schwender et al., 2004a). This special pathway generates 20% more acetyl-CoA, a precursor for fatty acid biosynthesis, in comparison to glycolysis and saves 40% of the carbon that would otherwise be lost as CO₂.

CONTRIBUTION OF AMINO ACID METABOLISM TO THE ENERGY STATUS OF DEVELOPING SEEDS

Amino acids are constituents of proteins and hence essential components for the life of all organisms. Yet, in response to specific

developmental and stress-associated conditions, amino acids also serve as energy donors through their catabolism in the TCA cycle (Araujo et al., 2010; Angelovici et al., 2011; Kirma et al., 2012). In vegetative tissues, photosynthesis is the major source of energy during daytime, and thus during daytime amino acids are used for the synthesis of proteins and, as precursors of multiple secondary metabolites (Less and Galili, 2008). Yet, during night-time or in response to stresses that cause major energy shortages due to the lack of or reduction in photosynthesis, amino acids also serve as important energy sources through their catabolism via the TCA cycle (Araujo et al., 2011). Therefore, the contributions of amino acid catabolism to the energy status requirements of developing seeds appears even more critical than in vegetative tissues, due to the limits of oxygen diffusion.

CONTRIBUTION OF Lys SYNTHESIS AND CATABOLISM IN THE TCA CYCLE TO SEED ENERGY STATUS

Insight into the potential importance of Lys catabolism to the energy status of developing seeds was obtained in research aiming to enhance the nutritional quality of seeds by increasing Lys accumulation (Zhu and Galili, 2003). Lys is an essential amino acid that serves a vital role in human food and livestock feed, since humans and some livestock (such as chicken and pigs, i.e., mono-gastric livestock) are unable to synthesize Lys (Kirma et al., 2012). The synthesis of Lys in plants (**Figure 1**) is subject to post-translational regulation, where increasing Lys feedback inhibits the activity of dihydrodipicolinate synthase (DHDPS), which catalyzes the first committed step in the Lys biosynthetic branch of the Asp-family pathway. Plants possess two DHDPS isozymes (DHDPS1 and DHDPS2), with DHDPS2 accounting for the majority of the total DHDPS activity (Jones-Held et al., 2012). Because Lys is an essential amino acid, an attempt was made to increase Lys in seeds of the model plant *Arabidopsis*, using a recombinant gene encoding in a seed-specific manner a mutant bacterial DHDPS2 enzyme insensitive to Lys feedback inhibition (Zhu and Galili, 2003). This approach yielded only a relatively mild increase in seed Lys, leading to the hypothesis that this amino acid is not an end product metabolite, but rather might be catabolized in the TCA cycle to generate energy. To test this hypothesis, the same bacterial feedback-insensitive DHDPS was expressed in seeds of a transgenic *Arabidopsis* genotype that lacks the capacity for Lys catabolism due to a knockout mutation in the gene encoding the bi-functional enzyme lysine-ketoglutarate reductase/saccharopine dehydrogenase (LKR/SDH), which contains the first two enzymes of Lys catabolism linked as a single polypeptide. In this combined genotype, seed Lys content was nearly 1000-fold higher than wild type (WT), indicating that developing seeds have a strong flux of Lys synthesis as well as catabolism into the TCA cycle (Zhu and Galili, 2003).

Developing seeds possessing significantly enhanced Lys levels due to increased Lys synthesis and suppression of Lys catabolism also exhibited notable differences in their transcriptomes and primary metabolomes, indicating that Lys metabolism (synthesis and catabolism) is well connected to the TCA cycle (Angelovici et al., 2009, 2011). For example, compared to WT, the levels of the TCA cycle metabolites fumarate, citrate, and ketoglutarate

are lower in the genotype possessing enhanced Lys synthesis and a block of Lys catabolism, compared to the wild-type, genotype (Angelovici et al., 2009, 2011). Lys catabolism into the TCA cycle is apparently used to generate energy essential for seed development. As shown in **Figure 1**, Lys is not the only amino acid of the Asp-family pathway that feeds into the TCA cycle. A second branch of the Asp-family pathway leads to the synthesis of Thr and Met, which are further metabolized into Ile, which also feeds into the TCA cycle and serves as a major substrate for energy generation (Joshi et al., 2006; Kochevenko and Fernie, 2011).

In the developing seed, the upstream substrate that feeds the Asp-family pathway on route to the TCA cycle is Asn. Asn is transported from vegetative tissues to developing seeds where it is converted by asparaginase into Asp, the starting point metabolite of the Asp-family pathway (**Figure 1**; Credali et al., 2013). Indeed, the asparaginase level is generally stimulated during early seed development (Dickson et al., 1992; Credali et al., 2013).

AMINO ACID CATABOLISM FACILITATES RESPIRATION UNDER STRESS CONDITIONS

Under normal conditions, respiration depends on the oxidation of carbohydrates. However, during situations in which carbohydrate supply is limited, the plant cell can modify its metabolism to utilize alternative respiratory substrates. Among these substrates are proteins. Protein degradation is a highly regulated process, involving a multitude of cellular reactions, such as ubiquitinylation and degradation *via* the proteasome, the autophagy machinery and nutrient sensing by the TOR pathway. The product of protein degradation, free amino acids, can be further catabolize to generate energy (ATP; Zhu and Galili, 2003; Joshi et al., 2006; Araujo et al., 2011; Kochevenko and Fernie, 2011). Indeed, it has been shown that under abiotic stress there is increased transcription of amino acid catabolic genes (Less and Galili, 2008).

In mammals, the mitochondrial protein, electron-transfer flavoprotein:ubiquinone oxidoreductase (ETFQO), accepts electrons from electron transfer flavoprotein (ETF) to reduce ubiquinone. ETF serves as an obligatory electron acceptor for nine mitochondrial flavoprotein dehydrogenases. The ETF/ETFQO system facilitates electron transfer from these flavoprotein dehydrogenases to the main respiratory chain (Ishizaki et al., 2005, 2006). Homologs of ETF and ETFQO have been characterized in plants, as well as two flavoprotein dehydrogenases: isovaleryl-CoA dehydrogenase (IVDH) and 2-D-hydroxyglutarate dehydrogenase (D2HGDH; Ishizaki et al., 2005, 2006; Araujo et al., 2010). T-DNA insertion mutants of each of these genes display increased sensitivity to prolonged darkness, a condition that leads to carbon starvation. In addition, metabolic analysis of these mutants under prolonged darkness revealed an accumulation of several amino acids and an intermediate metabolite of Leu catabolism in comparison to WT. These results suggest a role for amino acid catabolism in supplying respiratory intermediates during carbon starvation (**Figure 2**; Ishizaki et al., 2005, 2006). It has been demonstrated that IVDH is apparently predominantly responsible for the transport of electrons from breakdown products of phytol and branched-chain amino acids (BCAA: Ile, Leu, and Val), while D2HGDH

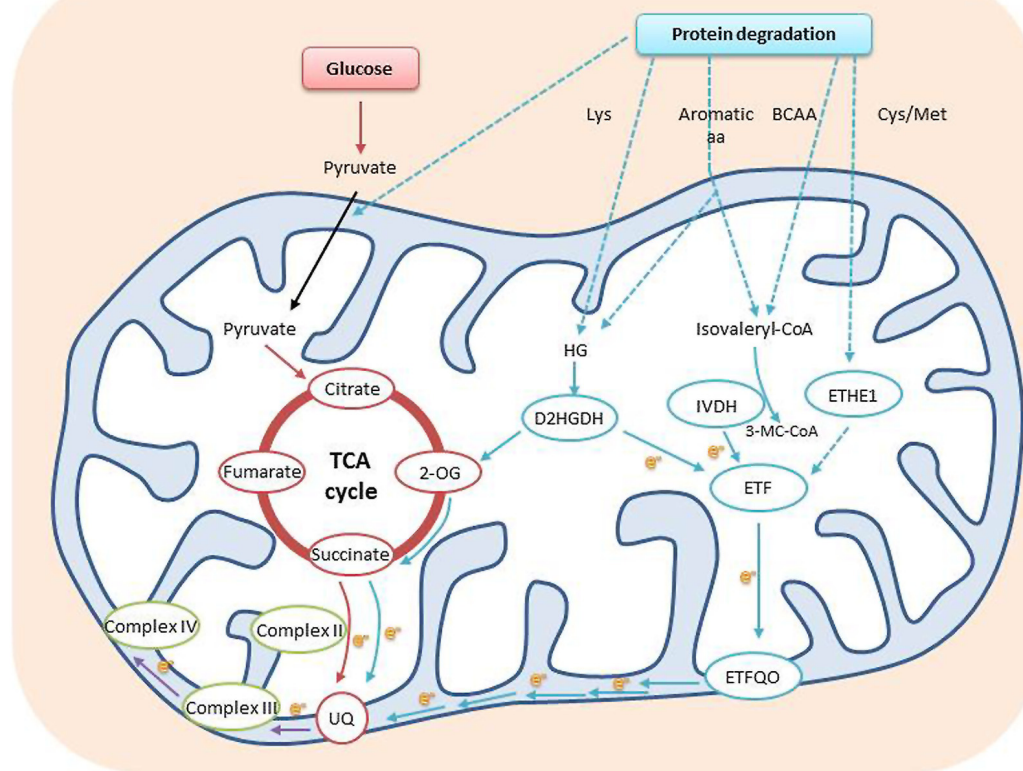


FIGURE 2 | Amino acids can be used as electron donors to the mitochondrial electron transport chain. Protein degradation yields a range of amino acids that are further metabolized either into isovaleryl-CoA or HG. Isovaleryl-CoA can be produced by catabolism of the branched chain and aromatic amino acids and by both phytol and Lys degradation, whereas HG can be produced by aromatic amino acid degradation or from the Lys derivative L-pipecolate. The electrons generated are transferred to the respiratory chain through to the ubiquinol pool via an ETF/ETFQO system. Possible involvement of sulfur containing amino acids has also been implicated by the phenotype of ETHE1 knockdown plants. Some amino acids can facilitate energy production via the TCA cycle,

either by conversion to pyruvic acid or acetyl-CoA or by direct conversion to TCA cycle intermediates, such as 2-OG, and direct electron supply to the ubiquinol pool of the mitochondrial electron transport chain in plants. Dotted arrows represent possible transport processes and multi enzymatic reactions. Abbreviations: BCAA, branched chain amino acids; D2HGDH, 2-D-hydroxyglutarate dehydrogenase; e⁻, electron; ETF, electron transfer flavoprotein; ETFQO, ETF:ubiquinol oxidoreductase; ETHE1, ethylmalonic encephalopathy protein1; HG, hydroxyglutarate; IVDH, isovaleryl-CoA dehydrogenase; 3-MC-CoA, 3-methylcrotonyl-CoA; 2-OG, 2-oxoglutarate; TCA cycle, tricarboxylic acid cycle; UQ, ubiquinol (Adapted from Araujo et al., 2011; Krüssel et al., 2014).

is responsible for the transport of electrons from breakdown products of Lys (Figure 2). This last finding is interesting, as it demonstrates the ability of Lys degradation products to contribute electrons directly to the mitochondrial electron transport chain, as well as supply intermediates to the TCA cycle (Araujo et al., 2010).

Although a direct role for the ETF/ETFQO system in seed development has not yet been demonstrated, considerable experimental evidence has accumulated to support this hypothesis. First, the existence of hypoxic conditions and lack of photosynthesis in some seeds point to the need for alternative electron donors in seeds for the mitochondrial electron transport chain. Secondly, analysis of a mutant with high levels of 12 out of the 20 amino acids in seeds was shown to be IVDH defective, further strengthening the role of this enzyme in the regulation of free amino acid homeostasis during seed development (Gu et al., 2010). Thirdly, a recent publication highlighted the role of BCAT2, a BCAA catabolic enzyme,

in establishing the variation of BCAA levels in different *Arabidopsis* accessions (Angelovici et al., 2013). BCAT2 was shown to localize in the mitochondria, and its expression was shown to increase during seed development, suggesting the involvement of BCAA catabolism in seed development, possibly via the ETF/ETFQO system (Angelovici et al., 2013). Additional evidence suggesting the involvement of the ETF/ETFQO system in seed development was obtained using genetic manipulation of amino acid delivery to pea (*Pisum sativum*) embryos. When an increase of amino acid delivery was induced, transcripts of the ETF complex were most highly induced (Weigelt et al., 2008). It is important to note that *etf* and *etfqo* mutants display lower seed set and shorter siliques when grown under long day conditions (Ishizaki et al., 2005, 2006). This phenotype is attributed to the maternal tissue, as demonstrated by reciprocal crosses of *etfqo* mutants and WT plants (Ishizaki et al., 2005). Another finding strengthening the role of the ETF/ETFQO system in seed development is

a recent publication describing ETHE1, a mitochondrial sulfur dioxygenase. ETHE1 is a matrix protein that has been shown to be involved in the detoxification of sulfur compounds derived from sulfur-containing amino acids (Cys and Met). A complete knockout of ETHE1 is embryo lethal and ETHE1 knockdown plants are viable, but present a delay in seed development. Surprisingly, ETHE1 knockdown plants display higher sensitivity to carbon starvation, reminiscent of the ETF/ETFQO system T-DNA mutants (**Figure 2**) and have been shown to accumulate BCAA under these conditions. These data suggest a possible role for ETHE1 in the ETF/ETFQO system as well as hinting at the importance of the enzyme, *per se*, during seed development (Krüssel et al., 2014).

In summary, in this review we discussed a number of studies that have enhanced our understanding of the parallel roles of photosynthesis and amino acid-derived respiratory catabolic processes in meeting the demands for normal energy status during seed development. In respect to amino acids, we focused on Lys degradation and highlighted the involvement of the ETF pathway. Technical advances, including improved understanding of sub-cellular compartmentization of metabolism (Sweetlove and Fernie, 2013), alongside mathematical approaches to understand whole plant physiology as well as metabolite-metabolite associations (Toubiana et al., 2012; Grafahrend-Belau et al., 2013) are now available. These will greatly enhance our understanding of these enzymatic processes. Furthermore, metabolite imaging techniques, such as genetically encoded metabolite sensors (Okumoto et al., 2012), nuclear magnetic imaging (Borisjuk et al., 2013), and flux profiling techniques (Schwender et al., 2004b), alongside miniaturization of respiration measurements (Sew et al., 2013), will additionally enhance our understanding of the shifts in plant energy metabolism that occur during the process of seed development. Our potential to metabolically engineer seeds in a highly tailored manner will be radically improved once such information is available and integrated with our current knowledge.

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Proteome balancing of the maize seed for higher nutritional value

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Most flowering plant seeds are composed of the embryo and endosperm, which are surrounded by maternal tissue, in particular the seed coat. Whereas the embryo is the dormant progeny, the endosperm is a terminal organ for storage of sugars and amino acids in proteins and carbohydrates, respectively. Produced in maternal leaves during photosynthesis, sugars, and amino acids are transported to developing seeds after flowering, and during germination they nourish early seedlings growth. Maize endosperm usually contains around 10% protein and 70% starch, and their composition ratio is rather stable, because it is strictly regulated through a pre-set genetic program that is woven by networks of many interacting or counteracting genes and pathways. Endosperm protein, however, is of low nutritional value due mainly to the high expression of the α -zein gene family, which encodes lysine-free proteins. Reduced levels of these proteins in the *opaque 2* (*o2*) mutant and α -zein RNAi (RNA interference) transgenic seed is compensated by an increase of non-zein proteins, leading to the rebalancing of the nitrogen sink and producing more or less constant levels of total proteins in the seed. The same rebalancing of zeins and non-zeins has been observed for maize seeds bred for 30% protein. In contrast to the nitrogen sink, storage of sulfur is controlled through the accumulation of specialized sulfur-rich proteins in maize endosperm. Silencing the synthesis of α -zeins through RNAi fails to raise sulfur-rich proteins. Although overexpression of the methionine-rich δ -zein can increase the methionine level in seeds, it occurs at least in part at the expense of the cysteine-rich β - and γ -zeins, demonstrating a balance between cysteine and methionine in sulfur storage. Therefore, we propose that the throttle for the flow of sulfur is placed before the synthesis of sulfur amino acids when sulfur is taken up and reduced during photosynthesis.

Keywords: nitrogen, lysine, sulfur, storage proteins, RNAi

STORAGE PROTEINS IN MAIZE SEED

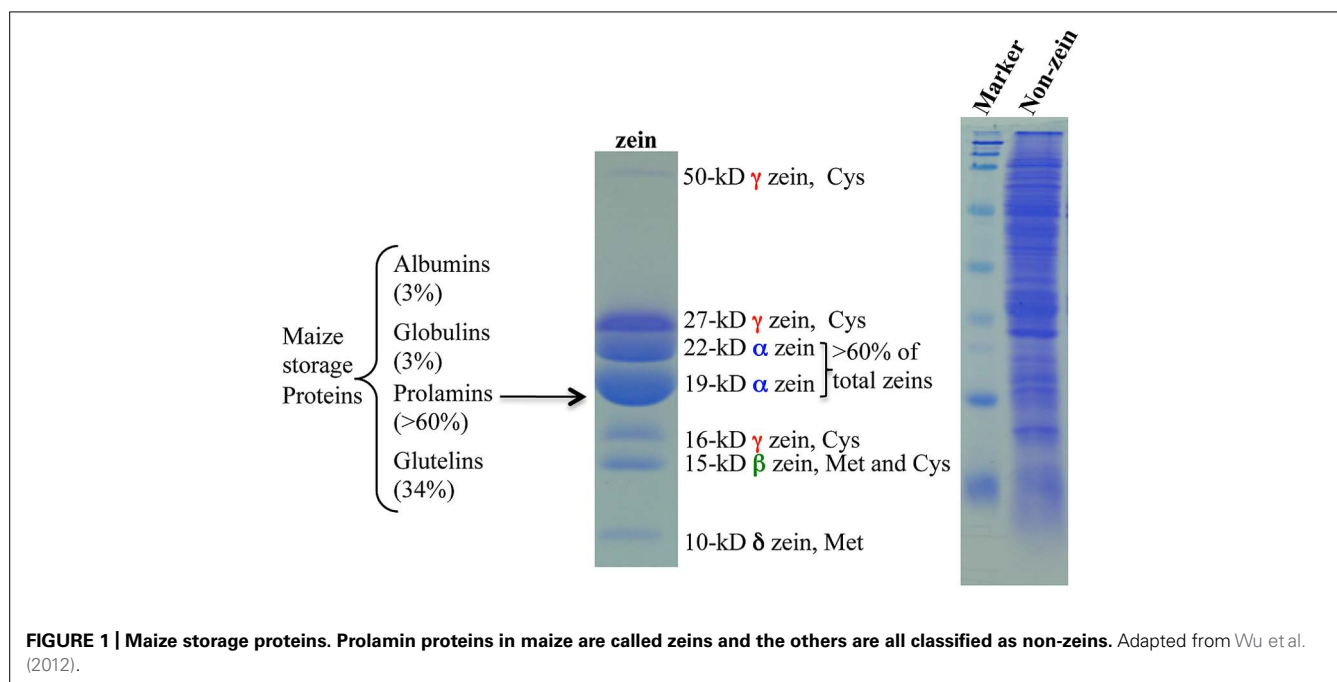
Angiosperm seeds result from double fertilization and are usually the primary mode of reproduction. Besides their vital biological function, seeds are the most frequently harvested organs in agriculture. Therefore, their production has tremendous economic importance for humans and livestock. For this reason, maize has become one of the most productive cereal crops in the world in respect to yield per acreage. Maize seeds mainly consist of endosperm and embryo, which account for 90 and 10%, respectively, of the whole dry seed weight (Flint-Garcia et al., 2009). Starch and protein are mainly stored in endosperm, whereas most of the oil accumulates in the embryo.

Maize seeds contain ~10% proteins and ~70% of them are classified as storage proteins (Flint-Garcia et al., 2009). Based on their solubility in different solvents, endosperm proteins are divided into four groups: albumins, globulins, glutamines, and prolamins. The latter, called zeins, make up > 60% of total proteins (Figure 1). Zeins can be divided into four subfamilies, α (19 and 22 kDa), γ (50, 27, and 16 kDa), β (15 kDa), and δ (18 and 10 kDa; Esen, 1987; Coleman and Larkins, 1998; Figure 1). A common feature of all prolamins is internal tandem variable repeats of blocks of amino acids with primarily

proline and glutamine, as first observed in a maize α -zein (Geraghty et al., 1981). Because of this feature, α -zeins lack essential amino acids like lysine, methionine, and tryptophan. Due to the high expression of α -zein genes in maize endosperm, the final levels of these three essential amino acids in total protein are very low (Osborne and Mendel, 1914). Therefore, maize cannot serve as a balanced dietary protein source for humans and monogastric animals and has to be supplemented with these amino acids, raising the cost of food supply worldwide (Mertz et al., 1964). Interestingly, the level of one amino acid, methionine, can reach sufficient levels in some cultivars, making supplements redundant (Messing and Fisher, 1991). The reason for this is that minor zeins, β , γ , and δ , have a high proportion of sulfur-rich amino acids and can vary in expression levels among maize cultivars. The δ -zeins are very rich in methionine, whereas the γ -zeins are abundant in cysteine; β -zein has high percentages of cysteine and methionine, while α -zeins lack both of them (Wu et al., 2012).

PROTEOME BALANCING IN MAIZE ENDOSPERM

Maize domestication from its wild ancestor, teosinte, can be traced back to the Tehuacan Valley of Mexico as early as 8,000 years ago.



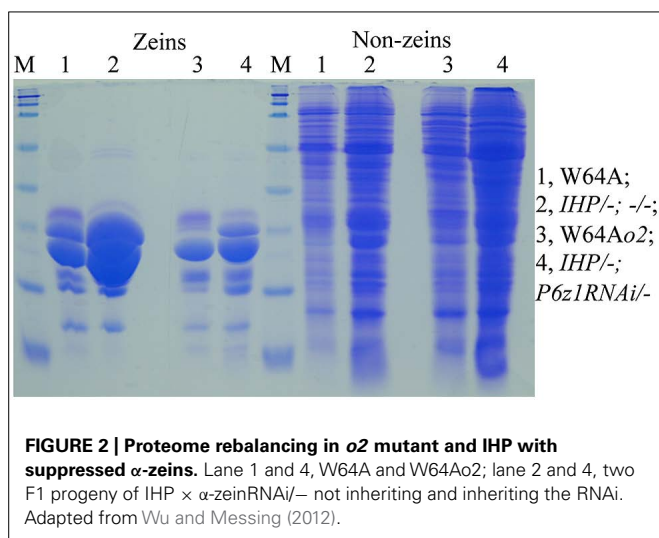
During this process, teosinte underwent dramatic changes, not only in plant morphology, but also in seed composition (Flint-Garcia et al., 2009). Teosinte contains ~30% protein and has a high level of the methionine-rich δ -zeins (Swarup et al., 1995), but modern maize has only ~10% total protein and a low level of methionine-rich proteins in cultivars grown for consumption. Although one can achieve among all crops the highest yields of grain with maize, its protein level is much lower than soybean, which contains ~35% protein with sufficient lysine levels.

To investigate whether artificial selection can significantly change seed compositions, a long-term selection experiment has been carried out for more than one century at the University of Illinois. This has yielded four strains with substantially different protein levels: Illinois high protein (IHP), Illinois low protein (ILP), Illinois high protein reverse (IHPR), and Illinois low protein reverse (ILPR) with protein levels of 30, 4, 7, and 15%, respectively (Hopkins, 1899; Dudley and Lambert, 2004; Moose et al., 2004; Dudley, 2007). However, elevated protein levels are mainly due to zeins, which of course lack lysine (Osborne and Mendel, 1914). Therefore, IHP contains even relatively lower lysine levels (Lys_{rel}) than those in normal maize (Wu and Messing, 2012).

An unexpected finding was when zein levels are lowered by the *opaque-2* mutation the relative lysine content was improved to a nearly sufficient level. This mutation affects an endosperm-specific transcription factor belonging to the bZIP family that is required for transactivation of several zein gene subfamilies (Schmidt et al., 1992; Cord Neto et al., 1995). The reduction in zein gene expression results in seeds with an opaque appearance. In the *o2* mutant, the main zein components, the α -zeins, are reduced by more than 60% in certain inbred lines. However, the total protein level remains almost unchanged by a compensatory increase of non-zein proteins with higher lysine levels (Holding and Larkins, 2009). As a consequence, the percentage of overall

lysine is elevated. This compensation phenomenon indicates that nitrogen storage is controlled at the level of protein synthesis, leading to a more or less constant amount of total protein. However, as *o2* is recessive, pleiotropic and its penetration can vary in different α -zein haplotypes (Song and Messing, 2003), this trait requires two parental lines that are homozygous for *o2* and have additional QTLs for seed quality for hybrid seed production. Such QTLs, namely *o2* modifiers, are required to convert the starchy *o2* endosperm, which is unfavorable for storage and transport of large volumes of maize, to a hard kernel texture. This modified *o2* maize mutant is known as “Quality Protein Maize” or QPM (Vasal et al., 1980; Holding et al., 2008). Because of the loss of the opaque phenotype in QPM, it becomes difficult for breeders to maintain *o2* homozygosity through visual scoring. To simplify QPM breeding, high lysine maize lines can be created with RNA interference (RNAi) mutants, which reduce α -zein mRNA in a dominant and more targeted fashion. However, in the absence of *o2* modifiers, the resulting transgenic seeds also present an opaque phenotype (Segal et al., 2003; Huang et al., 2006; Wu and Messing, 2011).

Although QPM has a hard endosperm and contains higher lysine than normal (Vasal et al., 1980), the total protein levels are still lower than in soybeans (Prasanna et al., 2001). If one could create maize lines that rival the nutritional quality of soybeans being high-protein and high-lysine, while having a hard-endosperm texture, one could investigate whether total protein could also be rebalanced by the mechanism operating in IHP. Indeed, when an α -zein RNAi event was crossed with IHP, the total protein level was maintained, although zeins were substantially reduced. Consequently, the non-zein fraction was dramatically increased to compensate for the loss of zeins (Figure 2). Moreover, suppression of zeins with an α -zein RNAi is incomplete, leaving a



considerable amount of residual zeins that provide a hard vitreous endosperm texture without the need for *o2* modifiers (Wu and Messing, 2012).

What could be the mechanism underlying rebalancing the seed proteome? Sugars and amino acids produced during photosynthesis are transported to seeds for deposition as starch and protein. It seems that developing maize seeds possess compensatory mechanisms that sense protein content when zein synthesis is interrupted, leading to translation of other mRNAs instead of zein mRNAs. This transfer of ribosomes to a different mRNA pool could be as simple as mass action, or involve an intracellular signal transduction to attain a predetermined protein level. Such signal transduction would likely occur, although not exclusively, at the transcriptional, posttranscriptional or translational levels (Frizzi et al., 2010; Jia et al., 2013). No matter how proteome rebalancing operates to alter seed composition, breeders had to take a long-term selection approach to accumulate QTLs to regulate this tightly controlled program (Dudley and Lambert, 2004). When synthesis of soybean's major storage proteins, glycinin and conglycinin, were suppressed in knockdown mutant lines, the seeds maintained nearly identical levels of total protein compared to the untransformed soybean cultivars, with similar seed size and weight (Schmidt et al., 2011), suggesting that proteome rebalancing in seeds might be a rather common event, providing a constant sink for reduced nitrogen during seed maturation. In addition, plant seeds seem to possess the ability to overcome a protein shortage by remodeling their protein composition for use during germination and early seedling growth. Profiling non-zein accumulation in *o2* and α -zeinRNAi mutants appears to follow two distinct patterns, with an overall slight increase of proteins in general and significant overexpression of several specific proteins (Holding and Larkins, 2009; Wu et al., 2012; Jia et al., 2013). Among the specifically enhanced expressed proteins, eIF2 and GAPDH have been identified as high-lysine containing proteins, which were thought to add a substantial contribution to the overall lysine elevation (Habben et al., 1993, 1995; Jia et al., 2013). However, what regulates their expression when zeins are suppressed remains unclear.

SULFUR REBALANCING IN MAIZE ENDOSPERM

Sulfur amino acid deficiency differs from lysine deficiency in several ways. The essential amino acid methionine is the only amino acid that is currently chemically synthesized for supplementation of animal feed, because even soybean proteins do not provide sufficient levels in a dietary ration. However, in contrast to lysine, maize produces β - and δ -zein proteins that are very high in methionine residues. But in most maize inbreds, they just do not accumulate at sufficient levels although it has been shown that increased levels of sulfur in the soil can increase synthesis of sulfur-rich proteins in peas (Beach et al., 1985). Screens of seeds from different maize genetic backgrounds by germinating in the presence of lysine and threonine (LT) resulted in the discovery of one LT-resistant line (Phillips, 1985), where the δ -zein gene, rich in methionine codons, was overexpressed (Kirihaara et al., 1988). It also was shown that this differential expression was subject to parental imprinting in hybrid crosses (Chaudhuri and Messing, 1994). This high δ -zein line was sufficient to replace synthetic methionine in a regular feed for chickens, with a direct impact on weight and feather quality (Messing and Fisher, 1991). Interestingly, the high expression of the δ -zein gene is not due to transcription, but rather to post-transcriptional regulation of its mRNA (Schickler, 1993). In fact, it appears that the regulation occurs via the un-translated regions (UTRs) of the mRNA, which was shown in transgenic seeds when the δ -zein mRNA UTRs were replaced by other sequences (Lai and Messing, 2002).

The allele-specific regulation of the methionine content, however, would unlikely be a pathway for rebalancing protein composition in seeds. In fact, high-lysine maize lines, like the *o2* mutant, where lysine-free α -zein proteins are reduced with a compensatory increase of other proteins, have failed to show any increase but rather somewhat of a decreased methionine level (Mertz et al., 1964; Phillips, 1985; Wu et al., 2012). This could also be an effect on the transcription of δ -zeins by *O2* itself, as it also regulates another methionine-rich zein gene, the β -zein. Indeed, in knock-out mutants of δ -zeins in combination with a knock-down of β -zein, the accumulation of methionine is 40% less than that in normal maize lines (Wu et al., 2012). To eliminate the pleiotropic effects of *O2* and only reduce the expression of α -zeins, methionine levels were also evaluated in the presence of α -zein RNAi. In this case, the methionine level did not increase along with lysine, showing that non-zein proteins are not as rich in sulfur amino acids as in lysine. Indeed, only 8% of the proteins in the maize protein database have methionine residues above 4%, while about 57% have lysine residues above 4% (Wu et al., 2012). Therefore, it appears that the sink for reduced nitrogen and sulfur operate differently during seed development.

There is no apparent inferior kernel phenotype in high-methionine maize, in contrast to high-lysine α -zein RNAi maize, indicating that single gene manipulation could add a stable trait without agronomic compromises. Indeed, after several backcrosses of the chimeric δ -zein gene to a maize line that is low in methionine, overexpression of the 10-kDa zein gene remained stable (Lai and Messing, 2002). However, the transgenic line exhibited an interesting biochemical difference compared to normal maize (Wu et al., 2012). Unexpectedly, the accumulation of cysteine-rich

γ - and β -zeins was dramatically suppressed (**Figure 3**). A recent study also found that selecting high-methionine variants from a maize population apparently resulted in low accumulation of the cysteine-rich 27-kDa γ -zein (Newell et al., 2014). These results suggest that increased methionine storage requires increased flow of reduced sulfur from cysteine to methionine, thereby reducing the translation of 27-kDa γ -zein mRNA. However, this shift could also be achieved with RNAi against γ - and β -zeins.

Perhaps, this could be explained as follows. Methionine and cysteine are the only two sulfur-containing amino acids among the twenty protein-containing L-amino acids. Sulfur is one of the essential elements for plant growth and is absorbed by root as sulfate (SO_4^{2-}) with an oxidation state +6. Sulfate has to be reduced to -2 through several enzymatic steps to form the intermediate product, cysteine. Because γ - and β -zeins are the cysteine-rich storage proteins, silencing their expression causes a significant reduction in cysteine level, indicating these proteins are the main sink for cysteine storage (Wu et al., 2012). If free cysteine is the first stable

product with reduced sulfur, the majority of which is incorporated into cysteine-rich proteins, like γ -zeins and the excess would flow into methionine, its concentration would drive the translation of the δ - and β -zein (β -zein is rich both in cysteine and methionine) mRNA. Indeed, in RNAi against γ - and β -zeins, one can observe a boost in the accumulation of δ -zeins. Therefore, depriving the cysteine sink or increasing the methionine sink has the same result in that the flux of reduced sulfur flows through cysteine to methionine. This balance is made possible through the expression of different single/low copy number genes specialized for storage of these two amino acids (Wu et al., 2012).

Based on the above hypothesis, the major bottleneck for increasing seed methionine content is the capacity of sulfur absorption by roots and the efficiency by which sulfur can be reduced in the leaves during photosynthesis. Three enzymes ATP sulfurylase, APS reductase (APR) and sulfite reductase in this pathway combine coordinately to reduce sulfate with oxidation state +6 to sulfide with oxidation state -2 (**Figure 4**). Meanwhile, O-acetylserine (OAS), the other precursor for cysteine synthesis, is formed from serine and acetyl-CoA catalyzed by serine acetyltransferase (SAT). And last, sulfide reacts with OAS, producing the end assimilation product of cysteine catalyzed by OAS thiol-lyase (Leustek et al., 2000). We propose such capacity of sulfur reduction could be enhanced by specific overexpression of the committing enzymes APR and SAT in leaf bundle sheath cells, where the sulfur reduction occurs and as a consequence improve cysteine and methionine sinks in seed.

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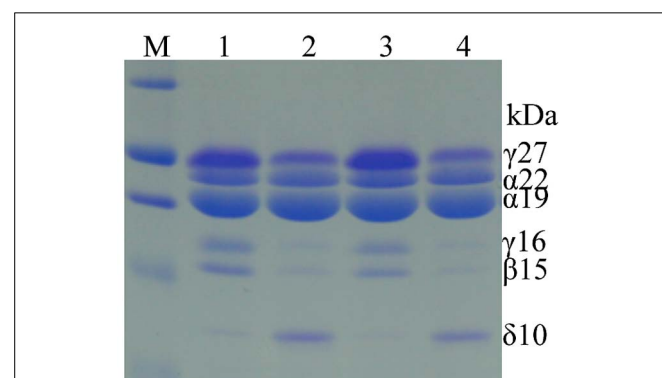


FIGURE 3 | Accumulation patterns of zeins in high-methionine transgenic and WT seeds. Hi-Met transgenic seeds in lane 2 and 4 express much higher levels of the 10-kDa δ -zein, but lower levels of β - and γ -zeins than WT in lane 1 and 4. Adapted from Wu et al. (2012).

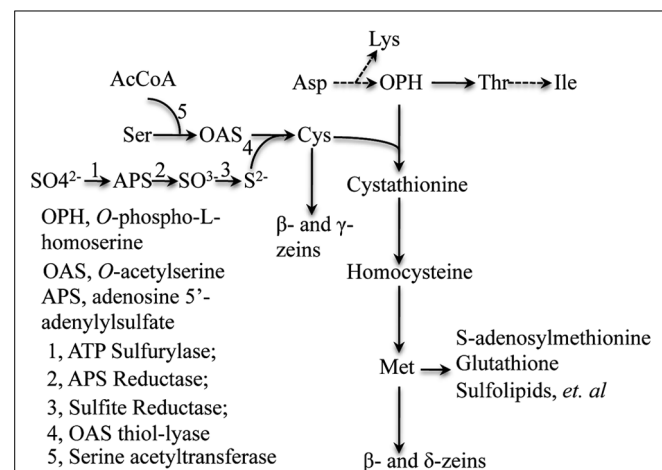


FIGURE 4 | Sulfate reduction and synthesis of cysteine and methionine pathways. The flow of sulfur is shown to illustrate sink source relationship. Adapted from Wu et al. (2012).

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Soybean seed proteome rebalancing

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The soybean seed's protein content and composition are regulated by both genetics and physiology. Overt seed protein content is specified by the genotype's genetic framework and is selectable as a breeding trait. Within the genotype-specified protein content phenotype soybeans have the capacity to rebalance protein composition to create differing proteomes. Soybeans possess a relatively standardized proteome, but mutation or targeted engineering can induce large-scale proteome rebalancing. Proteome rebalancing shows that the output traits of seed content and composition result from two major types of regulation: genotype and post-transcriptional control of the proteome composition. Understanding the underlying mechanisms that specifies the seed proteome can enable engineering new phenotypes for the production of a high-quality plant protein source for food, feed, and industrial proteins.

Keywords: protein, proteome, seed, storage protein, soybean

SOYBEANS ARE A GLOBAL PROTEIN COMMODITY

Among the global commodity of crops, soybean has an almost unique role, being high enough in protein content to provide the nitrogen (N) needed for efficient large-scale animal feed production. Soybeans possess economically valued oil and protein and is an archetype seed used to dissect the processes that specify seed compositional output traits. Over the past decade, considerable public and industry funds have been invested to create soybean community resources, including genomic, transcript, SNP and SSR maps, proteomics, as well as supported a broad range of bioactivity, biochemical, nutritional, and agronomic projects.

PROTEIN CONTENT AS A GENOTYPE

The genome of soybean specifies the genetic framework for seed formation and maturation, and it controls the expression, mix, and timing for synthesis of the storage metabolite traits (Wilson, 2004 for general information; Hartwig and Kilen, 1991; Wilcox and Shibles, 2001; Chung et al., 2003; Nichols et al., 2006; Bolon et al., 2010). Plant breeding has shown that different soybean genotypes specify a standardized, often line/cultivar-specific protein content (Wilson, 2004). The genetic program that produces seeds is simultaneously manifested in the embryo, endosperm, and maternal plant. Genetic marker analysis, using SNPs, has identified QTLs that demonstrate the overt protein and oil content has a strong genetic determinant (see Diers et al., 1992; Cregan et al., 1999; Zhao-Ming et al., 2011 for examples); these traits have supported generations of breeders who have enhanced soybean as a crop (Brim and Burton, 1979; Carter et al., 1986; Cober and Voldeng, 2000; Wilson, 2004).

Of the three individual components that comprise seeds, two are reproductive progeny: the endosperm and the zygotic embryo, which result from the double fertilization and are enclosed in the maternal-origin seed coat that connects the maturing seed to the maternal plant. Each reproductive-phase soybean plant consists of a coordinated network of embryos and endosperms for the common goal of maximizing reproductive output. Historically,

breeding programs have selected traits for enhancement of seed productivity, storage metabolite content, and important agronomic performance traits of the maternal plant. One way to view seed production by plants is as a population that produces (maternal) and distributes (maternal and endosperm) nutrient metabolites to the embryonic sink. During soybean seed development the endosperm undergoes progressive programmed cell death that is completed prior to the accumulation of stored metabolites. By the onset of protein and oil accumulation, only a single cell layer of aleurone remains from the endosperm that encapsulates the embryo, separating it from the inner surface of the maternal seed coat. But the physiological role, if any, of the aleurone in regulating nutrient flux to the developing embryo has not been investigated. Viewed in this way, the soybean plant's progeny are a population of aleurones and embryos interacting with the metabolite flux. The non-synchronized developing population of seeds must both compete and synchronize with the common maternal nutrient source. To assure the mature seeds are nearly all equivalent in composition, independent of their particular position on the maternal plant, their developmental program and physiological regulation must be coordinated along with the capacity of the maternal plant to nourish them.

The embryo's genotype specifies maturation-stages (Fehr et al., 1971) that are controlled by transcription factors that provide the developmental framework for storage substance accumulation (Hill and Breidenbach, 1974; Goldberg et al., 1981a,b; Mienke et al., 1981; Walling et al., 1986; Naito et al., 1988; Harada et al., 1989; Perez-Grau and Goldberg, 1989; Nielsen and Nam, 1999; To et al., 2006). A large number of soybean seed-specific DNA binding proteins have been identified (<http://casp.rnet.missouri.edu/soydb/>), and some of these have been shown to regulate specific seed maturation specific genes. (Chen et al., 1986; Jofuku et al., 1987; Allen et al., 1989; Lessard et al., 1991; Bäumlein et al., 1992; Kwong et al., 2003; Wang et al., 2007). A key role of some transcription factors is to regulate the metabolic and developmental processes that support

storage substance accumulation (Kroj et al., 2003; Gutierrez et al., 2007; Santos-Mendoza et al., 2008 for reviews). Understanding how cooperation between the embryo, endosperm, and maternal organs is integrated at the level of gene expression and cross-regulation of metabolism is important for creating models of the source-sink relationship of seed-fill.

NUTRIENT SOURCE DEFINES SEED PROTEIN ACCUMULATION

Whole plant physiological experiments demonstrate that nutrient distribution to seeds is highly regulated. The seed protein output trait is primarily regulated by controlling the composition of seeds, with the total number of seeds being a consequence of nutrient availability. The average size of seeds from small size plants compared with larger size plants, differs only a little, but the total number of seeds produced is directly related to the total biomass of the maternal plant and its mobilized metabolite source potential. In an agronomic context, this defines yield. From the perspective of the plant, the protein content genotype maximizes the potential of an individual seeds with the overall yield of seeds depending on the available biomass/growth conditions.

Although the maternal plant, endosperm, and embryo function in concert to form the seed, their metabolic interaction occurs without a direct, contiguous flow of nutrients, as each is apoplastically isolated from the other (Thorne, 1980; Thorne and Rainbird, 1983; Egli and Bruening, 2001; Patrick and Offler, 2001 for review). The metabolite flux from the maternal plant through the aleurone to the embryo results from coordinated secretion from the source and uptake by the sink, and this potentially determines the storage output trait (Borisjuk et al., 2003, 2004). In annual plants, such as soybean, the maternal plant must grow rapidly and produce nutrient-capture organs (i.e., roots and leaves).

The relationship between the maternal plant (source) and the seed (sink) has been investigated with increasingly more sophisticated tools and concepts for the past 40 years. For soybean, early studies focused on accumulation of vegetative proteins, primarily in foliage, as the nitrogen store that is mobilized to the seed and determines the accumulation of storage substances. This model of resource acquisition parallels that of most other seed plants, where metabolites in foliage are later mobilized to the seed. The amount of carbon fixed during photosynthesis is highly responsive to the environment, and the maternal plant manages carbon flux so it can distribute nutrients based on their availability and the demand of the seed (endosperm/embryo) sink (see Fellows et al., 1979; Borchers-Zampini et al., 1980 for early examples). A number of studies have shown that leaf proteins, predominantly Rubisco, accumulate over time (Schaefer et al., 1981a,b). In addition, soybean leaves accumulate a vegetative storage protein (VSP), a member of the vacuolar acid phosphatase family (DeWald et al., 1992; Staswick et al., 1994). VSP accumulation is highly responsive to nitrogen availability (Franceschi and Giaquinta, 1983; Franceschi et al., 1983; Staswick, 1989a,b), and it increases with depodding, i.e., removal of the seed sink. This observation led to proposals that VSP is a necessary adjunct that provides additional nitrogen resources for the seed. By silencing the VSP gene, it was later shown that VSP does not appear to make a difference in soybean seed protein content (Staswick et al., 2001).

Accumulated leaf proteins are mobilized by specific proteases (see Ragster and Chrispeels, 1979, 1981a,b) found in leaf cell vacuoles and plastids; the enzymes mediate the hydrolysis of Rubisco and VSP as well as other less abundant leaf proteins. Removal of all maturing seeds, except in one portion of the plant, leads to redistribution of source leaf nutrient flux (Carlson and Brun, 1984) indicating there must be (unknown) feedback-regulation between the seed and the nutrient source that is manifested through a long distance signal. Systems biology approaches could determine how the source size/composition is regulated, and how its mobilization is coordinated with the draw of the sink.

Leaf photosynthate and the products of protein hydrolysis produce a metabolite flux consisting predominantly of sucrose, glutamine and asparagine (Hsu et al., 1984; Rainbird et al., 1984; Krishnan et al., 2011); for nitrogen-fixing legumes in particular, there are also ureides from xylem fluid. With respect to the amino acid flux, the input from glutamine and asparagine has different characteristics. Skokut et al. (1982), using ^{15}N -NMR showed that there is no discrimination between the amino and amide N of glutamine, but for Asn the amino N is incorporated into protein twice as efficiently as the amide N, indicating a key role of asparagine in transamination. Asn may also be directly incorporated into proteins, with dual labeled ^{13}C and ^{15}N Asn being incorporated directly without scrambling the labels (Schaefer et al., 1981a,b). Within the seed, free Asn accounts for a larger fraction of amino acids (33–49%), with the fractional amount varying by genotype (Schaefer et al., 1981a,b). Asn dominates seed coat free amino acid efflux, assayed as apoplastic fluid, from the seed cup, i.e., the seed coat with embryo removed (Gifford and Thorne, 1985; Murray, 1987; De Jong et al., 1997; Hernández-Sebastià et al., 2005; Pandurangan et al., 2012). It is unclear whether the tissue source used for these experiments was derived from the inner surface of the aleurone or the maternal seed coat, or a combination of both, since the aleurone often adheres to the inner side of the seed coat. This shows that distinct from the embryo, the seed coat (perhaps comprising aleurone and seed coat) has an amino acid composition similar to the source (assayed as xylem sap), containing Asn as the dominant N-source, and is about 10-fold higher in abundance than Gln (Thorne and Rainbird, 1983; Lohaus et al., 1998; Zhang et al., 2010; Krishnan et al., 2011; Pandurangan et al., 2012).

PROTEIN COMPOSITION PLASTICITY AND THE SEED PROTEIN CONTENT GENOTYPE

The soybean seed protein output trait has two primary components: total protein content and the composition of individual proteins (the proteome). For soybeans, like many other seeds (Herman and Larkins, 1999 for review), the two major storage proteins, glycinin (11S legumin type) and conglycinin (7S vicilin type), dominate the proteome. The soybean seed proteome also includes many moderately abundant proteins that are bioactive and allergenic, such as the Kunitz and Bowman-Birk trypsin inhibitors, lectin, P34 allergen, sucrose binding protein, urease, oleosins (Herman and Burks, 2011) and several thousand low abundance proteins, including enzymes that mediate metabolism, synthesize storage substances, and create the structural framework of the cell. The specific mix of proteins and each protein's abundance

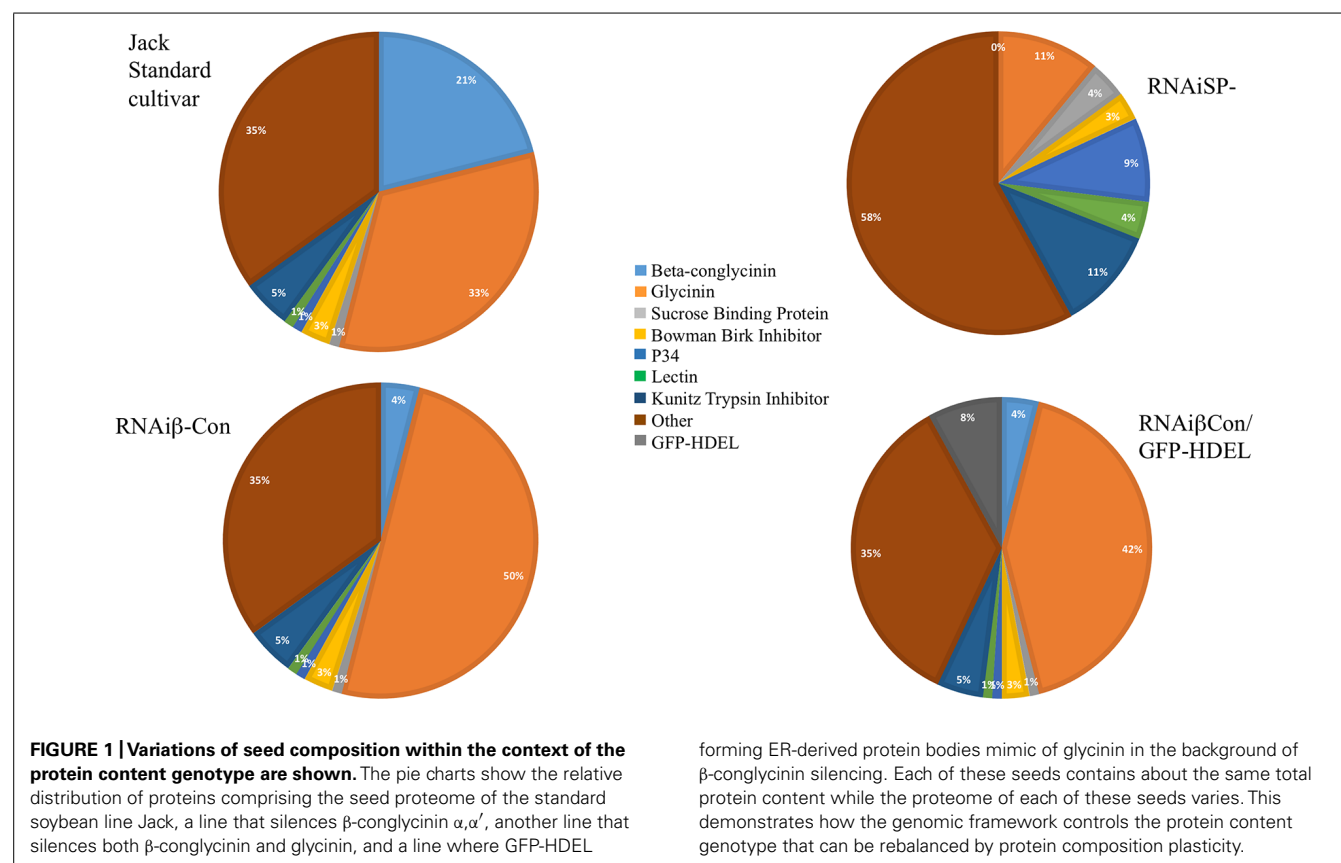
within the proteome determines the total amino acid composition trait.

Since the development of plant transformation techniques, there have been many attempts to express genes to induce accumulation of large quantities of foreign proteins in seeds. The goals of these projects were often to alter the nutritional quality of seeds, by increasing essential amino acids such as methionine in soybean, or to use the seeds as protein bioreactors. Even with strong storage protein promoters to regulate the transgene expression, the most frequent outcome of such experiments was to produce relatively small amounts of the heterologous protein (about 1% of total) and for the protein and amino acid composition to be little altered compared to control. These minor composition changes occurred whether the protein was targeted to the vacuole or accreted in ER-derived protein bodies, suggesting the limit of protein accumulation is independent of its deposition site. The observed heterologous protein production, compared to the expectations of the engineering design, indicated there must be seed regulatory mechanisms that limit foreign protein production so as not to significantly alter the seed protein content phenotype.

The converse experiment is to silence the intrinsic major storage protein genes and assess the impact on the seed's protein content. Kinney et al. (2001) showed total soybean protein content was conserved after silencing conglycinin, which constitutes about 20% of the total seed protein. The resulting seeds accumulated more glycinin, which apparently compensated for the

missing conglycinin. Of the five glycinin-genes in the soybean genome, the protein encoded by the glycinin A4 gene tends to accrete in the ER, producing protein (ER)-bodies (Herman and Schmidt, 2004; Herman, 2008), which are not normally found in soybean (Kinney et al., 2001). Mori et al. (2004) showed similar observations in a conglycinin mutant obtained from screening a collection that exhibited the same phenotype of "glycinin rebalancing," and for some of this protein to remain as proglycinin and to accumulate ER-derived protein bodies. Schmidt and Herman (2008) showed that introducing a gene encoding a foreign protein into the conglycinin-glycinin rebalancing increased the accumulation of the heterologous protein. A GFP-HDEL gene, as a glycinin-gene mimic allele with a glycinin promoter and terminator, was constructed. The addition of the HDEL ER-retention sequence was intended to promote accretion of the protein in the ER to form ER-(protein)-bodies and mimic the accreting glycinin ORF by substituting the GFP-HDEL protein. The expression of GFP-HDEL in the standard cv *Jack* soybean background resulted in about 1% of the total seed protein accumulated as GFP in protein bodies, a level typical of experiments of heterologous protein production in seeds. However, introgressing the GFP-HDEL glycinin mimic allele into the conglycinin-silenced line resulted in about eightfold increased accumulation of GFP as the glycinin mimic was utilized to compensate for the conglycinin shortfall (Figure 1).

To further test regulation of the protein content genotype and its capacity to allow for proteome alterations, RNAi silencing of



both the glycinin and conglycinin storage proteins (*SP*- or storage protein minus) lines were created that eliminated over two thirds of the protein content of standard soybean seeds (Schmidt et al., 2011). *SP*- seeds exhibited a number of different phenotypes that included conserving the same seed protein content as the parental line, due to compensatory increases of other vacuolar proteins, including Kunitz Trypsin Inhibitor, Lectin, P34, and sucrose binding protein (Figure 1). These compensating proteins accumulated at levels up to 11X more than normal, and each protein's increase occurred without a parallel increase in its steady-state RNA transcript abundance. This suggests that the protein content trait is determined by genotype but the abundance of proteome members occurs at the translational level.

FREE ASN IS AN INDICATOR OF ALTERED PROTEIN CONTENT AND COMPOSITION

Free Asn is correlated with soybean seed protein content and composition. One line of experimental evidence has shown that in soybean seed cultivars with a range of protein contents there is a positive correlation between high free Asn and high protein content (Hernández-Sebastià et al., 2005; Pandurangan et al., 2012). For the *SP*- storage protein silenced soybean, free Asn increased 5.8X over the standard type (Schmidt et al., 2011). Perhaps in response to the elevated free Asn, the steady-state transcript (RNAseq) level for asparaginase increased 6.5X over the conventional controls. In standard lines the asparaginase level was previously correlated with protein content in standard lines (Wan et al., 2006). Together, these observations suggest there is a correlation of protein increase, whether by genotype selection for higher protein content or by increased abundance of individual proteins within the context of the protein genotype, with changes in free Asn and asparaginase. This suggests the free Asn level is a nitrogen status indicator (Miller et al., 2008), either as a regulator of, or as a component of, the processes that specify protein content and composition.

CULTURED SOMATIC AND ZYGOTIC EMBRYOS EXHIBIT AN EXCESSIVE GROWTH TRAIT

Ex vivo zygotic embryo and somatic embryo cultures are often used as proxies for seed maturation; however, there are significant differences in metabolic behavior of embryos that form *in vivo* and *in vitro* (see Thompson et al., 1977; Obendorf et al., 1983, 1984; Raper et al., 1984; Finer, 1988; Hayati et al., 1996; Santarem et al., 1997; Chanprame et al., 1998; Pipolo et al., 2004; Iyer et al., 2008; Nishizawa and Ishimoto, 2009; Allen and Young, 2013). RNA expression profiling showed that somatic embryos produce a relatively standard set of seed-specific transcripts (Thibaud-Nissen et al., 2003). *Ex vivo* cultures exhibited fidelity with *in planta* seeds, but exhibit differences in the content of accumulated reserve substances (Pipolo et al., 2004). Gln has been shown to be an effective N-input source for these cultures (Saravitz and Raper, 1995; Schmidt et al., 2005) and is often used as the experimental N-source in nutrition-flux studies (He et al., 2011; Allen and Young, 2013; Truong et al., 2013, for recent examples), even though it is Asn that accounts for the large majority of the actual maternal source N *in planta* (Lea and Mifflin, 1980; Lohaus et al., 1998; Lima and Sodek, 2003). A recent paper by Allen and Young (2013)

showed in cultured zygotic soybean embryos that ^{14}C -Gln supplied 36–46% of the carbon of amino acids. In another study using somatic embryos, Truong et al. (2013) showed that increasing Gln in extrinsic culture media resulted in increased protein content, without greater oil content, showing that Gln is preferentially used to synthesize protein. This is consistent with older NMR observations on ^{13}C and ^{15}N that showed the amino and amido N for Gln as well as the carbon, is non-discriminatory when incorporated into the protein sink (Schaefer et al., 1981b; Skokut et al., 1982).

Taken together, these observations support a model where the maternal source supplies Asn (Pandurangan et al., 2012) as the N-source for zygotic embryos, but experimental *ex vivo* embryos can effectively use Gln. The difference between Asn and Gln may be important in the context of the morphological and compositional differences between *in planta* zygotic and cultured somatic and zygotic embryos. The media used for soybean culture varies, although Gln as the N-source dominates (Haga and Sodek, 1987), particularly in SHaM media (Schmidt et al., 2005), which was developed for transgenic embryo maturation (see Schmidt and Herman, 2008; Schmidt et al., 2011 for examples of its use). It is also used in some *ex vivo* nutritional studies (Truong et al., 2013). The media used for immature somatic embryo culture and transformation (Finer, 1988; Finer and McMullen, 1991; Walker and Parrott, 2001) has Asn as the N source. Tissue culture embryos used for transformation and regeneration, freed from the physical and metabolic constraints of the endosperm/aleurone and seed coat, exhibit aberrant growth (Figures 2 and 3), supporting



FIGURE 2 | The comparison of the size and morphology of a mature seed and a mature somatic embryo is shown. Note that the somatic embryo can exceed the seed's size, and the axis is enlarged compared to the cotyledon.

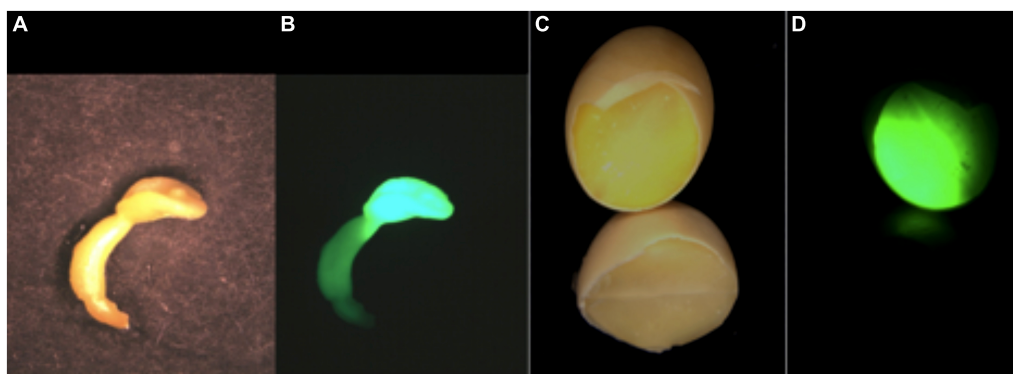


FIGURE 3 | A comparison of the expression of the storage protein trait in somatic embryos and seeds is shown as a GFP-HDEL glycinin mimic allele expressed as a storage protein proxy. The somatic embryo in white light (A) and UV fluorescence (B) shows that the primary GFP expression site is in the cotyledon that is reduced in size compared to cotyledons of seed. In seeds the cotyledons comprise the large majority of the seed's mass shown

as a chipped seed illuminated with white light (C) and UV for GFP fluorescence (D). The comparative expression the same glycinin promoter-regulated GFP in somatic embryos and seeds shows that while somatic embryos are a good proxy for seed expression there are challenges in interpreting somatic embryo results as an accurate proxy for a seed's in planta protein content and composition.

a regulatory role for the endosperm and/or seed coat in seed development (Garcia et al., 2003, 2005; Berger et al., 2006). In culture, somatic embryos form “monster” embryos with an enlarged embryonic axis and diminished, sometimes fused, cotyledons. Somatic embryos grown in the SHaM media are deemed “healthy,” (i.e., large, green, well-formed), often exceeding in size a fully formed seed. Similar observations are obtained by culturing immature zygotic cotyledons that enlarge to a size that exceeds that of *in planta* seed cotyledons. This suggests the more an embryo is fed, the larger it grows, even beyond the size in a standard seed. Cultured embryos favor the accumulation of carbonaceous over nitrogenous metabolites, yielding less protein per mass than zygotic embryos. For *ex vivo* zygotic and somatic embryos, the genotype-specific protein content and its proteome phenotype appears to be less regulated, and instead the storage substance accumulation appears to have a direct relationship with nutrient input. The differences between *in planta* and *ex vivo* embryo development and storage substance accumulation indicates the significance of the *in planta* circumstance of each seed as an interactive member of a larger population.

SEED PROTEIN CONTENT AND ITS VARYING PROTEOME

For seed crops, of which soybean is a prominent example, historic and modern breeding has selected for enhanced storage substance accumulation. Generations of breeders have established that protein content is a genetically determined trait that can be selected. How protein content is regulated in relationship with protein composition appears to be a multilevel process, with the genotype establishing protein content. The rebalancing of proteome occurs in both dicots and monocots as shown by observations on soybean and maize (Wu and Messing, 2014). From the perspective of the seed that has to establish the next generation of an annual plant, its capacity to make compositional choices in response to altered metabolic circumstances has selective advantages. Understanding the processes that control proteome plasticity within the context of the protein content phenotype can enable biotechnologists to

create enhanced soybeans optimized for specific end uses, such as species-specific feed or as protein bioreactors.

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The dynamic behavior of storage organelles in developing cereal seeds and its impact on the production of recombinant proteins

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Cereal endosperm is a highly differentiated tissue containing specialized organelles for the accumulation of storage proteins, which are ultimately deposited either within protein bodies derived from the endoplasmic reticulum, or in protein storage vacuoles (PSVs). During seed maturation endosperm cells undergo a rapid sequence of developmental changes, including extensive reorganization and rearrangement of the endomembrane system and protein transport via several developmentally regulated trafficking routes. Storage organelles have been characterized in great detail by the histochemical analysis of fixed immature tissue samples. More recently, *in vivo* imaging and the use of tonoplast markers and fluorescent organelle tracers have provided further insight into the dynamic morphology of PSVs in different cell layers of the developing endosperm. This is relevant for biotechnological applications in the area of molecular farming because seed storage organelles in different cereal crops offer alternative subcellular destinations for the deposition of recombinant proteins that can reduce proteolytic degradation, allow control over glycan structures and increase the efficacy of oral delivery. We discuss how the specialized architecture and developmental changes of the endomembrane system in endosperm cells may influence the subcellular fate and post-translational modification of recombinant glycoproteins in different cereal species.

Keywords: endosperm, molecular farming, recombinant glycoproteins, cereal biotechnology, storage organelles

INTRODUCTION

The endosperm is a short-lived tissue adapted for nutrient storage, which is found in both dicotyledonous and monocotyledonous seeds. However, its relative contribution to the mass of the mature seed varies greatly in different species. In cereals, the endosperm occupies the major part of the seed and consists of starchy inner endosperm cells, which are dead at the time of full maturation, and one or several outer layers of living aleurone cells, which secrete the enzymes needed to break down reserves following germination (Young and Gallie, 2000).

The endomembrane system of the developing cereal endosperm is clearly influenced by its functional specialization. Storage protein synthesis requires a highly active and well-developed endoplasmic reticulum (ER), and different types of storage organelles are rapidly formed during endosperm development to accommodate various types of storage proteins (Muntz, 1998; Shewry and Halford, 2002). ER-derived protein bodies mostly contain prolamin aggregates, whereas protein storage vacuoles (PSVs) tend to accumulate different storage protein classes, typically in separate phases, and often incorporate the content of ER-derived storage bodies (Shewry et al., 1995; Galili, 2004; Tosi et al., 2009). At the peak of storage protein production, programmed cell death occurs in the inner endosperm to generate a starchy endosperm core. In the surrounding aleurone cells, PSVs are converted into lytic vacuoles as germination commences (Bethke et al.,

1998) and programmed cell death is delayed until a few days later.

To accommodate this sequence of intracellular changes in developing and germinating seeds, the endomembrane system must be extremely flexible and capable of rapid morphological and functional adaptation. Seed development and germination are therefore ideal platforms to study endomembrane plasticity and reshaping, and to follow the transition from PSV to lytic vacuole, representing a shift between resource accumulation and redistribution.

Techniques that allow the real-time visualization of membranes and organelle markers within the endosperm tissue are particularly suitable for this type of analysis because they provide insight into membrane dynamics during seed development and germination. For example, several transgenic cereal lines are now available expressing fluorescent subcellular markers and tagged or mutated storage proteins (Mohanty et al., 2009; Onda et al., 2009; Tosi et al., 2009; Ibl et al., 2014; Oszvald et al., 2014) and other fluorescent probes have been developed that can track organelles in living cells and report the subcellular organization and dynamics *in vivo* (Landrum et al., 2010). These techniques can be combined with transcriptional analysis and proteomics, which help to identify the molecular regulators for storage organelle development in cereals (Walley et al., 2013).

The mechanisms of protein trafficking and deposition in cereal endosperm can also be investigated using recombinant proteins,

particularly glycoproteins (Stoger et al., 2005a; He et al., 2012; Wakasa and Takaiwa, 2013). Seeds are an attractive platform for the production of high-value recombinant pharmaceutical proteins, an approach known as molecular farming, because the specialized storage organelles allow such proteins to accumulate to high concentrations in small-volume compartments that contain molecular chaperones and disulfide isomerases to facilitate protein folding and maintain stability (De Jaeger et al., 2002; Stoger et al., 2005a; Ramessar et al., 2008a). This supportive intracellular environment means that the recombinant proteins are inert, and can be stored for long periods of time in the form of dry seeds without losing stability or activity. The accumulation of inert proteins in seeds also allows the expression of toxic proteins because these are inactive and are not expressed in vegetative tissues and therefore they do not impact on plant growth and development. The accumulation of proteins is also boosted by the triploid genome and the several rounds of endoreduplication that occur in the endosperm, thus increasing the effective number of transgene copies (Sabelli and Larkins, 2009). On this basis, many recombinant proteins have been produced successfully in cereal seeds, including commercial products such as lactoferrin, lysozyme, and human serum albumin (HSA) produced in rice by Ventria Bioscience (Fort Collins, CO, USA; Ramessar et al., 2008b; He et al., 2011b) and human growth factor for cosmetic use produced in barley by ORF Genetics (Iceland; Erlendsson et al., 2010).

Storage organelles in cereal seeds provide a clear advantage for the production of recombinant proteins, but the plasticity and remodeling of endomembrane organelles affect the accumulation and modification of proteins and so a better understanding of species-dependent and development-specific factors is needed to optimize cereal seeds for molecular farming applications. In this review article, we summarize the key features of the endomembrane organelles in major cereal species, and address the issues of cargo trafficking to these organelles in the developing endosperm

of cereal species, endomembrane reshaping, and vacuolar transition during development and germination. Finally, we discuss how these endosperm-specific features affect the production of recombinant glycoproteins in plants.

STORAGE ORGANELLES AND ENDOMEMBRANE TRAFFIC IN DIFFERENT CEREAL SPECIES

The endomembrane system in the developing cereal endosperm is highly specialized to accommodate different storage proteins, and differences are observed between cereal species. A representative endosperm cell from each of the four major cereals is shown in **Figure 1**. The vacuolar storage compartment can be identified easily in wheat (**Figure 1A**) and barley (**Figure 1B**) because large prolamins deposits are found in a central vacuole. In contrast, rice and maize endosperm cells do not have a single prominent protein storage site. Rice endosperm cells uniquely separate globulins and prolamins into separate compartments: globulins are sorted into numerous small PSVs whereas prolamins accumulate in ER-derived protein bodies (**Figure 1C**). Both compartments are evenly distributed within the endosperm cell cytoplasm. Maize, like wheat and barley, predominantly stores prolamins, which in this species are known as zeins. These form highly conserved protein bodies derived from the ER (Lending et al., 1989) and fill up the cytoplasm of endosperm cells together with a small number of vacuolar compartments that accumulate globulins (Woo et al., 2001; Arcalis et al., 2010; **Figure 1D**).

SECRETION VS. STORAGE IN ENDOSPERM CELLS

The endosperm tissue of many plants is composed of uniform, living reserve cells that secrete hydrolytic enzymes to degrade the endosperm cell walls, allowing the radicle to emerge during germination. In contrast, cereal endosperm contains a core of mature starchy endosperm cells that are already dead before germination, and the enzymes that break down reserves are secreted by the cells in the aleurone layer (Leubner-Metzger et al., 1995; Nonogaki and

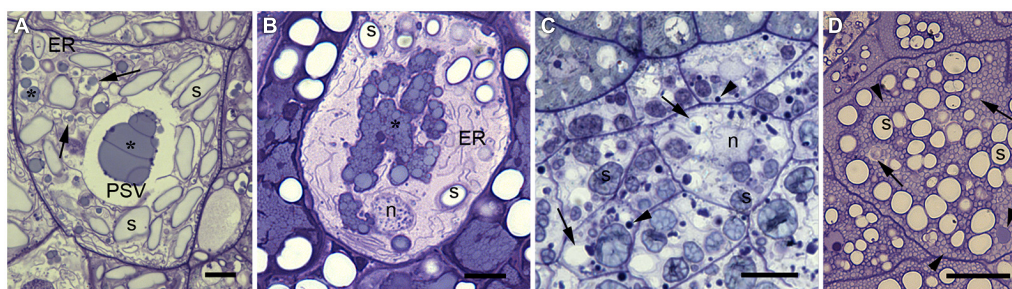


FIGURE 1 | Comparison of endosperm cells from the subaleurone layer at mid-maturation stage in wheat (A), barley (B), rice (C), and maize (D). Semithin sections (1 μm in thickness), stained with toluidine blue for light microscopy (Arcalis et al., 2004). **(A)** Wheat endosperm cells show a predominant, large central PSV. Note the huge prolamins aggregates stained in light blue (*) and the scarce globulin (triticin) bodies stained in dark blue at the periphery of the prolamins. Several smaller vacuolar compartments containing prolamins can also be observed (arrows), and well developed endoplasmic reticulum (ER) and abundant spindle like starch grains (s). **(B)** Barley endosperm cells show abundant protein deposits forming a multiphasic protein body (see the different shades of blue), habitually within a PSV. Note

the abundant ER, the spheroidal starch grains (s) and an apoptotic nucleus (n). **(C)** Rice endosperm cells are the smallest depicted in this figure. Rice endosperm accumulates mainly glutelins in protein storage vacuoles (arrows). Note the abundant PSVs containing a blue stained inclusion, normally close to the tonoplast and the spherical, densely packed prolamins bodies or PB-I (arrowheads). Starch (s). **(D)** Maize endosperm stores mainly prolamins in ER-derived protein bodies (zein bodies). Zein bodies (arrowheads) reach a diameter of 1 μm , are very abundant and appear evenly spread within the cytoplasm. Several storage vacuoles can be also observed (arrows) either completely filled or with peripheral protein deposits. Starch grains (s) are spheroidal and similar in size to the PSVs. Scale bar equals 10 μm .

Morohashi, 1996; Chen and Bradford, 2000; Brown and Lemmon, 2007). Secretory activity is therefore less likely in the starchy cereal endosperm, as has indeed been reported when cereal seeds are used for the expression of recombinant proteins. Recombinant proteins such as fungal phytase and the HIV-neutralizing antibody 2G12, carrying a signal peptide directing them to the endomembrane system but no further targeting signal, were shown to be transported to the PSV via the Golgi apparatus as evidenced by immunoelectron microscopy and glycan analysis in wheat, rice, and maize (Arcalis et al., 2004, 2010; Drakakaki et al., 2006; Peters et al., 2013). The same phytase protein, carrying the same targeting information, was secreted to the apoplast in leaves of transgenic rice plants (Drakakaki et al., 2006). These results suggest that the final destination for otherwise secreted proteins in the cereal endosperm is the PSV, although it is also possible that signal sequences are recognized and interpreted differently by cereal leaf mesophyll and seed endosperm cells.

TRANSPORT BETWEEN THE ER AND PSV

The tracking of proteins in different storage compartments has shown that the PSVs in cereal endosperm cells are not simply post-Golgi compartments. Prolamins such as wheat glutenins, barley hordeins and oat avenins are initially deposited in ER-derived protein bodies, but later they are also found in the PSVs (Cameron-Mills and Wettstein, 1980; Lending et al., 1989; Rechinger et al., 1993; Shewry et al., 1995; Galili, 2004; Tosi et al., 2009; Ibl et al., 2014). How they get there is a matter of controversy, but it appears that both Golgi-dependent and Golgi-independent routes are involved. Levanony et al. (1992) initially suggested, based on a series of electron micrographs, that ER-derived prolamins in wheat endosperm are eventually incorporated in the PSV through an autophagy-like process that bypasses the Golgi apparatus. This is supported by the presence of internal membranes in barley endosperm PSVs, including ER-derived membranes associated with individual and clustered protein bodies, suggesting that also hordein transport to the PSV at least partially bypasses the Golgi (Ibl et al., 2014). Ectopic zein bodies are also sequestered into PSVs in tobacco endosperm cells (Coleman et al., 2004). Reyes et al. (2011) proposed a Golgi-independent, autophagy-like route for the vacuolar delivery of zeins based on the presence of pre-vacuolar compartments that would sequester zein bodies and deliver them to the PSV in aleurone cells. Although the lipidation of ATG8 was observed, which is consistent with the macroautophagic mechanism (Klion-sky et al., 2008; Rubinsztein et al., 2009; Chung et al., 2010), there was no subsequent vacuolar degradation of lipidated ATG8, indicating that the vacuolar delivery of zeins to the PSVs of maize aleurone cells does not use the typical ATG8-dependent macroautophagic process, but rather an atypical autophagy-like sequence of events (Aamodt et al., 2011). As an alternative to this model, Rogers (2011) proposed a mechanism by which membrane-containing vesicles bud from the ER as pre-vacuolar organelles that subsequently deliver materials into the PSV, which has been documented in dicots (Oufattole et al., 2005).

The direct route from the ER to PSVs in seeds involves a lot of traffic. Torres et al. (2001) reported the presence of the ER-resident

molecular chaperone calreticulin in the rice endosperm PSV, providing evidence for a Golgi-independent pathway. Accordingly, KDEL-tagged recombinant proteins are often found at least partially in PSVs, e.g., a single chain antibody fragment (scFv) in rice (Torres et al., 2001) and HSA in wheat (Arcalis et al., 2004). The direct ER-to-PSV transport of recombinant proteins has also been reported in dicot seeds (Petrucelli et al., 2006; Floss et al., 2009; Loos et al., 2011a; Morandini et al., 2011; Arcalis et al., 2013). The endogenous KDEL-tagged proteinase sulphhydryl-endopeptidase (SH-EP) behaves in a similar manner in the cotyledons of germinating mung bean seeds (Toyooka et al., 2000; Okamoto et al., 2003), and storage protein precursors in pumpkin seeds are delivered to PSVs in precursor-accumulating (PAC) vesicles (Hara-Nishimura et al., 1998). PAC-like vesicles have also been described in rice endosperm by Takahashi et al. (2005). They are larger than the PAC vesicles in pumpkin seeds but they also arise directly from the ER and contain storage proteins destined for the PSV, such as glutelins and globulins (Takahashi et al., 2005). Viotti (2014) recently speculated that PAC vesicles may be the precursors of PSVs that slowly acquire their final size and identity via Golgi-mediated and post-Golgi-mediated transport, similar to the transition from pro-vacuoles to lytic vacuoles (Viotti et al., 2013; Viotti, 2014). Indeed, the main vacuolar proton pumps (H^+ -ATPase, VHA-a3 and H^+ -PPase AVP1) appear to follow a Golgi-independent route from the ER to the PSV in *Arabidopsis* seeds (Viotti et al., 2013), and alpha-TIP may follow the same, brefeldin A (BFA)-insensitive route. Considering this possibility, the trafficking of storage proteins and the relationships between the different storage compartments in cereal seeds could be reinterpreted, well in line with a model proposed earlier for barley aleurone PSVs (Bethke et al., 1998). In this model, it has been proposed that the ER membrane producing the neutral lipid may also serve as the site of storage protein accumulation and could mature into a PSV, supported by the observation that oleosomes forming on the surface of the ER are later found surrounding PSVs.

DEVELOPMENTAL CHANGES OF PROTEIN TRAFFICKING ROUTES

A number of studies have suggested that the intracellular trafficking and distribution of storage proteins may change during seed development (Shy et al., 2001; Vitale and Hinz, 2005; Tosi et al., 2009). Accordingly, the fates of the recombinant glycoprotein phytase, and the endogenous vacuolar corn proteins legumin-1 (CL-1) and α -globulin (CAG), were found to change during maize endosperm development (Arcalis et al., 2010). All three proteins were found in the PSVs during early development as expected, but closer to maturity they were found at the periphery of the ER-derived zein bodies. In the case of recombinant phytase, the switch in localization was accompanied by a switch in the glycan profile, consistent with a stage-dependent protein trafficking behavior comprising a Golgi-dependent pathway to the PSVs in younger cells switching to the deposition in ER-associated compartments later. There was also a significant reduction in the number of PSVs during development (Arcalis et al., 2010), suggesting a net decrease in number or a change in appearance reflecting the different content. There was no significant decline in the number of Golgi organelles in developing maize, although

in wheat the number of transcripts representing Golgi-associated proteins was shown to decline during seed maturation (Shy et al., 2001).

The endomembrane system of specialized and transient tissues such as endosperm should therefore not be considered as a static and rigid structure, but rather as a plastic and dynamic system that involves interactions between organelles and changes in protein trafficking to fulfill distinct developmental functions.

SPATIOTEMPORAL MORPHOLOGICAL CHANGES OF STORAGE ORGANELLES IN CEREAL SEEDS

ARCHITECTURAL CHANGES IN THE ENDOMEMBRANE SYSTEM DURING DEVELOPMENT AND GERMINATION

The massive reorganization of the endomembrane system during seed development involves significant morphological changes to the endosomal and storage organelles (Hoh et al., 1995; Wang et al., 2010; Ibl et al., 2014). The observation of *in vitro* transgenic maize endosperm cultures has shown that the ER changes from its typical reticulated distribution pattern into a more punctate architecture during the development of both starchy endosperm and aleurone cells, probably representing the formation of ER-derived protein bodies (Aamodt et al., 2011). In barley, the aleurone ER remains predominantly reticulated, whereas prominent protein bodies appear in the subaleurone and central starchy endosperm ERs (Ibl et al., 2014). In the germinating grain, the synthesis of secretory proteins in the living aleurone cells is accompanied by the proliferation of the ER to form stacks, an increase in the size and complexity of the Golgi apparatus, a reduction in the number of oleosomes and an increase in the number of glyoxysomes and mitochondria (reviewed by Fath et al., 2000).

Conventional studies of subcellular structures, intracellular pathways and protein storage organelles in cereal seeds involve the acquisition of static images based on immunofluorescence and electron microscopy (Cameron-Mills and Wettstein, 1980; Arcalis et al., 2004, 2010; Gubatz et al., 2007; Holding et al., 2007; Fukuda et al., 2013; Tian et al., 2013). This reveals little about the dynamic restructuring events during endosperm development, which have to be inferred from samples at different developmental stages. However, fluorescent membrane markers can be used to follow the dynamic morphological changes *in situ* by live cell imaging. This was reported in the context of barley endosperm development, comparing PSVs in the aleurone, subaleurone and central starchy endosperm layers (Ibl et al., 2014). Whereas the spherical PSVs in the aleurone remain constant, those in the subaleurone and central starchy endosperm cells undergo substantial but cell type-specific morphological changes. In both the subaleurone and central starchy endosperm cells, the PSVs initially appear as large compartments. In the subaleurone, they subsequently go through cycles of fusion and rupture, first allowing the protein bodies to form larger, composite aggregates within the vacuole, and finally producing unconfined protein bodies and ER-derived as well as TIP3-labeled membrane fragments (Figures 2A,B). In contrast, PSVs in the starchy endosperm become smaller so that the protein bodies are tightly enclosed, and later in development some of the PSV membranes lose their integrity. This membrane degeneration may be induced by the desiccation process. The aleurone is protected against desiccation-induced injury (Stacy et al., 1999) but membrane dehydration may contribute to the dynamic behavior of membranes in the starchy endosperm due to the physical impact on

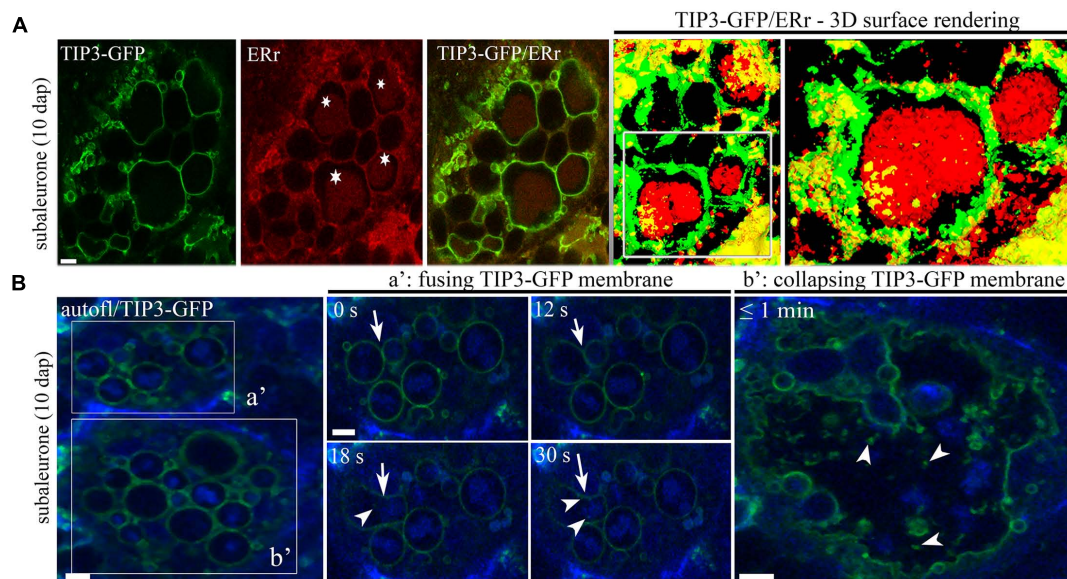


FIGURE 2 | TIP3-GFP-labeled PSVs contain protein bodies and are involved in fusion and rupture in barley endosperm. (A) TIP3-GFP-labeled PSVs comprise large protein bodies stained with ER-TrackerTM red (asterisks). Note the three-dimensional surface rendering (and the magnified inset) of 16 sections with a step size of 0.5 μ m. **(B)** Live cell

imaging of TIP3-GFP-labeled PSVs show fusion (a') and collapse (b') processes in the subaleurone at 10 DAP. Note the presence of TIP3-GFP-labeled vesicles (a', arrowheads) after PSV fusion (a', arrows). Images were acquired every 6 s. Scale equals 5 μ m. Figure partially reproduced from Ibl et al. (2014).

membrane lipids, including demixing, fluid-to-gel phase transition, increasing cytosolic viscosity, protein denaturation, and membrane fusion (Bryant et al., 2001; Hoekstra et al., 2001). In rice endosperm, the synthesis of large amounts of disulfide-rich storage proteins during seed development is accompanied by the production of H_2O_2 , which causes the peroxidation of membrane lipids (Onda et al., 2009). This promotes lipid chain fracture, which alters intrinsic membrane properties such as fluidity and permeability, finally leading to the leakage of small molecules and electrolytes (Sattler et al., 2006; Onda et al., 2009; Sharma et al., 2012). Notably, mutant rice seeds that cannot produce normal amounts of sulfhydryl groups generate less H_2O_2 and desiccate more slowly than wild-type seeds (Onda et al., 2009). The production of H_2O_2 in the ER of endosperm cells may also induce programmed cell death during seed desiccation and maturation (Onda, 2013).

THE ALEURONE AS A STORAGE TISSUE

In addition to providing hydrolases for the breakdown of reserves in the starchy endosperm, the aleurone is also a storage tissue in its own right (Ritchie et al., 2000). Aleurone cells are filled with spherical PSVs that retain a constant appearance during endosperm development (Cameron-Mills and Wettstein, 1980; Bethke et al., 1996; Ibl et al., 2014). PSVs in the barley aleurone contain storage proteins, phytate (which is rich in phosphorus, potassium and magnesium) as well as storage carbohydrates (Jacobsen et al., 1971). *In situ* hybridization, RT-PCR and immunoblot analyses have shown that zein transcripts and proteins are present in the aleurone (Woo et al., 2001; Aamodt et al., 2011). Subcellular localization studies have revealed the presence of zeins, α -globulin and legumin-1 in maize aleurone cells at 18 and 22 days after pollination (DAP), predominantly as large inclusions within PSVs and small ER-derived protein bodies (Aamodt et al., 2011). As reported for the barley aleurone, PSVs and lipid bodies occupy most of the aleurone cellular volume in maize, along with multi-vesicular bodies (MVBs) and double-membrane autophagosome-like structures. Electron tomography has shown that aleurone cells at 22 DAP also contain one or more globoids (crystals of phytic acid salts) and a large system of intravacuolar membranes, possibly derived from the ER (Aamodt et al., 2011). Moreover, typical ER-resident proteins were detected in the PSVs (Aamodt et al., 2011). The dynamic analysis of the intravacuolar membrane system and the zein-rich inclusions in the maize aleurone revealed developmental changes in the PSV size, the total membrane surface area and the percentage corresponding to the intravacuolar membranes (Aamodt et al., 2011). The PSVs were smaller and more homogeneous at 14 DAP compared to 22 DAP. The total membrane surface area declined by $\sim 50\%$ during this interval, whereas zein-rich inclusions occupied almost 10-fold more of the PSV lumen at 22 DAP (Aamodt et al., 2011). The content and intravacuolar membrane system of maize aleurone PSVs therefore appears exquisitely dependent on the developmental stage.

MORPHOLOGICAL CHANGES WITHIN THE ALEURONE DURING GERMINATION

Following imbibition, the embryo releases gibberellic acid (GA_3), which diffuses into the aleurone layer and induces the highly

differentiated and specialized aleurone cells to synthesize and secrete digestive enzymes that subsequently mobilize the insoluble reserves in the starchy endosperm (Ritchie et al., 2000). During this process, the aleurone cells break down their storage proteins and use the resulting amino acids to synthesize a spectrum of hydrolases (Jones and Jacobsen, 1991; Bethke et al., 1998). After a few days, the storage reserves of the endosperm are depleted and the aleurone cells die.

The process is accompanied by profound morphological changes in the endomembrane system of aleurone cells (Jacobsen et al., 1985). De-embryonated half-grains, isolated aleurone layers and aleurone protoplasts were used to study the responses of cereal aleurone cells to hormones and to understand molecular and cellular aspects of signaling and regulation in the aleurone (reviewed by Ritchie et al., 2000; Bethke and Jones, 2001).

Barley aleurone protoplasts treated with GA_3 undergo dramatic morphological changes. Freshly isolated aleurone protoplasts contain many small PSVs, but 4 days of hormone treatment causes them to coalesce into one large central PSV (Jacobsen et al., 1985; Bush et al., 1986; Swanson and Jones, 1996; Fath et al., 1999). This GA_3 -dependent vacuolation process correlates strongly with the duration of GA_3 treatment and is completed after 5 days of incubation (Bethke and Jones, 2001; Hwang et al., 2005). Granules within the vacuoles accumulate in larger numbers as the vacuoles increase in size. These morphological changes reflect a functional transition from nutrient-storing compartments to lytic organelles. Noninvasive measurements of the vacuolar pH in barley aleurone protoplasts showed that protoplasts respond to GA_3 , acidifying the vacuole lumen in the course of a few hours from pH 6.6 to 5.8 or below (Swanson and Jones, 1996; Swanson et al., 1998). The cells also showed an abrupt loss of membrane integrity (Fath et al., 2000). The prolonged incubation of aleurone protoplasts with GA_3 was lethal.

Interestingly, gene expression profiling studies show that GA_3 and abscisic acid (ABA) are both synthesized during seed maturation and germination and build a possible interaction network during seed germination (Sreenivasulu et al., 2006, 2008). GA_3 and ABA signals also appear to influence the activity of a subset of stored proteases and the expression of further proteases and cell wall-loosening enzymes during grain maturation and germination. ABA antagonizes the events induced by GA_3 in the aleurone at many levels, indicating a sensitive balance between these hormones involving a spatiotemporal interaction network of key regulators involved in storage organelle dynamics. Isolated aleurone protoplasts and layers have been used to study aleurone characteristics, especially the roles of GA_3 and ABA in the regulation of vacuolar dynamics (Swanson and Jones, 1996; Swanson et al., 1998). Even if the same cellular events occur in imbibed whole grains and GA_3 -treated aleurone layers or protoplasts, the timing of events is faster in isolated aleurone layers and protoplasts and the model is simplified by the absence of interacting tissues and the application of GA or ABA, rather than their spatiotemporal ratios found *in vivo* (Bethke and Jones, 2001). The characteristics of aleurone protoplasts may also vary according to culture conditions (Jacobsen et al., 1985). These aspects emphasize the importance of confirming that results obtained using isolated cell cultures are also relevant in intact seeds.

IDENTIFYING MOLECULAR REGULATORS OF STORAGE ORGANELLE BEHAVIOR

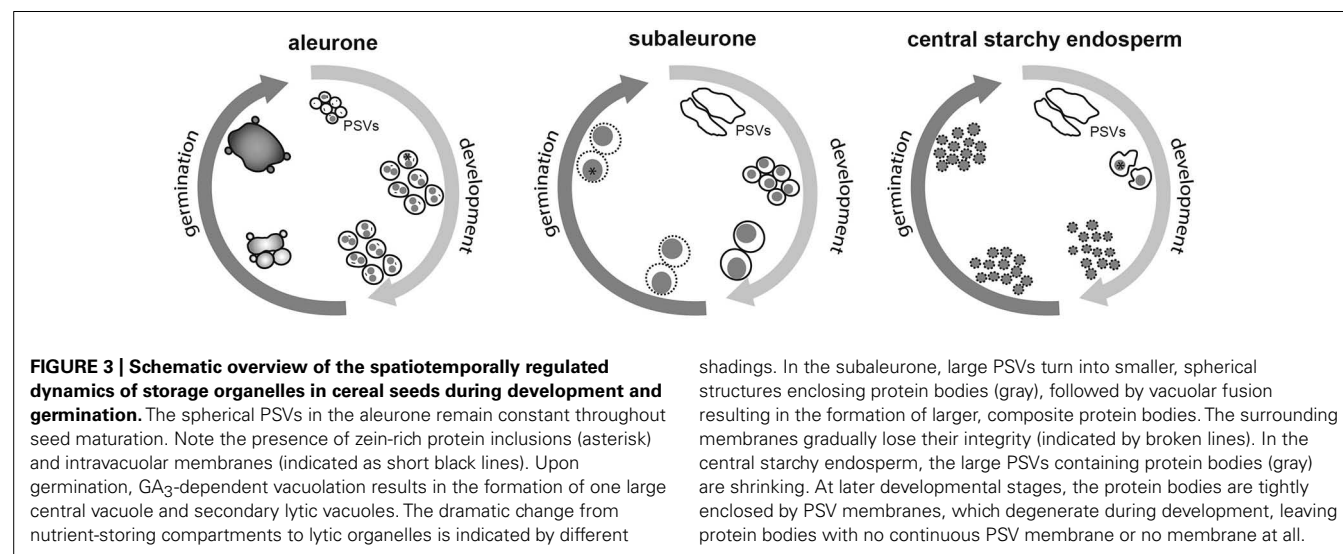
As discussed above, the dynamic behavior of storage organelles in cereal seeds strongly indicates the presence of a spatiotemporal regulatory network (**Figure 3**). Transcriptomics and proteomics have been instrumental in many areas of cereal research (reviewed by Pechanova et al., 2013). One opportunity to identify the molecular regulators of storage organelle-reshaping events is the transcriptional and/or proteomic analysis of developing and germinating seeds, to build an atlas of proteotypes. This has recently been reported for maize seeds, resulting in an atlas comprising ~14,000 proteins (Walley et al., 2013). Total protein was extracted from dissected maize seeds at seven stages of development, including separated embryo, endosperm and aleurone/pericarp tissues. Normalized and averaged data showed that peptide homologs of *Arabidopsis* TIP3 were minimally expressed in the endosperm after 12 DAP, but increased in the endosperm and in the aleurone/pericarp tissue by 27 DAP. Similarly, the comparative transcriptional analysis of two tissue fractions during barley grain maturation, desiccation and germination (starchy endosperm/aleurone vs. embryo/scutellum) revealed that TIP3 expression increases steadily during maturation and declines steadily throughout germination (Sreenivasulu et al., 2008). Because the storage endosperm dies during late maturation, any increase in transcript abundance in this fraction during germination must depend on RNA that is newly synthesized in the aleurone (Sreenivasulu et al., 2008).

Precise sampling for the more specific spatial analysis of expressed proteins is challenging and a system that can differentiate between aleurone and starchy endosperm cells is necessary. Laser microdissection (LMD) overcomes the heterogeneous distribution of different tissues and cells by allowing spatially resolved sampling of individual cells, cell populations or tissues (Fang and Schneider, 2013). This approach was recently used for the tissue-specific transcriptomic analysis of barley seeds, allowing the detection of transcriptional networks in the context of endosperm development (Thiel et al., 2011). In combination with studies

using transgenic lines with fluorescent marker proteins for cellular compartments, LMD-based transcriptomics provides a promising strategy to investigate the spatiotemporal regulation of storage organelle dynamics.

Recent developments in high-resolution, two-dimensional gel electrophoresis (2DE), multidimensional liquid chromatography and mass spectrometry (MS) have also helped to characterize the dynamic cereal seed proteome, e.g., in maize (Mechin et al., 2004) and barley (Finnie et al., 2004; Finnie and Svensson, 2009). Specialized extraction procedures allow the enrichment of enzymes and other proteins that control seed metabolism and storage product mobilization, in some cases allowing selective extraction from specific tissues and compartments such as the aleurone plasma membrane and starch granule proteomes in barley (Boren et al., 2004; Hynek et al., 2006). The resulting spatiotemporal profiling of the barley seed proteome during grain filling and germination allowed proteins to be assigned to distinct functional categories (Finnie and Svensson, 2003; Bonsager et al., 2007; Finnie et al., 2011). In maize, the availability of different mutants has facilitated proteomic analysis (Damerval and Devienne, 1993).

More insight into the dynamic nature of the seed proteome has been gained using comparative proteomics, and particularly quantitative proteomics. For example, comparative 2DE has been used to study the time course of protein mobilization during rice seed germination, revealing that germination causes the radical reprogramming of the proteome, not only by consuming protein reserves but also rebuilding defense pathways and inducing morphological changes (Yang et al., 2007; He et al., 2011a). Isobaric tags for relative and absolute quantification (iTRAQ) has been used to determine precise quantitative changes in the proteome during seed development (Lan et al., 2011; Owiti et al., 2011), and the same technique has been combined with multiple reaction monitoring (MRM) and gene ontology (GO) classification to profile the rice embryogenesis-dependent proteins, thus providing a dataset that could be used to investigate the molecular basis of rice embryogenesis (Zi et al., 2013).



RECOMBINANT PROTEIN PRODUCTION IN CEREAL ENDOSPERM

UNUSUAL TRAFFICKING BEHAVIOR OF RECOMBINANT PROTEINS

Protein trafficking and organelle reshaping can also be investigated by looking at the behavior of recombinant proteins, including storage proteins fused to fluorescent tags (Tosi et al., 2009; Saito et al., 2012; Shigemitsu et al., 2013; Wakasa and Takaiwa, 2013) or foreign proteins that have been produced in the context of molecular farming. Endogenous glycoproteins are rarely found in the endosperm (Woo et al., 2001) and are difficult to follow due to the lack of appropriate detection antibodies, so recombinant glycoproteins are particularly useful because they can be traced through intracellular pathways by immunolocalization and by characterizing their glycan modifications (Drakakaki et al., 2006; Arcalis et al., 2010).

A better understanding of the peculiar rules of protein trafficking in the cereal endosperm is also desirable for the production of valuable recombinant proteins such as pharmaceuticals, which need to be produced in a predictable and homogeneous form (Stoger et al., 2014). Targeting sequences that have been shown to work in vegetative plant organs do not always guarantee the predictable trafficking of recombinant proteins to a given compartment in cereal endosperm cells (Arcalis et al., 2004; Takaiwa et al., 2009; Wakasa and Takaiwa, 2013). For example, the same protein may be secreted from rice leaf cells, but sequestered in PSVs within the endosperm (Drakakaki et al., 2006). The addition of a KDEL signal usually targets proteins to the ER lumen in vegetative tissues, but in the endosperm the final destination appears to differ by species and protein, such as in the case of endogenous prolamins accumulating in the ER and ER-derived protein bodies in rice (Wakasa and Takaiwa, 2013) and maize (Rademacher et al., 2008), or in the PSVs of wheat endosperm (Arcalis et al., 2004). Storage protein fusions usually accumulate in predictable compartments, i.e., protein bodies or PSVs (Sugita et al., 2005; Wakasa and Takaiwa, 2013). Storage organelles are generally a desirable target site for recombinant proteins because they have evolved to facilitate stable protein accumulation and thus offer a protective environment for recombinant proteins, which can remain stable in dry cereal seeds at ambient temperatures for several years (Stoger et al., 2005b). Secondly, the accumulation of recombinant proteins into storage organelles can protect the protein not only from degradation within the plant cell but also beyond harvest. For example, prolamins are highly resistant to gastrointestinal digestion *in vitro* and *in vivo*, resulting in the excretion of significant numbers of prolamins, making them suitable for bioencapsulation (Tanaka et al., 1975; Ogawa et al., 1987). It should be borne in mind that the trafficking of recombinant proteins can change during seed development and affect the glycan profile as discussed above, so the harvesting time can significantly affect the characteristics of the purified protein (Arcalis et al., 2010).

Another factor that may impact not only the expression, but also the subcellular localization and modification of recombinant proteins in the endosperm is the choice of promoter to drive transgene expression. The structure and arrangement of storage organelles varies according to the tissue layer within the endosperm (Tosi et al., 2009; Ibl et al., 2014), and

endosperm-specific promoters also vary significantly in their spatiotemporal activity (Qu and Takaiwa, 2004), which should make possible to favor recombinant protein expression in cell types with a specific organelle architecture. Endosperm-specific promoters often have minimal or no activity in the aleurone (Lamacchia et al., 2001), so their use can be contrasted with constitutive or even aleurone-specific promoters such as the amylase promoter, which has been used to drive the expression of a recombinant enzyme during malting in barley (Nuutila et al., 1999). The secretory profile and *N*-glycoproteome differ markedly between the aleurone and the inner maturing endosperm (Barba-Espin et al., 2014). However, recombinant protein production during malting/germination is challenging because of the higher intrinsic proteolytic activity in the tissue at this stage, which affects the stability of the product.

Finally, the fate of a recombinant protein in developing seeds may occasionally be affected by interactions with endogenous storage proteins. Proteins with free cysteine residues and multimeric proteins that assemble via disulfide bonds (such as antibodies) are particularly prone to covalent interactions with prolamins. For example, free antibody chains interact with zeins (Peters et al., 2013), and a cysteine-rich peptide was shown to mediate protein retention in rice prolamins bodies (Takaiwa et al., 2009).

THE BIOENCAPSULATION IN STORAGE ORGANELLES

Plant tissue can provide some protection from proteolytic enzymes in the gut, and the sequestration of recombinant proteins in rice protein bodies appears to extend the protection from digestive proteolysis following oral administration in an animal model. This was shown by directly comparing the digestibility of a model oral tolerogen from three sources: ER-derived protein bodies in rice endosperm, glutelin bodies (PSVs) in rice endosperm and a chemically synthesized peptide (Takagi et al., 2010). Both endosperm-derived peptides were more resistant to *in vitro* digestion with pepsin than the soluble form, but the prolamins bodies were more resistant than that from PSVs. Similar results were reported in feeding studies, indicating that bioencapsulated forms of the tolerogen significantly enhanced its immunological efficacy. The cholera toxin B subunit (CTB) also accumulated within protein bodies and the PSV in rice endosperm, and was similarly protected from *in vitro* pepsin degradation when fed to mice, allowing the induction of CTB-specific serum IgG and mucosal IgA antibodies (Nochi et al., 2007).

These studies suggest that protein storage organelles offer natural bioencapsulation strategies compatible with oral vaccines or prophylactic mucosal antibodies for passive immunization against gastro-intestinal disease. Oral vaccines must be protected from digestion to ensure sufficient amounts of the antigen reach the Peyer's patches (lymphoid tissue in the ileum), which is necessary for the induction of an oral immune response. Storage proteins such as zeins have already been considered as *in vitro* protein encapsulation reagents for slow-release pharmaceuticals (Lai and Guo, 2011; Lau et al., 2013), thus naturally occurring protein bodies may provide the ideal encapsulation platform for recombinant pharmaceuticals produced in plants.

ER STRESS AND NOVEL ER-DERIVED COMPARTMENTS

Some recombinant proteins have been shown to induce the formation of additional, prolamin-free ER-derived protein bodies, e.g., a modified house dust allergen and a modified birch pollen allergen expressed in rice seeds (Yang et al., 2012a; Wang et al., 2013). Similarly, human IL-10 expressed in rice seeds was found to be localized in ER-derived prolamin bodies and aberrant ER-derived compartments (Fujiwara et al., 2010; Yang et al., 2012b). The aberrant deposition of recombinant proteins in newly formed ER-derived structures has also been observed in other plant seeds, including a scFv-Fc antibody that was partially localized in ER-derived compartments delimited by ribosome-associated membranes in *Arabidopsis* seeds (Van Droogenbroeck et al., 2007). Similar observations have been reported for other scFv-Fc molecules with or without KDEL signals (Loos et al., 2011b). These novel ER-derived compartments may play a protective role in the host cell, and may be induced preferentially by aggregation-prone protein candidates. Although additional factors such as protein expression levels may also come into play, seeds could be more prone to the induction of ER-derived compartments because the mechanism that generates ER-derived protein bodies is already prevalent, especially in the endosperm.

Recombinant protein expression can sometimes elicit an ER stress response reflected by the coordinated expression of ER-resident molecular chaperones (Oono et al., 2010; Wakasa et al., 2012). This correlates with the appearance of distorted protein bodies at the microscopic level (Yang et al., 2012b; Wang et al., 2013). In some cases, there is also a specific grain phenotype at the macroscopic level, such as the opaque phenotype with floury and shrunken features reported in transgenic rice seeds (Oono et al., 2010), phenotypically similar to the maize *floury2* mutant that is also characterized by an ER stress response (Hunter et al., 2002). It is unclear whether seeds are more prone to ER stress induced by recombinant protein expression than vegetative tissues, perhaps due to the temporally confined high protein expression levels, or whether the stress symptoms are more obvious and therefore more frequently noticed in seeds due to the opaque phenotype.

UNUSUAL N-GLYCAN STRUCTURES

N-glycan structures on recombinant proteins vary according to the final subcellular location and the trafficking route (Lerouge et al., 1998). The lack of secretion in cereal endosperm often results in a distinct lack of typical apoplast N-glycan structures such as GnGnXF, which are abundant in proteins expressed in leaves (reviewed in Samyn-Petit et al., 2003; Arcalis et al., 2013). Glycoproteins that have not passed through the Golgi apparatus typically bear oligomannosidic structures (high-mannose glycans) whereas those in post-Golgi locations tend to bear complex, xylosylated and fucosylated N-glycans. The ratio between these glycan classes sometimes correlates with the distribution of a protein between ER-derived protein bodies and PSVs, but this is not necessarily the case because the direct ER-to-PSV transport route discussed above may allow a proportion of proteins deposited in the PSV to bypass the Golgi apparatus completely. Interestingly, a number of recent studies involving the analysis of glycopeptides, rather than N-glycans digested off glycoproteins prior to analysis,

have revealed significant proportions of aglycosylated seed-derived recombinant glycoproteins (Van Droogenbroeck et al., 2007). This may reflect the rapid production of high levels of the recombinant protein based on temporally confined extreme transcriptional and translational activities, but it may also indicate the limited capacity of the glycosylation machinery in maturing seeds. Under-glycosylation may also be linked to ER-stress and result in the formation of small, ER-derived organelles as discussed above.

Another, perhaps more puzzling phenomenon, is the abundance of trimmed N-glycan structures consisting of only a single GlcNAc residue, which may be useful for specialty applications but may not support the functionality of some recombinant proteins such as antibodies with effector functions (Umana et al., 1999; Schuster et al., 2007). These structures are often found on KDEL-tagged proteins, and most likely reflect the activity of Endo- β -N-acetylglucosaminidase (ENGase) on oligomannosidic N-glycan substrates (Fischl et al., 2011). Single GlcNAc residues have been detected on glycoproteins produced in maize, and may even represent the predominant glycoform suggesting a high level of ENGase activity in cereal seeds (Rademacher et al., 2008; Ramessar et al., 2008a; Arcalis et al., 2010). Indeed, ENGase activity has been observed in cereal seeds (Vuylsteker et al., 2000), and free oligomannosidic glycan structures, which are released by ENGase activity, have been identified in seeds of diverse plant species (Kimura and Kitahara, 2000; Kimura et al., 2002) and a physiological role for them in plant development, fruit and seed maturation has been proposed (Priem and Gross, 1992; Kimura and Kitahara, 2000). However, *Arabidopsis* plants lacking ENGase activity showed no obvious morphological phenotype (Fischl et al., 2011; Kimura et al., 2011).

It is still unclear why ENGase, an enzyme with a presumed cytosolic localization (Suzuki et al., 2002; Fischl et al., 2011), can access substrates that accumulate within endomembrane organelles. Although we cannot completely exclude the possibility that glycan trimming occurs during extraction, our preliminary data instead support the *in vivo* action of the enzyme. In addition, based on the fact that endomembrane structures break down and compartments rupture, possibly in response to oxidative stress and desiccation (Ibl et al., 2014), combined with the incorporation of cytosolic material into the interior of vacuoles via atypical pre-vacuolar compartments during autophagy (Reyes et al., 2011), it could be speculated that these events might also allow ENGases to come into contact with glycoprotein substrates. Further investigations are required to determine whether this is the case, perhaps providing a better understanding of the physiological role of ENGases in plant seeds and increasing the spectrum of its endogenous substrates.

CONCLUSION

Endosperm is a short-lived tissue that undergoes a rapid sequence of developmental changes, including extensive endomembrane system reorganization and rearrangement. The development and maturation of storage organelles is linked with storage protein synthesis and protein transport via several developmentally regulated trafficking routes. The investigation of spatially and temporally regulated gene expression will provide insight into the underlying

molecular mechanisms, and transgenic cereal plants expressing fluorescent marker proteins combined with live cell imaging techniques allow the investigation of dynamic membrane reorganization events. The analysis of recombinant protein transport, deposition and glycosylation provides additional information about cargo trafficking to storage organelles. By understanding these processes, we will be able to control the production of recombinant proteins and design optimized production strategies for molecular farming that exploit the unique bioencapsulation properties of storage organelles.

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Protein body formation in the endoplasmic reticulum as an evolution of storage protein sorting to vacuoles: insights from maize γ -zein

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The albumin and globulin seed storage proteins present in all plants accumulate in storage vacuoles. Prolamins, which are the major proteins in cereal seeds and are present only there, instead accumulate within the endoplasmic reticulum (ER) lumen as very large insoluble polymers termed protein bodies. Inter-chain disulfide bonds play a major role in polymerization and insolubility of many prolamins. The N-terminal domain of the maize prolamin 27 kD γ -zein is able to promote protein body formation when fused to other proteins and contains seven cysteine residues involved in inter-chain bonds. We show that progressive substitution of these amino acids with serine residues in full length γ -zein leads to similarly progressive increase in solubility and availability to traffic from the ER along the secretory pathway. Total substitution results in very efficient secretion, whereas the presence of a single cysteine is sufficient to promote partial sorting to the vacuole via a wortmannin-sensitive pathway, similar to the traffic pathway of vacuolar storage proteins. We propose that the mechanism leading to accumulation of prolamins in the ER is a further evolutionary step of the one responsible for accumulation in storage vacuoles.

Keywords: disulfide bonds, endoplasmic reticulum, evolution of the secretory pathway, seed storage proteins, *Zea mays*

INTRODUCTION

Seed storage proteins, the major food proteins, have unique characteristics that allow very high accumulation during seed development, low digestibility by predators, but rapid hydrolysis during germination. Despite these shared features, as well as structures that strongly suggest an evolution through variable combinations of very few domain types (Shewry et al., 1995; Adachi et al., 2001; Xu and Messing, 2008; Gu et al., 2010), the different seed storage proteins have specific assembly, solubility, and intracellular localization properties and can thus be divided into three major classes: (i) 2S albumins (the number refers to the sedimentation constant) are monomeric and soluble in water, (ii) 7S and 11S globulins are homotrimers and homohexamers, respectively, and are soluble in salt water, (iii) prolamins, the most heterogeneous class, are soluble in strong alcohol/water solution or after reduction of disulfide bonds. How the evolution of biochemical properties relates to that of subcellular localization is still not clear (Ibl and Stoger, 2012). All storage proteins are co-translationally inserted into the endoplasmic reticulum (ER), where 7S and 11S globulins rapidly trimerize. The ER is the port of entry of the secretory pathway: from here, proteins traffic through the Golgi complex and are secreted by default, unless they have structural features/signals that sort them to intracellular compartments of the pathway. Albumins and globulins follow traffic pathways shared by the other soluble vacuolar proteins and are sorted to storage vacuoles of cotyledonary cells, where they accumulate (Vitale and Hinz, 2005). Endoproteolytic cleavage of 11S globulin polypeptides occurring in the vacuole

promotes further assembly of trimers into the final 11S hexamers. Most prolamins, instead, form large polymers that in many cases rapidly become insoluble and do not proceed along the secretory pathway, accumulating as protein bodies (PB) within the ER lumen of endosperm cells (Shewry et al., 1995; Herman, 2008). The developmentally programmed use of the ER as a protein storage compartment seems to be unique to plants, whereas the formation of insoluble protein accretions in the ER is associated to many human diseases (Anelli and Sitia, 2010). Storage albumins and globulins are present throughout land plant evolution, but prolamins have been found only in cereals and are therefore much less ancient (Xu and Messing, 2008). In all cereals, each PB contains many different prolamin polypeptides, indicating promiscuous interactions among the products of the different prolamin genes. When expressed individually in vegetative tissues of transgenic plants, some prolamins form homotypic PBs within the ER, indicating that they contain all the information sufficient to form an ER-retained polymer, whereas others remain soluble and are delivered to the vacuole. Examples of these two different destinies are maize 27 kD γ -zein and wheat γ -gliadin, respectively (Geli et al., 1994; Napier et al., 1997). Individual storage globulins can also be retained in the ER as large accretions, instead of being sorted to storage vacuoles, if the synthesis of other members of the family is suppressed (Kinney et al., 2001). Altogether, these data suggest a close relationship between the mechanisms of storage protein accumulation in vacuoles or the ER, and that the latter may have evolved directly from the former.

The 27 kD γ -zein (hereon termed γ -zein, for simplicity) is among the most ancient maize prolamins (Xu and Messing, 2008, 2009); it is therefore a good model to study the early events that may have caused a shift of accumulation from the vacuole to the ER. After co-translational removal of the signal peptide for entry into the ER, mature γ -zein consists of two major regions, each corresponding to about half of the polypeptide (Prat et al., 1985). As schematically illustrated in **Figure 1A**, the N-terminal region is characterized by eight repeats of the hexapeptide PPPVHL (the repeated hexapeptide is also VHLPPP, because the last of the eight PPPVHL sequences is followed by PPP) and seven Cys residues involved in inter-chain bonds. A synthetic (VHLPPP)₈ peptide forms *in vitro* an amphipathic structure that has affinity with lipids derived from plant ER (Kogan et al., 2004). The C-terminal region is homologous to 2S albumins (Shewry et al., 1995), which are characterized by three domains named A, B, and C, containing eight Cys that form four inter-chain disulfide bonds (**Figure 1A**). Consistently, when a fusion between thioredoxin and the C-terminal domain of γ -zein was expressed in *E. coli*, these eight Cys residues formed the intra-chain bonds typical of 2S albumins (Ems-McClung et al., 2002). The presence of a repeated sequence, as well as the 2S albumin domains, are common features of many prolamins (Shewry et al., 1995).

Early study established that γ -zein is soluble only in the presence of reducing agents (Vitale et al., 1982). The N-terminal region is retained in the ER if the 2S albumin-like region is deleted, whereas efficient secretion occurs when most of the N-terminal region is deleted (Geli et al., 1994). When a fragment (amino acids 24–112, from the translation start) that includes the eight Pro-rich repeats and the first six Cys residues was fused to the C-terminus of the vacuolar 7S storage globulin of common bean, phaseolin, the chimeric construct, termed zeolin, formed polymers with the main features of γ -zein: they are insoluble unless reduced and accumulate as homotypic PB in the ER (Mainieri et al., 2004). The Zera sequence, which consists of amino acids 1–112 of γ -zein, similarly promotes the formation of PB in the ER when fused to the N-terminus of a number of proteins (Torrent et al., 2009). Collectively, these experiments indicate that the N-terminal region of γ -zein forms inter-chain disulfide bonds and contains information sufficient for ER retention, independently of its position in fusion proteins.

When the six Cys residues of zeolin were mutated to Ser, efficient secretion occurred from transiently transfected protoplasts (Pompa and Vitale, 2006). Consistently, *in vivo* treatment with the reducing agent 2-mercaptoethanol caused secretion of zeolin from protoplasts of transgenic tobacco (Pompa and Vitale, 2006). Therefore, the inter-chain disulfide bonds are necessary for zeolin retention in the ER. This result was confirmed and extended by mutagenesis of the fluorescent chimera Zera-ECFP (Llop-Tous et al., 2010): when all the six Zera Cys residues were mutated or all eight repeats were deleted, PB formation was totally impaired, leading to efficient secretion, indicating cooperation between hydrophobic interactions and disulfide bonds in the formation of PB. Progressive mutagenesis of Cys residues or deletion of the Pro-rich repeats caused parallel gradual decrease in the size and abundance of Zera-ECFP PBs and increased secretion. The first two N-terminal Cys residues were identified

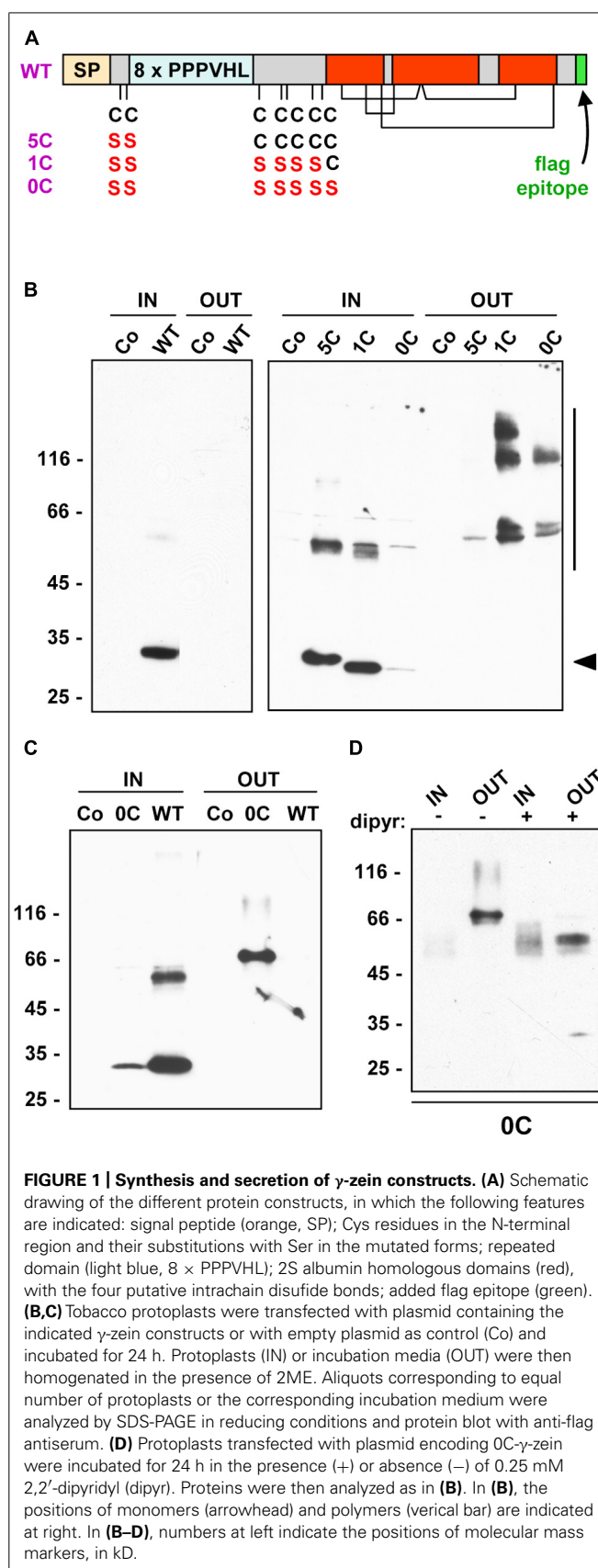


FIGURE 1 | Synthesis and secretion of γ -zein constructs. (A) Schematic drawing of the different protein constructs, in which the following features are indicated: signal peptide (orange, SP); Cys residues in the N-terminal region and their substitutions with Ser in the mutated forms; repeated domain (light blue, $8 \times$ PPPVHL); 2S albumin homologous domains (red), with the four putative intrachain disulfide bonds; added flag epitope (green). **(B,C)** Tobacco protoplasts were transfected with plasmid containing the indicated γ -zein constructs or with empty plasmid as control (Co) and incubated for 24 h. Protoplasts (IN) or incubation media (OUT) were then homogenized in the presence of 2ME. Aliquots corresponding to equal number of protoplasts or the corresponding incubation medium were analyzed by SDS-PAGE in reducing conditions and protein blot with anti-flag antiserum. **(D)** Protoplasts transfected with plasmid encoding OC- γ -zein were incubated for 24 h in the presence (+) or absence (–) of 0.25 mM 2,2′-dipyridyl (dipy). Proteins were then analyzed as in **(B)**. In **(B)**, the positions of monomers (arrowhead) and polymers (vertical bar) are indicated at right. In **(B–D)**, numbers at left indicate the positions of molecular mass markers, in kD.

as critical, since their mutagenesis was sufficient for full secretion, as visualized by fluorescence microscopy (Llop-Tous et al., 2010).

Using the full length γ -zein as a model, we have studied here the relationships between prolamins solubility, assembly, and intracellular traffic. We found a progressive change in subcellular location from the ER, to the vacuole, to secretion, that casts light on the structural features that may have allowed the evolutionary shift of storage protein localization from the vacuole to the ER, thus giving rise to a new subcellular compartment.

MATERIALS AND METHODS

PLASMID CONSTRUCTION

To prepare WT γ -zein for transient expression and detection with anti-flag antiserum, plasmid pBSKS.G1L (Bellucci et al., 1997), which contains the coding sequence of 27 kD γ -zein, was PCR amplified with the following oligos: 5'-TGTAGTGACATGAGGGTGTGCTCGTTGCCCT-3' (termed forward1, the SalI restriction site is underlined) and 5'-ACATGCATGCCTATCATTACTTGTCTCGTCGTCCTTGTA-GTCGTGGGGGACACCGCCGCGAGCA-3', (termed reverse1, the SphI restriction site is underlined, the reverse complement of the codons encoding the flag epitope DYKDDDDK is double underlined). The sequence was restricted with SalI and SphI and inserted into the transient expression vector pDHA (Tabe et al., 1995). 1C γ -zein was constructed starting from pDHAzeolin(Cys⁻), see Pompa and Vitale (2006), first by amplifying its zein domain with the oligos 5'-TGTAGTGACATGAGGGTGTGCTCGTTGCCCTCGCTCTCCTGGCTCTCGCTGCGAGCGCCACCTCCACGCATACAAGCGGCGGTAGCGGATCTCAGCCA-3' (forward2, the SalI site is underlined, the translation start ATG is in *Italic*, the codons that substitute the first two Cys with Ser are double underlined) and 5'-AAAACTGCAGTTGCGACGGACTAGGATGAGG-3' (reverse2, the PstI site is underlined). The amplified sequence was restricted with SalI and PstI and used to substitute the corresponding fragment of WT γ -zein inserted into pDHA. To construct 5C γ -zein, WT γ -zein inserted into pDHA was amplified with the oligos forward2 and reverse1, restricted with SalI and SphI and reinserted into pDHA. 0C γ -zein was constructed using a QuickChange protocol, starting from 1C γ -zein inserted into pDHA, using the oligos 5'-CAACAGGGAACCTCCGGCGTTGGCAGC-3' (forward3, the codon that substitutes the last Cys of the N-terminal domain of γ -zein with Ser is double underlined) and its reverse complement (reverse3).

TRANSIENT EXPRESSION IN PROTOPLASTS

Protoplasts were isolated from small (4–7 cm) leaves of tobacco (*Nicotiana tabacum*) SR1 plants grown in axenic conditions and subjected to polyethylene glycol-mediated transfection as described (Pedrazzini et al., 1997). Unless otherwise stated in the Results section, 40 μ g of plasmid were used to transform 10^6 protoplasts. Transformed protoplasts were resuspended in K3 medium [Gamborg's B5 basal medium with minimal organics (Sigma), supplemented with 750 mg/L CaCl₂ 2H₂O, 250 mg/L NH₄NO₃, 136.2 g/L sucrose, 250 mg/L xylose, 1 mg/L 6-benzylaminopurine, and 1 mg/L 1-naphthalenetic acid, pH 5.5],

supplemented with 150 μ g/ml bovine serum albumin as a competing substrate for extracellular proteases, and were incubated in the dark at 25°C. After the desired time, the incubation medium containing secreted proteins was carefully collected with a 2 ml syringe and protoplasts were washed and concentrated by the addition of three volumes of ice-cold W5 medium (154 mM NaCl, 5 mM KCl, 125 mM CaCl₂ 2H₂O, and 5 mM glucose) and centrifugation at 60 g for 10 min. The incubation medium and the protoplast pellet were frozen in liquid nitrogen and stored at -80°C, but freezing of protoplasts was avoided when subcellular fractionation was performed. When needed, inhibitors of protein trafficking brefeldin A (BFA: Roche; final concentration 10 μ g/ml) or wortmannin (Sigma-Aldrich; final concentration 10 μ M), were added to the protoplast incubation medium 1 h after transfection and maintained at the same concentration throughout the incubation. To inhibit prolyl hydroxylation, transfected protoplasts were incubated in the presence of 0.25 mM 2,2'-dipyridyl (dipyr), a chemical that inhibits *in vivo* activity of prolyl-4-hydroxylase (Moriguchi et al., 2011).

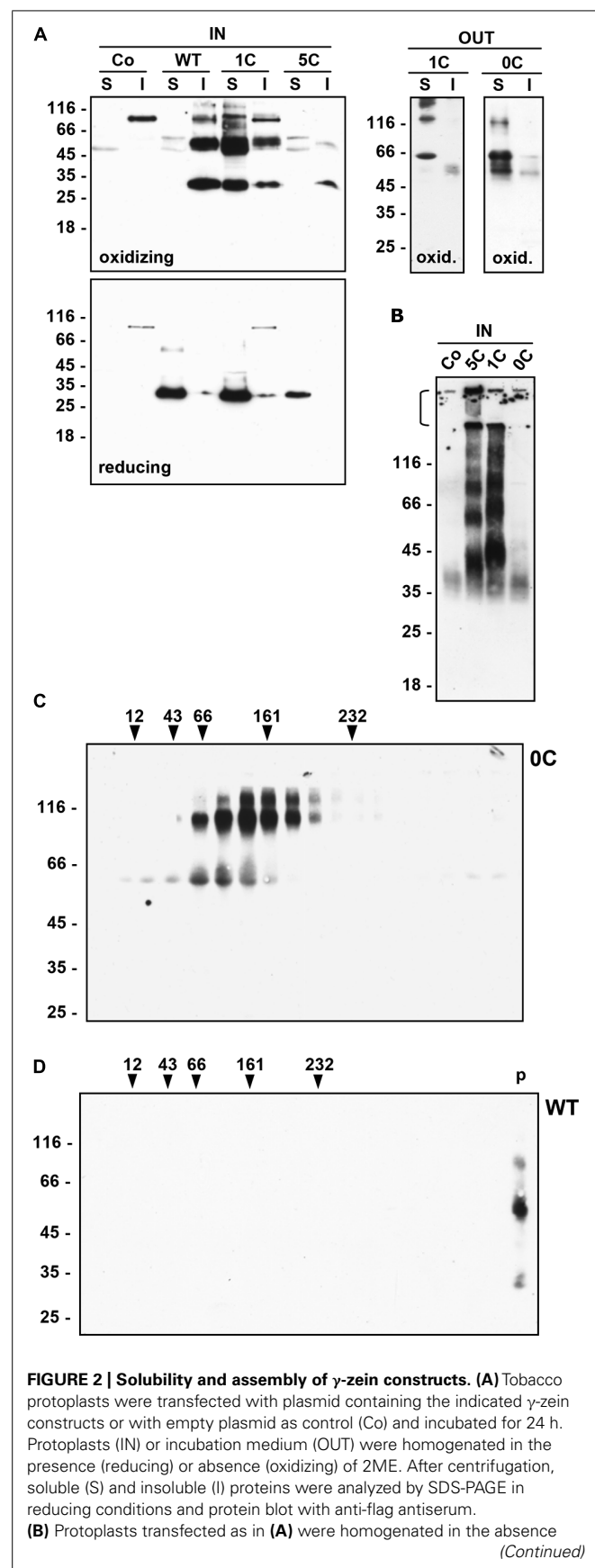
PROTEIN ANALYSIS

Protoplasts and incubation media were homogenized in homogenation buffer [150 mM Tris-Cl, pH 7.5, 150 mM NaCl, 1.5 mM EDTA, 1.5% Triton X-100, Complete protease inhibitor cocktail (Roche)], supplemented (reducing conditions) or not (oxidizing conditions) with 4% (v/v) 2-mercaptoethanol (2-ME). Separation of soluble and insoluble proteins was performed by centrifugation at 1,500 g, 10 min, 4°C. In the experiment shown in **Figure 2B**, the oxidizing homogenation buffer was supplemented with the alkylating agent iodoacetamide (Sigma-Aldrich, final concentration 70 mM). To analyze proteins, the homogenates were adjusted to 20 mM Tris-Cl pH 8.6, 1.0% SDS, 4% 2-ME, 8% glycerol (denaturation buffer), heated at 90°C for 5 min and separated by 15% acrylamide SDS-PAGE. For SDS-PAGE in non-reducing conditions, 2-ME was omitted from the denaturation buffer. Gels were blotted to Hybond-P membrane (GE Healthcare) and proteins revealed using with anti-flag rabbit polyclonal antibodies (Sigma-Aldrich; 1:2,000 dilution), anti-BiP rabbit antiserum (Pedrazzini et al., 1997, 1:10,000 dilution) or anti-endoplasmic reticulum rabbit antiserum (Klein et al., 2006, 1:2,500 dilution) and the Super-Signal West Pico Chemiluminescent Substrate (Pierce Chemical, Rockford, IL, USA). Protein Molecular Weight Markers (Fermentas, Vilnius, Lithuania) were used as molecular mass markers.

For velocity ultracentrifugation, the incubation medium of protoplasts expressing 0C γ -zein was homogenized with oxidizing homogenation buffer and centrifuged 1,500 g, 10 min, 4°C. The supernatant was loaded on top of a linear 5–25% (w/v) Suc gradient made in 150 mM NaCl, 1 mM EDTA, 0.1% Triton X-100, 50 mM Tris-Cl, pH 7.5. After centrifugation at 200,000 g average, 4°C for 20 h, an equal aliquot of each gradient fraction was analyzed by SDS-PAGE and protein blot. An identical gradient loaded with molecular mass markers was run in parallel.

SUBCELLULAR FRACTIONATION AND VACUOLE PURIFICATION

Separation of microsomes derived from the different subcellular compartments was performed by protoplast homogenation in



10 mM KCl, 100 mM Tris-Cl, pH 7.8, 2 mM MgCl₂, 12% (w/w) sucrose, followed by isopycnic centrifugation using linear 16–55% (w/w) sucrose gradient in the same buffer, as described (Mainieri et al., 2004). Isolation of vacuoles by floatation in Ficoll/betaine gradients (Dombrowski et al., 1994) and determination of the activity of the vacuolar marker α -mannosidase (Foresti et al., 2008) have also been described.

RESULTS

SOLUBILITY AND SECRETION OF γ -ZEIN ARE INVERSELY RELATED TO THE NUMBER OF Cys RESIDUES IN THE N-TERMINAL REGION AND THE EXTENT OF OLIGOMERIZATION

Three mutated constructs were produced, in which the first two, first six or all seven Cys residues of the N-terminal region were mutated to Ser (Figure 1A). The positions of these Cys residues, from the translation start, are 26, 28, 83, 101, 103, 111, and 117. To facilitate detection by protein blot, the flag epitope DYKDDDDK was added to the C-terminus of these constructs and of WT γ -zein. For brevity, here on the constructs will be called based on the number of remaining Cys residues of the N-terminal region: 5C indicates γ -zein^{C26,28S}, 1C indicates γ -zein^{C26,28,83,101,103,111S}, and 0C indicates γ -zein^{C26,28,83,101,103,111,117S}; WT indicates wild type γ -zein. All constructs were transiently expressed in tobacco leaf protoplasts under the control of the constitutive CaMV 35S promoter.

To first test whether the mutations promoted traffic of γ -zein, at 24 h after transfection proteins were extracted from protoplasts or the incubation media in the presence of non-ionic detergent and the reducing agent 2-mercaptoethanol (2-ME), separated by SDS-PAGE and detected with anti-flag antiserum. Polypeptides of the expected size, migrating between the 25 and 35 kD molecular mass markers (Figure 1B, arrowhead), as well as higher molecular mass forms that indicated oligomer formation or post-translational modifications, in part related to secretion (Figure 1B, vertical bar), were detected in protoplasts transfected with all γ -zein constructs, but not when transfection was performed with the empty plasmid. WT γ -zein was exclusively recovered in protoplasts, as expected, whereas a progressive decrease in the number of Cys residues caused a parallel, gradual increase in secretion (Figure 1B). In the experiment shown in Figure 1B, secretion of 0C- γ -zein was almost complete. This was not always the case in fully independent transfections, probably

reflecting variability in intracellular redox balance among the different protoplast preparations (Lombardi et al., 2012), but the ratio of secreted/intracellular recombinant protein was always $0C > 1C > 5C \geq WT$ γ -zein, where secreted WT γ -zein was always virtually 0% (Table 1). Even in experiments in which the total amount of WT γ -zein synthesized was clearly higher than that of 0C, the former was not secreted at all, indicating that the differences in the traffic properties are not dependent on expression levels (Figure 1C).

The γ -zein forms migrating around 50–60 kD could represent dimers particularly difficult to denature, whereas the larger forms, that are mainly detected extracellularly, could indicate further oligomerization or post-translational modifications related to traffic (Figure 1B). Higher molecular mass forms difficult to denature have also been detected to variable extents upon expression of γ -zein or protein fusions containing the N-terminal γ -zein domain in transgenic plants (Geli et al., 1994; Bellucci et al., 2000; Mainieri et al., 2004; Torrent et al., 2009; Virgili-López et al., 2013).

Some of the γ -zein oligomerizations/modifications are clearly dependent on the presence of Cys residues in the N-terminal domain, as can be appreciated comparing secreted 1C- and 0C- γ -zein, but others are not (Figure 1B). It has been suggested that hydroxylation of proline residues could occur on γ -zein (Geli et al., 1994). *In vivo* inhibition of prolyl-4-hydroxylase abolished most of the differences between intracellular and secreted 0C- γ -zein (Figure 1D), indicating that the increase in molecular mass beyond 50–60 kD was indeed dependent on this modification, possibly followed by O-glycosylation of hydroxyproline occurring only along the route to secretion or extracellularly.

The inverse relationship between the number of Cys residues and secretion suggested that the removal of Cys residues increases γ -zein solubility in the naturally oxidizing ER environment. Homogenation in the absence or presence of 2-ME was therefore performed (Figure 2A, oxidizing and reducing, respectively), followed by centrifugation to separate soluble and insoluble material (S and I samples in Figure 2A), denaturation of all samples and analysis by SDS-PAGE in reducing conditions. Putative dimers were much more evident if extraction was performed in oxidizing conditions. WT γ -zein was insoluble unless extracted in the presence of reducing agent, as expected (Vitale et al., 1982), whereas decreasing the number of Cys residues caused a

parallel increase in solubility: a very small proportion of intracellular 5C, more than 50% of intracellular 1C, and more than 90% of secreted 0C- and 1C- γ -zein were solubilized also in the absence of reducing agent (Figure 2A, compare S and I for each sample).

Analysis by non-reducing SDS-PAGE indicated that soluble 1C- γ -zein and, even more, 5C- γ -zein undergo oligomerization beyond the dimer stage (Figure 2B; notice that a relevant proportion of 5C γ -zein does not even enter the separating gel). Oligomerization of the very small proportion of intracellular 0C- γ -zein was difficult to determine (notice that the diffused band around 40 kD is present also in the control and is thus irrelevant), but the native molecular mass of secreted 0C γ -zein polypeptides analyzed by velocity gradient ultracentrifugation corresponded roughly to that determined by SDS-PAGE, indicating that dimers particularly difficult to denature are formed by all constructs and that 0C- γ -zein does not form larger oligomers beyond dimers (Figure 2C). WT γ -zein could not be analyzed by non-reducing SDS-PAGE because of its insolubility, but upon velocity centrifugation it migrated at the bottom of the tube, indicating that it formed very large disulfide-bonded polymers, as expected (Figure 2D).

It can be concluded that γ -zein expressed in leaf protoplasts is insoluble unless reduced, as in maize endosperm, and that lowering the number of Cys residues progressively reduces the ability to form large disulfide-bonded polymers, resulting in increased solubility and ability to traffic along the secretory pathway.

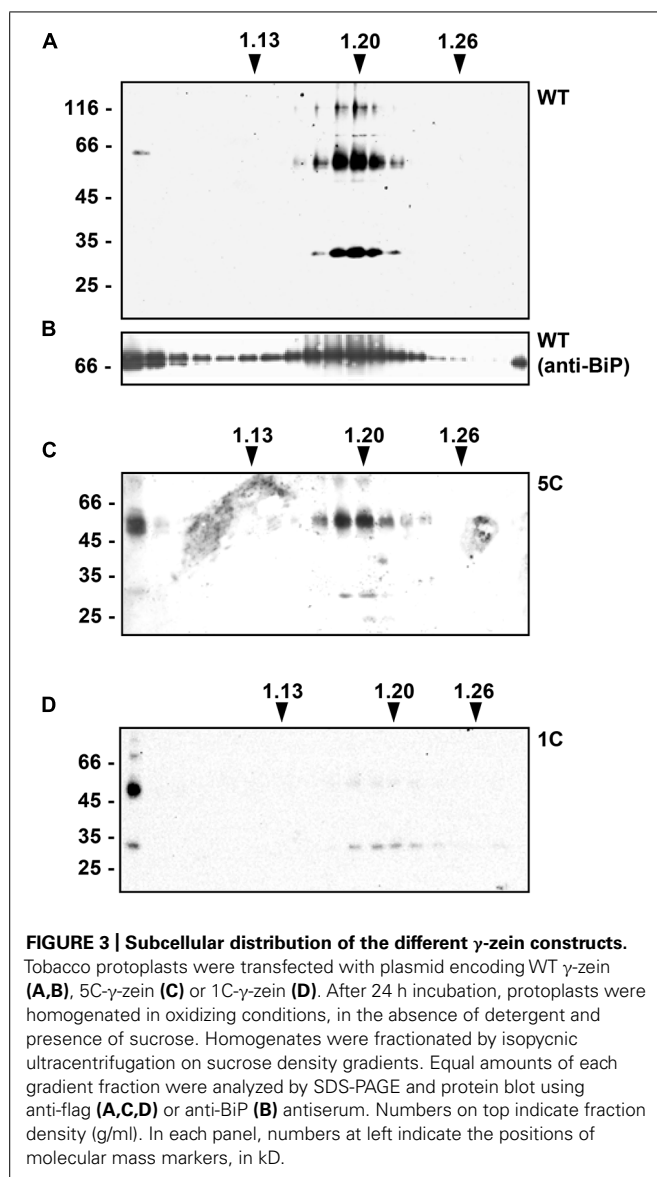
SOLUBLE γ -ZEIN TRAFFICS IN PART TO THE VACUOLE UNLESS ALL N-TERMINAL Cys RESIDUES ARE MUTATED

To determine whether the introduced mutations also changed the intracellular distribution of γ -zein polypeptides that were not secreted during the 24 h incubation, transfected protoplasts were homogenized in the absence of detergent and the homogenate subjected to isopycnic gradient centrifugation to separate sub-cellular compartments. Protein blots were analyzed using either anti-flag serum or serum against the chaperone BiP, a major soluble protein of the ER. WT γ -zein migrated as a clear peak in the region around density 1.20 g/L, which contained also BiP molecules (Figures 3A,B). This is an expected behavior for a protein forming PBs in the ER. An extremely low proportion of putative dimers migrated at top of the gradient (Figure 3A, first lane at left, faint band below the 66 kD marker). The chaperone BiP is commonly also found at top of isopycnic gradients, possibly due to partial *in vitro* release from broken ER membranes before they seal into microsomes (Figure 3B; see Gomord et al., 1997; Frigerio et al., 2001). Both 5C- γ -zein (Figure 3C) and 1C- γ -zein (Figure 3D) formed a peak at the same density of WT γ -zein, but they were also present at top of the gradients in much more relevant proportions compared to WT γ -zein, more markedly in the case of 1C- than 5C- γ -zein. This could indicate *in vitro* release from the ER; however, leaf vacuoles completely break during homogenation and release their soluble content, which remains on top of isopycnic gradients together with cytosolic soluble proteins (Pedrazzini et al., 1997; Frigerio et al., 2001). We therefore verified whether mutated, soluble γ -zein polypeptides

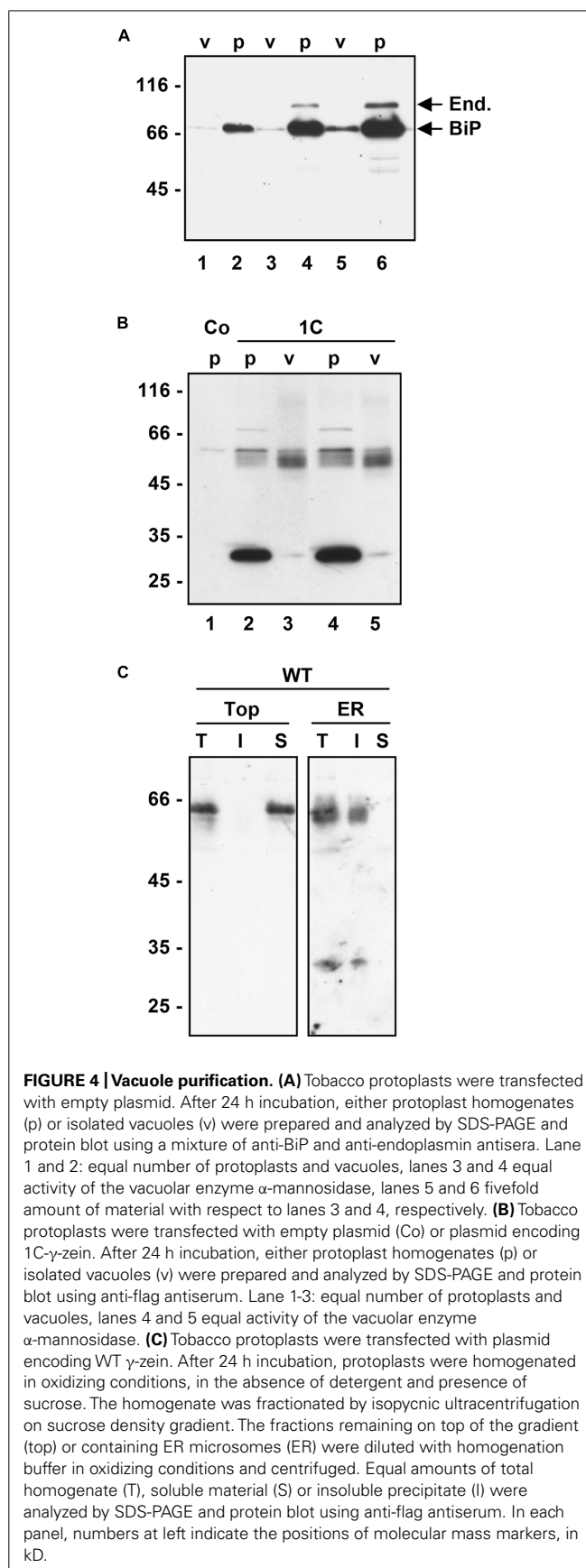
Table 1 | Secretion levels of γ -zein constructs.

γ -zein construct	WT	5C	1C	0C
	Percentage of recombinant protein that was secreted			
Experiment 1 ^a	0	0	5	79
Experiment 2	0	10	68	90
Experiment 3	0	0	32	51

^aExperiments 1, 2, and 3 are three fully independent protoplast preparation and transfection experiments.



are in part delivered to the vacuole. Protoplasts were subjected to gentle lysis, followed by centrifugation in buffers that allow vacuole floatation. These preparations of intact vacuoles contain very low proportions of the major soluble ER chaperones BiP and endoplasmic reticulum, indicating almost no contamination by microsomes originating from other endomembranes (Figure 4A). Vacuoles prepared from protoplasts expressing 1C- γ -zein were highly enriched in γ -zein dimers, indicating that this mutated protein is in part delivered to the vacuole (Figure 4B) and suggesting that also 5C- and WT γ -zein dimers present at top of isopycnic gradients (Figure 3) are located in the vacuole. Consistently, the extremely low amount of WT γ -zein dimers at top of isopycnic gradients (see the first lane in Figure 3A) are fully soluble in the absence of reducing agent, whereas those in the ER fraction are insoluble (Figure 4C). This indicates that WT γ -zein polypeptides can, albeit extremely rarely, remain soluble and available for vacuolar delivery.



SECRETION OF SOLUBLE γ -ZEIN IS INHIBITED BY BREFELDIN A AND STIMULATED BY WORTMANNIN

Most soluble seed storage proteins are delivered to storage vacuoles following a traffic pathway that involves the Golgi apparatus and multivesicular bodies (MVB, also termed prevacuolar compartment). The chemicals BFA and wortmannin affect this pathway: BFA blocks the traffic step from the ER to the Golgi apparatus and therefore inhibits vacuolar delivery as well as Golgi-mediated protein secretion (Gomez and Chrispeels, 1993; Jones and Herman, 1993; Pedrazzini et al., 1997); wortmannin inhibits the recycling of vacuolar sorting receptors from MVB to the Golgi/trans Golgi network, thus inducing default secretion of soluble proteins that use these receptors to reach vacuoles (daSilva et al., 2005). However, highly condensed insoluble prolamins can be delivered to vacuoles by autophagy (Levanony et al., 1992; Coleman et al., 1996; Reyes et al., 2011); furthermore, vacuoles can also be reached by BFA-insensitive vesicular traffic pathways that seem to bypass the Golgi apparatus or MVB (Gomez and Chrispeels, 1993; Hara-Nishimura et al., 1998; Pedrazzini et al., 2013). We have therefore investigated the effects of BFA and wortmannin on γ -zein trafficking. Treatment of protoplasts with BFA fully inhibited the secretion of 1C- and 0C- γ -zein as well as the modifications that increase the molecular mass of dimers, indicating that secretion occurs via the Golgi apparatus and that the post-translational modifications require traffic (Figure 5). There was no evident increase in accumulation of intracellular polypeptides, most probably because the drug also partially inhibits protein synthesis (Mellor et al., 1994; de Virgilio et al., 2008); consistently, WT γ -zein, which is not secreted by untreated protoplasts, accumulated at lower amounts upon BFA treatment (Figure 5). Wortmannin markedly stimulated the secretion of 1C- and to a much less extent that of 0C- γ -zein, whereas no WT γ -zein could be detected in the protoplast incubation medium even upon treatment with this drug (Figure 5). This indicates that the vacuolar delivery of a relevant proportion of 1C- γ -zein polypeptides occurs through the same pathway followed by most vacuolar storage proteins. In agreement with the other data presented in this study, the results of wortmannin treatment also indicate that WT γ -zein does not enter this traffic pathway and that traffic of 0C- γ -zein leads mainly to secretion rather than vacuolar delivery.

DISCUSSION

In all cereals, PBs contain the products of many different prolamins genes. Detailed characterization of maize seed development showed that zein genes have distinct temporal patterns of expression (Woo et al., 2001) and produce proteins with distinct ordered locations within individual PBs (Lending and Larkins, 1989). Characterization of the *floury1* (Holding et al., 2007) and *opaque1* (Wang et al., 2012) mutations indicated that specific proteins of the ER membrane and of the acto-myosin system are also involved in the shaping of PBs with normal size and morphology. These features indicate that a natural PB is assembled through a sequence of complex molecular interactions, whose details remain in large part unknown. The discovery that the ectopic expression of certain individual prolamins is sufficient to form large electron-dense

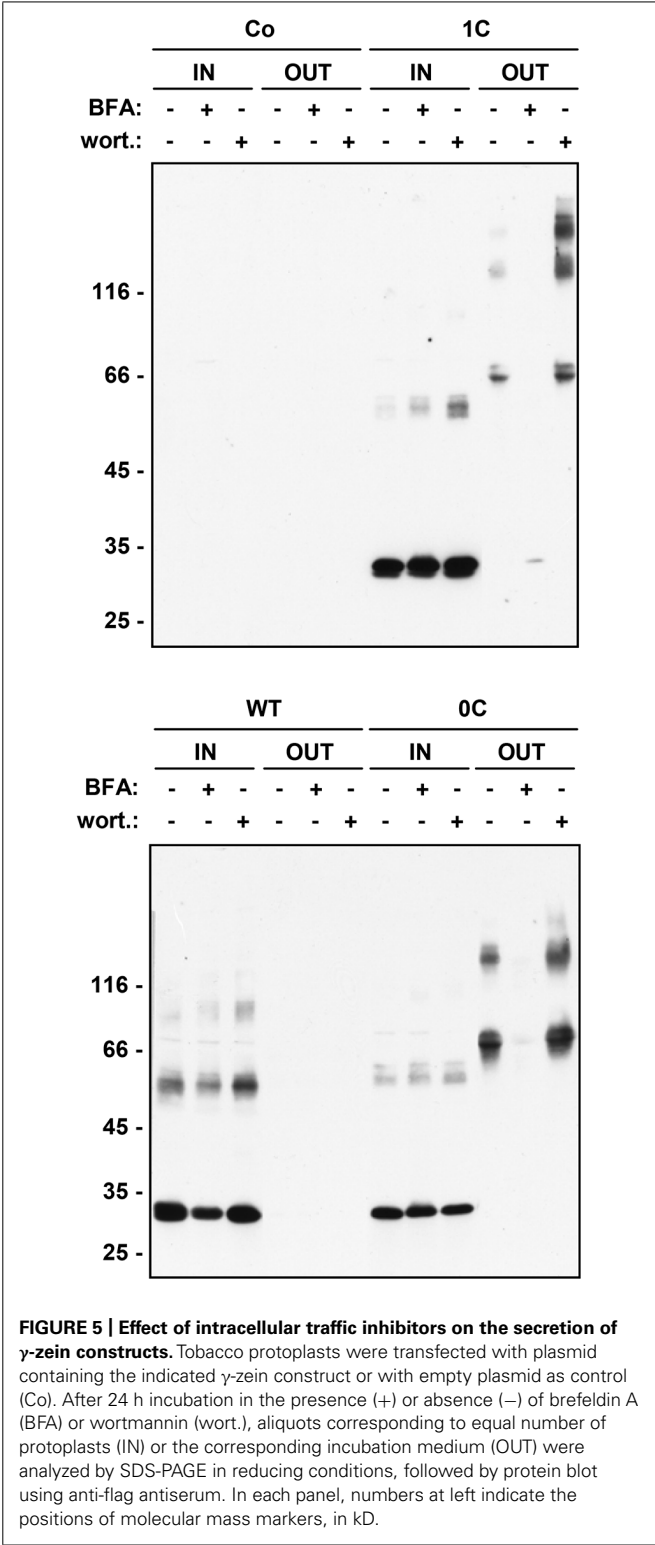


FIGURE 5 | Effect of intracellular traffic inhibitors on the secretion of γ -zein constructs. Tobacco protoplasts were transfected with plasmid containing the indicated γ -zein construct or with empty plasmid as control (Co). After 24 h incubation in the presence (+) or absence (–) of brefeldin A (BFA) or wortmannin (wort.), aliquots corresponding to equal number of protoplasts (IN) or the corresponding incubation medium (OUT) were analyzed by SDS-PAGE in reducing conditions, followed by protein blot using anti-flag antiserum. In each panel, numbers at left indicate the positions of molecular mass markers, in kD.

accretions in the ER has, however, opened the way to a reductionist approach toward understanding prolamins assembly into polymers and their ER retention (Geli et al., 1994; Bagga et al., 1995). The 27 kD γ -zein, perhaps the best characterized of these proteins, is among the most ancient prolamins (Xu and Messing, 2008, 2009),

is synthesized starting at very early stages of seed development and is specifically localized at the PB periphery, in proximity to the ER membrane, in mature PBs (Lending and Larkins, 1989). Elimination of 27 kD γ -zein by RNAi or induced gene deletion does not abolish maize PB formation, but strongly alters their morphology, size, and number, and has a general effect on endosperm texture (Wu and Messing, 2010; Yuan et al., 2014). Therefore, 27 kD γ -zein is both sufficient to form a homotypic PB and necessary for the normal assembly of a natural PB. Altogether, the features described above make 27 kD γ -zein an excellent model to define the structural requirements to initiate PB formation.

DISULFIDE BONDS, INSOLUBILITY AND INABILITY TO TRAFFIC

Deletions of γ -zein domains (Geli et al., 1994), amino acid substitutions carried out on fusions between the γ -zein N-terminal domain and otherwise soluble proteins (Pompa and Vitale, 2006; Llop-Tous et al., 2010), as well as *in vivo* treatments with reducing agent (Pompa and Vitale, 2006), all pointed to the importance of the Cys residues in the N-terminal region of the polypeptide in promoting γ -zein insolubility and ER retention, but this had not been demonstrated for the full-length protein. The results reported here demonstrate that 0C- γ -zein is fully soluble and very efficiently secreted, indicating that the presence of the C-terminal, 2S albumin-like domain and the N-terminal repeated region are not sufficient to form insoluble polymers and for ER retention in the absence of the seven N-terminal Cys residues. This efficient secretion also indicates that 0C- γ -zein is not a misfolded protein disposed by ER quality control. Indeed all constructs studied here are able to form dimers, suggesting a similar folding pathway. Forms that could represent dimers have also been detected in transgenic plants expressing γ -zein (Geli et al., 1994; Bellucci et al., 2000) as well as upon expression of zeolin (Mainieri et al., 2004) and Zera (Torrent et al., 2009) fusions. Intracellular dimers and further polymers are detected in much higher proportions when extraction is performed in the absence of reducing agent. The detection of dimers of 0C- γ -zein and polymers of 1C- γ -zein suggest that either the intra-chain disulfide bonds of the 2S albumin-like region allow an overall conformation that favors inter-chain hydrophobic interactions or, perhaps surprisingly, the Cys residues present in this region are also directly involved in inter-chain bonds.

The results presented here confirm those obtained by Zera-ECFP mutagenesis regarding the direct relationship between number of Cys residues in the N-terminal domain and ability to form ER-located PB (Llop-Tous et al., 2010). However, the high importance of the first two N-terminal Cys in Zera-ECFP was not confirmed in full-length γ -zein: mutagenesis of these residues in Zera-ECFP resulted in full secretion (Llop-Tous et al., 2010), whereas 5C γ -zein is largely insoluble and ER-located, and it is almost unavailable for secretion. This indicates that the contribution of individual Cys residues of the N-terminal region to PB formation are less strict in full length γ -zein, as also suggested by domain deletion experiments (Geli et al., 1994).

As mentioned in the Introduction, synthetic (VHLPPP)₈ forms an amphipathic helix that interacts *in vitro* both with itself and with liposomes (Kogan et al., 2004). The inter-chain disulfide

bonds may thus determine folding properties that stabilize and further promote similar interactions *in vivo*. The affinity with lipids may explain the natural position of γ -zein at the periphery of the PB, in close contact with the luminal face of the ER membrane, its ability to form stable PBs also when expressed alone, and the altered PB shape in maize mutants that lack γ -zein. Thus, even if the very abundant α -zeins also assemble into disulfide bonded polymers and do not seem to interact covalently with γ -zein (Vitale et al., 1982), the latter seems fundamental to provide a scaffold that favors the stable architecture of a natural PB.

POLYMERIZATION AND VACUOLAR SORTING

As two, six or all seven Cys residues of the N-terminal domain were mutated, a parallel increase in BFA-sensitive secretion was observed. However, unlike WT γ -zein, intracellular 5C- and 1C- γ -zein were not exclusively located in the ER. The presence of a relevant proportion of protein at top of isopycnic gradients suggested a vacuolar localization, confirmed by vacuole isolation. The polypeptides delivered to the vacuole are soluble. Treatments with wortmannin indicated that this vacuolar delivery is due to traffic rather than autophagy and that the route is the same followed by most 2S albumins and 7/11S globulins. Very efficient secretion of 0C- and partial vacuolar sorting of 1C- γ -zein indicate that Cys¹¹⁷ acts as a determinant for vacuolar sorting. These results support a model of the evolution of PB formation from the mechanism of storage protein sorting to vacuoles and not directly from default secretion.

The γ -zein fragments used in zeolin and Zera constructs never included Cys¹¹⁷, because they stopped a few amino acids ahead of it. We do not know whether any other Cys residue of the N-terminal region would be sufficient in promoting vacuolar sorting of full-length γ -zein, but the following observations indicate that this promotion occurs because the Cys residue stabilizes polymerization events that require other γ -zein domains. First, a γ -zein deletion construct that lacks most of the N-terminal region is very efficiently secreted but still contains Cys²⁶, Cys²⁸, and Cys¹¹⁷ (Geli et al., 1994), indicating that these residues are not sufficient *per se* to drive vacuolar sorting or ER retention. Second, experiments performed on the bean 7S globulin phaseolin indicate that the short C-terminal hydrophobic peptide that acts as a vacuolar sorting signal and promotes transient polymerization events (Frigerio et al., 1998; Holkeri and Vitale, 2001; Castelli and Vitale, 2005) can be at least in part replaced by a Cys residue that forms an inter-chain bond (Pompa et al., 2010). There is thus a striking similarity between the effect of the presence of a single additional Cys in 1C- compared to 0C- γ -zein and the artificial addition of a single Cys to a mutated, secreted phaseolin: in both cases vacuolar sorting is stimulated. It should be underlined that addition of Cys residues in phaseolin domains distant from the C-terminal end does not have any effect, indicating that disulfide bonds are formed when close interactions anyway exist, as expected (Pompa et al., 2010). In γ -zein, these interactions clearly require the Pro-rich amphipathic, repeated region.

AN EVOLUTIONARY MODEL

Prolamins have been divided into three groups, named I, II, and III starting from the most recently evolved (Xu and Messing, 2009).

The γ - and β -zeins have been assigned to group II. Their synthesis during seed development starts before that of the α - and δ -zeins, which belong to group I (Lending and Larkins, 1989). Maize does not have group III members. The 27 kD γ -zein is therefore among the most ancient maize prolamins (Xu and Messing, 2008, 2009). The A, B, and C domains that are common to 2S albumins and to other vacuolar seed proteins – such as trypsin inhibitor – are the most common feature of group II and III prolamins, indicating an evolution involving regions of vacuolar proteins (Xu and Messing, 2008). It has been hypothesized that conversion of Cys residues of the A, B, or C domains from an involvement in intra-chain disulfide bonds to inter-chain bonds may have been important events in this evolution (Kawagoe et al., 2005). The results shown here indicate a different model, in which at least one of the key mechanisms was the addition of new Cys residues that further increase and stabilize inter-chain interactions otherwise involved in vacuolar sorting (Figure 5). According to this model, the progressive addition reached a level that promoted the formation of large, insoluble polymers unable to traffic out of the ER (Figure 6).

The ER is the port of entry of the secretory pathway; intuitively, the development of a mechanism for protein accumulation in this compartment would be both more rudimentary and more energy-saving than using protein trafficking and sorting to vacuoles. However, the very complex array of players and molecular interactions involved in productive protein folding and quality control in the ER, the main functions of this

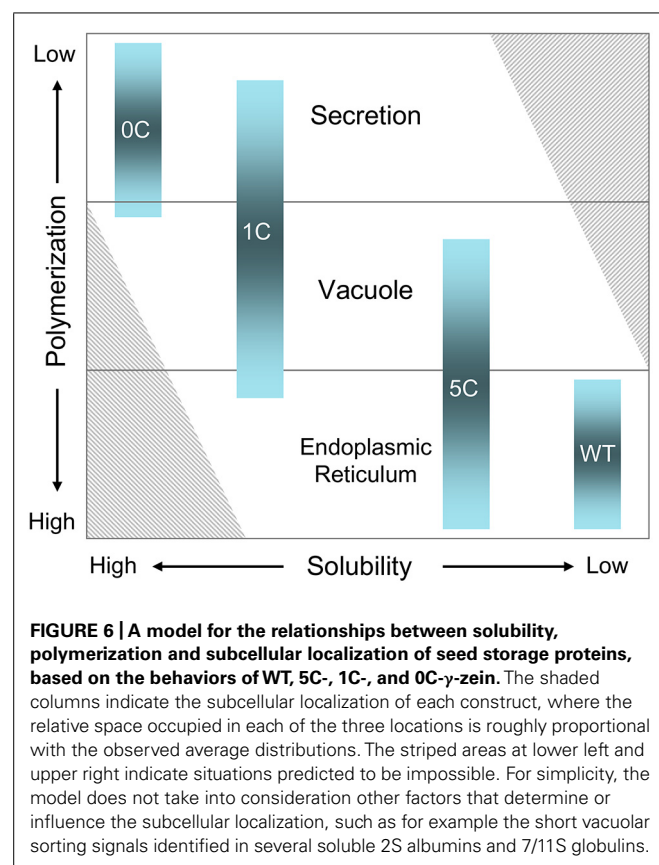
compartment, may be negatively affected, at least in theory, by the presence of large amounts of stored material. Evolution of proteins that accumulate in the ER as insoluble polymers, apparently a very unusual event in any kingdom, may have been favored by the fact that the endosperm, unlike cotyledons, undergoes programmed cell death at the late stages of cereal seed development, making thus irrelevant the final location of stored proteins for what regards their mobilization during germination. It should, however, be underlined that the many experiments in which proteins that accumulate in the ER were ectopically expressed in vegetative tissues indicate that the plant ER is anyway very tolerant for what regards protein accumulation (Herman, 2008), another feature that may have allowed protein body formation in plants but not in members of other kingdoms.

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Recent advances in the study of prolamin storage protein organization and function

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Prolamin storage proteins are the main repository for nitrogen in the endosperm of cereal seeds. These stable proteins accumulate at massive levels due to the high level expression from extensively duplicated genes in endoreduplicated cells. Such abundant accumulation is achieved through efficient packaging in endoplasmic reticulum localized protein bodies in a process that is not completely understood. Prolamins are also a key determinant of hard kernel texture in the mature seed; an essential characteristic of cereal grains like maize. However, deficiencies of key essential amino acids in prolamins result in relatively poor grain protein quality. The inverse relationship between prolamin accumulation and protein quality has fueled an interest in understanding the role of prolamins and other proteins in endosperm maturation. This article reviews recent technological advances that have enabled dissection of overlapping and non-redundant roles of prolamins, particularly the maize zeins. This has come through molecular characterization of mutants first identified many decades ago, selective down-regulation of specific zein genes or entire zein gene families, and most recently through combining deletion mutagenesis with current methods in genome and transcriptome profiling. Works aimed at understanding prolamin deposition and function as well as creating novel variants with improved nutritional and digestibility characteristics, are reported.

Keywords: zein, kafirin, prolamin, storage protein, endosperm, QPM, protein body, deletion mutagenesis

INTRODUCTION

Although prolamins are the dominant class of seed storage protein in many cereals, this article illustrates their function and organization in maize and sorghum, the first and fifth most globally important cereal crops. Maize and sorghum are physically distinct in terms of their vegetative and reproductive architecture with maize having separate male and female reproductive organs and sorghum having hermaphroditic flowers that produce seed less than one tenth of the size of domestic maize seed. Sorghum is also usually more water use efficient and has potential for increased cultivation in marginal lands for this reason. Despite these differences, maize and sorghum are genetically more closely related than to other grasses. This is best shown by the phylogenetic relationships between their zein and kafirin prolamin-encoding genes (Xu and Messing, 2008).

PROLAMIN GENES

Prolamins were initially distinguished as a group of proteins soluble in 70% ethanol (Osborne, 1897). However, differences in aqueous solubility and ability to form disulfide interactions, were later used to classify prolamin sub-families. The zeins are grouped into α , β , γ , and δ types based on these properties (Esen, 1987; Coleman and Larkins, 1999). Similarly, the kafirins are grouped into α , β , γ , and δ types based on their molecular weight, solubility, and gene sequence (Shull et al., 1991). Alpha zeins are encoded by four different gene sub-families (Z1A, Z1B, Z1C, and Z1D) that in the B73 reference line contain more than 40 genes in six chromosomal locations (Feng et al., 2009). There is,

however, copy number and expression variation across different maize backgrounds. While substantial α -kafirin gene duplication also occurred in sorghum, all 20 α -kafirin genes are clustered at one chromosome 5 location in the BTx623 genome (Xu and Messing, 2008).

Alpha prolamins resolve at ~19- and 22-kDa on SDS-PAGE gels in both maize and sorghum. In maize, the 19-kDa α -zeins are encoded by the Z1A, Z1B, and Z1D subfamilies while the 22-kDa α -zeins are encoded by the Z1C subfamily (Song et al., 2001; Song and Messing, 2002). In sorghum, 19-kD α -kafirins are encoded by the K1 α 19 subfamily while the 22-kD α -kafirins are encoded by the K1 α 22 subfamily (Xu and Messing, 2009). Alpha prolamins cluster in a broad phylogenetic group (Group 1) as do the δ -zein genes. 10-kD and 18-kD δ -zeins are encoded by z2 δ 10 and z2 δ 18 genes in maize and k2 δ 2 and k2 δ 18 genes in sorghum (Xu and Messing, 2008, 2009). γ - and β -prolamins cluster within Group 2 (Xu and Messing, 2008, 2009). Unlike α -prolamins, Group 2 prolamin genes exist as single copies rather than highly duplicated gene families. In maize, this group consists of z2 γ 16 and z2 γ 27, encoding 16- and 27-kD γ -zeins, and z2 γ 50, encoding a 50-kD γ -zein. Similarly, k2 γ 27 and k2 γ 50 encode 27- and 50-kD γ -kafirins in sorghum although there is no 16-kD γ -kafirin. The maize z2 γ 16 gene is thought to derive from an unequal crossing-over event that occurred after allotetraploidization (Xu and Messing, 2008). Maize and sorghum also have genes encoding a 15-kD β -prolamin (z2 β 15 and k2 β 15) which are related to the γ -prolamins within Group 2 (Xu and Messing, 2008).

PROLAMIN ACCUMULATION, THEIR EFFECT ON GRAIN TEXTURE, FUNCTIONALITY, AND PROTEIN QUALITY

Sorghum kernels are usually much smaller than maize kernels and both, but especially sorghum, show considerable heterogeneity in seed size across varieties (**Figure 1**). Despite this variability, maize and sorghum seed have similar endosperm composition having a high proportion of glassy or vitreous endosperm at the periphery of the mature kernel and a central opaque region (**Figure 1**). Vitreous endosperm is important for resistance to insect and fungal damage, resilience during harvest and storage, and many end use characteristics. Although we are still learning how vitreous endosperm is formed during kernel maturation, considerable evidence suggests that accumulation and packaging of prolamins into endoplasmic reticulum (ER) protein bodies play a central role. For example, in maize the vitreous outer region of the endosperm contains much more zein than the soft, opaque interior, and environmental conditions that cause reduced zein synthesis, such as nitrogen depletion, result in kernels that are soft and starchy throughout (Tsai et al., 1978). Sorghum kernels grown in limited nitrogen conditions are smaller and lack vitreous endosperm (**Figure 1**). Duvick (1961) proposed that in the periphery of the developing starchy endosperm, there is a certain ratio of starch grains, protein bodies, and viscous cytoplasm which dries down to form a rigid glass-like structure at kernel maturity (the vitreous endosperm; **Figure 1**). Toward the center of

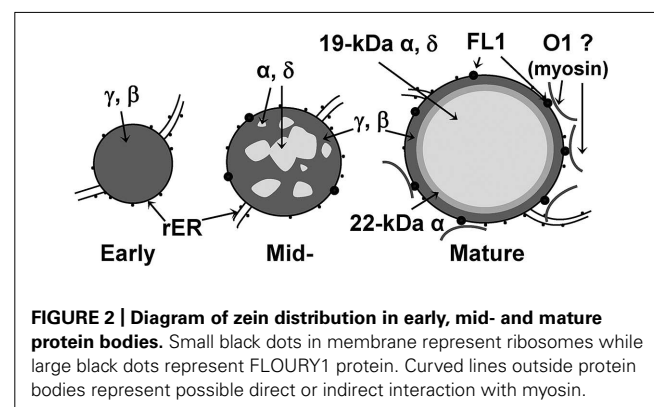
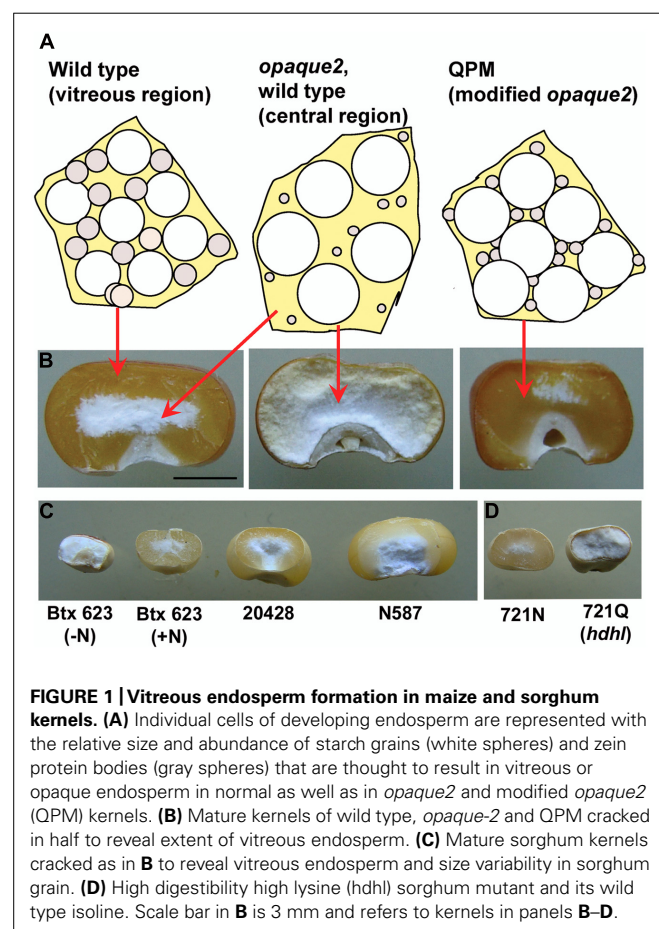
the endosperm, where zein protein bodies are smaller and less abundant, the rigid matrix is not formed during kernel desiccation, which results in the formation of the friable, opaque kernel center (**Figure 1**; Duvick, 1961). In opaque mutants, the central opaque region extends to the periphery of the endosperm (**Figure 1**).

Protein body formation in maize is controlled at several levels, including the temporal and spatial regulation of zein gene expression, the level of transcription and interactions that occur between the different types of zein proteins (Woo et al., 2001; Kim et al., 2002). Zeins are devoid of the essential amino acids, lysine and tryptophan (Mertz et al., 1964), but account for more than 70% of maize endosperm protein. This results in an overall protein content that is especially deficient in these amino acids. The equally dominant sorghum kafirins, share this nutritional deficiency, but it is compounded by their poor digestibility (Aboubacar et al., 2001) that results from their high degree of disulfide cross-linking.

Our knowledge of how prolamins are packaged at such high levels comes largely from maize. Zeins are retained as discretely layered membrane bound accretions in the ER (Lending and Larkins, 1989; **Figure 2**). Protein bodies start as small accretions consisting entirely of γ -zein, consistent with the slightly earlier onset of γ -zein gene expression (Woo et al., 2001). As protein bodies expand, α - and δ -zeins are sequestered into the protein body core, where they become encapsulated in a shell of γ -zeins. The 19-kD α -zeins are the most abundant class and immunological evidence suggests that the 22-kD α -zeins form an intermediary layer between the central 19-kD α -zeins and the γ -zein periphery (Holding et al., 2007). Although the γ -zeins have some functional redundancy, selective down-regulation has suggested they also have specialized roles as described below (Guo et al., 2013).

MUTATIONS IN PROLAMIN GENES AND RELATED FACTORS SHED LIGHT ON PROLAMIN FUNCTIONAL ORGANIZATION

Natural and engineered mutants exhibiting reduced kernel hardness offer the opportunity to dissect the various biochemical and biophysical processes that affect vitreous endosperm formation, and consequently their study is of significant agronomic importance. Kernels of these mutants are opaque since they do not transmit light and often show defects in the accumulation of zeins or their packaging into ER-localized protein bodies. However, it is now clear that other factors are also important determinants



of kernel texture since several recent studies have shown that vitreous endosperm can be disrupted by processes that do not affect zein synthesis and protein body structure. For example, vitreous endosperm formation is abolished in the *floury1* mutant as a result of knocking out a protein body ER membrane protein which seems to be involved zein organization (Holding et al., 2007). Therefore, it is likely that further protein body-related organizational factors remain to be identified. Other opaque mutants are the result of genetic aberrations in processes unrelated to protein body formation such as amino acid biosynthesis, plastid development and cytoskeletal function (Holding et al., 2010; Myers et al., 2011; Wang et al., 2012). This indicates that further functional genomics is needed to generate a more complete understanding of the factors which control late endosperm development.

The most well-known of the maize opaque mutants is *opaque2* (*o2*) which has been widely studied because of the increased lysine and tryptophan accumulation (Mertz et al., 1964) resulting from its reduced accumulation of alpha zeins. Cloning of the *O2* gene revealed that it encodes a transcription factor that regulates α -zeins (Schmidt et al., 1990) as well as other genes such as pyruvate Pi dikinase (Maddaloni et al., 1996). Although the soft kernels and yield penalty of *o2* prevented its commercial success, subsequent breeding projects, including those in Mexico (Vasal et al., 1980) and South Africa (Geevers and Lake, 1992), led to the development of hard kernel *o2* varieties called quality protein maize (QPM). QPM kernels maintain the low levels of α -zeins and thus, retain the high levels of lysine and tryptophan but the genetic basis of *o2* endosperm modification is complicated and poorly understood. The most prominent biochemical feature of QPM endosperm is the accumulation of the 27-kD γ -zein at 2–3 fold higher levels than in wild type and *o2* (Wallace et al., 1990; Geetha et al., 1991; Lopes and Larkins, 1991). Although the genetic or epigenetic mechanism of this increase is unknown, the degree of QPM endosperm vitreousness closely correlates with the level of 27-kD γ -zein protein (Lopes and Larkins, 1991). Furthermore, the 27-kD γ -zein gene maps to the most significant QTL for endosperm modification in QPM located on chromosome 7 (Lopes and Larkins, 1995; Lopes et al., 1995; Holding et al., 2008, 2011). QPM endosperm accumulates larger numbers of small, γ -zein rich protein bodies (Figure 1) which are proposed to allow the formation of a rigid glassy matrix similar in texture to mature wild type endosperm (Figure 1). γ -zein is known to be essential for endosperm modification in QPM (Wu et al., 2010), although the extent to which it is alone sufficient is unknown.

Although the functional redundancy resulting from the multi-member α -zein gene families has prevented the identification of recessive mutants, several dominant opaque mutants have been characterized. The phenotypes in these mutants result from the accumulation of defective prolamins that interfere with normal prolamins deposition and cause ER stress responses (Coleman et al., 1997; Kim et al., 2004, 2006; Wu et al., 2013). *Floury-2* (*fl2*), *Defective endosperm B30* (*De-B30*), and *Mucronate* (*Mc*) are caused by dominantly acting mutations in zein genes. *fl2*, *De-B30*, and *Mc* show pleiotropic effects and result in a general reduction of all zeins (causing increases in lysine-containing

proteins as in *o2*) and lobed protein bodies (Lending and Larkins, 1992). In the case of *fl2* and *De-B30*, this result from mutations that cause the signal peptides to remain attached in the 22-kD α -zein and 19-kD α -zein respectively, resulting in aggregation of these proteins at the ER membrane (Gillikin et al., 1997; Kim et al., 2004). The *Mc* mutant (Soave and Salamini, 1984) results from a 38 bp deletion that leads to a frame-shift mutation in the 16-kD γ -zein (Kim et al., 2006). The abnormal zeins produced in these mutants result in ER stress and cause a constitutive unfolded protein response (UPR), as shown by the dramatic up-regulation of a number of UPR-associated genes (Hunter et al., 2002). In fact, elevated markers for endosperm stress is a common feature of all opaque mutants studied irrespective of discernible changes in zeins and zein protein bodies (Hunter et al., 2002). This leads to the suggestion that endosperm stress and a resulting energy crisis may be at least partially responsible for disrupting vitreous endosperm formation (Guo et al., 2012).

Zein and kafirin proteins are packaged into protein bodies that are inherently recalcitrant to digestion. This results from the disulfide cross-linked nature of the γ -prolamins themselves and the fact that they form a shell of relatively low surface area in relation to the amount of prolamins packaged. The poor digestibility of prolamins is especially pronounced in sorghum. An opaque kernel sorghum mutant was identified in an EMS mutagenized population that had increased lysine content as a result of reduced kafirin accumulation, and most notably, a marked increase in protein digestibility (Oria et al., 2000). Called the “high digestibility high lysine” (*hdhl*) variant (Figure 1), this mutant has significant potential to improve the utility of sorghum as a human staple and livestock feed. The increased digestibility apparently results from increased protease accessibility caused by reticulation of kafirin protein body shape, in a manner reminiscent of *fl2*, *De-B30*, and *Mc* in maize. Furthermore, developing *hdhl* kernels also exhibit a defined UPR. These phenotypic similarities to the maize mutants prompted a directed cloning approach in which the mutation was first mapped to an alpha kafirin gene cluster and extensive genomic and cDNA sequencing identified a mutant-specific α -kafirin copy harboring point mutation (Wu et al., 2013). The mutation causes a threonine substitution of an alanine residue, that is strictly conserved at position 21 of the signal peptide of all known α -prolamins (Wu et al., 2013). This substitution causes a dominant-negative response through low level accumulation of an uncleaved α -kafirin (Wu et al., 2013).

The characterization of opaque mutants has shown that vitreous endosperm formation depends on the correct expression and processing of prolamins themselves but also on factors that may have indirect roles in prolamins protein bodies such as *Floury-1* and *Opaque-1* (Holding et al., 2007; Wang et al., 2012). *Floury-1* was identified as a protein body ER membrane-specific protein, through a *Mutator* knock-out line that displays normal amounts of zein proteins and normal protein body size and shape, but slightly disorganized zein organization (Holding et al., 2007). *Floury-1* contains a domain of unknown function (DUF593) for which the location inside or outside the ER lumen was not determined (Holding et al., 2007). Recently, screens for

endomembrane proteins that bind myosin XI proteins in *Ara-bidopsis* identified myosin receptor proteins that bind myosin through DUF593 (Peremyslov et al., 2013). This suggests that FL1 may function to attach protein bodies to the cytoskeleton and may explain the absence of a severe protein body phenotype in *fl1*. Similar to *fl1*, *o1* also does not have reduced zein accumulation but has a reduced number of slightly smaller protein bodies (Wang et al., 2012). *O1* was identified by positional cloning and encodes a myosin XI protein that is associated with cisternal and protein body ER (Wang et al., 2012). Although it has not been demonstrated, this suggests there may be a direct or indirect functional interaction between FL1 and O1 (**Figure 2**) and may suggest that the cytoskeleton plays an essential role in endosperm maturation.

Factors unrelated to prolamins are also essential for vitreous endosperm formation as demonstrated by opaque mutants such as *mtol40*, *o7*, and *o5* (Holding et al., 2010; Miclaus et al., 2011a; Myers et al., 2011). *MTO140* encodes a member of the maize arogenate dehydrogenase family that are involved in tyrosine biosynthesis (Holding et al., 2010), while *O7* encodes an acyl-CoA synthetase-like protein (Miclaus et al., 2011a). *O5* encodes the major biosynthetic enzyme for synthesis of chloroplast membrane lipids, monogalactosyldiacylglycerol synthase and the mutant is specifically defective in galactolipids necessary for amyloplast and chloroplast function (Myers et al., 2011). As described in the section on deletion mutagenesis below, kernel opacity is a pleiotropic characteristic of kernel mutants also displaying other phenotypes such as small kernel, rough kernel, defective kernel, viviparous, and partial empty pericarp.

TRANSGENIC EFFORTS TO OFFSET AMINO ACID DEFICIENCIES IN MAIZE

Various types of biotechnological approaches have been considered for improving the amino acid composition of maize (Holding and Larkins, 2008). In order to increase the methionine content, Lai and Messing (2002) created transgenic maize plants expressing a chimeric gene consisting of the coding region of 10-kD δ -zein and the promoter and 5' untranslated region of the 27-kDa γ -zein. Although the effects on synthesis of endogenous high-sulfur zeins were not reported, uniformly high levels of 10-kDa δ -zein and methionine were observed and maintained over five backcross generations. Initial poultry feeding studies suggested that the transgenic grain was as effective as non-transgenic grain supplemented with free methionine.

For increasing the lysine content in maize, either non-maize, lysine-rich proteins can be expressed in an endosperm specific manner, or the zein sequences themselves can be manipulated to contain lysine. The former approach has been tried with a number of proteins which have mostly been expressed using γ - or α -zein promoters (Kriz, 2009). In order to make a significant difference to mature kernel lysine content, transgenic proteins must be driven to accumulate in very high amounts, in forms that do not interfere with the normal timing and pattern of endosperm programmed cell death and in a manner that does not induce UPR or kernel opacity. Furthermore,

candidate proteins must meet stringent standards for potential allergenicity.

For the above reasons, perhaps the most promising way to elevate endosperm lysine is by modifying the coding sequences of the zein genes themselves. Lysine-containing zeins are more likely to be stored in their native ER protein body form and potentially in high enough quantities to significantly impact lysine levels. Preliminary studies in modifying a 19-kD α -zein with lysine residues, showed the transgenic protein to accumulate in protein body-like structures in *Xenopus* oocytes. Since the 19-kD α -zein is by far the most abundant zein, being packaged in the center of protein bodies (Holding et al., 2007), it may only be necessary to substitute a fraction of the native protein with a modified protein to make a significant impact on kernel protein quality. The 27-kD γ -zein, with its suspected role as the initiator of protein body formation, and as the major *o2* modifier, as well as its abundant accumulation, is also a good candidate for substituting certain amino acids with lysine. One study showed, using transient transformation of maize, that a 27-kD γ -zein in which (Pro-Lys)_n sequences were inserted contiguous to or in substitution of the Pro-Xaa region, that the modified γ -zein co-localized with endogenous α - and γ -zeins (Torrent et al., 1997). We are further investigating this type of approach using custom gene synthesis and the latest protein modeling programs that can assist in selection residues for substitution than are least likely to adversely affect normal zein packaging. To increase the chances of lysine-rich transgenic proteins being driven to accumulate at significant levels, it may be necessary to reduce the accumulation of native α -zeins. An effective way to do this is using RNA interference (RNAi) as described below.

Zeins are much less likely to invoke allergic reactions than the wheat prolamins, the glutens. However, when considering potential transgenic bio-fortification approaches, allergen databases must be consulted. Among several allergenic maize seed proteins, precursors of α - and β -zein have both been shown to be allergenic (Pastorello et al., 2009).

RNA INTERFERENCE LINES HAVE ALLOWED DISSECTION OF REDUNDANT AND NON-REDUNDANT PROLAMIN FUNCTION

Naturally occurring and induced opaque mutants have been extensively studied because of their potential for grain nutritional improvement and have created an understanding of prolamins packaging in ER protein bodies and its relationship to ER protein quality control and UPR. However, opaque mutants carrying nutritional benefits such as *o2* and *fl2* also carry negative pleiotropic characteristics. Furthermore, the extensive gene duplication and gene redundancy, especially in the α -prolamin classes, have resulted in a lack of recessive prolamins mutants, and an inability to infer the relative prolamins functional redundancy and non-redundancy. RNAi has been an effective tool for further addressing maize and sorghum nutritional potential as well as providing new information regarding functions of specific prolamins classes (Holding and Messing, 2013).

Initial use of RNAi to eliminate α -zeins revealed the possibility of creating dominant, non-pleiotropic low-zein lines for lysine improvement. The dominance of such transgenes circumvents one

of the limitations of *o2* based varieties which is that the *o2* allele must be maintained in the homozygous mutant state, which is easily lost through wild type pollen contamination, and is especially problematic in an open pollinated QPM setting. Originally, the 22-kD α -zein was targeted and transgenic lines had considerably reduced α -zein and concomitant increase in lysine (Segal et al., 2003) despite lines accumulating substantial amounts of 19-kD α -zein. Protein bodies were of reduced size due to reduced α -zein filling and notably, exhibited distorted lobed appearances. Similarly, a study in sorghum aimed to increase lysine content and digestibility by removing α -kafirins (Kumar et al., 2012). Like the maize study, only one class of α -kafirins (22-kD) was targeted. Though a reduction in protein body size was not reported, the transgene resulted in protein body lobing similar to the 22-kD α -zein RNAi lines and dominant α -zein signal peptide mutants (Kumar et al., 2012). This suggests that 22-kD α -prolamins may be essential for correct packaging of the 19-kD α -prolamins and is consistent with the observed peripheral location of the 22-kD α -zeins relative to the 19-kD α -zeins (Holding et al., 2007). Later works targeting both the 19- and 22-kD α -zeins did not address the morphological effects on protein bodies (Huang et al., 2006; Wu and Messing, 2011). Using a chimeric α -zein RNAi cassette, comprised of \sim 250 bp regions of the most abundantly expressed Z1A, Z1B, Z1C, and Z1D α -zein family members in B73, and the 27-kD γ -zein promoter and the cauliflower mosaic virus 35S terminator, we suppressed both 22- and 19-kD α -zeins to low levels. This resulted in very small protein bodies but did not suppress protein body number per unit area suggesting that while α -zeins drive protein body filling, they are not involved in protein body initiation (Guo et al., 2013; **Figure 3**). In contrast to suppression of 22-kD α -zein alone, no lobing or distortion of protein bodies was observed in support of the suggestion that such phenotypes are generated by inappropriately located or unconstrained α -zeins. Similarly, in *o2* where all α -zeins are reduced, protein bodies are small but not misshapen (Geetha et al., 1991).

Apart from the *Mc* mutant, which accumulates a dominant-negative 16-kD γ -zein with a nonsense C-terminus as a result of a frame-shift mutation (Kim et al., 2006), mutants of γ -prolamins have not been described. This may be partly due to some functional redundancy of different γ -prolamins but knowledge of their roles is very limited aside from their ability to form the cross-linked outer shell of ER-protein bodies. A specialized role for the 27-kD γ -zein in protein body initiation has been inferred from its increase in QPM endosperm and concomitant increase in protein body number. This is also supported by the *o15* mutant in which reduced 27-kD γ -zein leads to reduced protein body number (Dannenhoffer et al., 1995).

RNA interference lines have provided functional insight about different γ -zeins. Transgenic events that targeted the 27-/16-kD γ -zeins, whose genes share sequence similarity, as well as a separate 15-kD β -zein RNAi event caused minor morphological changes to protein bodies (Wu and Messing, 2010). Although an incidence of very small protein bodies was shown in both cases, the majority of protein bodies were of normal size and no changes in protein body number were reported (Wu and Messing, 2010). The 50-kD γ -zein was not targeted in this study since it was assumed to have

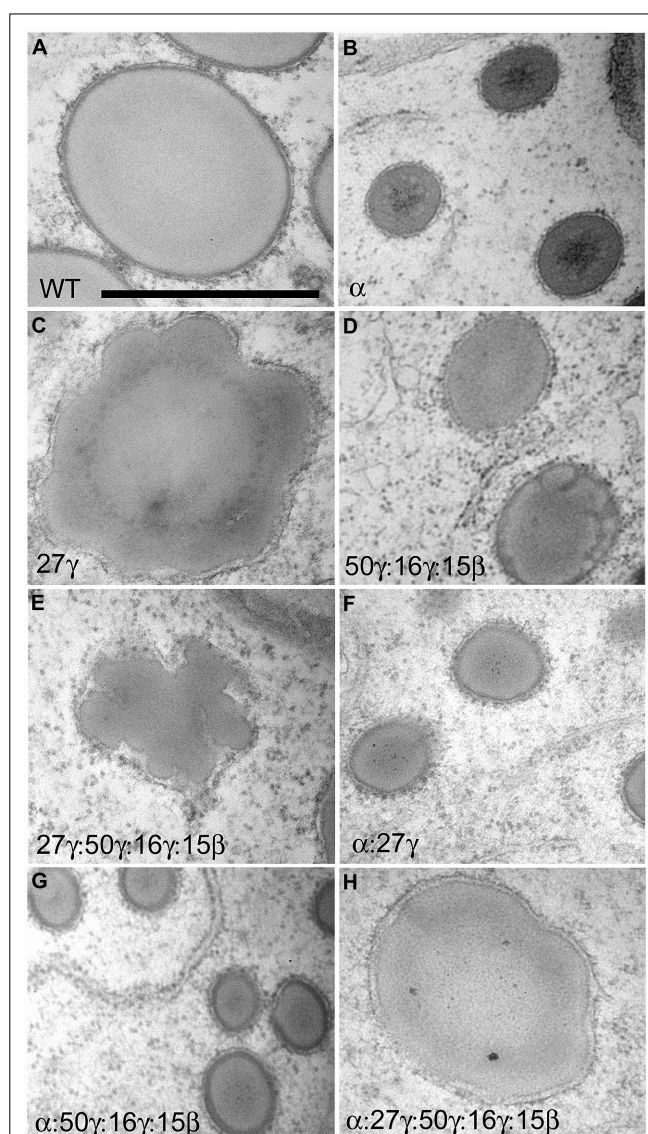


FIGURE 3 | TEM analysis showing protein body size and morphology in the fourth sub-aleurone starch layer of 18 DAP endosperm in zein RNAi lines and their crosses. Scale bar in **A** is 1 μ m and refers to all panels. RNAi transgenes present are shown in bottom left of each panel in **A–H**. Figure copyright of American Society of Plant Biologists.

a minor role in protein body formation due to its low abundance. In fact, by manipulating the ethanolic extraction procedure, it has been shown that the 50-kD γ -zein has comparable abundance to other γ -zeins except the dominantly abundant 27-kD γ -zein (Guo et al., 2013).

We made RNAi constructs to dissect the role of 27-kD γ -zein with respect to other γ -zeins. The first was a complete 27-kD γ -zein gene RNAi (27- γ) driven by its native promoter and terminated by the cauliflower mosaic virus 35S terminator, and this almost completely inhibited synthesis of 27-kD γ -zein and, because of sequence similarity, significantly reduced 16-kD γ -zein. A second transgene was a synthetic RNAi gene consisting of \sim 250 bp regions of the 16- and 50-kD γ -zein and the 15-kD

β -zein (16/50/15- γ) that were selected to have the least similarity to 27-kD γ -zein. In this case, the promoter of a dominantly expressed 22-kD α -zein gene was used in this case, to avoid potential co-suppressive effects on the 27-kD γ -zein level that could have resulted from using the 27-kD γ -zein promoter. The 16/50/15- γ transgene reduced all target proteins to very low levels while leaving 27-kD at high levels (Guo et al., 2013). Protein bodies in developing endosperm of 16/50/15- γ events were of normal shape but were of reduced size, and accumulated in normal numbers (Figure 3; Guo et al., 2013). This illustrates that while the 16/50/15-kD γ -zeins are necessary for protein body filling and α -zein encapsulation, they are not involved in protein body initiation. Conversely, the 27- γ RNAi did not reduce protein body size and induced undulations in protein body shape (Figure 3), suggesting that the 27-kD γ -zein is not necessary for the bulk of protein body filling and that other γ -zeins can fulfill this role. Most notably however, protein bodies in 27- γ events were of much lower number than control, suggesting that the 27-kD γ -zein alone has the role of protein body initiation (Guo et al., 2013). Combining the γ -zein transgenes resulted in addition of the reduced number/distortion phenotypes of the 27- γ RNAi with the reduced size phenotype of the 16/50/15- γ transgene (Guo et al., 2013; Figure 3). Similarly, combining either of the γ -zein RNAi transgenes with the α -zein RNAi resulted in small protein bodies (Figure 3) with the 27- γ transgene reducing protein body number more significantly than the 16/50/15- γ transgene (Guo et al., 2013). When all three transgenes were combined to reduce all zeins proportionately, while protein body number was very low, protein bodies had a normal size and relatively normal morphology (Figure 3; Guo et al., 2013). This showed that maintenance of an appropriate ratio of all zeins is critical for their proper storage.

FUNCTIONAL GENOMICS OF MAIZE ENDOSPERM MATURATION USING DELETION MUTAGENESIS

While RNAi transgenes as well as different types of mutation often result in leaky expression, gene deletion mutagenesis, though random, has the advantage creating complete nulls. We investigated γ -irradiation for its potential to identify genome regions containing *o2* modifier genes in a QPM background. A small population of \sim 300 M3 families contained a number of recessive opaque revertant mutants (Figure 4) thus demonstrating its utility for identifying *o2* modifier genes as well as genes generally involved in kernel maturation (Yuan et al., 2014). This non-pleiotropic and non-lethal class of kernel mutants had varying effects on zein accumulation (Figure 5). The two most striking of these opaque mutants generated were unlike any previously described zein variants. The first of these, line 107, which has been thoroughly characterized at the molecular and phenotypic levels, is a null mutant of 27-kD γ -zein (Yuan et al., 2014). The second mutant, line 198, reduces 19-kD α -zeins to very low levels, in addition to the already low 22-kD α -zein caused by the *o2* mutation. Line 107 showed a complete absence of 27-kD γ -zein on SDS-PAGE gels, and the 50-kDa γ -zein was also undetectable. This was a preliminary indication that a deletion spanned both genes since they are known to be separated by only 27 kbp on chromosome 7 (Holding et al., 2008). Subsequent RT-PCR

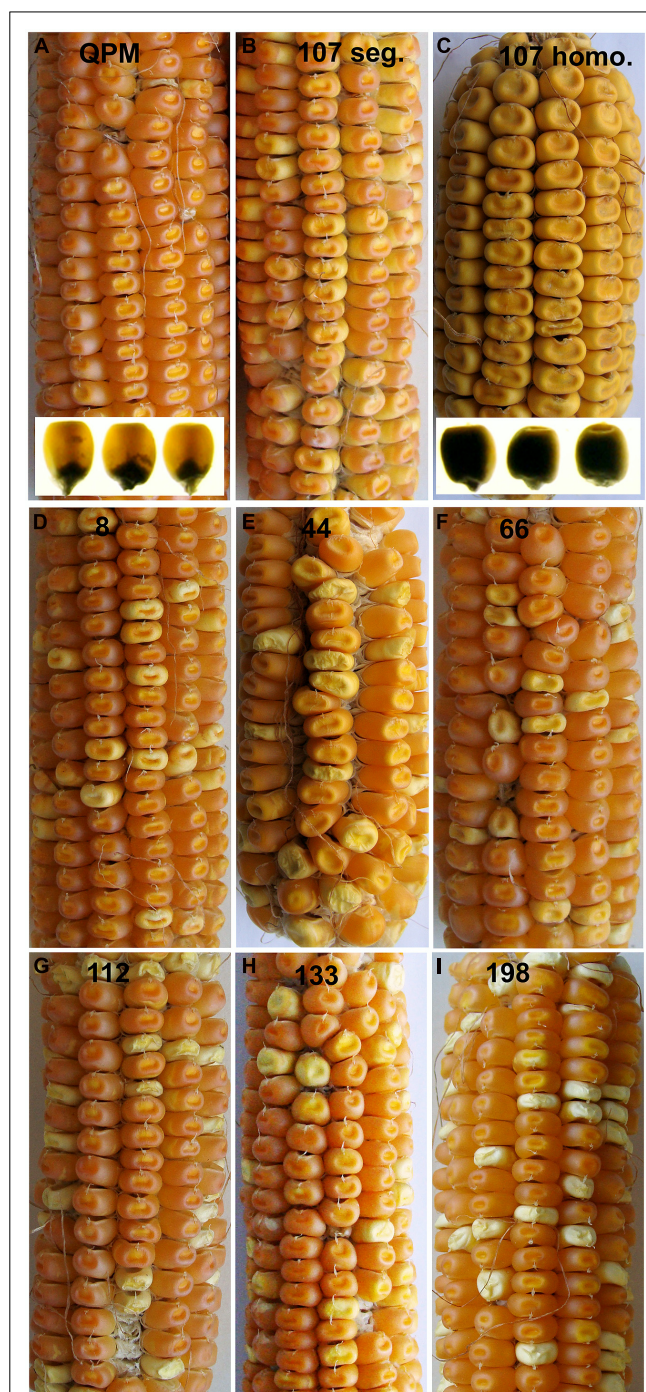
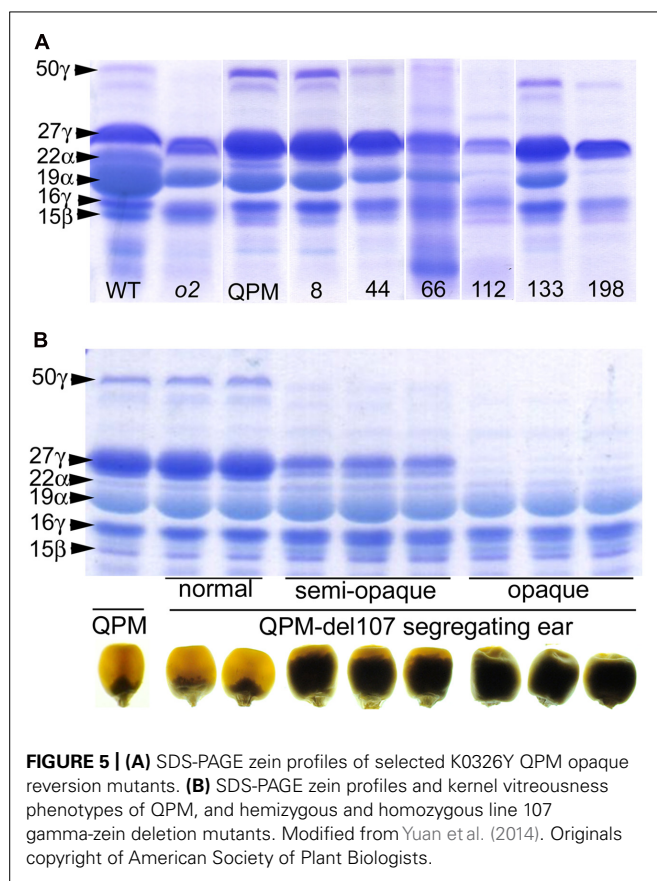


FIGURE 4 | M3 ear phenotypes of selected segregating K0326Y opaque deletion mutants. K0326Y mutant line number is shown at the top center of each panel in A–I. Inserts in A,C show light box phenotypes. Modified from Yuan et al. (2014).

and PCR confirmed the absence transcripts and genes, while the unlinked 16-kD γ -zein was unaffected (Yuan et al., 2014). Illumina sequencing of exon-enriched genomic DNA showed that line 107 has a 1.2 Mbp deletion on chromosome 7.02 that includes both the 27- and 50-kD γ -zein genes. The increase in



27-kD γ -zein in QPM and its map position within the largest QTL for *o2* endosperm modification has long been known, but we also observed an increase in 50-kD γ -zein in QPM, possibly demonstrating a contribution to this QTL. The homozygous γ -zein deletion completely abolished endosperm modification since kernels were fully opaque. Interestingly, hemizygous kernels with a single copy of each gene accumulated intermediate amounts of both γ -zeins and were semi-modified (**Figure 5**), indicating a haploinsufficiency effect in which high level expression from both copies of these genes are necessary for vitreous endosperm formation in QPM. This unequivocally establishes 27-kD γ -zein as *o2* modifier gene. More recent work indicates that the haploinsufficiency of the 27-kD γ -zein does not apply to normal vitreous endosperm formation in a wild type (*O2/O2*) background, since kernels hemizygous for the 27-kD γ -zein deletion are fully vitreous.

The 19-kD α -zeins are encoded by genes within the Z1A1, Z1A2, Z1B, and Z1D families residing at four different loci (Miclaus et al., 2011b). Though the expression of all these genes is not equivalent within B73 and varies dramatically between genetic backgrounds (Feng et al., 2009), the very low abundance of 19-kD α -zein in QPM deletion line 198 endosperm is unlikely to result from a physical deletion at one of the four loci. Indeed, our data do not suggest a physical Z1 deletion in line 198. All Z1 classes including Z1C (22-kD α -zein) show substantially reduced transcript abundance compared with the non-mutagenized control. However, exon sequencing and RNA-seq did not reveal any

physical Z1 gene deletions, cDNA sequencing did not identify missing species and bulked segregation analysis maps the mutation to a chromosome not containing Z1 loci. The more likely scenario is that the causative mutation in line 198 is within an *Opaque-2* unrelated gene with a direct or indirect role in regulating alpha-zein abundance. For other opaque mutants shown in **Figures 4** and **5**, mapping populations have been made and map positions are being used to guide prioritization of candidate gene deletions from exon-seq and RNA-seq data already generated.

Since even a small population of ~ 300 families in the QPM population yielded a more than 20 new opaque and small kernel mutants, we made a second mutagenized population in the B73 reference line. This population is much larger and resulted in 1793 M2 (second generation) ears. Rather than just *o2* modifier genes, the scope of this population is for more general seed functional genomics and direct manipulation of grain quality (such as by direct deletion of alpha zein sub-family loci). Since mutants are isogenic with the reference B73 genome, it will be considerably easier to assemble and utilize DNA and RNA-seq data when surveying the nature and extent of deletions within mutants.

The cells that give rise to the ear and the cells that give rise to the tassel are already specified and are physically separate in the embryonic maize shoot apical meristem (Poethig et al., 1986), and so a given mutation will not be present both ear and tassel of an M1 plant. Thus, M2 kernels will be hemizygous for such a mutation, and only show a kernel phenotype if it is dominant. Consequently, M3 families must be propagated to identify segregating recessive mutants. Among families already advanced to the M3 (10–15 plants each), there is substantial overlap between the seed phenotypes observed, since the majority of opaque mutants show some degree of reduced kernel size. Molecular genetic and biochemical characterization of these mutants will increase our understanding of the processes controlling kernel filling and its proper maturation. One priority is to identify mutants that have alterations in the ratio of zein and non-zein fractions and several mutants that have relatively increased amounts of non-zein proteins, with or without a corresponding decrease in zein proteins have been identified. F1 outcrosses are being made to Mo17 and subsequently F2 mapping populations will be used to map the causative mutations to a chromosome bin through Bulk Segregant Analysis. Map positions will be used to guide interpretation of Illumina HiSeq2500 DNA- and RNA-seq data as well as LC-MS/MS quantitative complete proteome profiling data.

CONCLUDING REMARKS

Studies of opaque mutants, especially *opaque-2* and QPM, were fueled by the prospect of maize varieties with improved protein quality. Though QPM varieties have been bred and are in use in many developing countries, their potential has not been realized in the U.S. Furthermore, characterization of other opaque mutants, especially those that do not improve protein quality, has been slow until recently. Our knowledge of the mechanisms of protein body formation and the role of zein storage proteins and other unknown factors in vitreous endosperm formation

in both wild type and QPM contexts, has been limited. However, over the last decade, several technological developments have accelerated our understanding of these processes. Mutator transposon induced opaque mutants led to the identification of several non-zein factors with roles in endosperm maturation. An enhanced ability to perform map-based cloning in maize has resulted in several very old, broadly mapped opaque mutants being cloned in recent years. RNAi studies have also shed light on the redundant and non-redundant roles of zeins in protein body formation. Deletion mutagenesis is emerging as an additional way to confirm suspected *opaque-2* modifier genes and potentially lead to identification of unknown ones. We are using this approach to generate new kernel mutants that will hasten seed functional genomics when paired with current genetic mapping resources, DNA- and RNA-sequencing capacities and proteomics.

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Conserved *cis*-regulatory modules in promoters of genes encoding wheat high-molecular-weight glutenin subunits

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The concentration and composition of the gliadin and glutenin seed storage proteins (SSPs) in wheat flour are the most important determinants of its end-use value. In cereals, the synthesis of SSPs is predominantly regulated at the transcriptional level by a complex network involving at least five *cis*-elements in gene promoters. The high-molecular-weight glutenin subunits (HMW-GS) are encoded by two tightly linked genes located on the long arms of group 1 chromosomes. Here, we sequenced and annotated the HMW-GS gene promoters of 22 electrophoretic wheat alleles to identify putative *cis*-regulatory motifs. We focused on 24 motifs known to be involved in SSP gene regulation. Most of them were identified in at least one HMW-GS gene promoter sequence. A common regulatory framework was observed in all the HMW-GS gene promoters, as they shared conserved *cis*-regulatory modules (CCRM) including all the five motifs known to regulate the transcription of SSP genes. This common regulatory framework comprises a composite box made of the GATA motifs and GCN4-like Motifs (GLMs) and was shown to be functional as the GLMs are able to bind a bZIP transcriptional factor SPA (Storage Protein Activator). In addition to this regulatory framework, each HMW-GS gene promoter had additional motifs organized differently. The promoters of most highly expressed x-type HMW-GS genes contain an additional box predicted to bind R2R3-MYB transcriptional factors. However, the differences in annotation between promoter alleles could not be related to their level of expression. In summary, we identified a common modular organization of HMW-GS gene promoters but the lack of correlation between the *cis*-motifs of each HMW-GS gene promoter and their level of expression suggests that other *cis*-elements or other mechanisms regulate HMW-GS gene expression.

Keywords: *cis*-elements, conserved *cis*-regulatory modules (CCRM), high-molecular-weight glutenin subunits (HMW-GS), transcriptional regulation, seed storage proteins (SSPs), transcription factors (TFs), wheat (*Triticum aestivum* L)

INTRODUCTION

Wheat is one of the three most economically important crops in the world with maize and rice, with a global annual production of about 700 Mt in 2012 (FAOSTAT; <http://faostat.fao.org/>). Wheat is a broad term for crops including tetraploid species ($2n = 28$) like durum wheat (*Triticum turgidum* spp. *durum*) and hexaploid species ($2n = 42$) like bread wheat (*T. aestivum* spp. *aestivum*). Wheat is one of the most important sources of carbohydrates and vegetable proteins in human diets as it accounts for about 20% of all calories and proteins consumed. It is mostly transformed before it is consumed, and each type of transformation depends on the unique visco-elastic properties of gluten, a network formed by water and seed storage proteins (SSPs). It is mainly the SSPs that determine the technological quality of wheat flour (for instance, see reviews by Shewry et al., 2002 and Shewry, 2009). Prolamins, the major component of wheat SSPs, comprise monomeric gliadins and polymeric glutenins. The latter have both low- (LMW-GS) and high- (HMW-GS) molecular-weight

subunits. Glutenins account for 30–50% of the total SSP content of grain, with HMW-GS alone representing up to 12% of the total. Glutenins strongly influence dough elasticity (Payne et al., 1987; Shewry et al., 2002), with HMW-GS more so than LMW-GS (Branlard and Dardevet, 1985; Gupta and MacRitchie, 1994; He et al., 2005).

As glutenins are so important for technological quality, the genes coding for HMW-GS have been extensively studied. The genome of the hexaploid bread wheat is divided into three sub-genomes (called A, B, and D) forming three homoeologous groups. HMW-GS are encoded by the three loci *Glu-A1*, *-B1* and *-D1* located on the long arms of the group 1 chromosomes. As confirmed by the sequencing of these three regions (Gu et al., 2006), each locus consists of two closely linked paralogous genes, *Glu-1-1* and *Glu-1-2*, that encode x-type and y-type HMW-GS, respectively. Thus, bread wheat HMW-GS form a small multi-gene family of six genes with two orthologous sets of *Glu-1-1* and *Glu-1-2* genes (Allaby et al., 1999). HMW-GS genes are highly

polymorphic (e.g., Payne and Lawrence, 1983). These six genes are not always all expressed. *Glu-A1-2* is silent so from three to five HMW-GS genes are usually expressed in grain. A duplication of *Glu-B1-1* is observed in lines with the overexpressed Bx7 HMW-GS giving an additional expressed gene (Ragupathy et al., 2008). SSPs are specifically expressed in the endosperm and all HMW-GS have similar patterns of expression and represent 60–65% of the total RNA from the endosperm between 10 and 30 days post anthesis (Shewry et al., 2009).

SSP synthesis is primarily controlled both spatially and temporally at the transcriptional level. Transcription factors (TFs) bind specifically to short conserved DNA sequences (5–15 nucleotides) called *cis*-regulatory elements or *cis*-elements, which are usually located in the proximal promoter of genes and characterized by a consensus motif. In barley (*Hordeum vulgare*), the regulatory mechanisms of SSP genes have been extensively studied by transient expression experiments using an hordein promoter (Mena et al., 1998; Vicente-Carbajosa et al., 1998; Oñate et al., 1999; Diaz et al., 2002, 2005; Isabel-La Moneda et al., 2003; Rubio-Somoza et al., 2006a,b; Moreno-Risueno et al., 2008) and have been described as a network of *cis*-elements and their interacting TFs (Rubio-Somoza et al., 2006a). This network is conserved in other cereals as reviewed by Verdier and Thompson (2008) and Xi and Zheng (2011). It consists of five *cis*-elements able to recognize eight TFs belonging to four families (bZIP of the Opaque-2 family, and the B3, DOF, and MYB proteins), which are all reported to be activators of SSP genes. More precisely, the GCN4 like-motif (GLM, 5'-ATGAG/CTCAT-3') and the prolamin box (P-box, or PB, 5'-TGTAAG-3'), also called the endosperm motif, constitute the bipartite endosperm box, which plays a key role in activating the expression of prolamin genes as also shown in wheat (Hammond-Kosack et al., 1993). GLM is recognized by bZIP TFs, like BLZ1 and BLZ2 in barley (Vicente-Carbajosa et al., 1998; Oñate et al., 1999) or SPA (Storage Protein Activator) in wheat (Albani et al., 1997), while the P-box is bound by PBF and SAD, both DOF-type TFs (Vicente-Carbajosa et al., 1997; Mena et al., 1998; Diaz et al., 2005). Two additional *cis*-elements, 5'-AACA/TA-3' and 5'-TATC/GATA-3' core sequences, are able to bind R2R3-MYB (notably GAMYB) and R1MYB (MCB1 and MYBS3) TFs, respectively (Diaz et al., 2002; Rubio-Somoza et al., 2006a,b). The last *cis*-regulatory sequence is the RY repeat (5'-CATGCATG-3'), which binds FUSCA3, a B3 protein (Bäumlein et al., 1992; Moreno-Risueno et al., 2008). In addition to these DNA-protein interactions, protein-protein interactions consolidate the formation of larger complexes that regulate SSP expression (Rubio-Somoza et al., 2006b).

Wheat promoters of α -gliadin classes (Van Herpen et al., 2008), LMW-GS (Hammond-Kosack et al., 1993; Conlan et al., 1999), and HMW-GS (Norre et al., 2002) have been functionally analyzed. Van Herpen et al. (2008) reported differences in regulatory-elements between promoter sequences of α -gliadin genes from A and B genomes. The LMW-GS promoter studied is characterized by a tandem repeat of two endosperm motifs known as the long endosperm box that is important for controlling endosperm-specific expression (Hammond-Kosack et al., 1993). Thomas and Flavell (1990) and Norre et al. (2002) analyzed extensively the promoters of *Glu-D1* by transient expression

assay in tobacco and maize. A 38-bp enhancer element has been identified (Thomas and Flavell, 1990). In addition, the promoter of *Glu-D1-1* contains an atypical endosperm box where the P-box is associated with a G-like box of the ACGT family able to bind bZIP proteins (Norre et al., 2002). Moreover, these authors suggested that the enhancer element may act with the G-like box to increase reporter gene expression.

The exponential growth of genomic sequence databases, and the development of specialized databases of *cis*-acting elements in plants (Higo et al., 1999; Rombauts et al., 1999), coupled with the development of bioinformatics tools to discover specific motifs in DNA or protein sequences (e.g., MEME; Bailey et al., 2006), greatly facilitate the *in silico* analysis of promoters. However, the discovery of *cis*-regulatory elements is hindered by the variability within their sequences, which typically tolerate nucleotide substitutions without a loss of functionality. There are ways of taking this variability into account when predicting the presence of *cis*-regulatory elements (Stormo, 2000). Another aspect to consider is that, in higher eukaryotes, TFs often regulate gene expression by binding DNA in cooperation with other regulatory proteins. As reviewed by Armone and Davidson (1997), separate *cis*-elements of a given promoter often interact with different parts of an overall regulatory complex. This type of organization of *cis*-elements in a region of up to a few 100 bases in the vicinity of the gene being regulated is called a *cis*-regulatory module (CRM), where the relative positions of *cis*-elements and the distances between them are crucial.

Recently, the LMW-GS and HMW-GS gene promoters have been analyzed *in silico* (Juhász et al., 2011; Makai et al., 2013). The *cis*-acting elements present in published sequences of LMW-GS genes, mainly ESTs, were computationally retrieved and differences in the numbers and combinations of specific sequences were highlighted allowing the identification of conserved non-coding sequence regions (CRMs). Models for the transcriptional regulation of LMW-GS genes were then proposed (Juhász et al., 2011). The promoter profiles of HMW-GS genes are highly conserved in the Triticeae family despite differences between paralogous genes (Makai et al., 2013). Here the aim was to understand in more detail the transcriptional regulation of HMW-GS genes through a comparative promoter analysis. The promoters of the main alleles at each HMW-GS gene were analyzed *in silico* for the predicted presence of *cis*-regulatory elements. The organization of these elements within orthologous (homoeologous) and paralogous copies was compared. This work shows the presence of conserved CRMs (CCRMs). In addition, the HMW-GS gene promoters were sequenced in a set of wheat lines to determine whether their sequence variability correlates with the organization of *cis*-elements and hence the expression levels of these genes. A functional analysis of conserved regions consisting of *cis*-motifs potentially able to bind bZIP TFs was carried out by using transient expression and electrophoretic mobility shift assays (EMSA).

MATERIALS AND METHODS

DIVERSITY ANALYSIS

Forty-two lines representative of the genetic diversity (Haseneyer et al., 2008; Ravel et al., 2009) and of the main electrophoretic

alleles of HMW-GS of the INRA worldwide hexaploid wheat (*Triticum aestivum* L.) core collection (Balfourier et al., 2007) were analyzed (Table 1). Genomic DNA was extracted from leaves as described in Ravel et al. (2009) and used for PCR amplification of the proximal promoter of HMW-GS genes. Fragments of approximately 700–1100 nucleotides were obtained (Supplementary Table 1) and sequenced. We did not amplify *Glu-A1-2* genomic DNA as it was silent in all the 42 lines. Diversity indices including nucleotide diversity (π), number of segregating sites (θ), number of haplotypes (H), haplotype diversity (Hd), and Tajima's *D*-test of neutral evolution were calculated for each sequence with SNIPlay (Dereeper et al., 2011).

EXPRESSION ANALYSIS

To quantify HMW-GS gene expression, RNA was extracted from developing grains harvested at 400°C days after anthesis from 13 lines representing the main promoter alleles (Table 1). Lines were cultivated in the greenhouse as described in Ravel et al. (2009). For each of the four lines 964, 1288, 2135, and 4874, four independent biological replicates were obtained. Two independent biological replicates were used for each of the nine remaining accessions. Quantitative-real-time PCR (qRT-PCR) was performed as described in Ravel et al. (2009) using a LightCycler® 480 II sequence detection system and the LightCycler 480 SYBR Green I Master (Roche) according to the manufacturer's instructions. Primer pairs used for qRT-PCR and their amplification efficiency are given in Supplementary Table 2. The specificity of each primer pairs was confirmed by a single peak in the real-time melting temperature curves for each gene.

Amplification plots and predicted threshold cycle values were obtained with LightCycler 480 SW 1.5 software (Roche). Genes coding for glyceraldehyde 3-phosphate dehydrogenase (GAPDH), elongation factor 1 alpha (eF1 α), β -tubulin, and 18S RNA were used as internal controls to normalize expression results (Ravel et al., 2009). The geometric mean of control gene expression was calculated so that HMW-GS gene expression could be quantified and normalized also taking into account the efficiency of each primer pair.

PROMOTER ANNOTATIONS

Twenty motifs known to participate in the regulation of SSP and two light responsive motifs were selected from the PLACE *cis*-motif database, which contains 469 entries (Table 2; Higo et al., 1999). We included a light responsive (Abox) and a circadian rhythm-responsive (CIACADIANLELHC) motif because diurnal fluctuations in carbohydrate pools and Opaque 2 (O2) binding activity during seed filling may impact SSP synthesis (Ciceri et al., 1997, 1999; Carman and Bishop, 2004). We also added two additional motifs, 5'-AACNNA-3' and 5'-TATAWA-3', which were not in the PLACE database. The first motif is able to bind a MYB protein from rice (*Oriza sativa*) belonging to the GAMYB sub-family (Takaiwa et al., 1996). The second motif is the TATA-variant sequence of SSP genes involved in the formation of a transcription initiation complex (Fauteux and Strömvik, 2009; Bernard et al., 2010).

Both strands of the 1-kb region upstream of the start codon for the six HMW-GS genes from cv. Renan retrieved from public

databases (DQ537335.1, DQ537336.1, and DQ537337.1 for *Glu-A1*, *Glu-B1*, and *Glu-D1*, respectively; Gu et al., 2006) and the promoter sequences of the five (i.e., all but *Glu-A1-2*) HMW-GS genes obtained in this study for 42 lines (including cv. Renan) of the INRA worldwide hexaploid wheat core collection were annotated using a custom-made PERL program (named PlantPAD) that extracts the name, sequence and coordinates of the motifs and produces a graphical representation of the query sequence on which the starting position of each *cis*-motif is plotted. Based on the assumption that functional *cis*-motifs are conserved among HMW-GS genes, we used PlantPAD to search for co-occurrence of *cis*-motifs in these genes. To build the consensus, the program considers each motif and its coordinates (the position of its first nucleotide relative to the start codon). Any motif that appears at the same coordinates (± 5 bp) in all the sequences being annotated is considered to be conserved. As insertion-deletion events (indels) within a sequence cause motifs to shift along the gene, the program also recognizes conserved motifs which appear in all the sequences with the same coordinates plus or minus the shift size (the length of indels). The consensus is then plotted and the distances between conserved motifs corresponding to those found in more than 50% of the sequences are analyzed. Such a consensus is designed to highlight the conserved regulatory regions. This approach was used to analyze separately both sets of orthologous genes and produce a consensus plot for each of them. These consensus were then used to generate an overall consensus annotation of HMW-GS gene promoters.

FUNCTIONAL VALIDATION

Particle bombardment was performed in developing wheat endosperm to validate *cis*-motifs potentially able to bind bZIP TFs. The promoter of *Glu-B1-1* gene (hereafter termed PrBx7) was amplified and cloned using the primers from cv. Renan given in Supplementary Table 1. A total of 747-bp upstream fragment of the start codon was used. In addition, to assess the role of the distal conserved regulatory regions of this promoter, the 597-bp fragment from the start codon (hereafter termed tPrBx7) was synthesized.

All constructs used for transient expression assay were obtained using Gateway technology (Invitrogen). Three entry clones were used (pDONRP4-P1R, pDONR221, and pDONRP2R-P3). pDONRP4-P1R contained the rice actin promoter, PrBx7 or tPrBx7, while pDONR221 and pDONRP2R-P3 contained a reporter gene (either GUS or GFP, respectively) and the 3'-terminator nopaline synthase gene (3'-NOS). Three expression pDEST4-R3-based vectors (pAct-GFP, pPrBx7-GUS, and pTPrBx7-GUS) were created. A transient promoter activation assay based on co-bombardment with pPrBx7-GUS or pTPrBx7-GUS and pAct-GFP constructs was performed using immature endosperm from cv. Récital collected at 230°C day after anthesis from plant grown in the greenhouse under optimal growth conditions. Seeds were surface-sterilized and endosperms were carefully isolated. Endosperms were cultured on Murashige and Skoog medium supplemented with maltose (100 g L⁻¹) for 2–3 h for subsequent bombardment. Gold particles (0.6 μ m in diameter; Bio-Rad) were prepared with 500 ng of a 1:1 molar ratio mixture of pAct-GFP and pPrBx7-GUS or pTPrBx7-GUS.

Table 1 | Country of origin, protein coding alleles, and haplotypes of the promoters of five HMW-GS genes for 42 accessions of the INRA worldwide hexaploid wheat core collection.

Name ^a	Country of origin ^b	Glu-A1-1		Glu-B1-1		Glu-B1-2		Glu-D1-1		Glu-D1-2	
		Protein ^c	Promoter ^d	Protein ^c	Promoter ^d	Protein ^c	Promoter ^d	Protein ^c	Promoter ^d	Protein ^c	Promoter ^d
A4 (748)	AFG	1	h1	7	h1	8	h1	3	h1	12	h1
Aifeng NO 4 (822)	CHN	1	h1	7	h1	HZ	h1	HZ	h2	HZ	h1
ARCHE (964)	FRA	null	h2	6	h2	8	h2	2	h2	12	h1
AUORE (1110)	AUS	2*	h3	7	h1	9	h1	2	h2	12	h1
BALKAN (1192)	YUG	2*	h3	7	h1	9	h1	5	h3	10	h2
BARBU DU FINISTERE (1323)	FRA	null	h2	20	h1	20	h3	2	h2	12	h1
BELLIE 590 (1288)	HUN	2*	h3	7	h1	9	h1	5	h3	10	h2
CHINESE SPRING (2135)	CHN	null	h2	7	h1	8	h1	2	h2	12	h1
CHORTANDINKA (2153)	RUS	null	h1	HZ	h1	HZ	h1	HZ	h3	HZ	h2
CHYAMTANG (2171)	NPL	null	h2	7	h1	8	h1	2	h2	12	h1
COPPADRA (2330)	TUR	2*	h3	7	h1	8	h1	3	h2	12	h1
COTIPORA (2353)	BRA	2*	h3	N	h1	N	h3	2	h2	12	h1
COURTOT (2358)	FRA	2*	h3	7	h1	8	h1	2	h2	12	h1
DI7202-103 (2526)	FRA	1	h1	7	h1	8	h1	5	h3	10	h2
GLENLEA (3358)	CAN	2*	h3	7OE	h1	8	h1	5	h3	10	h2
GODOLLOI 15 (3366)	HUN	null	h2	N	h1	N	h4	5	h3	10	h2
JO3045 (3942)	FIN	2*	h3	7	h1	9	ND	2	h2	12	h1
M708//G25/N163 (4482)	ISR	2*	h4	HZ	h1	HZ	h1	2	h2	12	h1
MARS DE SUEDE ROUGE BARBU (4645)	FRA	null	h2	7	h1	8	h1	2	h2	12	h1
MISKAAGANI (4874)	LBN	2*	h3	N	h1	N	h1	2	h2	12	h1
MOCHO DE ESPIGA BRANCA (4901)	PRT	2*	h3	13	h3	16	h1	2	h2	12	h1
N46 (5088)	ISR	null	h2	7	h1	8	h1	2	h2	12	h1
NABU EPI BLANC (5102)	NPL	null	h2	7	h1	8	h1	2	h2	12	ND
NANKING 25 (5116)	CHN	null	h2	7	h1	8	h1	2	h2	12	h1
NEPAL 84 (5166)	NPL	null	h2	7	h1	8	h1	2	h2	12	h1
NP120 (5308)	IND	null	h2	17	h1	18	h1	2	h2	12	h1
NYU BAY (5399)	JPN	null	h2	7	h1	8	h4	2	h2	12	h1
OPAL (5486)	DEU	1	h1	7	h1	9	h1	5	h3	10	h2
PITIC 62 (5748)	MEX	1	h1	7	h1	8	h1	2	h2	12	h1
RECITAL (6027)	FRA	2*	h3	6	h2	8	h2	5	h3	10	h2
RENAN (6086)	FRA	2*	h3	7	h1	8	h1	5	h3	10	h2
SEU SEUN 27 (6529)	KOR	null	h2	7	h4	8	h1	4	h2	12	h1
RALET (8048)	FRA	null	h5	20	h1	20	h3	2	h2	12	h1
ZANDA (8058)	BEL	1	h2	20	h1	20	h3	2	h2	12	h1
HOPEA (9048)	FIN	1	N	6	h2	8	h2	2	h2	12	h1
FRUH-WEIZEN (13310)	DEU	null	h2	22	h5	22	h5	5	h3	10	h2
ORNICAR (13471)	FRA	2*	h3	6	h2	8	h2	5	h3	10	h2
TALDOR (13476)	FRA	2*	h3	7	h1	8	h1	4	h2	12	h1
APACHE (13481)	FRA	null	h2	7	h1	8	h1	3	h2	12	h1
OPATA 85 (13811)	MEX	2*	h3	7	h1	9	h1	5	h3	10	h2
SYNTHETIQUE-W7984 (13812)	MEX	null	h6	7	h1	8	h1	N	h4	N	ND
BLE DE REDON BLANC 1/2 LACHE 1 1 (15658)	FRA	1	h1	13	h3	16	h1	2	h5	12	h1

Accessions used for expression studies are shown in bold.

^aAccession no. in the INRA Triticeae Genetic Resources Collection (<http://www6.clermont.inra.fr/umr1095>) is given in brackets.

^bCountry names are given as three-letter ISO codes (<http://www.unc.edu/~rowlett/units/codes/country.htm>).

^cProtein coding allele for the x- or y-type HMW-GS identified by SDS-PAGE. HZ, heterozygous.

^dHaplotype of the promoter for HMW-GS genes. ND, no data.

Table 2 | Characteristics of *cis*-motifs from PLACE database and bibliographic references used to annotate the promoters of HMW-GS genes.

Names	Name used in PLACE	Sequence	Binding transcription factor ^a	References
DOF				
DOF core	DOFCOREZM	AAAG	DOF SAD, <i>PBF</i> , BPBF <u>WPBF</u>	Hammond-Kosack et al., 1993; Yanagisawa and Schmidt, 1999
Pbox1	PROLAMINBOXOSGLUB1	TGCAAAG		Wu et al., 2000; Isabel-La Moneda et al., 2003
Pbox2	300CORE	TGTAAAG		Thomas and Flavell, 1990
Pbox3	–300ELEMENT	TGHAAARK		Marzábal et al., 1998
bZIP				
GLM 1	GCN4OSGLUB1	TGAGTCA	bZIP <i>O2</i>	Albani et al., 1997; Vicente-Carbajosa et al., 1998; Wu et al., 2000
GLM 2	–300MOTIFZMZEIN	RTGAGTCAT	BLZ1, BLZ2	Thomas and Flavell, 1990; Oñate et al., 1999
GLM 3	GLMHVCHORD	RTGASTCAT	<u>SPA</u>	Norre et al., 2002
ACGT core	ACGTATERD1	ACGT		
G-box motif 1	ABREATCONSENSUS	YACGTGGC		Kang et al., 2002; Choi et al., 2000
G-box motif 2	ABRELATERDI	ACGTG		
CAAT	CAATBOX1	CAAT	bZIP ^b	Shirsat et al., 1989
RY-REPEAT				
RY_core	RYREPEATLEGUMINBOX	CATGCAY	AB3/VP1 FUSCA3	Fujiwara and Beachy, 1994; Moreno-Risueno et al., 2008; Van Herpen et al., 2008
AACA MYB				
AACA motif 1	AACACOREOSGLUB1	AACAAAC	R2R3-MYB GaMYB <u>GaMYB</u>	Takaiwa et al., 1996; Suzuki et al., 1998; Wu et al., 2000; Diaz et al., 2002
AACA motif 2	ANAERO1CONSENSUS	AAACAAA		
MYB1AT	MYB1AT	WAACCA		
AACA motif 3	Not referred in PLACE	AACNNA		
GATA MYB				
GATA box 1	GATABOX	GATA	R1MYB MCB1 MYBS3	Rubio-Somoza et al., 2006a
GATA box 2	MYBST1	GGATA	MYB	Baranowskij et al., 1994
OTHERS				
E box	EBOXBNNAPA	CANNTG	bHLH	Chaudhary and Skinner, 1999
CCAAT	CCAATBOX1	CCAAT	HAP <u>CBF</u>	Albani and Robert, 1995
ESP	ESPASGL01	ACATGTCATCATGT	Not identified	Vickers et al., 2006
TATA-variant	Not referred in PLACE	TATAWA	TATA-box-binding proteins	Fauteux and Strömvik, 2009
CIACADIANLELHC	CIACADIANLELHC	CAANNNNATC		Piechulla et al., 1998
ABox	PALBOXAPC	CCGTCC		

^aTranscription factor families are indicated in bold followed by the name of corresponding transcription factor in maize (*italics*), barley, wheat (underlined), or other species (*italics and underlined*).

^bInteraction not functionally validated.

Bombardments were conducted at a distance of 6 cm from the stopping plate using a biolistic helium gun device (PDS-1000, Bio-Rad) with a pressure of 6.21 MPa. Following bombardment, endosperms were incubated for 2 days in the dark at 24°C in a Murashige and Skoog medium supplemented with 3% (w/v) sucrose and 0.15 mM of each of the 20 proteinogenic amino acids. For GUS expression, endosperms were stained with 5-bromo-4-chloro-3-indolyl glucuronide according to Jefferson et al. (1987). Endosperms were observed using a MZ16 F stereomicroscope equipped with a DFC300 FX digital

camera (Leica Microsystems) and GUS and GFP activities were determined by counting the number of blue and green cells, respectively. Expression results were normalized by dividing the number GUS foci by the number of GFP foci. For each construct, 10 independent bombardments of eight endosperms each were performed. The pAct-GFP construct was used to determine the efficiency of bombardment as proposed by Eini et al. (2013).

The DNA-binding activity of *cis*-motifs with SPA was studied by EMSA. The SPA protein was expressed in *E. coli* (BL21 AI strain) by cloning *Spa* cDNA into the pDEST17 plasmid vector

(Invitrogen) producing pHis-SPA. *Spa* expression was induced with 0.2% (w/v) arabinose for 3 h. Proteins extracts were obtained after re-suspension of the induced cells in a 10 mM Tris buffer (pH 8) containing 6 M urea and 100 mM NaH_2PO_4 (10 mL g^{-1} pellet). Purification of the recombinant protein was achieved by loading protein extracts onto a Ni^{2+} -NTA resin and bound proteins were eluted in a 10 mM Tris buffer (pH 4.5) containing 6 M urea and 100 mM NaH_2PO_4 . The eluate was dialyzed against a 10 mM Tris buffer (pH 8.3) containing 2 M urea, 100 mM NaH_2PO_4 , 100 mM KCl, 0.02% Tween-20, 10% glycerol, and 0.5 mM phenylmethylsulfonyl fluoride (PMSF) for 36 h to renature the recombinant protein and then against a 10 mM Tris buffer (pH 7.5) containing 50 mM KCl, 1 mM dithiothreitol, 0.02% Tween[™] 20, 10% glycerol, and 0.5 mM PMSF for 16 h. The dialysate was then concentrated with an Amicon 10 kDa filter (Millipore).

DNA oligonucleotides able to bind bZIP TFs (GLM and G-box) used in EMSA are described in Supplementary Table 3. Each single-strand oligonucleotide was labeled using the Biotin 3' End DNA Labeling Kit (Pierce) following the manufacturer's instructions and hybridized for 30 min at the annealing temperature of the probes. The labeled dsDNA probe (20 fmol) was incubated with 560 ng to 4 μg of recombinant His-SPA protein in 20 μL of a binding buffer containing 10 mM Tris (pH 7.5), 2 mM dithiothreitol, 100 mM KCl, 10% glycerol, 0.05% nonyl phenoxypolyethoxyethanol, 2 mM ethylenediaminetetraacetic acid, 100 ng μL^{-1} poly(dLdC), 250 ng μL^{-1} fish sperm DNA, 0.5 mM PMSF for 30 min at room temperature. DNA-protein complexes were analyzed by non-denaturing 6% polyacrylamide gel electrophoresis in a 45 mM Tris, 45 mM Borate, and 1 mM ethylenediaminetetraacetic acid buffer (pH 8.3). After separation (100 V, 1 h at 4°C), gels were electroblotted to nylon membranes using the same buffer (380 mA, 45 min at 4°C). The biotin end-labeled DNA was detected using streptavidin, horseradish peroxidase conjugate following the manufacturer's instructions (LightShift Chemiluminescent EMSA kit, Pierce).

STATISTICAL ANALYSES

All statistical analyses were done using R 3.0 software (R Core Team, 2013). The normality of and homogeneity of variances of expression data were tested by the Shapiro–Wilk and Bartlett's tests, respectively. Depending on the results of previous analyses, expression data were submitted to non-parametric or parametric variance analysis with the Kruskal–Wallis or the general linear model procedure. Multiple comparison tests between groups after Kruskal–Wallis tests were done with the *Kruskalmc* function while the Student–Newman–Keuls test was used to compare means after the general linear model procedure. The Kruskal–Wallis and Student–Newman–Keuls tests used were those available in the R “agricolae” (version 1.1-8) package (De Mendiburu, 2014), all other tests were done using the R “Stats” (version 2.15.3) package. All the data were used in a first analysis based on a model with one factor (gene). In a second step, analyses were carried out gene per gene to study the promoter haplotype factor.

To analyze the differences in expression of HMW-GS genes and haplotypes one-way ANOVA were performed. First, an ANOVA

with the gene as the main factor was carried out. The four lines with the null allele at *Glu-A1-1* and the line with protein allele 7 overexpressed (7OE) at *Glu-B1-1* were excluded from this analysis to avoid bias. Secondly, ANOVAs with the promoter haplotype as the main factor were performed for each gene (including the null allele at *Glu-A1-1*).

Differences in normalized expression from transient expression assays were analyzed using *t*-test. All statistically significant differences were judged at 5%.

RESULTS

THE VARIABILITY OF THE PROMOTER IS NOT SYSTEMATICALLY CONNECTED WITH PHENOTYPIC VARIABILITY

The variability in the nucleotide sequence of the promoters of the five HMW-GS genes was extensively studied by sequencing a set of 42 lines representative of the diversity present in the INRA worldwide hexaploid wheat core collection. The following results deal with the noncoding DNA region upstream of the start codon given that for HMW-GS genes the transcription start site (TSS) is about 60 bases upstream of the start codon for translation. In some cases, the hybridization sites of reverse primers were downstream of the start codons, so the sizes of the upstream fragments studied ranged from 467 to 1138 bp. A total of 36 single-base changes, 2 single-base insertion-deletions (indels) and 1 larger indel were identified in an average of 3858 bp promoter sequence per line (Table 3, Supplementary Table 4). These specific regions have an average of one polymorphism every 100 bases. The number of polymorphisms varied between promoters. *Glu-B1-2* promoter has one polymorphism every 58 bp, three-fold more frequently than the *Glu-D1-2* promoter, which has one polymorphism every 145 bp. One large deletion of 54 bp spanning from 291 to 344 upstream of the start codon in the *Glu-B1-1* promoter was observed in two lines (accession nos. 4901 and 15658). Thus, nucleotide diversity estimated by the mean pairwise difference (π) varied from one promoter to another, ranging from 1.5×10^{-3} for *Glu-D1-1* to 3.0×10^{-3} for *Glu-B1-1*. Except for *Glu-D1-2*, we observed that the nucleotide diversity (π) and the number of segregating sites (θ) are about equal in values as confirmed by the non-significant Tajima's D statistic (Table 3). This suggests that there has been no particular pattern of selection in these regions.

The polymorphisms are linked by a high level of linkage disequilibrium (data not shown). Therefore, for all loci, most of the lines clustered into two main haplotypes with the remaining haplotypes being generally represented by single lines. Notably, the number of haplotypes found for each promoter fits the number of protein coding alleles for *Glu-D1-2* only (Table 1, Figure 1). For *Glu-B1-1*, we observed more protein coding alleles than promoter haplotypes. For the three other *Glu1* genes, we observed more promoter haplotypes than protein coding alleles. Each electrophoretic allele, except for *Glu-B1-2* alleles, tends to have a more-frequent promoter haplotype (Figure 1).

THE VARIABILITY OF THE HMW-GS GENE PROMOTER IS OFTEN CONNECTED WITH THE LEVEL OF GENE TRANSCRIPTION

To assess whether the gene transcription level is influenced by the promoter haplotype of each HMW-GS gene, HMW-GS

Table 3 | Number of electrophoretic alleles revealed by SDS-PAGE, haplotype and diversity statistics for the promoters of five HMW-GS genes from 42 accessions of the INRA worldwide hexaploid wheat core collection.

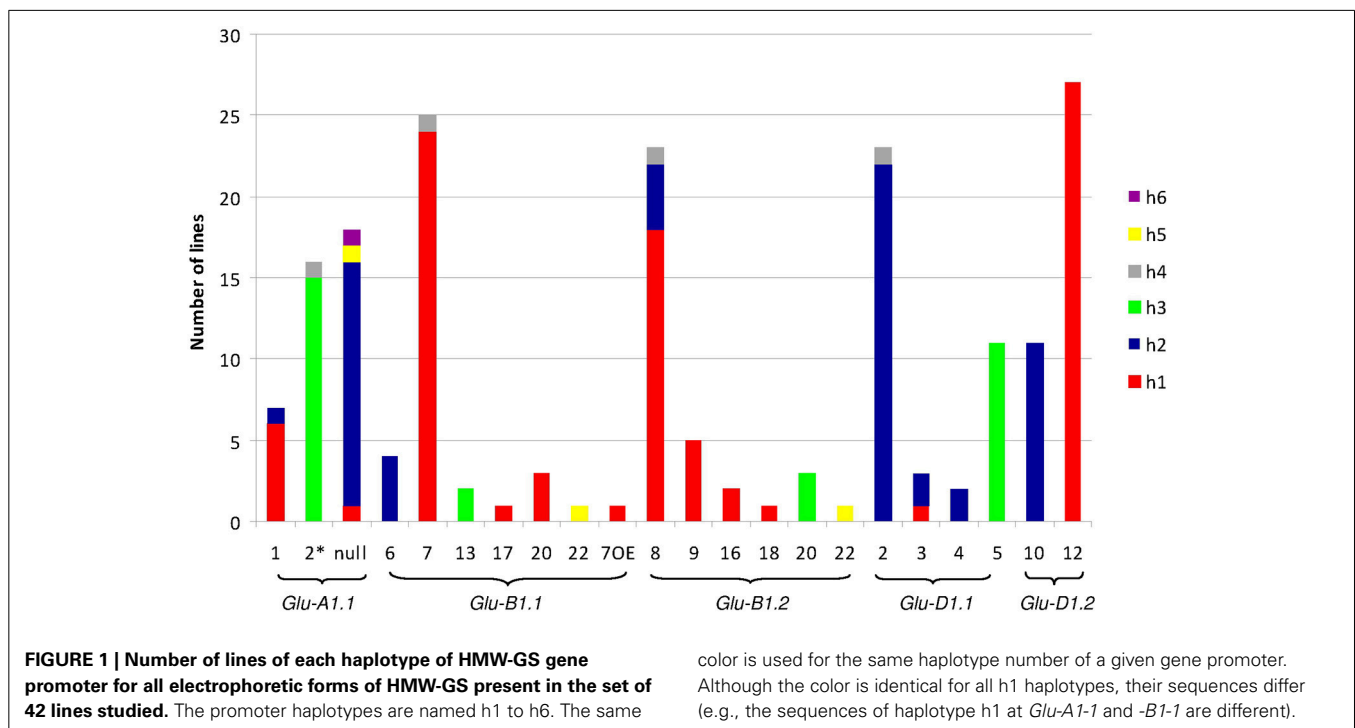
Genes	No. of electrophoretic alleles ^a	Promoter length (bp)	No. of polymorphic sites/No. of indels ^b	No. of haplotypes ^c	Haplotype diversity, Hd	Nucleotide diversity, π	No. of segregating sites, θ	Tajima's statistic
<i>Glu-A1-1</i>	3	878	7 (4)/0	6 (3)	0.71	1.51×10^{-3}	1.60×10^{-3}	NS ^d
<i>Glu-B1-1</i>	7	747	10 (3)/1 (0) 54	5 (2)	0.34	2.67×10^{-3}	3.16×10^{-3}	NS
<i>Glu-B1-2</i>	6	465	7 (2)/1 (0) 1	5 (1)	0.45	3.03×10^{-3}	3.03×10^{-3}	NS
<i>Glu-D1-1</i>	4	667	5 (3)/0	5 (2)	0.49	1.48×10^{-3}	1.52×10^{-3}	NS
<i>Glu-D1-2</i>	2	1163	7 (0)/1 (0) 1	2 (0)	0.43	2.93×10^{-3}	1.39×10^{-3}	$P < 0.05$

^aProtein coding allele for the x- or y-type HMW-GS identified by SDS-PAGE.

^bThe number of singletons (i.e., a polymorphism found in a single line) is given in brackets; the size of indels is indicated in italics.

^cThe number of haplotypes including a single line is indicated in brackets.

^dNS, not significant.



transcripts were quantified at 400°C days after anthesis for 13 lines by qRT-PCR (Table 1). The five HMW-GS genes had different levels of transcription ($P = 2 \times 10^{-16}$). On average, *Glu-B1-1* and *Glu-D1-1* showed a higher level of transcription than the remaining genes, while *Glu-D1-2* was expressed at lower levels (Table 4). The two x-type HMW-GS genes were expressed up to 10-fold higher than the genes coding the y-type. The transcription of *Glu-A1-1* was intermediate.

Among the four accessions with the null allele at *Glu-A1-1*, three harbor the h2 promoter haplotype and one the h5 haplotype. These two haplotypes differ by only one single nucleotide polymorphism (SNP) and their transcription was close to zero (Table 5). The transcription of the two other promoter haplotypes for *Glu-A1-1* were not different ($P = 0.95$). One line (accession no. 8058) harbors the h2 haplotype but has the protein

allele 1 and had a transcription close to that of the h1 and h3 promoter haplotypes. For *Glu-B1-1*, once the line with the Bx7OE protein allele was discarded, the promoter haplotype effect was significant ($P = 0.014$). The transcription for the h1, h3, and h4 haplotypes was similar and, on average, 2.6-fold higher than that for haplotype h2 (Table 5), which only includes the Bx6 protein allele (Figure 1). The line with the Bx7OE protein allele has the h1 promoter haplotype, as most of the Bx7 protein alleles, but it expressed *Glu-B1-1* at a level (195.33 ± 29.25 , $n = 2$) twice that of Bx7 lines. For *Glu-B1-2*, the haplotype effect was significant ($P = 0.023$) and transcription from h1 was higher than from h3 (Table 5). For this gene, the promoter haplotypes were not linked with separate protein alleles (Figure 1). The RNA expression of the *Glu-D1-1* and *Glu-D1-2* alleles was not influenced by their promoter haplotypes (data not shown).

Table 4 | Comparison of the transcription levels of HMW-GS genes at 400°C days after anthesis for 13 lines of INRA worldwide hexaploid wheat core collection.

Genes	No. of lines ^a	RNA expression levels ^b
<i>Glu-A1-1</i>	9 (22)	56.70 ± 3.99 (B)
<i>Glu-B1-1</i>	12 (32)	83.64 ± 7.65 (A)
<i>Glu-B1-2</i>	13 (34)	17.14 ± 0.97 (C)
<i>Glu-D1-1</i>	13 (34)	83.69 ± 5.02 (A)
<i>Glu-D1-2</i>	13 (34)	8.063 ± 0.42 (D)

Data are means ± 1 SE.

^aThe number of data points is indicated in brackets.

^bDifferent letters in brackets indicate a significant difference ($\alpha = 5\%$) calculated according to a Kruskal–Wallis non-parametric test followed by the Kruskal multiple comparisons test.

Table 5 | Multiple comparison of the mean levels of RNA expression from promoter alleles of HMW-GS genes at 400°C days after anthesis.

Genes	Promoter haplotype	No. of lines ^a	RNA expression levels ^b
<i>Glu-A1-1</i>	h1	1 (2)	58.25 ± 1.83 (B)
	h2 (null) ^d	3 (10)	1.40 ± 0.18 (A)
	h2 (1) ^d	1 (2)	57.38 ± 7.70 (B)
	h3	6 (16)	58.56 ± 5.19 (B)
	h5	1 (2)	1.41 ± 0.32 (A)
<i>Glu-B1-1</i> ^c	h1	7 (20)	102.27 ± 9.08 (A)
	h2	3 (8)	35.36 ± 3.43 (B)
	h3	1 (2)	87.23 ± 7.35 (A)
	h4	1 (2)	86.94 ± 11.50 (A)
<i>Glu-B1-2</i>	h1	8 (22)	18.96 ± 1.24 (A)
	h2	3 (8)	14.74 ± 1.28 (AB)
	h3	2 (4)	11.89 ± 1.45 (B)

Data are means ± 1 SE.

^aThe number of data points is indicated in brackets.

^bDifferent letters in brackets indicate a significant difference ($\alpha = 5\%$) calculated according to a Kruskal–Wallis non-parametric test followed by the Kruskal multiple comparisons test.

^cThe line accession no. 3358 with the 7OE allele was discarded.

^dFor *Glu-A1-1* haplotype 2, results for the null and 1 protein alleles (indicated in brackets) were treated as two different haplotypes in the ANOVA.

These results highlight different RNA expression levels for different HMW-GS genes and, for three HMW-GS genes, the effects of the promoter haplotype. Thus, differences in the regulation of these genes might stem from the organization of the *cis*-motifs in their promoters.

COMMON *cis*-MOTIFS ORGANIZATION OF HMW-GS GENE PROMOTERS

To analyze the organization of *cis*-motifs in HMW-GS gene promoter, we first searched for similar patterns in the 1-kb promoter region of the six HMW-GS genes of cv. Renan, as HMW-GS genes have similar expression patterns during development and

in response to environmental factors. We then compared the consensus organization of *cis*-motifs found for cv. Renan with that found for the haplotypes of each gene to relate differences in *cis*-motifs organization with differences in gene expression.

In all six HMW-GS gene promoters of cv. Renan we found all the 24 *cis*-motifs we annotated but the Pbox2 and ESP motifs. Most of these motifs were annotated several times and a total of 44 (for *Glu-B1-2*) to 54 (for *Glu-D1-2*) *cis*-motifs per gene were annotated. All the *cis*-motifs able to bind all TFs known to regulate the expression of SSP genes were present, but the typical bipartite endosperm box was not found. The number of *cis*-motifs found was over-estimated as the sequences of a few motifs (Table 2) were nested within some others. Most of the nested *cis*-motifs bind TFs of the same family (Table 2). Therefore, we took into account only the longest motif where nested motifs were predicted, which reduced the number of *cis*-motifs per gene by 15–24%. Motifs able to bind MYB TFs (GAMYB, MCB1, MYBS3) were predominant, with 9–14 *cis*-motifs per gene, followed by motifs able to bind bZIP TFs, with 9–13 *cis*-motifs per gene, and DOF TFs (PBF, SAD), with 4–8 *cis*-motifs per gene. The CAAT *cis*-motif accounted for about two-thirds of the total number of *cis*-motifs able to bind bZIP TFs (Table 6).

The organization of orthologous promoters from cv. Renan showed few differences (Figures 2A,B) on the plus strand. For x-type HMW-GS genes, the organization was well conserved between 0 and –400 (nucleotide position relative to the start site). The TATA-box was at –90. A few differences were detected like an AACA motif at –144 in *Glu-A1-1* and *-D1-1*, which was absent in the orthologous B sequence. Between –400 and –1000, the organization was also well conserved but a 55-bp insertion in the *Glu-B1-1* promoter shifted the *cis*-motif upstream (i.e., at a more negative nucleotide position) of the insertion. Interestingly, we discovered a composite box named the GLM-GATA box. This box includes two repeated units, each of them made of a GATA motif and a GLM separated by a third GGATA motif. The relative positions of the constitutive *cis*-motifs in this box were conserved among the three orthologous sequences of cv. Renan (Figure 2). An ACGT motif was present a few bases upstream of this box in the B and D sequences. About 50 and 200 nucleotides upstream of this box, a DOF core motif (AAG) and an AACA motif (able to bind R2R3-MYB TFs), respectively, were detected in all the homoeologs. Downstream of this box, we found an AACA motif able to bind R2R3-MYB and the RY repeat.

Similar observations were made for the y-type sequences (Figures 2B,C). *Cis*-motifs organization presented many similarities between positions 0 and –400, although the promoter of *Glu-B1-2* includes some additional motifs at about position –150. In addition, the entire composite GLM-GATA box was lacking in the promoters of *Glu-A1-2* and *-B1-2*, the latter containing only a single copy of the GLM. None of these three sequences included the ACGT motif near the GLM-GATA found in the x-type HMW-GS gene promoters. We observed a composite motif at position –400, which was conserved in these three homoeologous sequences, composed of a G-box and three consecutive MYB motifs (two GATA and one AACA motifs). At about position –400, a deletion shortened the distances between the motifs at –400 and the adjacent ones on the *Glu-A1-2* promoter causing

Table 6 | Number of motifs in the upstream 1000-bp region of the six HMW-GS genes from the hexaploid wheat cv. Renan.

Motif sequence	Binding transcription factor	<i>Glu-A1-1</i>	<i>Glu-B1-1</i>	<i>Glu-D1-1</i>	<i>Glu-A1-2</i>	<i>Glu-B1-2</i>	<i>Glu-D1-2</i>
DOF							
AAAG	DOF	6	4	4	7	4	5
TGCAAAG	DOF		1	1	1		1
TGHAAARK	DOF	1		2			1
bZIP							
ACGT ^a	bZIP		1	1	2	3	2
ACGTG ^a	bZIP	1					
RTGAGTCAT ^b	bZIP				1	1	
TGAGTCA ^b	bZIP	2	2	2			2
YACGTGGC ^b	bZIP		1	1	1	1	1
CAAT	bZIP ^c	7	9	7	6	6	7
AACA MYB							
AAACAAA	R2R3-MYB	2	1	2	1	1	1
WAACCA	GAMYB			1	2	2	1
AACNNA	R2R3-MYB	1	1	1	1	1	1
GATA MYB							
GGATA	MYB/R1MYB	8	7	9	7	8	7
RY REPEAT							
CATGCA	AB3/VP1	2	2	2	3	1	2
OTHERS							
CANNTG	bHLH	4	4	4	7	5	4
CCAAT	HAP	2	3	2	2	2	2
TATAWA	TATA-box-Binding Proteins	1	1	1	1	1	1
CAANNNNATC		1	2	2	2	2	2
CCGTCC		1	1		1		1
Total		39	40	42	45	38	41

^a Related to GLM.^b Related to G-box motifs.^c Interaction not functionally validated.

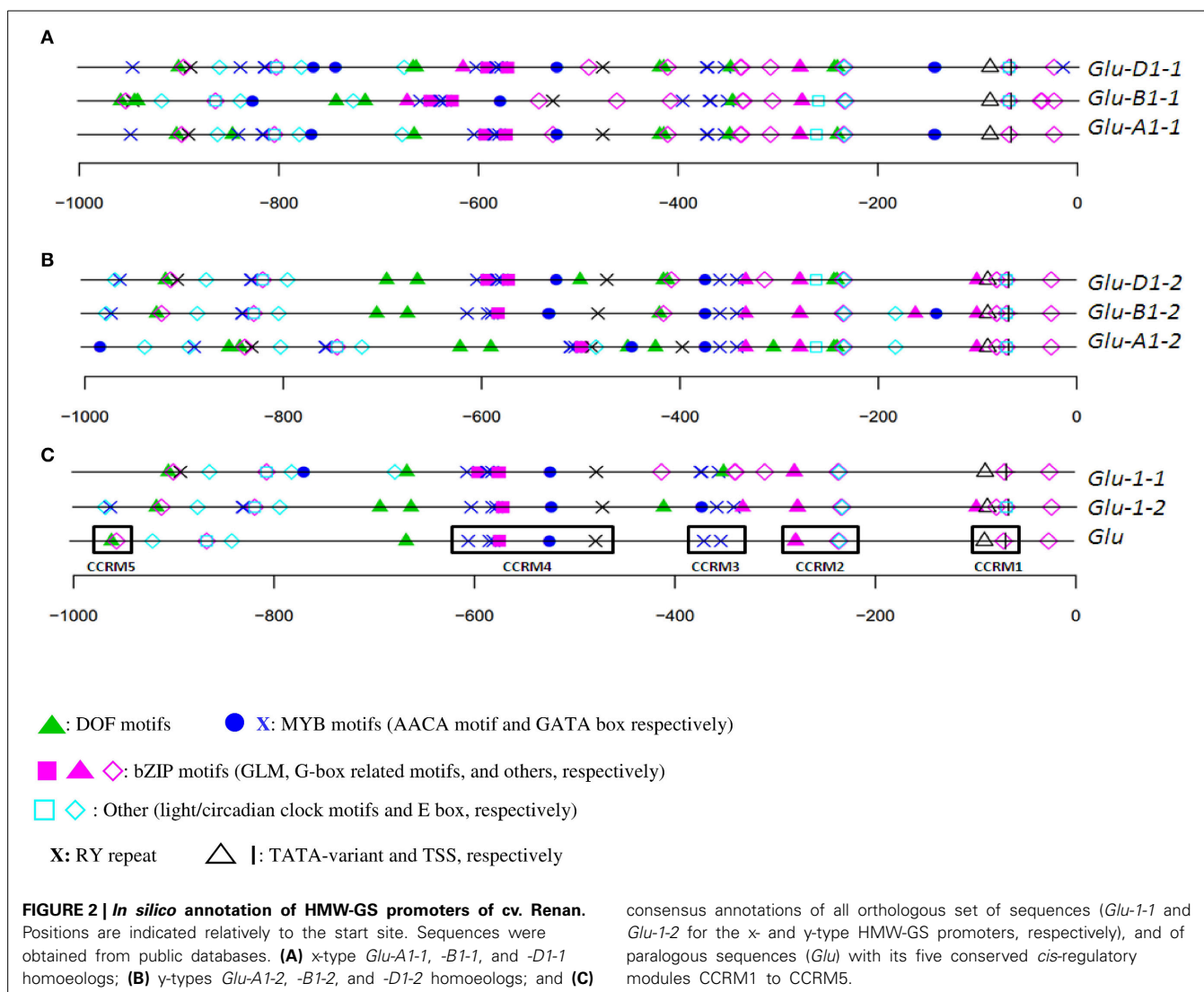
a deletion of a few motifs. For the three y-type homoeologous genes, an RY repeat and an AACA motif (binding R2R3-MYB) were located between position −400 and the GLM-GATA box.

The overall consensus generated from all HMW-GS genes of cv. Renan (**Figure 2C**) consisted of 21 motifs including motifs able to bind all the TFs known to regulate SSP synthesis so far. They were organized into five CCRMs. CCRMs were numbered from 1 to 5 from the start codon and composed of two to five *cis*-elements. As expected, CCRM1, a few nucleotides upstream of the TSS, was composed of the TATA-box variant and the CAAT motif. CCRM2 included a G-box-like motif and a CAAT motif, nested into an E-box (CANNTG), while CCRM3 clustered two GATA boxes. CCRM4 was the most interesting module. It included the incomplete GLM-GATA box, an AACA motif and the RY repeat. The GLM-GATA box was incomplete because of a missing GLM in the cv. Renan allele at *Glu-B1-2*. The fifth module, CCRM5, has a DOF motif and a CAAT box nested into an E-box and is located between positions −900 and −1000 in all promoters. A few bases downstream of CCRM5, E-boxes and circadian motifs were conserved. No typical bipartite endosperm box was detected.

On the minus strand, we noted an over-representation of the DOF core AAAG motif (data not shown).

For each HMW-GS gene, except *Glu-B1-1*, the annotation of haplotypes was almost identical (**Figures 3, 4**). Three groups were observed for *Glu-B1-1*. Haplotypes h2 and h5 have identical annotations, but compared to the other haplotypes, they contain an additional RY repeat at position −160. The second group contains h1 and h4, which are distinct from h3 because of an indel. Distances between motifs upstream and downstream of position −400 are therefore shorter in h3 than in the other haplotypes. In addition, a bZIP motif present in the insertion is deleted in h3. The haplotype h3 of *Glu-D1-1* promoter differs from other haplotypes as it has two additional bZIP motifs, one being a G-box.

The relative position of the GLM-box was conserved in all haplotypes of the three orthologous sequences of the x-type HMW-GS genes (**Figure 3**) and the y-type *Glu-D1-2* gene (**Figure 4**). For *Glu-B1-2*, the region sequenced in this study did not cover the GLM-GATA box (**Figure 4**), but the analysis of *Glu-B1-2* promoter sequences of cv. Chinese Spring (KC20630) and Xiaoyan



54 (EU137874), available in public databases, shows that, in these cases, the relative position of the GLM-box is also conserved in this gene (data not shown).

THE GLM-GATA BOX IS INVOLVED IN THE REGULATION OF *Glu-B1-1* EXPRESSION

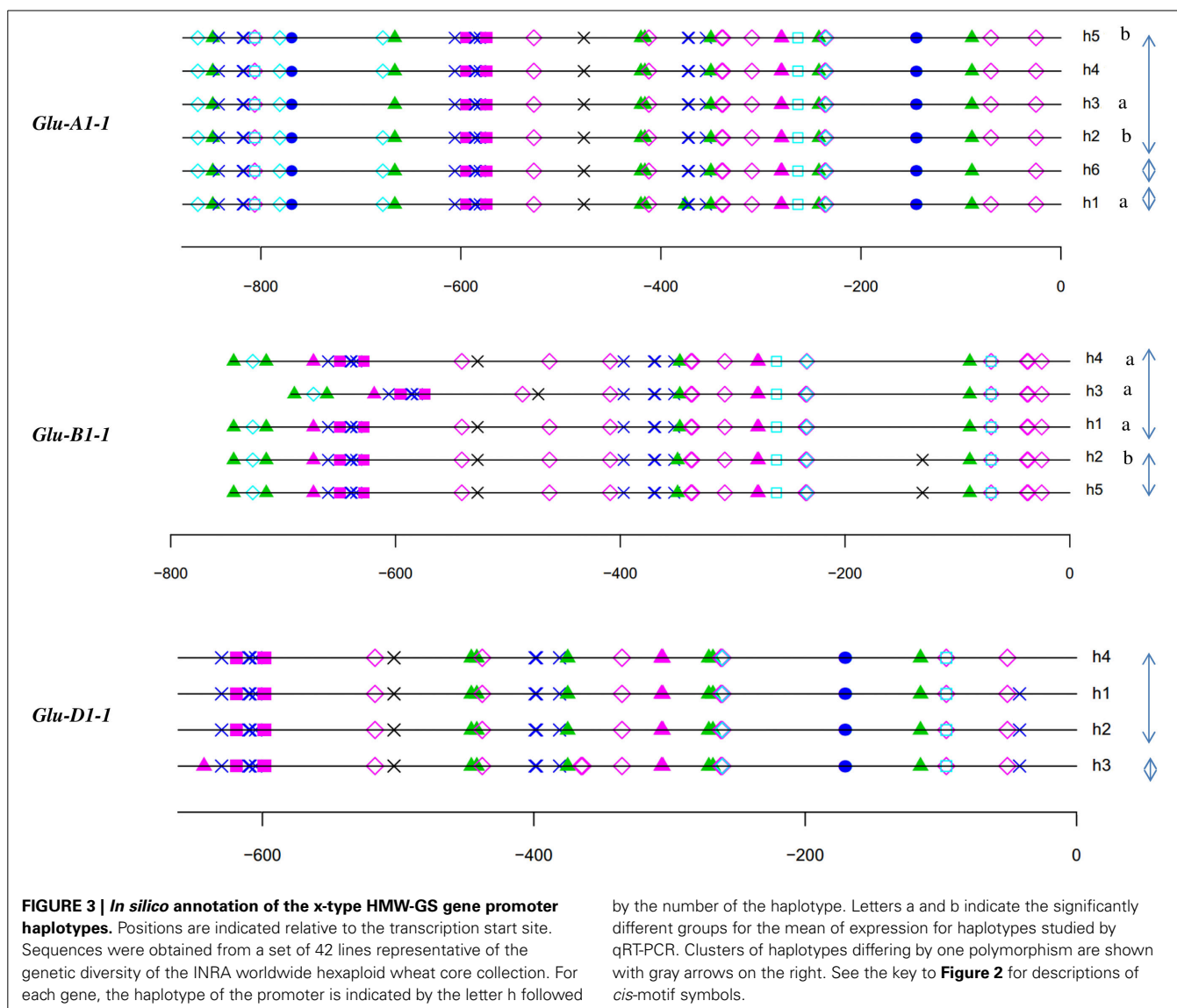
To investigate the involvement of the GLM-GATA box in the regulation of HMW-GS gene expression, we analyzed the effect of the 5' deletion from positions -747 to -597 (fragment carrying the GLM-GATA box) by transient expression experiment (Figures 5, 6). The deletion of the GLM-GATA box reduced normalized GUS expression by 59%.

To verify the potential binding activity of the two GLMs (GLM1 and GLM2 at positions -647 and -626 , respectively) present in the GLM-GATA box of the *Glu-B1-1* gene promoter, we performed EMSAs with synthetic oligonucleotides and a recombinant SPA protein expressed as a His fusion in *E. coli* (Figure 7). We also determined the *in vitro* binding of SPA to the G-box motif, which was previously shown to bind bZIP proteins (Norre

et al., 2002). As shown in Figure 7A, arabinose treatment induced expression of a protein of 50–75 kDa that was not present in uninduced cell extracts. The apparent size of the recombinant protein determined by SDS-PAGE was larger than the expected 48 kDa molecular mass of the His-tagged SPA fusion protein. A similar apparent increase in size on SDS gels was already reported by Albani et al. (1997) in their study of SPA. The recombinant His-SPA protein was purified to near homogeneity and used for binding assays. A DNA-protein complex was clearly observed with the GLM2 motif, while the shifted band detected for the GLM1 and the G-box was considerably fainter (Figure 7B). No shifted band was observed when incubation was carried out with the mutated probes (*glm1*, *glm2*, and *G-box*). DNA-binding affinity of the recombinant protein seems to be greater with the GLM2 probe than the other probes tested.

DISCUSSION

Here we characterized and annotated wheat HMW-GS gene promoters. The expression of these genes in developing grain was

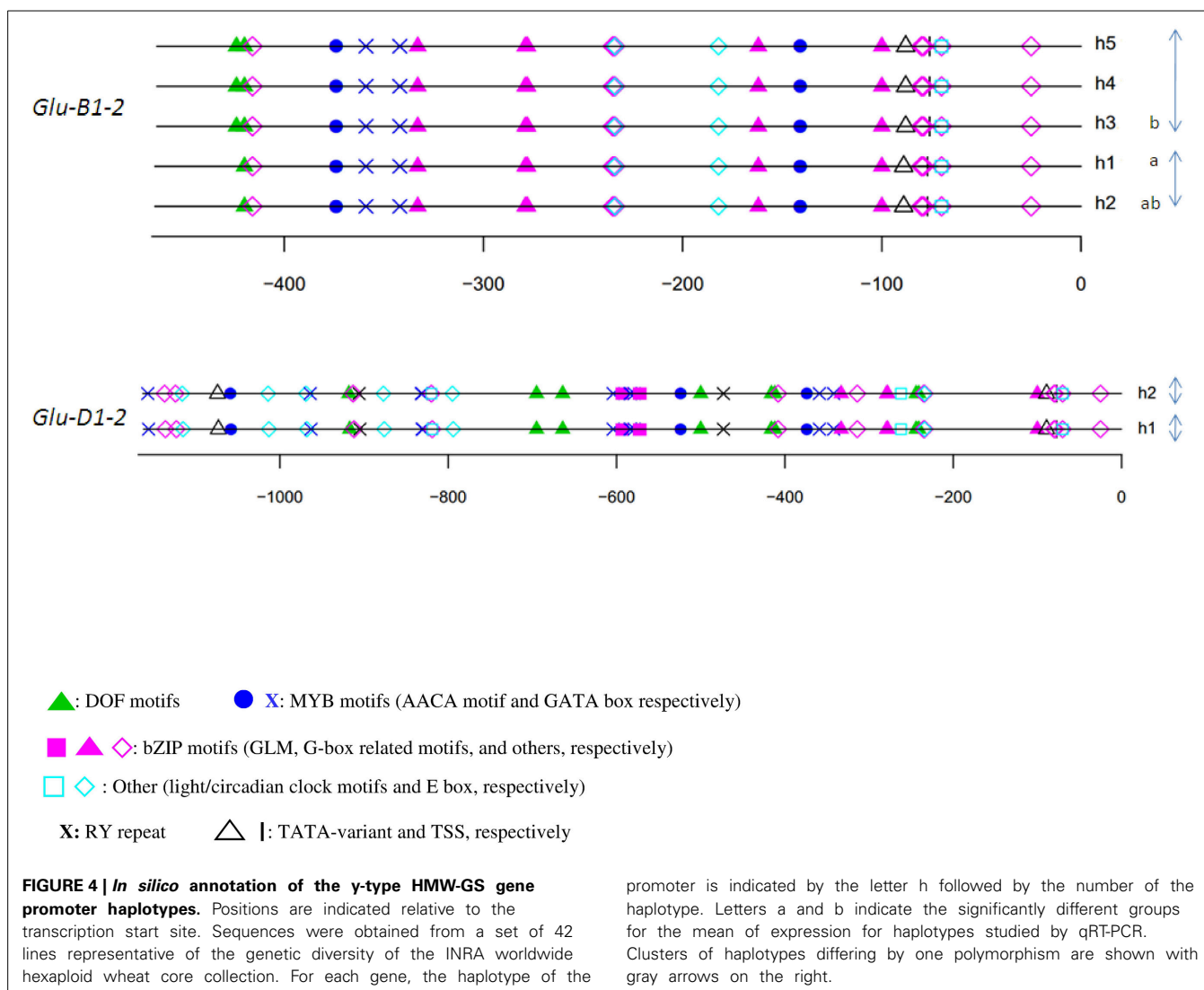


quantified by qRT-PCR and the correlations between the variability in expression and the variability in predicted *cis*-element motifs of the corresponding promoter were also analyzed. We considered regions of 467–1138 bp upstream of the start codon. In *Arabidopsis thaliana*, based on the density of polymorphisms in gene upstream regions, functional promoters require 250–500 nucleotides upstream of the TSS (Korkuć et al., 2014). Under the assumption that promoter length is conserved, the lengths of the regions surveyed here provide a reasonable coverage of functional SSP gene promoters in wheat. Moreover, we analyzed the role of the GLM-GATA box of the *Glu-B1-1* gene promoter by transient expression assay and evaluated the functionality of the *cis*-motifs reported to bind bZIP TFs.

VARIABILITY OF HMW-GS PROMOTER HAPLOTYPES CANNOT BE USED DIRECTLY TO SCREEN FOR ELECTROPHORETIC ALLELES

In *A. thaliana*, the nucleotide variability in promoters varies depending on the function of their downstream gene (Korkuć

et al., 2014). It is higher for genes involved in adaptive processes and transcriptional regulation than for genes involved in housekeeping functions. In wheat, the diversity of promoters is not widely documented so far. The range of nucleotide diversity observed for HMW-GS promoters, approximately one polymorphism every 100 bases, is comparable to that reported for the SPA promoter (Ravel et al., 2009), but is higher than the overall level of polymorphism of one SNP every 212 nucleotides reported for promoters of other genes (Ravel et al., 2006). Although upstream gene regions are somewhat constrained as they are involved in gene regulation, they are reported to show higher variability than coding regions. Constraints most likely apply to *cis*-regulatory elements (Korkuć et al., 2014). As they affect short regions, mutations could occur with little or no incidence, whereas the entire coding sequence has to withstand greater constraints. In addition, the modular organization of *cis*-elements, together with their redundancy, may buffer the effects of mutations (reviewed by Purugganan, 2000). These reasons probably explain why the



diversity is higher in promoter regions than in coding sequences. As usually reported (e.g., Chao et al., 2009), the level of diversity was the lowest in HMW-GS sequences from the D genome with 1 polymorphism every 145 base for *Glu-D1-2*, whereas the highest level of diversity was observed for HMW-GS promoters from the B genome with, on average, one polymorphism every 60 bases.

SDS-PAGE is still routinely used for characterization of HMW-GS alleles. Developing diagnostic SNPs to identify electrophoretic forms of HMW-GS from any part of young plants would be a valuable tool to support breeding for improved flour quality. However, there are up to four haplotypes promoter sequences per electrophoretic allele or only one haplotype for several alleles. Anderson et al. (1998) already reported two different alleles for the Bx7 promoter. The promoter haplotypes perfectly match the protein alleles only for *Glu-D1-2*. Currently, the identification of a set of SNPs from the other HMW-GS promoter sequences as a shortcut to distinguish between different protein forms is not possible, so the search for diagnostic SNPs needs to continue.

A MINIMAL FRAMEWORK FOR THE TRANSCRIPTIONAL REGULATION OF HMW-GS GENES IS REVEALED

We screened for *cis*-elements known to regulate SSP synthesis among all the HMW-GS gene promoters of cv. Renan. By annotating these promoters we found that they had a few regulatory elements in common, mostly organized into five CCRMs. Since HMW-GS genes show similar patterns of spatial and temporal expression, these common *cis*-elements might be involved in their global regulation and consequently may provide a minimal regulatory framework needed for the developmental and environmental (i.e., in response to nitrogen supply) regulation of HMW-GS gene expression. Like the long endosperm box described in some LMW-GS gene promoters, which consists of two repeats of the endosperm box (Albani et al., 1997; Juhász et al., 2011), the GLM-GATA box described here for the first time is also formed by two motifs (GATA and GLM) repeated twice in most of the promoters of HMW-GS. Our results demonstrate that the GATA-GLM box has an activator effect. Its two GLMs were able to bind SPA and were thus functional *cis*-motifs. GATA

and GLM motifs are reported to bind R1MYB and bZIP TFs. Modules able to bind MYB and bZIP proteins belong to the seven best-known combinations of *cis*-motifs and are also very well represented in *A. thaliana* and poplar promoters (Ding et al., 2012). However, these modules generally bind R2R3-MYB TFs and thus include AACA rather than GATA motifs.

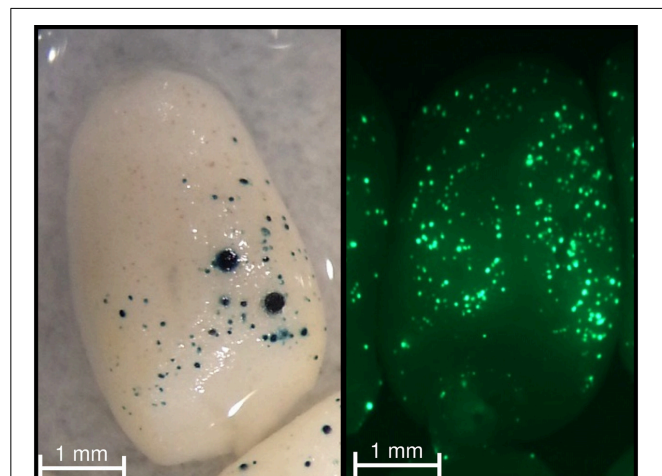
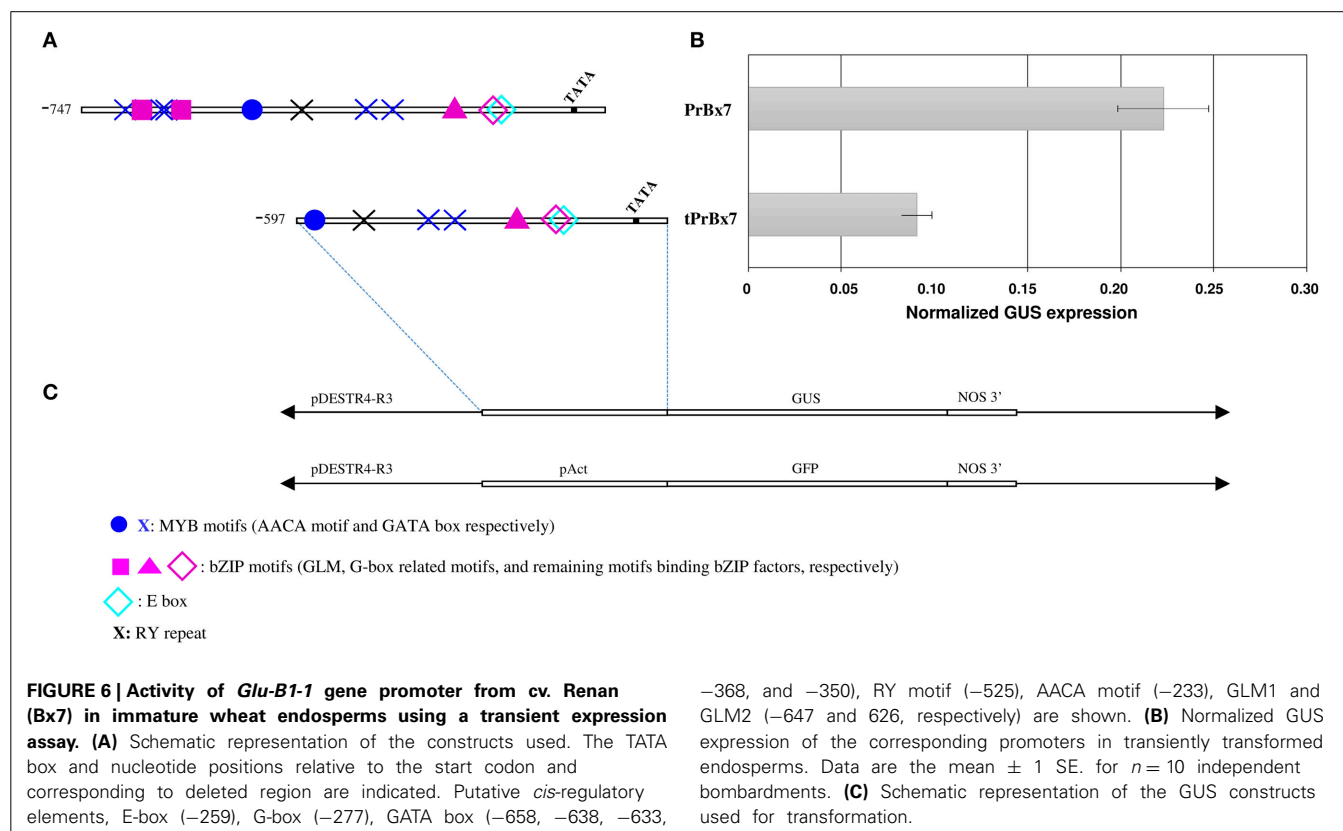


FIGURE 5 | GUS and GFP activities in wheat immature endosperm. Immature endosperm was co-bombarded with the pPrBx7-GUS and pAct-GFP constructs. Note the blue (bottom panel) and green (top panel) foci across the dorsal surface.

This GLM-GATA box is included in a CCRM with an AACA motif and a RY repeat. Notably, this conserved module is able to bind all the *cis*-motifs reported to regulate SSP synthesis. The minimal regulatory framework contains no P-box like those responsible for endosperm-specific expression of LMW-GS genes. However, several motifs have been reported to be involved in endosperm-specific expression like the CAAT, AACA and ESP motifs (Shirsat et al., 1989; Takaiwa et al., 1996; Vickers et al., 2006). The minimal regulatory framework also contains CAAT motifs. Possibly the G-box acts like the GLM in rice, which has been demonstrated to be an essential element conferring endosperm-specific expression, while P-box and AACA motifs are involved in quantitative regulation (Wu et al., 2000). In addition, the HMW-GS framework contains motifs involved in circadian rhythms. The E-box, which is able to bind bHLH and other TFs, has been reported to be involved in circadian transcriptional rhythms (Seitz et al., 2010), although exactly the same E-box sequence (5'-CATCTG-3') was not found in the HMW-GS promoters.

Previous reports demonstrated that the 277 bp immediately upstream of the TSS are sufficient for temporal and tissue-specific regulation (Halford et al., 1989; Norre et al., 2002). There is also strong evidence indicating that mutations in this region are responsible for the silencing of *Glu-A1-2* (Halford et al., 1989). However, we did not find any mutation that could alter *cis*-motifs known to be involved in SSP gene regulation. In addition, the mutations specific to *Glu-A1-2* promoter did not create or alter any of the *cis*-motifs of the PLACE database. This suggests that



gene is inactive (De Bustos et al., 2000). However, this does not explain the low levels of expression of these haplotypes as the qRT-PCR primers used to detect transcripts in this analysis are located upstream of this mutation. The very low transcription level of this null allele may be due to sequence polymorphism in the promoter as it has been demonstrated for the null *Glu-A1-2* allele (Halford et al., 1989). There were no obvious differences in our annotation of haplotypes of the *Glu-A1-1* promoter that could explain the large differences in expression observed. This is unlike the case of *Glu-A1-2*, which is silent and shows a particular *cis*-motif organization upstream of position -370 when compared with other *y*-type HMW-GS genes. However, a 277-bp fragment immediately upstream of the *GluA1-2* TSS was not able to generate any transcriptional activity (Halford et al., 1989). The organization of this fragment is quite similar to that of other expressed *y*-type promoters, so it is difficult to hypothesize how the gene is silenced. As expected, *Glu-B1-1* in Glenlea (line accession no. 3358) strongly expresses the Bx7 subunit transcript. This over-expression is explained by a 10.3-kb duplication including a second copy of *Glu-B1-1* (Ragupathy et al., 2008). Again, our annotation of the promoter alone does not show obvious differences that could explain the different levels of expression. In agreement with the results of Halford et al. (1989), the deletion found in the h3 haplotype does not impact the level of expression, which confirms that it plays no role in transcriptional regulation.

These results suggest that other mechanisms are able to modulate HMW-GS gene expression, such as *cis*-elements located further upstream of the region studied here. This would agree with results of Wang et al. (2013), who described the presence of key regulatory sequences in the distal sequence of *Glu-B1-1*, especially a Py-rich stretch at about position -2000. This sequence has been reported to cause a high level of expression in tomato (Daraselia et al., 1996). Methylation of DNA may also be involved in HMW-GS expression regulation, as shown for hordein genes in barley (Sorensen et al., 1996; Radchuk et al., 2005), even though no CpG islands were detected in the wheat promoter regions studied here using the PlantPAN search engine (Chang et al., 2008).

In conclusion, this work reveals a minimal regulatory framework shared by all the wheat HMW-GS gene promoters. The *cis*-elements organization is conserved, including all the motifs known to be involved in the regulation of SSP genes. The conservation of this regulatory framework strongly suggests that it is involved in the regulation of this gene family. The bipartite endosperm box was not found but a CCRM with the GATA-GLM box with an RY repeat and an AACA motif is present in all the promoters. The CCRMs, which occur at similar relative positions in all the promoters of this small family, presumably have a common evolutionary origin, suggesting that they may be functional. However, validating their functional roles requires further experiments. The “*in silico* footprint” described here will help to select motifs for functional validation, as shown here by transient expression assays of *Glu-B1-1* promoter. Our annotations do not directly account for differences in expression among promoter haplotypes, suggesting that other mechanisms may be involved in regulating HMW-GS gene expression.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <http://www.frontiersin.org/journal/10.3389/fpls.2014.00621/abstract>

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Analogous reserve distribution and tissue characteristics in quinoa and grass seeds suggest convergent evolution

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Quinoa seeds are highly nutritious due to the quality of their proteins and lipids and the wide range of minerals and vitamins they store. Three compartments can be distinguished within the mature seed: embryo, endosperm, and perisperm. The distribution of main storage reserves is clearly different in those areas: the embryo and endosperm store proteins, lipids, and minerals, and the perisperm stores starch. Tissues equivalent (but not homologous) to those found in grasses can be identified in quinoa, suggesting the effectiveness of this seed reserve distribution strategy; as in cells of grass starchy endosperm, the cells of the quinoa perisperm endoreduplicate, increase in size, synthesize starch, and die during development. In addition, both systems present an extra-embryonic tissue that stores proteins, lipids and minerals: in gramineae, the aleurone layer(s) of the endosperm; in quinoa, the micropylar endosperm; in both cases, the tissues are living. Moreover, the quinoa micropylar endosperm and the coleorhiza in grasses play similar roles, protecting the root in the quiescent seed and controlling dormancy during germination. This investigation is just the beginning of a broader and comparative study of the development of quinoa and grass seeds. Several questions arise from this study, such as: how are synthesis and activation of seed proteins and enzymes regulated during development and germination, what are the genes involved in these processes, and lastly, what is the genetic foundation justifying the analogy to grasses.

Keywords: coleorhiza, endosperm, grass seed, micropylar endosperm, perisperm, quinoa seed

INTRODUCTION

Cereals, e.g., rice (*Oryza sativa* L.), wheat (*Triticum aestivum* L.), maize (*Zea mays* L.), barley (*Hordeum vulgare* L.), oat (*Avena sativa* L.), rye (*Secale cereale* L.) are members of the monocot family Poaceae, which are cultivated for the edible components of their grains or caryopses and consist of a single seed enclosed by dry and indehiscent pericarp, firmly adhered to the rest of the integuments.

Pseudocereals are dicots (thus not cereals) and include species of the Amaranthaceae (e.g., quinoa, *Chenopodium quinoa* Willd.), and different species of the genus *Amaranthus* and Polygonaceae (e.g., buckwheat, *Fagopyrum esculentum* Moench) families, also cultivated for the edible components of their grains. The dispersal unit in pseudocereals is the grain botanically called achene, which consists of a single seed enclosed in a dry and indehiscent pericarp (Figures 1 and 2). According to Prego et al. (1998), in quinoa the pericarp is very thin; as a result, the achene is also referred to as utricle.

Quinoa seeds are highly nutritious due to the quality of their proteins and lipids and the wide range of minerals and vitamins they store. The ability of quinoa to produce high-quality proteins under extreme environmental conditions makes it an important crop not only for Andean communities but also for the diversification of future agricultural systems. Cereals and quinoa are grain crops and thus essentially full of starch, but

they also contain significant quantities of proteins, oil, and minerals. In quinoa and grasses, the distribution of main storage reserves is clearly divided and three main storage compartments can be distinguished in the mature seed: (i) a tissue that stores mainly starch, which is the perisperm in quinoa and the starchy endosperm in grasses, with (ii) an embryo that stores principally proteins and lipids, and (iii) a non-embryonic tissue that stores proteins, lipids, and minerals, which is the aleurone layer in gramineae and the micropylar cone in quinoa. In this study we demonstrate that tissues equivalent (but not homologous) to those found in grasses can be identified in quinoa (Figure 3), thus suggesting the effectiveness of this seed reserve compounds distribution strategy and justifying the advantages that led evolutionary distant plants to develop seeds with analogous nutrients distribution.

This investigation is part of a broad comparative study of the development of quinoa and grass seeds. Several questions arise from this investigation, such as: how are synthesis of seed proteins and enzymes regulated during development and germination, what are the genes involved in these processes, and lastly, what is the genetic foundation for the analogy with grasses.

THE FRUIT

According to Prego et al. (1998), in quinoa the pericarp is made up of papillose cells derived from the outer epidermis of the ovary

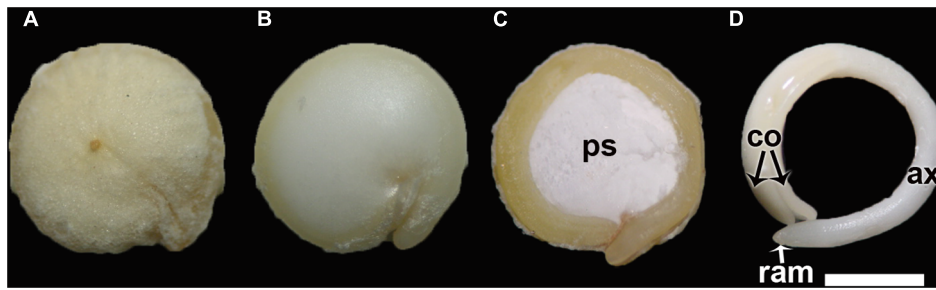


FIGURE 1 | (A) Quinoa grain; **(B)** Quinoa seed (without pericarp); **(C)** Longitudinal midsection of a quinoa seed; **(D)** Excised embryo. ax, hypocotyl-radicle axis; co, cotyledon; ps, perisperm; ram, root apical meristem. Bar: 1 mm.

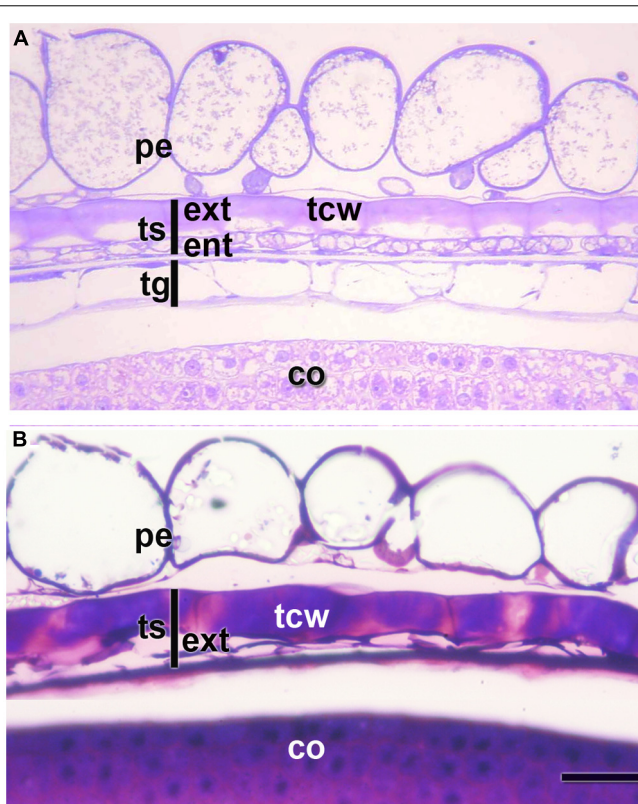


FIGURE 2 | Pericarp and integuments at two stages of quinoa seed development. (A) Young seed (torpedo stage). **(B)** Mature seed. Grains were fixed using a mixture of 2% paraformaldehyde and 1% glutaraldehyde in 0.1 M phosphate buffer, pH 7.2, and embedded in London Resin White resin, according to López-Fernández and Maldonado (2013b). Semithin sections (2 μ m thick) were stained with 0.5 % Toluidine Blue. co, cotyledon; ent, endotesta; ext, exotesta; pe, pericarp; tcw, tangential cell wall of the cells from the outer layer of the outer integument; tg, tegmen; ts, testa.

and an inner discontinuous layer with tangentially stretched cells (**Figure 2**). The seed coat derives from ovule integuments, each one constituted by two to three layers. The seed coat consists of a testa and a tegmen, each one two layers thick. During seed development, the endotesta layer and both layers of the tegmen are almost completely consumed (**Figure 2B**); on the contrary,

cells of the exotesta enlarge and develop thick tangential cell walls; these cells remain intact and are dismantled just after germination (**Figure 2**).

In grasses, the pericarp is adhered to the remains derived from the ovule integuments, which are, at maturity, usually reduced to a thin layer (Morrison, 1976). The anatomy of the pericarp is remarkably similar in all the grasses studied to date (Rost, 1973). It is composed of an outer epidermis with a thick cuticle layer and one to several subjacent cell layers (Bessey, 1894; Narayanaswami, 1953, 1955a,b,c, 1956; Rost, 1973). Even though cells of the subjacent layers are crushed, two types of cell layers, both typically containing cells with thick walls can be identified: a cross-cell layer, adjacent to the inner epidermis, whose cells are elongated transversely to the long axis of the caryopsis; and a tube cell layer, derived from the inner epidermis, whose cells are elongated parallel to the caryopsis axis (Krauss, 1933; Kent and Evers, 1994).

THE SEED

THE QUINOA SEED

The ovule is amphitropous (i.e., ovule is bent by the formation of a basal body, then both micropylar, and chalazal ends are near each other), bitegmic (with two integuments), and crassinucellate (archesporial cell cuts off a parietal cell, and parietal cell derivatives make the megasporocyte deep-seated in the ovule; Davis, 1966). The seed contains a peripheral, curved embryo surrounding a perisperm or basal body and is covered by integuments and pericarp (**Figure 1**). A micropylar endosperm forming a cone surrounds the root apical meristem of the embryo (**Figure 3**). The embryo consists of a hypocotyl–radicle axis and two cotyledons (**Figure 1D**). In the axis, both the root apical meristem, with the root cap, and the shoot apical meristem are differentiated. The shoot apical meristem forms a conical structure between the two cotyledons lacking leaf primordia (Prego et al., 1998; Burrieza et al., 2012). All embryo cells, including those of the apical meristems, store abundant proteins and lipids in the form of protein and lipid bodies, respectively. During germination, the radicle grows through the center of the cone, in the space previously occupied by the suspensor.

The suspensor connects the embryo to the nucellus during early seed development, holding the growing embryo in a fixed position within the seed and allowing nutrients to be transported to the embryo (Bozhkov et al., 2005). It is a short-lived tissue, only active

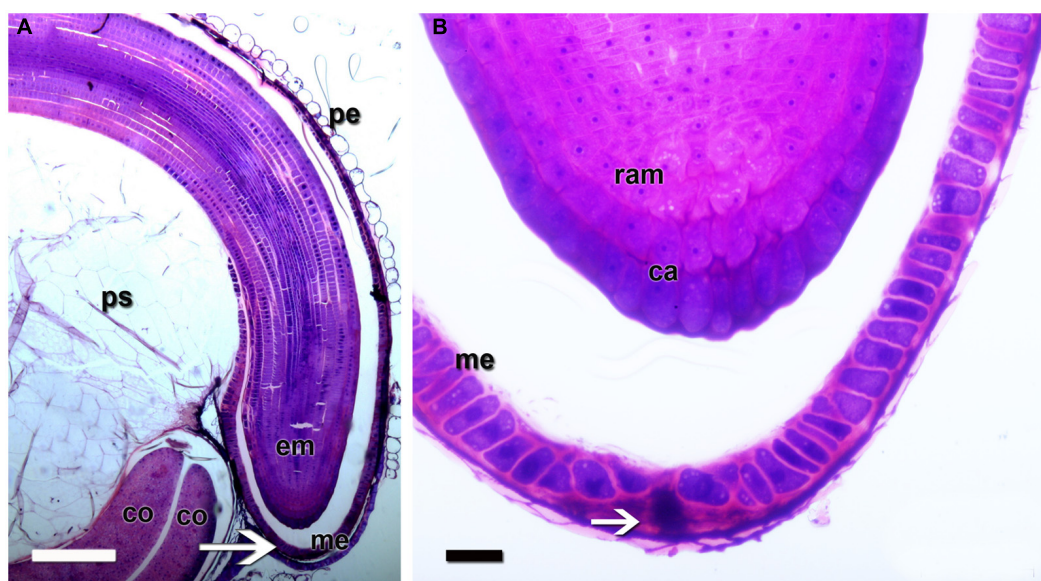


FIGURE 3 | Quinoa micropylar endosperm (in a mature seed). (A) The white arrow indicates the center of the micropylar cone; *co*, cotyledon; *em*, embryo; *me*, micropylar endosperm; *pe*, pericarp; *ps*, perisperm. (B) Detail of (A). The white arrow indicates the central channel of the micropylar cone,

which is occupied by the remains of the suspensor. *ca*, caliptra; *me*, micropylar endosperm; *ram*, root apical meristem. Semithin section (2 μ m thick) was obtained from a fixed, resin-embedded, sectioned, and stained seed, as described in **Figure 2**.

in early embryogenesis. In quinoa, it is constituted by (1) a neck that connects the suspensor to the embryo proper, which is made up of cells with small vacuoles; and (2) a knob, which is composed of a set of larger basal cells that protrude into the micropylar endosperm (**Figures 4 and 5**). The knob is formed by transfer cells on the outside, with ingrowths in their outer cell walls (**Figure 4**), dense cytoplasm, and numerous small vacuoles (López-Fernández and Maldonado, 2013b). When the embryo finishes accumulating reserves its cells degenerate leaving, however, visible remains in the center of the micropylar cone (**Figure 3**). During germination, this remnant of the suspensor presumably offers less mechanical resistance and might help facilitate radicle protrusion during germination.

The perisperm is derived from the nucellus of the ovule; this portion of the nucellar tissue is not consumed by the development of the embryo sac and persists after fertilization, becoming the main nutritive tissue of the seed (**Figure 5A**). During quinoa perisperm development, three major developmental phases can be distinguished: (1) early development of the nucellus, including mitotic activity, the last stage of which takes place before anthesis, establishing the final cell number and tissue configuration; (2) cellular differentiation, which can be broken down into the partly overlapping processes of cellular expansion, endoreduplication, accumulation of starch reserves, and programmed cell death (PCD); and (3) maturation, which comprises the shutdown of biosynthetic processes, desiccation induction, and quiescence (López-Fernández and Maldonado, 2013a). Through endoreduplication, DNA content usually peaks at 8°C but some nuclei can reach up to 16 and 32°C (López-Fernández and Maldonado, 2013a). At maturity, the perisperm consists of uniform, non-living, thin-walled cells. Nuclei and other cytoplasmic organelles

are absent at this stage. Cells are full of compound starch grains and simple starch grains occupy the space between compound grains (Prego et al., 1998).

Endosperm development in quinoa, as in cereals, is of the nuclear type. According to Olsen (2004), syncytial and cellularization phases of nuclear endosperm development are conserved among all groups of angiosperms. Endosperm development has only recently begun to be studied in quinoa (López-Fernández and Maldonado, 2013b). In the endosperm mother cell, nuclear divisions occur freely in the parietal cytoplasm surrounding the central vacuole. Cellularization is associated with the initiation of periclinal divisions, which occur in a centripetal direction, thereby shrinking the vacuole. While divisions are ongoing, nuclei grow in size and endoreduplicate, with the DNA content peaking at 6°C (López-Fernández and Maldonado, 2013b). When the endosperm reaches its final size, three domains are differentiated: a micropylar domain, comprising six to eight cell layers; a peripheral domain of two cell layers; and a chalazal domain of six or seven cell layers. The embryo grows at the expense of the endosperm, i.e., the chalazal and peripheral endosperms, as well as the inner layers of the micropylar endosperm are progressively dismantled (**Figure 5A**). Cells destined to be consumed during embryo development do not accumulate storage reserves. In mature seeds, the remaining endosperm forms a micropylar cone, crossed in the center by the suspensor (**Figure 4**). According to López-Fernández and Maldonado (2013b), throughout development, two major cell types make up the quinoa endosperm: the micropylar endosperm, which is constituted by a cone covering the radicle, and the ephemeral endosperm: the tissue located on either side of the growing embryo (**Figure 4**). During seed development, cells of the ephemeral endosperm

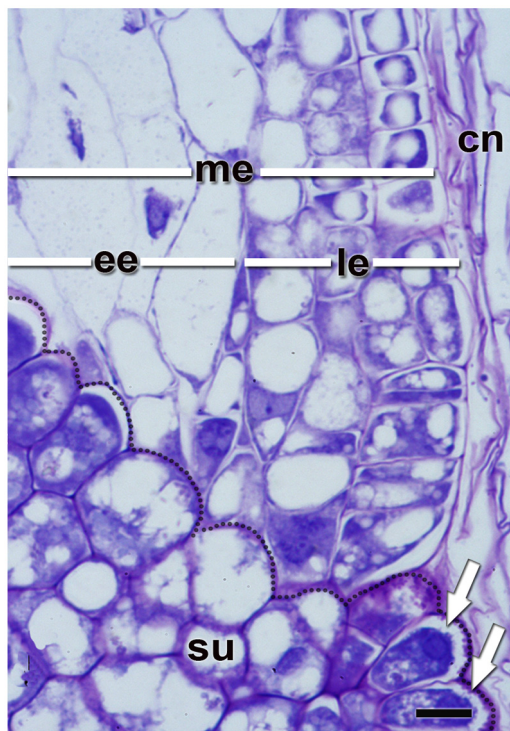


FIGURE 4 | Quinoa micropylar endosperm (at the torpedo stage). *cn*, crushed nucellus; *ee*, ephemeral endosperm; *le*, lasting endosperm; *me*, micropylar endosperm; *su*, suspensor. Semithin section (2 μm thick) was obtained from a fixed, resin-embedded, sectioned, and stained seed as described in **Figure 2**. The border between the suspensor and endosperm has been highlighted with a dotted line. White arrows indicate the "festooned" outer cell walls in the transfer cells of the suspensor. Bar: 10 μm .

are crushed and finally disintegrated. In contrast, cells of the micropylar cone (**Figure 3**), which is one or two cell layers thick, store lipids and proteins that are used by the embryo during germination.

THE GRASS SEED

The ovule is hemianatropous (the hemianatropous condition results from the curvature of the ovule such that the micropyle comes to lie at right angles to the funiculus), bitegmic (with two integuments), and tenuinucellate (i.e., the archesporial cell enlarges to form the megasporocyte, then megasporocyte is subdermal; Davis, 1966). The seed contains the embryo on the adaxial face of the caryopsis, which is unilaterally covered by the endosperm (**Figure 5B**).

The endosperm is almost completely preserved as reserve tissue in mature seeds. According to Olsen (2004), throughout development, four major cell types constitute the grass endosperm, i.e., aleurone, starchy endosperm, basal endosperm transfer cells, and embryo-surrounding region (**Figure 5B**). Similar to quinoa endosperm, after fertilization, the initial endosperm nucleus divides repeatedly without cell wall formation in the parietal cytoplasm surrounding the central vacuole (Brown et al., 1994; Olsen, 2004).

Cellularization is associated with the initiation of periclinal divisions, which occur in a centripetal direction, progressively shrinking the vacuole until its disappearance (Brown et al., 1994, 1996; Olsen, 2001, 2004). The first periclinal division round is formative, originating both the aleurone and starchy initials (Brown et al., 1996).

Aleurone cells form a sheet generally composed of cells that store proteins, lipids, and mineral nutrients to be used up during germination (Jones, 1969a; Lonsdale et al., 1999). In some species, the peripheral layer undergoes rounds of periclinal divisions before assuming aleurone cell characteristics. Thus, the amount of aleurone layers varies according to the species, e.g., maize and wheat have one layer, rice has one to several layers, and barley has three layers (Buttrose, 1963; Hoshikawa, 1993). Aleurone cells accumulate proteins and lipids in protein vacuoles and lipid bodies, respectively. Upon seed germination, it is assumed that storage proteins provides the amino acids necessary for the synthesis of hydrolytic enzymes required for starch mobilizing in the starchy endosperm and that aleurone cells die by autophagy (Jones, 1969b,c; Jones and Price, 1970; Taiz and Jones, 1970; Taiz and Honigman, 1976; for reviews see Bethke et al., 1998; Becraft and Gibum, 2011).

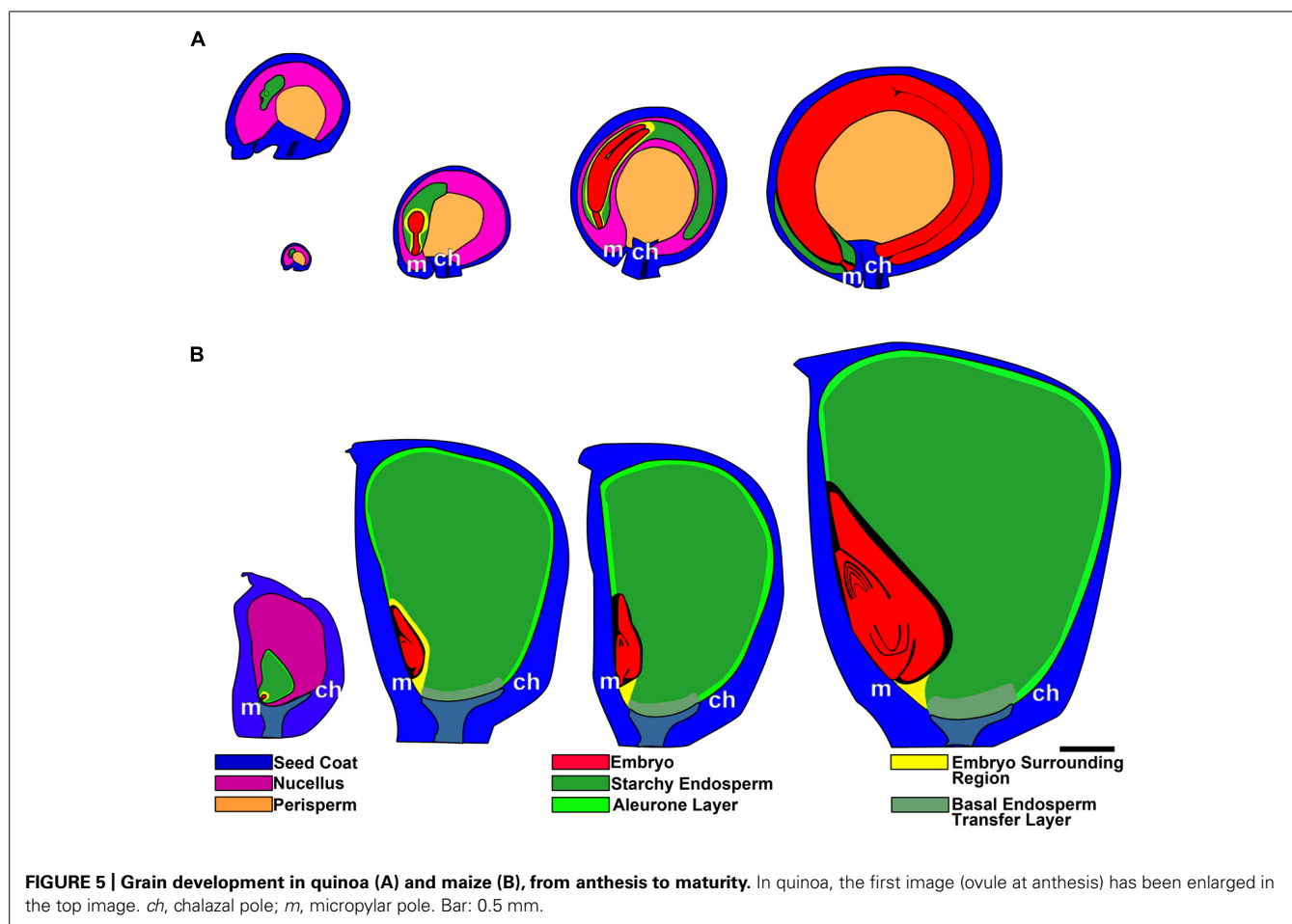
At maturity the starchy endosperm cells consist of uniform, non-living, thin-walled cells full of starch grains but they also contain protein bodies (Reyes et al., 2011; for review see Olsen et al., 1992). During development, these cells simultaneously accumulate storage reserves and degenerate, both processes mediated by a program of developmentally controlled cell death. Starchy endosperm cells accumulate starch in plastids and prolamins in protein bodies.

Endoreduplication occurs in starchy endosperm. In maize, DNA content usually peaks at 6 and 12°C, but some nuclei reach 24, 48, 96, and 192°C (Kowles and Phillips, 1985; Kowles et al., 1990; Larkins et al., 2001; Sabelli and Larkins, 2009; Sabelli, 2012). Endoreduplication precedes and accompanies two programs that occur simultaneously in this tissue: (i) accumulation of storage reserves, and (ii) PCD (Young et al., 1997; Young and Gallie, 2000; Domínguez and Cejudo, 2014).

The region of the transfer cells is located in the basal endosperm close to the vascular tissues of the placenta (**Figure 5B**), facilitating solute transfer from the vascular bundle of the pedicel toward the endosperm (Thompson et al., 2001). Two or three cells derived from the outer layer during the process of cellularization assume transfer cell identity, developing cell wall ingrowths (Thompson et al., 2001).

The embryo-surrounding region comprises several cell layers that completely envelop the young embryo (**Figure 5B**) and are characterized by their dense cytoplasm contents, abundance of small vacuoles, and a complex membrane system but they do not accumulate storage reserves and their death generates a space filled with crushed endosperm cells surrounding the embryo (Olsen, 2004; Sabelli and Larkins, 2009). The embryo grows at the expense of these cells, causing their degradation.

The single cotyledon of grasses is transformed into the absorptive scutellum which lies between the endosperm and the embryo axis. Many grasses possess a small scale-like appendage opposite the scutellum, the so-called epilates (Saha, 1957). The shoot apical



meristem is covered by the coleoptile and contains several leaf primordia.

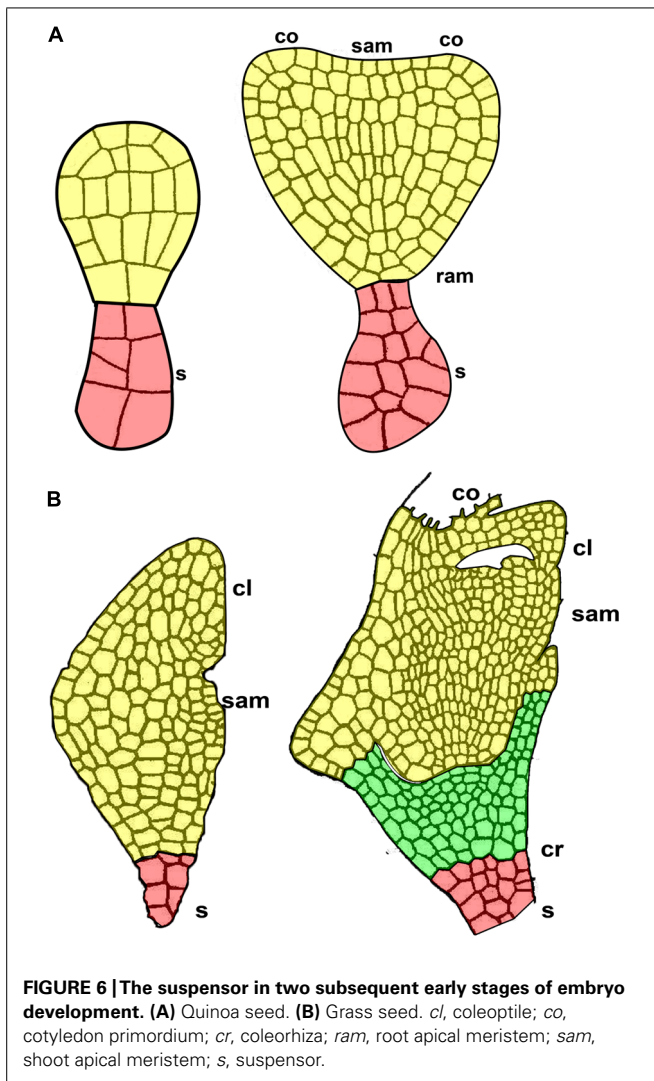
The coleorhiza is a non-vascularized, multicellular embryonic tissue that covers the cereal root apical meristem. It is an embryonic tissue located between the root apical meristem and the suspensor, characteristic of the grass embryo and absent in quinoa embryo (Figure 6). The coleorhiza originates together with the root cap and the suspensor (Johansen, 1950), but later in development it is separated from the radicle by a cleft (Figure 6B).

Although coleorhiza is involved in germination and successful establishment of all grass seedlings, information on its morphology, anatomy, and function is very sparse. In rye, Sargent and Osborne (1980) describe coleorhiza in the mature rye seed as made up of parenchymatic quiescent cells lacking vacuoles and containing a cytoplasm densely packed with ribosomes, lipid bodies largely confined to a peripheral position, a greatly reduced endomembrane system, mitochondria with a few cristae, and nuclei in which the heterochromatin is condensed. During germination of rye (Sargent and Osborne, 1980) and barley (Barrero et al., 2009) seeds, coleorhiza cells elongate and separate from each other, thereby forming intercellular spaces after consuming their own storage reserves. Eventually, the growth of embryonic roots (primary and adventitious) dismantles the tissue (Millar et al., 2006).

MICROPYLAR ENDOSPERM VS. COLEORHIZA

In quinoa, the micropylar endosperm is the only part of the tissue that persists in the mature seed, forming a cone covering the root apical meristem (Figure 5A). In other species (e.g., tomato, *Datura ferox*), the micropylar endosperm is just the micropylar portion of a larger tissue covering the root apical meristem. The micropylar endosperm has been studied in the species *Arabidopsis thaliana* (Millar et al., 2006; Okamoto et al., 2006), cress (Müller et al., 2006), *Datura ferox* (Mella et al., 1995; Arana et al., 2007), tomato (Toorop et al., 2000; Wu et al., 2000), coffee (Da Silva et al., 2004), cucumber (Amritphale et al., 2005; Salanenka et al., 2009), and lettuce (Nascimento et al., 2000).

In the mature seed, cells of the micropylar endosperm store hemicelluloses in cell walls, and proteins, lipids and minerals in the cytoplasm. Hemicelluloses strengthen and harden the tissue, and germination is only possible after this tissue has been sufficiently weakened (i.e., hydrolyzed) and the radicle can overcome its resistance (Psaras et al., 1981; Psaras and Georgiou, 1983; Watkins and Cantliffe, 1983; Groot and Karssen, 1987; Sánchez et al., 1990). In quinoa, control of radicle protrusion during germination is mediated, at least in part, by micropylar endosperm weakening, but its emergence occurs via the channel occupied by suspensor remains (unpublished observations).



On the other hand, endosperm weakening, as well as radicle growth potential, are known to be regulated by plant hormones (Linkies et al., 2010): abscisic acid (ABA) inhibits endosperm weakening while gibberellins (GA) act as its antagonists in a complex network integrating environmental signals such as light, temperature, water availability, and nutrient status (Kucera et al., 2005); ethylene and brassinosteroids also counteract ABA, but their effects on endosperm weakening are unknown.

In grasses, there is no micropylar endosperm, and the coleorhiza plays a role in protecting emerging roots during germination (Sargent and Osborne, 1980). According to Nishimura (1922), Howarth (1927), Walne et al. (1975), and Debaene-Gill et al. (1994), the coleorhizae also act in water and nutrient uptake, as a water reserve during dehydration and as a storage tissue. Barrero et al. (2009) propose a new role for the coleorhiza, i.e., to regulate germination in dormant seeds. Recent studies have shown that ABA 8-hydroxylase gene expression is strong and uniform in barley coleorhizae, thus suggesting a key role for this tissue in dormancy control, equivalent to that of the micropylar endosperm (Millar

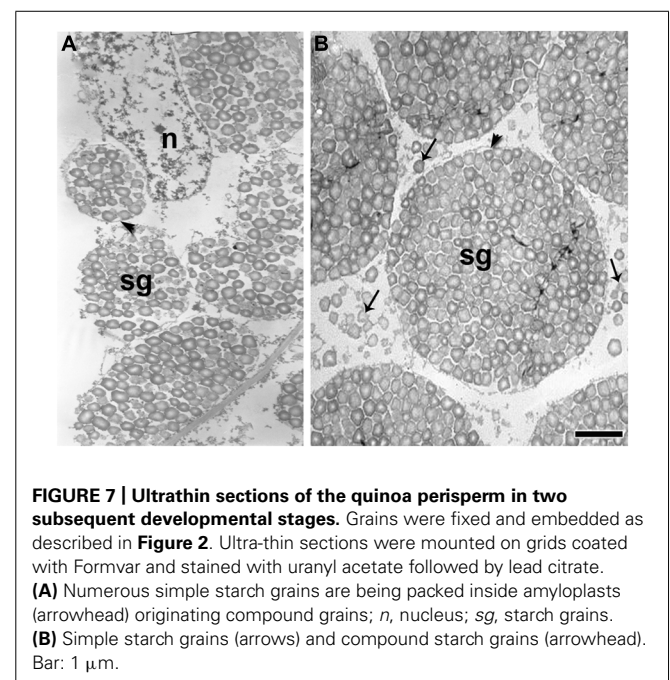
et al., 2006). In fact, several alternative catabolic pathways exist for the inactivation of ABA (Zhou et al., 2004; Nambara and Marion-Poll, 2005), but the reaction catalyzed by ABA 8'-hydroxylase is considered to be predominant in ABA catabolism (Nambara and Marion-Poll, 2005). ABA 8'-hydroxylase gene expression occurs in the coleorhiza and does not occur anywhere else in the barley embryo (Millar et al., 2006).

SEED STORAGE RESERVES

STARCH

In quinoa perisperm, starch accumulates forming compound and simple grains (Prego et al., 1998). In cereal starchy endosperm, compound grains have been reported in barley, rice, and wheat (Matsushima et al., 2010; Yun and Kawagoe, 2010). In wheat and barley, two types of starch grains are present: the large and lenticular A-type, which contains higher amylose concentrations, and the small spherical or ovoid B-type (Peng et al., 1999). In maize, according to Katz et al. (1993), starch grains are simple grains, but during development, Shannon et al. (1998) report the presence of both simple (larger) and compound (smaller) amyloplasts.

In quinoa, compound starch grains originate inside the amyloplasts by aggregation of single grains (Figure 7A). At the end of development, single grains are deposited in the extraplastidial space (Figure 7B). TEM images suggest that they are cytosolic in origin, but further studies are needed, considering that, to our knowledge, the formation of starch grains in the cytosol has not been previously reported. In rice endosperm, compound grains are generated by divisions of amyloplasts, which occur simultaneously at multiples constriction sites, and small amyloplasts bud from their surface (Yun and Kawagoe, 2009). More recently, Yun and Kawagoe (2010) demonstrated that a septum-like structure containing inner envelope membrane divides granules in the



amyloplast and that proteins of organelle division, (including FtZ, Min, ARC5, and PDV2) play roles not only in amyloplast division but also in compound granule synthesis (Yun and Kawagoe, 2009, 2010). These results strongly suggest that amyloplast division and compound granule synthesis in rice are closely related. This needs to be investigated further, since starch biosynthesis is an essential function in plant metabolism and is highly conserved throughout the plant kingdom.

Starch is synthesized from sucrose as a result of the combined action of four distinct enzymes: ADP-Glc pyrophosphorylase (AGPase), starch synthase (SS), starch-branching (BE), and starch-debranching (DBE) enzymes (Hannah, 2007). The complement of starch biosynthetic enzymes is well conserved between plastids of tissues that make different types of starches, i.e., transitory starch (made in chloroplasts) and storage starch (made in amyloplasts; Tetlow, 2010; for review see Geigenberger, 2011). In dicot storage tissue, the synthesis of ADP-glucose by the enzyme ADP-glucose AGPase occurs entirely within plastids, as reported in potato tuber (Sweetlove et al., 1996), pea embryo, and root (Denyer and Smith, 1988; Smith, 1988). In contrast, in monocots/cereals, i.e., in maize (Denyer et al., 1996; Huang et al., 2014), barley (Thorbjørnsen et al., 1996), rice (Sikka et al., 2001), and wheat (Tetlow et al., 2003), there is evidence indicating the presence of AGPase enzymes corresponding to plastidial and cytosolic isoforms (for reviews see Hannah and James, 2008; Comparot-Moss and Denyer, 2009; Geigenberger, 2011). Furthermore, whereas SS, BE, and DBE enzymes are found within amyloplasts, AGPase activity (which represents the rate-limiting step in starch biosynthesis) is confined almost exclusively to the cytosol. According to Beckles et al. (2001), the cytosolic localization of AGP in cereal endosperm may have functional significance for partitioning large amounts of carbon into starch when sucrose is plentiful.

In quinoa, it has yet to be determined if the synthesis of ADP-glucose by the enzyme ADP-glucose AGPase occurs entirely in plastids, as in the rest of dicotyledons studied to date. However, in advanced stages of quinoa seed development, once compound starch grain formation is complete, simple starch grains do form filling the space between amyloplasts (López-Fernández and Maldonado, 2013a; **Figure 7B**).

In cereal starchy endosperm dead cells, protein bodies, which mainly store prolamins, are present in the extraplastidial space. Conversely, in dead cells of quinoa perisperm, starch is the only storage reserve.

PROTEINS, MINERALS, AND LIPIDS

In quinoa, embryo and micropylar endosperm cells store proteins and lipids in the form of protein storage vacuoles (PSVs) and lipid bodies (Prego et al., 1998; Carjuzaá et al., 2008; López-Fernández and Maldonado, 2013b), respectively. PSVs contain one or more phytin crystals in the proteinaceous matrix and proplastids contain clusters of particles of phytoferritin (Prego et al., 1998). Brinegar and Goundan (1993) describe the protein composition of quinoa seeds and report an 11S-type globulin.

A 2S cysteine-rich globulin (8–9 kDa) is also described for quinoa seeds by Brinegar et al. (1996). More recently, Castellón et al. (2008) confirm these results. Likewise, Balzotti et al.

(2008) report the genomic and cDNA sequences for two 11S genes from the quinoa genome; in addition, on the basis of comparison with orthologous 11S sequences from other species, they describe the characteristics of the genes and their encoded proteins.

During development, proteins are transported from the lumen of the rough endoplasmic reticulum (RER) to the vacuole through the Golgi apparatus and PSVs are formed when vacuoles fragment (**Figure 8**). For each PSV, several electron-dense globoid crystals are formed (**Figure 8**). Before globoid formation, vesicles of phytic acid can be observed as bubbles concentrated on the outside of the PSV (**Figures 8A,B**); there, phytic acid associates with ions to form electron-dense globoids of phytin. To our knowledge, the formation of globoid crystals in the PSV had not been previously photo-documented in angiosperm seeds. Energy dispersive X-ray (EDX) analysis of globoid crystals reveals the presence of P, K, and Mg (Prego et al., 1998).

In cereals, globulins are synthesized in both the aleurone layer and starchy endosperm, and prolamins synthesized within the starchy endosperm rather than in the aleurone layer (Kriz and Schwartz, 1986; Kriz, 1989; Kriz and Wallace, 1991; for review see Shewry and Halford, 2002). On the other hand, protein body formation is tissue specific: in the aleurone layer, the pathways for all globulins and some albumins are similar to that described for quinoa, i.e., protein vesicles are transported from the lumen of the RER to the vacuole by way of the Golgi apparatus, and PSVs are formed by the subsequent fragmentation of the vacuole. Prolamins accumulate in protein bodies inside the endoplasmic reticulum (ER) of starchy endosperm cells, excluding the Golgi and vacuoles (Levanony et al., 1992; Rechinger et al., 1993; Reyes et al., 2011). Crystal globoids, which are included in the PSVs, are detected in the scutellum and aleurone layer but not in the starchy endosperm (Tanaka et al., 1973; Ogawa et al., 1977).

Lipid bodies are found in the quinoa embryo and micropylar endosperm, as well as in grass aleurone and embryo tissues. Lipid bodies originate in the ER (Schwarzenbach, 1971; Wanner et al., 1981; Hsieh and Huang, 2004). Lipids (triacylglycerides) accumulate between the bilayer leaflets at ER specific sites and, when they reach a certain size, bud off from the ER. Oleosin proteins are small (~15–30 kDa) and abundant proteins in the seeds of plants that bind to the surface of lipid bodies (Chapman et al., 2012). The synthesis and incorporation of oleosins occurs as triacylglycerides are deposited within the lipid bodies (Hsieh and Huang, 2007). During quinoa seed development, lipid bodies originate from the ER at the same time as the PSVs (**Figure 8**).

ENDOPOLYPLOIDY AND PROGRAMMED CELL DEATH IN STORAGE SEED TISSUES: QUINOA PERISPERM VS. CEREAL STARCHY ENDOSPERM

Quinoa perisperm consists of uniform, non-living, thin-walled cells full of starch grains. In grass starchy endosperm cells are full of starch grains, but also contain prolamins protein bodies. Thus, the two storage tissues are similar in terms of general characteristics and function, although genetically different.

During perisperm and endosperm development, two important aspects of both quinoa perisperm and cereal starchy endosperm are endoreduplication (for a review see Larkins et al.,

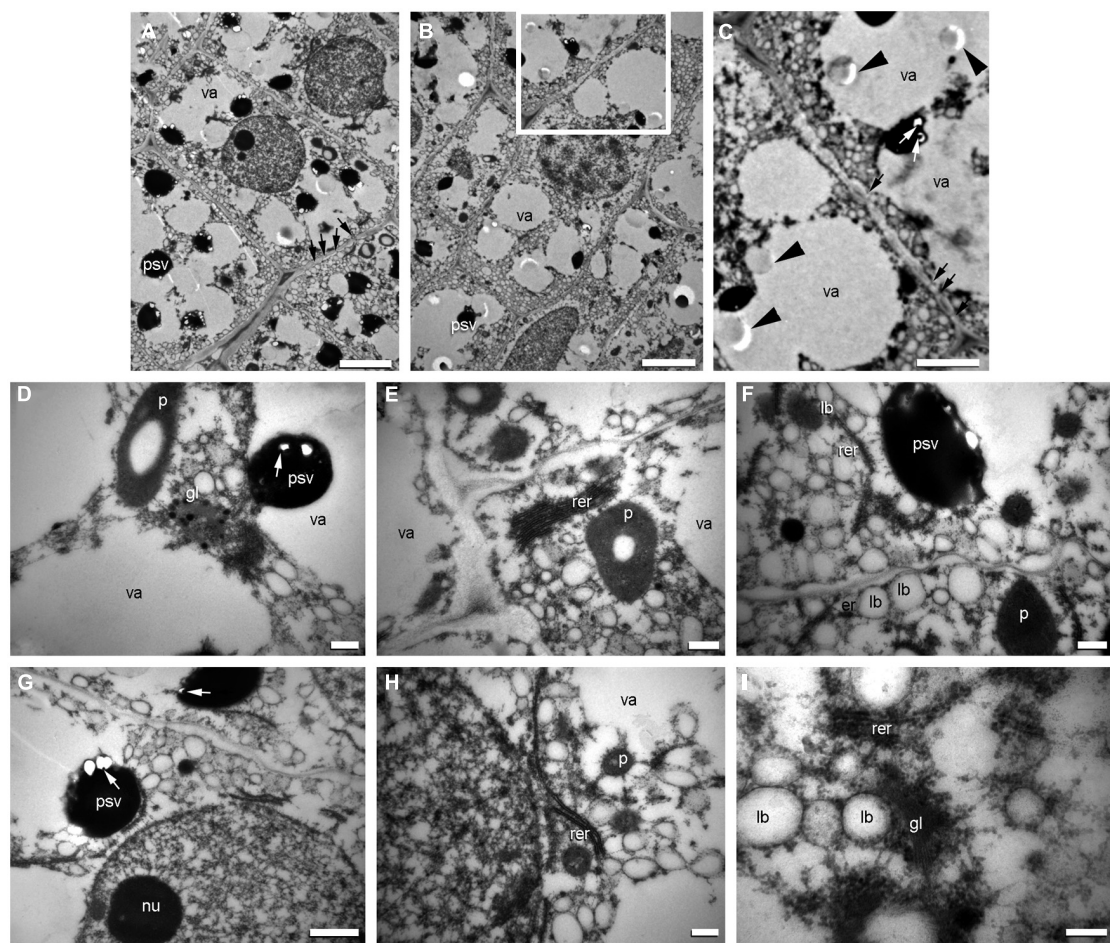


FIGURE 8 | Origin of protein storage vacuoles (PSVs) and lipid bodies in quinoa embryo. Excised embryos (torpedo stage) were processed as indicated in **Figure 7**. **(A)** Cells from the ground meristem. **(B)** Cells from the procambium. **(C)** detail of **(B)**. **(D–I)** Details of cytoplasm and organelles in cells from the ground meristem. In the different images, intense biosynthetic activity in cytoplasm can be inferred by the presence of abundant cisternae of rough endoplasmic reticulum (*rer*), numerous PSVs originating from the vacuoles (*va*); globoids (white arrows) can be seen inside PSV; the empty

areas inside PSV contained globoid crystals before they were dissolved during treatment of tissue fixation; numerous lipid bodies (*lb*) associated with endoplasmic reticulum; frequent dictyosomes, or Golgi (*gl*) and circular vesicles with electronically dense content in proximity to the dictyosomes (see **D**); nuclei with one or more nucleoli (*nu*). Arrowheads indicate the presence in the vacuole of the precursor salts of the globoids; white arrows indicate globoids; black arrows indicate plasmodesmata. *p*, plastid. Bars: **A–B**, 2 μm ; **C**, 1.5 μm ; **D–I**, 0.5 μm .

2001) and PCD (Young et al., 1997). In both tissues, cell death and dismantling are temporally separated, a process that can take years depending on when germination takes place (Young et al., 1997; Young and Gallie, 1999, 2000; López-Fernández and Maldonado, 2013a). In both cases, cell death occurs during seed formation and is not due to a complete process of autophagy since the cell remains intact until germination, when the starch reserves are mobilized and the dead tissue is finally dismantled. According to van Doorn and Woltering (2005), this type of cellular death does not seem to be autophagic in the strict sense of the term. In a more recent classification, based on morphological criteria, van Doorn et al. (2011) recognize two major classes of cell death that occur in plant tissues: vacuolar cell death and necrosis. However, PCD in grass starchy endosperm (Van Doorn, 2011; van Doorn et al., 2011) and quinoa perisperm, does not strictly fall into these two categories and are classified as separate modalities (van Doorn et al., 2011).

CONCLUDING REMARKS

In spite of their different origins, quinoa perisperm and grass starchy endosperm exhibit similar developmental programs and functional fates, i.e., endoreduplication, starch accumulation, and programmed cell death. Given the conservation of this seed developmental trajectory in quinoa and cereals, we infer the existence of convergent evolution in these two phylogenetically distant taxa.

The micropylar endosperm of quinoa and the coleorhiza of cereals serve the same role during germination: both tissues store reserves, protecting the root apical meristem in the quiescent seed and control dormancy during germination.

Because of the supposedly independent origin of monocotyledons and dicotyledons, efforts to solve questions related to seed evolution and particularly that of what determines the fate of storage tissues should be furthered for both grasses and quinoa. Hence, the present study may constitute a contribution toward a more

complete understanding of seed biology and thus may provide support for broader phylogenetic studies.

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Programmed cell death (PCD): an essential process of cereal seed development and germination

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The life cycle of cereal seeds can be divided into two phases, development and germination, separated by a quiescent period. Seed development and germination require the growth and differentiation of new tissues, but also the ordered disappearance of cells, which takes place by a process of programmed cell death (PCD). For this reason, cereal seeds have become excellent model systems for the study of developmental PCD in plants. At early stages of seed development, maternal tissues such as the nucellus, the pericarp, and the nucellar projections undergo a progressive degeneration by PCD, which allows the remobilization of their cellular contents for nourishing new filial tissues such as the embryo and the endosperm. At a later stage, during seed maturation, the endosperm undergoes PCD, but these cells remain intact in the mature grain and their contents will not be remobilized until germination. Thus, the only tissues that remain alive when seed development is completed are the embryo axis, the scutellum and the aleurone layer. In germinating seeds, both the scutellum and the aleurone layer play essential roles in producing the hydrolytic enzymes for the mobilization of the storage compounds of the starchy endosperm, which serve to support early seedling growth. Once this function is completed, scutellum and aleurone cells undergo PCD; their contents being used to support the growth of the germinated embryo. PCD occurs with tightly controlled spatial-temporal patterns allowing coordinated fluxes of nutrients between the different seed tissues. In this review, we will summarize the current knowledge of the tissues undergoing PCD in developing and germinating cereal seeds, focussing on the biochemical features of the process. The effect of hormones and redox regulation on PCD control will be discussed.

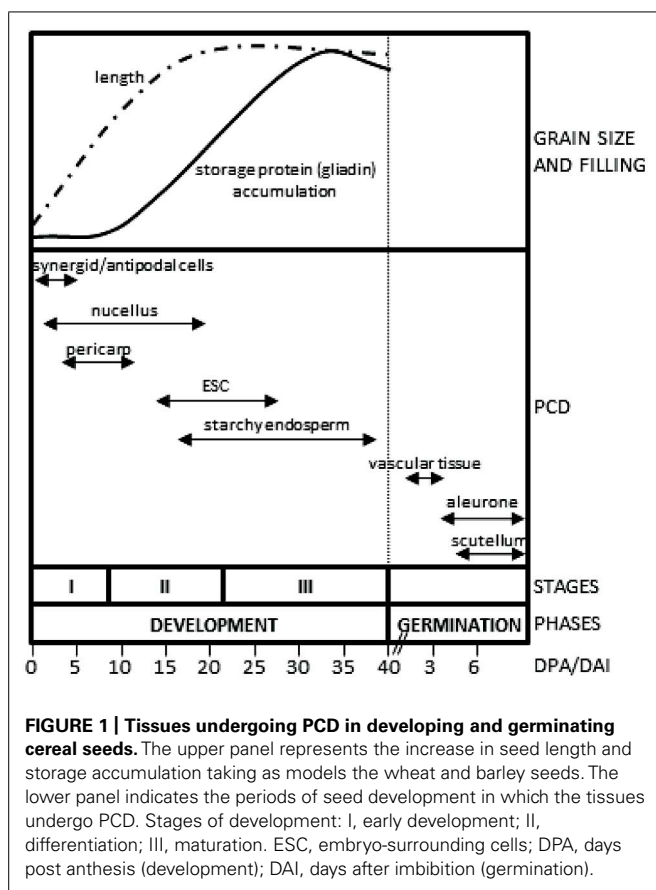
Keywords: cereal, development, germination, plant, programmed cell death, seed

INTRODUCTION

Two phases may be distinguished in the life cycle of the cereal seeds, development and germination. Seed development is initiated by the fertilization events and culminates with the formation of a mature seed, which has a low content of water and remains in a quiescent status. Upon imbibition, the quiescent seed initiates the phase of germination in which the reserves stored in the starchy endosperm are remobilized to support the initial stages of seedling growth. The phase of development may be subdivided in three stages (**Figure 1**): (I), early development, which includes double fertilization, syncytium formation and endosperm cellularization; (II), differentiation, which comprises the formation of the different cell types of the seed (embryo-surrounding cells, transfer cells, starchy endosperm and aleurone), endoreduplication and accumulation of storage reserves in the endosperm; and (III), maturation, which includes desiccation and dormancy (Sabelli and Larkins, 2009). At the morphological level, early seed development is characterized by a large increase in seed size, which reaches about 80% of its final length at this stage (**Figure 1**; Bosnes et al., 1992; Domínguez and Cejudo, 1996). Seed length increases predominantly due to the elongation of the pericarp cells in the longitudinal direction; this growth making room to accommodate the growing endosperm (Radchuk et al., 2011). Prior to the stage of storage accumulation in the growing

endosperm, a remobilization of nutrients from maternal tissues takes place, which involves the participation of a complex set of hydrolytic enzymes, including proteases (Domínguez and Cejudo, 1996) and starch-degrading enzymes (Radchuk et al., 2009). Following germination, a large process of remobilization of the storage compounds of the starchy endosperm occurs. This process, which supports early seedling growth until the new plant becomes autonomous, requires the synthesis and secretion of hydrolytic enzymes initially by the scutellum epithelium cells. Then, the aleurone cells, which surround the starchy endosperm, become activated and secrete a large amount of hydrolases (Fincher, 1989), in a process regulated by gibberellins synthesized by the scutellum and then released into the starchy endosperm (Appleford and Lenton, 1997).

Although the formation of a new seed, as well as the generation of a new plant upon germination, requires the generation and differentiation of a large number of cells, the ordered disappearance of cells is also of high relevance. Cell degeneration takes place by programmed cell death (PCD), which may be considered as an ordered process of selective removal of cells. There are several reasons that make PCD an important process for the successful completion of seed development and germination. Both seed development and germination rely on a continuous remobilization of nutrients, which is supported by cell degeneration. This



is the case of antipodal, nucellar and pericarp cells, which degenerate at early stages of seed development (Domínguez et al., 2001; An and You, 2004; Radchuk et al., 2011). The starchy endosperm undergoes PCD during the final stages of seed development; however, this tissue remains intact after cell death in the mature seed and the reserves stored therein will be mobilized only after germination. PCD also has the important function of creating new structures, such as nucellar projection cells at middle stages of seed development (Domínguez et al., 2001), and the vascular tissue of the scutellum, the differentiation of which is completed immediately after imbibition (Domínguez et al., 2002). Finally, PCD of pericarp cells is associated with the enlargement of the seed, facilitating the growth of the endosperm (Radchuk et al., 2011) and the formation of the seed cuticle, which has a protective function.

In summary, PCD is an essential process for the successful completion of cereal seed development and germination and, thus, cereal seeds have become an important model system for the study of cell death in plants. Based on morphological characteristics, two categories of plant PCD were recently proposed: vacuolar PCD, which includes autophagy, and necrosis, in conjunction with some forms of PCD that present mixed features and are not clearly ascribed to these categories (van Doorn et al., 2011). Most of the tissues that undergo PCD in cereal seeds show features of vacuolar PCD in agreement with the notion that cell death is part of developmental programs that characterize the formation and

germination of the seed. In this review we will summarize the present knowledge of the tissues undergoing PCD in developing and germinating cereal seeds, emphasizing their morphological and biochemical characteristics. In addition, we will focus on the function of the process of PCD for the successful completion of these developmental programs.

PCD OF MATERNAL TISSUES IS AN IMPORTANT PROCESS OF CEREAL SEED DEVELOPMENT

In monocots, fertilization is a double event that results in a diploid embryo and a triploid endosperm (Olsen, 2004). The formation of the seed involves the generation, growth and differentiation of new tissues; however, the ordered disappearance of cells plays as well an important function in this complex developmental process. In particular, several maternal tissues undergo PCD to help the formation of the seed; among them, it is worth mentioning the deaths of cells of the embryo sac, the nucellus, the pericarp, and the nucellar projections, which take place sequentially, as outlined in Figure 1. It follows below a brief description of how these cells undergo PCD.

SYNERGID AND ANTIPODAL CELLS

The embryo sac is composed of an egg cell, which is accompanied by two synergid cells at one pole and three antipodal cells at the opposite pole. Synergid cells are the first to undergo PCD at this initial stage of seed development (Figure 1). This death process occurs shortly before the pollen tube discharges and seems to be important to guide the growth of the pollen tube (An and You, 2004). In *Arabidopsis*, it was shown that the signaling cascade leading to the death of one of the two synergids is initiated by the contact with the pollen tube (Sandaklie-Nikolova et al., 2007). Synergids control sperm delivery through the *FERONIA* signaling pathway to initiate and modulate their distinct calcium signatures in response to calcium dynamics and growth behavior of the pollen tube (Ngo et al., 2014). PCD of antipodal cells occurs later, at 2–3 days post-anthesis (DPA), and contributes to the development of the adjacent free-nuclear endosperm. Nuclear materials from the dying antipodal cells support the nuclear divisions in the growing coenocyte (Engell, 1994; An and You, 2004).

NUCELLUS

At early stages of cereal seed development, the nucellus is among the first tissues to degenerate; nucellar cells undergoing a process of PCD, which has been well characterized at the morphological and biochemical levels (Domínguez et al., 2001; Radchuk et al., 2011). After the double fertilization event, the endosperm nucleus suffers several rounds of divisions to form a multinucleate syncytium surrounding the characteristic central vacuole (Figure 2). The technique of terminal deoxynucleotidyl transferase dUTP end labeling (TUNEL), which allows the direct staining of fragmented DNA and, thus, the visualization of nuclei from cells undergoing PCD, has been of great aid in characterizing the pattern of PCD in early developing seeds. The TUNEL assay allowed the identification of degenerating nuclei of the inner cell layers of the nucellus very early after anthesis; the degenerative process spreading to the outer nucellar layers at 2 DPA (Radchuk et al., 2011). It has been proposed that PCD of the nucellus serves for the remobilization

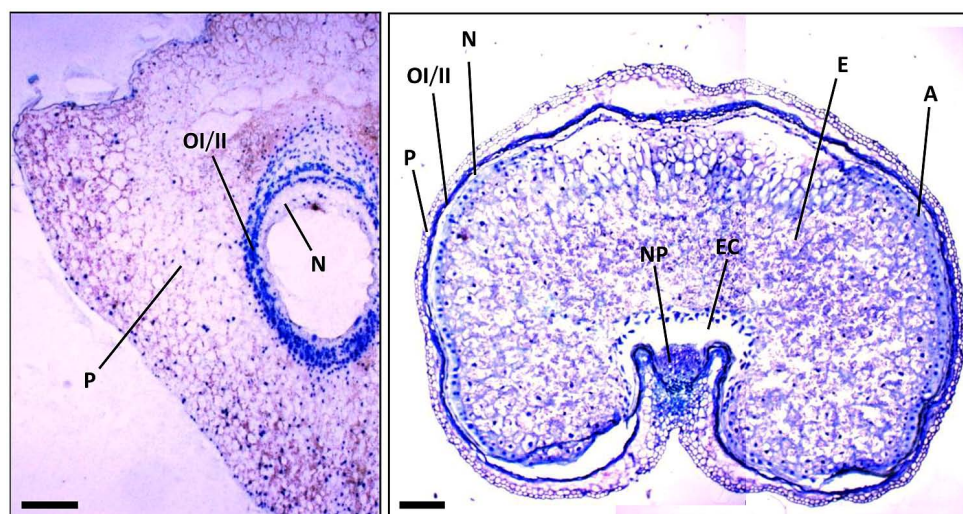


FIGURE 2 | Sections of wheat seeds at 3 DPA (left) and 16 DPA (right) stained with toluidine blue. Note the different tissues and how they change between these stages of seed development. P, pericarp; Ol,

outer integument; II, inner integument; N, nucellus; NP, nucellar projections; A, aleurone; E, starchy endosperm; EC, endosperm cavity. Bars, 100 μ m.

of its cellular contents, which are needed for the nourishment of the growing coenocyte and the cellularization process. Additional markers of cell degeneration are the expression of different hydrolytic enzymes, such as the aspartic protease nucellin (Chen and Foolad, 1997), a cathepsin B-like protease (Domínguez and Cejudo, 1998), the vacuolar processing enzyme nucellain (Linnesstad et al., 1998), and the α -amylase AMY 4 (Radchuk et al., 2009). A gradient from internal to external layers is observed in the degeneration of the nucellus in developing wheat grains that culminates when only the nucellar epidermis remains. At 5 DPA, the nucellar parenchyma is completely disorganized, and TUNEL-labeled nuclei of the nucellar epidermis and the two-cell layer inner integuments are observed (Figure 3; Domínguez et al., 2001). At 15 DPA, the nucellus is reduced to a single-cell layer, which shows high level of expression of genes encoding cathepsin B-like thiol protease and serine carboxypeptidase III, suggesting a high hydrolytic activity in this tissue (Domínguez and Cejudo, 1998). It is noteworthy that besides that of genes involved in the hydrolytic activity, these nucellar cells also show the expression of genes encoding enzymes involved in biosynthetic metabolism. This is the case of phosphoenolpyruvate carboxylase (PEPC), which is expressed at high level at early stages of seed development (5 DPA) in the nucellus, the multinucleate syncytium and the vascular tissue. This activity may generate carbon skeletons to support the demand of amino acid biosynthesis in the growing endosperm (González et al., 1998).

PERICARP

In the case of wheat and barley seeds, the pericarp is a tissue of maternal origin which, at early stages of development, is formed by several layers of parenchymatic cells, a two-cell-layer chlorenchyma and the inner epidermis (Figure 2). During the pre-storage phase (0–10 DPA), this tissue shows a decrease in cell divisions, which is accompanied by twofold to threefold

increase in cell elongation, while the rows of parenchymatic cells localized between the inner integument and the outer epidermis are reduced twofold to fourfold (Radchuk et al., 2011). The first symptoms of pericarp cell degeneration appear at 4 DPA (Domínguez et al., 2001; Radchuk et al., 2011). Then, during the period of 6–10 DPA, PCD is extended to the whole tissue (Radchuk et al., 2011), so that by 15 DPA the pericarp is reduced to several layers of cuticle, as shown for the case of the wheat seed (Figure 3). Biochemical analyses showed the presence of proteolytic activities in the pericarp of wheat seeds at early stages of development (Domínguez and Cejudo, 1996). Furthermore, transcriptomic analyses performed in barley seeds revealed the expression of different genes encoding proteolytic enzymes in this tissue (Sreenivasulu et al., 2006), including the vacuolar processing enzyme VPE4 (Radchuk et al., 2011), suggesting that the degeneration of these cells occurs by a process of PCD. In addition, the expression of α -amylases suggests the existence of starch degradation in the pericarp (Radchuk et al., 2009). Indeed, pericarp PCD is accompanied by dynamic changes in starch accumulation patterns (Figure 3); starch granules being synthesized, deposited and degraded in plastids temporarily until their utilization by the growing endosperm (Zhou et al., 2009). PCD of the maternal tissues at these stages of seed development may have two purposes: to make room for the expanding endosperm and to support the nourishment of this tissue.

NUCELLAR PROJECTIONS

The nucellar projections cells form a complex tissue of great relevance during seed development. These cells differentiate into transfer cells, thus enabling the transfer of nutrients from the pericarp to the endosperm cavity (Figure 2). Based on morphological features, several stages of differentiation through the radial axis can be established: roundish meristematic cells close to the pigment strand and adjacent to the vascular tissue (stage I); middle

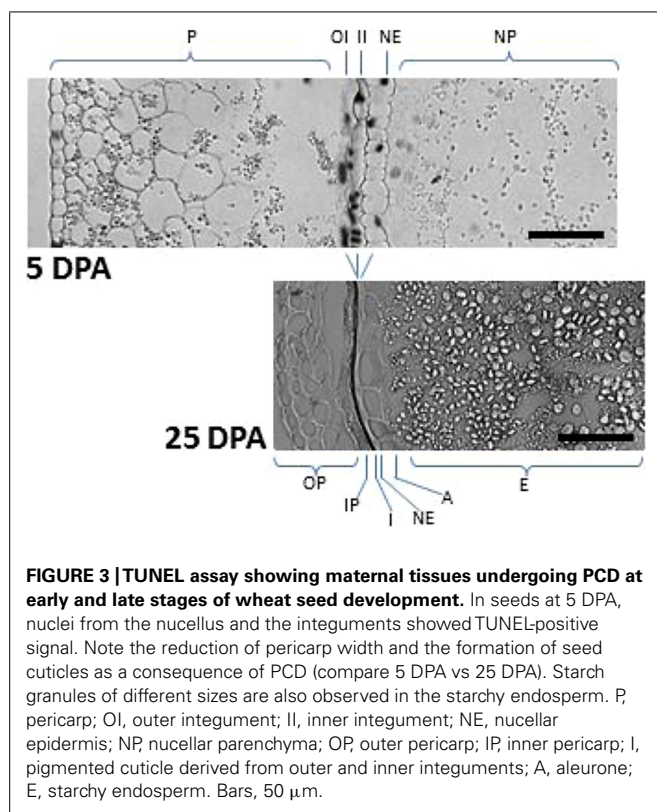


FIGURE 3 | TUNEL assay showing maternal tissues undergoing PCD at early and late stages of wheat seed development. In seeds at 5 DPA, nuclei from the nucellus and the integuments showed TUNEL-positive signal. Note the reduction of pericarp width and the formation of seed cuticles as a consequence of PCD (compare 5 DPA vs 25 DPA). Starch granules of different sizes are also observed in the starchy endosperm. P, pericarp; OI, outer integument; II, inner integument; NE, nucellar epidermis; NP, nucellar parenchyma; OP, outer pericarp; IP, inner pericarp; I, pigmented cuticle derived from outer and inner integuments; A, aleurone; E, starchy endosperm. Bars, 50 μ m.

zone with elongated cells (stage II); transfer cells with peculiar cell wall invaginations (stage III); and autolysing cells adjacent to the endosperm cavity (stage IV). PCD plays a relevant function in this process of differentiation (Domínguez et al., 2001). While nucellar projection cells show no symptoms of PCD at early stages of development (5 DPA), most cells show TUNEL-stained nuclei as seed development progresses (13 DPA). At 18 DPA, TUNEL staining is restricted to nucellar projection cells adjacent to the pigment strand, because cells located near the endosperm cavity seem to be completely degraded (Domínguez et al., 2001). The high level of expression of cathepsin B-like thiol protease (Domínguez and Cejudo, 1998) and the vacuolar processing enzyme nucellain (Linnestad et al., 1998) in nucellar projection cells at 9–16 DPA is in agreement with the known role of these proteases in the process of cell degeneration. Another marker of the differentiation and PCD of the nucellar projections is the JEKILL protein (Radchuk et al., 2006). The increase in the level of this protein has been associated with structural changes in the nucellar projections, so that a gradient is generated from the crease region to the autolysing cells close to the endosperm cavity. Repression of the gene encoding JEKILL impairs the differentiation of the nucellar projections, which affects the exchange of nutrients between the pericarp and the endosperm (Radchuk et al., 2006). The gradient observed in the nucellar projections, from the crease region to the endosperm cavity, has also been observed by large-scale *in situ* hybridization expression analyses (Drea et al., 2005) and by laser micro-dissection pressure catapulting-based transcriptome analyses (Thiel et al., 2008). At 8 DPA, the meristematic zone (stage I of differentiation) shows the expression of genes characteristic

of tissues with high mitotic activity. Genes involved in cell wall biosynthesis and expansin/extensin genes are expressed along the elongation zone (stage II); finally, genes involved in PCD-related proteolysis and nitrogen remobilization are expressed in the disintegration zone (stages III and IV). Several genes associated with the degeneration of the nucellar projection cells have been identified (Domínguez and Cejudo, 1998; Linnestad et al., 1998; Radchuk et al., 2006), however, little is known about upstream regulatory factors controlling their patterns of expression. The MADS29 transcription factor was proposed to play a relevant function in the control of nucellus and nucellar projection cells degeneration (Yin and Xue, 2012; Yang et al., 2012). The MADS29 gene is expressed at high levels in the nucellus at early stages of seed development, up to 3 DPA. At later stages, 3–10 DPA, this gene shows a high level of expression in nucellar projection cells but not in the pericarp, integuments and endosperm (Yin and Xue, 2012). Under-expression of the MADS29 gene provokes abnormal development and formation of shrunken seeds with reduced rate of grain-filling and altered starch granules. Histological analysis of these seeds revealed that the degeneration of the nucellar projection cells and other maternal tissues is blocked (Yang et al., 2012; Yin and Xue, 2012), suggesting that MADS29 directly regulates the expression of several PCD-related genes (Yin and Xue, 2012). Nutrient transport in temperate cereals, such as wheat and barley, occurs along the entire length of the grain through a single vascular band embedded in the maternal pericarp. This vascular band distributes nutrients to the endosperm cavity through the nucellar projection. However, in tropical crops, such as maize and sorghum, the transfer of nutrients occurs through a placento-chalazal layer localized in the basal region of the grain. Interestingly, like the nucellar projections, the placento-chalazal layer also degenerates during maize seed development (Kladnik et al., 2004).

FILIAL TISSUES UNDERGO PCD IN DEVELOPING AND GERMINATING CEREAL SEEDS

With regard to the processes of PCD of filial tissues, these may be classified in those that occur during seed development, such as in the suspensor, embryo-surrounding layers and the starchy endosperm, and those taking place after germination, which include PCD in the parenchymal, epithelial, and vascular tissue of the scutellum, and the aleurone layer (Figure 1).

SUSPENSOR AND EMBRYO-SURROUNDING LAYERS

In cereals such as maize, the first asymmetric division of the diploid zygote produces an apical cell, which develops into the embryo proper, and a basal cell, which generates the suspensor. The analysis of the pattern of expression of different genes suggests a marked regionalization in the differentiation of the embryo (Okamoto et al., 2005), which might also be affected by auxin transport (Forestan et al., 2010). Several tissues undergo PCD during embryogenesis. This is the case of the suspensor, which participates in the transfer of nutrients from maternal tissues to the developing embryo proper. The suspensor undergoes PCD in conjunction with PCD in the embryo-surrounding tissues. In maize seeds at 14 DPA, the scutellum cell layers that surround the shoot primordium, as well as the coleoptile and

the root cap, show TUNEL-stained nuclei. Nuclei of the shoot primordium-surrounding layers appear completely degraded by 17 DPA (Giuliani et al., 2002). The suspensor undergoes a process of PCD, which is extended between 14 and 27 DPA defining a top-to-bottom gradient of DNA fragmentation, chromatin condensation and nuclei degeneration (Giuliani et al., 2002). In the so-called *emb* (embryo-specific) mutants of maize, which show arrested embryo development but a normal endosperm, the process of PCD in the suspensor is impaired (Consonni et al., 2003). More in-depth analyses at the molecular level have been carried out in non-cereal crops such as in the gymnosperm *Norway spruce* (Filonova et al., 2000). In this system it was identified a metacaspase, termed mclI-Pa, which has autoprocessing activity and is translocated from the cytoplasm to the nucleus in embryo cells undergoing PCD. Cell death thus relies on the proteolytic activity of metacaspase mclI-Pa, which acts as an executioner of PCD (Bozhkov et al., 2005). The death of the embryo suspensor requires the activation of autophagy-related components downstream of metacaspase mclI-Pa, as shown by the fact that the genetic suppression of the metacaspase-autophagy pathway promotes a switch from vacuolar PCD to necrosis. This suppression results in failure of suspensor differentiation and embryonic arrest (Minina et al., 2013). In addition, VEIDase, a caspase-6-like activity, was also identified in *Norway spruce* embryogenesis. The activity of this protease increases at early stages of embryo development and it has been proposed to participate in embryo pattern formation. When VEIDase activity is inhibited, the differentiation of the embryo-suspensor is blocked and the development of the embryo arrested (Bozhkov et al., 2004). VEIDase activity was also detected in barley developing embryo (Boren et al., 2006), suggesting common PCD mechanisms in gymnosperms and monocots. In tobacco, it was shown that the molecular mechanism triggering suspensor PCD is based on the antagonistic actions of two proteins: the cystatin NtCYS, a protease inhibitor, and its target, the cathepsin H-like protease NtCP14. NtCYS prevents precocious PCD in the basal cell of the proembryo by inhibiting NtCP14 protease. Transcriptional down-regulation of NtCYS leads to an increase in NtCP14 activity, which promotes PCD (Zhao et al., 2013). Silencing of the NtCYS inhibitor or overexpression of NtCP14 protease genes provoke precocious cell death with consequent embryonic arrest and grain abortion (Zhao et al., 2013).

ENDOSPERM

In wheat seeds, the expansion of the endosperm is preceded by PCD in cells adjacent to the nucellar projections. The endosperm cavity is thus formed, allowing the transfer of nutrients from the vascular bundle embedded in the pericarp to the growing endosperm. The development of the endosperm in cereal seeds encompasses different processes, such as endoreduplication, accumulation of storage materials and PCD. During endoreduplication, DNA replication is not followed by cytokinesis, resulting in an altered cell cycle and polyploidy (Sabelli, 2012). In maize seeds, endoreduplication is initiated in the central area of the endosperm around 8–10 DPA; the process being extended toward the periphery and producing a high level of polyploidy in endosperm cells at 20 DPA (Sabelli, 2012). It should be noted that endoreduplication

is not a homogeneous process since central endosperm cells have higher levels of polyploidy than external cells (Sabelli, 2012). The progression of PCD in the endosperm of developing maize seeds follows a two-wave pattern: the first wave begins around 16 DPA in central cells, coincident with an increase in DNA content; the second starts at the upper crown and progresses toward the base of the seed between 24 and 40 DPA, paralleling the pattern of starch accumulation (Young et al., 1997). In contrast with maize seeds, the pattern of PCD in the endosperm of developing wheat seeds progresses randomly; PCD being initiated by 16 DPA and extended in a random manner until 30 DPA, when the entire endosperm is affected (Young et al., 1997). Retinoblastoma-related (RBR) proteins and cyclin-dependent kinase (CDK) have been identified as fundamental players in cereal endosperm development. The retinoblastoma-related pathway seems to play a major role in endosperm development of maize seeds since it is involved in the control of processes such as endoreduplication, cell proliferation, cell size and cell death (Sabelli et al., 2013).

EMBRYO VASCULAR TISSUE

In cereals, the differentiation of the scutellum vascular tissue proceeds only to the provascular stage of seed development, and is completed following germination. This pattern of differentiation has the purpose of avoiding translocation of nutrients from the scutellum to the embryonic axis before grain maturation (Swift and O'Brien, 1970, 1971). However, a fully functional vascular system is needed immediately after seed germination. Therefore, differentiation of the scutellar tracheary elements is completed in seeds at 2–3 days after imbibition (DAI), forming the characteristic annular thickenings, in a process that involves PCD (Domínguez et al., 2002). Differentiation of the tracheary elements implies the participation of endo- and exopeptidases. Up to six genes encoding carboxypeptidases have been identified in cereals (Dal Degan et al., 1994; Washio and Ishikawa, 1994); some of them being expressed in the embryo of germinating grains. Only the GA₃-induced serine carboxypeptidase III, which was isolated from wheat aleurone cells (Baulcombe et al., 1987), has been shown to participate in vessel formation. The pattern of expression of this gene, as determined by in situ hybridization, shows a clear coincidence with TUNEL-stained nuclei in the tracheary elements of the scutellum, which suggests a role for this carboxypeptidase as executioner in this PCD process (Domínguez et al., 2002). The participation of the serine carboxypeptidase III in the differentiation of vascular tissues of other organs, such as shoots and roots, has also been suggested (Domínguez et al., 2002).

ALEURONE

The differentiation of the aleurone layer, the outermost cell layer of the endosperm, initiates in developing seeds around 8 DPA (Bosnes et al., 1992; Figure 2). In contrast with the endosperm, which undergoes a process of PCD at later stages of seed development (Young et al., 1997; Young and Gallie, 1999), the aleurone layer and the embryo remain alive in the mature seed. In wheat seeds, both tissues show the expression of protease inhibitors (Corre-Menguy et al., 2002), which may have a protective function since the surrounding pericarp shows intense proteolytic activity

during seed development (Domínguez and Cejudo, 1996). Following germination, the aleurone layer displays a high metabolic activity to synthesize and secrete hydrolytic enzymes, which are released into the starchy endosperm and promote the degradation of storage reserves (Cejudo et al., 1992, 1995; Domínguez and Cejudo, 1995, 1999). Once this function is completed, the aleurone undergoes a process of PCD (Domínguez et al., 2004). DNA fragmentation in aleurone layer nuclei was observed in seeds after 4 DAI, and then increased progressively. TUNEL assays revealed a very characteristic spatial pattern of aleurone layer PCD; the process being initiated in cells proximal to the embryo and extended to distal cells, both in wheat and barley (Wang et al., 1998; Domínguez et al., 2004). In contrast to wheat and barley, the process of aleurone PCD was delayed in maize seeds; DNA laddering being detected only after 12 DAI (Domínguez et al., 2004). This delay may reflect differences in the germination strategies of both types of grains. In this regard, it should be noted that the scutellum is larger in maize than in wheat or barley seeds and, thus, may have a more relevant function supporting the initial stages of seedling growth. The progression of PCD in the aleurone layer is a tightly regulated process, which takes place only when these cells have completed the synthesis and secretion of hydrolytic enzymes. Indeed, this function of the aleurone cells is essential for germination as shown by the fact that the aleurone-deficient maize mutant seeds, *dek1*, are unable to germinate (Domínguez et al., 2004).

SCUTELLUM

Although, as mentioned above, some of the tissues surrounding the embryo undergo PCD during embryogenesis in developing seeds, the bulk of scutellum PCD occurs after germination (Domínguez et al., 2012). This process was analyzed in wheat seeds in which the first symptoms of PCD appear at 4 DAI and increase progressively up to 7 DAI, affecting both the epidermal and parenchymal cells. The spatial progression of scutellum PCD in wheat grains occurs with an apical-to-basal gradient. PCD is initiated in the apical zone once the adjacent aleurone cells have completed PCD (Domínguez et al., 2012). This pattern of PCD progression suggests that one of the major functions of the scutellum in germinated seeds, which is the transfer of nutrients from the starchy endosperm to support the initial seedling growth (West et al., 1998; Aoki et al., 2006), does not cease abruptly (Domínguez et al., 2012). In fact, the degeneration of the scutellum seems to be coordinated with the sequential production of hydrolases. In wheat seeds at early stages of germination (1 DAI), the *AmyI* gene, which encodes the α -amylase I isoform, is expressed exclusively in the scutellar epithelium; its expression being transient and independent of GA₃. At a later stage (2 DAI), *AmyI* expression in the scutellar epithelium decreases while it increases in the aleurone layer (Cejudo et al., 1995). In contrast, the gene encoding a cathepsin B-like is expressed in scutellum parenchymal cells but not in the epithelium of wheat seeds at 2 DAI (Cejudo et al., 1992), thus suggesting a function for this protease other than mobilization of the starchy endosperm. Whether cathepsin B-like is involved in a lysosomal-like function, in the final degradation of peptide products of the proteases secreted into the endosperm, or in pro-death roles, is not yet known. As mentioned above, the gene

encoding the serine carboxipeptidase III is expressed during the differentiation of the scutellum vascular tissue (Domínguez et al., 2002). Therefore, PCD progression in scutellar parenchyma and epithelium appears as the last events in nutrients remobilization before the autonomous growth of the embryo (Domínguez et al., 2012).

DIFFERENT HALLMARKS CHARACTERIZE THE PROCESS OF PCD IN CEREAL SEEDS

The well-defined patterns of PCD in developing and germinating cereal seeds, as well as the variety of cells undergoing PCD, has favored the use of these systems to study PCD at the biochemical level. One of the more characteristic hallmarks of PCD in most developmental processes is the fragmentation of DNA, which is highly dependent of the level of DNA packaging (Domínguez and Cejudo, 2012). Nuclear DNA is packed into chromatin loops of ca. 50 kb, six of which are grouped in a rosette-like structure. In cereal seeds at initial stages of endosperm development (4–6 DPA), the identification of DNA fragments of 50–300 kb suggests the participation of proteases that cleave chromatin folding points of the rosette-like structure as an early event in DNA fragmentation and PCD (Young and Gallie, 2000). The second stage of DNA degradation corresponds to the internucleosomal fragmentation, which results in the typical ladder of multimers of 180–200 bp. The analysis of endosperm PCD in developing cereal seeds identified internucleosomal laddering only at late stages of seed development (20 DPA to the end of maturation); this process being thus an irreversible phase in cell death (Young et al., 1997; Young and Gallie, 1999, 2000). Finally, a third stage of DNA fragmentation of the starchy endosperm cells occurs in germinated seeds, which yields completely digested nuclear DNA. Internucleosomal fragmentation of nuclear DNA, which is a hallmark of animal apoptosis, is a clear feature of PCD in cereal seeds as shown in maternal tissues (Domínguez et al., 2001; Domínguez and Cejudo, 2006) and starchy endosperm cells (Young et al., 1997; Young and Gallie, 1999, 2000) during development, as well as in aleurone layer (Wang et al., 1996; Domínguez et al., 2004) and epithelial and parenchymal cells of the scutellum (Domínguez et al., 2012) following germination.

The fact that DNA fragmentation is central to cell death implies the participation of nucleolytic enzymes in this process. Biochemical analyses of cells undergoing PCD in cereal seeds have allowed the identification of nuclear- and cytoplasmic-localized endonucleases. While nuclear-localized nucleases promote the cleavage of nuclear DNA into high- and low-molecular weight fragments, cytoplasmic-localized endonucleases participate in the degradation of naked, double- or single-stranded DNA fragments as the final step that culminates the complete degradation of the cellular DNA. The action of nuclear-localized endonucleases seems to be a key event in pre-mortem nuclear dismantling, whereas cytoplasmic-localized endonucleases seem to carry out the completion of DNA degradation after vacuolar tonoplast disruption during post-mortem nuclear dismantling (Domínguez and Cejudo, 2012). Wheat grains have been a model system to identify nuclear-localized factors involved in internucleosomal DNA fragmentation. Two nuclear-localized neutral Ca²⁺/Mg²⁺ endonucleases of ca. 30 and 50 kDa were identified, respectively,

in aleurone (Domínguez et al., 2004) and nucellus cells undergoing PCD (Domínguez and Cejudo, 2006). An acid Zn^{2+} -dependent endonuclease of ca. 70 kDa was also identified in the nucleus of wheat scutellum cells undergoing PCD (Domínguez et al., 2012). The differences in cation requirement, electrophoretic mobility and optimal pH reveal that internucleosomal DNA fragmentation is performed by different nucleases in the different tissues of the wheat grain (Domínguez et al., 2004, 2012; Domínguez and Cejudo, 2006). Among the so-called waste-management endonucleases responsible for a third level of DNA fragmentation, it is worth mentioning the nucleases acting in the starchy endosperm cells of germinating barley seeds (Brown and Ho, 1986, 1987).

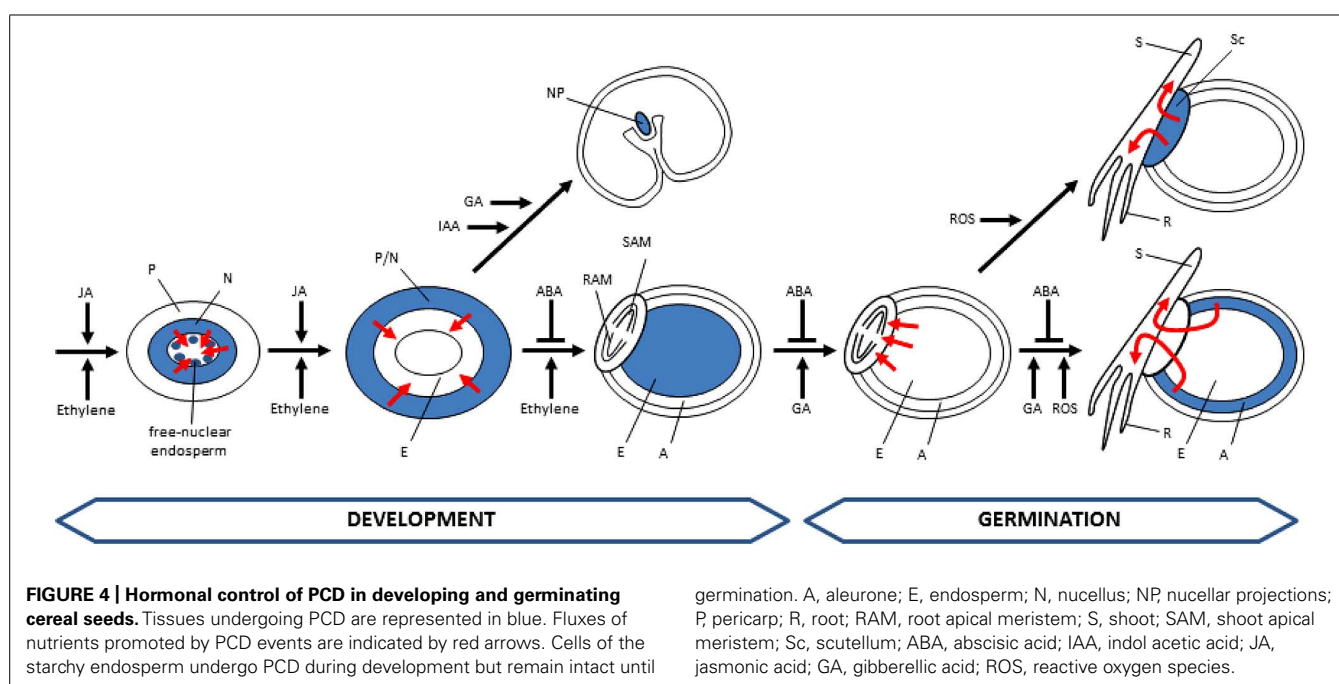
Finally, caspases are very well characterized proteases that participate as initiators and executioners in the process of apoptosis in animals. Because of this central role in the execution of apoptosis, the search for caspase counterparts has been a central focus of PCD studies in plants. Different approaches have revealed the complex set of endoproteolytic activities that participate in cell death in cereal seeds. These include serine-endoproteases in maternal tissues at early stages of development (Domínguez and Cejudo, 1996), and thiol-proteases in aleurone layer, scutellum, and starchy endosperm following germination (Domínguez and Cejudo, 1995). A caspase 6-like proteolytic activity, which acts at the sequence VEID, was identified in starchy endosperm and embryo cells from developing barley seeds (Boren et al., 2006). This VEIDase activity has been localized to autophagosome-like vesicles in randomly distributed cells of the starchy endosperm of barley seeds (Boren et al., 2006), in parallel with the progression of PCD in wheat (Young and Gallie, 1999). Therefore, VEIDase activity might be considered as an executioner with caspase-like activity in cereals. Nuclear-localized proteases have also been identified in cells undergoing PCD from developing wheat seeds. This is the case

of a serine endoprotease of ca. 60 kDa identified in nuclear extracts from maternal tissues, which might be potentially responsible for the cleavage of structural proteins in the nucleus (Domínguez and Cejudo, 2006).

HORMONAL REGULATION OF PCD IN DEVELOPING AND GERMINATING CEREAL SEEDS

The spatial-temporal patterns of PCD affecting different tissues of developing and germinating cereal grains, as described above, suggest the participation of mechanisms able to orchestrate these complex patterns of cell death. Although it is presumed that different factors are involved in the regulation of PCD in cereal seeds, hormonal action seems to be an obvious candidate. Yet the information concerning their participation in controlling the patterns of PCD in cereal seeds is scarce. Here, we summarize results showing the involvement of hormones in the control of PCD (Figure 4).

At early stages of *Arabidopsis* seed development, synergid cell death has been associated with the activation of the ethylene signaling pathway that takes place during the process of fertilization, in which EIN3 and EIN2 have been identified as critical factors (Völz et al., 2013). Ethylene appears also to be a crucial hormone controlling endosperm development in cereal seeds. During cereal seed development, two peaks of ethylene production occur; the first one being coincident with the onset of PCD in the central region of the endosperm, whereas the second one is associated with the increase in endonucleolytic activity (Young et al., 1997). Exogenously added ethylene results in the acceleration of cell death and DNA fragmentation in maize and wheat developing seeds, while treatments with inhibitors of ethylene biosynthesis or perception have the opposite effect (Young et al., 1997; Young and Gallie, 1999). The positive effect of ethylene on PCD induction was confirmed with the *shrunk2* mutant of maize, a starch-deficient



mutant that accumulates sugars, thereby producing ethylene levels threefold to fivefold higher than in wild-type seeds, which shows accelerated PCD (Young et al., 1997).

Two hormones, jasmonic acid (JA) and ethylene, have been proposed to participate in the control of pericarp PCD, based on the high level of expression of genes involved in the biosynthesis and signaling of both hormones during PCD of maternal tissues (Sreenivasulu et al., 2006). Lipases, lipid transfer proteins and lipo-oxygenases, which are involved in biosynthesis of JA precursors, were found among the genes with increased expression in barley seeds at 6–12 DPA. In addition, genes of the ethylene signal transduction pathway are also induced at these stages of seed development. The genes showing a higher level of expression include the ethylene receptor (ETR3), the raf-like protein kinase (CTR1), a MAP kinase, the ethylene-insensitive (EIN2) and the ethylene response factor ERF2 (Sreenivasulu et al., 2006).

Gibberellins and auxins have also been proposed to participate in the control of PCD of maternal tissues, such as the nucellar projections. The gradient of differentiation observed in nucellar projection cells in wheat seeds at 8 DPA is coincident with the expression patterns of genes involved in GA biosynthesis and signaling (Thiel et al., 2008). In addition, the auxin-dependent MADS29 transcription factor appears as a key regulator of early seed development by stimulating the expression of a Cys-protease and other PCD-related proteins participating in the degradation of the nucellus and the nucellar projections (Yin and Xue, 2012).

The important function of ABA in the control of cereal seed maturation is well known. During seed development, ABA biosynthesis takes place both in the developing embryo and the endosperm with the participation of different members of the aldehyde oxidase gene family (Sreenivasulu et al., 2006). Furthermore, ABA plays an essential role in the acquisition of desiccation tolerance of the embryo by stimulating stress-responsive genes, such as those encoding late-embryogenesis abundant proteins and dehydrins (Sreenivasulu et al., 2006). The implication of ABA in cereal endosperm PCD was demonstrated with two maize *viviparous* (*vp*) mutants, the ABA-insensitive *vp1* and the ABA-deficient *vp9* mutants. It should be noted that ethylene levels in the developing endosperm of these mutants are twofold to fourfold higher than in wild-type seeds, and thus ethylene might promote an acceleration of cell death in these mutants. The treatment of wild-type seeds with fluridone, an inhibitor of ABA biosynthesis, also promoted DNA fragmentation and cell death. Based on these findings, ABA was proposed as a negative regulator of ethylene biosynthesis and/or action during maize development (Young and Gallie, 2000). Thus a balance between ABA and ethylene regulates the onset and progression of PCD during cereal endosperm development (Young et al., 1997; Young and Gallie, 1999, 2000).

While ABA has a key function in seed maturation by inhibiting precocious germination, gibberellins have the opposite function and are the most relevant hormones promoting seed germination. The aleurone layer, the only endosperm tissue that remains alive in mature cereal seeds, shows a high sensitivity to gibberellins. The response of aleurone cells to gibberellins may be subdivided in two phases. In the short term, gibberellins stimulate

the metabolic activation of these quiescent cells upon seed imbibition. In response to gibberellins, aleurone cells induce the expression of genes encoding hydrolytic enzymes, such as amylases and proteases, which are secreted into the starchy endosperm (Cejudo et al., 1992, 1995; Domínguez and Cejudo, 1995, 1999). In addition, the hormone triggers the acidification of the starchy endosperm, thus facilitating the mobilization of storage compounds (Domínguez and Cejudo, 1999). Once the metabolic activation is achieved, aleurone cells show a long-term response to gibberellins, which involves the induction of PCD, a process that is counteracted by ABA (Wang et al., 1996, 1998; Bethke et al., 1999; Domínguez et al., 2004). Treatments of wheat grains with paclobutrazol, an inhibitor of gibberellin synthesis, delayed germination and avoided DNA fragmentation (Domínguez et al., 2004). Similarly, aleurone protoplasts treated with LY83583, which has an antagonistic effect on gibberellin signaling, showed no symptoms of PCD (Bethke et al., 1999). The activating role of gibberellins in PCD was corroborated with the analysis of the wheat gibberellin-insensitive mutant *Rht*, which shows altered post-germination, including delayed aleurone PCD (Domínguez et al., 2004). Taken into account the spatial-temporal gradients observed in the wheat aleurone layer, which affect the expression of genes encoding hydrolytic enzymes (Cejudo et al., 1992, 1995; Domínguez and Cejudo, 1999), the acidification of the starchy endosperm (Domínguez and Cejudo, 1999), and the process of DNA fragmentation and cell death (Domínguez et al., 2004), a model was generated to explain the action of gibberellins during the different PCD phases of a single aleurone cell: (1) quiescent phase, which is the status of aleurone cells in mature grains prior to gibberellin perception; (2) active phase, in which gibberellin perception induces the synthesis of hydrolytic enzymes and the acidification of the starchy endosperm; and (3) death phase, in which aleurone cells undergo PCD (Cejudo et al., 2001). According to this model, the aleurone layer of germinating grains is composed by a heterogeneous group of cells: those located adjacent to the embryo are the first to perceive and respond to gibberellins and, thus, to enter the death phase, whereas those located far from the embryo may be still in the quiescent phase (Cejudo et al., 2001).

REDOX REGULATION OF PCD IN DEVELOPING AND GERMINATING CEREAL SEEDS

In addition to hormone control, redox regulation has been considered to play an important role in establishing the patterns of PCD in cereal seeds. Aerobic metabolism inevitably generates reactive oxygen species (ROS), including hydrogen peroxide, superoxide anion and hydroxyl radicals. These compounds show reactivity with almost all cellular macromolecules and, hence, their accumulation above certain levels may have a harmful effect causing oxidative stress (Bailly, 2004). At the end of the phase of development, the cereal seed enters a phase of desiccation, which involves a massive loss of water that provokes oxidative stress in tissues that remain alive in the mature seed, such as the embryo and the aleurone layer. Moreover, these tissues also suffer oxidative stress in germinating seeds due to resumption of respiration (Serrato and Cejudo, 2003). ROS, in conjunction with hormones, has been proposed to exert an important regulatory role in the regulation

of PCD of cereal aleurone cells (Bethke and Jones, 2001; Fath et al., 2002). The GA-induced progression of PCD in these cells is accelerated in the presence of internally generated or exogenously applied hydrogen peroxide, whereas antioxidant agents, such as ascorbic acid or dithiothreitol, have the opposite effect (Bethke and Jones, 2001). Nitric oxide (NO) has the effect of delaying PCD of aleurone cells, most probably by counteracting the accelerating effect of ROS (Beligni et al., 2002). To avoid the harmful effect of ROS and prevent precocious PCD, aleurone cells are equipped with detoxification systems based on the scavenger activity of catalase, ascorbate peroxidase and superoxide dismutase (Fath et al., 2001), as well as haem oxygenase (Wu et al., 2011), some of which are down-regulated before the process of PCD is initiated (Fath et al., 2001). A nuclear detoxification system has also been described in wheat seed cells suffering oxidative stress, which is composed by an NADPH thioredoxin reductase (NTR) and a 1-Cys-peroxiredoxin (1-Cys Prx; Stacy et al., 1996, 1999; Pulido et al., 2009). This nuclear-localized redox system may have the function of preventing oxidative damage to DNA and nuclear structures, as suggested by DNA protection assays *in vitro*. In addition, this redox system may control the level of hydrogen peroxide in the nucleus, thus having a potential signaling function. Besides nuclear-localized detoxification systems, wheat aleurone cells also display a set of gibberellin-induced glycosylases participating in the base excision repair pathway to remove non-bulky DNA base lesions generated by ROS (Bissenbaev et al., 2011). Under the oxidant conditions generated in germinating seeds, the 1-Cys Prx undergoes a progressive inactivation by overoxidation of its catalytic cysteine residue (Pulido et al., 2009). This inactivation would promote a further accumulation of hydrogen peroxide; the nuclear environment becoming more oxidant and promoting cell death.

CONCLUDING REMARKS AND PERSPECTIVES

The cereal seed constitutes an excellent example illustrating the essential function of cell death for developmental programs in plants. Different techniques, such as TUNEL staining of nuclei of dying cell, have been a valuable aid in identifying tissues undergoing PCD and also in studying the spatial-temporal patterns of PCD in developing and germinating cereal seeds. Moreover, although most of the tissues undergoing PCD in cereal seeds present autophagic-like morphology, other tissues such as the starchy endosperm show peculiar characteristics. The identification of proteolytic and nucleolytic activities associated with PCD in the different tissues reveal the biochemical complexity of cell death in this plant model system. PCD in cereal seeds occurs with very well-defined spatial-temporal patterns, which are established by different factors; hormones playing a relevant function. So far, most of the knowledge of PCD in cereal seeds has been obtained from descriptive approaches. However, the last decade has brought impressive advance in our understanding of the cereal genomes that have been sequenced. In cereal models such as rice and *Brachypodium*, larger collections of mutants are available; in addition, genetic transformation of cereals is becoming a routine technology. All these molecular and genetic tools now available for cereals are expected to facilitate functional approaches applied to the study of PCD, which may allow a more precise

dissection of the process in this plant system and, eventually, the identification of genes acting as key regulators of cell death in plants.

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Physical, metabolic and developmental functions of the seed coat

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The conventional understanding of the role of the seed coat is that it provides a protective layer for the developing zygote. Recent data show that the picture is more nuanced. The seed coat certainly represents a first line of defense against adverse external factors, but it also acts as channel for transmitting environmental cues to the interior of the seed. The latter function primes the seed to adjust its metabolism in response to changes in its external environment. The purpose of this review is to provide the reader with a comprehensive view of the structure and functionality of the seed coat, and to expose its hidden interaction with both the endosperm and embryo. Any breeding and/or biotechnology intervention seeking to increase seed size or modify seed features will have to consider the implications on this tripartite interaction.

Keywords: seed development, nutrients supply, seed photosynthesis, PCD, maternal-filial interface

INTRODUCTION

The evolution of sexual reproduction and the seed underlies much of the evolutionary success of the flowering plants. The most distinctive characteristic of the angiosperms is the double fertilization event, followed by the development of a seed encased in maternal tissue, referred to as the seed coat (or testa). The enclosure of the developing embryo affords it protection and thereby enhances its chances of reaching maturity and establishing the subsequent generation; this feature has not been achieved by species belonging to other clades of the plant kingdom. The progenitor structure of the angiosperm seed on the female side is the ovary, and its final form comprises an embryo, an endosperm, and the seed coat. The embryo results from the fusion between an egg cell and a sperm nucleus, while the endosperm develops from the fusion between the two central cell nuclei and a second sperm nucleus to produce (in diploid species) a triploid structure. The seed coat is entirely maternal in origin. When fertilization fails, the structure degenerates rapidly, thereby ensuring that the assimilate invested in an aborted seed is recycled (Roszak and Köhler, 2011). Post fertilization, the development of the seed relies on a coordinated interaction between the seed coat, the embryo, and the endosperm. The molecular basis of seed development has been intensively studied (Lafon-Placette and Köhler, 2014), but until now, the lack of suitable *in vivo* analytical methods has hampered systematic investigations of either the metabolism occurring or the internal structures developing within the growing seed. Here, a description is given of our current understanding of the functional role of the seed coat in the developing seed.

FROM OVULE TO SEED COAT

The seed coat originates from cell layers surrounding the ovule. The analysis of a number of *Arabidopsis thaliana* mutants has

revealed its structure and function, as well as identifying many of the genes involved in its development (Haughn and Chaudhury, 2005; Figueiredo and Köhler, 2014). Seed coat development is repressed prior to fertilization by dosage-sensitive, sporophytically active polycomb-type-proteins that are expressed in the maternal tissue surrounding the female gametophyte (Roszak and Köhler, 2011). The fertilization generates a signal that relieves the polycomb type protein-mediated repression, resulting in the initiation of seed coat formation (Roszak and Köhler, 2011).

The *A. thaliana* seed coat is composed of five cell layers: the three-layered inner integument and the two-layered outer integument; each of these layers follows a distinct path during seed development. The endothelium (the innermost cell layer) synthesizes proanthocyanidins (PAs), which first condense into tannins, then oxidize to impart the brown pigmentation seen in the mature seed of many species (Lepiniec et al., 2006). The two adjacent cell layers are crushed together as the seed expands (Nakaune et al., 2005). The outer integument undergoes extensive differentiation, regulated by the YABBY family transcription factor *INNER NO OUTER* (Kelley and Gasser, 2009), going on to form the sub-epidermal and epidermal cell layers. The former of these generates a thickened wall on the side facing the epidermis (Haughn and Chaudhury, 2005), while the latter produces a pectinaceous carbohydrate referred to as mucilage (Arsovski et al., 2010; Haughn and Western, 2012). The outer integument is associated with a suberized layer, and the endothelium with a cutin-like polyester layer (Molina et al., 2008). In leguminous species, the seed coat is typically a multi-layered structure, including both macro- and osteosclerids in its outer integument and parenchyma in its inner integument (van Dongen et al., 2003; Verdier et al., 2012). In the cereal grain (strictly a caryopsis rather than a seed, since the ovary wall is fused with the seed coat), the endothelium and the outer

integument each form a pair of cell layers, while the enlarged pericarp takes over some of the key functions of the seed coat (Sreenivasulu et al., 2010). The various impacts of the seed coat are illustrated for a contrasting set of species in **Figure 1**.

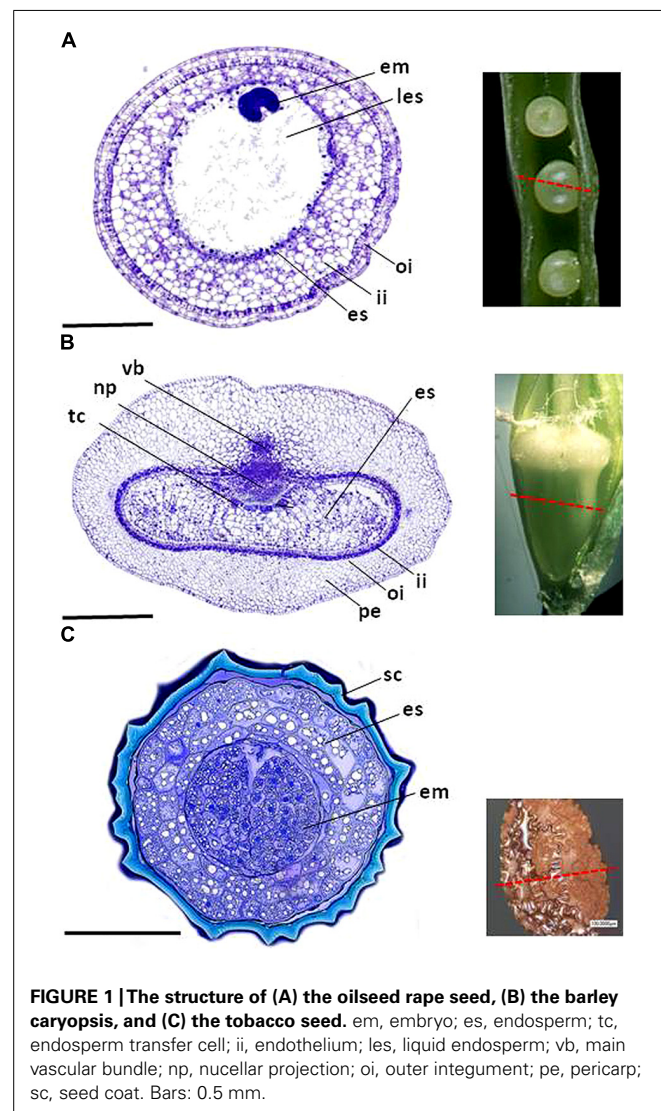
The development of the endothelium has been revealed by the analysis of *A. thaliana* mutants impaired in seed coat pigmentation. A number of relevant genes have been isolated, classified for the most part into either transcription factors or genes required for the synthesis and compartmentation of PA flavonoid compounds (Haughn and Chaudhury, 2005). Comprehensive transcriptomic descriptions of the developing *A. thaliana* seed coat have provided a wealth of information relevant to how the process occurs in other species (Dean et al., 2011). The *Medicago truncatula* myb transcription factor gene *MtPAR* has been shown to be a key regulator of PA synthesis, and its transcription co-localizes with the site of PA accumulation in the seed coat (Verdier et al., 2012). Key *M. truncatula* genes along with the precursor transporter *MATE1* (involved in PA synthesis) have been isolated and characterized by Zhao and Dixon (2009). Orthologs of *BANYULS*,

which encodes anthocyanidin reductase (Albert et al., 1997), have been identified in oilseed rape and its close relatives *Brassica rapa* and *B. oleracea* (Auger et al., 2010). The transcriptional regulation of flavonoid metabolism is less well understood in legumes and cereals, perhaps because the genes underlying PA synthesis have been lost during domestication, with the result that white-seededness is commonplace in these taxa. Consequently, in contrast to its wild relatives, cultivated barley (similarly to rice and wheat) does not accumulate substantial amounts of PA (Sang, 2009). The relationship of secondary PA metabolism with both developmental regulation and the stress response has the potential to contribute significantly to future crop improvement and is being investigated by a number of research groups (Debeaujon et al., 2000; Bassoi and Flinham, 2005; Lepiniec et al., 2006; Gao et al., 2013).

Elucidation of the development of the *A. thaliana* outer integuments has relied on mutants that produce either less mucilage than the wild type or those which produce mucilage of a different composition. Both regulatory and structural genes have been recognized (Haughn and Chaudhury, 2005; Arsovski et al., 2010; Haughn and Western, 2012). The set of WD repeat, bHLH and myb transcription factors that regulate outer integument development partially overlaps with the factors controlling trichome initiation and development, the regulation of anthocyanin production and endothelial development, although the relevant interaction partners are distinct (Schiefelbein, 2003; Bernhardt et al., 2005; Haughn and Chaudhury, 2005; Gonzalez et al., 2008). For example, outer integument differentiation is controlled by the proteins TTG1, myb5/TT2, and TT8/EGL3, which also drive the transcription of *ABE1*, *ABE4*, *GH*, *GL2*, and *mybL2* (Gonzalez et al., 2008; Li et al., 2009). The *A. thaliana* model has been informative for understanding the molecular basis of the synthesis of cotton fibers, which arise from the epidermal cells of the outer integument and are distributed all over the seed's surface (Lee et al., 2007; Liu et al., 2012; Ruan, 2013). Several of the regulatory genes involved in fiber initiation have proven to be homologs of *A. thaliana* genes (e.g., *TTG1* and *GL2*) responsible for trichome formation and the differentiation of the outer integument. The current understanding is that a transcriptional myb/bHLH/WD repeat complex is required for this initiation process (Yang and Ye, 2013). A full understanding of the regulatory machinery operating in the epidermal cells will aid in achieving further improvement in a number of cotton seed traits (Yan et al., 2009; Efe et al., 2010) as well as the development of sustainable means of processing seeds and the fibers (Kimmel and Day, 2001; Stiff and Haigler, 2012).

NO LIFE WITHOUT PROTECTION

In many seeds, the epidermal layer of the seed coat generates a cuticle which represents a physical barrier between the seed and its external environment. Neither viruses nor bacteria are able to penetrate an intact mature seed cuticle (Singh and Mathur, 2004; Gergerich and Dolja, 2006). The only entry points into a mature seed of this type for a pathogen are the micropyle – which represents the point of entry of the pollen tube – and the funiculus, which links the maternal vascular system to the seed integument. The immature seed coat is less robust, so it offers



less protection against pathogen penetration, which can occur via either the ovary wall or the stigma. Mechanically damaged cuticles offer an alternative path for pathogen invasion (Singh and Mathur, 2004). Integrity of seed coat surface is extremely important for seed quality and fitness during seed storage or germination, and diverse technologies are available for preserving and enhancing of seed surface (Black and Halmer, 2006; Brooker et al., 2007).

An additional layer of protection is provided in certain seeds by the deposition of toxic compounds such as cyanogenic glycosides, terpenoids, and flavonoids. The issue of seed coat chemistry has especial resonance in relation to the presence of glucosinolates in brassicaceous crops (Bohinc et al., 2012). The accumulation of phenolics in plant tissues is considered to be an adaptive response to adverse environmental conditions (Lattanzio et al., 2006; Vermerris and Nicholson, 2007).

Since plants lack mobile defender cells, they are forced to rely on the innate immunity of every cell and on the production of signal molecules by invaded cells and their subsequent sensing (Jones and Dangl, 2006). The small and highly stable cysteine-rich peptides referred to as defensins actively inhibit pathogen invasion in both plants and animals (Stotz et al., 2009). Defensins genes induced by pathogen infection have been identified in a number of plant species (Thomma et al., 2002; Lay and Anderson, 2005; Carvalho and Gomes, 2009). Their products are concentrated mainly in the peripheral/bordering cells, as typified in barley and rice (Kovalchuk et al., 2010), and are released following tissue damage (Thomma et al., 2002; Lay and Anderson, 2005). Defensin production can also be promoted by certain abiotic stress agents, and also by exposing plants to the phytohormones methyl jasmonate, ethylene, or salicylic acid (Lay and Anderson, 2005). The expression of defensins in response to a variety of biotic and abiotic stimuli implies the possibility of cross-talk between distinct signal transduction pathways and gene expression programs involved in cellular signaling and growth regulation (Hanks et al., 2005; Okuda et al., 2009). Plant defensins have become the focus of a considerable body of biotechnological research (Carvalho and Gomes, 2009; Kovalchuk et al., 2010).

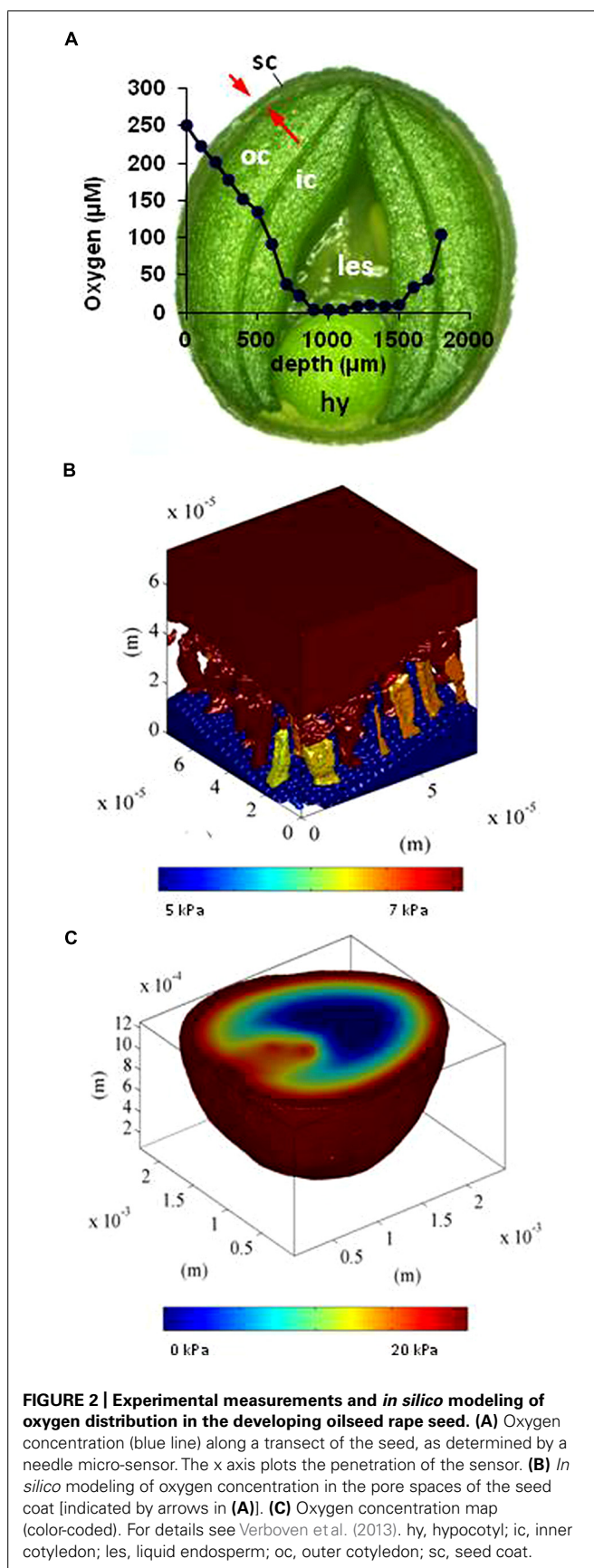
The barrier function of the seed coat does not extend to gases, since it is in most cases at least semi-permeable (Welbaum and Bradford, 1990; Beresniewicz et al., 1995). The seed coat epidermis in the mature seed features no, or at best only scarce, functional stomata (Cochrane and Duffus, 1979; Geisler and Sack, 2002). In conjunction with the chemical composition of the cuticle, this implies a rather limited capacity for gas exchange (Nutbeam and Duffus, 1978; Sinclair et al., 1987; Sinclair, 1988). It was already demonstrated some 40 years ago that most of the gas exchange activity occurring within the pea seed is located in the micropylar region (Wager, 1974). The diffusivity of carbon dioxide through plant tissue is much higher than that of oxygen, since (unlike oxygen) carbon dioxide is readily soluble in water and so can move from cell to cell in the form of the carbonate ion. The presence of gas-filled intercellular spaces is therefore likely to be essential for translocation of oxygen within the seed. Synchrotron X-ray computer tomography has identified such spaces in the developing seeds of both *A. thaliana* (Cloetens et al., 2006) and oilseed rape *in vivo* (Verboven et al., 2013). In the latter species, both the

seed coat and the hypocotyl are well supplied with void spaces, unlike the cotyledons, where the spaces are small and only poorly inter-connected (**Figure 2**). *In silico* modeling has revealed a three orders of magnitude range in oxygen diffusivity from the seed coat to particular embryonic tissues (Verboven et al., 2013). The multiple void spaces present in the seed coat suggest that gas exchange is effective within this part of the seed. There is a lack of any interconnectivity with the embryo, so the seed coat void network is likely to be autonomous. Both the seed cuticle and the lipid-containing aleurone layer of the endosperm have been identified as barriers to oxygen exchange, the former between the seed coat and external atmosphere and the latter between the seed coat and the endosperm/embryo. The oxygen pool stored in the voids of oilseed rape seed is consumed about once per minute. Since the developing seed has a high respiratory rate, it requires an additional supply of oxygen to maintain aerobic respiration.

Oxygen micro-sensor measurements made within the seed of faba bean, pea (Rolletschek et al., 2002, 2003) and soybean (Borisjuk et al., 2005), and within the grains of barley (Rolletschek et al., 2004), wheat (van Dongen et al., 2004), and maize (Rolletschek et al., 2005) have established that hypoxia is the norm. In the developing seed, it may be advantageous to keep the oxygen level low, because the bioenergetic efficiency of mitochondria is usually increased at low oxygen levels (Gnaiger et al., 2000). Thus, a low internal oxygen concentration in the seed may stimulate carbon use efficiency. Low oxygen levels help to avoid the formation of toxic concentrations of reactive oxygen species, which damage cellular structures and require the expenditure of energy for repair (Borisjuk and Rolletschek, 2009). In maize, the level of expression of detoxification genes (encoding glutathione *S*-transferase, superoxide dismutase, and ascorbate peroxidase) decreases during grain development (Méchin et al., 2007), consistent with a reduction in oxygen availability. To summarize, maintaining a low oxygen level within the seed has been proposed to provide a means for the developing seed to control the local level of metabolic activity (Borisjuk and Rolletschek, 2009). Deep within the mature seed, the inhibition of gas exchange can generate a state of near-anoxia, which may help to ensure the remarkable longevity of seeds (Shen-Miller, 2002). While the mechanistic basis of seed longevity is not fully understood, an important component is likely the control of oxidation (Hendry, 1993; Smirnoff, 2010; Bailly and Kranner, 2011). Practical methods to prolong seed viability in *ex situ* gene banks exploit this natural phenomenon by hermetically sealing the seed in order to maintain a high level of carbon dioxide within; this is combined with careful drying down and refrigeration, which help to slow seed metabolism/respiration and suppress oxidation processes (Kranner et al., 2010).

PERCEIVING ENVIRONMENTAL CUES

The seed coat's function is simultaneously to protect the embryo and to transmit information regarding the external environment. An impenetrable seed coat may help to keep the embryo safe, but at the same time it would exclude the sensing of environmental cues. The evolutionary solution to this dilemma is to combine certain structural features with appropriate levels of metabolic and photosynthetic activity in the seed coat.



As plant species vary so much with respect to the distribution and amount of chlorenchyma in their developing seed, it is difficult to make meaningful generalizations regarding seed photosynthesis. However, out of 19 major crop species, only maize grains lack chlorophyll (Bewley and Black, 1994). Both the seed coat and embryo of pea (Tschiersch et al., 2012), soybean (Saito et al., 1989), oilseed rape (Borisjuk et al., 2013) and faba bean (Rolletschek et al., 2003) are photosynthetically active during seed development. The immature caryopsis of barley, wheat, rice and other grasses features a photosynthetically active pericarp (Bewley and Black, 1994; Rolletschek et al., 2004). The site of photosynthetic electron transport coincides with that of chlorophyll (Tschiersch et al., 2012), as for example in the barley pericarp (Figures 3A,B). When exposed to light, the chloroplasts (Figure 3C) produce sufficient ATP and NADPH to meet local energy demand. Given the very short half life of both ATP and NADPH, it is likely that little long distance transport occurs from their site of synthesis. Non-photosynthetic plastids within the pericarp depend entirely on an external supply of ATP, just as is the case for other non-photosynthetic tissues (Möhlmann et al., 1994; Möhlmann and Neuhaus, 1997). The spatial separation between the endosperm and the photosynthetically active pericarp implies that seed photosynthesis does not make any direct energy contribution to assimilate storage in the endosperm.

Photosynthetic activity in the seed coat, as in the leaves, fixes carbon dioxide (Nutbeam and Duffus, 1978; Caley et al., 1990), and generates oxygen (Rolletschek et al., 2004; Tschiersch et al., 2012). This process is saturated in seeds at a light intensity some fivefold below that applicable for leaves. Oxygen production and carbon dioxide fixation combine to maintain a

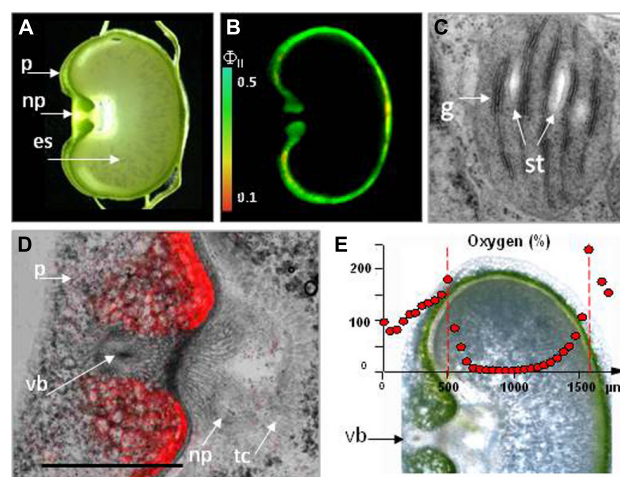


FIGURE 3 | Photosynthesis in the barley pericarp. (A) Cross-section of a grain. (B) The effective quantum yield of photosystem II (FII) across a cross-section of a 12-day-old caryopsis, measured at a light intensity of $160 \mu\text{mol quanta m}^{-2} \text{s}^{-1}$. The scale shows the relationship between the color and FII. (C) A transmission electron micrograph of seed chlorenchyma plastids. (D) Chlorophyll auto-fluorescence within the crease region of the pericarp. (E) Oxygen levels within the caryopsis, as measured by a micro-sensor. For details see Tschiersch et al. (2012). es, endosperm; g, grana; np, nucellar projection; p, pericarp; st, starch grain; tc, transfer cell; vb, vascular bundle.

consistent gaseous environment within the seed. The effect of photosynthetic oxygen evolution exceeding the oxygen demand of the respiring seed coat is an increase in the internal oxygen level (Patrick et al., 1995; Rolletschek et al., 2002, 2003), which serves to relieve hypoxic stress and thereby enhances the synthetic activity of the seed (Greenway and Gibbs, 2003; Rolletschek et al., 2005). Importantly, the tissues through which nutrients are transported to the endosperm/embryo are oxygen depleted (Melkus et al., 2011). In the dark, the oxygen level can fall below 0.1% of the ambient atmospheric concentration (Rolletschek et al., 2011), but the chlorenchyma layer that surrounds the region ensures that the level of oxygen present is much higher in the light than this (**Figures 3D,E**). Both nutrient transport to, and storage activity within the endosperm rely heavily on respiratory energy and thus on a steady supply of photosynthetically derived oxygen. Experiments tracking the incorporation of labeled sucrose into starch have shown that the process is stimulated by both light and oxygen (Gifford and Bremner, 1981), underlining the dependence of storage activity on a supply of oxygen. Similarly, assimilate supply to the dicotyledonous seed is also oxygen-dependent, as shown by phloem unloading experiments (Thorne, 1982).

The seed coat's high rate of respiration, along with its low permeability with respect to carbon dioxide, contributes to elevating the seed's internal level of carbon dioxide. However, high concentrations of carbon dioxide do promote phosphoenolpyruvate carboxylase activity, which serves to encourage carbon dioxide re-fixation and so restricts its loss (Wager, 1974; Harvey et al., 1976; Flinn, 1985; Araus et al., 1993; Golombek et al., 1998). Limiting carbon dioxide loss in this way can make an important contribution to the seed's overall carbon budget (Vigeolas et al., 2003; Rolletschek et al., 2004). In addition, re-fixation of carbon dioxide is mediated by Rubisco activity during photosynthesis (Goffman et al., 2004; Ruuska et al., 2004). The seed's rate of carbon dioxide uptake from the atmosphere is much lower than the leaf's (Brar and Thies, 1977; Watson and Duffus, 1988), in line with both a lower activity of photosynthesis-associated enzymes (Duffus and Rosie, 1973) and a limited rate of metabolic turn-over (Schwender and Ohlrogge, 2002; Sriram et al., 2004). Critical factors should be considered such as (1) the low density of stomata on the surface of the developing seed, and (2) the low amount of chlorenchyma. Most relevant experiments have disregarded the re-assimilation of internally produced CO₂ and hence probably underestimated the actual sizes of the occurring fluxes (Araus et al., 1993). Nevertheless, the generally held conclusion still stands that the contribution of seed photosynthesis to dry matter production (via net CO₂ fixation) is low.

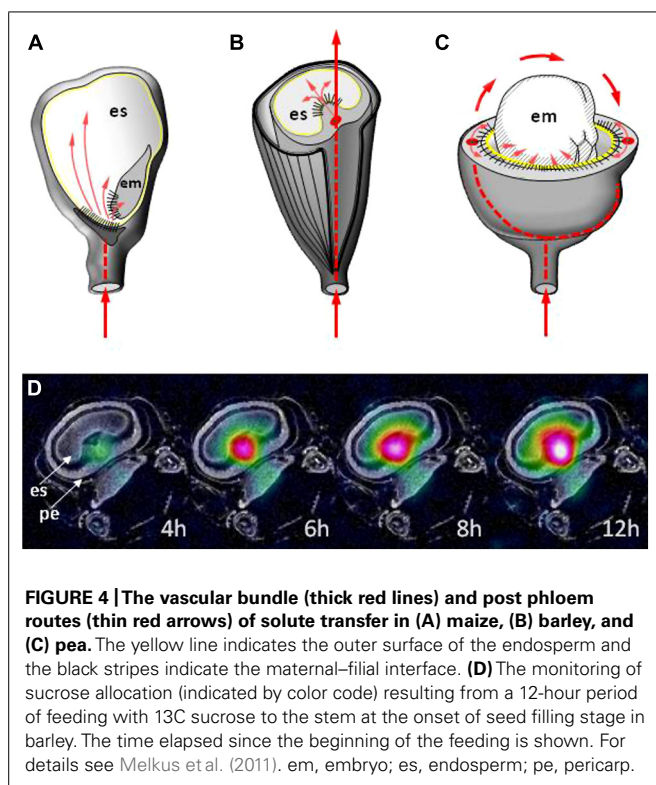
One likely hypothesis regarding the evolutionary significance of retaining photosynthetic capacity in the seed coat suggests that the interception and processing of light by the seed coat gives the seed the means to sense its external environment, which is integrated with the hormonal, metabolic, and other signals brought to the seed through the phloem. Assimilate generated in the leaf is exported into the phloem in the form of sugar. The developing seed can benefit from the capacity to anticipate a burst of sugar arriving via the phloem, since this would facilitate the seed's rapid adjustment to its synthesis of storage products. Photosynthesis has

a marked effect on the entrainment and maintenance of robust circadian rhythms (Haydon et al., 2013). In this way, the retention of seed photosynthesis can provide a means of tuning the seed's metabolism to the quantity and quality of the light available to the mother plant.

HIGHWAYS AND BYWAYS TRAVELED DURING SOLUTE TRANSFER

Assimilates produced by the mother plant are delivered to the developing seed via the same conduit, the vascular system, which brings hormonal signals and the necessary protein- and RNA-based messages. Collectively, this enables the coordination of physiological and developmental processes at the whole organism level (van Bel et al., 2013). As the vascular system does not extend beyond the seed coat (Patrick et al., 1995), the embryo and the endosperm are apoplastically isolated from the mother plant and are therefore somewhat autonomous. Several pathways for nutrient flow are available, depending on seed size and structure. The smallest seeds (orchid seeds can be as small as 200 µm in diameter) have no vascular structure; rather, the zygote forms a haustorium which extends toward the terminus of the mother plant's vascular system. Slightly larger seeds form a bundle of pro-vascular elements. Medium-sized seeds develop a simple, well developed collateral bundle (van Dongen et al., 2003). Finally, in large-seeded species, the vascular bundle is bulky enough to anastomose, thereby allowing for the distribution of nutrients throughout the seed (Vinogradova and Falaleev, 2012). In the *A. thaliana* seed, the vascular tissue terminates at the junction of the funiculus and ovule, and in the maize kernel, the vascular bundle terminates at the placenta–chalazal region (**Figure 4A**; Dermastia et al., 2009; Gómez et al., 2009; Costa et al., 2012). In contrast, wheat, barley and rice grains form a vascular system that extends over the whole length of the grain (**Figure 4B**; Sreenivasulu et al., 2010). The vascular architecture of *Fabaceae* species seeds is highly variable, ranging from a single chalazal vein in the *Viciae* and *Trifolieae* to an extensive anastomosed arrangement in the *Phaseoleae* (**Figure 4C**; van Dongen et al., 2003; Weber et al., 2005; Verdier et al., 2013).

Vascular structures are typically embedded within parenchymatous tissue. Adjacent parenchyma cells are interconnected by plasmodesmata, forming a symplastic continuum (domain). The plasmodesmata within these domains are larger than elsewhere in the seed (Ruan and Patrick, 1995; Oparka et al., 1999; Stadler et al., 2005a,b), which facilitates the movement of small molecules such as sugars and peptides. The maternal symplasm represents the major route for nutrients to reach the seed (Wang and Fisher, 1994; Borisjuk et al., 2002; van Dongen et al., 2003). In *A. thaliana*, each integument forms an independent symplasm (Stadler et al., 2005a; Ingram, 2010), which acts as an extension of the phloem (Stadler et al., 2005a,b). In common bean, faba bean, and pea, assimilate unloading sites are distributed throughout the seed coat parenchyma, with the possible exception of the branched parenchyma (Patrick and Offler, 1995). In the small grain crops, the nucellar projection is the focus of a well organized transport route. The cellular architecture of the nucellar projection has been described in wheat (Wang and Fisher, 1994) and barley (Thiel



et al., 2008; Melkus et al., 2011). A characteristic feature of tissues adjacent to the nutrient transport route is the presence of multiple symplastic junctions, large intercellular spaces and cell wall invaginations. The cells of the nucellar projection are extended toward the endosperm, thereby directing the flow of nutrients into the seed. With the exception of the crease region, a thick cuticular layer borders the pericarp and encloses the whole endosperm. In rice, two routes have been identified for nutrients to reach the developing grain: one is analogous to the nucellar projection, while the second passes through the nucellar epidermis (Oparka and Gates, 1981; Krishnan and Dayanandan, 2003).

The structure of the seed impedes the direct visualization of the site of the interaction between maternal and filial tissue. Various dyes and fluorescence- or isotope-labeled substances have been employed to follow nutrient (mainly sucrose) transport (Fisher and Cash-Clark, 2000; Stadler et al., 2005a,b). However, this experimental approach has the major disadvantage of being destructive. Invasive methods inevitably risk inducing artifacts with respect to both metabolite distribution and enzymatic activity. Non-invasive technologies, in the form of biosensors or imaging platforms like Foerster resonance energy transfer (FRET), Positron Emissions Tomographie (PET), and nuclear magnetic resonance (NMR) provide potentially superior alternatives (Frommer et al., 2009; Jahnke et al., 2009; Borisjuk et al., 2012). Real-time information on signaling and metabolite levels with subcellular granularity can be obtained *in vivo* with the help of genetically encoded FRET nanosensors (Frommer et al., 2009). PET does appear to be an appropriate platform for *in planta* analysis (Jahnke et al., 2009). When ^{11}C is the target isotope, its spatial resolution of 1.4 mm (Phelps, 2004) suits it for the study of long distance

translocation. NMR – and especially ^{13}C NMR – is less sensitive than PET, but it delivers a fivefold higher level of in-plane resolution than PET, and can be used for real time monitoring (Melkus et al., 2011). The dynamic NMR-based imaging of sucrose in barley seed was integrated with flux balance analysis (FBA), which operated with more than 250 biochemical and transport reactions occurring in the cytosol, mitochondrion, plastid, and extracellular space. This approach has helped to unravel the complex biochemical processes affecting sucrose distribution in the grain (Melkus et al., 2011; Rolletschek et al., 2011).

DELIVERING NUTRIENTS ACROSS THE MATERNAL–FILIAL INTERFACE

Some experimental evidence has been obtained to support the view that the delivery of metabolites to the embryo bypasses the endosperm (Yeung and Meinke, 1993; Weijers et al., 2003; Stadler et al., 2005a; Morley-Smith et al., 2008; Ungu et al., 2008; Pignocchi et al., 2009). However, other data suggest that the process is, in fact, mediated by the endosperm, largely because compromised endosperm development is so often associated with aberrant embryo growth (Chaudhury et al., 2001; Choi et al., 2002; Garcia et al., 2005; Ingouff et al., 2006). In either case, the inter-generational transfer of materials occurs via the apoplastic space. The specialized cellular structures developed at the tissue margins coordinate nutrient delivery from the seed coat into the seed itself. Transfer cells develop invaginated cell walls, thereby increasing the surface area of their plasma membrane and hence their capacity to transport nutrients (Andriunas et al., 2013). Nutrient transporters such as sucrose transporter 1 (Weber et al., 2005; Melkus et al., 2009) and amino acid permease 1 (AAP1; Tegeder, 2014) are typically present in both maternal and filial cells. Often they appear as tissue-specific isoforms: examples are the tonoplast intrinsic proteins (TIPs) for water (Gattolin et al., 2010) and Siliques Are Red 1 (SIAR1) for amino acids (Ladwig et al., 2012); some can change from efflux to influx mode in response to metabolic signals (Ladwig et al., 2012). The transfer cells positioned on either side of the apoplast (Zhang et al., 2007) act as the gateway for nutrient flow, as demonstrated *in vivo* by NMR in the barley caryopsis (Figure 4D; Melkus et al., 2011; Rolletschek et al., 2011).

The maternally located efflux transfer cells are responsible for the release of nutrients into the apoplast, and form cell wall ingrowths which direct the flow toward the seed (Stadler et al., 2005b; Zhang et al., 2007). The plasma membranes in these cells are enriched with respect to aquaporins, membrane transporters, and channels for sugars, amino acids and peptides, inorganic ions, and other compounds (Zhang et al., 2007; Thiel et al., 2008; Bihmidine et al., 2013). These efflux cells, like the cells of the barley and wheat nucellar projections, typically undergo programmed cell death (PCD; Zhou et al., 2009; Radchuk et al., 2011), which contributes to nutrient transfer to the filial tissue. In the maize seed coat placenta–chalazal region, PCD is coordinated with endosperm cellularization and is completed prior to the beginning of the storage phase. In this way, PCD functions as an adaptive process to facilitate the passage of solutes (Kladnik et al., 2004). In barley, the extensive vacuolization of cells

in the nucellar projection allows for the transient accumulation of sucrose, which is released together with the complete cell contents to the apoplast after cell disintegration. A defective nucellar projection compromises nutrient flow into the endosperm, resulting in a reduction in final grain size (Radchuk et al., 2006; Melkus et al., 2011; Yin and Xue, 2012). Although important for the seed's fate, the identity, and mechanics of efflux constituents and transporters are only poorly understood (Braun, 2012; Patrick et al., 2013).

The influx transfer cells in monocotyledonous species lie on the surface of the endosperm, directly opposite the maternal unloading site (Thiel et al., 2008; Monjardino et al., 2013; Lopato et al., 2014). The development and function of these transfer cells have been comprehensively and recently reviewed (Lopato et al., 2014; Thiel, 2014). In dicotyledonous species, the transfer cells usually face the seed coat (Borisjuk et al., 2002; Offler et al., 2003; Olsen, 2004). A delay in the *trans*-differentiation of the embryonic epidermal cells to form transfer cells in the pea mutant *E2748* has a negative impact on embryo growth and seed viability (Borisjuk et al., 2002). Maize grains defective for the formation of basal endosperm transfer cells exhibit a shrunken kernel phenotype, as exhibited in the mutants *reduced grain filling 1* (Maitz et al., 2000), *globby1* (Costa et al., 2003), *baseless1* (Gutiérrez-Marcos et al., 2006), *empty pericarp 4* (Gutiérrez-Marcos et al., 2007), and *miniature1* (Kang et al., 2009).

The coordinated differentiation of opposing transfer cells requires a functional interaction between them, so presumably relies on an effective signaling mechanism. How this interaction operates is unclear, but a possible sequence of events has been suggested by Weber et al. (2005) and Andriunas et al. (2013). In the dicotyledonous seed, the expanding cotyledon makes contact with the seed coat, after which the innermost thin-walled parenchyma cells are gradually crushed (Offler et al., 1989; Harrington et al., 1997). The stress, akin to wounding, may induce an ethylene burst (Harrington et al., 1997; Zhou et al., 2010). In response, a secondary ethylene burst in the adjacent embryo cells could be mediated by the auto-regulated expression of 1-aminocyclopropane-1-carboxylic (ACC) synthase (Chang et al., 2008). The process initiates the *trans*-differentiation of epidermal cells into transfer cells (Zhou et al., 2010). Crushing of the seed coat is also coupled with a decrease in the activity of extracellular seed coat-specific invertase (Weber et al., 1996a,b), which leads to a local reduction in the level of intracellular glucose (Borisjuk et al., 1998). The lowered glucose level, sensed via a hexokinase-dependent pathway, removes the glucose-induced repression of ethylene-insensitive 3 (EIN3) and triggers an ethylene-signaling cascade, driving transfer cell differentiation (Dibley et al., 2009; Andriunas et al., 2011). As shown in both *in vitro* and *in vivo* experiments, transfer cell formation across a wide range of plant species involves an interaction between phytohormones, sugar, and reactive oxygen species (Dibley et al., 2009; Forestan et al., 2010; Zhou et al., 2010; Andriunas et al., 2012; Xia et al., 2012). The signals and signaling pathways responsible for the induction of transfer cell formation may be conserved across the monocotyledon/dicotyledon divide (Andriunas et al., 2013). When the promoter of the maize transfer cell-specific transcription factor *ZmMRP1* (Gómez et al., 2009) was fused to a *GUS* reporter

gene and inserted into maize, *A. thaliana*, tobacco, and barley, *GUS* activity could be identified in regions of active transport between source and sink tissues in each of these species (Barrero et al., 2009), supporting the idea that the processes involved in transfer cell differentiation are similar across a diversity of plant species, and that differentiation is initiated by conserved induction signals.

COMMUNICATING BETWEEN ADJACENT SEED COMPARTMENTS

Coordination of seed development clearly requires communication between seed compartments, and in particular a level of feedback between the seed coat and the endosperm/embryo. Transporters localized at the embryo surface seem to be regulated by the metabolite concentrations present in the seed apoplast, but it is unclear how these transporters contribute to coordinating carbon partitioning between the maternal and filial tissues of the seed. For example, storage protein synthesis in the *A. thaliana* embryo and final seed weight depend on nitrogen availability and are mediated by AAP1, which is expressed in both the embryo and the seed coat. In both the seed coat and the endosperm of the *aap1* loss-of-function mutant, amino acid levels are higher than in the wild type, whereas in the embryo, the content of storage proteins and carbohydrate is lower (Sanders et al., 2009). Similarly, phloem amino acid concentrations regulate nitrogen loading into the oilseed rape seed (Lohaus and Moellers, 2000; Tilsner et al., 2005; Tegeder, 2014).

Nutrient release from the seed coat needs to be precisely tuned via a fast and sensitive mechanism such as, for example, cell turgor, which directly depends on the activity of vacuolar sucrose transporters (Walker et al., 2000). A turgor-homeostatic mechanism in the seed coat could sense a loss of solute from the seed apoplast and then could act to balance this by adjusting efflux activity (Patrick and Offler, 2001). The growth of the endosperm, therefore, may trigger a feedback signal to the seed coat, which is then transmitted via a calcium signaling cascade (Zhang et al., 2007) to drive cell elongation. Such a mechanism could allow the endosperm to coordinate aspects of seed development (Borisjuk et al., 2002; Melkus et al., 2009).

Sucrose, hexoses, and amino acids can all provide a regulatory signal (Koch, 2004; Weber et al., 2005; Ruan et al., 2010). Sugar responsiveness is a prominent feature of genes contributing to the sink strength of developing organs, and provides an important mechanism for sink adjustment to source delivery (Xiong et al., 2013b). A number of genes involved in sucrose metabolism are up-regulated by sugars (Smidansky et al., 2002; Kang et al., 2009). As a result, the strongest sink is the one most efficiently up-regulated by the supply of assimilate (Bihmidine et al., 2013). A balancing via down-regulation is also feasible (Kang et al., 2009). An invertase prominent in regulating sucrose unloading (Cheng et al., 1996; Weber et al., 2005; Chourey et al., 2011) has been proposed to enhance sugar signaling in the context of establishing assimilate sinks (Weber et al., 1996a, 2005; Ruan et al., 2010; Aoki et al., 2012). The expression of the myb-like transcription factor *ZmMRP-1*, a key regulator of transfer cell differentiation (Gómez et al., 2009), is modulated by various carbohydrates, with glucose being the most effective inducer (Barrero et al., 2009). *ZmMRP1*

transcriptionally activates a number of transfer cell-specific genes in the maize endosperm (Gómez et al., 2002); one of these is *Meg1*, which encodes a small cysteine-rich peptide localizing to the plasma membrane of differentiating endosperm transfer cells, where it regulates the expression of *cell wall invertase 2* (Costa et al., 2012). The strong maternal influence over placental-like functions is conferred by genomic imprinting, which has been attributed to maternal–filial co-adaptation (Wolf and Hager, 2006; Gehring et al., 2009). *Meg1* is one of more than a hundred imprinted genes active in the endosperm (Raissig et al., 2011; Waters et al., 2011; Wolff et al., 2011; Zhang et al., 2011), and is the first to have been identified as having a role in regulating the flow of nutrients to the embryo (Costa et al., 2012). *Meg1* also acts in tripartite (seed coat–endosperm–embryo) interaction and regulates maternal nutrient uptake, sucrose partitioning, and seed weight.

MAINTAINING A LEVEL OF CONTROL OVER SEED SIZE

The developing maternal tissue has an effect on endosperm filling and thus also final seed size. Several genes associated with seed size in *A. thaliana* are expressed in the seed coat (Haughn and Chaudhury, 2005; Roszak and Köhler, 2011). Among them are the transcription factors *ARF2/MNT* [which restricts seed size by suppressing cell proliferation in the integuments (Schruff et al., 2006; Li et al., 2008)], *AP2* (Jofuku et al., 2005; Ohto et al., 2005, 2009), *TTG2* and *EOD3/CYP78A6*, which control cell expansion in the integuments (Garcia et al., 2005; Ohto et al., 2009; Fang et al., 2012) and *KLUH/CYTOCHROME P450 78A5*, which stimulates cell proliferation in the endothelium. The up-regulation of *KLUH* increases seed size, produces larger seedlings and increases seed oil content (Adamski et al., 2009). *NARS1* and *NARS2* are expressed in the outer integument, acting redundantly to regulate seed shape and embryogenesis (Kunieda et al., 2008); the seed of the *nars1 nars2* double mutant are abnormally shaped.

At least 400 quantitative trait loci (QTL) related to grain size have been identified in rice and candidate genes have been identified for some of these (Huang et al., 2013). *Dwarf1* is strongly transcribed in the early developing pericarp and only weakly in the endosperm (Izawa et al., 2010). This gene encodes the α sub-unit of the heterotrimeric G protein (Ashikari et al., 1999; Fujisawa et al., 1999), which is suspected of controlling cell number, since its loss-of-function mutant displays a ubiquitous reduction in cell number (Izawa et al., 2010). A second candidate gene, *gif1*, encodes a cell wall invertase required for carbon partitioning during early grain filling (Wang et al., 2008). Its transcript is only detectable in the (maternal) vascular tissue, suggesting that its role is associated with sucrose unloading (Wang et al., 2008). The expansion of parenchymatous cell layers seen in a faba bean accession (large-versus small-seeded) may reflect the activity of cell wall invertase 1 (Weber et al., 1996a).

Several factors involved in ubiquitin-related activity have been shown to influence seed size (Li and Li, 2014). In rice, a ubiquitous RING-type protein displaying E3 ubiquitin ligase activity (encoded by *GW2*) negatively regulates grain size by restricting cell division. Its loss-of-function mutant forms an enlarged spikelet hull, which allows for a greater contact area between the endosperm and the seed coat (Song et al., 2007).

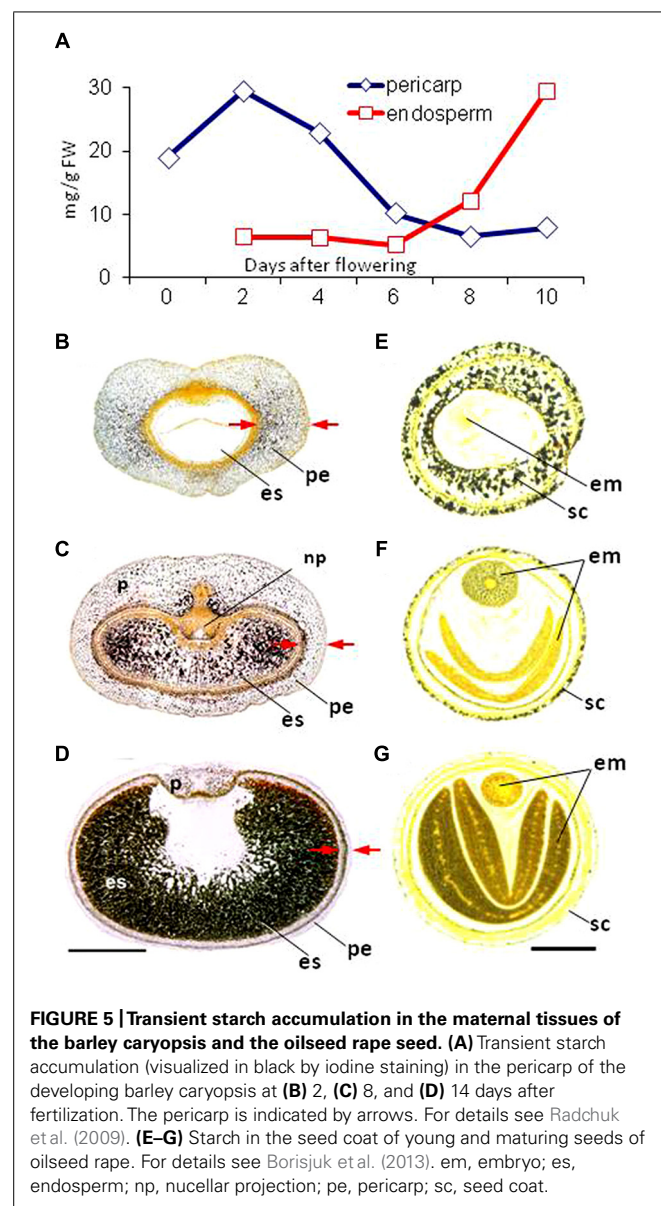
An uncharacterized protein, encoded by a candidate gene for a QTL for seed width mapping to chromosome 5, interacts with polyubiquitin, and acts to limit grain size, possibly by its involvement in the ubiquitin-proteasome pathway (Weng et al., 2008). However, because ubiquitin-related genes are so widely expressed – including within the endosperm – it is unclear whether their function is exclusively under maternal control. The *A. thaliana* gene *DA2* is a homolog of *GW2*; it acts in the maternal tissue to restrict the growth of the seed. The *da1* mutant produced larger and heavier seeds than wild type (“da” means “large” in Chinese; Li et al., 2008). The growth-restricting factor *DA1* is an ubiquitin receptor which determines final seed size by restricting the period of integument cell proliferation (Li et al., 2008; Xia et al., 2013). The gene underlying a major grain length QTL in rice encodes a putative phosphatase 2A-type protein harboring a Kelch-like repeat domain. Its effect is manifested by inducing a higher cell density on the outer surface of the glumes and the ovary (Zhang et al., 2012).

The influence of the maternal tissue on caryopsis size has been well documented in cereals, although quite how this is achieved at the molecular and metabolic level remains unresolved (Huang et al., 2013). The extensive synteny and conserved gene structure among cereals has allowed much of the knowledge gained from rice to be exploited in crops such as maize, wheat, and barley. In particular, orthologs of *GW2* have been identified in both wheat (Su et al., 2011) and maize (Li et al., 2010).

SMALL PROVISIONS FOR GOOD REASON

At an early developmental stage, the seed coat in dicots, and the pericarp in monocots accumulate a significant amount of starch (Figure 5). In *A. thaliana*, oilseed rape, and pea, starch accumulation occurs in the cells of the outer integument during the growth phase (Abirached-Darmency et al., 2005; Haughn and Chaudhury, 2005; Borisjuk et al., 2013). In the *A. thaliana* seed coat, the most abundant transcript level of the genes encoding starch synthesis enzymes are observed during the pre-globular and globular developmental stages (Khan et al., 2014). Starch granules in the chalazal part of the seed coat are smaller and less abundant than in the distal part, a trait which is mirrored by a differential starch synthesizing enzyme transcript profile (Khan et al., 2014). In *M. truncatula*, an abundance of starch granules accumulates transiently in the seed coat from the embryo heart stage all the way up to mid-maturation (Verdier et al., 2013). Based on the behavior of pea seeds lacking ADP-Glc pyrophosphorylase activity, it appears that transiently produced starch is required for sink acquisition, maximal embryo growth and final seed size (Rochat et al., 1995; Vigeolas et al., 2004). The role of this transient starch is not completely clear. Young maternal tissue may perhaps have evolved a starch storage function to ensure a sufficient assimilate sink strength, which becomes redundant once the growing seed's own sink is established (Radchuk et al., 2009). Accumulating assimilate in the form of starch is energetically highly efficient (Schwender, 2008), so it is unsurprising that the transient maternal sink accumulates starch rather than protein or lipid.

Transient starch is utilized for the growth and development of the maternal tissue (Xiong et al., 2013a), for example, by providing a source of carbohydrate to reinforce the cell wall with



pectinaceous mucilage (Khan et al., 2014). It may also help support the growth of the endosperm and embryo (Radchuk et al., 2009; Verdier et al., 2013). In *Zingiberales* and *Caryophyllales* species, the nucellus, rather than degenerating, accumulates large amounts of starch (López-Fernández and Maldonado, 2013), forming a so-called perisperm which persists until the seed is mature. In quinoa and the grain amaranth, the perisperm consists of dead, thin-walled cells completely filled with starch granules, producing a structure which strongly resembles the cereal endosperm (López-Fernández and Maldonado, 2013).

The synthesis of transient starch is performed by a similar set of genes as is used in the leaf (Radchuk et al., 2009). Its mode of breakdown in the cereal pericarp is distinct between living and dying cells. In living chlorenchyma cells, it most likely occurs via a pathway similar to that followed in the photosynthesizing leaf; this involves the phosphorylation of the starch granule surface, making

it accessible for the degrading enzyme β -amylase. Plastid-localized BAM5, BAM6, and BAM7 β -amylases are thought to produce maltose, acting either at the granule surface or on linear malto-oligosaccharides. The action of iso-amylase 3 on the granule, on the other hand, releases soluble malto-oligosaccharides, which can be metabolized by disproportionating enzyme 1 (DPE1), liberating glucose, and larger malto-oligosaccharides for continued degradation. After its transport to the cytosol, maltose can be further converted to glucose by DPE2. In dying cells, the mode of starch breakdown resembles that occurring in the germinating grain, which requires a combination of α - and β -amylase activity. AMY1 is active in the pericarp and nucellar tissue of a developing grain and is responsible for most of the α -amylase activity seen in germinating grains (Radchuk et al., 2009). A plausible starch degradation pathway in dying pericarp cells involves the joint activity of AMY1 and AMY4. Linear malto-oligosaccharides released by the action of these enzymes should provide an appropriate substrate for β -amylase 2. The molecular identity of the gene/enzyme responsible for the conversion of maltose to glucose remains to be identified.

Seed coat tissues may also serve as a transient depot for proteins and microelements. In faba bean, the storage protein legumin B is deposited in the seed coat at mid-embryogenesis (Panitz et al., 1995), while the wheat pericarp and nucellus accumulate significant quantities of calcium, copper, iron, molybdenum, magnesium, manganese, and phosphorus (Wu et al., 2013; Xiong et al., 2013a). The physiological significance of this accumulation has not yet been elucidated.

DYING QUIETLY

Because cell division in the maternal tissue ceases soon after fertilization, further enlargement only occurs through cell expansion (Radchuk et al., 2011; Figueiredo and Köhler, 2014). The rapid growth of the endosperm and embryo requires the triggering of PCD to remove maternal cells in order to allow seed expansion. In both dicotyledonous and monocotyledonous seeds, the early stages of endosperm expansion are at the expense of the nucellus (Domínguez et al., 2001; Greenwood et al., 2005; Lombardi et al., 2007; Zhou et al., 2009; Radchuk et al., 2011). After the cereal nucellus has degenerated, the next tissue to undergo PCD is the pericarp, starting from its innermost cell layer (Radchuk et al., 2011). The chlorenchyma is retained in a viable, functional state almost up to physiological maturity. In *A. thaliana* and the castor oil plant, PCD occurs first in the endosperm and later in the integuments (Greenwood et al., 2005; Nakaune et al., 2005).

As in animal cells, the molecular basis for PCD in plants relies on caspase-like activity. Although no caspase homologs have been identified in plants, plants do harbor proteases sharing some similarity to animal caspases. Caspase-1-like, caspase-3-like, and caspase-6-like activities have all been detected in the degenerating chayote (*Sechium edule*) nucellus (Lombardi et al., 2007). Vacuolar processing enzyme (VPE, also referred to as legumain) has caspase-1-like activities (Hara-Nishimura et al., 2005), while phytaspase possesses caspase-6-like activity (Chichkova et al., 2010). A seed specific δ VPE produced by *A. thaliana* is present in the two inner cell layers of the seed coat. In a mutant defective for

δ VPE, PCD is delayed and the seed coat remains thick throughout development. In contrast, in the wild type, the two layers undergo PCD very early during seed development, reducing their thickness by more than 50% (Nakaune et al., 2005). The spatial and temporal patterns of *HvVPE4* transcription coincides with the onset of PCD in the barley pericarp (Radchuk et al., 2011). The product of *HvVPE2a* (also called nucellain), together with those of *HvVPE2b*, *HvVPE2c*, and *HvVPE2d*, are important for the timely degeneration of the nucellus and the nucellar projection (Linnestad et al., 1998; Radchuk et al., 2011). *HvVPE2b* possesses caspase-1 like activity (Julián et al., 2013). The supposed role of the barley VPEs in grain development still requires experimental confirmation. Novel technologies (Tsiatsiani et al., 2012) might help to identify the target(s) of VPE.

A large number of proteases are present in degenerating maternal tissue, some of which may be active components of PCD (Sreenivasulu et al., 2006; Thiel et al., 2008). The ricinosome, a castor oil plant specific organelle, contains a large quantity of a pro-cysteine endopeptidase (CysEP), which serves to disintegrate the nucellar cells, leaving crushed and folded cell wall residues in the apoplastic space (Greenwood et al., 2005). Nuclear DNA fragmentation has been detected in the nucellus of the castor oil plant (Greenwood et al., 2005), chayote (Lombardi et al., 2007), barley (Linnestad et al., 1998; Radchuk et al., 2011) and wheat (Domínguez et al., 2001), as well as in the *A. thaliana* endothelium (Nakaune et al., 2005).

The transcription factor *OsMADS29* has been described as a regulator of PCD in the rice nucellus (Yang et al., 2012; Yin and Xue, 2012). *OsMADS29* transcripts are concentrated in the nucellus and the nucellar projection (Yin and Xue, 2012), but are also detectable in the inner layers of the pericarp, in other maternal seed tissues and in the embryo (Yang et al., 2012; Nayar et al., 2013). PCD is slowed in an *OsMADS29* knockdown line, leading to a reduction in starch accumulation in the endosperm and the production of shrunken or aborted grain (Yin and Xue, 2012). An alternative role for this transcription factor – in relation to hormone homeostasis, plastid biogenesis and starch synthesis – has been suggested by Nayar et al. (2013). *OsMADS29* is thought to bind to the promoters of cysteine protease genes (Yin and Xue, 2012). The down-regulation of *OsMADS29* suppresses the transcription of *VPE* genes in the grain (Yang et al., 2012). As yet, however, there is no consensus regarding the localization of either its transcript or its gene product, its primary target(s) or its likely function during grain development. The transcription of its barley homolog, *HvMADS29*, is restricted to the nucellus and the nucellar projection and coincides with that of *Jekyll* and *HvVPE2a*. The promoter regions of *Jekyll*, *HvVPE2a*, *HvVPE2b*, and *HvVPE2d* contain the same CARG-like regions recognized by *OsMADS29*, which implies that they are all transcriptionally regulated by *HvMADS29*. *Jekyll* is a key player in grain development (Radchuk et al., 2006), and is also active in nurse tissues, where it mediates the gametophyte-sporophyte interaction in both the gynoecium and the androecium (Radchuk et al., 2012). Its down-regulation slows PCD in the nucellus and nucellar projection, although the mechanistic basis of this effect is unclear. The *Jekyll* product, which is unique to *Pooideae*, is a small, cysteine-rich protein deposited within the intracellular membranes (Radchuk et al.,

2012). It has no significant similarity to other proteases or any protein of known function, and has no *in vitro* protease activity.

IMPROVING THE CHANCES OF SEED SURVIVAL

The capacity of the seed coat to limit water loss and to protect against mechanical damage persists beyond seed maturation. The mechanical strength of the seed coat is achieved primarily by the accumulation of sclerenchyma. Cell walls containing lignin, cellulose, and sometimes silica are effective in providing protection against attacks by fungi, insects, and herbivores (Lanning and Eleuterius, 1992). Seed coat constituents (e.g., PAs in *Brassica napus*) impair the digestibility and are being targeted by genetic and molecular approaches to improve nutritional value of seeds (Auger et al., 2010; Yu, 2013).

The seed coat can also contribute to seed dispersion: some species produce winged seed, where the wing structure is formed by outgrowths of the seed coat, while others produce hairy seed. Some of the compounds found on the seed coat have industrial applications. Under natural conditions, the cotton boll (its fibers are almost pure cellulose) will tend to increase the dispersion of the seeds, and indeed the use of cotton for fabric is known to date to prehistoric times. Genetically modified cotton has increased yield, but further improvements are needed (Molina et al., 2008; Kathage and Qaim, 2012; Ruan, 2013).

The seed coat, along with the endosperm, is the primary determinant of seed dormancy (Debeaujon et al., 2000; Bethke et al., 2007; Iglesias-Fernández et al., 2007), which represents a physiological adaptation to environmental uncertainty (Bewley et al., 2013). Dormancy dictates the environmental conditions required to trigger germination (Finch-Savage and Leubner-Metzger, 2006). The acquisition of seed dormancy is under complex genetic control, but it is vital as a means of assuring the survival of natural plant populations (Penfield and King, 2009; Graeber et al., 2012). Seed dormancy can be a critical trait for breeders (Fuller and Allaby, 2009; Gao et al., 2013; Smýkal et al., 2014) and would represent a prime target for biotechnology intervention, provided that its regulation were better understood (Flintham, 2000; Graeber et al., 2012).

A combination of external factors, such as light, temperature, water, and chemicals play an important role in breaking seed dormancy. Many small seeded species, the seeds of which contain little stored energy, are triggered to germinate by exposure to light. In some cases the minimum duration of exposure required can be measured in milliseconds (Quail, 1997). Phytochromes represent the main vehicle for seeds to sense light (Smith, 2000; Mochizuki et al., 2009). The linkage between the light-regulated trigger and the hormone-mediated induction of germination in *A. thaliana* has been explored by Cho et al. (2012). A rapid adaptation to light fluctuation can represent a key competitive advantage in natural plant populations. A particularly striking example of how the seed coat contributes to seed survival is provided by species that have adapted to bushfires. Australian *Banksia* species are destroyed when burnt, but the fire stimulates the opening of their seed-bearing follicles and promotes the germination of buried seed. The smoke from bushfires contains as many as 5000 different compounds (Nelson et al., 2012), including a number of substances proven to stimulate germination (Nelson et al.,

2012). While volatiles such as ethylene and nitric oxide are not very persistent in the soil, other smoke compounds (in particular, karrikins, and cyanohydrins) are quite stable in the upper layers of the soil where dormant seeds tend to be found. The seed coat of a mature *Banksia* sp. seed is permeable to these molecules. The seeds of hundreds of plant species have been tested with many smoke compounds, and the mode of action of some has been elucidated in *A. thaliana* (Nelson et al., 2010; Flematti et al., 2013). It has even been suggested that some of these compounds have been co-opted through evolution as signals for germination (Nelson et al., 2012; Challis et al., 2013).

CONCLUDING REMARKS

During seed development, the seed coat (dicots) and pericarp (monocots) serve a number of functions, most of which have evolved to protect the seed and to promote the development of the embryo and the endosperm within it. The architecture, chemical composition and metabolism of the seed coat work together to ensure effective responses to both biotic and abiotic factors. Nutrients passing from the mother plant to the developing embryo and endosperm must traverse the seed coat, which therefore controls seed development and seed filling. Specialized tissues have developed in a coordinated fashion on either side of the apoplast to direct and facilitate nutrient flow toward the growing embryo and endosperm. The seed coat and the endosperm act together to determine final seed size. The fine-tuning of nutrient flow from the seed coat to their endosperm and embryo is controlled at the genetic, epigenetic, and metabolic level, but how the interplay is achieved *in vivo* remains to be clarified.

Photosynthesis in the seed coat provides oxygen to the hypoxic regions deep within the developing seed. The overwhelming proportion of the nutrition supplied to the seed is provided by the leaf of the mother plant, the delivery of which is tied to the circadian rhythm. Adapting the seed's metabolism to this uneven flow of nutrition is facilitated by the seed's ability to sense light. In the course of seed development, the maternal tissues undergo PCD, thereby providing both the space and nutrients for the growth of the filial tissue. Finally, an outer seed envelope is built which is important for providing protection for the mature seed, enabling the establishment of dormancy and aiding in seed dispersal.

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The role of the testa during development and in establishment of dormancy of the legume seed

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Timing of seed germination is one of the key steps in plant life cycles. It determines the beginning of plant growth in natural or agricultural ecosystems. In the wild, many seeds exhibit dormancy and will only germinate after exposure to certain environmental conditions. In contrast, crop seeds germinate as soon as they are imbibed usually at planting time. These domestication-triggered changes represent adaptations to cultivation and human harvesting. Germination is one of the common sets of traits recorded in different crops and termed the “domestication syndrome.” Moreover, legume seed imbibition has a crucial role in cooking properties. Different seed dormancy classes exist among plant species. Physical dormancy (often called hardseededness), as found in legumes, involves the development of a water-impermeable seed coat, caused by the presence of phenolics- and suberin-impregnated layers of palisade cells. The dormancy release mechanism primarily involves seed responses to temperature changes in the habitat, resulting in testa permeability to water. The underlying genetic controls in legumes have not been identified yet. However, positive correlation was shown between phenolics content (e.g., pigmentation), the requirement for oxidation and the activity of catechol oxidase in relation to pea seed dormancy, while epicatechin levels showed a significant positive correlation with soybean hardseededness. myeloblastosis family of transcription factors, WD40 proteins and enzymes of the anthocyanin biosynthesis pathway were involved in seed testa color in soybean, pea and *Medicago*, but were not tested directly in relation to seed dormancy. These phenolic compounds play important roles in defense against pathogens, as well as affecting the nutritional quality of products, and because of their health benefits, they are of industrial and medicinal interest. In this review, we discuss the role of the testa in mediating legume seed germination, with a focus on structural and chemical aspects.

Keywords: domestication, dormancy, hardseededness, legumes, proanthocyanidins, seed coat, testa, water permeability

LEGUMES

Legume seeds are the second most important plant protein source, on a world basis, after cereals. While in cereals the major storage molecule is starch, which is deposited in the endosperm, in most of the grain legumes (pulses) the endosperm is transitory and consumed by the embryo during seed maturation, which contains a high proportion of proteins (20–40%), and either lipids (soybean, peanut) or starch (or both) as a further carbon source. Nutritionally, they are generally deficient in sulfur-containing amino acids (cysteine and methionine), but unlike cereal grains, their lysine content is relatively high. The major storage proteins are globulins, which account for up to 70% of the total seed nitrogen. The ability of legumes to fix atmospheric nitrogen allows them to colonize poor soils; however adequate nitrogen reserves in the seed are vital to allow the seedling to survive the heterotrophic growth phase before nitrogen fixation is established in root nodules. Fabaceae, the third largest family of flowering plants, are divided into three subfamilies: Caesalpinioideae, Mimosoideae,

and Papilionoideae, all together with 800 genera and 20,000 species (Lewis et al., 2005). The latter subfamily contains most of the cultivated major food and feed crops (Smýkal et al., 2014). It is a diverse family with a worldwide distribution, encompassing a broad range of plant forms, from annual and perennial herbs to trees and lianas. This variation is also reflected by widely diverse seed shapes and sizes, ranging from 1-mm seeds of the native Australian legume species *Pycnospora lutescens* to 18-cm seeds of the coastal tree *Mora oleifera* (Gunn, 1981). Legume seeds develop either within pods (e.g., legume), or less frequently, samara (Lewis et al., 2005), which can have several functions; protective, dispersal, and nutritive, can comprise a significant source of remobilized nutrients during seed filling.

DORMANCY CONCEPTS

The function of a seed is to establish a new plant but it can do this only once, because the completion of germination essentially is an irreversible process. Plants have evolved several dormancy

mechanisms to optimize the time of germination (Foley, 2001). Since seed dormancy is a physiological adaptation to environmental heterogeneity, it is a primary factor that influences natural population dynamics (reviewed in Bewley et al., 2013). Dormancy provides a strategy for seeds to spread germination in time in order to reduce the risk of plant death and possible species extinction in an unfavorable environment. Dormancy occurs in three ways: (1) Seeds are dispersed from the parent plant with different degrees of dormancy. Frequently, the variation in dormancy is reflected by the appearance of the seeds or dispersal units in terms of color, size, and thickness of the coat. (2) Through the dependence of dormancy breakage on environmental factors. (3) Through seed dispersal via animals, wind or water (reviewed in Bewley et al., 2013). A classical concept of seed dormancy was formulated by Harper (1957) who distinguished three types: (1) Seeds born as dormant (innate); (2) Those with achieved dormancy (induced); and (3) Seeds with dormancy thrust upon them (enforced). Moreover, Harper distinguished two categories of plants living in a community; those which are growing at present and those which are dormant (in the form of a soil seed bank). A problem in distinguishing dormancy-relieving factors from factors stimulating or initiating germination is that the actual state of dormancy cannot be measured directly (Thompson and Ooi, 2013). Vleeshouwers et al. (1995) defined dormancy as: “a seed characteristic, the degree of which defines what conditions should be met to make the seed germinate” (Vleeshouwers et al., 1995). Consequently, seeds of many species that form a persistent seed bank exhibit annual changes in dormancy (Karssen, 1982; Milberg and Andersson, 1997). This phenomenon of dormancy cycling (Baskin and Baskin, 1985) is regulated by various factors such as temperature. Moreover, the intensity of dormancy within a given species varies at several levels: among populations, within populations and between seeds collected in different years from the same population (Foley, 2001; Lacerda et al., 2004). There is also heterogeneity in dormancy among seeds at the level of the individual plant (reviewed in Matilla et al., 2005), depending on the age and the nutritional status of the mother plant during seed maturation, seed position on the mother plant, seed size and shape, the time since seed harvest, and the duration of seed storage (Probert, 2000). Despite of all this variation, seed dormancy has a clear genetic basis (Graeber et al., 2012). Several dormancy classes were defined by Nikolaeva (1969, 1977) and more recently reviewed by Finch-Savage and Leubner-Metzger (2006). Morphological dormancy refers to seeds that have an underdeveloped embryo and require longer time to grow and germinate. Physiological dormancy, the most prevalent form of dormancy, appears to broadly involve abscisic acid (ABA) and gibberellins (GAs) metabolism. In addition, there are morphophysiological and combinational dormancies. In contrast to hormone-mediated seed dormancy, extensively studied in *Arabidopsis* or cereals, we have still limited knowledge of the regulation of physical dormancy, which involves the development of a water-impermeable seed coat (Baskin et al., 2000). This type of dormancy is found in at least 17 plant families, including agronomically important families like the Fabaceae, Malvaceae, Cannaceae, Geraniaceae, and Convolvulaceae (Baskin et al., 2000) and is present in the wild progenitors of cultivated legumes

(Dueberrn de Sousa and Marcos-Filho, 2001; Zohary et al., 2012; Abbo et al., 2014).

Germination begins with water uptake (imbibition) by the quiescent dry seed and is completed by radicle protrusion through the tissues surrounding the embryo. There are three phases of seed imbibition. Dry seeds have very low water potentials, which causes rapid water influx during phase I. As this process is driven by water potential, it also occurs in dead seeds. Similar phenomena can be observed in resurrection plants and pollen. The permeability of the testa, being the part of the seed that comes into contact with the ambient water, plays a central role in water uptake. Phase II encompasses the rupture of the testa, and during phase III endosperm rupture and radicle protrusion occur (Finch-Savage and Leubner-Metzger, 2006). Germination occurs when embryo growth overcomes the constraints imposed by the seed coat (Bewley et al., 2013).

In nature, exposure to high temperature or fluctuating temperatures is the most likely cause of release from seed dormancy. The interactions between seed dormancy mechanisms and accumulated and current environmental conditions determine whether and what fraction of seeds in a seed bank will germinate at a given time. Weather and soil physical characteristics largely determine the microclimate to which seeds are exposed. The most critical environmental factor is water. Seeds imbibe water from their surroundings, and the water potential of the soil determines the maximum water potential that the seeds can attain. Seed banks may be composed of seeds from different years, which experienced different after ripening- or dormancy-breaking regimes, resulting in multiple subpopulations with different dormancy characteristics. Temperature is the second most important environmental determinant of seed germination. In extreme cases this is associated with fire (Hanley and Fenner, 1998) or vegetation gaps that are hotter than the surrounding forest soils (Vázquez-Yanes and Orozco-Segovia, 1982). Moreover, water and temperature regimes interact and also light plays a role in the onset of germination via regulation of phytochrome activity. Other factors include oxygen and other gasses. Dependence on exogenous factors for the initiation of germination suggests that physically dormant seeds should be limited in their ability to spread germination risk over multiple time periods or “recruitment opportunities” (reviewed in Bewley et al., 2013). However, in a few taxa the responsiveness of seeds to dormancy-breaking cues varies seasonally (Karssen, 1982), which suggests temperature, rainfall and perhaps deciduous tree leaf-drop as key factors. In summary, seasonal germination patterns are largely controlled by the seeds’ responses to prevailing environmental factors, such as moisture, temperature, light, and various chemicals in conjunction with seasonal environmental factors (e.g., chilling, after-ripening) that sensitize the seeds to the environment.

LEGUME SEED COAT (TESTA) DEVELOPMENT AND STRUCTURE

The angiosperm seed develops from the fertilized ovule and depending on the stage of development is usually composed of (1) the embryo, arising by fertilization of the egg cell by one of the pollen tube nuclei; (2) the nutritive tissue of the endosperm, generated by the fusion of two polar nuclei of the embryo sac with the

other sperm nucleus; and (3) a protective seed coat (testa), derived from the inner, outer or both ovular integuments (Bradford and Nonogaki, 2009).

THE SEED COAT TISSUE COMPONENTS

The origin of the seed coat can be traced back to the L1 sporophyte layer of the ovule primordium (Schneitz et al., 1997) with an emerging network of regulatory pathways coordinating growth of the inner and/or outer integuments surrounding the ovule (Skinner et al., 2004; Galbiati et al., 2013; Kurdyukov et al., 2014). The number of ovule integuments varies depending on the species; legumes have two integuments (bitegmic ovules). The inner integument largely vanishes during development (Esau, 1965) while the outer one produces several distinct cell layers and establishes the “typical” seed coat structure. The chalazal region is an important part of the testa where connections of the vascular tissues of the maternal funiculus terminate. The scar where the funiculus was attached is called hilum (**Figure 1B**). Current seed identification criteria are based upon morphological characteristics including seed size, general shape, surface shape, color, pattern, hilum length and width. These are often used in taxonomical classifications (Lestern and Gunn, 1981; Chernoff et al., 1992; Güneş, 2013) and archeobotany (Zohary et al., 2012). Legume seed characters support the concept of one family (Fabaceae) as advocated already by de Candolle (1825). Although the seed coats of different species vary greatly in structure and composition, they undergo similar phases of development in relation to the embryo and endosperm (Butler, 1988). In legumes, the seed coat and endosperm develop first, followed by development of the embryo (Weber et al., 2005).

In spite of some known exceptions such as peanut (*Arachis hypogaea*) with lignified pod or *Archidendron* and *Pithecellobium*, which have a partly pulpy and edible testa (Gunn, 1981), there is a rather common blueprint of seed coat structure for the Fabaceae family (Lush and Evans, 1980). Interspecific variation comprises mainly the patterns of differentiation, dimensions, and modifications of cell walls of individual layers. There are a number of publications in this area (Pammel, 1899; Rolston, 1978; Lush and Evans, 1980) with considerable emphasis on economically important soybean.

THE OUTER INTEGUMENTS

The epidermis of the outer integument forms a single layer of tightly packed palisade of radially elongated sclereids (called Malpighian cells, macrosclereids, or palisade cells) with heavily and unevenly thickened cell walls (**Figure 1A**). The outer tangential cell walls are covered with cuticle and, because of specific cell wall thickening and modifications, they are commonly described as terminal caps. Their shape together with cuticle and waxy depositions determine the texture of the seed coat surface (Güneş, 2013). The architecture of this layer and the structure of its cuticle attract considerable attention as their properties are generally related to water-impermeability of hard seeds (White, 1908; Hamly, 1932, 1935; Riggio Bevilacqua et al., 1989; Argel and Paton, 1999). The cuticle forms a continuous layer covering the seed, except for the hilum, and is considered the outermost barrier to imbibition (White, 1908; Spurny, 1963; Ma et al., 2004;

Shao et al., 2007). Interestingly, the chemical composition of soybean cuticle seems to differ in fatty acid composition from the shoot cuticle (Shao et al., 2007). Its continuity, being a crucial feature of hardseededness, might be compromised by the emergence of cracks during seed expansion and development (Ranathunge et al., 2010). In some legume species, such as soybean, the seed surface is also modified by secretory activity of the fruit (pod) wall (Yaklich et al., 1986) which might deposit hydrophobic proteins on the cuticle (Clarkson and Robards, 1975; Gijzen et al., 1999).

THE SCLEREID LAYERS

There is frequently a lucent region of macrosclereid cell walls separating macrosclereid terminal caps from their basal parts. This border line, which extends transversally across the macrosclereid layer is named light-line or *linea lucida* (**Figure 1A**) in many species. Its appearance derives from local variation in refractive indices and stainability attributed to the modifications in polysaccharide deposition and/or impregnation of this cell wall region (Hamly, 1935; Harris, 1983; Bhalla and Slattery, 1984; Bevilacqua et al., 1987). The strength of the light line was related to seed coat impermeability (Stevenson, 1937; Harris, 1987). The lumen of macrosclereids is usually irregular and tapered toward the seed coat surface due to prominent cell wall thickening. Macrosclereids differentiation was followed in cytological detail in pea (Spurny, 1963; Harris, 1983), soybean (Harris, 1987), and clover (Algan and Büyükkartal, 2000). The length of macrosclereids seems to be under environmental control in soybean (Noodén et al., 1985). Unevenly distributed pores (pits) in soybean seed coat develop during the desiccation phase (Yaklich et al., 1986; Vaughan et al., 1987) and the presence of such cracks, pits and other irregularities on the seed coat surface, seems to be related to its water permeability (Wolf et al., 1981; Yaklich et al., 1986; Ma et al., 2004). A subepidermal layer of cells is differentiated into osteosclereids (bone-shaped cells), also termed by different authors columnar or pillar cells, hourglass cells or lagenosclereids (flask-shaped cells) depending on the shape of the cells. This layer includes conspicuous air-filled intercellular spaces (**Figure 1A**) resulting from cell shaping during testa differentiation and massive cell wall deposition in the middle part (Harris, 1983; Miller et al., 2010). Osteosclereids are the first major cell types during testa differentiation where cell death was detected, followed by parenchyma and macrosclereids (Ranathunge et al., 2010). In and around the hilum, the layer of osteosclereids merges with thick-walled, star-shaped parenchyma (**Figure 1C**). Continuity of the intercellular spaces may be related to seed desiccation and gas exchange.

THE PARENCHYMA OR NUTRIENT LAYER

The innermost part of the seed coat is composed of parenchyma cells (**Figure 1A**), which are elongated in tangential direction and result in abundant air-filled intercellular spaces. Frequently there are 5–12 cell layers of parenchyma with the inner layer in direct contact with the endosperm (Hamly, 1932, 1935). Some authors call the parenchymatous region “nutrient layer” owing to its function during embryo development (Van Dongen et al., 2003). The seed coat vascular systems are embedded into parenchyma layers and their structures vary amongst legumes; some species possess an extensive vascular systems that anastomose to form reticulated

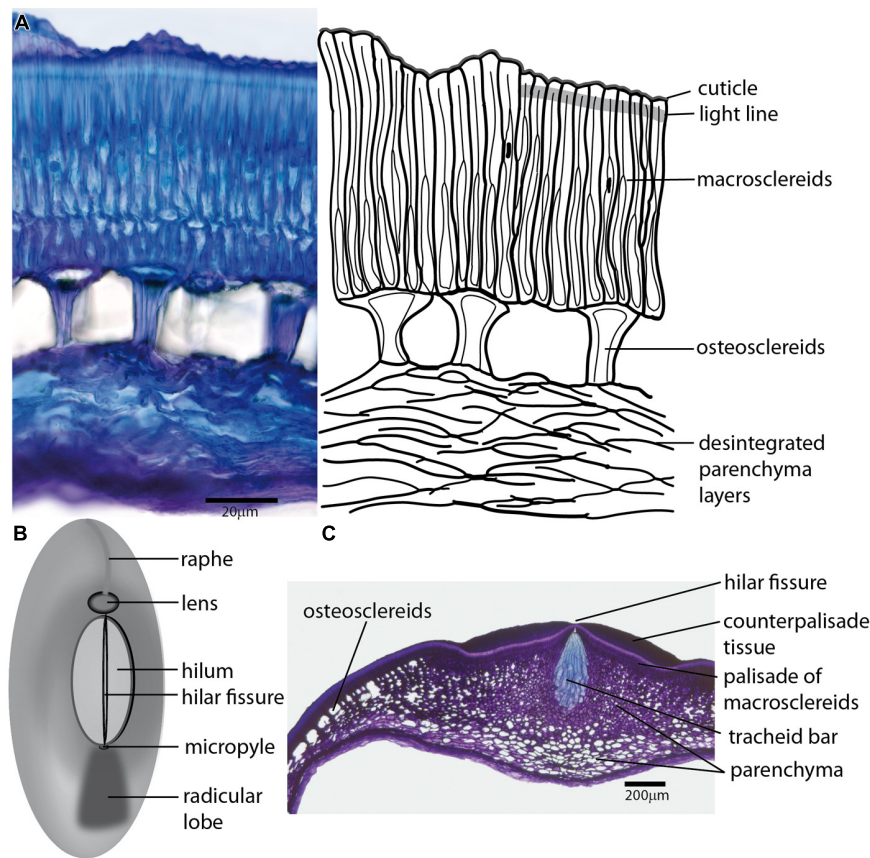


FIGURE 1 | The arrangement of Fabaceae seed coat share rather common structural features. (A) Transversal section of the seed coat of wild *Pisum sativum* subsp. *elatius* (left), with a schematic drawing (right); epidermal cells differentiate into macrosclereids, which are characterized by a cuticle-covered surface. The outer parts of the macrosclereids (sclereid caps) are frequently separated by a region of the cell wall (light line) with specific features, resulting in different optical and staining properties. The central part of the testa differentiates into osteosclereids with a specific shape caused by thickened secondary cell wall. The innermost layers of parenchymatous cells

frequently die during differentiation and only disintegrated fragments are left. **(B)** Generalized scheme of the seed coat morphology commonly found in Fabaceae seeds showing the most important structural features, including the hilum, lens differentiated on the raphe and micropylar pore. **(C)** Transversal section of a *Pisum sativum* seed coat in the area of the hilum. The macrosclereids of the hilum scar are covered with counter palisade tissue with a central fissure above the tracheid bar, which is surrounded by star-shaped parenchyma interconnected to intercellular spaces of a layer of osteosclereids.

networks throughout the entire seed coat (e.g., common bean, Offler and Patrick, 1984; soybean, Thorne, 1981), while other species have relatively simple vascular systems, with only a single chalazal vascular bundle and two lateral branches extending into the seed coats (e.g., pea, Spurny, 1963; Hardham, 1976; broad bean, Offler et al., 1989). During seed coat maturation, parenchyma cells lose the protoplast and the innermost layers might be crushed. Parenchyma layers are not generally related to water-impermeability. However, high callose levels in this layer might be related to low permeability of clover seed coat (Bhalla and Slattery, 1984), but a causal relationship remains to be determined.

THE MICROPYLE AND HILUM

The anatomical structure of the testa is rather homogenous except for the chalazal region (Figure 1B). The hilum is a distinctly oval or round abscission scar in the chalazal seed region, a relic of former connection of the seed to the maternal plant via the funiculus. There is another residual layer of palisade cells of funicular origin

termed counter-palisade, which are part of the hilum scar (Lackey, 1981). There is a central fissure (hilum groove) in the hilum palisade layer overlaying the tracheid bar (Figures 1B,C) from the micropyle to the ovular bundle on the other side. This strip of large, pitted and lignified tracheids is commonly found in legumes although there is some variability in structure and ovular bundle position (for more detail see Lersten, 1982). A role for the hilum groove as a hygroscopically activated valve was suggested (Hyde, 1954; Lush and Evans, 1980). The fissure in the hilum opens when relative humidity is low permitting the seed to dry out whereas high relative humidity causes the fissure to close preventing the absorption of moisture.

THE LENS (STROPHIOLE)

The micropyle, an entrance pore for the pollen tube (Figure 1B), is inconspicuous on mimosoid and casealpinoid seeds but is discernible (often of different color) on faboid seeds (Gunn, 1981). In some species, there is a residue of the micropylar opening covered

with a waxy lid (Vaughan et al., 1987). Specific outgrowth of raphe termed lens (strophiole) on the other side of the hilum (**Figure 1**) might be obvious in some species (Lersten and Gunn, 1982; Lersten et al., 1992). This structure is considered to act as a water gap (Baskin et al., 2000; Hu et al., 2009; Karaki et al., 2012) that might be open by external (e.g., heat, mechanical action, temperature variation; Baskin, 2003; Van Assche et al., 2003) or internal factors (Rolston, 1978; Argel and Paton, 1999). The palisade cells of the lens region are modified, narrower, longer and more variable than in the rest of testa. A loosely arranged cell structure on the lens-side of the hilum, a deeply grooved hilar fissure, and a narrow tracheid bar were considered to be associated with high initial water absorption in some common bean and *Psophocarpus* seeds (Deshpande and Cheryan, 1986).

Functionally, the main effects exerted by the tissues surrounding the embryo are: (1) the interference with water uptake, (2) mechanical restraint to radicle protrusion, (3) inference with gas exchange, (4) prevention of inhibitor leakage from the embryo, (5) supply of inhibitors to the embryo and (6) light penetration in species in which light plays a role in germination (Werker et al., 1979; Nowack et al., 2010; Bewley et al., 2013).

COORDINATED GROWTH OF THE THREE SEED COMPONENTS

The coordinated growth of the inner and outer integuments, which ensures that the ovule is surrounded by protective tissues, is regulated by several locally expressed transcription factors (TFs), which were first identified in *Arabidopsis* (Skinner et al., 2004). The integuments are initially undifferentiated, but rapidly undergo changes to produce a complex structure that protects the embryo and sustains its growth. In fact, differentiation of the seed coat from the ovular integuments includes some of the most dramatic cellular changes observed during seed development. Early seed coat development from the time of anthesis to seed maturation has been well described in soybean (Miller et al., 1999), pea (Van Dongen et al., 2003), *Medicago truncatula* (Wang and Grusak, 2005), and faba bean (Offler et al., 1989; Offler and Patrick, 1993; Borisjuk et al., 1995), and shows a relative homogeneity in term of ontogeny and final structure. During early legume seed development, the embryo and endosperm develop within the seed coat. The endosperm and embryo divide in parallel, with the endosperm occupying a larger volume until the beginning of seed filling or maturation, when the endosperm begins to degenerate and the embryo cells expand to accumulate storage products. Importantly, early embryo development and differentiation are controlled by the surrounding maternal tissue, and signals from the maternal plant must be transmitted through the seed coat and endosperm before they can reach the embryo. A model for the maternal control of embryo development through sugar metabolism that implicated seed coat invertases has been developed in legumes (reviewed in Weber et al., 2005). In *Arabidopsis*, mutations of the endosperm-specific LRR kinase HAIKU or the WRKY transcription regulator MINISEED3 result in limited growth of the endosperm, which in turns affects cell elongation in the seed coat resulting in smaller seeds. Conversely, mutation of the maternally expressed TF TTG2 restricts cell elongation in the seed coat, which limits endosperm growth. Whether homologous genes play a role in legume seeds remains to be shown.

DEVELOPMENT AND ACCUMULATION OF MAIN COMPONENTS OF THE TESTA

The different seed coat cell layers have three main physiological functions: (1) Production, transport, and download of metabolites for zygote development, including metabolite inter-conversions, transport of photosynthetic assimilates and photosynthesis, (2) synthesis and deposition of defense-related compounds, both phytoalexins and structural components, and (3) establishment of physical dormancy and mechanical protection. Seed coat development and structure in soybean and *Medicago truncatula* share some traits that differ from those of *Arabidopsis* (Miller et al., 1999; Wang and Grusak, 2005). Whereas *Arabidopsis* epidermal cells produce and secrete large quantities of mucilage, soybean and *Medicago* epidermal cells do not and show extensive cell wall thickening (Russi et al., 1992). The innermost seed coat cell layer, the endothelium, is a metabolically active cell layer and is the main site of synthesis of proanthocyanidins (PAs). In the *Arabidopsis* mature seed, a brown pigment layer (bpl) forms between the inner integument 1 (ii1) and the outer integument 1 (oi1) cell layers as a result of compaction of several parenchyma cell layers (Beeckman et al., 2000). The endothelium has been described in soybean (Miller et al., 2010) and was microdissected for transcriptomic analysis (Le et al., 2007). In faba bean, this layer has been termed thin-walled parenchyma (Miranda et al., 2001). Because the aleurone remains at maturity and is crushed against the innermost layer of the seed coat, it is often considered as part of the seed coat (Miller et al., 1999; Moïse et al., 2005). However, differences in their development and more importantly in their origin (maternal for the seed coat vs. zygotic for the aleurone) make these two tissues distinct entities with specific roles during seed development.

Seed coat development is tightly regulated, and several tissues present during embryogenesis and seed filling will not persist at maturity or will undergo important modifications. This is particularly true for the parenchyma layers derived from the inner ovular integuments, which proliferate and then collapse and are crushed (Miller et al., 1999; Nadeau et al., 2011). In pea, three parenchyma sub-layers can be distinguished during testa development: chlorenchyma, ground parenchyma, and branched parenchyma. Starch transiently accumulates in the plastids of these cell layers, the young seed coats being a transient storage organ for carbohydrates and proteins (Rochat and Boutin, 1992). A dramatic and transient expansion of the branched parenchyma occurs during the filling period followed by its complete compression and the formation of a boundary layer between the seed coat and the filial tissue (Van Dongen et al., 2003; Nadeau et al., 2011). In pea and common bean, branched parenchyma is the site of expression of extra-cellular invertases, and it has been suggested that the degradation of this layer initiates the storage phase through a switch from high to low ratios of hexose to sucrose in the developing seeds (Weber et al., 1997; Van Dongen et al., 2003). Important cellular changes are also observed in the testa outer cell layers and in specific cell wall thickening. Sclereids are characterized by extensive secondary cell wall formation and are usually non-living at maturity with a callose-rich wall area running parallel to the edge of the seed coat (Bhalla and Slattery, 1984; Serrato Valenti et al., 1993; Ma et al., 2004). In common

bean, cell vacuoles of the thick-walled epidermal cells are often completely filled with tannins, indicating that the macrosclereid cells play a key role in hardening of the seed coat (Algan and Büyükkartal, 2000). The contrasting cellular fates above are related to different functional requirements during the course of development: nutrient transport and metabolism to sustain embryo growth during embryogenesis and seed filling and physical and structural requirements as the seed matures to insure protection.

OMICS ANALYSIS: TOWARD A GLOBAL GENE ACTIVITY PROFILE OF SEED COAT DEVELOPMENT

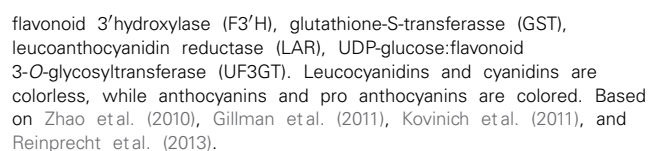
In general, development of the seed coat has not been characterized at the molecular level to the extent of the embryo and endosperm (Thompson et al., 2009). Transcriptomic and proteomic analyses have been used to dissect the molecular mechanisms underlying the development of the three major seed tissues, including the maternal seed coat in the legume model *Medicago truncatula* (Gallardo et al., 2007; Pang et al., 2007; Verdier et al., 2008) and in soybean (Le et al., 2007; Ranathunge et al., 2010; Miernyk and Johnston, 2013). Seed coat transcriptome and proteome were shown to be highly correlated in *Medicago* and quite distinct from that of the embryo or endosperm (Gallardo et al., 2007). Results highlighted a metabolic interdependence of these three seed components during seed filling, with certain metabolic steps or enzymes being restricted to a particular tissue. An example is several proteases specifically produced in the seed coat that may be important to provide amino acids for protein synthesis within the embryo (Gallardo et al., 2007). Similarly, seed coat specific TFs acting during early seed filling when seed coat and endosperm are active in supplying nutrients to the developing embryo were identified (Verdier et al., 2008) and could represent master regulators of seed coat development and function. More recently, a combined histology and transcriptomic analysis of the *Medicago* seed coat was performed (Verdier et al., 2013a) and a regulatory network-based analysis of transcriptome profiles during *Medicago truncatula* seed maturation was carried out (Verdier et al., 2013b). At 4 to 6 days after pollination (DAP), arrest of cell division occurs, which is compensated by cell elongation in the expanding seed coat. This cell size increase was associated with endopolyploidy and supported by transcriptomics data showing over-expression of “nucleotide metabolism” class genes. In addition, laser capture microdissection and transcriptional profiling were used to identify genes expressed in different sub-regions of soybean seeds (Le et al., 2007; <http://seedgenenetwork.net/soybean>). Transcriptomic data are not only available for nearly mature seed coat layers (hourglass, palisade, parenchyma) but also for the inner and outer integuments during early seed coat development, providing a source of candidate genes for further functional analyses.

POLYPHENOLIC COMPOUNDS BIOSYNTHESIS AND ACCUMULATION

The PAs, oligomers of flavan-3-ol units, have received particular attention due to their abundance in seed coats (Dixon et al., 2005; Zhao et al., 2010). PAs are also known as the chemical basis for tannins, polymeric flavonoids that comprise part of the broad and diverse group of phenolic compounds that plants produce as secondary metabolites (Winkel-Shirley, 2001). These are synthesized

in the inner integument or endothelium layer. PA biosynthesis and its regulation have been dissected in *Arabidopsis* using *transparent testa* (*tt*) mutants, which regulate production, transport or storage of PAs (Lepiniec et al., 2006), and 20 genes affecting flavonoid metabolism were characterized at the molecular level (reviewed in Bradford and Nonogaki, 2009). Most notably, a set of three types [(TT2, a myeloblastosis family of transcription factors (MYB) protein family member; TT8, a basic-helix-loop-helix (bHLH) proteins; and TTG1, a WD40 protein)] of TFs was characterized that interact to regulate transcription of anthocyanidin reductase (ANR; **Figure 2**), a key enzyme producing the epicatechin building block of PAs (Baudry et al., 2004). Many of these flavonoid biosynthesis pathway genes have been found to affect dormancy of *Arabidopsis* seeds, indicating the role of pigments in this process (Debeaujon et al., 2000). Whether these genes play a similar role in legume seeds remains to be shown. Tannins are also important nutritionally because they can complex with several minerals and proteins in the gastrointestinal lumen, reducing the absorption, digestibility and availability of these nutrients (Brune et al., 1989). In *Medicago truncatula*, seed coat-expressed genes involved in PA biosynthesis and transport (**Figure 2**) have also been identified (Pang et al., 2007; Zhao and Dixon, 2009; Zhao et al., 2010), and two genes implicated in the regulation of PA biosynthesis have been isolated, a WD40-repeat TF (Pang et al., 2009) and a MYB family TF (Verdier et al., 2012).

Legumes vary in the types of PA monomers that are polymerized to form tannins (**Figure 2**). The best studied *Medicago truncatula* PAs are composed primarily of epicatechin and/or catechin units (which yield cyanidin on hydrolysis), with much lower levels of epigallocatechin or galocatechin (yielding delphinidin) and epiafzelechin or afzelechin (yielding pelargonidin) units. In lentils, there is a balance between catechin and galocatechin units; and the polymer fraction was more abundant than the monomer and oligomer fraction (Dueñas et al., 2003). In contrast, common beans had mainly catechin monomers (60% on average) in their seed coat tissue, with minor and variable amounts of galocatechin and afzelechin (Díaz et al., 2010). Other genes affecting PA deposition play roles in the differentiation of the endothelium layer (Dean et al., 2011). This layer is for the most part a single cell layer, but in *Arabidopsis* limited periclinal divisions were observed in the micropylar region (Debeaujon et al., 2003). Interestingly, in *Arabidopsis*, PA accumulation begins in the micropylar region of young seeds approximately at the two-cell stage of embryo development, progressing through the seed body, and ending in the chalazal end at the heart stage of embryo development, a process reminiscent of the asynchronous differentiation of endosperm during seed development. The availability of an endothelium-specific promoter (*BANYULS* gene of *Arabidopsis*) permitted (Debeaujon et al., 2003) testing the effect of the ablation of this cell layer using a promoter:Barnase fusion. The seed, which completely lacked the pigment layer, remained viable, while embryo, and endosperm development were not being obviously affected, but testa-imposed dormancy was reduced. However, other mutants acting earlier (pre-fertilization) on the formation of the integument layers, do affect, or even prevent, seed development (Schneitz et al., 1997; Mizzotti et al., 2012). The



In common bean, the roles of seed coat color pattern genes such as *Bip* (*bipunctata*) and *Z* (*zonal*) genes in the accumulation of tannin also suggest that tannin first accumulate in the seed coat tissues nearest the hilum (Caldas and Blair, 2009). Patterned seeds require a *t/t* genotype for expression of a partial color, whereas a *T/-* genotype gives seeds that are totally colored. The types (form and extension) of colored patterns are then controlled by the interaction of the *t* gene with the two previously mentioned *Z* gene for patterned color expression on the testa, plus the genes *L* (*limiter*) and *J* (*joker*) which were found to be allelic to each other (Bassett, 1994, 2002, 2007). Finally, the *Z* gene is allelic with the *D* gene, which specifically determines hilum color (Bassett, 1999). Outside the legume family, 10 species were evaluated for condensed tannins in the hilum including species where no tannins were found in other regions of the seed coat (Marles and Gruber,

2004). The hilum is known to be the point of attachment of the seed to the placental tissue of the ovary, but it also is the place where seed water uptake often begins, a portion of the seed that would need to be protected by tannins which have roles as antifungal metabolites. Notably, white beans, which lack any coloration, usually have no tannins or very low tannin levels and are more susceptible to root rots and other diseases (Ma and Bliss, 1978; Guzmán-Maldonado et al., 1996).

In soybean, six independent loci (*I*, *T*, *R*, *Wp*, *Wl*, and *O*) control the color and distribution of pigments (Bernard and Weiss, 1973; Palmer and Kilen, 1987; Gillman et al., 2011). The best characterized *I* locus (for *inhibitor*, encoding chalcone synthase) inhibits the production and accumulation of anthocyanins and PAs in the epidermal layer of the seed coat (Bernard and Weiss, 1973). An allelic series for the *I* gene is present in soybean, where the absence of pigmentation is controlled by the dominant allele at the *I* locus, whereas the homozygous recessive *ii* genotype produces a totally pigmented seed coat, and the alternate *i¹* allele results in pigmentation of the hilum (Tuteja et al., 2004). Most cultivated soybean varieties are homozygous for the *I* gene, resulting in a yellow seed coat. To date, eight chalcone synthase genes have been identified in soybean, all expressed in seed coat (reviewed in Moïse et al., 2005). Chalcone synthase is the first enzyme of the branched pathway of flavonoid biosynthesis (Figure 2), and it plays a role in the synthesis of secondary metabolites functioning as UV protectants, phytoalexins, insect repellents, and symbiosis initiators in various plant tissues. Another locus, *T*, affects pubescence and hilum colors, and it induces seed coat cracking. It encodes flavonoid 3'-hydroxylase, which is necessary for the formation of quercetin from kaempferol (Figure 2) and is responsible for the hydroxylation of the 3' position of flavonoids, leading to the production of cyanidin pigments (Zabala and Vodkin, 2003). The *Wl* locus controls flower color and affects seed color only in an *iRT* background, where *Wl* and *wl* alleles give imperfect black and buff seed coat colors, respectively. The *Wl* allele encodes flavonoid 3',5'-hydroxylase (Zabala and Vodkin, 2007) and causes purple flower. The *Wp* locus was suggested to code for the flavanone 3-hydroxylase (Figure 2) based on microarray analysis (Zabala and Vodkin, 2005), where the recessive *wp* allele resulted in change from black (*iRTWp*) to light grayish (*irtwp*) color. The *O* locus affects the color of brown seed coat (*irTO*) and has been suggested to code for ANR (Yang et al., 2010). Finally, the *R* locus controls the presence (*R*) or absence (*r*) of anthocyanins in black (*iRT*) or brown (*irT*) seed coat, respectively (Nagai, 1921). The up-regulation of anthocyanidin synthase genes suggests that the *R* locus codes for a regulatory factor (Kovinich et al., 2011). Comparably less is known about pigmentation in pea, especially in relation to the testa. Mendel's *A* gene, conferring pea flower color and testa pigmentation, has been recently identified as a bHLH TF, exerting thus pleiotropic effects on flower, leaf axils and testa pigmentation (Hellens et al., 2010). However, these traits can be genetically uncoupled, e.g., pea with colored flowers can have nearly non-pigmented seed coat (Smýkal, unpublished). The *b* gene of pea was shown to encode a defective flavonoid 3',5'-hydroxylase, conferring pink flower color (Moreau et al., 2012). However, none of these two mutations result in alteration of seed dormancy, since they have been identified in cultivated pea lines.

Also in lupin, besides the hard-seeded gene *Mollis*, the blue flower and dark seed color gene *Leucospermus* (Clements et al., 2005) confers domestication trait. Although truly wild *Vicia faba* has not identified, a locus was found to be involved in seed dormancy (i.e., *doz*) linked to a locus controlling anthocyanin and pro-anthocyanidin synthesis (i.e., *sp-v*; Ramsay, 1997). Finally, in *Trifolium subterraneum* seeds, a relationship between color, phenolic content and seed coat impermeability was found (Slattery et al., 1982).

OTHER SEED COAT COMPOUNDS INVOLVED IN PROTECTION

Besides pigments, several active enzymes have been isolated from the legume seed coat. Chitinases were isolated from soybean and are expressed late during seed development (Gijzen et al., 2001). They have been suggested to play a role in plant defense against fungal pathogens (Schlumbaum et al., 1986). Peroxidase is a major component of the protein fraction in mature soybean seed coat where it accumulates in the hourglass cells of the epidermis. Initially involved in the synthesis or modifications of extracellular polymers such as lignin or suberin, peroxidase is believed to have a function in defense when released from the hourglass cells during seed imbibition (Moïse et al., 2005). Furthermore, polysaccharides, such as galactorhamnans, are present in the innermost layer of jack bean (*Canavalia ensiformis*) seeds, and are effective against seed beetles (Oliveira et al., 2001). A well-documented barrier for preventing water entry via the seed coat is suberin accumulation (Nawrath, 2002). Suberin is composed of two distinct types of insoluble polyesters of fatty acid and glycerol. Suberin has been found in the pea testa (Spurny, 1964). Genetic evidence shows that suberin deposition controls seed permeability (Beisson et al., 2007), and glycerol-3-phosphate acyltransferase (GPAT) gene candidates for a role in suberin biosynthesis have been identified in soybean (Ranathunge et al., 2010), *Medicago truncatula* (Verdier et al., 2013a), *Arabidopsis*, and *Melilotus* (Liang et al., 2006; Beisson et al., 2007).

ROLE OF SEED COAT IN SEED DEVELOPMENT

Thorne and Rainbird (1983) developed a method, adopted by several groups, for measuring phloem unloading from seed coats by excising the immature embryo and recovering assimilates unloaded into the embryo sac. Legume seed coats were thus shown to play a critical role in the lateral transfer of assimilates and other nutrients, prior to their release to the developing embryo (Lush and Evans, 1980; Offler and Patrick, 1984, 1993). The seed coat supplies the zygote with water and oxygen, minerals, certain phytohormones including ABA and IAA, and C and N assimilates in the form of sucrose and amino acids unloaded from the phloem terminals. Further, the legume seed coat is the site of inter-conversions of the principal amino acids unloaded from the phloem, asparagine and aspartate, via asparaginase and aminotransferases, to a composition better adapted for storage protein accumulation, before unloading into the embryo sac (Murray and Kennedy, 1980; Lanfermeijer et al., 1992). Similarly, sucrose is partly hydrolysed by extracellular invertases prior to entry into the embryo sac, contributing to the maternal control of legume seed development (reviewed in Weber et al., 2005).

Cell wall invertases promote assimilate unloading by increasing the sucrose concentration gradient in the unloading zones of the legume seed coat. The glucose released promotes embryo cell divisions, determinant of final seed size (Weber et al., 1997). Solute transfer is also facilitated by the differentiation of specialized transfer cells located in the coat parenchyma or cotyledon epidermis, i.e., at the interface between the seed coat and the embryo (Thompson et al., 2001), as found in the epidermis of faba bean and pea embryos (Bonnemain et al., 1991). Transfer cell development is accompanied by the increased expression of a sucrose- H^+ transporter gene. Both cell differentiation and gene expression have been suggested to be induced by signals coming from the maternal seed coat or to be elicited by tissue contact. Auxin, ethylene and reactive oxygen species (ROS) have been proposed as inductive signals for transfer cell differentiation (reviewed in Andriunas et al., 2013).

In addition to the production of PAs and other defense-related compounds, the seed coat is an important source of phytohormones for the developing seed, either synthesized *in situ*, or transported from the mother plant. In pea, Nadeau et al. (2011) analyzed GA content and transcript abundances of major enzymes of the GA biosynthesis pathway and studied the consequences of their inactivation in the three seed tissues during development. The results are consistent with a key role for GA in orchestrating seed coat differentiation via the production and turnover active GA forms in the seed coat during early and mid-phase seed development. In legume seeds, cytokinin (CK) concentrations are low (Slater et al., 2013), with a maximum during embryogenesis and at the beginning of the filling stage. Highest CK levels within the seed are found in the seed coat and in the liquid endosperm (Emery et al., 2000). Calculations of CK delivery rates from transport fluids to seeds suggest that CK is synthesized *in situ* in the seed coat and/or endosperm (Emery et al., 2000). CK was proposed to promote cell division and thus enhance sink strength, increasing solute unloading from the seed coat (Quesnelle and Emery, 2007). Auxin and its conjugated form IAA-Asp play essential roles in controlling pattern formation in the developing legume embryo, and were shown to be the major hormones present in the embryo during the early stage of development (Slater et al., 2013). In the Fabaceae tribe of legumes, 4-chloro auxin is the predominant auxin species (Reinecke, 1999). Seed-produced auxin is also transported to the pericarp, where it coordinates pod development with that of the seeds (Ozga et al., 2009; Park et al., 2010).

Abscisic acid accumulates within legume seed (Liu et al., 2010; Slater et al., 2013), and genes involved in ABA biosynthesis were found to be expressed during seed filling in *Medicago truncatula* seed coat, suggesting it could be a source of the hormone (Verdier et al., 2013a). ABA is required for the seed maturation program, acting via the “master regulator” TFs to control storage and late embryogenesis accumulating (LEA) protein deposition and the acquisition of desiccation tolerance (Verdier et al., 2013b). Seed coat-mediated dormancy in *Medicago truncatula* requires ABA (Bolingue et al., 2010), probably produced by maternal seed tissues, as shown in tobacco by the reciprocal crosses of *aba* mutants, defective in ABA synthesis (Karssen et al., 1983; Frey et al., 2004). Developmental signals often result from interactions between two or more hormones. Hence fertilization-stimulated

auxin production modulates synthesis of active GA (Dorcey et al., 2009), and the ratio of ABA:GA modulates seed filling (Liu et al., 2010). Liu et al. (2012) found a positive correlation between ABA and IAA concentrations and seed filling rate when comparing varieties of contrasting seed size.

ROLE OF SEED COAT IN IMPERMEABILITY TO WATER STRUCTURAL ASPECTS

In soybean, an anatomical study showed that the only features consistently correlating with seed coat permeability to water were small cuticular cracks (Ma et al., 2004). These cracks were present in soft but not hard seeds (within the studied cultivated genotypes). The initial penetration of water into soft seeds typically occurred on the dorsal side, the location of the majority of the cracks (Ma et al., 2004). Besides anatomical differences, chemical analysis resulted in the identification of a seed coat cutin with unusual chemical composition, lacking typical mid-chain hydroxylated fatty acids but being relatively rich in other types of hydroxylated fatty acids (Shao et al., 2007). The cuticle of the impermeable soybean cultivar (again, no wild soybean was studied) contained a disproportionately high amount of hydroxylated fatty acids relative to that of the permeable ones. According to the results of Shao et al. (2007) and those of Ma et al. (2004), the difference between hard and soft soybean seeds was based on the composition and continuity of the outermost seed cuticle and the presence of small cracks in the cuticles of the latter. The differences in chemical composition were rather subtle, and the authors speculated that crucial elasticity of soybean cuticle might be related to its association with carbohydrates (Ranathunge et al., 2010).

The site of water entry into the seed coat is still a matter of debate (Meyer et al., 2007; Ranathunge et al., 2010). Various explanations were proposed to account for the different permeability of the seed coats to water in hard and soft seeds including tightly bound palisade cells (Corner, 1951; Ballard, 1973), thickened seed coat tissues (Wyatt, 1977; Miao et al., 2001), lack of pits (Chachalis and Smith, 2001), presence of endocarp deposits (Yaklich et al., 1986), dark color (Wyatt, 1977), closed hilum and/or micropyle (Hyde, 1954; Ballard, 1973; Rolston, 1978; Hu et al., 2009), modifications of the outer tangential walls of palisade cells (Werker et al., 1979), a prominent light line of the palisade cells (Harris, 1984, 1987), presence of water gaps in the lens (Dell, 1980; Hanna, 1984; Serrato Valenti et al., 1986, 1989, 1993; Serrato-Valenti et al., 1995; Van Staden et al., 1989; Shen-Miller et al., 1995; Morrison et al., 1998; Baskin et al., 2000; Burrows et al., 2009; Hu et al., 2009), as well as cracks in the cuticle of the seed coat (Morrison et al., 1998; Hu et al., 2009). In some legume species, such as *Vigna*, *Robinia*, *Acacia*, and many tropical and sub-tropical legume species (Karaki et al., 2012), water enters the seed a specialized structures such as the hilar slit and water gap (e.g., strophiole or lens; Gopinathan and Babu, 1985; Kikuchi et al., 2006) opens. The morphological characteristics of these water gaps can vary between species. It is thought that water gap structures act as an environmental sensor to fine-tune germination to coincide with an environment that provides the best chance for seedling survival and ecosystem colonization. Water gaps are usually associated with areas of the seed coat where natural openings in the ovule occurred during the seed

development such as the hilum, micropyle, and chalaza. Although the soybean seed coat composition and structure are modified at the hilum and micropyle areas, these are thought not to contribute to the initial uptake of water (Ma et al., 2004). Instead, in soybeans, water mainly enters through small cracks in the seed coat to reach the embryo (Chachalis and Smith, 2000). There is some controversy on this issue, since other studies have suggested water uptake through the hilum (McDonald et al., 1988). In a related Phaseoleae tribe, the hilum, micropyle and lens have been proposed to be water entrance points for example, in *Phaseolus lunatus* (Korban et al., 1981) and *Phaseolus vulgaris* (Agbo et al., 1987).

In subfamilies Caesalpinioideae and Mimosoideae, cracks develop in the extrahilar region or in the hilum that allow water to enter the seed (Gunn, 1984, 1991; Hu et al., 2009). The hilum of faboid seed, except in flattened seeds, has a separation in palisade cells called the hilar groove (Lhotská and Chrtková, 1978), which is a diagnostic botanical feature. Hyde (1954) reported that this groove acts as hygroscopic valve, that prevents water entry from the outside but permits water to leave seed interior during maturation and drying. The seed coat becomes impermeable as drying occurs. Since the seed remains dry until released from dormancy, it has the potential to remain viable for many years. Seed dormancy not only prevents immediate germination, but it also regulates the time, conditions, and location where germination will occur.

The occurrence of precocious germination under humid conditions indicates that seeds can become germinable prior to maturation drying. There are contrasting results concerning whether some degree of drying is required for switching seeds from dormant to a germinative mode. Prior to desiccation, the seed undergoes developmental changes and mostly anabolic metabolism associated with formation of the embryo and its surrounding structures and the deposition of the major storage reserves. Following desiccation and rehydration, seed metabolism becomes largely catabolic to support germination. Thus, for most desiccation-tolerant (orthodox) seeds, including legumes, maturation drying clearly switches the seed to a germination mode upon subsequent rehydration. Desiccation-intolerant (recalcitrant) seeds can effect this switch without dehydration, as can orthodox seeds developing inside fleshy fruits (tomatoes, melons), having the capacity to germinate without maturation drying. However, premature removal of the seeds from the fruit inevitably severs the maternal connections. In the case of common bean and soybean seeds, it was reported that fresh developing seeds are unable to germinate without prior dehydration. On the other hand, it was found that *Phaseolus* seeds near the end of the seed filling period are capable of germinating within the fruit with their funicular connection intact if water was injected into the pods. To survive in dry state (with less than 10% moisture content on a dry-weight basis), a seed has to avoid damage to its cellular components, both during water loss and upon subsequent rehydration. Damage does occur, but is limited to a level that can be repaired and that involves accumulation of non-reducing sugars (sucrose, trehalose), oligosaccharides (raffinose) and other solutes such as proline, glycinebetaine (cited in Bewley et al., 2013). In addition to these metabolites, large number of LEA proteins, including dehydrins and heat shock

proteins (HSPs), are expressed, both responding positively to ABA.

SEED COAT PIGMENTATION AND DORMANCY

Seed coat pigmentation was shown to correlate with imbibition ability in several legumes. Browning of seed coat during maturation was found to be associated with its impermeabilization in common bean (Caldas and Blair, 2009; Díaz et al., 2010), chickpea (Legesse and Powell, 1996), yardlong bean (Kongjaimun et al., 2012), soybean (Liu et al., 2007), faba bean (Ramsay, 1997), and pea (Marbach and Mayer, 1974; Werker et al., 1979).

The genes or quantitative trait loci (QTLs) for seed color and loss of seed dormancy in azuki bean (*Vigna angularis*) were shown to be closely linked, and there is a significant correlation between these two traits (Isemura et al., 2007). A positive correlation has also been found between phenolic content, the activity of catechol oxidase and seed dormancy in wild pea seeds (Werker et al., 1979). Recently, epicatechin, cyanidin 3-O-glucoside, and delphinidin 3-O-glucoside were specifically isolated in wild but not in cultivated soybean seed coats, with epicatechin showing a significant positive correlation with hardseededness (Zhou et al., 2010). Combined analysis of seed coats of black vs. brown isogenic lines of soybean, indicated over-accumulation of anthocyanins, altered procyanidin, and reduced flavonol, benzoic acid, and isoflavone content in black seeds, as a result of altered transcription of numerous biosynthetic pathway genes (Kovinich et al., 2011). Increased β -1,3-glucans (callose) deposition in cell walls during maturation is associated with increased dormancy in a number of species (Finch-Savage and Leubner-Metzger, 2006), while β -1,3-glucanases, which break down callose are associated with dormancy release. Other soluble phenolic compounds, such as coumarin and chlorogenic acid, and their derivatives, or ferulic, caffeic, sinapic acids occur in the coats of many seeds. These may inhibit seed germination and could be leached out into the soil where they may inhibit neighboring seeds (a form of allelopathy). Phenolic compounds of legume seeds, however, participate in nodulation by acting as chemoattractants, promoting rhizobial growth, and inducing transcription of nodulation genes in symbiotic bacteria (Mandal et al., 2010).

GENETICS OF LEGUME SEED DORMANCY

Seed dormancy is a monogenic trait in lentil (Ladizinsky, 1985), narrowleaf lupin (Forbes and Well, 1968), yardlong (Kongjaimun et al., 2012), rice bean (Isemura et al., 2010), mungbean (Isemura et al., 2012), associated with one to two loci in common bean (Koinange et al., 1996), and two to three loci in pea (Weeden, 2007). In this last case, control of seed dormancy was via testa thickness, testa impregnation and structure of the testa surface. In azuki bean (Isemura et al., 2007; Kaga et al., 2008), four to six QTLs were associated with field germination, time of germination, testa permeability, winter survival of seeds in the soil, days to germination of winter-surviving seeds in the field and water content in seeds. In recently (~100 years) domesticated lupin, *Lupinus angustifolius*, the hard-seeded gene *mollis*, and the blue flower and dark seed color gene *leucospermus* (Clements et al., 2005) are two of the key domestication traits. A molecular marker linked to the recessive *mollis* gene was discovered and applied to lupin

breeding (Boersma et al., 2007; Li et al., 2012), where wild material was used to provide new diversity. Interestingly, Ladizinsky (1985) found that two different monogenic systems operated in crosses of *Lens orientalis* and *Lens ervoides*, with cultivated lens, *Lens culinaris*. In the former, the allele for dormancy was dominant, but in the latter it was recessive. The gene for dormancy in *Lens orientalis* appeared to be linked to another one controlling pod shattering. Similarly, interspecific crosses between *Vicia sativa*, and a closely related species, *Vicia cordata* suggested a two-gene system (Donnelly et al., 1972). Breeding has allowed the development of soft-seeded summer and hard-seeded winter lines of *Vicia sativa* (cited in Büyükkartal et al., 2013). As mentioned earlier, the testa is of maternal origin. The maternal control is clearly demonstrated when a soft-seeded (e.g., with no or low testa imposed seed dormancy) plant is used as a female parent and crossed with a hard-seeded wild type. The F₁ seed is soft-seeded, and all the resultant F₂ seeds are hard-seeded, including those individual seeds possessing the homozygous soft-seediness genotype, as shown in lupin (Li et al., 2012).

DORMANCY-BREAKING REQUIREMENTS OF LEGUME SEEDS

Many legume seeds are known to be long-lived, and they are frequently found in seed bank surveys. *Melilotus* seeds survived for 17 years in the soil (Bibbey, 1948), seeds of *Malva rotundifolia* (Malvaceae) lived for 120 years in burial seed experiment (Telewski and Zeevaert, 2002) and seeds of *Astragalus distortus* germinated 24 years after sowing under near-natural conditions (Baskin and Baskin, 2014). The breaking of dormancy under natural conditions is only partly understood. As mentioned above, water and temperature are two principal environmental regulators of seed germination. In many ecosystems, fire is also an important factor and there is no doubt that germination is promoted by fire-induced heat treatment in species such as *Acacia* sp. in the legumes family (Sabiiti and Wein, 1987; Hanley and Fenner, 1998). It is not understood, however, how germination is regulated in ecosystems with a temperate climate, where fire occurs very rarely and where fluctuations in daily soil temperature are rather limited to a maximum of 10–15°C. Since temperature is relatively constant in its seasonal variations, it is arguably the most important environmental factor to synchronize seed germination with conditions suitable for seedling establishment. This is certainly valid for seasonal climate types, but in arid and semi-arid regions water may be the most important factor, whereas in the humid tropics variations in temperature and water availability appear to be virtually absent. For temperate regions species, germination in summer is accompanied by a higher risk of seedling loss due to drought or shading by leaf canopies, whereas in autumn the seedlings experience a reduced length of the growing period and risk frost damage (Probert, 2000). It has been proposed that hard seeds become permeable to water after mechanical abrasion by soil particles, decomposition of the seed coat by microbial action, ingestion and passage through the digestive tracts of an animal or by cracks in the coat caused by partial seed consumption, but little evidence is available to support these views (Gogue and Emino, 1979; Baskin and Baskin, 2000; Dueberrn de Sousa and Marcos-Filho, 2001; Fenner and Thompson, 2005). Hardseededness has been shown to protect seeds during the passage through the digestive tract (Simao

Neto et al., 1987), to extend seed longevity (Mohamed-Yasseen et al., 1994) and persistence in soil seed banks (Shen-Miller et al., 1995). Dalling et al. (2011) postulated that species with physical seed dormancy rely on physical defenses to exclude predators and pathogens. In this case, rapid seed germination cannot be used to escape pathogens at the emergence stage. Recently, it was proposed that hard seeds are an anti-predator trait that evolved in response to selection by small mammal seed predators (Paulsen et al., 2013). Seeds of two legume species with dimorphic seeds (“hard” and “soft”), *Robinia pseudoacacia* and *Vicia sativa*, were offered to desert hamsters. Volatile compounds released from imbibed seeds attracted the hamsters to the seeds, but the animals could not detect buried hard or dry soft seeds. Correlations between the dormancy release mechanism and ecological habitat were tested in four legume species (van Klinken and Goulier, 2013): two wetland species (*Mimosa pigra* and *Parkinsonia aculeata*), both dispersed primarily by water and two terrestrial species (*Acacia nilotica* and *Prosopis pallida*), both dispersed primarily through vertebrate herbivores. Seed viability was largely unaffected by temperature or moisture regime, although it differed with species and was lower for non-dormant seeds.

There are two steps in breaking physical dormancy with high temperatures. At first, the preconditioning phase will occur if seeds are at constant temperatures, and the rate at which this stage is completed increases with an increase in temperature. Seeds prevented from drying (by blocking the hilum) during the first stage are more likely to become water-permeable in the second stage than those that dehydrate further during stage one. The second stage (when seeds become permeable) requires fluctuating temperatures for maximum loss of dormancy (Baskin and Baskin, 2014). Taylor (1981) suggested that thermal degradation occurs during the first stage, which results in weakening of the lens. In the second stage, physical expansion and contraction associated with temperature fluctuations cause cells in the lens to open. There are also two steps in breaking dormancy by low winter temperatures, as found in temperate-zone species. Study of *Melilotus alba*, *Vicia villosa*, and *T. pratense* showed that during a first step, low winter temperatures make seeds sensitive to alternating temperatures, and during a second step, these alternating regimes occurring in early spring cause the sensitive seeds to become water-permeable. Further, cycles of germination (but not dormancy break) occur because spring temperatures might not be adequate to open the water gap of sensitive seeds. Thus, seeds may lose their sensitivity and have to go through another winter to become sensitive again. Seeds can only respond to alternating spring temperatures if they become sensitive during the winter (Baskin and Baskin, 2014).

The alternating temperatures that break the physical dormancy of a seed depend on the amplitude of the fluctuation. Clover (*T. subterraneum*) seeds become sensitive in response to temperatures that fluctuate between 30 and 60°C over a period of several weeks or months, the fluctuations occurring on open soils in Mediterranean-line climates, and subsequently their seed coats become permeable for water (Quinlivan, 1971; Taylor, 1981, 2005; Moreno-Casasola et al., 1994; Taylor and Ewing, 1996; Taylor and Revell, 1999, 2002; de Souza et al., 2012). The proportion of soft/hard seeds seems to vary from year to year (Roberts and

Boddrell, 1985), presumably as a result of climatic effects. The influence of seasonal factors on the germination of impermeable seeds of 14 herbaceous legume species was studied by Van Assche et al. (2003). Six species (*Medicago lupulina*, *Melilotus*, *Lotus*, *T. pratense*, *T. repens*, and *Vicia cracca*) showed a marked seasonal cycle with high germination rates in spring. *Medicago arabica*, *T. dubium*, and *Vicia sativa*, which are typical winter annuals, germinated mostly in summer and autumn, while *Lathyrus aphaca*, *Lathyrus nissolia*, and *Vicia hirsuta*, germinated in all seasons except summer (Van Assche et al., 2003). The importance of daily temperature fluctuations in breaking physical dormancy was shown for several legume species. The percentages of impermeable seeds of *Stylosanthes humilis* and *Stylosanthes hamata* begun to decline in northern Australian pastures in September (early spring) when mean monthly maximum and minimum temperatures were about 67 and 28°C, respectively. The number of dormant seeds decreased until December (early summer) when rains stimulate all permeable seeds to germinate. Dormancy was not broken from January to August, when daily maximum and minimum temperatures were less than 55 and 25°C, respectively (McKeon and Mott, 1982). Impermeable seeds of *Indigofera glandulosa* become permeable (Bhat, 1968) by exposure to high temperatures (up to 60°C). Impermeable seeds of *Lupinus digitatus*, *Lupinus luteus*, *Medicago trilobus*, and *T. subterraneum* subjected to alternating temperature regimes had highest germination rates under temperature regimes of 60/15°C for 4 months (Quinlivan, 1961). Dormancy loss was determined by the maximum daily temperature, provided there was a minimum daily temperature fluctuation of at least 15°C. The maximum daily temperatures required for loss of dormancy varies with the species: *T. subterraneum*, 30°C; *T. hirtum*, *T. cherleri*, *T. cernum*, 40°C; *Medicago truncatula*, *Medicago littoralis*, *Medicago polymorpha*, 50°C; and *Lupinus varius*, 60°C (Quinlivan, 1968). Such temperature fluctuations are prevented by seeds shaded by plant litter or by soil burial. Continuous moisture of substrate could be an important clue for some seeds to become water permeable. However, this factor has received comparably less attention in the literature. Several species did not imbibe seeds for long periods, up to 3 years for *Stylobasium spathulatum* among Surianaceae (Baskin et al., 2006). The seeds of *Acacia nilotica*, which grows along rivers in Sudan and Egypt and is subjected to flooding, imbibe and germinate at best when soaked for 18 weeks (prolonged submersion decreases germination rates again), which corresponds to the average duration of annual flooding periods (Warrag and Eltigani, 2005). There is also a promoting effect of seed burial in soil which could be related to increased moisture or microbial action (Baskin and Baskin, 2000). Testing of seed germination in presence or absence (using sterilized seeds) of microbes resulted in increase of germination for the former. This was most pronounced in *Vigna minima* seeds, which imbibed within 186 h in the presence of soil suspension but failed to do so in pure water for 30 days (Gopinathan and Babu, 1985). Similarly, passage through the animal's digestive tract, often results in better germination of impermeable seeds. It is assumed that it acts via acid enzymatic digestion of testa or mechanical scarification (cited in Baskin and Baskin, 2014). Interesting interaction was found between the *Acacia sp.* seeds, bruchid beetles that lay eggs on the seeds and mammals and birds that feed on

the seeds. Gazelles feed on pods of *Acacia sp.* in the Negev Desert of Israel and disperse the seeds, which have superior germination as a result. Moreover, the seeds infected with bruchid larvae germinate with higher rates (Halevy, 1974). Seeds containing a bruchid beetle larvae are more likely to germinate before the parasite destroys the embryo if seeds go through the digestive tract of an animal (Pellew and Southgate, 1984). On the other hand, these insect larvae cause substantial proportion of the otherwise water-impermeable seeds to imbibe and germinate, despite part of the seeds have destroyed embryo as shown for *Acacia sp.*, *Vicia sativa*, *Ulex europaeus*, and *Gleditsia japonica* (cited in Baskin and Baskin, 2014).

Some species produce heterogeneously colored seeds with different degrees of hardness. For example, the tree legume species *Senna obtusifolia* produces 90% hard-coat seeds with 10% soft-coat seeds (in Baskin and Baskin, 1998). 82–93% of the soft-coat seeds germinated, while only 15–32% of the hard-seed-coat ones germinated. This heterogeneity may be an important eco-physiological strategy, since soft-coat seeds can germinate in the spring in temperate regions, whereas hard-coat seeds cannot germinate until late spring–summer, when high temperatures cause an increase in seed-coat permeability. The seeds of the legumes *Adenocarpus decorticans*, *Astragalus granatensis ssp. Granatensis*, and *Cytisus reverchonii* (all endemic to the Betic Cordillera, Spain) collected at different altitudes, required different temperature for germination (Angosto and Matilla, 1993).

Several artificial techniques are used to break physical dormancy in seeds, including mechanical, thermal and chemical scarification, enzymes, dry storage, percussion, low temperatures, radiation and high atmospheric pressures (Baskin and Baskin, 2014).

LEGUME SEED DORMANCY AND DOMESTICATION

The development of agriculture was one of the key transitions in human history, and a central part of this was the evolution of new plant forms that were selected and became domesticated crops. The domestication of wild plants into crop plants can be viewed as an accelerated evolution, the result of both human and natural selection (Abbo et al., 2012, 2014). Domestication is often described as a quality in which morphological (and genetic) changes are found amongst cultivated plants in comparison to those in wild populations (Hancock, 2012; Zohary et al., 2012). These domestication-triggered changes represent adaptations to cultivation and human harvesting, accompanied by genetic changes. A common set of traits has been recorded for domesticated, but otherwise un-related crops, which collectively have been called the “domestication syndrome” (Harlan, 1971; Hammer, 1984). These traits are linked to successful early growth of planted seeds and include loss of germination inhibition and increase of seed size (Figure 3). Members of the Fabaceae have been domesticated in parallel with cereal domestications (Abbo et al., 2009). One of the major differences between the wild progenitors of Near Eastern grain legumes and cereals concerns the low germination rate imposed by the hard seed coat of these legumes (Ladizinsky, 1979, 1985; Werker et al., 1979; Abbo et al., 2009, 2014; Fuller and Allaby, 2009). Timing of seed germination is thus one of the key steps both in natural and agricultural ecosystems and

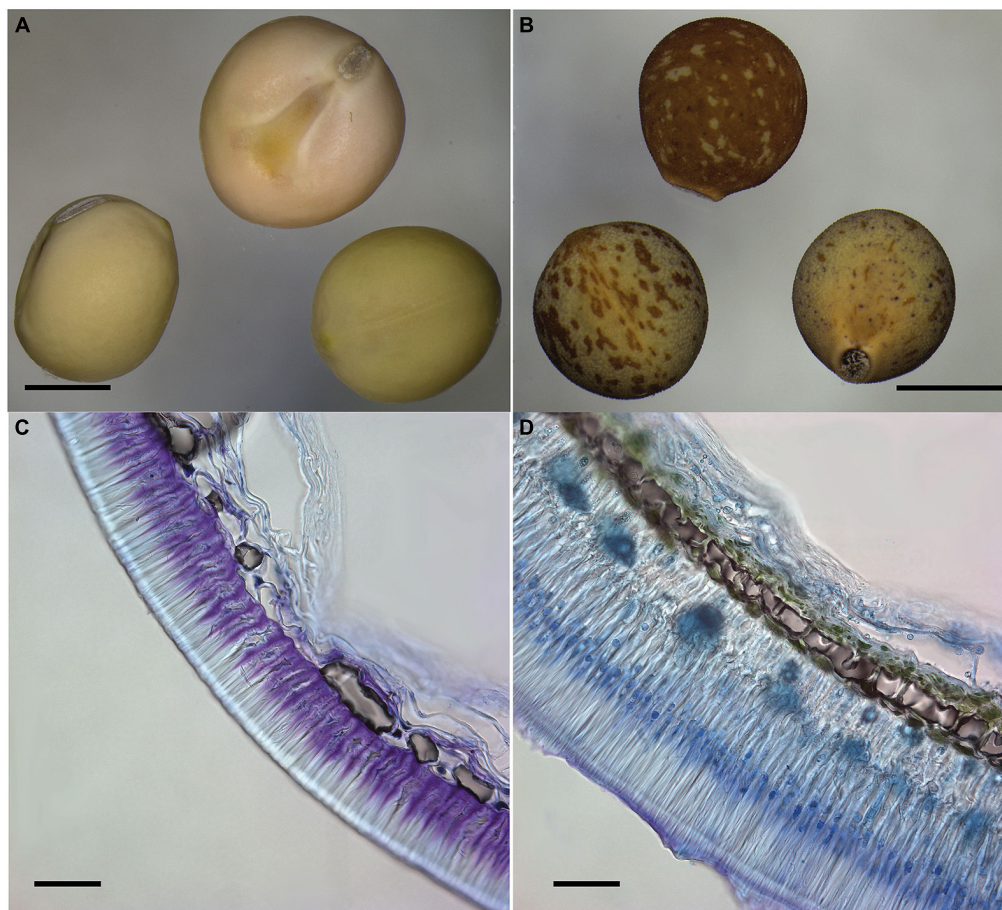


FIGURE 3 | Comparison of cultivated and wild pea seeds. Macrograph of modern cultivated pea cv. Cameor with transparent testa (**A**) and wild *Pisum sativum* subsp. *elatius* J164 with pigmented testa and visible rough (gritty)

testa surface (**B**). Scale bars = 3 mm. Transversal section of toluidine blue-stained seed coat of domesticated *Pisum sativum* cv. Cameor (**C**) and wild *Pisum sativum* subsp. *elatius* J164 (**D**). Scale bars = 50 μ m.

is a major factor for crop production. In contrast to wild species, crops tend to germinate as soon as they are imbibed and planted making seed dormancy a potentially unwanted trait. The selection acts on loss of dormancy during cultivation (Fuller and Allaby, 2009). Seed imbibition also has a crucial role in the ability of most grain legumes to undergo cooking. Hence, reduction of seed coat thickness has led to a concurrent reduction of seed coat impermeability. Ladizinsky (1987) argued that the very low germination rates in wild pulses, in particular lentil, would have precluded their successful cultivation on the basis of very low yields from planted seeds. He therefore suggested that hunter-gatherers must have selected wild mutants with quick germination for cultivation (Ladizinsky, 1987; Weiss et al., 2006). That germplasm could have been part of a “pre-cultivation domestication” process. The experimental harvest of wild lentils by Abbo et al. (2008) provided strong support for Ladizinsky’s (1985, 1987, 1998) arguments. This also holds true for peas, where intact wild seeds which have a germination rate of only 2.6–7% in a given year (Abbo et al., 2011, 2014). These results suggest that free germination was a more important trait for the domestication of wild pea (and possibly lentil and chickpea as well) than the mode of seed dispersal. However, too

low seed dormancy levels reduce seed quality and may trigger pre-harvest sprouting, which can occur in cereals. Therefore, seeds of crop plants require a well-balanced level of seed dormancy. Pre-harvest sprouting is rarely a problem in legume seeds since they are produced within a pod. Similarly, high-quality mungbean and common bean seeds are difficult to produce in humid tropical regions because of susceptibility to weather damage, which, however, can be mitigated by hardseededness (Hamphry et al., 2005). Whilst seed dormancy has been largely removed in grain legume crops, it remains in a number of important fodder crops and less domesticated species. Moreover, even in highly domesticated legume crops such as soybean, which has been selected for seeds that imbibe water rapidly and uniformly, some varieties produce some hard seeds (Rolston, 1978). This constitutes a major problem during food processing where rapid and uniform hydration is important for the production of quality foods.

CONCLUSION

The seed testa plays important roles in seed development and the beginning of a new plant generation. The seed coat provides not just structural and protective functions, but as discussed in

this review, has a decisive role in timing of seed germination of legumes by regulating water uptake. This control is fundamental under variable natural conditions where the establishment of young plants might influence the species evolutionary success. Such control was largely removed from domesticated crop plants, which are largely characterized by immediate seed germination. Moreover, water uptake allows us as well as early farmers, to cook and make legume seeds edible, thus providing important protein levels to the human diet. Although we have a good understanding of the genetic control of germination, we are just starting to identify the genes involved in this process. Although not formally demonstrated, the main testa pigments, PAs, are hypothesized to play a role in seed coat permeability. These pigments are also known as antioxidants with beneficial effects on human health, including cardioprotective, anticancer, and anti-inflammatory roles. These compounds also protect animals by binding to proteins in feed and slowing fermentation in the rumen, thereby reducing microbial production of methane.

Currently available analytical tools applied to a widening range of germplasm will help dissect germination in legumes more precisely. Detailed structural and chemical description of crop seed coats will provide the comparative basis for further studies and might lead to the identification of novel phenolic substances with potential health and nutritional benefits.

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Seed dormancy and germination—emerging mechanisms and new hypotheses

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Seed dormancy has played a significant role in adaptation and evolution of seed plants. While its biological significance is clear, molecular mechanisms underlying seed dormancy induction, maintenance and alleviation still remain elusive. Intensive efforts have been made to investigate gibberellin and abscisic acid metabolism in seeds, which greatly contributed to the current understanding of seed dormancy mechanisms. Other mechanisms, which might be independent of hormones, or specific to the seed dormancy pathway, are also emerging from genetic analysis of “seed dormancy mutants.” These studies suggest that chromatin remodeling through histone ubiquitination, methylation and acetylation, which could lead to transcription elongation or gene silencing, may play a significant role in seed dormancy regulation. Small interfering RNA and/or long non-coding RNA might be a trigger of epigenetic changes at the seed dormancy or germination loci, such as *DELAY OF GERMINATION1*. While new mechanisms are emerging from genetic studies of seed dormancy, novel hypotheses are also generated from seed germination studies with high throughput gene expression analysis. Recent studies on tissue-specific gene expression in tomato and Arabidopsis seeds, which suggested possible “mechanosensing” in the regulatory mechanisms, advanced our understanding of embryo-endosperm interaction and have potential to re-draw the traditional hypotheses or integrate them into a comprehensive scheme. The progress in basic seed science will enable knowledge translation, another frontier of research to be expanded for food and fuel production.

Keywords: chromatin remodeling, dormancy, embryo, endosperm, germination, hormone

INTRODUCTION

The ultimate role of seeds is to produce offspring and maintain species. Therefore, plants have evolved diverse strategies to ensure successful germination of this genetic delivery system. Proper distribution of seed germination, in both temporal and spatial manners, is critical for survival and proliferation of seed plants. Spatial distribution of germination is generally controlled through seed and fruit morphology, which enhances dispersal of the offspring from the maternal habitat. In contrast, temporal distribution of germination is controlled mainly by the physiological status of seeds. A variation among individual seeds in a population, in terms of physiological status, allows each seed to germinate at a different timing, which is an important strategy for seeds to avoid competition with their siblings or extinction of all individuals due to a disastrous condition. Plants have evolved seed dormancy, temporal suppression of germination under the conditions favorable to germination. Induction of seed dormancy during the maturation stage and its release at a dry state after a certain period of time, which is called “after-ripening,” are widespread phenomena observed in diverse species of seed plants (Bewley et al., 2013). There may be a universal mechanism of seed dormancy as well as a species-specific variation in the regulatory mechanisms.

Hormonal regulation may be a highly conserved mechanism of seed dormancy among seed plants. Induction and maintenance

of seed dormancy by abscisic acid (ABA) and dormancy release by gibberellin (GA) are observed in many species. The molecular mechanism of antagonistic function of these two hormones was unclear for many years. However, identification of the rate-limiting hormone metabolism genes, such as nine-*cis*-epoxycarotenoid dioxygenase (*NCED*), an ABA biosynthesis gene and *GA2ox*, a GA deactivation gene, and intensive analysis of their regulatory mechanisms in the last decade, have provided a comprehensive picture of ABA and GA involvement in the seed dormancy mechanisms (Seo et al., 2009). Now, we understand that seed response to light, which varies depending on species, is also controlled through hormone metabolism and signal transduction (Seo et al., 2009). Progress in seed dormancy and germination research is well summarized in recent review articles and textbooks (Graeber et al., 2012; Arc et al., 2013; Bewley et al., 2013). In this review, the main focus will be placed on the most recent discoveries from on-going research of seed dormancy and germination. Therefore, the contents of this review are not meant to be comprehensive but will highlight the “emerging” mechanisms and new hypotheses at the frontier of research.

EMERGING MECHANISMS OF SEED DORMANCY

Previously unknown seed dormancy-associated factors are emerging from on-going research, some of which enhance seed dormancy while others negatively affect it. The positive and

negative regulators of seed dormancy, which will be discussed in this section, are summarized in **Table 1**. There is a risk of over-simplifying gene function with the categorization of positive and negative regulators, because there are complex regulatory mechanisms of seed dormancy, in which a single gene product could exert both positive and negative effects, including negative feedback from a positive regulator. However, to highlight the discoveries of gene function in the original research, this categorization will be used for the discussion in this section.

POSITIVE REGULATION

***DOG1*—CENTRAL TO SEED DORMANCY BUT UNKNOWN FOR BIOCHEMICAL FUNCTION**

Quantitative trait locus (QTL) analysis using natural variation in *Arabidopsis* has identified the “seed dormancy-specific” loci, including the *DELAY OF GERMINATION* (*DOG*) genes (Alonso-Blanco et al., 2003; Bentsink et al., 2006, 2010), although some of them might not be strictly specific to dormancy (Chiang et al., 2013). One of them, *DOG1* has been characterized in detail. *DOG1* is expressed in seeds during the maturation stage. Loss of function of *DOG1* results in no dormancy (Bentsink et al., 2006). The genetic role of *DOG1* in seed dormancy and the significance of its expression in environment sensing and adaptation have been well documented (Kronholm et al., 2012; Footitt et al., 2013, 2014).

In contrast, the biochemical and molecular function of *DOG1* is still a mystery. *DOG1* encodes an unknown protein, for which only limited information is available. The *DOG1* cDNA shows highest similarity with a *Brassica napus* EST from an embryo library, however this gene also is not annotated. The protein with a known function that shows the highest similarity with *DOG1* is the wheat transcription factor Histone gene Binding Protein-1b (HBP-1b) (Bentsink et al., 2006). HBP-1b is a leucine zipper class transcription factor, which binds to the H3 hexamer motif ACGTCA in the promoter regions of wheat histone H3 genes (Mikami et al., 1989). This motif is required for transcription of the wheat H3 histone gene (Nakayama et al., 1989). *DOG1* has also been suggested to be a transcription factor, which is supported by its localization in the nucleus (Nakabayashi et al., 2012). However, the identity between *DOG1* and HBP-1b is not very high especially in the basic motifs and the heptad-repeat leucines in the leucine zipper structure (Tabata et al., 1991), which are conserved in HBP-1b and other H3 hexamer-binding proteins, such as tobacco Activation Sequence Factor-1 (ASF-1) (Lam et al., 1989) (**Figure 1**). Therefore, the biochemical function of *DOG1* is hardly predicted from its moderate similarity to HBP-1b. So far, direct target genes of *DOG1* that are clearly linked to the seed dormancy mechanisms have not been identified, although some dormancy up-(Dup) regulated genes [e.g., At5g43580 (*PR peptide*), At5g45540 (*unknown protein*), At5g45830 (*DOG1*), At5g47160 (*YDG/SRA domain-containing protein*)] or dormancy down-(Ddown) regulated genes [At4g19700 (*E3 ubiquitin ligase*), At5g04220 (*SYNAPTOTAGMIN3*), At5g46160 (*ribosomal protein*)] in the *DOG1* near isogenic line (NIL) have been identified (Bentsink et al., 2010).

POSSIBLE MODIFICATION AND PARTNERS OF *DOG1*

DOG1 transcript accumulates during the seed maturation stage with its peak around 14–16 days after pollination (DAP) (Bentsink et al., 2006), is reduced to about 20% in freshly harvested seeds, and disappears during imbibition (Nakabayashi et al., 2012). *DOG1* protein also accumulates during the maturation stage, however the protein level does not decrease toward the completion of seed maturation. As a consequence, freshly harvested seeds contain a relatively high level of *DOG1* protein. The protein level still remains relatively high even after 13 weeks of after-ripening when seed dormancy is already released (Nakabayashi et al., 2012). Thus, a correlation is lacking between the amount of *DOG1* protein and dormancy levels in after-ripened seeds. It has been proposed that the chemical property of *DOG1* protein, rather than its amount, is critical for *DOG1* to maintain seed dormancy and that its alteration to a non-functional form during after-ripening allows seed germination (Nakabayashi et al., 2012). In fact, there is a shift in the pI (isoelectric point) of the *DOG1* peptides prior to and following after-ripening (Nakabayashi et al., 2012).

Induction of *DOG1* in imbibed *dog1* mutant seeds with a heat-shock inducible system does not cause dormancy and allows 100% germination (Nakabayashi et al., 2012). This can be explained by the lack of protein modification discussed above. When *ABI5*, another key dormancy gene was overexpressed in *Arabidopsis* seeds, it was not sufficient to suppress germination. Only when the SnRK2 (Snf1-related protein kinase2), which activates *ABI5*, was induced in imbibed seeds, *ABI5* was able to suppress seed germination (Piskurewicz et al., 2008). Therefore, it is possible that the *DOG1* protein induced by the heat-shock system was missing necessary modification in the ectopic induction experiment.

Recently, a search for possible *DOG1* partners was conducted through a yeast two-hybrid screen, which identified multiple proteins, including the PDF1 protein phosphatase 2A (Miatton, 2012). *PDF1* expression is enriched in the vascular system of the embryo (Miatton, 2012), which mimics the *DOG1* localization (Nakabayashi et al., 2012). *PDF* expression has its peak around 16 DAP during the maturation stage and is reduced in mature seeds, which is similar to the *DOG1* expression mentioned above. Unlike the *dog1* mutant, the *pdf1* loss of function mutant exhibits an enhanced seed dormancy phenotype (Miatton, 2012), suggesting that *PDF1* is a negative regulator of seed dormancy and antagonizes *DOG1*. It is hypothesized that *DOG1* requires phosphorylation to be active, in terms of its function in seed dormancy induction and maintenance, and is dephosphorylated by *PDF1*, which could inactivate *DOG1* (Miatton, 2012). More analysis of *PDF1* and other *DOG1*-interacting proteins will potentially provide a breakthrough in seed dormancy research.

Regardless of posttranslational modification, an alternative hypothesis to explain the lack of seed dormancy in *DOG1*-induced *dog1* seeds is that *DOG1* functions mainly during the maturation stage and the *DOG1* protein contained in mature seeds might be residual. It is possible that *DOG1* affects seed dormancy through its effects on ABA levels during maturation (Nakabayashi et al., 2012). *DOG1* has been proposed to function in a pathway independent of plant hormones. However,

Table 1 | Seed dormancy associated genes described in this article.

Symbol	Gene name	Dormancy function	Related publications
<i>ABA1</i>	<i>ABA deficient 1</i>	Positive	Bentsink et al., 2006
<i>ABI3</i>	<i>ABA INSENSITIVE 3, 4, 5</i>	Positive	Zheng et al., 2012
<i>ABI4</i>		Positive	Liu et al., 2007
<i>ABI5</i>		Positive	Piskurewicz et al., 2008
<i>ACO1</i> <i>ACO4</i> <i>ACO5</i>	<i>1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE 1, 4, 5</i>	Negative Negative Negative	Wang et al., 2013
<i>AGO4</i>	<i>ARGONAUTE 4</i>	Negative	Singh and Singh, 2012; Singh et al., 2013
<i>ATXR7</i>	<i>ARABIDOPSIS TRITHORAX-RELATED 7</i>	Positive	Liu et al., 2011
<i>CYP707A</i>	<i>Cytochrome P450 707A</i>	Negative	Wang et al., 2013
<i>DEP</i>	<i>DESPIERTO</i>	Positive	Barrero et al., 2010
<i>DOG1</i>	<i>DELAY OF GERMINATION 1</i>	Positive	Bentsink et al., 2006, 2010; Nakabayashi et al., 2012
<i>ELF4</i> <i>ELF5</i>	<i>EARLY FLOWERING 4, 5</i>	Positive Positive	Liu et al., 2011
<i>ERF9</i> <i>ERF105</i> <i>ERF112</i>	<i>ETHYLENE RESPONSE FACTOR</i>	Negative Negative Negative	Wang et al., 2013
<i>GA3ox</i>	<i>GA3-oxidase</i>	Negative	Yano et al., 2013
<i>GA2ox</i>	<i>GA2-oxidase</i>	Positive	
<i>HD2B</i>	<i>HISTONE DEACETYLASE 2B, 6, 19</i>	Negative	
<i>HDA6</i> <i>HDA19</i>		Positive* Positive*	Wang et al., 2013
<i>HDAC1</i>	<i>HISTONE DEACETYLATION COMPLEX 1</i>	Negative*	Perrella et al., 2013
<i>HUB1</i>	<i>H2B MONOUBIQUITINATION 1</i>	Positive	Liu et al., 2007
<i>KYP</i>	<i>KRYPTONITE</i>	Negative	Zheng et al., 2012
<i>NCED4</i>	<i>NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 4, 9</i>	Positive	Wang et al., 2013
<i>NCED9</i>		Positive	Liu et al., 2007
<i>PDF1</i>	<i>PDF1 protein phosphatase 2A</i>	Negative	Miatton, 2012
<i>RDO2</i>	<i>REDUCED DORMANCY2 (=TFIIS)</i>	Positive	Liu et al., 2011
<i>RDO4</i>	<i>REDUCED DORMANCY2 (=HUB1)</i>	Positive	Liu et al., 2007
<i>Sdr4</i>	<i>Seed dormancy 4</i>	Positive	Sugimoto et al., 2010
<i>SNL1</i> <i>SNL2</i>	<i>SIN3-LIKE 1, 2</i>	Positive Positive	Wang et al., 2013
<i>SnRK2</i>	<i>Snf1-related protein kinase 2</i>	Positive	Piskurewicz et al., 2008
<i>SUVH4</i>	<i>SU(VAR)3-9 HOMOLOG4 (=KYP)</i>	Negative	Zheng et al., 2012
<i>TFIIS</i>	<i>Transcription elongation factor S-II</i>	Positive	Grasser et al., 2009
<i>VIP7</i> <i>VIP8</i>	<i>VERNALIZATION INDEPENDENCE 7, 8</i>	Positive Positive	Liu et al., 2011

*HDA6 and HDA9 are known to affect ABA sensitivity negatively, which could affect seed dormancy negatively.

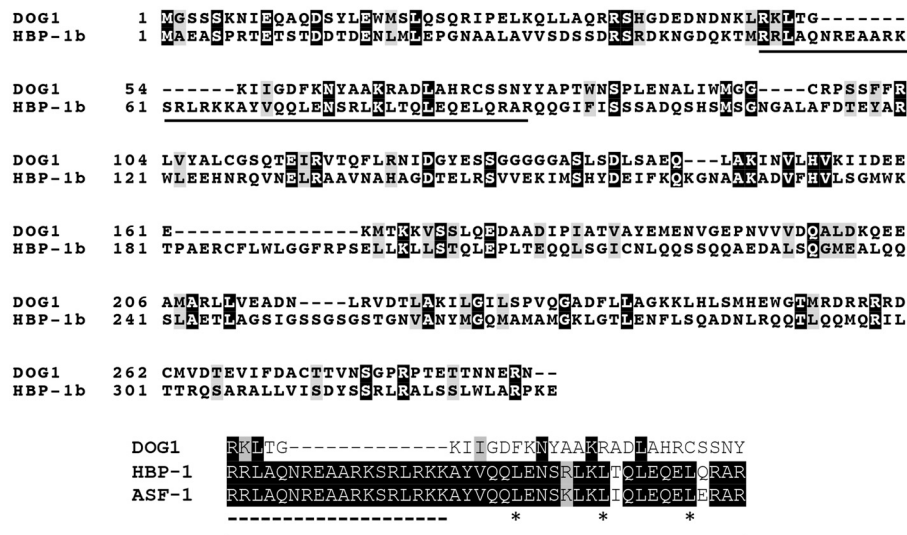


FIGURE 1 | Alignment of Arabidopsis *DOG1*, wheat HBP-1b and tobacco ASF-1. Arabidopsis *DOG1* (*DELAY OF GERMINATION1*) encodes an unknown protein, which shows some similarity to the wheat HBP-1b (Histone gene Binding Protein-1b), a leucine zipper class transcription factor (Bentsink et al., 2006). However, the *DOG1* protein does not show high identity to the leucine zipper domain in the HBP-1b (solid underline in the top

panel). This region (extracted as the bottom panel) contains the basic motifs (dashed underline) and the heptad-repeat leucines (asterisks) in the leucine zipper structure (Tabata et al., 1991), which are conserved among the wheat HBP-1b, tobacco ASF-1 (Activation Sequence Factor-1) and other leucine zipper transcription factors. Sequences were aligned using the ClustalW and boxshade programs (http://www.expasy.org/genomics/sequence_alignment).

DOG1 is not able to impose seed dormancy in *aba1-1*, an ABA-deficient mutant (Bentsink et al., 2006), indicating that *DOG1* function is dependent on ABA. ABA levels are reduced in *dog1* mutants while GA levels are enhanced (Bentsink et al., 2006; Nakabayashi et al., 2012), supporting the idea of possible links between the *DOG1* and hormone pathways in seed dormancy. More information is necessary to obtain a clear picture about the hormone dependent and independent pathways of seed dormancy. To date, induction of *DOG1* specifically at the right timing during seed maturation (14–16 DAP) has not been experimentally examined. Investigation of molecular consequences upon *DOG1* induction at the right timing, including gene expression, protein phosphorylation and epigenetic changes (discussed below), will provide useful information. It should be noted that there are other dormancy(-specific) genes recently discovered, such as *Seed dormancy 4* (*Sdr4*) in rice (Sugimoto et al., 2010) and *DESPIERTO* in Arabidopsis (Barrero et al., 2010), which were not discussed here. Those genes also appear to be central to the dormancy mechanisms and are important targets of seed dormancy research.

TRANSCRIPTION ELONGATION OF SEED DORMANCY GENES

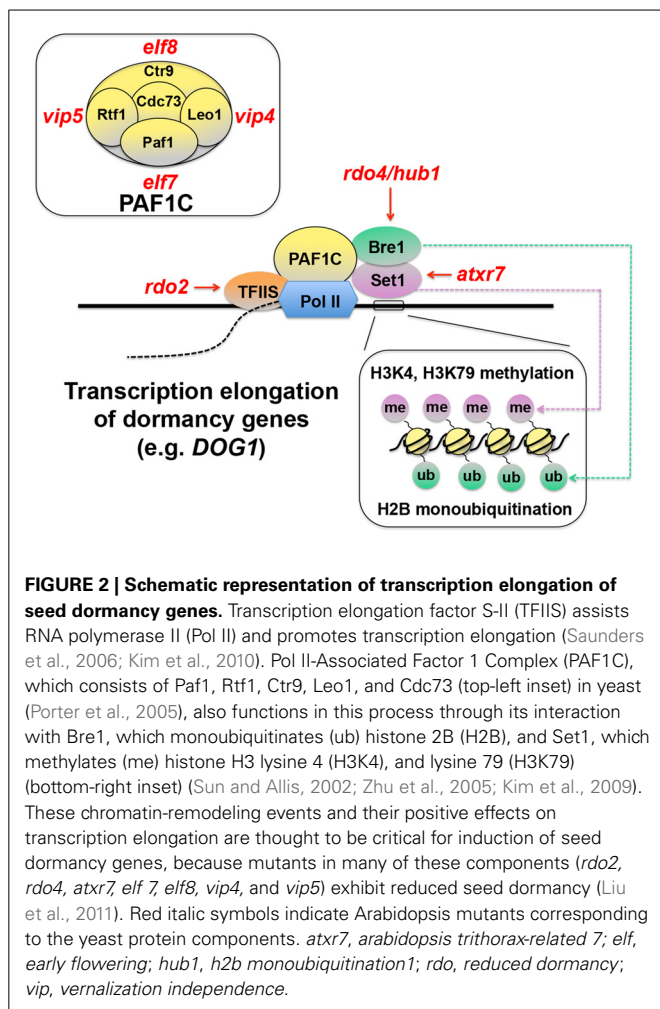
There is emerging evidence to suggest that regulation of transcriptional efficiency may be one of the core mechanisms of seed dormancy. Transcriptional efficiency is determined by recruitment of RNA polymerase II (Pol II) to the DNA template and the rate of transcription elongation after its binding to DNA. The efficiency of transcription elongation is influenced by an arrest of Pol II and its recovery from the arrest (Saunders et al., 2006). Transcription elongation factor S-II (TFIIS) assists Pol II to overcome the temporal arrest during elongation and enhances RNA

synthesis (Kim et al., 2010) (Figure 2). A mutagenesis screen for seed dormancy in Arabidopsis yielded *reduced dormancy* (*rdo*) mutants (Leon-Kloosterziel et al., 1996; Peeters et al., 2002). *RDO2*, one of the genes identified from this screening, encoded TFIIS (Liu et al., 2011). Another independent study also found that a mutation in *TFIIS* resulted in reduced seed dormancy (Grasser et al., 2009). These results suggest that transcription elongation may be a critical part of the dormancy mechanisms.

The phenotypes of other mutants also support this contention. TFIIS and Pol II interact with the Pol II-Associated Factor 1 Complex (PAF1C) (Kim et al., 2010) (Figure 2). In yeast, PAF1C consists of Paf1, Rtf1, Ctr9, Leo1, and Cdc73 (Penheiter et al., 2005; Porter et al., 2005) (Figure 2, top-left inset). The Arabidopsis orthologs of these yeast proteins EARLY FLOWERING7 (ELF7) (= Paf1), ELF8 (= Ctr9), VERNALIZATION INDEPENDENCE4 (VIP4) (=Leo1), VIP5 (= Rtf1) and PLANT HOMOLOGOUS TO PARAFIBROMIN (PHP) (= Cdc73) have been identified (Zhang and Van Nocker, 2002; He et al., 2004; Oh et al., 2004; Yu and Michaels, 2010). Seeds of the *elf7*, *elf8*, *vip4*, and *vip5* mutants all exhibit reduced dormancy (Liu et al., 2011), suggesting the importance of PAF1C and transcription elongation for seed dormancy.

HISTONE UBIQUITINATION AND METHYLATION ASSOCIATED WITH TRANSCRIPTION ELONGATION

PAF1C interacts with Bre1, a protein involved in histone 2B (H2B) monoubiquitination (Kim et al., 2009) (Figure 2). Interestingly, *rdo4*, another reduced dormancy mutant in Arabidopsis, which was isolated from the same mutagenesis screening as mentioned above, has a mutation in *H2B MONOUBIQUITINATION1* (*HUB1*) gene, an Arabidopsis ortholog of *Bre1* (Liu et al., 2007).



Bre1 interacts with Set1, which methylates histone 3 lysine 4 and lysine 79 (H3K4, H3K79) (Sun and Allis, 2002; Zhu et al., 2005) and promotes gene expression (Figure 2). A mutation in the *Set1* ortholog *ARABIDOPSIS TRITHORAX-RELATED 7* (*ATXR7*) also causes reduced dormancy in seeds (Liu et al., 2011). These results reinforce the idea that regulation of transcription elongation efficiency is an essential part of seed dormancy and suggest the significance of chromatin remodeling in the regulatory mechanisms.

H2B monoubiquitination and H3K4 and H3K79 methylation, which is dependent on H2B monoubiquitination (Nakanishi et al., 2009), are thought to activate gene expression (Henry et al., 2003). Since *hub1* (=bre1) seeds exhibit reduced dormancy, genes down-regulated in the *hub1* mutant are good candidates for seed dormancy-imposing genes, the expression of which is promoted through transcriptional elongation. *ABA INSENSITIVE4* (*ABI4*), *DOG1*, *NINE-CIS-EPOXYCAROTENOID DIOXYGENASE9* (*NCED9*) and other genes have been identified as possible targets of HUB1/RDO4 (Liu et al., 2007). *RDO2* (*TFIIS*) and *RDO4* (*HUB1*), two positive regulators of transcription are induced during the same stages of seed maturation (~18–19 DAP). There is a significant overlap

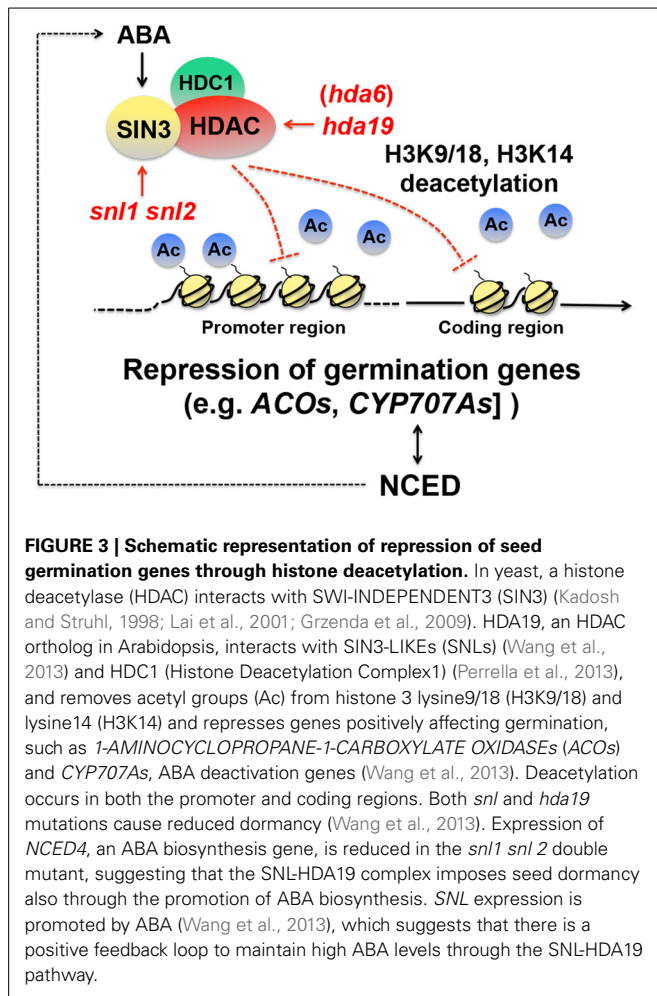
between *rdo2* and *rdo4*, in terms of differentially expressed genes in the mutants. These results suggest that RDO2 and RDO4 might share common targets. Intriguingly, *DOG1* is one of the genes commonly down-regulated in the two mutants (Liu et al., 2011). Activation of *DOG1* through chromatin remodeling and transcriptional elongation might be an important mechanism of seed dormancy.

The hypothesis that seed dormancy is regulated by the efficiency of transcription elongation of *DOG1* is also supported by the recent analysis of the *tfls* mutant, in which seed dormancy is reduced but reverted to the wild-type level by an extra copy of *DOG1* (Mortensen and Grasser, 2014). However, when the *hub1/rdo4* mutant is crossed with the NIL carrying *DOG1*-Cvi, which causes deep seed dormancy, the resulting seeds still show dormancy at a level between *hub1* and *DOG1*-Cvi NIL. Similar results are observed when the *hub1/rdo4* was transformed with the Cvi *DOG1* genomic fragment. The incomplete alleviation of dormancy from NIL *DOG1* by *hub1/rdo4* mutation in both cases suggests that *HUB1* is not epistatic to *DOG1*. In contrast, the combination of *hub1* and *DOG3*-Cvi resulted in no seed dormancy, suggesting that *HUB1* functions in the same pathway as *DOG3* to affect seed dormancy (Liu et al., 2007). More analyses of the specific targets of epigenetic modification and transcriptional elongation will be necessary to draw a clear picture about seed dormancy regulation through these processes.

REPRESSION OF SEED GERMINATION GENES THROUGH HISTONE DEACETYLATION

While activation of dormancy genes through transcription elongation appears to be critical for dormancy induction, continuous repression of seed germination-associated genes is also probably an essential part of dormancy maintenance. There is evidence that histone deacetylation is imperative for repression of genes positively affecting seed germination. In yeast and mammals, histone deacetylase (HDAC) interacts with SWI-INDEPENDENT3 (SIN3), an amphipathic helix repeat protein, removes acetyl groups from lysine in the histone tails, and creates a transcriptionally inactive state of chromatin (Kadosh and Struhl, 1998; Lai et al., 2001; Grzenda et al., 2009) (Figure 3). In Arabidopsis, SIN3-LIKE1 (SNL1) physically interacts with HDA19, an Arabidopsis HDAC ortholog, both *in vitro* and *in planta* (Wang et al., 2013). The Arabidopsis genome contains *SNL2*, which is partially redundant to *SNL1*. Seeds of the *snl1 snl2* double mutant exhibit reduced dormancy. A reduced dormancy phenotype is also observed in *hda19* mutant seeds (Wang et al., 2013). These results indicate that SNLs and HDA19 are positive regulators of seed dormancy. It appears that proper repression of the SNL-HDA19 targets, which are most likely germination-inducing genes, through histone deacetylation is essential for normal seed dormancy. Acetylation of H3K9/18 and H3K14 is increased in the *snl1 snl2* double mutant (Wang et al., 2013), which confirms that in wild-type seeds the SIN3-HDAC complex deacetylates histones and puts repressive marks on the chromatin (Richon and O'Brien, 2002) (Figure 3).

Global gene expression analysis between the *snl1 snl2* double mutant and wild-type seeds with RNA sequencing identified possible targets of SNL-HDA19. Ethylene biosynthesis



genes, such as *1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE1* (*ACO1*), *ACO4*, and *ACO5* and ethylene response genes, such as *ETHYLENE RESPONSE FACTOR9* (*ERF9*), *ERF105*, and *ERF112*, were up-regulated in the mutant (Wang et al., 2013). Quantitative PCR combined with chromatin immunoprecipitation with the H3K9/18 acetylation-specific antibodies showed that the *ACOs* and *ERFs* genes were indeed hyperacetylated in the mutant, which mainly occurred in the promoter region but were also found in the coding region (Wang et al., 2013). These results suggest that SNL-HDA19 causes seed dormancy by suppressing the ethylene pathway, which positively affects seed germination in Arabidopsis (Chiwocha et al., 2005; Arc et al., 2013).

In contrast, the same study suggests that SNL-HDA19 increases ABA levels and thereby enhances seed dormancy. *CYP707A1* and *CYP707A2*, ABA deactivation genes, which reduce ABA levels, were up-regulated in the *snl1 snl2* double mutants. Consistently, *NCED4*, an ABA biosynthesis gene, was down-regulated in the same mutant (Wang et al., 2013). These results suggest that SNL-HDA19 suppresses *CYP707As* and activates *NCED4* in wild type, both of which increase ABA levels and enhance seed dormancy. Interestingly, ABA stimulates *SNL1* and *SNL2* expression (Wang et al., 2013), which suggests that there

is positive feedback regulation to maintain high levels of ABA through the histone deacetylation pathway (**Figure 3**). While this study suggests that ABA levels are positively affected by SNL-HDA19, other studies suggest that ABA sensitivity is negatively regulated by HDA19 (and HDA6). Mutations in *HDA6* and *HDA19* cause ABA hypersensitivity during germination (Chen et al., 2010; Chen and Wu, 2010). Loss of function in Histone Deacetylation Complex1 (HDC1), another component of the SNL- and HDA19-containing complex, which physically interacts with HDA6 and HDA19 (**Figure 3**), also causes ABA hypersensitivity in seedlings. *HDC1* overexpression promotes seedling emergence (Perrella et al., 2013), although detailed information about *sensu stricto* germination and a dormancy phenotype of the mutant seeds is not available. The significance of the opposite effects of the HDAC multiprotein complex to ABA levels (positive) and sensitivity (negative) in the regulatory mechanisms of seed dormancy is not known. It is possible that the seemingly counterintuitive effects are associated with negative feedback regulation.

NEGATIVE REGULATION

REPRESSION OF DORMANCY GENES AND ACTIVATION OF GERMINATION GENES THROUGH HISTONE DEACETYLATION

HISTONE DEACETYLASE 2B (HD2B), another HDAC gene, is also involved in seed dormancy. In this case, it negatively affects seed dormancy (Yano et al., 2013). This discovery was made through a combination of genome-wide association mapping (GWA) (Atwell et al., 2010) and transcriptomics. The efficiency of QTL analysis using different accessions of *Arabidopsis*, such as Cvi, Ler, and Col, for seed dormancy is well exemplified by the successful identification and characterization of the *DOG* genes (Alonso-Blanco et al., 2003; Bentsink et al., 2006, 2010). Since the comparison of a few different *Arabidopsis* accessions is so powerful, multiplying this approach using many accessions with natural variations in seed dormancy is expected to produce fruitful outcomes in seed dormancy research, especially when it is combined with GWA, which identified a number of single nucleotide polymorphisms (SNPs) likely associated with various phenotypes (Atwell et al., 2010). Based on this concept, 113 accessions were analyzed to identify SNPs associated with natural variation in seed dormancy using GWA and transcriptomics, which identified *HD2B* as a strong candidate of a seed dormancy-associated gene. *HD2B* expression levels are significantly lower in 24 dormant accessions than 28 less-dormant accessions, although there are some exceptions. When the highly dormant Cvi line was transformed with the genomic fragment of Col *HD2B* (termed Col^{HD2B}/Cvi), mature seeds of Col^{HD2B}/Cvi exhibited reduced dormancy, which was not evident immediately after harvest without cold stratification but became clear when seeds were stratified or partially after-ripened (Yano et al., 2013).

Cold stratification releases seed dormancy through an increase in GA levels. *GA3ox1*, a rate-limiting GA biosynthesis gene, is induced by cold stratification (Yamauchi et al., 2004), which triggers expansion of cortex cells in the radicle/hypocotyl region and then generates growth potential of the embryo for germination (Ogawa et al., 2003). Evidence suggests that HD2B mediates this dormancy-releasing process. In ^{Col}*HD2B/Cvi* seeds, expression

of *GA3ox1* and *GA3ox2* and GA_4 levels are increased, while expression of *GA2ox2*, a GA deactivation gene, is reduced compared to wild-type Cvi seeds (Yano et al., 2013). Since HDAC represses gene expression through histone deacetylation, *GA2ox2* repression could be a direct effect of HD2B. In contrast, the up-regulation of *GA3ox* genes may be through repression of their upstream regulators or some other mechanisms. It is interesting that the three separate hormone pathways (ethylene, ABA, and GA) associated with seed dormancy are regulated by histone deacetylation. These results demonstrate that epigenetic regulation through chromatin remodeling is a robust mechanism to alter hormone levels in seeds.

SILENCING OF SEED DORMANCY GENES THROUGH HISTONE AND DNA METHYLATION

The studies mentioned above showed that HDAC could affect seed dormancy either positively (HDA19) or negatively (HD2B), depending on the target genes. Histone methylation also affects seed dormancy in both ways. While H3K4 and H3K79 methylation activates gene expression and causes seed dormancy as mentioned above (Set1 or ATXR7), dimethylation of H3K9 (H3K9me2), a repressive mark, occurs on the chromatin associated with seed dormancy genes. Analysis of gene silencing at the Arabidopsis *SUPERMAN* (*SUP*) locus identified the KRYPTONITE (*KYP*) methyltransferase, which causes H3K9me2 (Figure 4). The methylated histone recruits the DNA methyltransferase CHROMOMETHYLASE3 (*CMT3*) through its interaction with HETEROCHROMATIN PROTEIN1 (*HP1*) and triggers the methylation of cytosine nucleotides of DNA and silences the gene (Jackson et al., 2002; Johnson et al., 2007) (Figure 4). *KYP* is SU(VAR)3-9 (Rea et al., 2000) HOMOLOG 4 and is also called SUVH4. The *kyp-2* mutant seeds show enhanced dormancy, suggesting that *KYP/SUVH4* suppresses seed dormancy genes. Interestingly, again, *DOG1* is one of the up-regulated genes in the mutant, as well as *ABI3* (Zheng et al., 2012). These results suggest that histone methylation caused by *KYP/SUVH4* induces silencing of *DOG1* and *ABI3* through DNA methylation and negatively affects seed dormancy.

The *KYP-CMT3* gene-silencing pathway mediates RNA-directed DNA methylation (RdDM), which is triggered by small interfering RNAs (siRNAs) produced by DICER-LIKE3 (*DCL3*) and their loading onto ARGONAUTE4 (*AGO4*) (Zilberman et al., 2004; Tran et al., 2005) (Figure 4). AGO proteins are components of the RNA-induced silencing complex (RISC) and are involved in gene silencing. While AGO1 and AGO10 proteins function mainly in posttranscriptional gene silencing (PTGS) through the MIR (microRNA) and TAS (trans-acting siRNA) pathways, the AGO4/AGO6/AGO9 clade proteins are associated with transcriptional gene silencing (TGS) through RdDM (Mallory and Vaucheret, 2010). Little information is available for silencing of seed dormancy genes through RdDM, however a possible involvement of AGO4 in seed dormancy regulation has been suggested from studies of cereal seed dormancy. *AGO1003*, an ARGONAUTE (*AGO*)4_9 gene in barley, is expressed differentially in the embryos of dormant and non-dormant grains and is thought to function as a negative regulator of seed dormancy through RdDM (Singh and Singh, 2012). A separate study

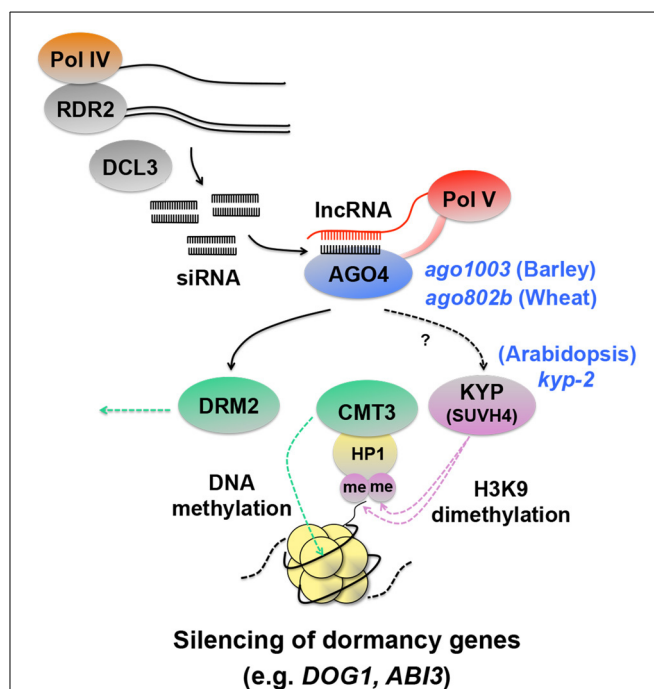
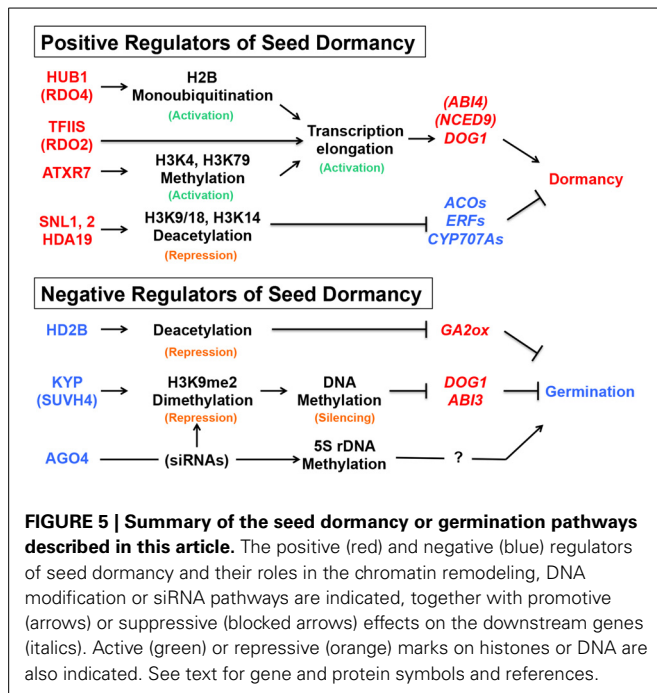


FIGURE 4 | Schematic representation of silencing of dormancy genes through histone and DNA methylation. RNA polymerase IV (Pol IV) transcripts are converted to double-stranded RNA by RNA-Dependent RNA polymerase 2 (RDR2), which are then processed into 24-nt siRNAs by DICER-LIKE3 (*DCL3*) (Xie et al., 2004; Herr et al., 2005; Onodera et al., 2005; Law et al., 2011). siRNAs are loaded onto ARGONAUTE4 (*AGO4*) (Qi et al., 2006) and interact with long non-coding RNAs (lncRNAs) produced by Pol V, which are thought to function as scaffold transcripts to guide siRNAs to specific loci to be silenced (Wierzbicki et al., 2008, 2009; Wierzbicki, 2012). In this way, the AGO4 complex containing siRNAs and lncRNAs triggers RNA-directed DNA methylation (RdDM) (Wierzbicki, 2012). A possible event downstream of AGO4 is histone 3 lysine 9 dimethylation (H3K9me2) by the KRYPTONITE (*KYP*), which causes HETEROCHROMATIN PROTEIN1 (*HP1*) to bind to the modified histone and recruit CHROMOMETHYLASE3 (*CMT3*), a DNA methyltransferase that induces gene silencing (Jackson et al., 2002; Zilberman et al., 2004; Tran et al., 2005; Johnson et al., 2007). A mutation in *KYP* in Arabidopsis causes enhanced dormancy and up-regulation of *DOG1* and *ABI3* (Zheng et al., 2012), suggesting that the seed dormancy genes are silenced by the *KYP-CMT3* pathway. The AGO4 complex is also involved in gene silencing by DOMAINS REARRANGED METHYLTRANSFERASE2 (*DRM2*) (Zilberman et al., 2004; Wierzbicki, 2012), although *DRM2* involvement in seed dormancy regulation is not known. Direct evidence for siRNAs and lncRNAs involvement in *DOG1* and *ABI3* regulation is lacking, however AGO4 has been shown to be a negative regulator of dormancy in barley and wheat seeds (Singh and Singh, 2012; Singh et al., 2013). The Arabidopsis, barley and wheat seed dormancy mutants corresponding to the protein components in the RdDM pathway are indicated by blue italic symbols.

in wheat supports this hypothesis. *AGO802B*, a wheat ortholog of *AGO4_9* gene is expressed during grain development (5–20 DAP). *AGO802B* expression is significantly lower in preharvest sprouting (PHS)-resistant (i.e., more dormant) varieties than in susceptible ones (Singh et al., 2013). This result also suggests that *AGO4* is a negative regulator of dormancy. It is not known whether specific coding genes are subjected to silencing through RdDM in wheat seeds. However, analysis of 5S



ribosomal DNA from PHS-resistant and susceptible varieties with the methylation-sensitive restriction enzyme *MspI* suggested that ribosomal DNA methylation was reduced in PHS-resistant varieties (Singh et al., 2013), supporting the hypothesis that AGO4 enhances histone and DNA methylation and acts as a negative regulator of seed dormancy.

The chromatin-remodeling factors mentioned above include both positive and negative regulators of seed dormancy, which could be considered as negative and positive regulators of seed germination, respectively. The description “activation of seed dormancy genes” or “repression of seed germination genes,” which could mean the same consequence (dormancy or no germination), is confusing. It is even more confusing when the description is combined with different terminology of histone modification, such as histone (de)acetylation, monoubiquitination or (de)methylation, because they could be either repressive or active marks depending on the position of residues in the histone tail. To avoid the confusion, the positive and negative regulators of seed dormancy, their roles in chromatin and DNA modification, and possible consequences in gene expression downstream are summarized in **Figure 5**.

NEW HYPOTHESES FOR GERMINATION EVENTS

REMAINING BARRIERS OF SEED GERMINATION

A quiescent state of the embryo is changed when molecular repression on seed germination genes is removed, which is probably orchestrated with silencing of dormancy genes. However, an active embryo is still unable to complete germination when the suppressive force, or mechanical resistance, of the covering tissues, such as the testa and endosperm, exceeds embryo growth potential. When the embryo is not dormant, it is the mechanical resistance of the covering tissues that mainly determines whether the embryo emerges from imbibed seeds.

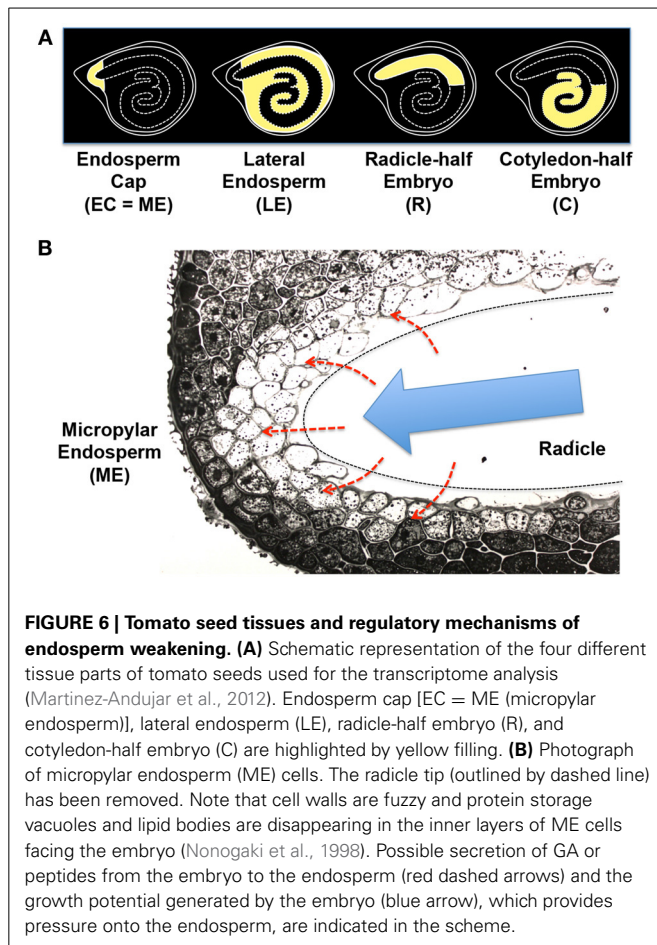
In fact, the embryos in dormant seeds in many species are able to grow when they are excised from seeds, which is called coat-imposed dormancy (Bewley et al., 2013). While further increase in embryo growth potential may still be necessary, alteration of the properties of covering tissues plays a significant role in germination. The testa in a mature seed is generally a non-living tissue, therefore the major reduction in the mechanical resistance of the covering tissues depends on physiological changes in the living endosperm. Changes in the properties of the endosperm significantly affect timing of radicle emergence in non-dormant seeds also. Therefore, the mechanisms of endosperm weakening have been a focal point in seed germination research.

Basic information about endosperm weakening is summarized in other literature (Linkies et al., 2010; Bewley et al., 2013). Briefly, the micropylar region of endosperm (ME) surrounds the radicle tip and provides an opposing force to it (**Figure 6**), which is reduced during germination through weakening. The mechanical resistance of ME is mainly due to the thick and rigid cell walls in this tissue. Therefore, cell wall modification is thought to play an essential role in ME weakening (Bewley et al., 2013). In fact, genes encoding cell wall-modifying proteins, such as xyloglucan endotransglycosylase/hydrolases (XTHs) and expansins (EXPs), are expressed exclusively in ME of *Arabidopsis* (Dekkers et al., 2013), *Lepidium sativum* (Voegelé et al., 2011) and tomato (Chen and Bradford, 2000; Chen et al., 2002) seeds during germination. While distinct cell wall architecture is observed in ME of seeds depending on plant species and family (Lee et al., 2012a), ME weakening by cell wall modifying proteins seems to be a widely conserved mechanism of germination.

EMBRYO-ENDOSPERM INTERACTION IN TOMATO SEEDS

A high throughput transcriptome analysis of germinating tomato seeds showed enrichment of cell wall-associated genes in ME (Martinez-Andujar et al., 2012), supporting the hypothesis discussed above. In this study, tomato seeds were dissected into the endosperm cap (EC, equivalent to ME), lateral endosperm (LE), radicle-half embryo (R), and cotyledon-half embryo (C) (**Figure 6A**). In addition to the cell wall-associated genes, PR (pathogenesis-related) or wound-response genes were detected as another major group of ME-enriched genes. The 5' upstream sequences of the ME-enriched PR genes contain the conserved sequences, including the DNA motifs targeted by ethylene response factors (ERFs). Interestingly, *Tomato ERF1* (*TERF1*), an experimentally validated upstream regulator of the PR genes, was also one of the ME-enriched genes in tomato seeds (Martinez-Andujar et al., 2012). These results suggest that *TERF1* is a major upstream regulator in ME and induces other ME genes, such as PR- or wound response genes and possibly cell wall-associated genes also.

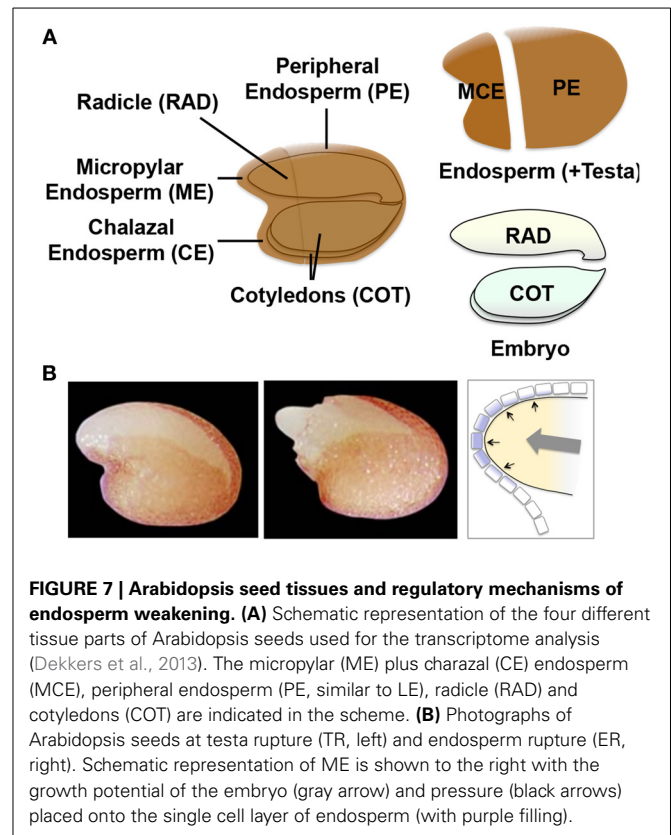
The degradation of cell wall in ME of tomato seeds, which is accompanied by disappearance of storage vacuoles and lipid bodies from the cells, is initiated at the inner cells adjacent to the radicle tips (**Figure 6B**), suggesting that ME activation is under the control of the embryo. A traditional view of the mechanism of ME gene induction is that diffusible signals, such as GA, or non-diffusible signals, such as peptide ligands, are secreted



from the embryo to ME (Figure 6B, red dashed arrows) and then stimulate gene expression in this tissue. However, the new finding about the TERF1 cascade and possible involvement of a PR- or wounding response in ME gene expression generated a new hypothesis of “mechanosensing.” In this hypothesis, pressure, rather than chemical molecules, which is generated by the embryo and placed onto ME cells (Figure 6B, blue arrow), triggers a wound response, *TERF1* expression, and then induction of the downstream genes in ME.

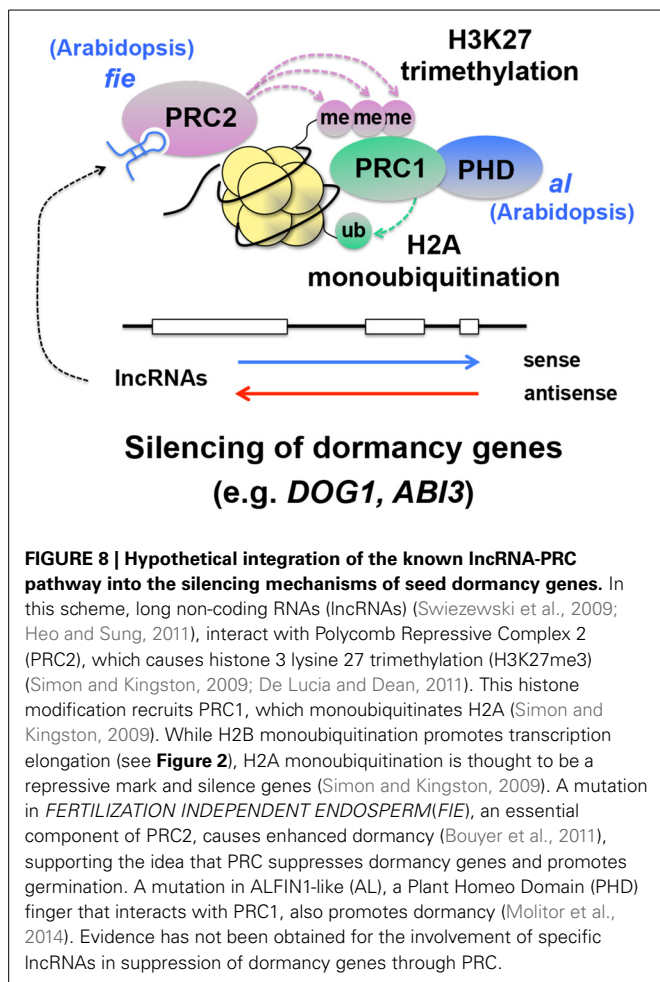
THE “TOUCH” GENES IN ARABIDOPSIS SEEDS

A similar but more comprehensive and dynamic transcriptomic analysis in Arabidopsis seeds provided supporting evidence for the mechanosensing hypothesis. It is technically difficult to dissect ME from Arabidopsis seeds. Therefore, in this study gene expression was compared for the micropylar and chalazal endosperm (MCE), peripheral endosperm (PE, similar to LE), radicle (RAD), and cotyledons (COT) (Dekkers et al., 2013) (Figure 7A). The high-resolution data set included many time points including those before and after testa rupture (TR) and endosperm rupture (ER), which are the signature events during germination and at the completion of germination, respectively (Figure 7B). This study demonstrated that TR was marked by activation of the specific genes in MCE, such as *TOUCH3* and *TOUCH4*, which are



known to be induced by touch or thigmotropism (Braam, 2005). The comparison of MCE genes at TR in Arabidopsis seeds with the genes up-regulated by touching the aerial part of Arabidopsis plants (Lee et al., 2005) showed significant overlaps. These results suggest that ME gene induction in Arabidopsis seeds is also caused by touch or mechanosensing (Dekkers et al., 2013).

No conclusive evidence has been obtained to date for the mechanosensing or touch hypothesis. However, the new findings have great potential to re-draw the traditional view of ME gene regulation, which is a core mechanism of germination. It is well known that GA stimulates ME gene expression in the GA-deficient *gib-1* tomato seeds, which absolutely require GA for radicle emergence (Groot and Karssen, 1987; Nonogaki et al., 2000). The GA requirement for ME gene expression can be substituted by co-incubation of ME with the embryonic axes, suggesting that the embryo produces GA and secretes it to the endosperm (Groot and Karssen, 1987). There seems to be no doubt that ME gene expression is under the control of GA and the embryo. However, it should be noted that exogenous GA stimulates gene expression in both ME and LE when tomato seeds are dissected, while only ME is responsive when GA is applied to intact seeds (Martinez-Andujar et al., 2012). This raises the question as to why LE in an intact seed remains unaffected by GA or why only ME is responsive to it? The new hypothesis (mechanosensing or touch) could answer these questions. If the GA-dependent embryonic effects on ME gene expression are not directly exerted through chemical secretion but are indirectly mediated by the pressure provided by the radicle tip, the highly localized gene

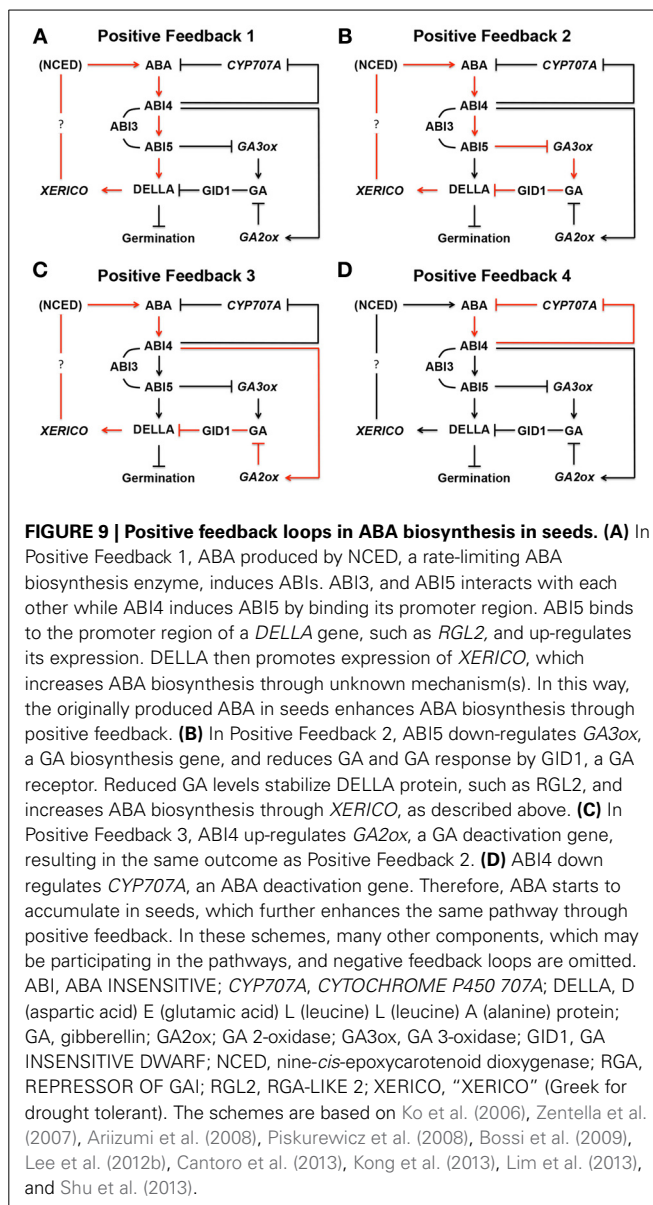


expression in ME, which is in close contact with the radicle tip, could be explained. Since generation of embryo growth potential, which causes the pressure onto ME, is dependent on GA (Ni and Bradford, 1993; Yamaguchi et al., 2001), the concept of pressure-triggered stimulation of ME gene expression is well integrated with the traditional concept (and evidence) of GA- and embryo dependency of ME gene expression. While the possibility of direct stimulation of ME by GA or insoluble secondary messengers should not be excluded, the recent data sets provided the new concept for embryo-endosperm interaction and opened the next phase of seed germination research.

PERSPECTIVES FOR BASIC RESEARCH AND KNOWLEDGE TRANSLATION

MORE DISCOVERIES EXPECTED THROUGH EPIGENETIC STUDY

A number of discoveries were made in the recent studies of seed dormancy and germination. More significant discoveries will probably be made from epigenetic studies of seed dormancy and germination over the next few years. While bioinformatics and systems biology could generate new hypotheses, the exciting discoveries happening from characterization of seed dormancy mutants look very convincing and promising. Exploring these emerging mechanisms with forward genetics and biochemical



and molecular approaches will result in more progress in seed dormancy research. The information obtained from individual mutants of chromatin remodeling was assembled into several schemes in this article to provide an overview of the frontier of this field. However, information to connect each component precisely in the schemes is still missing. For example, while histone methylation and subsequent silencing of *DOG1* by DNA methylation seems likely, contribution of *DCL3*, *AGO4*, and *RdDM* to the *DOG1*-dependent dormancy pathway is not clear (Figure 4). It is possible that siRNAs and long non-coding RNAs (lncRNAs), including antisense transcripts (Yamada et al., 2003; Liu et al., 2010; Sun et al., 2013), are involved in repression of key dormancy genes. Recent studies suggest that the Polycomb Repressive Complex (PRC), which is involved in histone methylation and gene silencing, also targets *DOG1* (Bouyer et al., 2011; Muller et al., 2012; Molitor et al., 2014). This is very interesting because

PRC is known to mediate gene silencing triggered by expression of long non-coding RNA, at least in the case of the flowering gene *FLOWERING LOCUS C* (Swiezewski et al., 2009; De Lucia and Dean, 2011; Heo and Sung, 2011). It is possible that some dormancy genes are regulated through the lncRNA-PRC pathway (Figure 8), which could maintain dormancy genes “dormant.” Missing information in the current schemes of regulatory mechanisms of seed dormancy and germination genes might already be emerging from other epigenetic studies. In addition, the current schemes, which seem to be separate pathways, could be combined with each other and integrated into a single comprehensive scheme, through more discoveries. The crosstalk between the histone deacetylation and DNA methylation pathways is known (To et al., 2011; Kim et al., 2012), however little is known about their interaction directly linked to the seed dormancy mechanisms. This might be one of the areas in which the major discoveries could be made in the future.

KNOWLEDGE TRANSLATION OF SEED HORMONE BIOLOGY

The topic of hormonal regulation of seed dormancy, such as the regulation of ABA or GA biosynthesis and deactivation enzymes by the environmental signals (e.g., light and temperature), was minimized in the discussion above, because it is well summarized elsewhere (Finkelstein et al., 2008; Seo et al., 2009) and this article focuses on emerging mechanisms and new hypotheses. Nonetheless, this is probably the area of seed biology that has been most advanced in the last decade, and from a knowledge translation point of view, this area has the greatest potential for agricultural application. For example, identification of the rate-limiting ABA biosynthesis gene *NCED* advanced our understanding of thermoinhibition of lettuce seed germination, which is a critical issue in agriculture. Now, we understand that thermoinhibition of germination at high temperature, which could induce secondary dormancy, is caused by *NCED* expression (Argyris et al., 2008, 2011). Likewise, screening of wheat populations for mutations in ABA 8'-hydroxylase, an ABA deactivation enzyme, has successfully identified the genetic lines, which are potentially resistant to PHS, another serious issue in agriculture (Chono et al., 2013). A separate screen for a mutation in the *ENHANCED RESPONSE to ABA* (*ERA*) gene also isolated PHS-resistant wheat lines (Schramm et al., 2013). The information about *MOTHER OF FT AND TFL1* (*MFT*) gene, which is a recently identified member of the ABA and GA signaling pathways in Arabidopsis (Xi et al., 2010), has already been translated into wheat (Nakamura et al., 2011; Lei et al., 2013; Liu et al., 2013).

More progressive efforts are being made to translate seed hormone biology. It has been demonstrated that direct manipulation of the rate-limiting enzymes in the hormone metabolism pathways can successfully be used to alter seed performance. Silencing *NCED* with RNA interference can promote germination in lettuce seeds (Huo et al., 2013). In contrast, chemical induction of *NCED*, a single gene, was sufficient to suppress precocious germination in Arabidopsis, which can also be applied to PHS prevention in cereal crops (Martinez-Andujar et al., 2011). While the latter approach was tested in the model system Arabidopsis, the gene induction experiments in this study were performed with the chemical ligand that has been approved for field application by

the U.S. Environmental Protection Agency, making the principle applicable to agriculture. Even more advanced system of *NECD* enhancement, which does not require chemical application, has been established recently, using a positive feedback mechanism. In this system, a chimeric *NCED* gene, which is designed to trigger positive feedback regulation, amplifies ABA biosynthesis and signaling in seeds and causes hyperdormancy in a spontaneous manner (Nonogaki et al., 2014). This positive feedback system was created based on the mechanisms emerged from, and the comprehensive understanding established by, the past research on the ABA metabolism and signaling pathway in seeds. The translational research unexpectedly revealed that a positive feedback mechanism is also present in the native system of *NCED* expression in seeds (Nonogaki et al., 2014), demonstrating the synergy between basic and translational research. Other positive feedback mechanisms in the hormonal regulation of seed dormancy and germination are also emerging from on-going discoveries (summarized in Figure 9). More findings and understanding of elegant pathways in nature will provide greater opportunities of knowledge translation, another frontier of research that should be expanded in the future.

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