**Supporting Information**

**Figure S1**



**Fig. S1** The sections were stained by phloroglucinol-HCl at six developmental stages. The fruit were collected at 20, 30, 35, 50, 80, 125 days after full bloom (DAFB) in 2020. Scale bar, 1 cm.

**Figure S2**



**Fig. S2** Stone cell production and lignin content were measured. The no treatment and Ca2+ treatment fruits were collected at 20, 30, 35, 50, 80, 125 DAFB in 2020. Data are shown as mean ± SE. Statistical significance was determined using Student’s *t*-test: \*, *P*<0.05.

**Figure S3**



**Fig. S3** Lignin biosynthesis related enzyme PAL (phenylalanine ammonialyase), 4CL (4-hydroxycinnamate-CoA ligase), C4H (cinnamate 4-hydroxylase), CAD (cinnamyl alcohol dehydrogenase), PRX (peroxidase) activity were measured. Data are shown as mean ± SE. Statistical significance was determined using Student’s *t*-test: \*, *P*<0.05.

**Figure S4**



**Fig. S4** Phylogenetic tree of *Pu**PRX42-like* sequences of different fruit crops, based on a conservative approximate alignment. The scale indicates the genetic distance.

**Figure S5**



**Fig. S5** RNA-seq data analysis of Ca2+-treated and control pear fruits of days after full bloom 35 d. (a) Volcano plot of differently expressed genes, red points represent up-regulated DEGs, The y-axis and x-axis present the -log10(pvalue) and the log2(fold change), blue points represent down-regulated DEGs, and gray points represent non-DEGs. (b) Enriched KEGG pathways among the DEGs. The y-axis and x-axis present the KEGG pathways and the rich factors, respectively. Dot size corresponds to the number of distinct genes, whereas dot color reflects the p-value.

**Table S1** Details of primers used for this study.

|  |  |  |
| --- | --- | --- |
| Primer name | Sequence (5’-3’) | Purpose |
| Dof2.5-AD-*EcoR*Ⅰ-F | GTACCAGATTACGCTCATATGATGGATACTGCTCAATGGCTGC | Y1H assay |
| Dof2.5-AD-*Nde*Ⅰ-R | ATGCCCACCCGGGTGGAATTCTCACCACGAGCCTCCACCT |
| PRX42-like-pABAi-*Sma*Ⅰ-F | CTTGAATTCGAGCTCGGTACCTTGATTTAGGTATCACGCAATTT |
| PRX42-like-pABAi-*Sac*Ⅰ-R | AGCACATGCCTCGAGGTCGACGGAAGAAGAAGAAGAAGCCATGGC |
| Dof2.5-pRi-*Sac*Ⅰ-F | TCTTCACTGTTGATACATATGATGGATACTGCTCAATGGCTGC | Transient in fruit |
| Dof2.5-pRi-*Nde*Ⅰ -R | CGATCGGGGAAATTCGAGCTCTCACCACGAGCCTCCACCT |
| PRX42-like-pRi-*Sac*Ⅰ-F | TCTTCACTGTTGATAATGGCTTCTTCTTCTTCTTCCAGA |
| PRX42-like-pRi-*Nde*Ⅰ-R | CGATCGGGGAAATTCCTAGTCCCGGATTTTATTGGCA |
| Dof2.5-pRi-*Sac*Ⅰ-F | TCTTCACTGTTGATACATATGATGGATACTGCTCAATGGCTGC | GUS transactivation assay |
| Dof2.5-pRi-*Nde*Ⅰ-R | CGATCGGGGAAATTCGAGCTCTCACCACGAGCCTCCACCT |
| PRX42-like-pbi-SalⅠ-F | GACCATGATTACGCCAAGCTTTTGATT TAGGTATCACGCAATTT |
| PRX42-like-pbi-BamHⅠ-R | ACTGACCACCCGGGGATCCGGAAG AAGAAGAAGAAGCCATGGC |
| ChIP-PRX42-like-S1-F | GATAATTTCAAATAGCGATATTCAGTTTT | ChIP PCR assay |
| ChIP-PRX42-like-S1-R | TTGATTTAGGTATCACGCAATTTTATT |
| ChIP-PRX42-like-S2-F | TGATGATTGCATGCCTCCTCA |
| ChIP-PRX42-like-S2-R | TGAAATTATCGTTTCCTCTAATAGTTTCT |
| ChIP-PRX42-like-S3-F | CAACACTCATTTTTTACACGTGTTGC |
| ChIP-PRX42-like-S3-R | CAATCATCATAGTTTTTGTGATGATGC |
| ChIP-PRX42-like-S4-F | TACAAGTATTCAGTATATTTTCTTAAAGTTTCTT |
| ChIP-PRX42-like-S4-R | ATGAGTGTTGCAGAAATGAGAATGT |
| ChIP-PRX42-like-S5-F | AGCATTCACCGCTCTAATTAAACTAC |
| ChIP-PRX42-like-S5-R | TACTTGTAGCTAACAGAAAACTTAATGCA |
| ChIP-PRX42-like-S6-F | GGAAGAAGAAGAAGAAGCCATGG |
| ChIP-PRX42-like-S6-R | GTGAATGCTGCGGTGAATCC |
| PRX42-like-full-F | ATGGCTTCTTCTTCTTCTTCC | Gene cloning |
| PRX42-like-full-R | CTAGTCCCGGATTTTATTGG |
| Dof2.5-full-F | ATGGATACTGCTCAATGGCTGC |
| Dof2.5-full-R | TCACCACGAGCCTCCACCT |
| PRX42-like-ex-F | TCTGTCAATCTGCTGCTGT | Gene expression |
| PRX42-like-ex-R | TCATTCAAATCAGCGTCT |
| CAD-ex-F | AAGGAAACTGAGGAGATGCTTGAAT |
| CAD-ex-R | TACTTTATTAAATAAGATTGCTGCCG |
| C4H-ex-F | GCACAGCAGAAGGGAGAAATC |
| C4H-ex-R | GTCGGGCTCTGTGATTTGTAC |
| PAL-ex-F | GAAGTGCTACAGAATCAG |
| PAL-ex-R | GAATCTTATGCCAGAGTAG |
| 4CL-ex-F | CATGCTCCTCCTCCAAAACAG |
| 4CL-ex-R | TCCTTCACCTTGTCCACGTAA |
| NAC1-ex-F | ACACAGACATACAGCGAC |
| NAC1-ex-R | TCGCAACCATGGCCATTG |
| MYB1-ex-F | CTGGAACTCCACGTTGAAGC |
| MYB1-ex-R | AACCGAACTCGTGCTCATCC |
| Dof2.5-ex-F | CGACGGTAGCAGGCACTTA |
| Dof2.5-ex-R | CTCTACTTCTTCAGGTCCA |
| WRKY2-ex-F | CACTCGAGCGTTCCAGAA |
| WRKY2-ex-R | ACAGTCGCAGTCCTCTTG |
| ERF1-ex-F | ACCCTTGCTATGTGACCC |
| ERF1-ex-R | GTTATCAGCTTCCCTCGC |
| Actin-F | GCTGGATTTGCTGGTGAT |
| Actin-R | GCTCACTATGCCGTGCTC |