Subcellular proteomics—where cell biology meets protein chemistry

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The development of compartments in eukaryotic cells and the distribution of nuclear-encoded proteins underlies the expansion of plant genomes, the proliferation of multigene families and the specialization of cellular functions. The exploration of the proteome of the cell in terms of the collection of its subcompartments is therefore both a practical approach and also a function led necessity that recognizes that proper interpretation of proteomic data requires information about compartmentation of protein machinery.

Subcellular proteomics decreases the complexity of proteome discovery. With the typical compartment representing 500–4000 proteins, its analysis by gel based and MS based systems approach the resolution of the analytical techniques. In contrast, whole cell proteomes of 12,000–40,000 proteins extend well beyond the ability of proteomic tools to resolve them, leaving whole cell proteome studies being "tip of the iceberg" activities. Current shotgun studies can identify ∼500–3000 proteins with 2–20 h of MS time, making organelle proteomes and their quantitative comparisons within the reach of many research laboratories that either perform their own MS or use MS services.

Subcellular proteomics stands on the shoulders of decades of biochemical research that has developed methods for isolation of subcellular compartments. Extensive laboratory work involving the tinkering with density, size, and charge separation techniques has enabled incremental limitation of contamination in isolation methods from a range of subcellular structures. However, in depth MS studies over the last decade have also revealed that typical 90–95% enrichment still leaves much room for contaminants in preparations (Eubel et al., 2007; Huang et al., 2009; Ito et al., 2014). Studies from relatively abundant, or easily isolated homogenous compartments dominate the literature. In this class of structures are plastids, mitochondria, peroxisomes, and nuclei. Currently over 8000 proteins have been experimentally identified in these organelles in Arabidopsis (Tanz et al., 2013). Many fewer studies have attempted to untangle the intracellular membrane systems of ER, golgi, and PM. Separate techniques for these are complex, lack high levels of enrichment, and the protein populations of these structures are often transitory and differ between tissue types. Currently over 6000 proteins have been experimentally identified in these membranes in Arabidopsis (Tanz et al., 2013). All these structures bathe in the cytosol of the cell that itself contains a large and complex proteome. Isolation of pure cytosol without breaking organelles is extremely challenging and thus cytosolic proteomes are best defined through subtractive analysis of soluble proteomes against enriched organelle datasets. Quantitative comparisons of fractions collected during the sub-compartment enrichment process, or across gradient separation of organelles, are key tools to differentiate the low level protein component from the small fraction of a contaminating protein from another location in the cell. Bringing together subcellular proteomics studies in aggregation databases has been very revealing to confirm location of proteins for which there are multiple conflicting claims in the literature (Tan et al., 2012; Tanz et al., 2013).

Analysis of multiple subcellular proteomes from the same tissues has begun to show the way in which multigene families have dispersed particular protein classes across subcellular boundaries to maintain translational, metabolic, signaling, and degradative machinery through the cell. Subcellular proteomes and targeted metabolic engineering are also showing how steps in metabolic pathways have been, and can be, redistributed in plants (compared to animals) to enable unique chemistries and accumulation of end-products in plants.

This special research topic aimed to bring together knowledge across sub cellular components and plant species to provide a basis for accelerated research in plant subcellular protein research. We have brought together a wide array of 26 publications including original research articles, reviews, and mini-reviews. They are focused on the model plants Arabidopsis (Parsons et al., 2012; Albenne et al., 2013; Bussell et al., 2013; Carroll, 2013; Lee et al., 2013a; Peters et al., 2013; Simm et al., 2013; Yadeta et al., 2013; Ito et al., 2014), rice (Huang et al., 2013; Komatsu and Yanagawa, 2013) and medicago (Kiirika et al., 2013; Lee et al., 2013b; Simm et al., 2013) as well as crop plants wheat, barley, maize, and tomato (Casati, 2012; Komatsu and Yanagawa, 2013; Petersen et al., 2013; Ruiz-May and Rose, 2013; Zhang et al., 2013). They include studies of the easily isolated subcellular proteomes of the chloroplast, mitochondria, peroxisome, and nuclei (Casati, 2012; Repetto et al., 2012; Bussell et al., 2013; Havelund et al., 2013; Huang et al., 2013; Lee et al., 2013a; Narula et al., 2013; Peters et al., 2013; Petersen et al., 2013; Simm et al., 2013), as well as less easily isolated golgi, plasma membrane, cytosolic ribosome, and cell wall proteomes(Parsons et al., 2012; Carroll, 2013; Takahashi et al., 2013; Yadeta et al., 2013; Zhang et al., 2013). Articles have also begun to investigate sub-organellar proteomes including the subcompartments of chloroplast (Simm et al.,

2013) and mitochondria (Peters et al., 2013), plasma membrane microdomains (Takahashi et al., 2013), and cell wall plasmodesmata (Salmon and Bayer, 2012). In addition to cataloguing these proteomes, researchers are beginning to investigate the post-translational modifications present on proteins in these locations (Havelund et al., 2013).

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