POLYPRENOL REDUCTASE 2 Deficiency is Lethal in Arabidopsis Due to Male Sterility

Short title

PPRD2 is vital for plant development

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Synopsis: Arabidopsis PPRD1 and -2, orthologues of human SRD5A3 (steroid 5α reductase type 3), encode polyprenol reductases responsible for conversion of polyprenol to dolichol.

Abstract

Dolichol is a required cofactor for protein glycosylation, the most common posttranslational modification modulating the stability and biological activity of proteins in all eukaryotic cells. We have identified and characterized two genes, *PPRD1* and *-2*, which are orthologous to human *SRD5A3* (*steroid 5α reductase type 3*) and encode polyprenol reductases responsible for conversion of polyprenol to dolichol in *Arabidopsis thaliana*. *PPRD1* and *-2* play dedicated roles in plant metabolism. *PPRD2* is essential for plant viability; its deficiency results in aberrant development of the male gametophyte and sporophyte. Impaired protein glycosylation seems to be the major factor underlying these defects although disturbances in other cellular dolichol-dependent processes could also contribute. Shortage of dolichol in *PPRD2*-deficient cells is partially rescued by *PPRD1* overexpression or by supplementation with dolichol. The latter has been discussed as a method to compensate for deficiency in protein glycosylation. Supplementation of the human diet with dolichol-enriched plant tissues could allow new therapeutic interventions in glycosylation disorders. This identification of PPRD1 and -2 elucidates the factors mediating the key step of the dolichol cycle in plant cells which makes manipulation of dolichol content in plant tissues feasible.

Introduction

Dolichol (Dol) is a member of the isoprenoids, which are functionally and structurally the most diverse group of natural products (Thulasiram et al., 2007). Dolichyl phosphate (Dol-P) as a cofactor is necessary for protein glycosylation, a ubiquitous post-translational modification found in all domains of life (Schwarz and Aebi, 2011; Pattison and Amtmann, 2009). Glycosylation is crucial for protein functioning since it modulates folding and quality control, and is a prerequisite for diverse biological recognition events (Liu et al., 2010; Moremen et al., 2012). The oligosaccharide precursor used for *N*-glycosylation of proteins is assembled on dolichyl diphosphate ($Glc_3Man_9GlcNAc_2$-PP-Dol) and the resulting tetradecasaccharide is co-translationally transferred to an asparagine residue (Asn-X-Ser/Thr sequence) of the growing polypeptide. In addition, the activated monosaccharides Dol-P-Man and Dol-P-Glc are also utilized during protein *N*-glycosylation, *O*- and *C*-mannosylation, and glycosylphosphatidylinositol (GPI) anchor biosynthesis.

In line with the indispensable role of Dol in protein glycosylation, impaired Dol and/or Dol-P biosynthesis leads to disorders called Congenital Disorders of Glycosylation Type I (CDG-I), while disruption of the subsequent steps of the formation of $Glc_3Man_9GlcNAc_2$-PP-Dol together with peptide glycosylation and glycan maturation are collectively called CDG-II (Lefeber et al., 2011 and references therein).

Besides their role in protein glycosylation, polyisoprenoid alcohols, i.e., Dols and their α-unsaturated counterparts - polyprenols, are involved in cell adaptation to adverse environmental conditions (Bergamini, 2003; Bajda et al., 2009). Whether polyisoprenoids protect senescing tissues via their highly increased accumulation upon aging (summarized by Swiezewska and Danikiewicz, 2005) remains a matter of debate. Dol is also suggested to be involved in the intracellular trafficking of proteins (Sato et al., 1999; Belgareh-Touze et al., 2003) and in macromolecular complex assembly (e.g., of glycan biosynthetic enzymes, Jones et al., 2009).

The biosynthesis of Dol comprises three steps: (I) formation of isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP) – five-carbon building blocks of isoprenoids biosynthesized in plant cells by a concomitant involvement of the mevalonate (MVA) and the methylerythritol phosphate (MEP) pathways, (II) formation of

farnesyl diphosphate (FPP) and its elongation *via* subsequent condensations of FPP with IPP molecules (performed by *cis*-prenyltransferase, CPT) leading to a mixture of homologous polyprenyl diphosphates with a species-dependent composition, and (III) hydrogenation of the double bond in the OH-terminal isoprene unit of polyprenol and/or polyprenyl diphosphate resulting in the formation of a corresponding mixture of Dols (Figure 1A). Among these, the last step in Dol biosynthesis was the least studied until the identification of members of the steroid α-reductase family, mammalian SRD5A3 and yeast Dfg10, as key enzymes responsible for polyprenol hydrogenation (Cantagrel et al., 2010). This was achieved by elucidation of the molecular basis of a rare Mendelian disease, demonstrating that mutations in the *SRD5A3* or *DFG10* genes cause increased polyprenol accumulation at the expense of Dol, leading to defective protein *N*-glycosylation. Moreover, a loss-of-function mutation the *Srd5a3* gene is embryo-lethal in mouse (Cantagrel et al., 2010). In the human, mutations in *SRD5A3* lead to a neurological disease with developmental delay, ataxia and early visual impairment with optic atrophy. In some cases, ichthyosiform dermatitis is reported with liver dysfunction and coagulation abnormalities (for summary see Buczkowska et al., 2015 and references therein).

Despite the fact that a considerable amount of Dol is accumulated in plant roots (Skorupinska-Tudek et al., 2003; Jozwiak et al., 2013), a plant polyprenol reductase has not been identified until now. In this study, two genes encoding polyprenol reductase (*PPRD-1* and *-2*), orthologues of *SRD5A3* and *DFG10*, were identified in Arabidopsis. The newly identified PPRDs were found to be involved in the regulation of plant growth and reproductive processes.

Results

Two genes encode functional polyprenol reductases in *Arabidopsis thaliana*

Three putative polyprenol reductases were found in the Arabidopsis proteome (gene loci At1G72590, At2G16530 and At3G43840) using BLASTP. The amino acid sequences of those putative Arabidopsis polyprenol reductases were similar to the human (47 - 54% similarity and 28 - 30% identity) and yeast (39 – 47% similarity and 26 – 27% identity, Supplemental Table 1) orthologues and the predicted POLYPRENOL REDUCTASE 1 (PPRD1) and PPRD2 polypeptides comprised 320 and 343 amino acids, respectively, while the putative PPRD3 contained 84 aa corresponding to the C-terminal part of PPRD1 and -2. A multiple sequence alignment of PPRDs from various plant species showed the presence of at least eight highly conserved regions (Supplemental Figure 1 and Supplemental Figure 2). Membrane topology analysis (TMHMM Server) predicted five transmembrane domains (TMD) in PPRD1 and PPRD2 proteins, similar to the six TMDs in SRD5A3 (Cantagrel et al., 2010), while only one TMD was predicted in PPRD3 (Supplemental Figure 3).

To determine whether Arabidopsis *PPRD1* and *PPRD2* are true orthologues of yeast *DFG10,* functional complementation of the yeast *dfg10* mutants (*dfg10Δ* and *dfg10-100* – a transposon insertion in *DFG10* promoter) was performed with *PPRD1* and *PPRD2* coding sequences and with *PPRD1* variants, *PPRD1-INT3* or *PPRD1-INT4* carrying intron 3 or intron 4, respectively (Supplemental Figure 4). Analysis of the *N*-glycosylation status of carboxypeptidase Y (CPY), which in the mature form contains four *N*-glycan chains, revealed that in contrast to WT (BY4741), hypoglycosylated (tri-, di- and mono-) CPY variants were clearly detectable for *dfg10* (Figure 1B). Transformation with *PPRD1* and *PPRD2*, similarly to *DFG10*, fully rescued the CPY hypoglycosylation, in contrast to *PPRD1-INT3* and *PPRD1-INT4*. Similar results were obtained for the both *dfg10* mutants and only those for *dfg10*Δ are shown (Figure 1B). These results indicate that *PPRD1* and *-2* are functional orthologues of the yeast *DFG10*.

To explore the biochemical effects underlying the yeast complementation, lipid profiles of *dfg10* strains and the transformants mentioned above were analyzed using HPLC/UV. The two *dfg10* mutants displayed a high polyprenol:Dol ratio in contrast to the

WT strain, suggesting a block in the polyprenol reduction step and confirming the literature data (Cantagrel et al., 2010). Transformation of the *dfg10*Δ strain with *DFG10*, *PPRD1*, or *PPRD2* almost completely rescued this chemotype – only traces of polyprenols were observed (Figure 1C). By contrast, transformation with *PPRD1-INT3* or *PPRD1-INT4* did not complement the Dol deficiency (Figure 1D) – most likely truncated non-functional PPRD1 proteins devoid of 86 or 53 C-terminal aa were expressed in those cases (Supplemental Figure 4). Similar results were obtained for complementation of the *dfg10-100* mutant (not shown). Thus, *PPRD1* and *PPRD2* are functional orthologues of yeast polyprenol reductase.

The catalytic domain of PPRD is localized at the C-terminus

In silico analysis of the PPRD1 and -2 aa sequences led to the identification of the catalytic 3-oxo-5-α-steroid 4-dehydrogenase domain (PF02544) in the C-terminal part of both PPRDs (Supplemental Figure 3) similarly to SRD5A3 (Cantagrel et al., 2010). Again, PPRD3 seemed to be a truncated form of PPRD1 and -2 comprising solely this domain (87% and 61% identity with C-terminal fragments of PPRD2 and PPRD1, respectively (Supplemental Table 2). Thus, only PPRD1 and -2 were subjected to further analysis.

To confirm the location of the catalytic domain, directional mutagenesis was performed aiming at substitution of conserved histidines, which are suggested to take part in the reduction reaction (Cantagrel et al., 2010; Wigley et al., 1994). PPRD2 mutants with His^{321} or His^{336}, corresponding to His^{296} or His^{309} in hSRD5A3, substituted by Leu were employed to complement the yeast *dfg10*Δ mutant (Supplemental Figure 3). For the H321L and double H321L H336L mutants, 47% and 45% of the WT reductase activity was recovered, respectively, supporting the C-terminal location of the catalytic domain. These results are also in line with the total loss of activity of the putative C-terminally truncated PPRD1 proteins encoded by *PPRD1-INT3* and *PPRD1-INT4* (Figure 1D). Nevertheless, these findings suggest that besides H^{321} and H^{336} other residues of PPRD2 might be involved in the reduction since H296G substitution in hSRD5A3 abolished its enzymatic activity (Cantagrel et al., 2010).

PPRD1 and PPRD2 catalyze reduction of polyprenol to Dol *in vitro*

To confirm the enzymatic activity of PPRDs as polyprenol reductases, an *in vitro*

assay using lysates containing the recombinant proteins expressed in the bacterial system was performed. *E. coli,* like most other bacteria, does not possess endogenous PPRD activity. The concentration of detergent, Triton X-100, used to solubilize exogenous Prenol-16 (Pren-16) required careful optimization to ensure the availability of the hydrophobic substrate to PPRD and simultaneously to avoid loss of its enzymatic activity. For both lysates from bacteria overexpressing either PPRD1 or PPRD2, a notable amount of Dol-16, the expected product of Pren-16 reduction (approx. 30 or 11% of the substrate for *PPRD2* or *PPRD1*, respectively) was detected while no Dol was formed in the presence of lysate from control bacteria (empty vector) (Figure 1E). Interestingly, in the strain expressing *PPRD2* endogenous bacterial P-11 was also reduced to Dol-11 (Figure 1E).

Taken together, these results confirm that *PPRD1* and *PPRD2* encode polyprenol reductases, which upon expression in heterologous systems catalyze efficient reduction of prenol (Pren) to Dol both *in vivo* and *in vitro*.

Polyprenol reductases are expressed in tissue-specific manner in Arabidopsis and are diversely localized within plant cell

Variable expression profiles of *PPRDs* were found in Arabidopsis organs - roots, leaves, stems, flowers and pollen - during the plant life span. The *e*xpression of *PPRD1* was consistently lower compared to that of *PPRD2.* Both genes were expressed in young seedlings (Figure 2A). In older plants, *PPRD1* was expressed only in the roots and flowers, unlike *PPRD2*, which was expressed in all organs analyzed (Figure 2A). With age, expression of *PPRD1* increased in the roots and decreased in the leaves while expression of *PPRD2* was fairly constant in the roots and decreased in the leaves. Interestingly, in pollen exclusively the *PPRD2* transcript was detected (Figure 2A). Expression of *PPRD1-INT3* and *PPRD1-INT4*, probably resulting from alternative splicing of *PPRD1*, was also observed in the leaves (Supplemental Figure 4).

To characterize further the expression pattern of *PPRD1* and *PPRD2*, a fusion of their promoter regions with the *β-glucuronidase* (*GUS*) reporter gene was employed. Substantial activity of the *PPRD1* promoter (*PPRD1*$_{pro}$*:GUS*) was detected mainly during the extensive development phase in tissues characterized by actively dividing cells (e.g., root apical meristem, root division and elongation zones, and leaf primordia) and

restricted only to a small number of cells (Figure 2B). The promoter activity of *PPRD2* (*PPRD2*$_{pro}$*:GUS*) was induced in a time-dependent manner - the older the tissue the higher the expression; it was virtually absent in four-day-old seedlings and expressed along the whole root in two-week and older plants, mostly in the junctions between lateral roots and the primary root, in the root division and elongation zones, in root cap (Figure 2B and Figure 2C). GUS staining was also visible in young stamen (Figure 2B).

Taken together, these results show that the expression of *PPRDs* is regulated temporally and in a tissue-specific manner, suggesting that the encoded enzymes might function in differentiation. The diverse patterns of expression of the two paralogues suggest divergent roles of these enzymes in the plant. In contrast to the more ubiquitously expressed *PPRD2*, *PPRD1* seems to undergo induction in particular tissues/cells in response to the current metabolic requirements.

To compare the intracellular localization of polyprenol reductases PPRD1:G3GFP and PPRD2:G3GFP constructs, encoding N-terminal fusions of the respective reductase with fluorescent protein, were transiently co-expressed with plant organelle markers (mCherry fusions) in *Nicotiana benthamiana*. The localization information for the ER:mCherry marker was provided by a well-established short targeting signal while plasma membrane (PM) labeling was based on the full-length coding region of At-PIP2A, a plasma membrane aquaporin (Nelson et al., 2007). Microscopic observations of transformed plants showed that PPRD2 was co-localized mostly with the marker of the endoplasmic reticulum (ER) while PPRD1 co-localized with that of the PM (Figure 2D, Supplemental Figure 5). Additionally, weak co-localization signals for PPRD2 with PM and PPRD1 with ER markers were also visible in all experiments (n=4); moreover weak co-localization signals for PPRD2 with Golgi:mCherry marker was observed in some (n=2) experiments too (not shown).

***PPRD2* knockout plants are not viable**

To analyze further the role of the polyprenol reductases, relevant PPRD T-DNA insertion lines were studied (Figure 3A). One line homozygous for *PPRD1* insertion was available (GabiKat_575B02) but it turned out to contain much higher (up to 600-fold) levels of the *PPRD1* transcript compared to WT plants in all organs (Figure 3B). Subsequent analysis revealed that in this line the T-DNA insert was localized in the

PPRD1 promoter region (Figure 3A). Such localization of the insert may actually lead to up-regulation of gene expression. Indeed, in this line Dol content was increased, reaching 213% and 126% of control in the leaves and roots, respectively. What is more, the increase of the dolichol content in the leaves seemed to occur at the expense of polyprenol - its content was decreased to 62% of WT, albeit no such phenomenon was observed in the roots (Figure 3E). Thus, the GabiKat_575B02 homozygous line will be further referred to as *PPRD1-OE* (overexpressing).

Two heterozygous T-DNA *PPRD2* insertion lines, *pprd2-1* (SALK_113221C) and *pprd2-2* (SALK_006421) (Figure 3A), were used in this study since no plants homozygous for *PPRD2* were found during genetic screens of *pprd2-1* or *pprd2-2* progeny (Table 1). In these lines, the expression levels of *PPRD1* and *PPRD2* were almost identical to those in WT plants (Figure 3B), as were the Dol and Pren contents (Figure 3E). Sequencing of the T-DNA insert confirmed its different location for *pprd2-1* and *pprd2-2* lines (Figure 3A).

To establish the reason for the inability to obtain homozygous *pprd2* plants, heterozygous mutant lines, *pprd2-1*$^{+/-}$ or *pprd2-2*$^{+/-}$, were self-pollinated and F1 progeny was genotyped. The lack of *pprd2* homozygotes among almost 200 plants of each mutant line suggested that disruption of this gene was lethal (Table 1). Segregation analysis of heterozygous *pprd2-1*$^{+/-}$ and *pprd2-2*$^{+/-}$ plants and X^2 test (Table 1) confirmed the lethality of the *pprd2*$^{-/-}$ (homozygous) state, which could be caused by pollen sterility since these lines produced siliques with seed number and germination rate comparable to those of WT (Supplemental Figure 6, Supplemental Table 3).

To gain a deeper insight into the *pprd2* lethality we performed reciprocal crosses of *pprd2-1*$^{+/-}$ and *pprd2-2*$^{+/-}$ with WT plants. For both the mutant alleles, pollination of the heterozygous stigma (♀) with WT pollen (♂) resulted in 50% of heterozygous and 50% WT plants in the offspring (Table 2). The reciprocal pollination of WT stigma (♀) with pollen from heterozygous plants (♂) produced only WT plants (Table 2). Therefore, the *pprd2*$^{+/-}$ plants are defective in the transmission of *pprd2* alleles through the male gametophyte.

To further elucidate the lethality of *pprd2* disruption, *pprd2-1*$^{+/-}$ stamens were pollinated with *PPRD1-OE* to produce double heterozygote *pprd2-1*$^{+/-}$ *PPRD1-OE*$^{+/-}$ (F1) plants

and in the next (F2) generation the double homozygote *pprd2 PPRD1-OE* was isolated. As expected, this mutant displayed no *PPRD2* expression and an increased (at least 200-fold) level of *PPRD1* mRNA (Figure 3C). This result suggests that overexpression of *PPRD1* can rescue the *pprd2* lethality since the *pprd2 PPRD1-OE* plants (double homozygote) displayed only mild morphological abnormalities (Figure 4A and Figure 4B).

By contrast, the *pprd2 PPRD1-OE*$^{+/-}$ (*PPRD1-OE* heterozygote) plants did show obvious growth defects, such as substantially delayed growth rate and flowering (Figure 4A and Figure 4B), undulation of some rosette leaves (Supplemental Figure 6), a significantly increased number of auxiliary branches at maturity (first- and higher order rosette branches and cauline branches) and no apical dominance (the length of the first-order branches was almost the same at different node positions) (Figure 4A). Both *pprd2 PPRD1-OE* and *pprd2 PPRD1-OE*$^{+/-}$ lines displayed problems with flower development (small petals, short stamen), pollination and silique maturation (short siliques with very few seeds - approx. 30% and 10% of WT for *pprd2 PPRD1-OE* and *pprd2 PPRD1-OE*$^{+/-}$, respectively), and in fact the latter plants were almost fully sterile (Supplemental Figure 6). The differences in *pprd2 PPRD1-OE* and *pprd2 PPRD1-OE*$^{+/-}$ phenotypes correlated well with the level of *PPRD1* transcript, which was considerably lower in all analyzed organs (including pollen) of *pprd2 PPRD1-OE*$^{+/-}$ compared to *pprd2 PPRD1-OE* (Figure 3C and Figure 3D). Moreover, DoI contents in the organs of *pprd2 PPRD1-OE* and *pprd2 PPRD1-OE*$^{+/-}$ lines were considerably different, namely for *pprd2 PPRD1-OE* plants DoI was 70.2% and 74.8% of the control WT while for *pprd2 PPRD1-OE*$^{+/-}$ DoI was 38.9% and 51.6% of control for stems and roots, respectively. Interestingly, DoI content was not changed in the leaves of these double mutant lines despite the increased transcript accumulation of *PPRD1* in this tissue. Additionally, Pren had highly increased accumulation in leaves of *pprd2 PPRD1-OE*$^{+/-}$ (approx. 2-fold) and especially in roots of *pprd2 PPRD1-OE* (approx.14-fold) and *pprd2 PPRD1-OE*$^{+/-}$ (approx.10-fold of control) (Figure 3E). Consequently, in roots of mutant lines (homozygous for *pprd2*) the ratio of Pren vs. DoI, calculated for the five most prevalent homologues Pren/DoI-14 – Pren/DoI-18, was increased from 0.05 for WT to approx. 2 for mutants (Figure 3E). Interestingly, the qualitative profile of

polyisoprenoids was not changed in these tissues. Thus, the shift of Pren:Dol ratio might indicate different mechanisms of regulation of PPRD enzymatic activity in leaves than in the other analyzed tissues.

Taken together, characterization of the *pprd2* mutant lines points to defects of the male gametophyte as the reason for *pprd2* lethality. Lack of PPRD2 is partially compensated for by overexpression of PPRD1, and this compensation is gene-dose dependent. Additionally, the impaired development of siliques of *pprd2 PPRD1-OE*$^{+/-}$ suggests some role of PPRD2 in female gametophyte function.

Lack of PPRD2 results in male sterility due to disturbed protein glycosylation and is rescued by exogenous Dol

Interestingly, the protein *N*-glycosylation status was clearly affected in the *pprd2 PPRD1-OE* and *pprd2 PPRD1-OE*$^{+/-}$ lines compared to WT as shown by specific staining of total leaf and flower proteins (Figure 4C and Supplemental Figure 7). This was additionally confirmed by the fate of SKU5 protein, involved in regulation of root growth and cell expansion, which in its native form is both *N*-glycosylated and GPI-anchored (Sedbrook et al., 2002). SKU5 was absent from flowers of *pprd2 PPRD1-OE* and *pprd2 PPRD1-OE*$^{+/-}$ plants, most probably due to proteolytic degradation of the unmodified polypeptide (Figure 4D) as earlier observed for *pnt1* mutant devoid of GPI-anchor biosynthesis (Gillmor et al., 2005). Similarly, mass spectrometry-based differential proteomics of WT and *pprd2 PPRD1-OE*$^{+/-}$ flower proteins revealed the absence of numerous proteins of vital physiological functions in *pprd2 PPRD1-OE*$^{+/-}$ plants (Supplemental Table 4).

Moreover, an elevated level of BiP2 protein, a marker of ER stress, was observed in both *pprd2 PPRD1-OE* and *pprd2 PPRD1-OE*$^{+/-}$ lines (Figure 4D). Consistent with this observation, *BiP2* expression was increased in flowers and especially leaves of *pprd2 PPRD1-OE*$^{+/-}$ plants, and, interestingly, the level of *BiP2* appeared to be negatively related with the level of *PPRD1* mRNA in individual plants (Supplemental Figure 6).

The development of male reproductive organs was monitored with Alexander staining – viable pollen grains are stained purple and dead ones green (Lalanne et al., 2004). Both WT and *pprd2-1*$^{+/-}$ anthers were full of purple pollen grains indicating that

pprd2-1$^{+/-}$ pollen was viable (Supplemental Figure 8). In parallel, *in vitro* pollen germination on solid medium revealed that approx. 43% of germinated *pprd2-1*$^{+/-}$ pollen grains displayed defects in tube growth and shape - swelling, shortening and branching (Figure 5B; Supplemental Table 5). By contrast, less than 4% of WT pollen produced abnormal pollen tubes (Figure 5B, Supplemental Table 5). These phenotypic differences were in accordance with the 50% decrease of *PPRD2* mRNA level in the pollen of heterozygous *pprd2-1*$^{+/-}$ plants compared to WT (Figure 5A). Aniline blue staining of WT pistils hand-pollinated with pollen of WT, *pprd2*$^{+/-}$ or *pprd2 PPRD1-OE* plants revealed inhibition of mutant pollen tube growth compared to WT, with more short tubes in the transgenic lines and fewer tubes reaching the bottom of the transmitting tract (Supplemental Figure 8).

To confirm that the shortage of functional PPRD was the reason for the pollen tube malformations, a rescue experiment was performed. Since Dol is the end-product of the enzymatic activity of PPRD, the solid medium used for pollen germination was supplemented with Dol or, in a control experiment, with polyprenol. Wild-type pollen displayed no abnormalities upon germination on either medium (Figure 5C). The supplementation of the growth medium with Dol resulted in an almost 100% rescue of the *pprd2-1*$^{+/-}$ pollen germination defect – the pollen tubes were of regular length and no malformations could be detected (Figure 5C). By contrast, the supplementation with Pren did not improve the pollen tube growth, confirming that specifically Dol, not just any polyprenol, was lacking in the *pprd2-1*$^{+/-}$ plants (Figure 5C, Supplemental Table 5).

To verify the mechanism of the effect of Dol shortage on pollen germination, WT pollen grains were germinated on solid medium supplemented with tunicamycin, an inhibitor of *N*-acetylglucosamine transferase (an essential enzyme of protein glycosylation) and inducer of ER stress. The morphology of tunicamycin-treated WT pollen tubes was almost identical to that of *pprd2*$^{+/-}$ pollen germinated on regular medium – swollen, shortened and branched tubes were noted (approx. 20 or 60% of total germinating pollen for 10 or 50 ng/ml tunicamycin, respectively, Figure 5D and Figure 5E, Supplemental Table 5). These pollen germination experiments strongly support the concept that the male sterility of *pprd2* plants is caused by shortage of Dol and consequent defects in protein glycosylation.

Additionally, scanning electron microscopy (SEM) examination revealed abnormalities in the exine structure of *pprd2-1*$^{+/-}$ pollen grain (Figure 6A). Consistently with the pollen germination results, approx. 38% of the observed grains were deformed (collapsed, shrunken, wrinkled) in contrast to WT pollen with only 3% deformed grains (Figure 6B). Upon a TEM analysis, the *pprd2-1*$^{+/-}$ pollen grains showed an abnormal cell wall of variable thickness, and some of the grains also had underdeveloped exine, uneven intine and slightly malformed ER structures. Furthermore, the electron density of lipid bodies was changed suggesting their modified composition (Figure 6C). In contrast, WT pollen showed a uniformly structured cell wall with clearly visible exine (T-shaped baculae and tecta) and regular intine structures and undisturbed cellular membranes. To summarize, mutations in the *PPRD2* gene lead to defects in pollen germination and development, and this explains the lack of functional pollen in *pprd2* mutants and the inability to obtain a homozygous *pprd2* sporophyte.

Discussion

Identification and functional characterization of *Arabidopsis thaliana* polyprenol reductases

Given the presence of Dols in plants, we undertook a search for polyprenol reductases (PPRDs) and identified two genes potentially encoding PPRD, *PPRD1* and *PPRD2* . Enzymatic activity of the corresponding PPRDs was confirmed both *in vivo* and *in vitro*. The catalytic domain was localized at their C-termini, similarly to hSRD5A3; in contrast to the human enzyme, however, the Arabidopsis PPRDs apparently had more than one catalytically active histidine residue.

Further studies are required to characterize PPRDs biochemically; however, the reduction of bacterial Pren-11 observed in this report together with the complex Dol mixture (Dol-7 to -35) present *in vivo* (Jozwiak et al., 2013; Surmacz et al., 2014) might suggest their broad substrate specificity. The function of the alternatively spliced *PPRD1* with persisting intron 3 or intron 4 remains unclear. Alternative splicing of *PPRD1* pre-mRNA might allow the plant to increase its adaptive potential in response to developmental and environmental cues, as suggested for other mRNA splice variants (Reddy et al., 2013). It might act, for instance, as a gene expression regulatory mechanism since alternatively spliced *PPRD1-INT3* and *–INT4* give rise to enzymatically inactive and/or unstable proteins.

Polyprenol reductase – a hitherto uncharacterized component of plant cell metabolism

Dol has been shown to participate in several vital cellular processes apart from protein glycosylation, e.g., aging and adaptation to adverse environmental conditions. Overexpression of *PPRD1* protects plants against environmental factors and ER stress caused by tunicamycin and, in line with this, expression of *PPRDs* (especially *PPRD2*) is enhanced upon stress (Supplemental Figure 9). Most probably an elevated Dol level compensates, at least partially, for the tunicamycin-induced disturbances in protein glycosylation, as clearly shown for pollen. Similarly, increased Dol-P-Man biosynthesis results in an increased resistance of *DPMS1*-OE plants to tunicamycin (Jadid et al., 2011). It seems worth mentioning that neither of the mutant lines characterized in this study, *pprd2-1*$^{+/-}$ and *pprd2-2*$^{+/-}$, showed hypersensitivity to ammonium salts (mentioned

earlier; Jadid et al., 2011). This discrepancy could result from differences in the experimental conditions used.

The enhancement of transcript accumulation of *PPRDs*, especially *PPRD2*, with plant age is in line with the increased Dol accumulation observed in senescing plant and mammalian tissues (summarized in Jones et al., 2009). Additionally, the tissue-specific expression pattern of *PPRDs* fits the Dol vs. polyprenol accumulation observed in the roots and leaves, respectively, even though the reason for this dichotomy remains obscure.

The differences between *PPRD1* and *-2* expression patterns suggest that they have specific roles in diverse organs. *PPRD2* mutants lack functional pollen as clearly shown by the results of reciprocal crosses and microscopic observations of pollen germination *in vivo* and *in vitro*. The defects due to *PPRD2* deficiency could be rescued by *PPRD1* overexpression only partially and in a gene-dose dependent manner. Thus, the development of sporophyte of *pprd2 PPRD1-OE*$^{+/-}$ (heterozygous for *PPRD1-OE*) was more severely affected than that of *pprd2 PPRD1-OE*, and similarly, seed formation, although considerably compromised in both lines, was substantially more efficient in the latter. This gene-dose effect is also mirrored at the molecular level - upon transcriptomic and lipid analysis of both lines. The partial compensation for PPRD2 deficit by PPRD1 suggests that these enzymes are not fully redundant. This seems understandable in light of their different cellular locations, of mainly the ER and the plasma membrane for PPRD2 and PPRD1, respectively, as suggested by the co-localization experiment. This result corroborates well with the *in silico* prediction (http://suba.plantenergy.uwa.edu.au/). Arabidopsis organelle proteome screening (Dunkley et al., 2006) has suggested that PPRD2 localizes to the ER, similarly to hSRD5A3 (Cantagrel et al., 2010; Sagami et al., 1993). The five TMDs predicted in the PPRDs makes ER membrane localization plausible. It seems likely, however, that besides these main cellular sites of residence, PPRDs might also undergo re-localization towards other cellular compartments. Dol biosynthetic machinery is involved in protein sorting and intracellular vesicular transport (Sato et al., 1999; Belgareh-Touze et al., 2003), and Dol overproduction resulting from PPDR expression might result in the enhancement of these processes. The ER localization of PPRD2 is in line with the

intracellular organization of Dol biosynthesis - formation of polyprenyl diphosphate, the substrate of PPRDs, is completed in ER (Skorupinska-Tudek et al., 2008). Moreover, Dol kinase is also localized in the ER of mammalian cells (Shridas and Waechter, 2006), and Dol-P thus produced is easily accessible to the ER-resident saccharide transferases biosynthesizing Dol-P-linked (oligo)saccharides (Supplemental Figure 10).

In summary, PPRD2 plays a crucial role in sporophyte growth and is critical for normal development of the male gametophyte, suggesting that protein glycosylation is required for reproductive processes.

Polyprenol reductase – a regulator of pollen development

The molecular mechanism linking the Dol cycle with biosynthesis of the pollen grain surface layer awaits clarification. Pollen wall comprises intine and exine (Quilichini et al., 2015). The intine is the innermost layer made up of cellulose and pectin. It maintains the structural integrity of pollen grains, as Arabidopsis plants with mutations in primary cell wall cellulose synthases (CESAs) produce collapsed or malformed pollen grains with aberrant pollen walls that lack or have uneven intine layer (Persson et al., 2007). Interestingly, the morphology of pollen grains of *pprd2* resembles that of mutants in genes encoding catalytic subunits of CESA (*cesa1-1* and *cesa3-1*). Moreover, the unevenly deposited cell wall of pollen grain, especially the intine layer, seems a common feature of *pprd2-1* and mutants in cellulose synthase-encoding genes (compare Figure 3F Persson et al., 2007 and Figure 6 this report). CESA requires *N*-glycosylated (Kang et al., 2008) KORRIGAN (KOR1) protein for activity (Mansoori et al., 2014), a fact that might explain the involvement of PPRD2 in intine formation.

The exine surrounding the intine is a complex structure made of sporopollenin (i.e. covalently cross-linked phenolics and polyhydroxylated aliphatics containing most probably also fatty alcohols, since fatty acid reductase encoded by *MALE STERILITY2* is required for exine formation). Sporopollenin provides the rigid and sculptured framework of the exine, which serves to encapsulate and protect the contents of spores/pollen, and to assist in stigmatic capture. Components of the exine are biosynthesized by the tapetal cells and deposited on the surface of developing microspores (Quilichini et al., 2015 and references therein). Recent identification of the involvement of GPI-anchored non-specific lipid transfer proteins in the biosynthesis or

deposition of sporopollenin (Edstam et al., 2013) might suggest the role of Dol, a compulsory cofactor of the biosynthesis of GPI-anchored proteins, in sporopollenin biosynthesis. Despite the observations described above, genes encoding proteins of the Dol cycle, e.g., *CPT*, *DOK*, *PPRD*, escaped identification within a large-scale genetic screen aimed at detection of those involved in pollen exine production (Suzuki et al., 2008; Dobritsa et al., 2011).

Although neither Dol nor Pren have ever been identified as components of pollen grain surface layers, this possibility has been raised based on the expression of the *cis*-prenyltransferase-encoding gene *LLA66* (accession No. DQ911525) of *Lilium longiflorum* in the microspores and the anther cell wall. Expression and activity of Ll-CPT correlated with tapetal growth and disintegration (Liu et al., 2011). Interestingly, the genes encoding close Arabidopsis homologs of Ll-CPT, namely CPT4 and CPT5 (Surmacz and Swiezewska, 2011), are expressed mainly in inflorescence, pollen and flower (Genvestigator). Their lipid products, polyprenyl diphosphates of not yet identified chain-length, might possibly serve as substrates for PPRD2.

Besides its putative role as component of pollen grain surface layer(s) Dol might also regulate the function of tapetum and/or other pollen grain surface layers via the biosynthesis of particular glycosylated and/or GPI-anchored proteins. So far, such a role might be predicted based on the presence of several potential *N*-glycosylation sites identified in the sequence of polygalacturonase inhibitory protein (Bc-MF19) expressed exclusively in the tapetal cells and microspores during anther development in Chinese cabbage Bc-MF19 (Huang et al., 2011). Even more interestingly, a gene encoding SKU5-SIMILAR18 (AT1G75790) protein possessing four potential *N*-glycosylation sites is coexpressed (TAIR) with *ACYL-COA SYNTHETASE5* (*ACOS5*), which is critical for pollen development and sporopollenin biosynthesis (Quilichini et al., 2015). Moreover, Dol deficiency might disturb the function of COBL10, a glycosylphosphatidylinositol (GPI)-anchored protein that is a component of pollen tube internal machinery critical for normal pollen tube growth and directional sensing in the female transmitting tract (Li et al., 2013). In line with this, an essential role of Dol kinase (DOK) in pollen development and the pollen tube reception pathway (Lindner et al., 2015) has been described very recently.

Taken together, these observations might explain the intine and exine malformations observed in the pollen grains of Dol-deficient *pprd2* mutants.

Polyprenol reductase – a component of the protein glycosylation machinery

Since Dol is an obligatory cofactor of protein glycosylation, mutations resulting in Dol deficiency should eventually lead to phenotypic aberrations observed for diverse mutants in this pathway. Indeed, developmental defects in male and female gametophytes leading to sterility similar to those observed for *PPRD2* disruption have been reported for several null mutants, both upstream and downstream of Dol (Supplemental Table 6), e.g., for Dol kinase deficiency (Kanehara et al., 2015). For the *pprd2* homozygous mutants, consistently with their Dol deficiency, defects in *N*-glycosylation were accompanied by degradation of some proteins, e.g. SKU5. Similarly, in Dol-P-Man synthase null mutants, reporter *N*-glycosylated and GPI-anchored proteins were affected (Jadid et al., 2011). The distinct phenotypes observed for various protein glycosylation-related mutants (Supplemental Table 6) are presumably caused by different degrees of hypoglycosylation of particular proteins.

Interestingly, in contrast to the mutations affecting the mevalonate (MVA) pathway, those compromising the second isoprenoid-generating route in plants, the methylerythritol phosphate (MEP) pathway, have not been shown to result in plant sterility.

The diverse clinical manifestations of *hSRD5A3* mutations do not include impaired fertility. Moreover, the excess of polyprenols accumulated in SRD5A3 patients' cells is considered toxic due to the polyprenol vs. Dol competition during polyisoprenoidPP-tetradecasaccharide assembly (Gruendahl et al., 2012). In Arabidopsis leaves, the content of polyprenols (Pren-10 dominating) highly exceeds that of Dols (Dol-16 dominating) (Gawarecka and Swiezewska, 2014), but the considerable difference of their chain-length suggests that the substrate specificity of Dol kinase and/or saccharyl transferases protects these cells against the potential toxicity of Pren excess. Moreover, sequestration of Pren in plastids might also serve as a salvage mechanism.

In conclusion, the PPRD2 polyprenol reductase is essential for the development of gametophytes and the sporophyte, and the *pprd2* knock-out mutation is lethal due to

male sterility. Defective protein glycosylation seems the major reason for these malfunctions although disturbances in other cellular Dol-dependent processes could also contribute. Additionally, involvement of PPRDs in other pathways besides the Dol cycle, e.g., reduction of other vital cellular substrates cannot be ruled out.

Supplementation of polyprenol reductase-deficient cells with Dol has been discussed as a method to compensate for deficiency in protein glycosylation, and, from a longer perspective, supplementation of the human diet with Dol-enriched plant tissues could allow new therapeutic interventions for glycosylation disorders. Complete elucidation of the Dol cycle in plant cells, via the current identification of PPRD1 and -2, renders manipulation of Dol content in plant tissues theoretically feasible.

The experimental model developed in this report, revealing beneficial effects of supplementation with exogenous Dol on PPRD2-deficient pollen tube development, might be suitable to test new therapeutic strategies of SRD5A3-CDG polyprenol reductase deficiency therapy since no such model is currently available.

Finally, an alternative albeit still not recognized pathway leading to Dol has been postulated in yeast and human to account for the residual Dol and partially retained protein glycosylation found in DFG10 and SDR5A3 and null-mutants (Cantagrel et al., 2010; Gruendahl et al., 2012). Whether a similar, SRD5A3/PPRD-independent Dol-producing pathway functions in plants awaits clarification (Supplemental Figure 10).

Materials and Methods

Plants and plant growth conditions

Arabidopsis thaliana ecotype Col-0 (WT control) as well as mutant lines *pprd2-1* and *pprd2-2* (SALK_113221C and SALK_006421, respectively) and *PPRD1-OE* (GK_575B02) were from the Nottingham Arabidopsis Stock Center.

Progeny of *pprd2-1, pprd2-2* and *PPRD1-OE* lines were genotyped and *PPRD1-OE* homozygous line was isolated. *pprd2* mutants were maintained as heterozygous segregating lines due to lethality of the homozygote.

In *pprd2-2*, an additional T-DNA insertion on the fifth chromosome was found, and after segregation, plants with single insertion located exclusively in *PPRD2* CDS on chromosome 2 (At2G16530 locus) were obtained. For the *pprd2 PPRD1-OE* and *pprd2 PPRD1-OE*$^{+/-}$ plants, *PPRD1-OE* was crossed to *pprd2-1*$^{+/-}$ and the F2 generation of the progeny was screened by PCR for homozygosity. F3 plants homozygous for both traits (*pprd2 PPRD1-OE*) or heterozygous for *PPRD1-OE* (*pprd2 PPRD1-OE*$^{+/-}$) were used. *PPRD1*$_{pro}$*:GUS* or *PPRD2*$_{pro}$*:GUS* expressing lines were constructed by Agrobacterium transformation of WT Arabidopsis Col-0 with gateway binary vector pGWB633 vector carrying *GUS* under native *PPRD1* or *PPRD2* promoter (Nakamura et al., 2010), sequences of the primers are listed in Supplemental Table 7. The fourth homozygous generation after transformation was used for experiments.

Plants for segregation analysis, phenotyping, and pollen collection were grown in a greenhouse under a long-day (16 h light) photoperiod at 21/18°C. Plants for RNA extraction, RT–PCR, lipid analysis and GUS histochemical analysis were grown in hydroponic culture in Gilbert medium in a growth chamber (AR-66L CLF Plant Climatics). Seedlings for GUS histochemical analysis were grown on plates with half-strength Murashige and Skoog (MS) medium supplemented with vitamins, 1% sucrose and solidified with 1.2% agar. To test the effect of stressors on seed germination standard ½ MS growth medium supplemented as above and with an appropriate stressor – sorbitol (final concentration 300 mM) or NaCl (150 mM) was used. To test the effect of tunicamycin on plant development 4-day-old seedlings grown on plates with standard ½ MS medium were transferred onto plates supplemented with tunicamycin (final concentration 200 ng/ml) and grown for 10 days.

Pollen for RNA extraction and gene expression analysis was collected as described earlier (Becker et al., 2003). Genotyping was performed with specific primers designed with the aid of T-primer design tool and LBb1.3 primer (Supplemental Table 7).

Cloning of *Arabidopsis thaliana* genes encoding polyprenol reductase, *PPRD1* and *PPRD2*

Putative genes encoding polyprenol reductases were identified in the Arabidopsis genomic sequence by searching with human gene encoding polyprenol reductase hSRD5A3. Total RNA from Arabidopsis roots was isolated and purified using the RNeasy Plant Mini Kit (Qiagen) according to the manufacturer's instructions. The mRNA was transcribed to cDNA, and *PPRD1* and *PPRD2* coding sequences (CDS) were amplified by PCR using specific primers (Supplemental Table 7). DNA fragments with CACC sequence at the 5'-end were cloned into the pENTR vector according to manufacturer's instructions (pENTR D-TOPO, Invitrogen).

Heterologous expression of *PPRD1* and *-2* and analysis of carboxypeptidase Y (CPY) glycosylation in *S. cerevisiae* transformants

PPRD1 and *PPRD2* CDS were recombined from pENTR to the yeast expression vector pYES-DEST52 using the LR Clonase enzyme mix according to manufacturer's instructions (Gateway LR Clonase II Enzyme mix, Invitrogen).

Yeast *S. cerevisiae* strains (BY4741, L5366 and mutant strains *dfg10*Δ and *dfg10-100* generated in the BY4741 and L5366 genetic background, respectively; Cantagrel et al., 2010) were grown on liquid minimal medium (0.67% Yeast Nitrogen Base, 2% galactose and appropriate amino acids without uracil) to stationary phase.

Protein extraction was done using post-alkaline extraction (Kushnirov, 2000).

Proteins were separated on 12% SDS-PAGE and transferred for 1 h to nitrocellulose membrane. The blots were incubated in a primary antibody solution (anti-CPY mouse antibody, Invitrogen, catalog number A6428, lot number 884879) at a dilution of 1: 2000 O/N in the cold room with agitation. They were then washed three times in PBS-T and incubated with secondary antibody (anti-mouse IgG HRP-conjugated, Sigma – Aldrich, catalog number A9044, lot number 031M4752) diluted to 1: 1000 for 1.5 h at room temperature with agitation. The blots were washed as above and developed for 1 min

with ECL detection reagent (SuperSignal West Pico Chemiluminescent Substrate, Thermo Scientific) according to the manufacturer's instructions.

Transformation with empty vector or native yeast *DFG10* was used as negative or positive control, respectively.

Site directed mutagenesis of *PPRD2*

Mutations in *PPRD2* CDS were introduced by PCR site-directed mutagenesis using specific primers with modified nucleotide sequence (Supplemental Table 7).

Polyisoprenoid profiling of yeast strains

Yeast strains were cultured in minimal media and harvested in log phase (OD_{600} 1). Cultures (100 ml, 48 h) were centrifuged for 10 min at 1500 x *g* (Allegra, Beckman). Supernatant was removed by decantation; the pellet was resuspended in 5 ml hydrolyzing mixture (0.5M KOH in 60% EtOH) and placed in hot water bath (85°C) for 1 hour. After cooling down, 15 ml water and 5 ml hexane were added. Lipids were extracted five times with 5 ml portions of hexane. Pooled organic fractions were evaporated under stream of nitrogen and dissolved in 200 µl propan-2-ol. Polyisoprenoid alcohols were analyzed as described previously (Jozwiak et al., 2013). Polyprenol and Dol standards were from the Collection of Polyprenols, IBB PAS, Warsaw.

Heterologous expression of *PPRD1* and *PPRD2* in *E. coli*

Plasmids harboring *PPRD1* or *PPRD2* were prepared by cloning appropriate nucleotide sequences into pGEX-4T-1 vector (GE Healthcare Life Sciences) cut blunt-ended with SmaI enzyme. The resulting vectors produced N-terminal GST fusions of PPRD1 or PPRD2 protein.

Escherichia coli BL21 strain was transformed with the above plasmids and grown on LB plates with ampicillin (100 µg/ml); empty pGEX-4T-1 vector was used as a negative control. Overnight bacterial culture (250 µl) was transferred to fresh medium (25 ml) and grown to OD600 of 1.0. Expression of *PPRD1* and *-2* was induced by the addition of 25 µl 0.1 M IPTG, followed by incubation for 4 h.

For protein purification and mass spectrometry analysis 20 ml bacterial cell culture was harvested by centrifugation, resuspended in lysis buffer (50 mM Tris pH 8.0, 10% glycerol, 0.1% Triton X-100, 100 µg/ml lysozyme, 1 mM PMSF, 2 mM $MgCl_2$), and incubated for 30 min on ice and sonicated – 5 x 1 min. Crude lysate was used for

enzymatic assay. Protein bands corresponding to PPRDs were excised from SDS-PAGE gel and analyzed by mass spectrometry.

In vitro reduction of polyprenol by PPRD1 or PPRD2

The assay was performed following the procedures described previously (Sagami et al., 1993, Cantagrel et al., 2010) with modifications. The reaction mixture consisted of 50 mM Tris-HCl (pH 8.0), 1 mM DTT, 50 mM KF, 20% glycerol, 2 mM $MgCl_2$, 0.1% Triton X-100, and 3.3 µg Pren-16 (C80) in 5 µl ethanol. After 25 min sonication in a water bath the reaction was initiated with the addition of 10 mM NADPH and 700 µg crude cell-extract proteins to give a final volume of 1250 µl. After incubation for 18 hours at 24°C, the samples were supplemented with 1 ml chloroform : methanol (2:1; v/v), and lipids were extracted and analyzed by HPLC/UV as described previously (Jozwiak et al., 2013). Polyprenol and Dol standards were from the Collection of Polyprenols, IBB PAS, Warsaw.

Cloning of promoters of _PPRD1_ and _-2_ and construction of lines expressing $PPRD1_{pro}$:_GUS_ and $PPRD2_{pro}$:_GUS_

To generate reporter constructs, the promoter regions of *PPRD1* (–1103 bp upstream of ATG) and *PPRD2* (–1041 bp upstream of ATG) were amplified from genomic DNA and cloned into the Gateway entry vector pENTR (Invitrogen). The promoter sequences were then subcloned into the binary plant transformation vector pGWB633, resulting in reporter constructs. The reporter constructs were used to transform *Agrobacterium*. The Agrobacterium transformants were used to generate lines expressing $PPRD1_{pro}$:*GUS* and $PPRD2_{pro}$:*GUS* using floral dip method as described previously (Bent, 2006).

Histochemical analysis of β-glucuronidase (GUS) activity

Histochemical localization of GUS in several independent transgenic lines harboring the $PPRD1_{pro}$:*GUS* or $PPRD2_{pro}$:*GUS* constructs was performed as described by Jefferson et al. (1987) with some modifications. Sample tissues were infiltrated with the reaction buffer (50 mM Na_2HPO_4–NaH_2PO_4 pH 7.0, 0.5 mM $K_3Fe(CN)_6$, 0.5 mM $K_4Fe(CN)_6$) containing 2 mM 5-bromo-4-chloro-3-indolyl-β-D-glucuronic acid (X-Gluc) as substrate under vacuum, and incubated at 37°C overnight. Plant pigments were extracted with

80% ethanol and the histochemical staining was analyzed under a binocular microscope (SMZ1500, Nikon).

Subcellular localization analysis of PPRD1 and PPRD2

Agrobacterium tumefaciens-mediated transient expression in *Nicotiana benthamiana* was employed. *PPRD1* and *PPRD2* were cloned into the pGWB451 gateway binary vector (Nakagawa et al., 2007). Cd3-959, cd-967 and cd3-1007 vectors were used as ER, Golgi and plasma membrane markers, respectively (Nelson et al., 2007). Recombinant plasmid (50 ng) was introduced into *Agrobacterium tumefaciens* strain GV3101 using the freeze/thaw method (Weigel & Glazebrook, 2002).

For infiltration, recombinant strains were grown overnight at 28°C with agitation in LB medium supplemented with spectinomycin (30 µg/ml) or kanamycin (30 µg/ml), respectively. Cells were pelleted at 3300 x *g* for 3 min at 20°C, resuspended in infiltration medium containing 10 mM MES (pH 5.6) and 10 mM $MgCl_2$ supplemented with 100 µM acetosyringone and diluted to OD600 of 0.4. After incubation at RT for 3 hours, cells were infiltrated by injection into the bottom side of the third or fourth leaf of 6-week-old *N. benthamiana* plants with a needless syringe. After 24-48 h, leaf discs of the infiltrated areas were observed under confocal microscope.

Quantitative (qPCR) analysis of expression of genes encoding polyprenol reductase and *BiP2*

Total RNA was isolated and purified using the RNeasy Plant Mini Kit (Qiagen) according to the manufacturer's instructions. First-strand cDNA synthesis was carried out with 2 µg of RNA using the RevertAid First Strand cDNA Synthesis Kit (ThermoScientific) and oligo-dT primers according to the manufacturer's procedure.

PPRD1, PPRD2 or *BiP2* expression analysis was performed in a total volume of 20 µl Luminaris Color HiGreen high ROX qPCR Master Mix (ThermoScientific) using gene-specific primers in a StepOnePlus Real-Time PCR System (Applied Biosystems) according to the manufacturer's instructions.

The cycle threshold (Ct) was used to determine the relative expression level of a given gene using the $2^{-\Delta\Delta Ct}$ method. The relative expression level of *PPRD1, PPRD2* and *BiP2* was normalized against *ACTIN2*. Statistical analysis of the qPCR data was performed using one-way ANOVA with Tukey's post test.

Analysis of protein glycosylation

Proteins were isolated according to Guillaumot et al., 2009. Protein extracts (30 µg/line) were separated by SDS-PAGE (10%) and subsequently two methods, using either Concanavalin A or Emerald 300, were employed to detect glycosylated proteins.

Concanavalin A method: the SDS-Page gels prepared in parallel were either stained with Coomassie Brilliant Blue or transferred to membrane as described above; the membrane was probed for 17 h with Concanavalin A labeled with horseradish peroxidase (1 µg/ml, Sigma – Aldrich, catalog number L6397, lot number SLBL8763V), washed with PBS for 50 minutes and developed for 5 seconds with ECL reagent (SuperSignal West Pico Chemiluminescent Substrate, Thermo Scientific) according to the manufacturer's instructions. Detection was performed with Molecular Imager ChemiDoc XRS+ with ImageLab Software (BioRad).

Emerald 300 method: SDS-PAGE gels prepared in parallel were stained with either Coomassie Brilliant Blue or Pro-Q®Emerald 300 Glycoprotein Gel and Blot Stain Kit (Invitrogen) according to the manufacturer's instructions.

Immunodetection of SKU5 and BiP2 by Immunoblotting

Proteins (30 µg/line) separated on 10% SDS-PAGE were transferred to membrane as described before and probed for 12h with either anti-SKU5 (1:1000, provided by Dr. J.C. Sedbrook, Illinois State University) or anti-BiP2 (1:2000, Agrisera) antibody (catalog number AS09 481). They were then washed three times in PBS-T and incubated with secondary antibody (anti-Rabbit IgG HRP-conjugated, Sigma – Aldrich, catalog number A0545, lot number 083M4752) diluted to 1: 1000 for 1 h at room temperature with agitation. The blots were washed and developed for 5 min with ECL detection reagent (SuperSignal West Pico Chemiluminescent Substrate, Thermo Scientific) according to the manufacturer's instructions.

Pollen *in vitro* germination

In vitro pollen germination and growth were performed on solid medium for 16 h at 22°C according to Boavida and McCormick (2007). For chemical complementation experiment Pren-16 or Dol mix (Dol-16 – Dol-21) (Collection of Polyprenols, IBB PAS) were added to the hot pollen germination medium at a final concentration of 10 mM.

Aniline blue staining of pollen tubes growing in the pistil

730 Hand-pollinated Arabidopsis pistils were collected 12 hours after pollination and placed
731 in Carnoy's solution (60% ethanol, 30% chloroform, 10% acetic acid). After approx. 3
732 hours, the fixative was changed to 70% ethanol and left for 10 min at room temperature.
733 After that, the same treatment was performed using 50, 30% ethanol and water. The
734 specimens were moved into alkaline solution (1 M NaOH) and left covered overnight at
735 RT. Pistils were washed with water for 10 minutes and then stained with 0.1% aniline
736 blue in 50 mM K_3PO_4 (pH 11) for 2 hours in darkness. The morphology of pollen tube
737 growth in the pistil was observed under an Eclipse E800 microscope (Nikon
738 Instruments).
739 **Staining of pollen anthers with Alexander stain**
740 Staining of pollen anthers with Alexander stain and microscopic observations were
741 performed as described earlier (Gutkowska et al., 2015).
742 **Microscopic observations**
743 The morphology of pollen germinating *in vitro* was observed under an Eclipse E800
744 microscope (Nikon Instruments) equipped with a CCD camera (Hamamatsu). Image
745 acquisition was performed with Lucia software (Laboratory Imaging). At least 10 visual
746 fields of material derived from 6 different plants obtained from three independent plant
747 cultivations were used for scoring in each case. The morphology of flowers and siliques
748 was studied under a Nikon D7000 camera equipped with a Nikon AF-S 60 f/2.8 G ED
749 Micro lens.
750 Subcellular localization of PPRD1 and PPRD2 was observed under a C1 confocal
751 microscope (Nikon Instruments). Images were recorded with the EZ C1 image
752 acquisition software (Nikon Instruments) and processed with EZ-C1 Viewer v.3.6 (Nikon
753 Instruments).
754 For TEM observations, flowers (green buds) were fixed in 2.5% glutaraldehyde in 100
755 mM cacodylate buffer (pH 7.2) overnight, rinsed once in the buffer, and post-fixed in 1%
756 osmium tetroxide overnight. Samples were rinsed, dehydrated in a graded ethanol
757 series (30, 50, 75, and 100%), and finally embedded in epoxy resin. Ultrathin sections
758 were cut with a diamond knife on an MTX ultramicrotome (RMC Boeckeler Instruments).
759 Specimens were examined using a LEO 912AB transmission electron microscope (Carl
760 Zeiss). Grains derived from the same *pprd2-1*$^{+/-}$ mutant plant were used to compare the

phenotypically WT vs. *pprd2-1* pollen. For SEM observations, pollen was spilled directly on microscope tables, coated with a thin layer of gold, and examined using a LEO 1430VP scanning electron microscope (Carl Zeiss).

Extraction of lipids from Arabidopsis tissues

Plant material (approx. 10g of fresh mass, collected from 3 plants) was supplemented with an internal standard (Prenol-19, 10 µl, 1 µg/µl, Collection of Polyprenols, IBB PAS) and 20 ml chloroform : methanol mixture (1:1, v/v) was added. The tissue was homogenized with an Ultra-Turrax apparatus (IKA Labortechnik). After dispersion, the mixture was agitated for 24 h at room temperature. The homogenate was filtered under reduced pressure, and the remaining tissue was re-extracted with 20 ml chloroform : methanol (2:1, v/v) and then 20 ml chloroform. The filtrates were pooled and evaporated under reduced pressure. Crude lipid extract was hydrolyzed, purified on a silica gel column and analyzed by HPLC-UV as described previously (Jozwiak et al., 2013). Each lipid extraction was performed in triplicate.

Bioinformatics

In silico analyses of Arabidopsis polyprenol reductases were performed using: BLAST P (comparison of protein sequences – identification of homologues), Clustal W (multiple sequence alignment, see Supplemental Data set 1), MEGA 6 (phylogenetic tree representation), TMHMM Server, v. 2.0 (topology prediction – prediction of membrane-spanning segments) and Pfam database (http://pfam.xfam.org/ - Wellcome Trust Sanger Institute, Cambridge, UK - identification of steroid 5α-reductase domains). PPRD protein sequences were aligned using a Gonnet matrix by the Clustal W (Larkin et al., 2007), with an open gap penalty of 10 and an extend gap penalty of 0.1 in pairwise alignments, an extend gap penalty of 0.2 in the multiple alignment, and a delay divergent setting of 30%. Phylogenetic relationships among the PPRDs were reconstructed using a neighbor-joining method by MEGA 6 (Tamura et al., 2013) with the Poisson amino acid substitution model. Two thousand bootstrap replicates were performed in each analysis to obtain the confidence support.

Accession Numbers

Sequence data from this article can be found in the Arabidopsis Information Resource (TAIR) under the following accession numbers: *PPRD1* (At1g72590), *PPRD2*

(At2g16530), *BiP2* (At5g42020), *ACTIN-2* (At3g18780) and for *SRD5A3* in the GenBank under the number NM_024592.4..

Supplemental Data

Supplemental Figure 1. Alignment of Amino Acid Sequences of Proteins with Steroid 5α-Reductase Domain from Human (hSRD5A3), Yeast *Saccharomyces cerevisiae* (Dfg10p) and 60 Plant Species.

Supplemental Figure 2. Evolutionary Tree of Proteins with Steroid 5α-Reductase Domain.

Supplemental Figure 3. Models of PPRDs.

Supplemental Figure 4. Schematic Representation and Expression of *PPRDs*.

Supplemental Figure 5. Subcellular localization of PPRD2 and PPRD1.

Supplemental Figure 6. Phenotypes of WT, *pprd2-1*$^{+/-}$, *PPRD1-OE*, *pprd2 PPRD1-OE* and *pprd2 PPRD1-OE*$^{+/-}$ Plants.

Supplemental Figure 7. Analysis of Glycosylated Proteins in WT, *pprd2-1*$^{+/-}$, *pprd2 PPRD1-OE* and *pprd2 PPRD1-OE*$^{+/-}$ Plants.

Supplemental Figure 8. Alexander Staining of Mature Anthers of WT and *pprd2-1*$^{+/-}$ Plants and Aniline Blue Staining of Pollen Tubes in the Pistil.

Supplemental Figure 9. Effect of At-*PPRD1* Overexpression on Plant Tolerance to Stress.

Supplemental Figure 10. Dol Cycle in Plant Cells.

Supplemental Table 1. Comparison of Amino Acid Sequences of Putative Arabidopsis PPRDs with Human and Yeast Polyprenol Reductases Based on the Alignment.

Supplemental Table 2. Localisation of Predicted 3-oxo-5-α-steroid 4-dehydrogenase Domain in Arabidopsis Polyprenol Reductases.

Supplemental Table 3. Seed Germination of *pprd2-1*$^{+/-}$ and *pprd2-2*$^{+/-}$ Plants on Solid Medium.

Supplemental Table 4. Mass Spectrometry-based Differential Proteomics of WT and *pprd2 PPRD1-OE*$^{+/-}$ Plants.

Supplemental Table 5. Effect of Polyprenol, Dol and Tunicamycin on Pollen Germination.

Supplemental Table 6. Phenotypes of Arabidopsis Mutants in Genes Encoding Elements of Isoprenoid Biosynthesis or Protein Glycosylation Pathways.

Supplemental Table 7. Primers Used for Genotyping, Cloning, Mutagenesis and Expression Studies.

Supplemental Data set 1. Text file of the alignment used for the phylogenetic analysis shown in Supplemental Figure 2.

Acknowledgments

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Author Contributions

A.J., M.G. and E.S. designed the research, A.J., K.G., L.S., A.B., M.L. and J.N. performed the research, and A.J., M.G. and E.S. analyzed data and wrote the paper.

Figure legends

Figure 1. Analysis of enzymatic activity of PPRD1 and PPRD2 *in vivo* and *in vitro.*

(A) Reduction of polyprenol to Dol - schematic representation; SRD5A3 and Dfg10 are the human and yeast enzymes, respectively.

Analysis of the glycosylation status of CPY (B) and polyisoprenoid profile (C) of the *dfg10*Δ yeast mutant transformed with either yeast *DFG10* or Arabidopsis *PPRD1*, *PPRD2*, *PPRD1-INT3* or *PPRD1-INT4* constructs; *dfg10*Δ and WT transformants with empty vector were used as a negative and positive control, respectively. The CPY glycosylation and Pren:Dol ratio of *dfg10*Δ are rescued by *DFG10*, *PPRD1* and *PPRD2* expression.

CPY (mature and hypoglycosylated forms) is detected by specific anti-CPY antibody. Positions of fully glycosylated CPY (mCPY) and the four hypoglycosylated forms (-1, -2, -3, -4) are indicated.

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(E) Reduction of exogenous Pren-16 *in vitro* by recombinant PPRD1 or PPRD2 produced in *E. coli*. Extracted lipids were analyzed by HPLC/UV. Black traces represent negative control reactions (bacteria transformed with an empty vector), red traces represent reactions with cell lysates from bacteria expressing PPRD1 or PPRD2. The rightmost chromatogram shows that Dol-11 is produced from endogenous Pren-11 in bacteria expressing PPRD2.

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Figure 2. Expression pattern of genes encoding polyprenol reductases in Arabidopsis and subcellular localization of PPRDs.

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Histochemical localization of GUS expression driven by the *PPRD1* or *PPRD2* promoter in transgenic Arabidopsis was analyzed at various time points. (B) 4, 10 and 14 days after germination, (C) in 31 day-old plants. In contrast to *PPRD1, PPRD2* promoter drives broad expression in Arabidopsis tissues.

(D) Co-localization of GFP-tagged PPRD2 or PPRD1 (green) with ER and PM markers – ER:mCherry and PIP2A:mCherry (red). Scale bar = 10 μm. Representative pictures are presented. See also Supplemental Figure 5.

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(A) Schematic representation of *PPRD1* and *PPRD2*. Grey and light grey boxes represent exons and 5'- and 3'-UTRs, location of T-DNA insertion in *PPRD1-OE*, *pprd2-1* and *pprd2-2* is shown. Positions of primers used for PCR-based genotyping or qPCR are indicated. Sequences of the borders of T-DNA inserts are provided.

(B-D) Expression of *PPRDs* in Arabidopsis. (B) Expression in various organs of 35-day-old Arabidopsis mutant plants normalized to the expression in leaves of same age WT plants. T-DNA *PPRD* gain-of-function (homozygous *PPRD1-OE*) and loss-of-function (heterozygous *pprd2-1*$^{+/-}$ and *pprd2-2*$^{+/-}$) mutant lines were analyzed;

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(E) Content of polyisoprenoid alcohols in leaves, stems and roots of WT, *PPRD1-OE*, *pprd2-1*$^{+/-}$, *pprd2-2*$^{+/-}$, *pprd2 PPRD1-OE* and *pprd2 PPRD1-OE*$^{+/-}$ plants, the rightmost panel shows the ratio of Pren vs. Dol content. Considerably increased ratio (higher polyprenol content) is observed for *pprd2 PPRD1-OE* and *pprd2 PPRD1-OE*$^{+/-}$ lines.

Values (±SD) represent mean of three, four and five independent experiments for roots, stems and leaves, respectively.
Statistically significant differences compared to WT plants are indicated; * - $P<0.05$ and ** - $P<0.01$.
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Figure 4. Phenotypic characteristics of *PPRD1-OE* and *pprd2*$^{+/-}$ plants and their crosses.
(A) Rosettes of 5-week-old plants (upper panel), flowers (middle panel), and whole 7-week-old plants (lower panel) are presented. Arrows indicate delayed flowering of *pprd2 PPRD1-OE* and *pprd2 PPRD1-OE*$^{+/-}$ lines. To illustrate that the *pprd2 PPRD1-OE*$^{+/-}$ plants show delayed rather than blocked development, the inset presents a 10-week-old plant; scale bar = 5 cm.
(B) Siliques of 7-week-old (WT, *pprd2-1*$^{+/-}$, *PPRD1-OE* and *pprd2 PPRD1-OE*) and 10 week-old (*pprd2 PPRD1-OE*$^{+/-}$) plants; scale bar = 1 cm.
Analysis of glycosylated proteins in WT, *pprd2-1*$^{+/-}$, *pprd2 PPRD1-OE* and *pprd2 PPRD1-OE*$^{+/-}$ plants. Protein extracts from leaves and flowers were separated by SDS-PAGE and blots were probed with (C) Concanavalin A labeled with horseradish peroxidase (left image). Gel stained with Coomassie Brilliant Blue is presented in right image. Marker lines contain PageRuler^{TM} Prestained Protein Marker. Asterisks mark bands present in WT extracts but absent in *pprd2* lines. Alternatively, blots were probed with (D) anti-SKU5 or anti-BiP2 antibody. In *pprd2* homozygotes, SKU5 protein is (nearly) absent while the BiP2 level is elevated compared to WT. Equal amounts of protein were loaded in all lanes.
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Figure 5. Development of pollen of the *pprd2-1*$^{+/-}$ line – effect of supplementation with Dol.
(A) Expression of *PPRD2* in WT and *pprd2-1*$^{+/-}$ pollen. Values are the means ± SD of three independent experiments.

Germination of pollen grains from WT and heterozygous *pprd2-1*$^{+/-}$ plants on regular medium (B), medium supplemented with polyprenol or Dol (C), or with tunicamycin (D, final concentration 10 or 50 ng/ml). Tube deformations (arrows), significantly more frequent for *pprd2-1*$^{+/-}$ than WT plants, are rescued by Dol but not Pren. Tunicamycin significantly increases number of deformed pollen tubes - scale bar = 100 μm.
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(C) Morphology and ultrastructure of pollen from *pprd2-1*$^{+/-}$ plants - TEM images. For phenotypic comparison, WT vs. *pprd2-1* pollen grains were derived from the same *pprd2-1*$^{+/-}$ mutant plant. Top row, general morphology of pollen grains; scale bar = 1 μm. Cell wall, intine and exine (middle row, scale bars = 500) and lipid bodies and ER (bottom row, scale bars = 250 nm) of *pprd2-1*$^{+/-}$ mutant are altered. Representative pictures are presented. In, Intine; Ne, Nexine; Se, Sexine; PM, plasma membrane; PC, pollen coat; PG, pollen grainLb, Lipid body; ER, endoplasmic reticulum.
See also Supplemental Figure 8 and Supplemental Table 5.

Tables

Table 1. Segregation of *pprd2* alleles.

SELF-POLLINATION					
pprd2-1, n=328			*pprd2-2,* n=196		
Genotype	**Expected**	**Observed**	**Genotype**	**Expected**	**Observed**
pprd2-1$^{+/-/-}$	82 (25%)	0	*pprd2-2*$^{+/-/-}$	49 (25%)	0
pprd2-1$^{+/-}$	164 (50%)	158 (48%)	*pprd2-2*$^{+/-}$	98 (50%)	96 (49%)
WT	82 (25%)	170 (52%)	WT	49 (25%)	100 (51%)
	X^2 =174.56***			X^2 =100.07***	

F1 progeny of self-pollinated *pprd2-1* and *pprd2-2* mutants. Analysis was performed by X^2 test against the H0 hypothesis that segregation is Mendelian. *** - significantly different from Mendelian, p<0.001

Table 2. Reciprocal crosses of *pprd2-1*$^{+/-}$ and *pprd2-2*$^{+/-}$ with the WT plants.

RECIPROCAL CROSSES				
Crosses		F1 genotypes, n=60		
Male	Female	WT	Heterozygote	Homozygote
pprd2-1$^{+/-}$	WT	60	0	0
WT	*pprd2-1*$^{+/-}$	30	30	0
pprd2-2$^{+/-}$	WT	60	0	0
WT	*pprd2-2*$^{+/-}$	31	29	0

Reciprocal crosses of *pprd2-1*$^{+/-}$ and *pprd2-2*$^{+/-}$ with the WT plants; 60 plants of each cross were genotyped.

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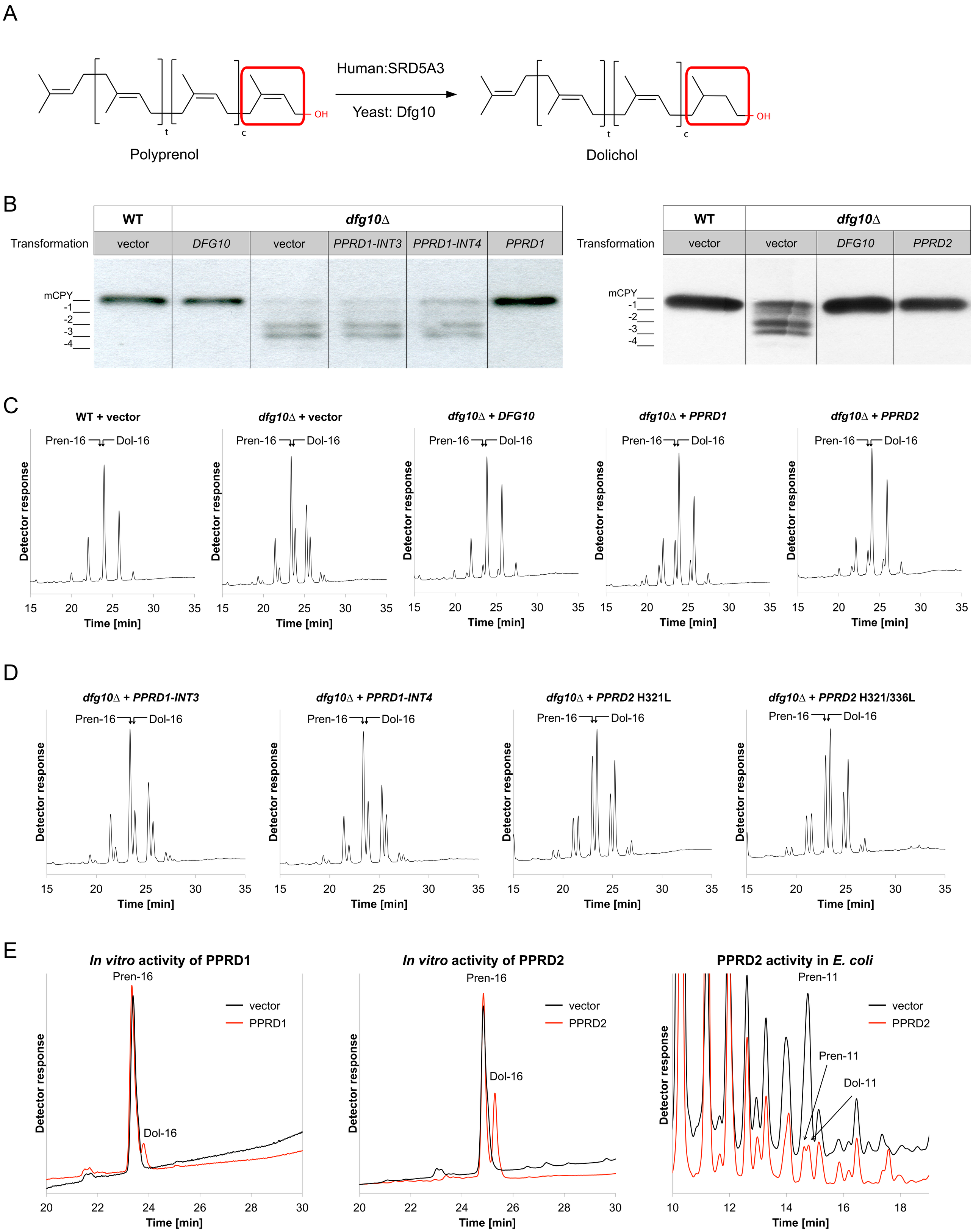

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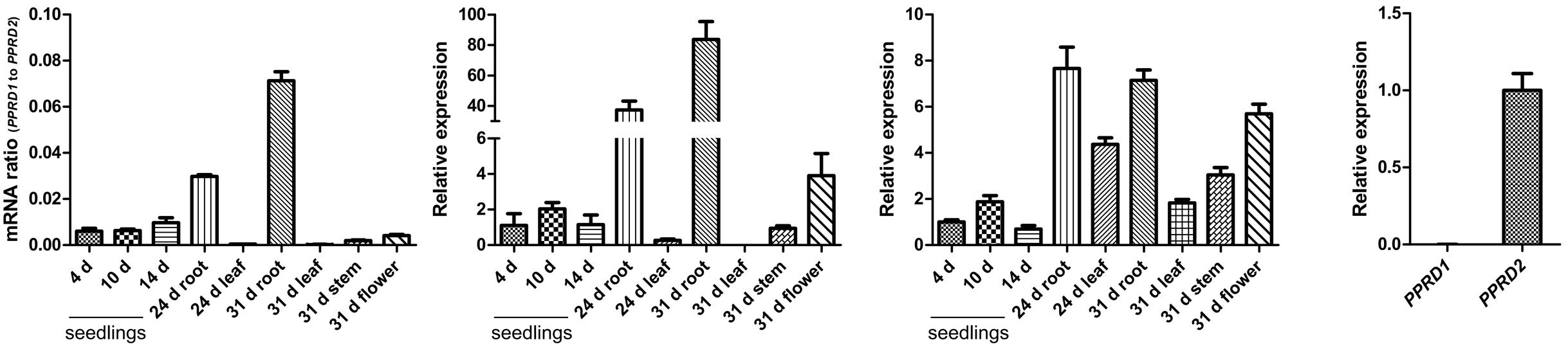

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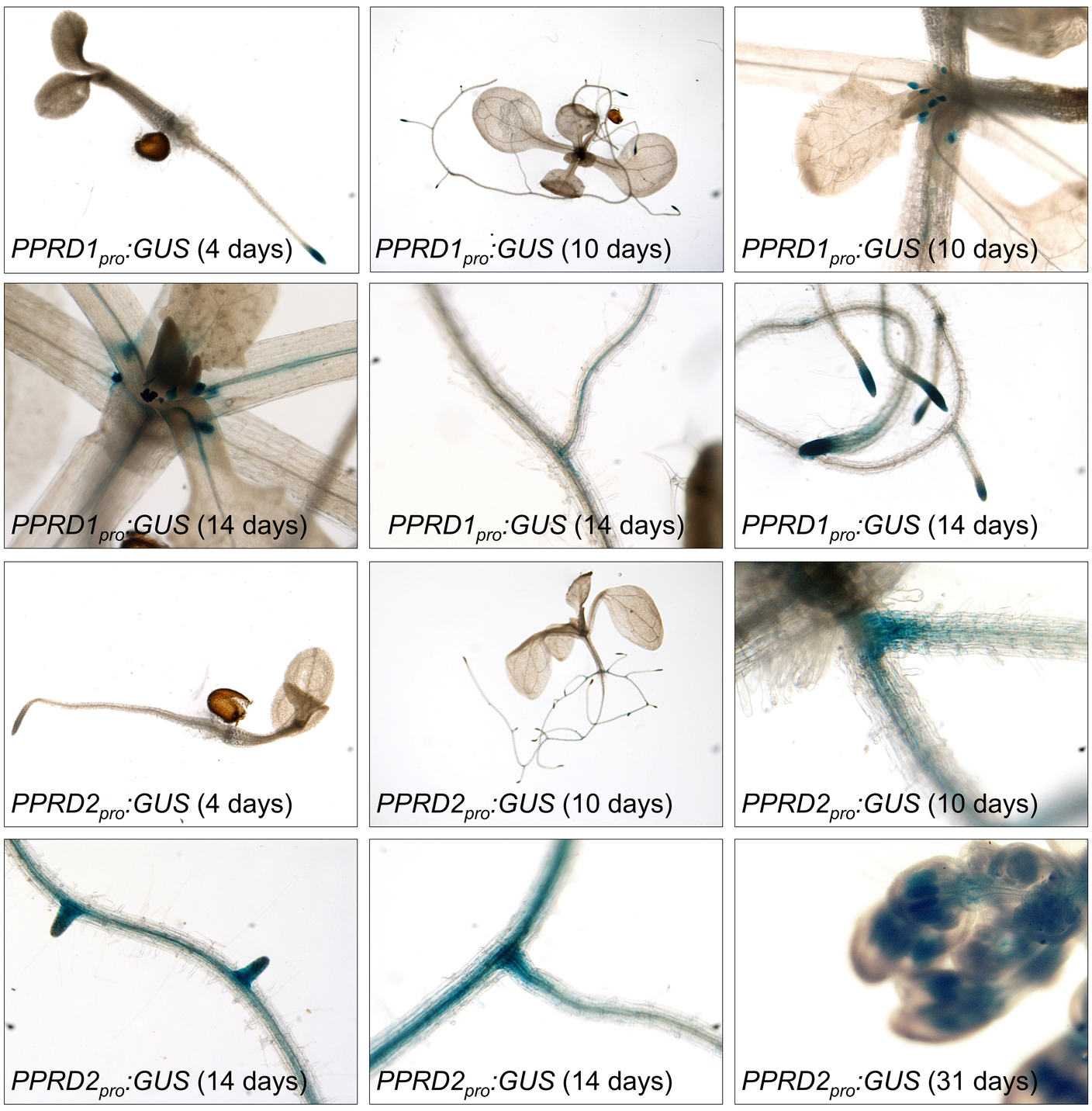

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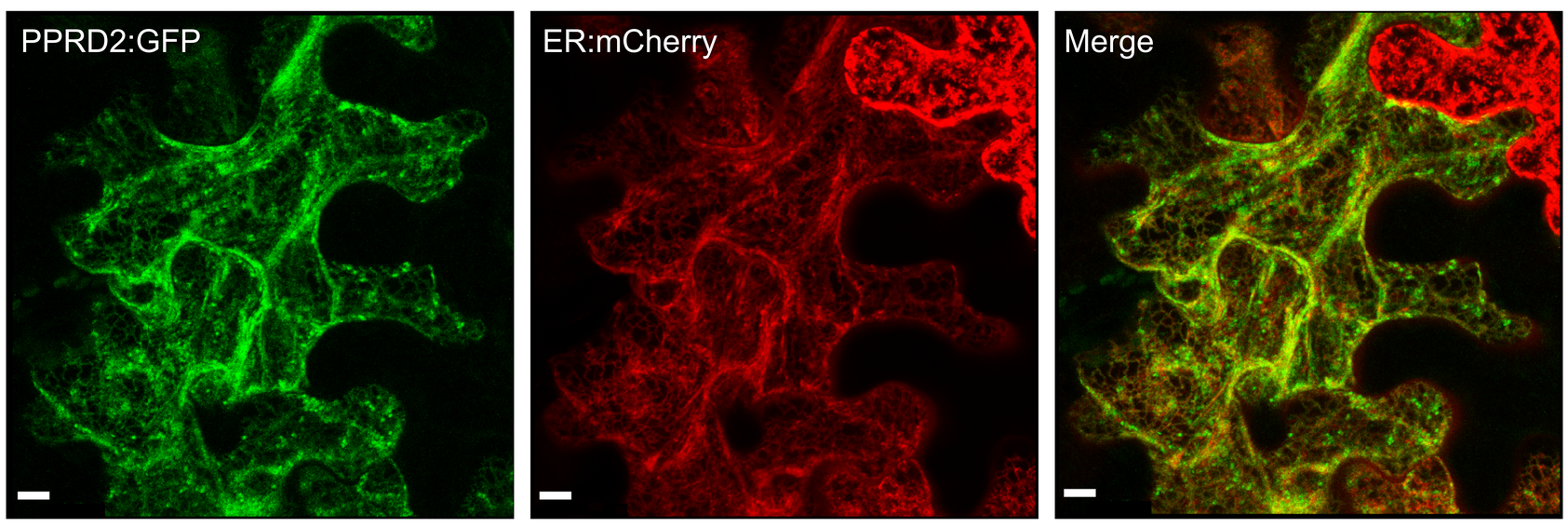

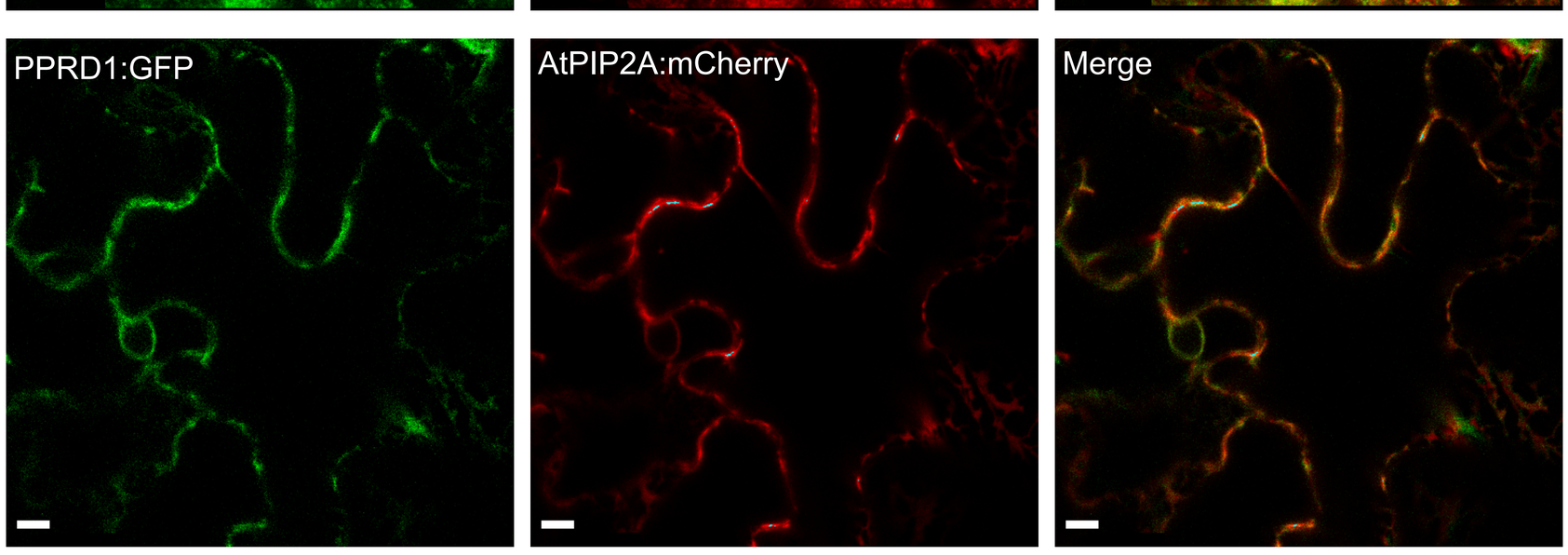

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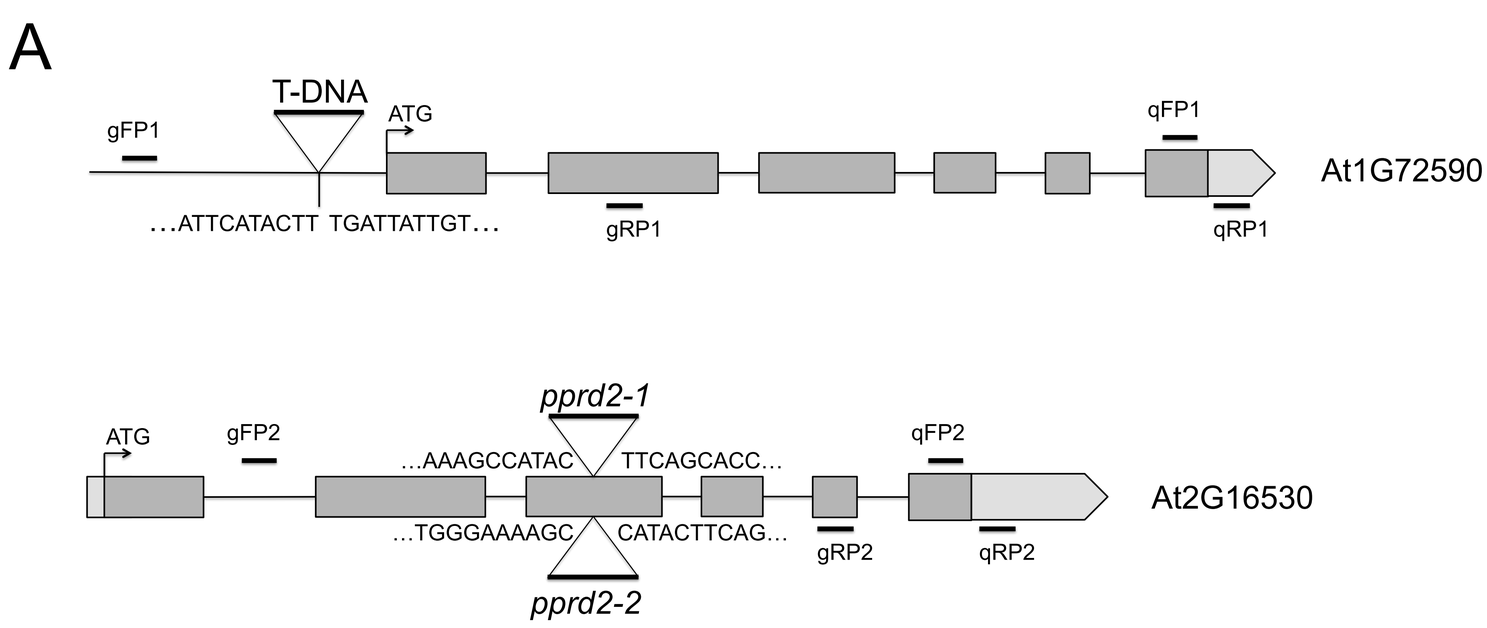

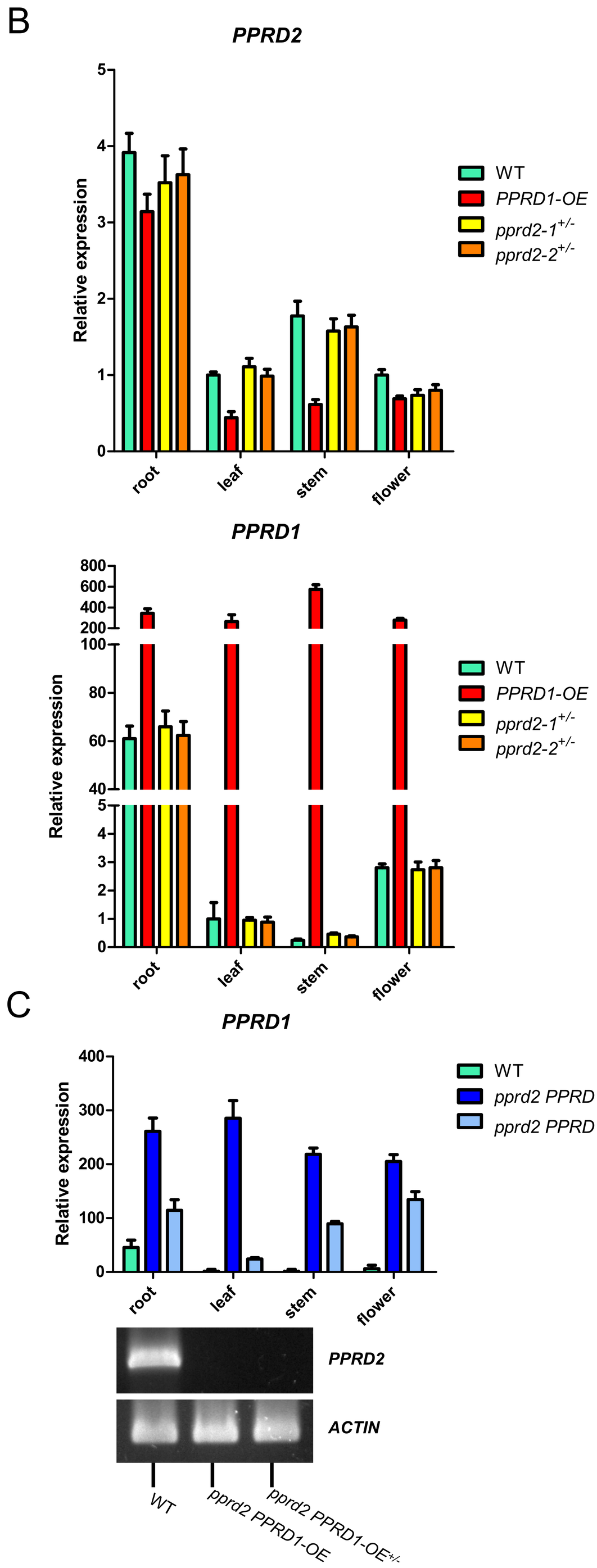

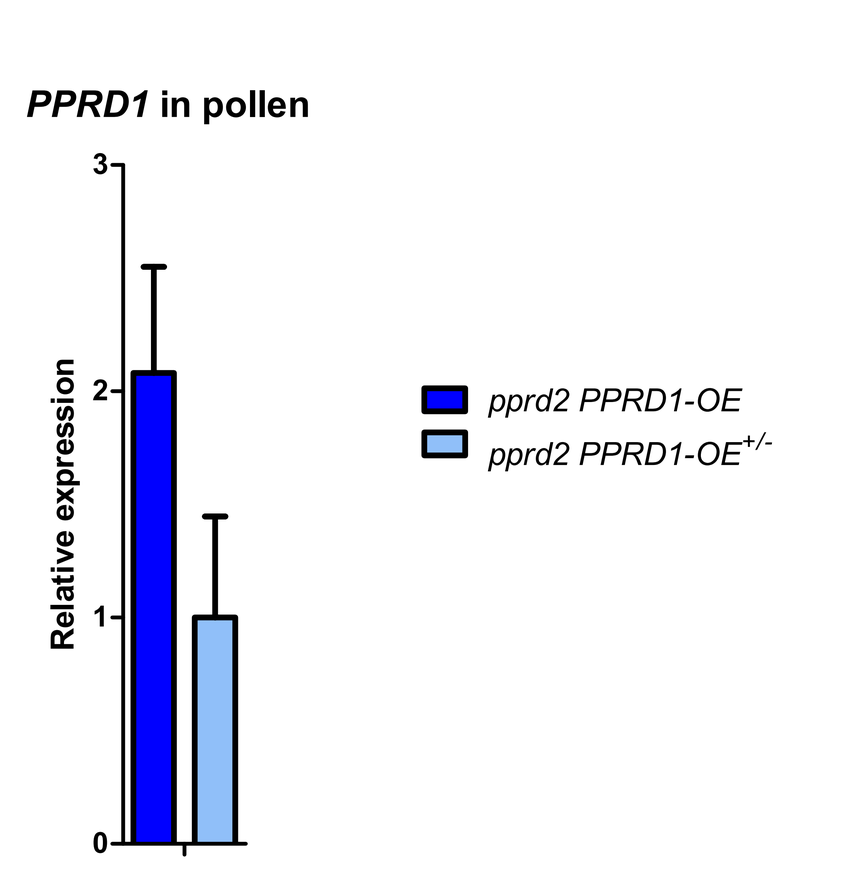

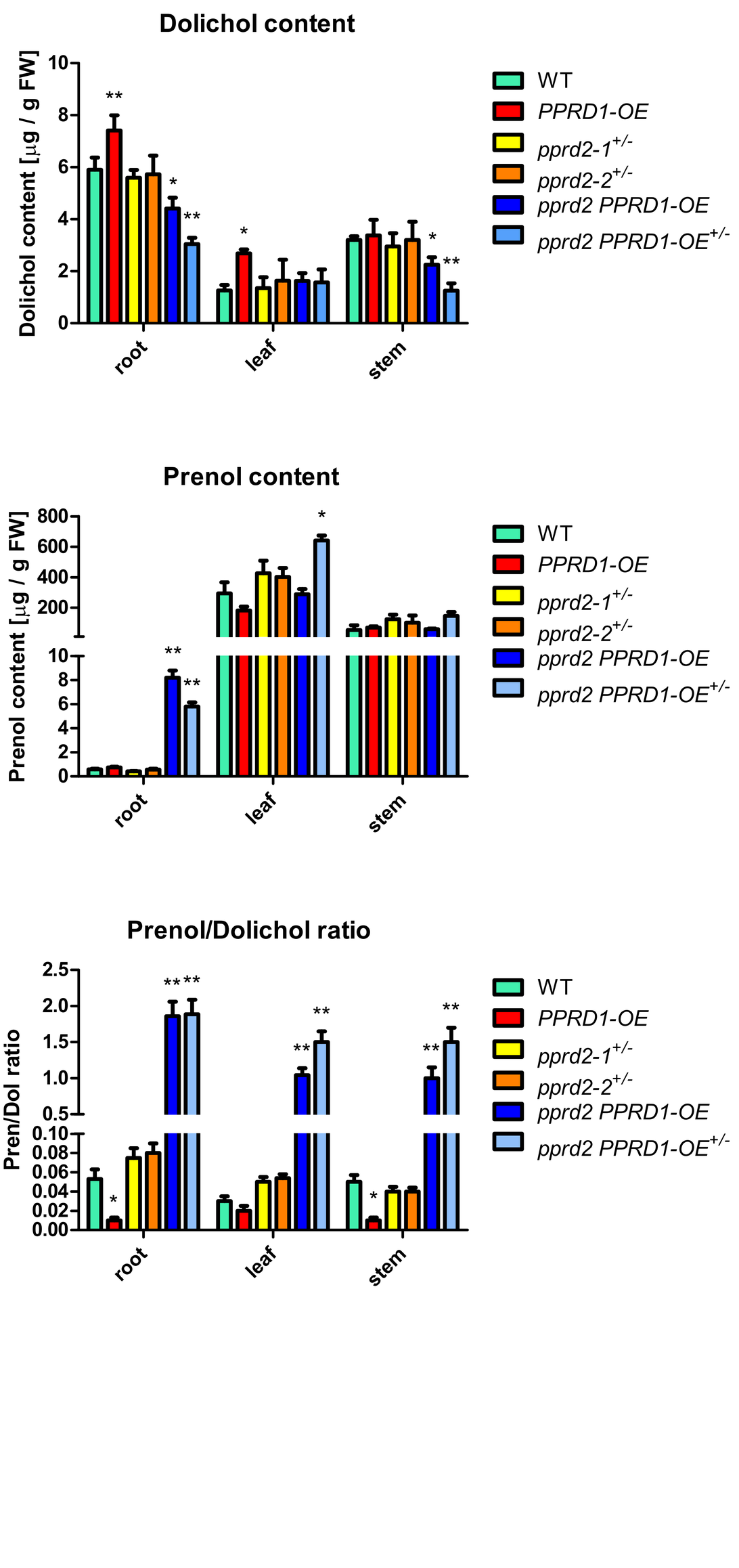

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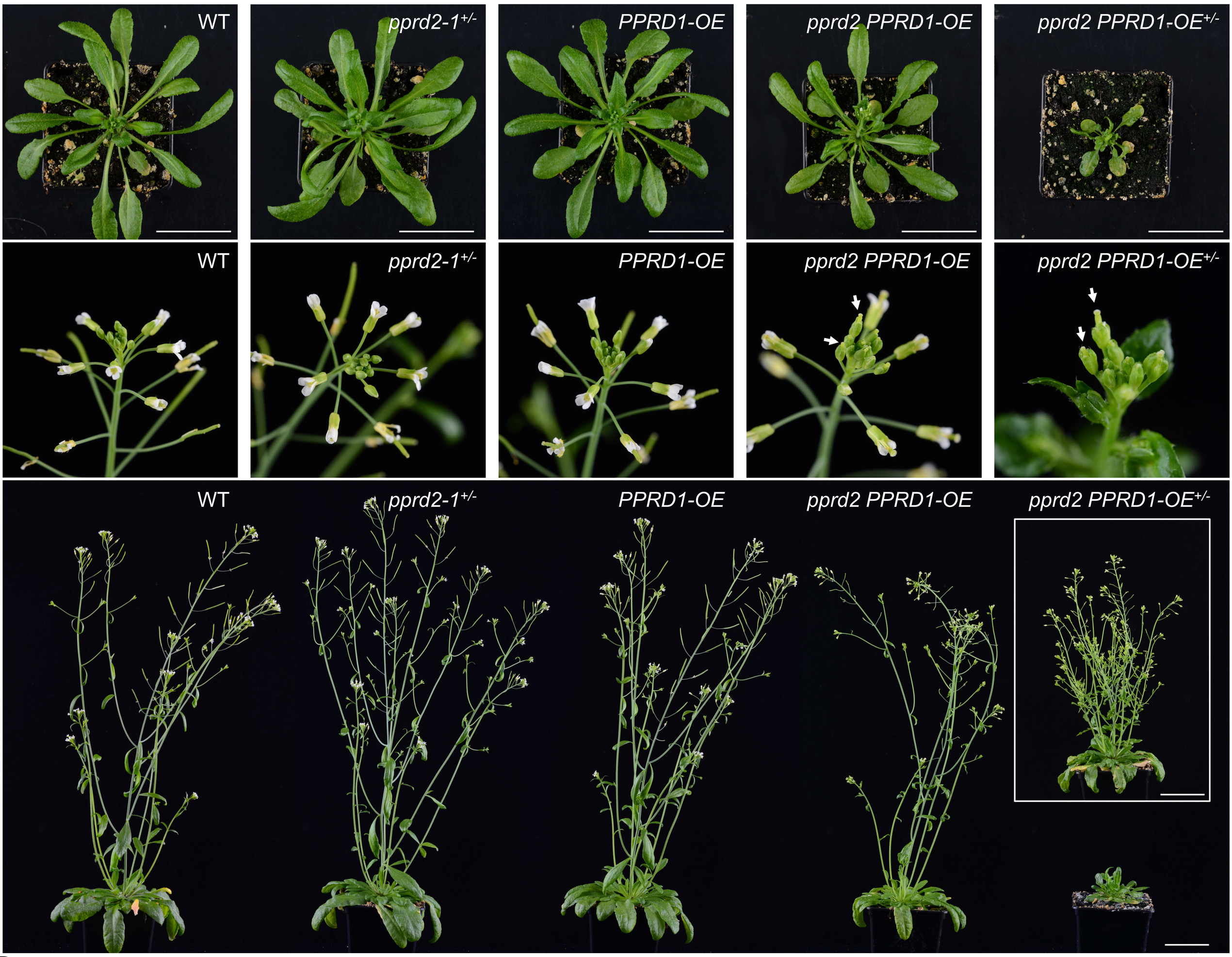

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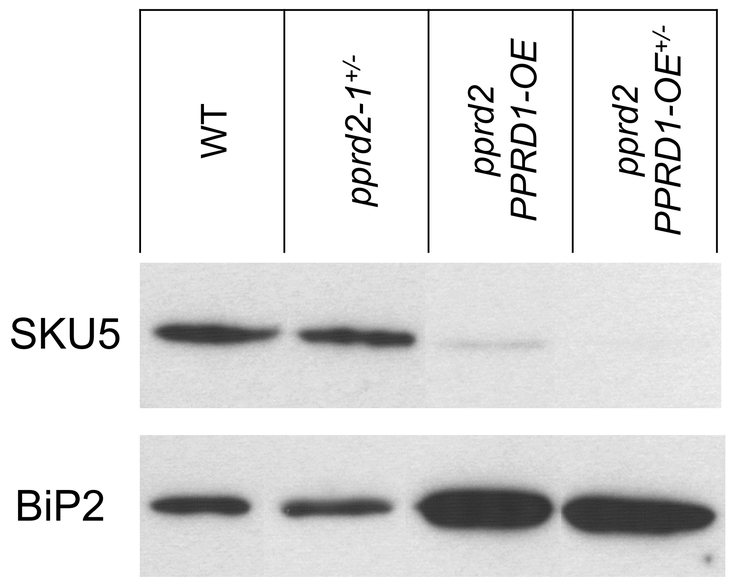

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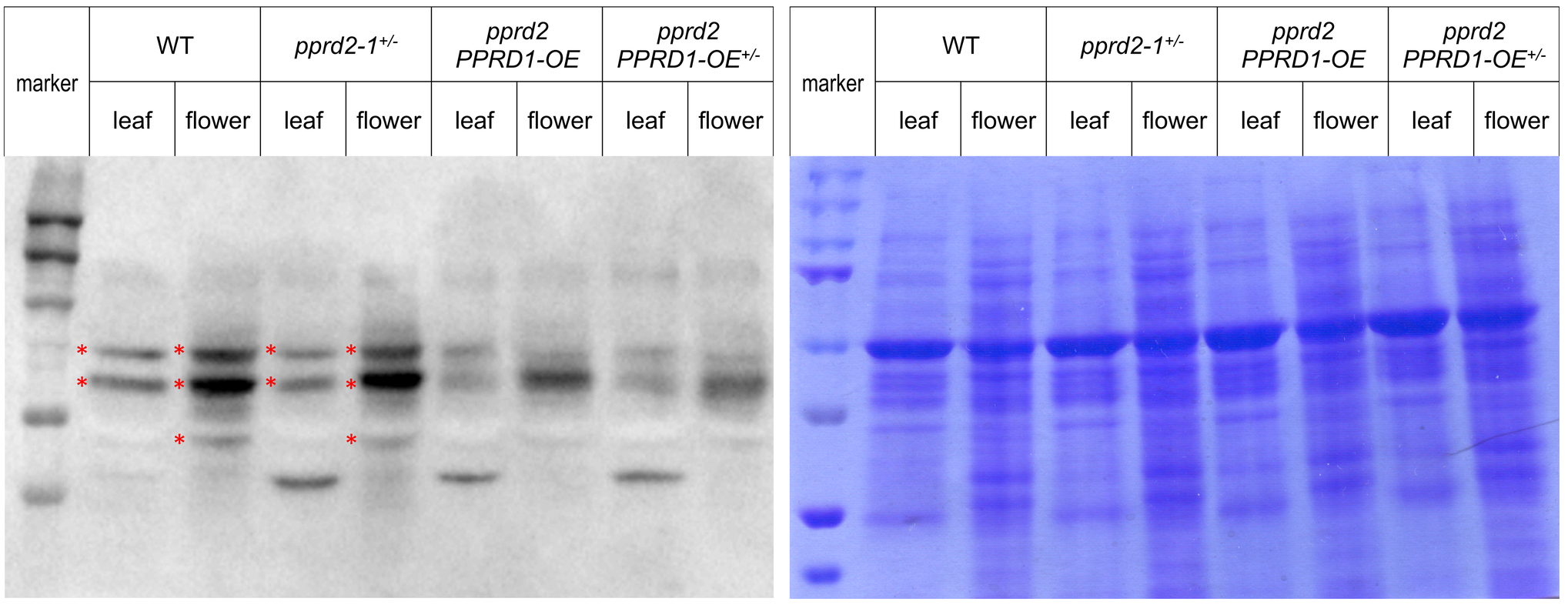

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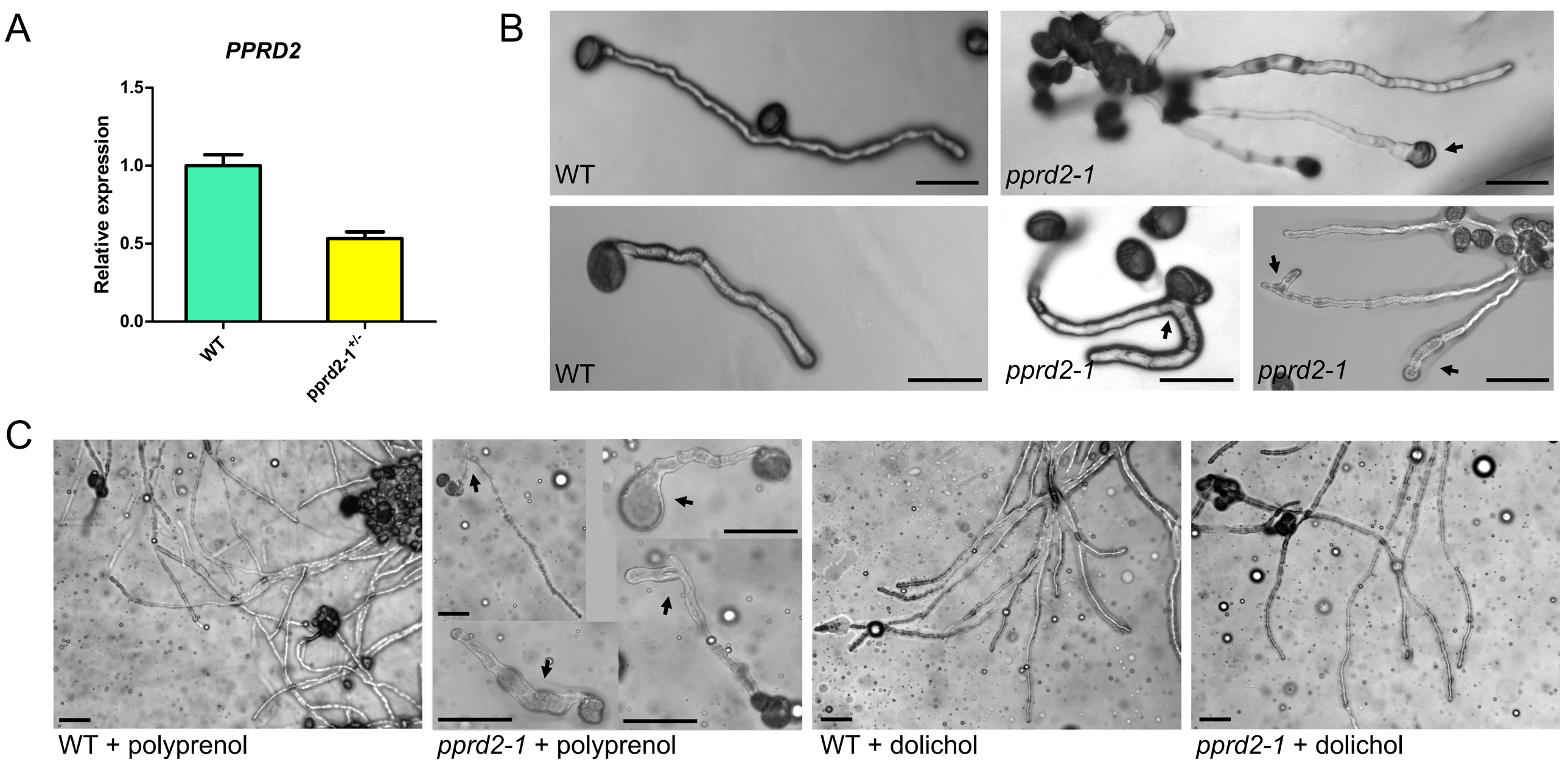

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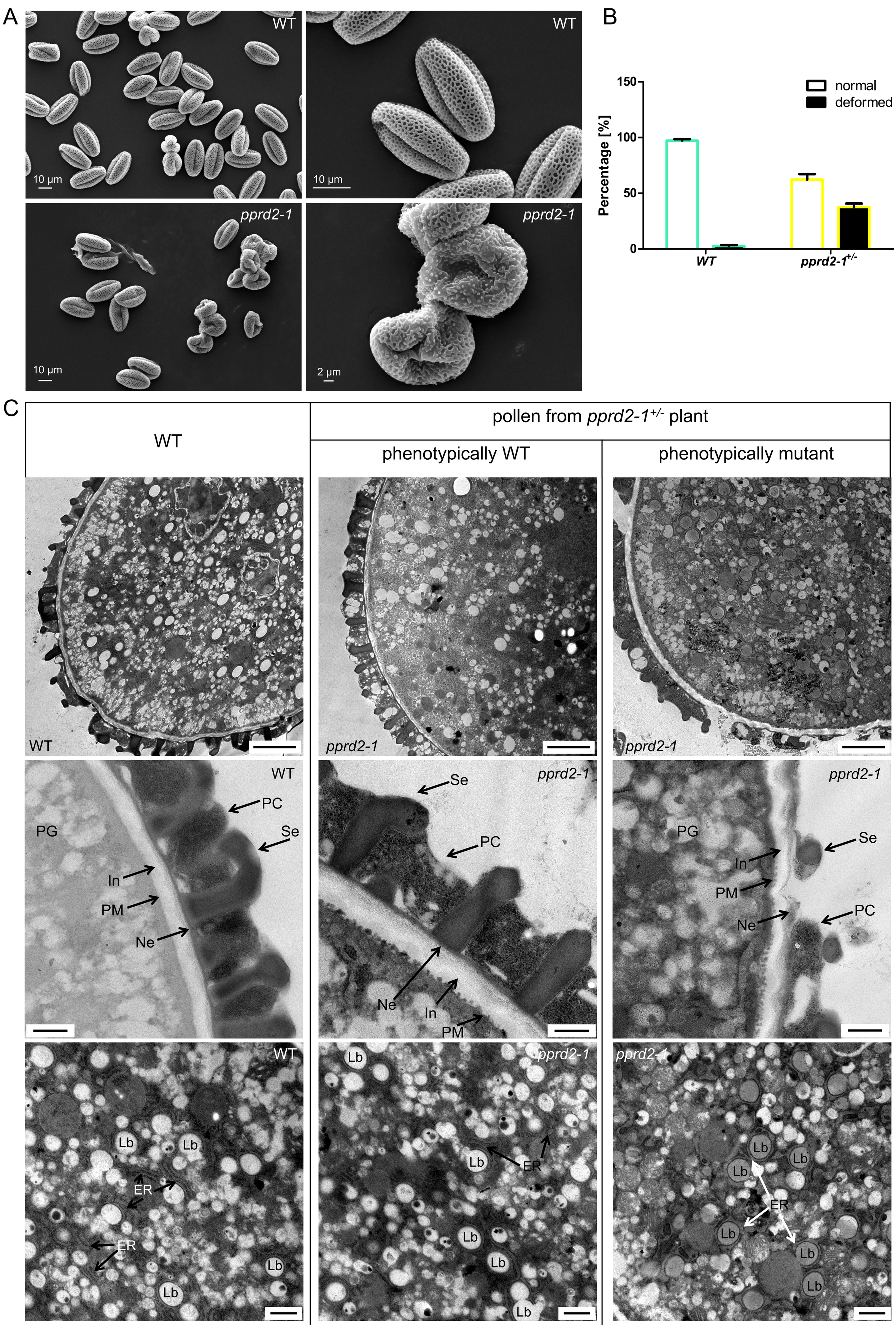

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