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***AtPDS* over-expression in tomato: exposing unique patterns of carotenoid self-regulation and an alternative strategy for the enhancement of fruit carotenoid content**

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Summary

The regulation of plant carotenogenesis is an active research area for both biological discovery and practical implementation. In tomato (*Solanum lycopersicum*) we demonstrate additional bottlenecks exist in the poly-*cis*-transformation of phytoene to lycopene in the context of ripening-induced PSY1 expression and activity, and reveal phytoene desaturase (PDS), as a target for manipulation toward elevated lycopene content in maturing tomato fruit. Over-expression of *Arabidopsis PDS*, *AtPDS*, elevated *PDS* transcript abundance in all aerial tissues resulting in both altered carotenoid accumulation and associated pathway gene expression in a tissue-specific manner. Significant increases in downstream carotenoids (all-*trans*-lycopene and β -carotene) and minimal changes in carotenogenic gene expression (carotenoid isomerase-like 1, *CRTIL1*) suggests over-expression of heterologous *AtPDS* in tomato circumvents endogenous regulatory mechanism observed with previous strategies. In transgenic leaves, depletion of the PDS substrate, phytoene, was accompanied by minor, but significant increases in xanthophyll production. Alterations in the leaf carotenogenic transcript profile, including the upstream MEP pathway, were observed revealing unique feedback and feedforward regulatory mechanisms in response to *AtPDS* over-expression. *AtPDS* over-expression in the background of the *tangerine* (carotenoid isomerase, *CRTISO*) mutant exposes its potential in elevating downstream *cis*-lycopene accumulation in ripe tomato fruit, as *cis*-lycopene is more bioavailable yet less abundant than all *trans*-lycopene in the wild type control. In summary, we demonstrate the limitation of PDS in ripening fruit, its utility in modifying carotenoid profiles toward improved quality, and reveal novel carotenoid pathway feedback regulation.

Introduction

Carotenoids (e.g. lutein, β -carotene and lycopene) and their catabolites (i.e. vitamin A and other apocarotenoids) are integral in the human diet as they ensure proper development and aid in the prevention of numerous age-related diseases (Rhinn *et al.*, 2012; Lian and Wang, 2008; Sharoni *et al.*, 2012; Ip *et al.*, 2013). Humans' inability to synthesize carotenoids *de novo* makes them dependent on plants as their primary source of dietary carotenoids, the acquisition of which is dependent upon both content in specific plant tissues and their ability to be absorbed in the digestive tract (bioavailability). The capacity of many fruits to accumulate elevated levels of carotenoids as they ripen, make fruits an important source of dietary carotenoids in many diets. Lycopene, the red carotenoid predominant in ripe tomatoes, has received increased attention as a target for manipulation due to evidence that lycopene-derived apocarotenoid signals aid in cancer prevention (Lian and Wang, 2008; Ip *et al.*, 2013).

In plants, carotenoids are essential for light absorption in photosynthetic tissues and as provisional colorants in flowers and fruit facilitating the attraction of pollinators and seed dispersing organisms (reviewed in Nisar *et al.*, 2015). The enhanced accumulation of carotenoids in ripening fruit is dependent on the switch from a photosynthetic to a non-photosynthetic-state, which embodies a remarkable transition of chloroplast to chromoplast rich cells, concurrent with strategic adjustments to the carotenoid profile within (Barry *et al.*, 2008; Barry *et al.*, 2012). Ripening associated carotenogenic gene expression in tomato is regulated by a complex symphony of transcription factors, the gaseous hormone ethylene and epigenome dynamics driving the flux of the pathway to all-*trans*-lycopene (and inhibition of its subsequent metabolism) conferring the typical red color of tomato (Vrebalov *et al.*, 2002; Eriksson *et al.*, 2004; Barry *et al.*, 2005; Vrebalov *et al.*, 2009; Martel *et al.*, 2011, Zhong *et al.*, 2013; Gallusci *et al.*, 2016; Giovannoni *et al.*, 2017). In the mature fruit, phytoene

synthase (the first committed step in carotenogenesis) is encoded by the highly regulated *PSY1* gene and is the major limiting activity for carotenoid flux (Fig. 1A) (Fraser *et al.*, 2002). Once synthesized by *PSY1*, phytoene undergoes a poly-*cis*-transformation conferred by 4 desaturation reactions catalyzed by phytoene desaturase (PDS) and ζ -carotene desaturase (ZDS) and 2 isomerizations facilitated by ζ -carotene isomerase (ZISO) and carotene isomerase (CRTISO) ultimately producing all-*trans*-lycopene (Fig. 1A) (Alba *et al.*, 2005; Yu *et al.*, 2010; Fantini *et al.*, 2013; Isaacson *et al.*, 2002). Subsequent processing of all-*trans*-lycopene is prevented through downstream repression of lycopene ϵ - and β -cyclases involved in synthesizing α -carotene (ϵ,β - rings), the precursor to lutein, and the provitamin A, β -carotene (β,β -rings) (Fig. 1A) (Ronen *et al.*, 1999; Ronen *et al.*, 2000, respectively). These combined activities, tightly regulated to push carotenoid flux toward specific products in the ripe fruit demonstrate finely tuned pathway regulation.

Multiple strategies have been pursued to enhance lycopene content in tomato deploying either plant or bacterial transgenes (reviewed in Fraser *et al.*, 2009). In carotenoid deficient staple crops (e.g. rice and potato) the use of the bacterial carotenoid desaturase, *CRTI*, has proven effective due to its ability to catalyze all six reactions required to convert phytoene to all-*trans*-lycopene (Misawa *et al.*, 1990; Ye *et al.*, 2000; Diretto *et al.*, 2007). Due to mechanisms yet to be defined, *CRTI* introduction *in planta* drives carotenogenesis beyond all-*trans*-lycopene to β -carotene via induced lycopene β -cyclase expression (Ye *et al.*, 2000; Römer *et al.*, 2000; Nogueira *et al.*, 2013; Enfissi *et al.*, 2017). In contrast to the successful applications in low carotenoid tissues, ectopic expression of *CRTI* was counterproductive for the enhancement of lycopene content in tomato fruit.

CRTI's structure has been solved facilitating characterization of its function as an FAD-dependent oxidase/isomerase (Schaub *et al.*, 2012). Two subsequent studies provided insight on the causal processes leading to β -carotene enhancement in the tomato including

CRTI protein localization (Nogueira *et al.*, 2013) in the plastid and lycopene-mediated pathway regulation (Enfissi *et al.*, 2017). Remaining unclear is the potential for an uncontrolled elevation of a foreign carotenogenic protein (i.e. CRTI) to disrupt one or more of the many protein interactions involved in plant carotenogenesis, thus negatively affecting carotenoid gene expression (reviewed in Shumskaya and Wurtzel 2013). Targeted manipulation of one or more of the four native plant enzymes carrying out limiting CRTI reactions in ripening fruit may facilitate enhanced all-*trans*-lycopene accumulation in an already high carotenoid tissue and provide insight into aspects of endogenous pathway regulation.

Here we 1) identify PDS within the poly-*cis*-transformation of phytoene to lycopene as a useful target for manipulation toward carotenoid enhancement in ripening tomato fruit 2) fully characterize the effect of *PDS* over-expression on carotenoid content and carotenoid gene expression in aerial organs and 3) demonstrate the utility of *PDS* over-expression combined with CRTISO repression via the *tangerine* (t^{3183}) mutation as a means to both elevate carotenoid levels and modify carotenoid accumulation profiles toward more bioavailable forms compared to wild-type control tomatoes (Cooperstone *et al.*, 2015).

Results

PDS becomes limiting once PSY1 is elevated during ripening

There is overwhelming evidence that PSY1 represents the major rate-limiting step in ripening-associated carotenogenesis (Nisar *et al.* 2015; McQuinn *et al.* 2015). The prevalence of intermediates in the poly-*cis*-transformation of 15-*cis*-phytoene to all-*trans*-lycopene as the fruit ripens, suggests additional points of pathway limitation providing targets to develop alternate strategies for enhancing flux to desired downstream carotenoids. In terms of amino-acid sequence identity and conserved domains, PDS and ZDS, enzymes are predicted to have

evolved from CRTI, with 41% and 30% identity, respectively, and both contain the same functional domains, NAD-binding domain and amine oxidase domain (NCBI Conserved Domains: <http://www.ncbi.nlm.nih.gov/Structure/cdd/cdd.shtml>) (Supplemental Fig. 1). In contrast, Z-ISO is considerably more distant and unrelated lacking both the NAD-binding and amine oxidase domains and instead contains a nitric acid domain (NCBI Conserved Domains: <http://www.ncbi.nlm.nih.gov/Structure/cdd/cdd.shtml>) (Supplemental Fig. 1). Furthermore, analysis of protein structure (TOPCONS.net) indicates Z-ISO is the only enzyme in this part of the pathway predicted as a transmembrane protein with multiple transmembrane domains, consistent with previous reports (Beltrán *et al.*, 2015). For these reasons and to gain a better understanding of the previously demonstrated metabolic constraints associated with CRTI over-expression, both PDS and ZDS were the focus of the efforts reported here, while ZISO, a more distant and distinct protein at the amino acid sequence and structural level (Beltrán *et al.*, 2015), was left for later examination.

In an effort to identify the optimal target for increasing carotenoid pathway flux post PSY1 activity, expression patterns of *PDS* and *ZDS*, were measured through four stages of fruit ripening (Mature Green, MG; Breaker, Br; and 3 and 7 days post breaker, 3DPB and 7DPB) using Quantitative Real-Time PCR. *PDS* was the lowest expressed gene in the fruit as compared to *ZDS* and *CRTISO* (Fig. 1B). While transcription does not determine enzyme activity, the elevated prevalence of PDS substrates (phytoene and phytofluene) compared to that of ZDS (9,9'-di-*cis*- ζ -carotene and neurosporene) in ripe fruit, as well as trace levels of PDS substrates observed in leaves (Table 1) suggest PDS activity may be limiting during carotenogenesis. PDS shares the substrate, phytoene, with CRTI allowing for the additional assessment of potential feedback or feedforward effects from depletion of a specific substrate (i.e. phytoene) or over accumulation of a specific downstream product (i.e. all-*trans*-lycopene) as speculated in previous reports (Kachanovsky *et al.* 2012; Fantini *et al.* 2013,

Enfissi *et al.* 2017). Together these observations suggested *PDS* as a high value target within the poly-*cis*-transformation for manipulation with the goal of elevating carotenoid accumulation.

Heterologous over-expression of *Arabidopsis PDS* in tomato enhances downstream carotenoid content in ripe fruit

The potential for activating an endogenous targeted gene repression system (e.g. siRNA-mediated gene silencing) in response to the introduction of a transgene, can be exacerbated due to high nucleotide sequence similarity between the endogenous gene and the transgene. The coding sequence of *AtPDS* shares only 72% of sequence identity with that of the endogenous *SlPDS*, reducing the potential for activating DNA sequence homology-based repression systems. For this reason, the *Arabidopsis* homolog of *PDS*, *AtPDS* (GenBank accession no. NM_202816), was deployed for over-expression rather than *SlPDS*, under the control of the constitutive CaMV 35S promoter in the wild-type tomato background cv. Ailsa Craig (AC++). Four independent homozygous transgenic lines (i.e. *AtPDS1A.1*; *AtPDS3.2*; *AtPDS4.2*; *AtPDS6.2*) displaying elevated levels of *AtPDS* transcripts in the three aerial plant organs analysed (i.e. leaves, flowers and ripe fruits) were propagated to the T₂ generation (Fig. 2A). The observed minimal effect on endogenous *PDS* transcript levels (Fig. 2A) indicated that any operating suppression systems had been bypassed. Ripe fruit from all four *AtPDS* over-expressing lines presented noticeably deeper red pigmentation compared to their wild-type counterparts (Fig. 2B).

Ripe fruit displayed the greatest increase in carotenoids downstream of *PDS*. Flowers and leaves had reduced and elevated lutein levels, respectively (Table 2). The metabolic effectiveness of *AtPDS* over-expression was evident in the reduction of steady state levels of phytoene and phytofluene, the substrate and intermediate of the *PDS* catalyzed reaction,

respectively, in both ripe tomato fruit (Table 2 and Fig. 3A) and leaves (Table 2 and Supplemental Fig. 3). Total lycopene and β -carotene were increased up to 31.1% and 42.8%, respectively (Table 2 and Fig. 3B, and C). With regards to the elevated total lycopene content, 31.1% equals an increase of 21.3 μ g/g fresh weight in this already high lycopene tissue (Fig. 3B). The observed increases in total lycopene and β -carotene content in *AtPDS* over-expressing ripe are not a consequence of reduced fruit size (Supplemental Fig. 4). The largest metabolic shifts were observed in the immediate products of the PDS enzymatic reaction where total ζ -carotene levels were > 160% higher than in wild-type fruit (Table 2 and Fig. 3A).

***AtPDS* over-expression in ripening fruit resulted in altered transcription of *CRTIL1*.**

Considering the previously observed deregulation of transcripts associated with carotenoid biosynthesis in *CRTI* over-expressing fruit (Römer *et al.*, 2000) it was necessary to quantify transcript abundance of genes throughout the biosynthetic pathway in ripe fruit of *AtPDS.OE* lines. A comprehensive analysis of the resulting carotenogenic transcript profile in *AtPDS.OE* ripe fruit was carried out via qRT-PCR with gene-specific primers (Supplemental Table 2) and compared to transcript abundance observed in the WT ripe fruit. Contrary to the observed off-target changes in carotenogenic gene expression in *CRTI* over-expressing fruit first described in Römer *et al.* (2000), no consistent or statistically significant changes in *PSY1*, *CRTL-B1* and *CRTL-B2* gene expression were identified (Fig. 4A). Analysis of relative transcript levels for the remaining carotenoid biosynthetic genes (*DXS*; *DXR*; *IDI1*; *PSY2*, *ZISO*; *ZDS*; *CRTISO*; *CRTIL1*; *CRTR-B1*; *CRTR-B2*; and *CRTL-E*) further shows limited impact of elevated PDS on carotenoid pathway self-regulation. A solitary significant change was observed in the reduction of *CRTIL1* transcript levels, a gene suggested to be involved in the isomerization of ζ -carotenes (Fantini *et al.*, 2013) (Fig. 4B). These results

indicate that PDS over-expression can provide a means for elevating carotenoid content in ripe fruit with limited feedback or feedforward effects on carotenoid gene expression and furthermore, that *CRTIL1* responds to changes in flux through early steps in the pathway during tomato ripening.

***AtPDS* over-expression in tomato leaves and flowers alters gene expression throughout the pathway.**

AtPDS over-expression in leaves enhanced carotenoid production in downstream xanthophylls, lutein, β -cryptoxanthin and zeaxanthin to small but measurable degrees (Fig. 5 A and B). Analysis of transcript levels of carotenoid biosynthetic genes by qRT-PCR revealed that *AtPDS* over-expression in tomato leaves had broad regulatory consequences and influenced multiple steps throughout the carotenogenic pathway. The gene representing the rate-limiting step of the MEP pathway (Rodríguez-Concepción and Boronat, 2002), deoxyxylulose 5-phosphate (DXP) synthase (*DXS*) was induced approximately 2 fold in the *AtPDS.OE* lines compared to the wild-type control (Fig. 5C). *PSY1* was also elevated in leaves, but to a lesser amount than *DXS* in *AtPDS.OE* leaves (Fig. 5C). Lycopene β -cyclase 1 (*CRTL-B1*) and β -carotene-hydroxylase 1 (*CRTR-B1*) were both expressed at higher levels in the *AtPDS.OE* leaves (Fig. 5C). *CRTR-B1* increased the most, (3-4 fold), and in combination with other changes in carotenoid gene expression provides insight into the mechanism underlying the elevated lutein, β -cryptoxanthin, and zeaxanthin content (Fig. 5). β -carotene content remained unchanged (Fig. 5).

Carotenoid biosynthetic gene expression analysis of the chromoplast rich flowers displayed limited alterations in response to heterologous PDS expression and this was again even more limited in the maturing fruit as noted above. The gene encoding the step immediately following *PDS*, ζ -carotene isomerase (*ZISO*), was elevated approximately 2 fold

compared to wild-type flowers (Fig. 6). *CRTR-B1* was reduced slightly in the *AtPDS.OE* flowers, potentially limiting the ability to increase xanthophyll content of the petals and anthers as confirmed by HPLC (Fig. 6).

***AtPDS* over-expression enhances *cis*-lycopene accumulation in *tangerine* (*CRTISO*) mutant ripe fruit**

In an effort to further amplify the value of the metabolic shift toward *cis*-carotenoids in *tangerine* (t^{3183}) mutant fruit, both *AtPDS3.2* and the *high pigment1* (*hp1*) mutations were crossed independently into the t^{3183} background. The *hp1* mutation in the tomato *DAMAGED DNA BINDING PROTEIN1* (*DDB1*) gene was selected as it confers an increase in plastid number resulting in elevated accumulation of carotenoids in ripe fruit (Liu *et al.*, 2004), a means of carotenoid elevation distinct from the direct increase of pathway flux conferred by *AtPDS* over-expression in tomato. $hp1;t^{3183}$ double mutant lines were also developed as a standard for comparison of metabolic pathway shift.

Plants homozygous for the *tangerine* (t^{3183}) mutation and positive for the *AtPDS* transgene or *hp1* were selected in F2 populations. All mutations and transgenes were nearly isogenic in the inbred Ailsa Craig background to minimize additional genetic variation in double mutant lines. Phenotypic and HPLC analyses were carried out on the ripe fruit of the *AtPDS3.2;t^{3183}* double mutant, the t^{3183} parent line, and the $hp1;t^{3183}$ double mutant. Compared to both the parental t^{3183} and $hp1;t^{3183}$ ripe fruit, *AtPDS3.2;t^{3183}* fruit were darker in color (Fig. 7A). The enhanced pigmentation associated with *AtPDS3.2;t^{3183}* was observed throughout the pericarp of cut fruit (Fig. 7B).

HPLC analysis revealed that *AtPDS* over-expression reduced steady state levels of phytoene and phytofluene by 64.8% and 61.8%, respectively, consistent with reductions observed when over-expressed in the wild-type background (Fig 7C and Table 2 and

Supplemental Fig. 5). *AtPDS* efficiency appears to be influenced by tissue type as *AtPDS3.2;t³¹⁸³* anthesis flowers only displayed a 30% reduction relative to *t³¹⁸³* phytoene and phytofluene levels (Fig. 7C and Supplemental Fig. 6). Both *AtPDS* over-expression and the *hp1* mutation led to a similar increase in 9,9'-di-*cis*- ζ -carotene content when combined with *t³¹⁸³* (Fig. 7C and Supplemental Fig. 5), while *AtPDS3.2;t³¹⁸³* alone displayed significant increases in products downstream of 9,9'-di-*cis*- ζ -carotene when compared to both *t³¹⁸³* and *hp1;t³¹⁸³* (Fig. 7C and Supplemental Fig. 5). Total neurosporene accumulates up to 84.5% higher in *AtPDS3.2;t³¹⁸³* compared to *t³¹⁸³* and 44.5% higher than *hp1;t³¹⁸³* (Fig. 7C and Supplemental Fig. 5). Additionally, tetra-*cis*-lycopene (prolycopene) levels are 30.3% and 42.2% higher than in *t³¹⁸³* and *hp1;t³¹⁸³*, respectively (Fig. 7C and Supplemental Fig. 5).

Total lycopene levels followed the same trend as prolycopene in the 3 genotypes with *AtPDS3.2;t³¹⁸³* displaying the highest levels (Fig. 7D and Supplemental Fig. 5). Subsequent lycopene isomer identification and quantification in the ripe fruit demonstrates genotype-specific effects on particular lycopene isomers (Fig. 7E and Supplemental Fig. 7 and Supplemental Table 2). Introduction of *AtPDS* over-expression and the *hp1* mutation in *t³¹⁸³* conferred elevations in two unidentified lycopene isomers and 5-*cis*-lycopene relative to the *t³¹⁸³* parental line (Fig. 7E). *AtPDS3.2;t³¹⁸³* tomatoes accumulate 2 and 7 times more 5,9(5',9') di-*cis*-lycopene and all-*trans*-lycopene, respectively, compared to levels found in *t³¹⁸³* tomatoes, while levels remain relatively unchanged in *hp1;t³¹⁸³* (Fig. 7E). The presence of genotype specific changes in *cis*-lycopene isomers and elevated total lycopene content observed in *AtPDS3.2;t³¹⁸³* demonstrates the potential for targeting PDS in a means that bypasses endogenous regulation in concert with CRTISO to enhance bioavailable *cis*-lycopene isomers in tomato.

Discussion

***AtPDS* over-expression effectively enhanced carotenoid accumulation in fruit and significantly alters the carotenoid gene expression pattern in a tissue specific manner.**

Carotenogenesis is heavily regulated regardless of plant organ, with PSY1 activity the major rate-limiting step in ripening-associated carotenoid biosynthesis (Nisar *et al.*, 2015; McQuinn *et al.*, 2015). This study demonstrates that in the context of normal ripening induction and function of PSY1, PDS activity becomes limiting and when elevated through deployment of a heterologous transgene, can significantly increase downstream carotenoid (i.e. ζ -carotene, lycopene, and β -carotene) accumulation and total carotenoid output (Table 2 and Fig.3). Moreover, when over-expressed in the ripening tomato, PDS metabolized 70% of the remaining phytoene in the plastid ultimately contributing to the elevated downstream carotenoids including the desired all-*trans*-lycopene (Table 2). The largest relative increase in carotenoid content was in ζ -carotene suggesting that as PDS activity was elevated, ZISO and ZDS now became limiting. These two genes thus present interesting targets for further carotenoid enhancement in ripening fruit with elevated PDS.

Importantly and in contrast to previous observations with transgenic tomatoes expressing the bacterial *CRTI* (Römer *et al.*, 2000; Nogueira *et al.*, 2013; Enfissi *et al.*, 2017), total carotenoid content was significantly elevated in *AtPDS.OE* ripe fruit (Table 2 and Figure 3D). Furthermore, *PSY1* transcripts did not decrease, nor did lycopene β -cyclase transcripts (*CRTL-B1* and *CRTL-B2*) increase across the 4 independent transgenic lines (Fig. 4). The lack of feedback regulation within the carotenogenic pathway may rely on the fact that an enzyme native to plants, PDS, was introduced rather than a more distant bacterial enzyme, CRTI. Given that both PDS and CRTI considerably deplete the phytoene pool in the plastids (based on observed steady state levels), the observed feedback regulation does not appear directly attributable to a response to lower substrate availability. It has recently been

suggested that this response may be due to an elevation in lycopene content (Enfissi *et al.*, 2017). PDS increases the accumulation of all-*trans*-lycopene in ripe tomato plastids more than with CRTI over-expression (Table 2 and Fig. 3B)(Römer *et al.*, 2000; Nogueira *et al.*, 2013; Enfissi *et al.*, 2017). While the lack of elevated lycopene in response to CRTI is due to enhanced lycopene β -cyclase activity, additional studies with *CRTB* (bacterial *PSY*) over-expressed in ripening tomatoes increased lycopene, absent increases in lycopene β -cyclase (*CRTL-B1* and *CRTL-B2*) expression (Fraser *et al.*, 2002; Nogueira *et al.*, 2013). It is possible that misregulation throughout the pathway in response to CRTI may be through means other than or in addition to elevated lycopene.

While PDS evolved from CRTI, PDS and CRTI function in contrast to each other with regards to maintenance of the FAD redox state and may differentially influence carotenoid pathway regulation in the ripening tomato fruit. It has been established that the plastid terminal oxidase, PTOX and the plastoquinone (PQ) pool controls the redox state and function of PDS in plants (Norris *et al.*, 1995; Carol *et al.*, 1999; Joet *et al.*, 2002; Josse *et al.*, 2003; Yu *et al.*, 2014). Moreover, while in photosynthetic chloroplasts alternative mechanisms appear to aid in the maintenance of PDS's redox state, in non-photosynthetic chromoplasts PDS is solely dependent on PTOX and the PQ pool (Shahbazi *et al.*, 2007). Norflurazon inhibits PDS activity by maintaining the FAD within PDS in a reduced state once it is lodged in the active site (Gemmecker *et al.*, 2015). In contrast, CRTI cannot be inhibited by norflurazon (Sandmann and Fraser 1993) and as suggested by Schaub *et al.* (2012) it remains unclear if CRTI can be oxidised similarly to PDS by PQ *in planta*. Therefore, in contrast to PDS over-expression, ripe fruit expressed CRTI protein may have the potential to disrupt the redox state of the PQ pool providing an alternative explanation for the observed carotenoid pathway misregulation.

AtPDS over-expression successfully circumvents the negative feedback mechanisms observed in response to bacterial CRTI. Indeed, *AtPDS* over-expression associated elevation of lycopene and β -carotene in the T₂ generation ripe fruit is improved compared to values observed with other strategies (Enfissi *et al.*, 2004; Fraser *et al.*, 2007). Lycopene content resulting from *AtPDS* over-expression are higher than reported in DXS over-expression lines in the T₁ generation while total carotenoid content stays comparable (Enfissi *et al.* 2004). Observations by Fraser *et al* (2007) demonstrated that PSY1 over-expression increases phytoene content in ripe transgenic fruit, but has no overall effect of the steady state levels of lycopene when compared to wild type fruit. In contrast, *AtPDS* over-expression overcomes the apparent limitation in the pathway at the PDS step and increases the steady state levels of lycopene in the ripe transgenic tomato fruit.

Many examples of pathway self-regulation have been reported including, but not limited to, the feedback regulation observed when CRTI is over-expressed in tomato fruit (Römer *et al.*, 2000; Nogueira *et al.*, 2013; Enfissi *et al.* 2017) and epistatic regulation of PSY1 in the spontaneous *tangerine* (*CRTISO*) mutation (Kachanovsky *et al.*, 2012; and reviewed in Cazzonelli and Pogson, 2010). Therefore, it was not surprising to observe tissue specific transcriptional perturbations of carotenogenic genes in response to *AtPDS* over-expression (Fig. 8). Interestingly, artificially increasing flux via elevated PDS triggered major alterations in gene expression throughout the carotenoid biosynthetic pathway in leaves (Fig. 5 and Fig. 8), while modifications in transgenic ripe fruit across all four independent *AtPDS.OE* lines were limited to a small change in *CRTIL1* (Fig. 4B and Fig. 8). Additionally, minor unique changes in pathway gene expression were also detected in the flowers but with no significant alterations in carotenoid content (Fig 6 and Fig. 8).

Considering the important protective roles of carotenoids in chloroplast stress tolerance, it is understandable that the carotenoid pathway would be more responsive to

perturbations within leaf chloroplasts. The transcript induction resulting from *AtPDS* over-expression was similar, yet distinct from gene expression changes in tomato leaves expressing *CRTI* reported in Nogueira *et al.* (2013). In the *AtPDS.OE* leaves, induced *DXS*, *PSY1*, *CRTL-B1* and *CRTR-B1* transcripts, and subsequent elevation of xanthophylls (i.e. lutein, β -cryptoxanthin, and zeaxanthin) are consistent with previous reports of elevated zeaxanthin levels in cyanobacteria from elevated PDS protein (Chamovitz *et al.*, 1993). However, the minimal changes observed in xanthophyll accumulation in response to the elevation in gene expression throughout the pathway is intriguing. Similar observations have been observed when manipulating PSY in photosynthetic tissues of *Arabidopsis* (Maass *et al.*, 2009; Zhou *et al.*, 2015; Lätari *et al.*, 2015). Whether via over-expression of PSY or the PSY activating ORANGE protein, carotenoid enrichment was limited to non-photosynthetic tissues (Maass *et al.* 2009; Zhou *et al.*, 2015). Lätari *et al.* (2015) demonstrate that over-expression of PSY in the *ccd4* mutant background results in xanthophyll accumulation to toxic levels, suggesting a role for CCD4 in controlling xanthophyll accumulation. PDS-associated enrichment of xanthophylls in tomato leaves may be similarly restricted via CCD4.

A strategy for enhancing lycopene content and bioavailability in tomato fruit.

Bioavailability as it is most commonly defined (Macrae *et al.*, 1993) equally depends on both the accessibility of the nutrient to the human body and its absorption properties therein. Impaired accessibility of carotenoids can negatively influence the overall effectiveness of carotenoid enhanced crops in addressing food security and nutritional concerns. Recent reports have suggested chromoplast ultrastructure and carotenoid sequestration effect the overall bioavailability of carotenoids, where bioavailability is improved via sequestration of carotenoids in a lipid-dissolved liquid-crystalline state (Schweiggert *et al.*, 2014; Schweiggert

et al., 2012). However in tomatoes and other all-*trans*-lycopene-rich fruits, all *trans*-lycopene forms long crystalline aggregates of approximately 15µm in length in the chromoplasts inhibiting its accessibility (Cooperstone *et al.*, 2015; Schweiggert *et al.*, 2014; Schweiggert *et al.*, 2012).

Chromoplast ultrastructure has been observed to be dependent on carotenoid composition (Harris and Spurr, 1969). Furthermore, an abundance of *cis*-carotenoids in chromoplast-rich tissues has been suggested to promote lipid-associated sequestration of carotenoids (Ben-Amotz *et al.*, 1988). Microscopic analysis of chromoplasts in *tangerine* mutant (t^{3183}) fruit demonstrates that the abundance of *cis*-lycopene isomers promote carotenoid sequestration in globular lipid-rich structures improving the accessibility of all lycopene isomers (Cooperstone *et al.*, 2015; Ben-Amotz *et al.*, 1988). Therefore, over-expression of *AtPDS* in the *tangerine* mutant (t^{3183}) of tomato provides a unique and effective strategy capable of elevating total lycopene content without complementing the *tangerine* mutation, thereby accumulating higher levels of the bioavailable *cis*-lycopene isomers (e.g. tetra-*cis*-lycopene; 5,9-di-*cis*-lycopene; 5-*cis*-lycopene, etc.) and maintaining enhanced accessibility of carotenoids, including all- *trans*-lycopene, sequestered in a lipid-dissolved liquid crystalline state (Cooperstone *et al.*, 2015; Schweiggert *et al.*, 2014; Schweiggert *et al.*, 2012; Ben-Amotz *et al.*, 1988). The strategy over-expressing *AtPDS* in the t^{3183} background reported here provides an initial step towards the enhancement of bioavailable carotenoids in fruit crops enabled in part by regulatory insights revealed through heterologous expression of PDS in tomato fruit.

Experimental Procedures

Plant Materials and Growth Conditions

Wild-type control, *tangerine* single mutant (LA3183) and *tangerine; high-pigment1* double mutant (LA3367) seed (*Solanum lycopersicum* cv Ailsa Craig) were obtained from the Tomato Genetics Resource Center, UC Davis (<http://tgrc.ucdavis.edu/>). Plants were grown in greenhouses at the Guterma Bioclimate Laboratory and Greenhouse Complex, Cornell University, Ithaca, NY. All plants were grown under natural light conditions consisting of 16hr day/ 8hr nights. *AtPDS* over-expression transgenic lines were carried on to the T2 generation. T2 generation plants showing the strongest consistent phenotypes were used for crosses to make double mutants / transgenics with *tangerine*. Leaf tissue was harvested from the 4th, 5th, and 6th leaves from the meristem of a two-month old plant. Whole petals and anthers were harvested from flowers at the point of anthesis/pollination. Ripe fruit were collected 7 days after tagging fruit at the first sign of color change at the blossom end (i.e. breaker stage). The tomato fruit ripening time course is represented by fruit collected at 4 stages of fruit ripening (Mature Green, MG; Breaker or onset of ripening, Br; and 3 [light red] and 7 days [full red] post breaker, 3DPB and 7DPB, respectively).

Development of Over-expression constructs and plant transformation

The *AtPDS* Over-expression (*AtPDS.OE*) construct was generated as described previously in Gleave (1992) using the pART7 and pART27 binary vector strategy. RNA from *Arabidopsis thaliana* (accession Columbia-0) leaf tissue was converted to cDNA via iScriptTM cDNA synthesis kit (Cat. No. 170-8891; BioRad; CA). Resulting cDNA was used to amplify the full length *AtPDS* ORF via FastStart High-fidelity PCR system (Cat No. 04-738-292-001; Roche Applied Sciences; IN) with *AtPDS-OE-KpnI.for* and *AtPDS-OE-XbaI.rev* primers (Supplemental Table 1). The resulting *AtPDS.OE* construct was sequence verified and

transformed into *S. lycopersicum* cv Ailsa Craig by *Agrobacterium tumefaciens* (strain LBA-4404) as previously described (Van Eck *et al.*, 2006).

DNA Isolation and Zygosity and Copy Number Analysis

Genomic DNA was isolated from fresh meristematic leaf tissue as previously described (Barry *et al.*, 2005). Verification of insertion events in T0 plants was confirmed via PCR using primers specific for the 35S promoter in the pHELLSGATE 2 vector, 35S-for and 35S-rev (**Supplemental Table 1**). Zygosity and copy number was determined in the T1 generation via Quantitative PCR relative to the single copy polygalacturonase 2a gene (PG2a, Accession No. X04583) using a modified protocol described in Haurogné *et al.* (2007). Quantitative PCR was performed in 5µl reactions containing 2.5µl SYBR® Green PCR Master Mix (Cat No. 4309155; Applied Biosystems; UK); 0.75µl of 10µM of each primer; and 1µl of gDNA using an ABI PRISM™ 7900HT Sequence Detection System (Applied Biosystems, CA) under the following reaction conditions: 48°C for 2 min; 95°C for 10 min; and 40 cycles of 95°C for 15 sec and 60°C for 1 min. Amplification was followed by a dissociation curve to verify specificity of the 35S promoter specific and PG gDNA specific primers used (**Supplemental Table 1**).

Identification of positive double mutants / transgenics was performed using a forward and reverse primers in the interior of the 35S promoter and AtPDS ORF (35S-internal-FOR and AtPDS-internal-REV, respectively) and primers spanning the deletion in the *tangerine* mutant (i.e. tangerine.mut-for and tangerine.mut-rev) (**Supplemental Table 1**). All positive double mutants/ transgenics were further verified by gene-expression via qRT-PCR and identification of appropriate flower and fruit phenotypes (Isaacson *et al.*, 2002).

RNA Isolation and Quantitative RT-PCR Analysis

Total RNA was isolated from all previously described tissue using a modified protocol from the RNeasy Minikit (Cat. No 74106, Qiagen Sciences, MD). RNA was extracted from 200-300mg of frozen powdered tissue via the addition of 800µl modified RLT buffer (4 M guanidine isothiocyanate; 0.2 M sodium acetate, pH 5.2; 25 mM EDTA; 2.5% (w/v) PVP-40) containing 1%(v/v) β-mercaptoethanol and 2% sarcosine, and separated upon the addition of 800µl chloroform. Total RNA in the upper aqueous phase was collected on the Econospin™ minispin column (Cat. No. 1920250; Epoch Life Sciences; TX). The column was washed twice with 500µl of RPE buffer (Cat. No. 1018013; Qiagen Sciences; MD) and RNA was eluted with 360µl of nuclease free water. DNase treatment of total RNA was achieved by adding 40µl DNase reaction buffer (60mM MgCl₂; 400mM Tris, pH 7.5) and 3µl of RQ1 DNase enzyme (Cat. No. M6101; Promega; WI) and allowed to incubate for 45 min at 37°C. Finally RNA samples were washed with an equal volume of phenol:chloroform solution (500g phenol crystals; 500ml chloroform; 20ml isoamyl alcohol; 0.5g 8-hydroxy-quinoline; equilibrated with 100mM Tris, pH 8.0) and lastly with an equal volume of chloroform. Total RNA was then precipitated overnight at -20°C and resuspended in 50-100µl of DEPC-treated water.

Quantitative Real-time PCR was performed using the Power SYBR® Green RNA-to-C_T™ 1-Step Kit (Cat No. 4309169; Applied Biosystems; NJ) in a 5µl reaction volume (2.5µl 2X Master Mix; 1µM forward and reverse primers; 1µl of total RNA; 0.46µl DEPC-treated water; 0.04µl RT enzyme mix). All tissue samples were represented by 3 biological replicates, each being carried out in triplicate. Gene specific primers were checked for efficiency using wildtype RNA (for primer sequence see **Supplemental Table 1**). To be able to apply the standard curve method described in User Bulletin #2 (Applied Biosystems, 1997) a standard curve was included on each plate for the specific gene being analyzed using

wildtype RNA (serial dilutions: 50ng; 5ng; 0.5ng; 0.05ng) in triplicates. For each gene analysis, template-free and negative-RT controls were included. Real-time PCR reactions were carried out using an ABI PRISM™ 7900HT Sequence Detection System (Applied Biosystems, CA) under the following reaction conditions: Reverse Transcription at 48°C for 30 min; enzyme activation at 95°C for 10 min; followed by 40 cycles of 95°C for 15 sec and 60°C for 1 min. A dissociation curve was added at the end of the run for verification of primer specificity.

ABI PRISM™ SDS version 2.3 software (Applied Biosystems, California) was used to determine gene specific threshold cycles (C_T) using the endogenous reference (18S rRNA) for every sample. C_T 's were extracted and the Standard Curve method (Applied Biosystems, 1997) was applied to calculate relative mRNA levels in comparison to the wildtype control or the reference sample (equal volume and concentration of RNA from each tissue combined), which was employed for the wild-type differential expression profile.

Carotenoid Extraction and Analysis

Carotenoids were extracted from 200mg of frozen tomato pericarp using a modified protocol from (Alba *et al.*, 2005). Carotenoid content of anthesis flowers was extracted from frozen petals and anthers of a single flower. The frozen tissue was homogenized in a Savant FP120 Fast Prep machine first with 15mg Mg-carbonate and 450μl of tetrahydrofuran (THF) twice and then a third time with 450μl of methanol containing 2,6-Di-tert-butyl-4-methylphenol (MeOH/BHT). The homogenate was then transferred and filtered through Spin-X centrifuge filters (0.45mm nylon filter; Corning/Costar #8170; NY). Tissue debris was re-extracted with an additional 500μl of THF to ensure complete extraction of carotenoids. The carotenoid/non-polar phase was separated from the aqueous phase through two separation steps, first with 375μl of petroleum ether and 150μl of 25% NaCl and next with 500μl of

petroleum ether. The two upper phase aliquots were combined and dried down in a vacufuge (Eppendorf). Prior to drying the flower extracts, xanthophylls went through a saponification as described in (Galpaz *et al.*, 2006). The dried extract from fruit was resuspended in 250µl of ethyl acetate, while dried flower extracts were resuspended in 500µl. All solvents used were HPLC-grade.

Carotenoid analysis was carried out using a Dionex HPLC machine (P680 HPLC pump, ASI-100 Automated Sample Injector, PDA-100 Photodiode Array Detector) and Chromeleon (v6.40) software package. Separation of Carotenoids was achieved under a polar to non-polar gradient (0-5min 100% Methanol:0.1%Ammonium Acetate; 6-25min ramp to 4% Methanol:Ammonium acetate and 96% Methyl t-butyl ether; 26-30min ramp to 100% Methanol:Ammonium acetate; 31-35min 100% Methanol:Ammonium acetate) through a guard cartridge (YMC Carotenoid S-5, 4.0 x 20mm DC guard; Waters; MA), C₃₀ column (YMC Carotenoid S-5, 4.6 x 250mm; Waters; MA) assembly. Seven channels were used for data acquisition, channel 1 (286nm); channel 2 (348nm); channel 3 (398nm); channel 4 (428nm); channel 5 (437nm) and channel 6 (450nm); channel 7 (464nm). Peak identification was performed as described in Alba *et al.* (2005). Lycopene isomers identification was determined relevant to results in Melendez-Martinez *et al.* (2013) (Supplemental Fig. 6 and **Supplemental Table 2**).

Accession Numbers

Arabidopsis thaliana: PDS (AT4G14210.1)

Solanum lycopersicum: DXS (Soly01g067890) PSY1, 2, and 3 (Soly03g031860, Soly02g081330, Soly01g005940, respectively); PDS (Soly03g123760); ZISO (Soly12g098710); ZDS (Soly01g097810); CRTISO (Soly10g081650); CRTIL1 (Soly05g010180); CRTL-E (Soly12g008980); CRTL-B1, and 2 (Soly04g040190,

Solyc06g074240, respectively); *CRTR-B1*, and 2 (Solyc06g036260, Solyc03g007960, respectively).

Seed stocks

Wild-type cv. Ailsa Craig (LA2838A)

tangerine single mutant (LA3183)

tangerine; high-pigment1 double mutant (LA3367)

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Table 1. Available carotenoid content ($\mu\text{g/g}$ FW) in the poly-*cis*-transformation of phytoene to *all-trans*-lycopene in leaves, flowers, and ripe fruit from wild type (AC) tomato plants. ($n \geq 5$)

	PDS		ZDS		CRTISO
	15' <i>cis</i> -phytoene	<i>cis</i> -phytofluene	9,9' di <i>cis</i> -z-carotene	<i>cis</i> -neurosporene	Prolycopene
Leaf	0.07 $\pm$ 0.004	n.d.	n.d.	n.d.	n.d.
Flower	n.d.	n.d.	n.d.	n.d.	n.d.
Ripe Fruit	1.72 $\pm$ 0.11	0.95 $\pm$ 0.06	0.23 $\pm$ 0.03	n.d.	n.d.

Carotenoid content is presented as $\mu\text{g/g}$ fresh weight (FW). Values represent the mean of a minimum of five biological replicates $\pm$ standard error. n.d. denotes not detected.

Table 2. Carotenoid composition in ripe fruit (7DPB), flower petals, and leaves of stable T2 generation AtPDS.OE tomato plants compared to wild type (AC) tomato plants.

Carotenoid composition (% of control $\pm$ SEM, $n \geq 5$)								
Genotype	Phytoene	Phytofluene	z-carotene	Lycopene	b-carotene	Lutein	Xantho- phylls	Total Carotenoids/ Xanthophylls
Fruit (7DPB)								
<i>Ailsa Craig</i> (WT)	100.0 $\pm$ 6.4	100.0 $\pm$ 6.5	100.0 $\pm$ 13.9	100.0 $\pm$ 3.9	100.0 $\pm$ 2.6	100.0 $\pm$ 7.2		100.0 $\pm$ 3.7
<i>AtPDS.OE.1A.1</i>	28.5 $\pm$ 1.9	24.9 $\pm$ 1.7	234.6 $\pm$ 23.8	110.1 $\pm$ 6.4	123.4 $\pm$ 9.7	90.9 $\pm$ 6.4		108.3 $\pm$ 6.3
<i>AtPDS.OE.3.2</i>	30.0 $\pm$ 3.0	26.1 $\pm$ 2.2	228.6 $\pm$ 24.1	121.9 $\pm$ 7.0	131.2 $\pm$ 11.5	102.9 $\pm$ 3.2		119.4 $\pm$ 6.3
<i>AtPDS.OE.4.2</i>	32.1 $\pm$ 3.2	28.5 $\pm$ 2.4	262.6 $\pm$ 24.3	131.1 $\pm$ 3.5	142.8 $\pm$ 6.9	101.6 $\pm$ 0.9		128.5 $\pm$ 3.0
<i>AtPDS.OE.6.2</i>	35.3 $\pm$ 4.7	30.7 $\pm$ 3.8	213.2 $\pm$ 28.3	100.8 $\pm$ 5.8	108.4 $\pm$ 5.7	86.9 $\pm$ 7.8		99.2 $\pm$ 5.5
Flower Petals								
<i>Ailsa Craig</i> (WT)					100.0 $\pm$ 6.2	100.0 $\pm$ 3.5	100.0 $\pm$ 4.9	100.0 $\pm$ 4.5
<i>AtPDS.OE.1A.1</i>					110.9 $\pm$ 5.8	92.4 $\pm$ 3.3	106.3 $\pm$ 4.6	105.7 $\pm$ 4.2
<i>AtPDS.OE.3.2</i>					100.7 $\pm$ 6.5	92.3 $\pm$ 5.4	101.8 $\pm$ 4.0	101.2 $\pm$ 3.5
<i>AtPDS.OE.4.2</i>					95.5 $\pm$ 5.1	89.1 $\pm$ 3.1	103.8 $\pm$ 5.1	102.2 $\pm$ 4.7
<i>AtPDS.OE.6.2</i>					109.6 $\pm$ 4.2	95.4 $\pm$ 3.2	108.5 $\pm$ 2.6	107.8 $\pm$ 2.4
Leaves								
<i>Ailsa Craig</i> (WT)	Trace				100.0 $\pm$ 6.4	100.0 $\pm$ 2.9	100.0 $\pm$ 3.0	100.0 $\pm$ 3.3
<i>AtPDS.OE.1A.1</i>	n.d.				102.3 $\pm$ 6.4	118.2 $\pm$ 6.6	115.0 $\pm$ 4.5	113.3 $\pm$ 4.7
<i>AtPDS.OE.3.2</i>	n.d.				101.8 $\pm$ 4.6	110.9 $\pm$ 4.2	103.6 $\pm$ 3.5	104.0 $\pm$ 3.6
<i>AtPDS.OE.4.2</i>	n.d.				108.3 $\pm$ 2.8	117.6 $\pm$ 2.8	104.1 $\pm$ 2.7	106.6 $\pm$ 2.5
<i>AtPDS.OE.6.2</i>	n.d.				102.4 $\pm$ 4.1	106.4 $\pm$ 5.9	92.4 $\pm$ 5.0	96.1 $\pm$ 4.9

Carotenoid contents are presented as percent of control (*Ailsa Craig* (WT)) unless otherwise indicated. Values represent a mean of a minimum of 5 biological replicates $\pm$ SEM. Trace denotes detected at very low levels. n.d. denotes not detected. (Representative chromatograph and UV spectrums of carotenoids detected in the wildtype ripe tomato shown in Supplemental Fig. 2)

Figure 1. PDS is limiting in carotenogenesis during tomato fruit ripening.

(A) Carotenoid biosynthetic pathway with enzymes abbreviated in bold: PSY1, 2, and 3, phytoene synthase 1, 2, and 3; PDS, phytoene desaturase; ZISO, ζ -carotene isomerase; ZDS, ζ -carotene desaturase; CRTISO, carotene isomerase; CRTL-E (LCY-E), lycopene ϵ -cyclase; CRTL-B1, and 2 (LCY-B and BCYC, respectively), lycopene β -cyclase; CYP97A3, carotene ϵ -hydroxylase; CRTR-B1, and 2, carotene β -hydroxylase 1 and 2; ABA is abscisic acid.

(B) Transcript levels of *PDS*, *ZDS* and *CRTISO* relative to a reference sample (combination of equal amounts of RNA from each tissue analysed) ($n=3$, in triplicate; Error bars, +SEM). Abbreviated tissues represent different stages of fruit ripening, mature green fruit, MG; Breaker or onset of ripening, Br; and 3 and 7 days post breaker, 3DPB and 7DPB, respectively.

Figure 2. Over-expression of *AtPDS* enhances tomato fruit color.

(A) Transcript levels of tomato and *Arabidopsis* *PDS* (*SlPDS* and *AtPDS*, respectively) in *AtPDS* over-expression lines relative to the wild-type control (cv. Ailsa Craig). Ripe fruit represents 7DPB ($n=5$, in triplicate; Error bars, +SEM).

(B) Visual phenotypes of the chromoplast rich 7DPB fruit of the *AtPDS.OE* lines compared to the wild-type control (cv. Ailsa Craig).

Figure 3. *AtPDS* over-expression pushes residual phytoene toward synthesis of downstream carotenoids in ripe tomato fruit.

(A) Phytoene; phytofluene; and ζ -carotene content ($\mu\text{g/g}$ FW) in ripe fruit of *AtPDS.OE* lines compared to wild-type ($n=5$, Error bars +SEM) (All *AtPDS.OE* values significant with a p -value <0.001).

(B) Lycopene content ($\mu\text{g/g}$ FW) in ripe fruit of *AtPDS.OE* lines compared to wild-type ($n=5$, Error bars +SEM) (* $p<0.05$; ** $p<0.01$; *** $p<0.001$).

(C) β -carotene content ($\mu\text{g/g}$ FW) in ripe fruit of *AtPDS.OE* lines compared to wild-type ($n=5$, Error bars +SEM) (* $p<0.05$; ** $p<0.01$; *** $p<0.001$).

(D) Total carotenoid content ($\mu\text{g/g}$ FW) in ripe fruit of *AtPDS.OE* lines compared to wild-type ($n=5$, Error bars +SEM) (* $p<0.05$; ** $p<0.01$; *** $p<0.001$).

Figure 4. Carotenoid gene expression changes limited to *CRTL1* in *AtPDS.OE* ripe fruit.

(A) Transcript levels of *PSY1*, *CRTL-B1* and *CRTL-B2* in the ripe fruit of *AtPDS.OE* lines relative to the wild-type control (cv. Ailsa craig).

(B) Transcript levels of *CRTL1* in the ripe fruit of *AtPDS.OE* lines relative to the wild-type control (cv. Ailsa craig).

Figure 5. Enhanced photoprotective xanthophyll content in young leaves of *AtPDS.OE* lines.

(A) Lutein and β -carotene content in young leaves of *AtPDS.OE* lines compared to wild-type ($n=5$, Error bars +SEM) (* $p<0.05$; ** $p<0.01$; *** $p<0.001$).

(B) zeaxanthin and β -cryptoxanthin content in young leaves of *AtPDS.OE* lines compared to wild-type ($n=5$, Error bars +SEM) (* $p<0.05$; ** $p<0.01$; *** $p<0.001$).

(C) Endogenous regulation of carotenoid biosynthetic genes, deoxyxylulose 5-phosphate (DXP) synthase, *DXS*; phytoene synthase 1, *PSY1*; chloroplast specific lycopene β -cyclase *CRTL-B1*; and chloroplast specific carotene β -hydroxylase, *CRTR-B1* ($n=5$, in triplicate; Error bars +SEM).

Figure 6. Deregulation of *ZISO* and *CRTR-B1* in *AtPDS.OE* flowers.

Transcript levels of *ZISO* and *CRTR-B1* in the anthesis flowers of *AtPDS.OE* lines relative to the wild-type control (cv. Ailsa craig).

Figure 7. Over-expression of *AtPDS* enhances downstream *cis*-carotenoid accumulation in the *tangerine* mutant.

(A) External visual phenotype of *tangerine* (t^{3183}) compared to *AtPDS3.2*; t^{3183} and *hp1*; t^{3183} double mutants.

(B) Cross-sections of ripe fruit display internal pericarp pigmentation in t^{3183} , *AtPDS3.2*; t^{3183} and *hp1*; t^{3183} .

(C) *Cis*-carotenoid content ($\mu\text{g/g}$ FW) from the poly-*cis*-transformation of phytoene to all-*trans*-lycopene in t^{3183} , *AtPDS3.2*; t^{3183} and *hp1*; t^{3183} 7DPB fruit ($n=5$; Error bars, +SEM) (* $p<0.05$; ** $p<0.01$; *** $p<0.001$).

(D) *Cis*- and all-*trans*-lycopene content ($\mu\text{g/g}$ FW) accumulating in 7DPB fruit of t^{3183} , *AtPDS3.2*; t^{3183} and *hp1*; t^{3183} ($n=5$; Error bars, +SEM) (* $p<0.05$; ** $p<0.01$; *** $p<0.001$).

All carotenoid names identify peaks with similar characteristics and retention timing as those identified in Melendez-Martinez et al.²¹

(E) Total lycopene content in 7DPB fruit of t^{3183} , *AtPDS3.2*; t^{3183} and *hp1*; t^{3183} ($n=5$; Error bars, +SEM) (* $p<0.05$; ** $p<0.01$; *** $p<0.001$).

Figure 8. Model of feedback and feedforward regulation induced by *AtPDS* over-expression in ripe fruit; leaves; and flowers.

Enzymes within the simplified MEP pathway are abbreviated in bold. DXS, deoxyxylulose 5-phosphate (DXP) synthase; DXR, DXP reductase; HDR, 4- hydroxy-3-methylbut-2-enyl diphosphate reductase. Enzyme products are abbreviated as follows: GAP, glyceraldehyde 3-

phosphate; DXP, deoxyxylulose 5-phosphate; MEP, methyl-d-erythritol 4-phosphate; HMBPP, 4-hydroxy-3-methylbut-2-enyl diphosphate; IPP, isopentenyl diphosphate; DMAPP, dimethylallyl diphosphate; and GGPP, geranylgeranyl diphosphate. Carotenoid biosynthetic enzymes are abbreviated in bold: PSY1, 2, and 3, phytoene synthase 1, 2 and 3; PDS, phytoene desaturase; ZISO, ζ -carotene isomerase; ZDS, ζ -carotene desaturase; CRTISO, carotene isomerase; CRTIL1, CRTISO-like 1; CRTL-E (LCY-E), lycopene ϵ -cyclase; CRTL-B1, and 2 (LCY-B and BCYC, respectively), lycopene β -cyclase; CYP97A3, carotene ϵ -hydroxylase; CRTR-B1, and 2, carotene β -hydroxylase 1 and 2; and ABA is abscisic acid. Black dotted bars designate negative impacts on gene expression in response to *AtPDS* over-expression in ripe fruit. Dark grey arrows designate positive impacts by *AtPDS* over-expression in leaves. Light grey arrows/bars designate positive/negative impacts by *AtPDS* over-expression in anthesis flowers.

Figure 1

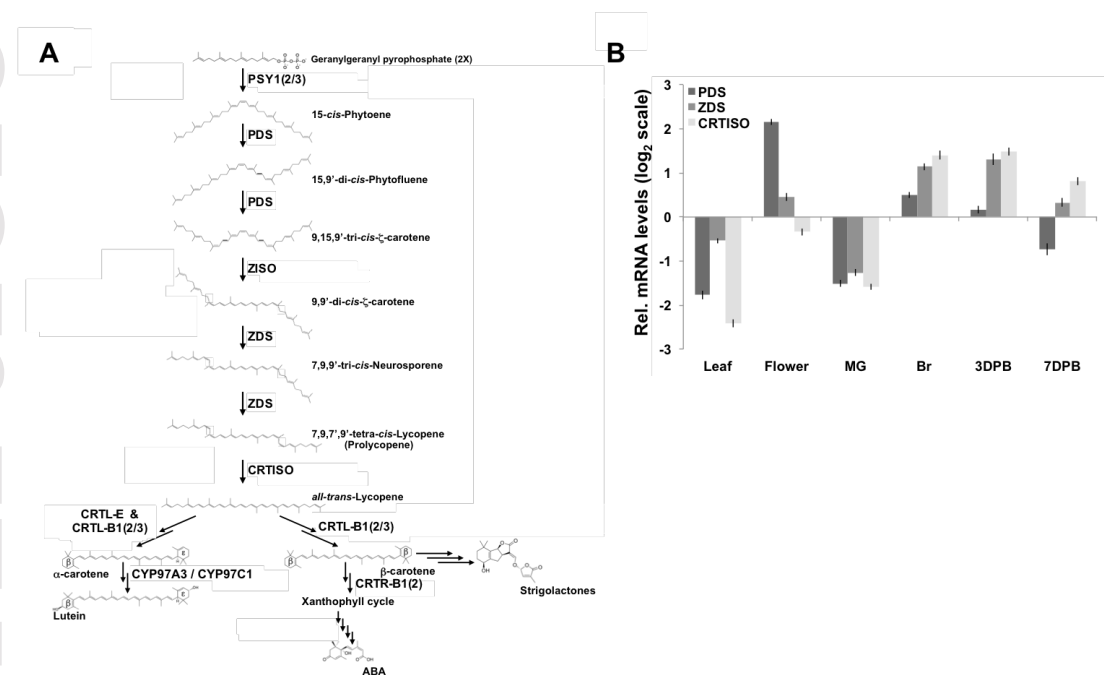


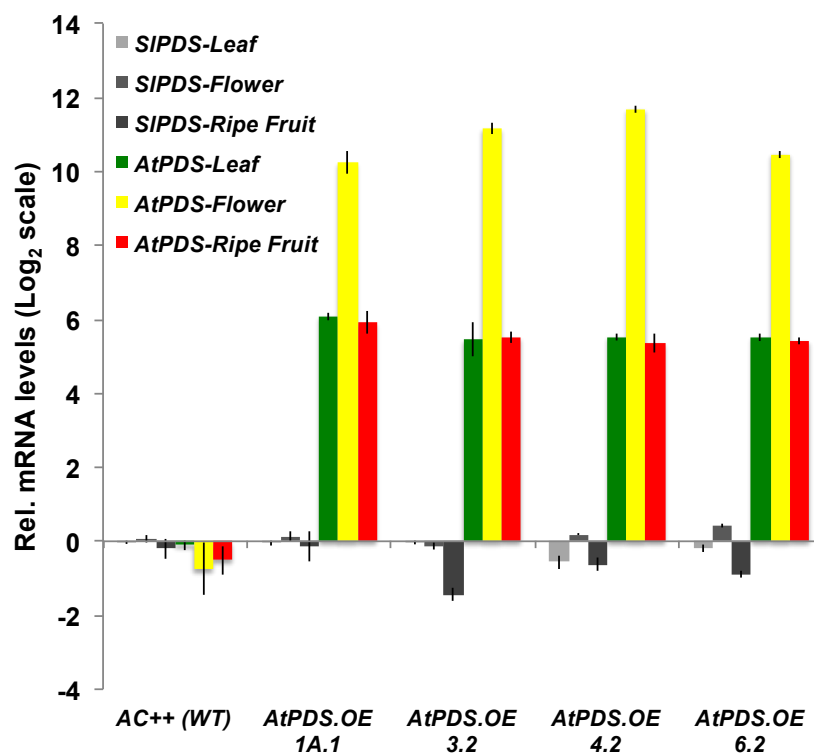
Figure 1. PDS is limiting in carotenogenesis during tomato fruit ripening.

(A) Carotenoid biosynthetic pathway with enzymes abbreviated in bold: PSY1, 2, and 3, phytoene synthase 1, 2, and 3; PDS, phytoene desaturase; ZISO, ζ -carotene isomerase; ZDS, ζ -carotene desaturase; CRTISO, carotene isomerase; CRTL-E (LCY-E), lycopene ϵ -cyclase; CRTL-B1, and 2 (LCY-B and BCYC, respectively), lycopene β -cyclase; CYP97A3, carotene ϵ -hydroxylase; CRTR-B1, and 2, carotene β -hydroxylase 1 and 2; ABA is abscisic acid.

(B) Transcript levels of *PDS*, *ZDS* and *CRTISO* relative to a reference sample (combination of equal amounts of RNA from each tissue analysed) ($n=3$, in triplicate; Error bars, +SEM). Abbreviated tissues represent different stages of fruit ripening, mature green fruit, MG; Breaker or onset of ripening, Br; and 3 and 7 days post breaker, 3DPB and 7DPB, respectively.

Figure 2

A



B

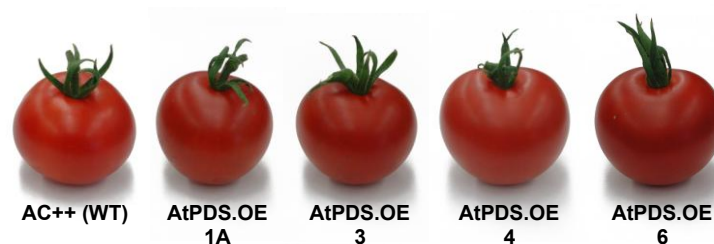


Figure 2. Over-expression of *AtPDS* enhances tomato fruit color.

(A) Transcript levels of tomato and *Arabidopsis PDS* (*SIPDS* and *AtPDS*, respectively) in stable, T₂ generation *AtPDS* over-expression lines relative to the wild-type control (cv. Ailsa Craig). Ripe fruit represents 7DPB ($n=5$, in triplicate; Error bars, +SEM).

(B) Visual phenotypes of the chromoplast rich 7DPB fruit of the stable, T₂ generation *AtPDS.OE* lines compared to the wild-type control (cv. Ailsa Craig).

Figure 3

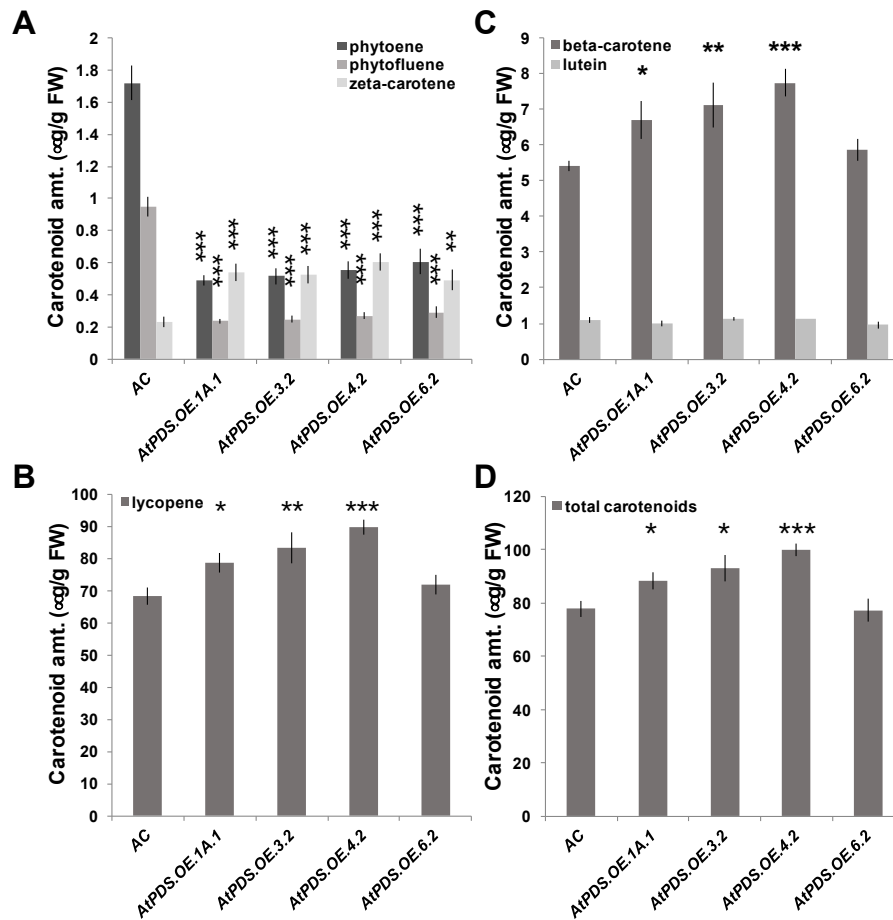


Figure 3. *AtPDS* over-expression pushes residual phytoene toward synthesis of downstream carotenoids in ripe tomato fruit.

(A) Phytoene; phytofluene; and ζ -carotene content ($\mu\text{g/g FW}$) in ripe fruit of stable, T_2 generation *AtPDS.OE* lines compared to wild-type ($n=5$, Error bars $\pm\text{SEM}$) (* $p<0.05$; ** $p<0.01$; *** $p<0.001$).

(B) Lycopene content ($\mu\text{g/g FW}$) in ripe fruit of stable, T_2 generation *AtPDS.OE* lines compared to wild-type ($n=5$, Error bars $\pm\text{SEM}$) (* $p<0.05$; ** $p<0.01$; *** $p<0.001$).

(C) β -carotene content ($\mu\text{g/g FW}$) in ripe fruit of stable, T_2 generation *AtPDS.OE* lines compared to wild-type ($n=5$, Error bars $\pm\text{SEM}$) (* $p<0.05$; ** $p<0.01$; *** $p<0.001$).

(D) Total carotenoid content ($\mu\text{g/g FW}$) in ripe fruit of stable, T_2 generation *AtPDS.OE* lines compared to wild-type ($n=5$, Error bars $\pm\text{SEM}$) (* $p<0.05$; ** $p<0.01$; *** $p<0.001$).

Figure 4

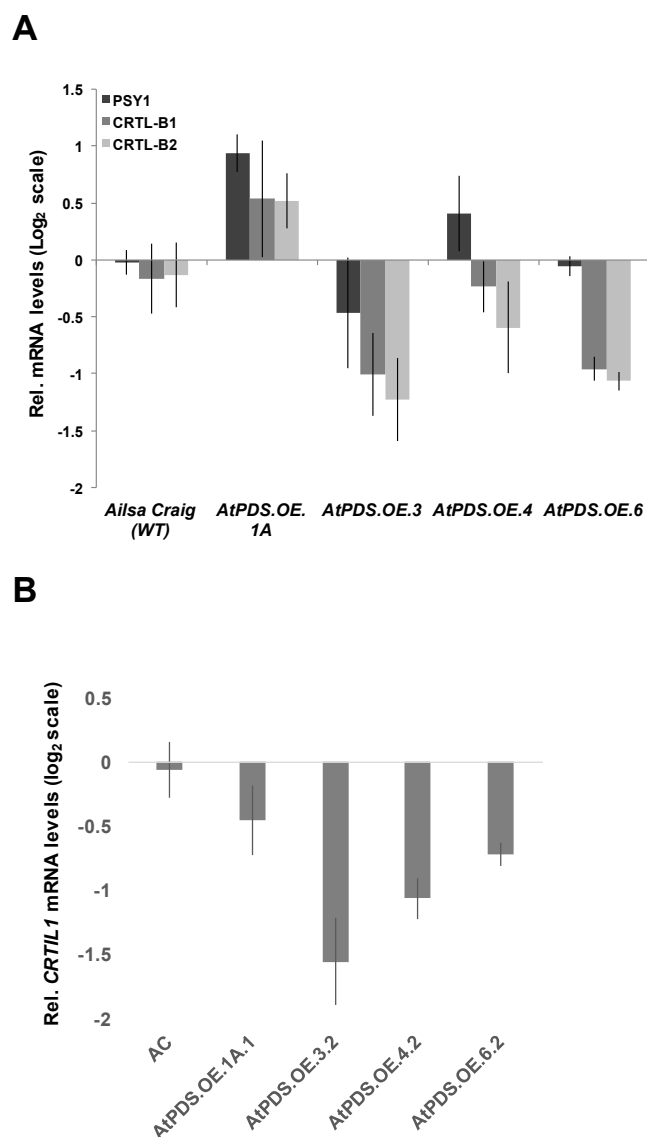


Figure 4. Carotenoid gene expression changes limited to *CRTIL1* in *AtPDS.OE* ripe fruit.

(A) Transcript levels of *PSY1*, *CRTL-B1* and *CRTL-B2* in the ripe fruit of stable, T₂ generation *AtPDS.OE* lines relative to the wild-type control (cv. Ailsa craig) ($n=3$, in triplicate; Error bars $\pm$ SEM).

(B) Transcript levels of *CRTIL1* in the ripe fruit of stable, T₂ generation *AtPDS.OE* lines relative to the wild-type control (cv. Ailsa craig) ($n=3$, in triplicate; Error bars $\pm$ SEM).

Figure 5

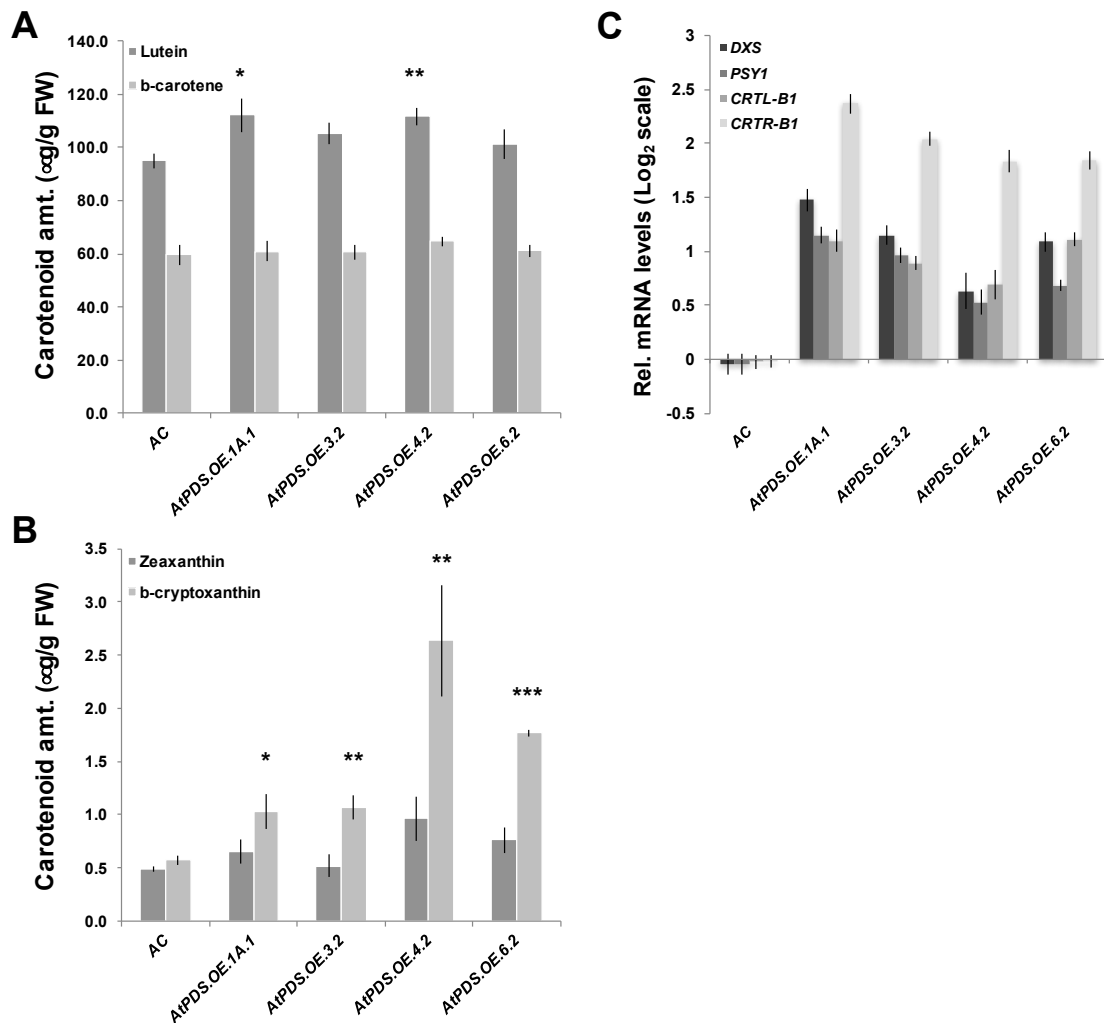


Figure 5. Enhanced photoprotective xanthophyll content in young leaves of *AtPDS.OE* lines.

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(B) zeaxanthin and β -cryptoxanthin content in young leaves of stable, T₂ generation *AtPDS.OE* lines compared to wild-type ($n=5$, Error bars $\pm$ SEM) (* $p<0.05$; ** $p<0.01$; *** $p<0.001$).

(C) Endogenous regulation of carotenoid biosynthetic genes, deoxyxylulose 5-phosphate (DXP) synthase, *DXS*; phytoene synthase 1, *PSY1*; chloroplast specific lycopene β -cyclase

CRTL-B1; and chloroplast specific carotene β -hydroxylase, *CRTR-B1* ($n=5$, in triplicate; Error bars $\pm$ SEM).

Figure 6

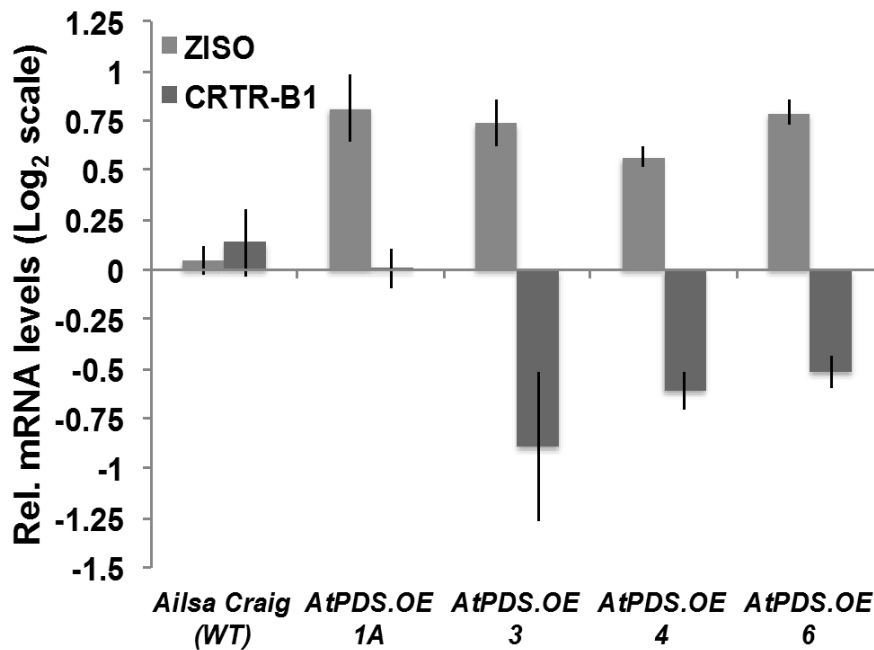


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Transcript levels of *ZISO* and *CRTR-B1* in the anthesis flowers of stable, T₂ generation *AtPDS.OE* lines relative to the wild-type control (cv. Ailsa craig) ($n=3$, in triplicate; Error bars $\pm$ SEM).

Figure 7

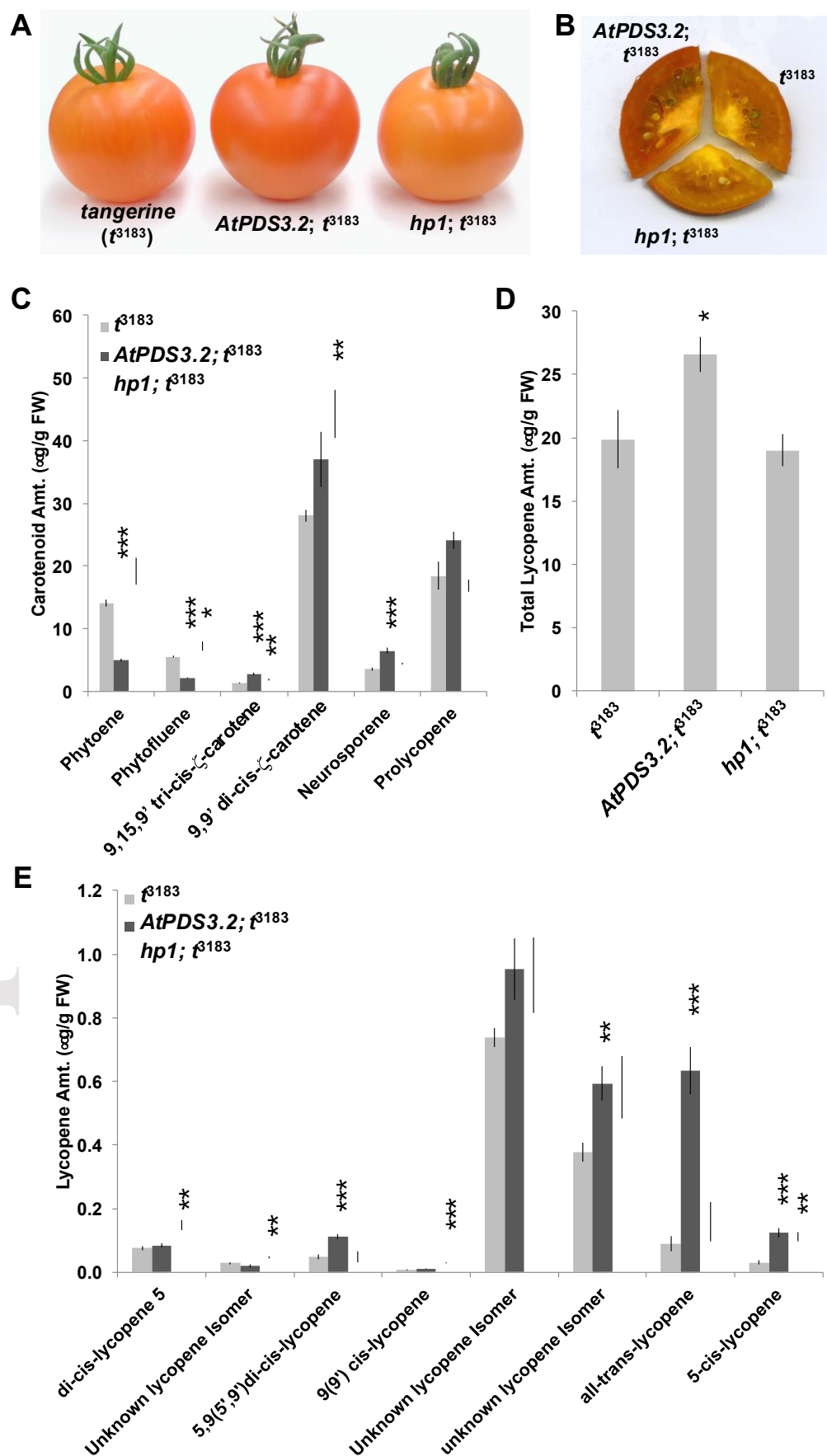


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(D) Total lycopene content in 7DPB fruit of t^{3183} , *AtPDS3.2*; t^{3183} and *hp1*; t^{3183} ($n=5$; Error bars, $\pm\text{SEM}$) (* $p<0.05$; ** $p<0.01$; *** $p<0.001$).

(E) *Cis*- and all-*trans*-lycopene content ($\mu\text{g/g}$ FW) accumulating in 7DPB fruit of t^{3183} , *AtPDS3.2*; t^{3183} and *hp1*; t^{3183} ($n=5$; Error bars, $\pm\text{SEM}$) (* $p<0.05$; ** $p<0.01$; *** $p<0.001$).

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Figure 8

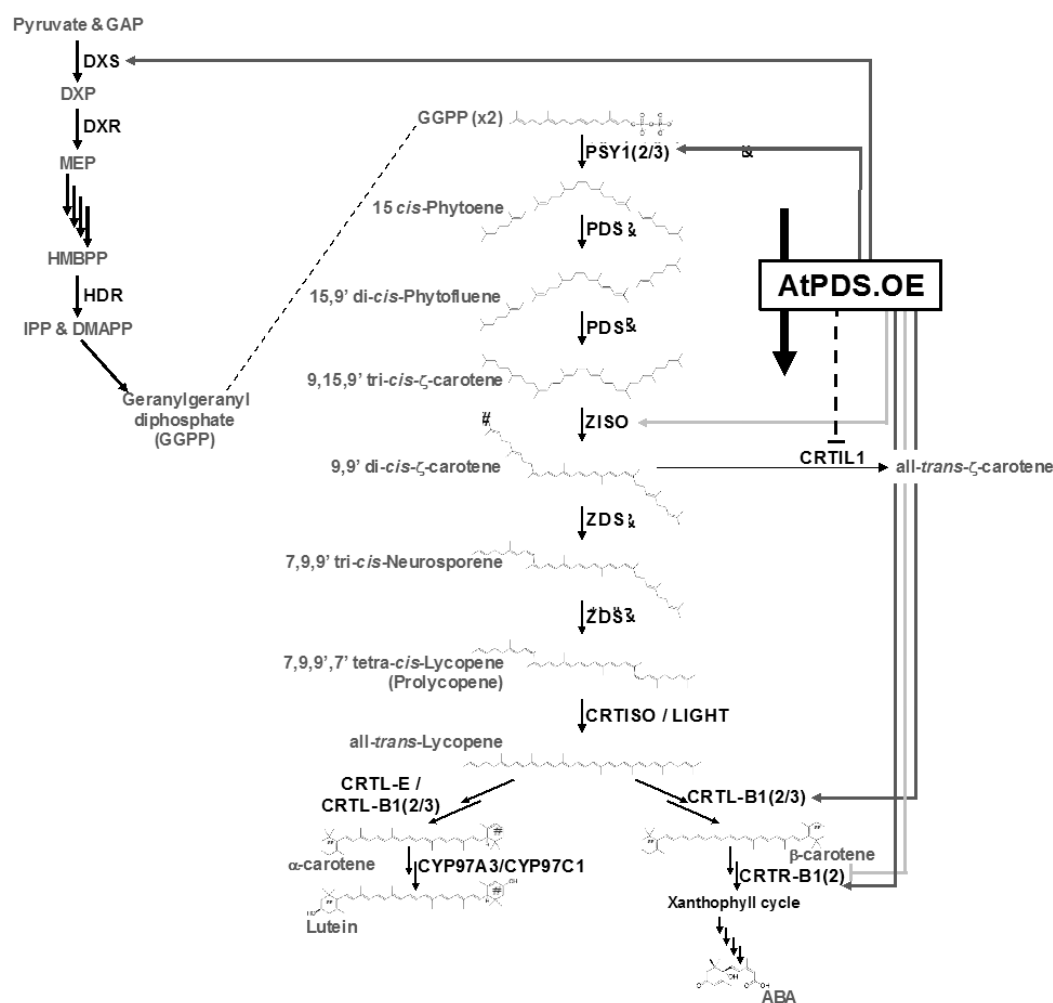


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CRTISO, carotene isomerase; CRTIL1, CRTISO-like 1; CRTL-E (LCY-E), lycopene ϵ -cyclase; CRTL-B1, and 2 (LCY-B and BCYC, respectively), lycopene β -cyclase; CYP97A3, carotene ϵ -hydroxylase; CRTR-B1, and 2, carotene β -hydroxylase 1 and 2; and ABA is abscisic acid. Black dotted bar represents negative impacts on gene expression in response to *AtPDS* over-expression in ripe fruit. Dark grey arrows designate positive impacts by *AtPDS* over-expression in leaves. Light grey arrows/bars designate positive/negative impacts by *AtPDS* over-expression in anthesis flowers.