Short Title. PGKs are co-regulated to adjust central metabolism

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Phosphoglycerate kinases are co-regulated to adjust metabolism and to optimize growth

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ONE SENTENCE SUMMARY. Photosynthetic and glycolytic phosphoglycerate kinase mutants are transcriptionally co-regulated to achieve metabolic homeostasis and to optimize growth in Arabidopsis.

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ABSTRACT

In plants, phosphoglycerate kinase (PGK) converts 1,3-bisphosphoglycerate into 3-phosphoglycerate (3-PGA) in glycolysis, but also participates in the reverse reaction in gluconeogenesis and the Calvin-Benson cycle. In the databases we found three genes that encode putative PGKs. PGK1 was localized exclusively in the chloroplasts of photosynthetic tissues, while PGK2 was expressed in the chloroplast/plastid of photosynthetic and non-photosynthetic cells. PGK3 was ubiquitously expressed in the cytosol of all studied cell types. Measurements of carbohydrate content and photosynthetic activities in PGK mutants and silenced lines corroborated that PGK1 was the photosynthetic isoform, while PGK2 and PGK3 were the plastidial and cytosolic glycolytic isoforms, respectively. The *pgk1.1* knock-down mutant displayed reduced growth, lower photosynthetic capacity and starch content. The *pgk3.2* knock-out mutant was characterized by a reduced growth, but a higher starch levels than the wild-type. The *pgk1.1 pgk3.2* double mutant was bigger than *pgk3.2*, and displayed an intermediate phenotype between the two single mutants in all measured biochemical and physiological parameters. Expression studies in *PGK* mutants showed that *PGK1* and *PGK3* were down-regulated in *pgk3.2* and *pgk1.1*, respectively. These results indicate that the down-regulation of photosynthetic activity could be a plant strategy when glycolysis is impaired to achieve metabolic adjustment and optimize growth. The double mutants of *PGK3* and the triose-phosphate transporter (*pgk3.2 tpt3)* displayed a drastic growth phenotype, but were viable. This implies that other enzymes or non-specific chloroplast transporters could provide 3-PGA to the cytosol. Our results highlight both the complexity and the plasticity of the plant primary metabolic network.

INTRODUCTION

Glycolysis was the first metabolic pathway to be fully elucidated biochemically in the 1940s (Plaxton, 1996). It is a central pathway in most living organisms, where it provides energy in the form of ATP and reducing power, pyruvate to fuel the tricarboxylic acid cycle (TCA), and precursors for secondary metabolism, amino acid, and fatty acid biosynthesis (Plaxton, 1996). In plants glycolysis is more complex than in animals, since it occurs independently in two compartments, the plastid and the cytosol. Besides, according to the genome databases (https://www.arabidopsis.org/), there is more than one isoform for each glycolytic reaction, and some of them are represented by more than 40 annotations. In spite of the important advances made in the functional characterization of both cytosolic and plastidial glycolytic enzymes (Sparla et al., 2005; Fermani et al., 2007; Muñoz-Bertomeu et al., 2009; Chen and Thelen, 2010; Prabhakar et al., 2010; Zhao and Assmann, 2011; Guo et al., 2012; Wakao et al., 2014), the relative contribution and the degree of integration of both pathways in different cell types are still far from being completely understood. In addition, some of the reactions of the plastidial glycolytic pathway are shared by the Calvin-Benson cycle although operating in the opposite direction. Specifically, glyceraldehyde-3-phosphate dehydrogenase (GAPDH) and phosphoglycerate kinase (PGK) could participate in the same compartment and/or at the same time in photosynthetic and glycolytic/gluconeogenic reactions (Fig. 1). For this reason, the functional characterization of both GAPDH and PGK isoforms is of crucial importance.

Plant GAPDH isoforms have been extensively characterized at genetic, biochemical and molecular levels (Sparla et al., 2005; Hajirezaei et al., 2006; Fermani et al., 2007; Holtgrefe et al., 2008; Muñoz-Bertomeu et al., 2009, 2010; Guo et al., 2012; Guo et al., 2014; Anoman et al., 2015; Han et al., 2015). However, little attention has been paid to the functional characterization of PGKs. These enzymes are essential in the metabolism of most living organisms and their sequence has remained highly conserved throughout evolution (Longstaff et al., 1989). They catalyze the reversible transfer of a highly energetic phosphate group at position one of the 1,3-bisphosphoglycerate to ADP to give rise to 3-phosphoglycerate (3-PGA) and ATP, and *vice versa*. PGKs from different species have been isolated in both animals and plants (Krietsch and Bucher, 1970; McCarrey and Thomas, 1987; Longstaff et al., 1989; Kopke-Secundo et al., 1990; McMorrow and Bradbeer, 1990; Lobler, 1998). Two PGK isoforms (PGK1 and PGK2) encoded by two genes have been identified in humans. PGK1 is expressed in all somatic cells, including red blood cells (Willard et al., 1985; McCarrey and Thomas, 1987; Chiarelli et al., 2012), while PGK2 is sperm-cell specific (Boer et al., 1987). PGK1 has been implicated in the metabolism of tumor cells (Lay et al., 2000; Hwang et al., 2006; Zieker et al., 2008, 2010; Ai et al., 2011), and also in nuclear DNA replication and repair (Popanda et al., 1998). PGK2 is essential for sperm motility and fertility (Danshina et al., 2010).

In plants, PGKs are involved in not only glycolysis/gluconeogenesis but also in photosynthetic carbon metabolism. Two highly conserved PGK isoforms were initially identified in wheat (Longstaff et al., 1989). One of them being located primarily in the cytosol, while the other was plastid-localized (Anderson and Advani, 1970). Although the two PGKs could theoretically catalyze both the forward and reverse reactions, it was assumed that the cytosolic isoform is involved in glycolysis and gluconeogenesis, while the plastidial isoform participates, at least in photosynthetic cells, in both the Calvin-

Benson cycle and plastidial glycolysis (Anderson et al., 2004). However, this latter assumption has not been thoroughly investigated to date. Subsequently, a second cytosolic PGK isoform from *Helianthus annus* was cloned (Troncoso-Ponce et al., 2012), and in the Arabidopsis genome an additional putative PGK isoform with a N-terminal plastid/chloroplast localization signal was identified (Ouibrahim et al., 2014). The presence of two PGKs in the plastid/chloroplast could lead to a specialization so that one of them could be involved in photosynthesis and the other in glycolysis, which seems to be the case of GAPDH isoforms (Anoman et al. 2015). Indeed a mutant of one of the Arabidopsis plastidial isoforms (At1g56190; *AtPGK2*) has been described as lethal (Myouga et al., 2010; Ouibrahim et al., 2014), which suggests that the two plastidial isoforms are not functionally redundant and likely play different roles in plant metabolism. Moreover, chloroplastic and cytosolic PGKs proteins were localized in the nucleus by immunocytolocalization experiments in peas (Anderson et al., 2004) which is in keeping with the presence of functional nuclear localization signals in the cytosolic PGK (Brice et al., 2004). This fact has led to the hypothesis that PGKs are able to act as "moonlighting" proteins playing other roles apart from their participation in metabolism. Accordingly, plastidial PGK2 has been shown to play a role in tolerance to abiotic (Liu et al., 2015; Joshi et al., 2016) and biotic (Ouibrahim et al., 2014) stresses. PGK2 has proven to be necessary for watermelon mosaic virus infection (Ouibrahim et al., 2014). Specifically, PGK2 could mediate the transport of viruses to the chloroplast (Lin et al., 2007; Cheng et al., 2013). The *in vitro* regulation of some PGK isoforms has been studied (Troncoso-Ponce et al., 2012; Morisse et al., 2014). It has been shown that the chloroplastic isoform of *Chlamydomonas reinhardtii* could be light-regulated by thioredoxins (Morisse et al., 2014). Furthermore, at the biochemical level, glycolytic PGKs activity has been reported to increase in sunflower developing embryos in conjunction with the oil content (Troncoso-Ponce et al., 2009). It has also been shown that PGK and enolase are two of the activities implicated in the differences in oil content between standard and low oil content sunflower lines (Troncoso-Ponce et al., 2010). Yet to date, no genetic or molecular evidence has been found to support the metabolic function of specific PGKs. In this work, we have followed a loss-of-function approach to functionally characterize all the glycolytic and photosynthetic isoforms annotated in the Arabidopsis genome at both molecular and physiological levels. We unraveled the specific contribution of each isoform to the primary metabolism of aerial parts (AP) and roots, and concluded that both glycolytic and photosynthetic isoforms are co-regulated to maintain the equilibrium between catabolic and anabolic processes.

RESULTS

Expression analysis and subcellular localization of the PGK family

In the Arabidopsis Information Resource database (TAIR; http://www.arabidopsis.org) we found three genes encoding putative PGKs: At3g12780, At1g56190 and At1g79550. According to the literature we named the proteins coded by these genes PGK1, PGK2 and PGK3, respectively. PGK1 displays 91% and 84% of amino acid identity with PGK2 and PGK3, respectively, while the amino acid identity between PGK2 and PGK3 is 85%. The three isoforms show 100% identity in all residues that form the putative catalytic site and the ligand binding domain (Supplemental Fig. S1A). The cladogram confirmed that PGK1 and PGK2 are more closely related to one another than to PGK3 (Supplemental Fig. S1B). We next assessed the expression patterns of the *PGK* family genes by quantitative real-time (RT) PCR and by analysis of promoter-GUS fusions in

both seedlings and adult plants. *PGK1* was expressed mainly in the leaves, and very poorly in roots at both seedling and adult stages (Fig. 2A and B). *PGK2* was also expressed mainly in leaves especially at the seedling stage, but at the adult stage its relative expression in roots, siliques and flowers was higher than that of *PGK1*. By contrast to *PGK1* and *PGK2*, *PGK3* was highly expressed in roots, especially at the seedling stage. At the adult stage its expression pattern was the most homogeneous of all three PGKs, being expressed similarly in all organs studied. These data confirm publically available microarray expression data (http://bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi). The promoter-GUS analysis revealed a generalized expression of *PGK1* in leaves and cotyledons, especially in guard cells and the surroundings of the vasculature, in petals and sepals, and confirmed the lack of *PGK1* expression in reproductive organs and roots (Fig. 2C and Supplemental Fig. S2). *PGK2* was strongly expressed in leaf veins and margins, in the root vasculature, and in floral organs (pedicel, petals, sepals and stigma) (Fig. 2C and Supplemental Fig. S3). *PGK3* was homogeneously expressed in all plant tissues with a high expression in veins and distal zones of leaves, and all over the roots, siliques and flowers (Fig. 2C and Supplemental Fig. S4). According to the ChloroP prediction server (http://www.cbs.dtu.dk/services/ChloroP/), both PGK1 and PGK2 harbor a N-terminal plastid/chloroplast localization signal (Emanuelsson et al., 1999). To investigate the subcellular localization of the PGK family proteins, we stably expressed PGK-GFP fusion protein constructs under the control of the PGKs endogenous promoters in Arabidopsis (*ProPGK1:PGK1-GFP*, *ProPGK2:PGK2-GFP*, *ProPGK3:PGK3-GFP)*. PGK1 was expressed mainly in the cloroplasts of mesophyll cells and no signal was observed in roots (Fig. 3). PGK2 was expressed in leaf plastids/chloroplasts. In roots, PGK2 was not homogenously expressed, but displayed a high expression in the columnela plastids. PGK3 was similarly expressed in the cytosol of both root and leaf cells (Fig. 3). PGK3 could also be localized in the nucleus as confirmed by the nuclear Hoechst marker (Supplemental Fig. S5).

Phenotypic characterization of *PGK* mutants

In order to shed light on the *in vivo* function of *PGKs*, a loss-of-function approach was followed. T-DNA insertion lines for each *PGK* gene were identified in the databases. The genomic location of the T-DNA insertions was verified by PCR with genomic DNA and sequencing of PCR products (Fig. 4A and Supplemental Table S1). In *pgk1.1* (GK_172A12) and *pgk1.2* (GK_908E11), the T-DNA insertions were located in the 5'UTR region (Fig. 4A). In *pgk2.1* (SALK_016097), the T-DNA insertion was located in the first exon. In *pgk3.1* (SALK_062377) and *pgk3.2* (SALK_066422), the T-DNA insertion was located in the fourth and fifth exon, respectively (Fig. 4A). Based on PCR genotyping, the segregation analysis of about 200 seeds from self-fertilized heterozygous plants for *PGK1* or *PGK3* mutant alleles *pgk1.1*, *pgk1.2*, *pgk3.1* and *pgk3.2* displayed a typical Mendelian ratio of 1:2:1 [homozygous mutant: heterozygous: wild-type (WT)]. RT-PCR analysis indicated that *PGK3* mutants were knock-out while both *PGK1* mutants were knock-down (Fig. 4B). The mutant *pgk1.1* showed the lowest *PGK1* expression and was chosen for further analysis (Fig. 4B).

The analysis of *pgk2.1* seedlings from self-fertilized heterozygous plants identified a population of albino individuals when grown in plates with sucrose, which were associated with the mutant homozygous genotype (mutant: WT phenotype ratio of 1:3). This phenotype could indicate that the homozygous *pgk2.1* individuals are lethal, as formerly observed in two different T-DNA insertion lines (SALK_016097 and Salk_071724) (Myouga et al., 2010; Ouibrahim et al., 2014). *PGK2* expression in

pgk2.1 was null (Fig. 4B). However, it was not possible to complement *pgk2.1* with any of the different constructs used herein (a *PGK2* cDNA under the control of the *35S* or native *PGK2* promoter, a genomic *PGK2* sequence) suggesting that there was probably more than one mutation associated with this line. Attempts to separate the albino phenotype from the T-DNA insertion by back-crosses with WT individuals were unsuccessful. As a genotype-phenotype correlation was not found, this mutant allele was discarded for further experiments. Instead *PGK2* down-regulated lines were made using artificial microRNAs (amiRNA). Fifteen lines overexpressing an amiRNA directed against the *PGK2* in a WT background were obtained, and two lines were selected on the basis of having the lowest *PGK2* transcript level (Supplemental Fig. S6A).

Growth parameters were quantified in homozygous mutants at different stages of development *in vitro* or in greenhouse conditions (Fig. 5). *PGK3* mutants presented a significant reduction in all growth parameters measured as compared to WT controls at all growth stages analyzed (Figs. 5A, B, C and D). *pgk1.1* displayed a trend to a reduced growth in plates which was significant in greenhouse conditions, where irradiance was higher (Fig. 5C). To support that the reduction of growth in *pgk1.1* was associated with a lower *PGK1* expression, amiRNA silenced lines were obtained (Supplemental Fig. S6B). The reduced growth of these lines corroborated the relation between *PGK1* expression level and growth (Figs. 5A, B and C). The *amiRNA-PGK2* lines displayed milder phenotypes than mutants from other genes, and only one of the two selected lines with the lowest *PGK2* expression level showed a significant reduction of rosette fresh weight as compared to controls (Fig. 5C). No changes in photosynthetic activities were observed in these lines (Supplemental Table S2).

Lower photosynthetic capacity was observed in 20- and 30-day-old *pgk1.1* plants, as inferred from the decreased net photosynthetic rate, and effective and maximum photochemical yield of PSII (Table 1). These results, together with the observed plastidial localization of PGK1, would suggest a role of this isoform in the Calvin-Benson cycle. Accordingly, lower starch content was measured in *pgk1.1* plants (Figure 6A). No differences in photosynthetic parameters were observed in 20-day-old plants of *pgk3.2* in comparison to WT (Table 1). In this mutant, starch levels were higher than in WT. These results alongside the localization studies, would support the hypothesis that PGK3 is involved in the cytosolic glycolysis. However, in 30-day-old plants, the photosynthetic activity decreased in *pgk3.2*, which suggest that low cytosolic glycolytic activity affects photosynthesis in the long term (Table 1).

To further corroborate the genotype-phenotype correlation of *pgk1.1* and *pgk3.2*, we transformed the mutants with a construct carrying the native *PGK1* or *PGK3* cDNA under the control of the endogenous or the *35S* promoter, respectively. We were able to complement the growth phenotypes associated with both the *pgk1.1* and *pgk3.2* mutations (Fig. 5E). Accordingly, the photosynthetic parameters were completely or partially recovered in *pgk1.1* and *pgk3.2* complemented lines (Table 1).

Metabolomics profile of down-regulated *PGK* lines

To understand the contribution of the PGKs to the primary metabolism, we studied the metabolomics profile of the *PGK* mutants. A clearly altered metabolite content in the AP and roots of mutants was observed (Fig. 7 and Supplemental Table S3).

In the *pgk1.1* AP, the most important changes were found in the amino acid pool. Many amino acids (threonic acid, alanine, aspartate, proline) increased by more than 40% as compared to the WT (Fig. 7 and Supplemental Table S3). Sugars were not so strongly affected and none of them varied by more than 40% as compared to the WT, although glucose and sucrose increased by 29% and 24%, respectively. In roots, the pattern of metabolite modifications differed from that obtained in the AP and the sugar levels were especially affected (Fig. 7 and Supplemental Table S4), with all the quantified sugars and sugar derivatives, with the exception of glyceraldehyde-3-phosphate, being significantly increased. Quantitatively, the most striking changes were those in the levels of fructose (103% increase) and glucose (71% increase).

The *pgk3.2* AP showed a general increase in amino acids and sugar levels (Fig. 7 and Supplemental Table S3). Of the 21 amino acids detected, the increases were significant in seven, while the decreases were significant only in three. Some, e.g., glutamine and *O*-acetyl serine, increased by more than 40%. In addition, increases were observed in more than half of the quantified sugars, and the increases in fructose (up to 164%) and glucose (113%) levels were particularly noteworthy. In the *pgk3.2* roots the most prominent changes were observed in certain organic acids, e.g, succinic and citric, which increased 52% and 108%, respectively (Fig. 7 and Supplemental Table S4). As for soluble sugars, the increase was higher than that observed in the AP, especially the increases in glucose (167%) and fructose (287%). Similar changes in the *pgk3.2* AP and roots were also found in the glyceric and phosphoric acid contents, which decreased in both organs.

Significant changes were found in the *amiRNA-PGK2* lines, but they were generally less dramatic than in the other studied mutants (Fig. 7 and Supplemental Tables S3 and S4). In the *amiRNA-PGK2* AP, there was a general trend towards a decrease in the metabolite content, but only raffinose reduced by more than 40%. In roots, an increasing trend was noted in metabolite content but, once again, changes were not as drastic as in the other mutant lines (approximately 10% different from WT levels).

The *PGK1* and *PGK3* double mutation compensates the growth defects and metabolic disorders of single mutants

Transcriptomics data provided in the databases (http://bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi) and our own RNA-seq data indicate that *PGK1* is the most abundant PGK transcript in Arabidopsis leaves (*PGK1:*945, *PGK2*:118, *PGK3*:102 counts in the AP). PGK cytosolic activity accounts for 5-10% of total PGK activity in barley and spinach, while chloroplastic activities account for 90-95% (Kopke-Secundo et al., 1990; McMorrow and Bradbeer, 1990). These activity data well agree with the transcript abundance of PGK isoforms in the Arabidopsis AP.

We observed a significant reduction in PGK total activity in the AP of 20-day-old *pgk1.1* seedlings and a non-significant trend to a reduction in *pgk3.2* (Figure 6B). Since *PGK1* is the most abundant transcript in the AP, changes in the activity of other isoforms could be masked or be difficult to detect in this organ. However in roots, where *PGK3* transcripts are the most abundant (*PGK1*:46, *PGK2*:62, *PGK3*:262 counts in the roots), a reduction of about 75% of total PGK activity was observed in *pgk3.2*, while no activity changes were observed in *pgk1.1* as compared to WT. Since *pkg3.2* is knock-out, the remaining 25% of PGK activity measured in the mutant roots could be to both PGK1 and PGK2 isoforms. There were no differences in *amiPGK2* PGK activity

in either AP or roots, which may imply that the silencing is not absolute and/or that it is a global minoritary isoform in both organs, as evidenced by the transcriptomics data.

In 30-day-old plants, a significant reduction in the AP PGK activity was observed in both *pgk1.1* and *pgk3*.2. Besides, this reduction was more marked in 30-day-old than in 20-day-old *pgk1.1* plants as compared to controls. Differences in total PGK activity in the mutant at seedling (20 day-old) and adult (30-day-old) stage could be related to changes in PGK gene expression. For this reason, we studied the *PGK* family gene expression in the different mutant backgrounds at different developmental stages (Fig. 6C). At the seedling stage only *PGK1* expression was slightly reduced in *pgk3.2*. However, in adult plants *PGK1* and *PGK3* expressions were dramatically down-regulated in *pgk3.2* and *pgk1.1*, respectively. The reduction in photosynthetic activity observed in 30-day-old *pgk3.2* (Table 1) could be associated with the repression of *PGK1* in the mutant at this developmental stage.

All these results could indicate that PGKs expression is regulated at the transcriptional level to adjust metabolism. To corroborate this hypothesis, a double mutant of *pgk1.1* and *pgk3.2* was generated and subsequently studied. *pgk1.1 pgk3.2* did not show more dramatic phenotypes as compared to single mutants. On the contrary, the *pgk1.1 pgk3.2* growth phenotype was less severe than that of *pgk3.2* (Figs. 5C and D), and the starch levels and photosynthetic activities were less affected as compared to *pgk1.1* (Fig. 6A and Table 1). Double mutants improved their growth and photosynthetic activities as compared to single mutants as plants were getting older, suggesting a long term compensatory effect of the double mutation (Figs. 5A, B, C and D, Table 1).

The metabolite analysis confirmed a compensatory effect of the double mutation (Fig. 7 and Supplemental Tables S3 and S4). For instance, some metabolites such as alanine and proline, increased in the *pgk1.1* AP by more than 40% compared to WT, but did not differ significantly in the *pgk3.2* AP. In *pgk1.1 pgk3.2*, the AP contents of such metabolites did not significantly differ from those in the WT either (Fig. 7 and Supplemental Table S3). In the *pgk3.2* AP, the metabolites that varied more than 40% but whose content did not differ with respect to WT in *pgk1.1*, were glutamine (80%) and fructose (164%) (Fig. 7 and Supplemental Table S3). In *pgk1.1 pgk3.2*, the glutamine content was significantly higher than in the control, but decreased to 30%, whereas the fructose content did not show significant differences. Finally, the contents of those metabolites that changed in the same direction in both single mutants (succinic acid, aspartate, *O*-acetyl-serine, citric acid and glucose) were not superior in the double mutant to those of the single mutants, but were rather intermediate or more similar to WT. The trend described above for the AP was additionally observed in roots (Fig. 7 and Supplemental Table S4).

Blocking the flux of 3-PGA between the plastid and the cytosol accentuates the *pgk3.1* phenotypes

PGK3 should provide the 3-PGA needed for the essential reactions of the glycolytic cytosolic pathway. In spite of PGK3 being the sole cytosolic PGK isoform, the knock-out *pgk3.2* was viable. The relative 3-PGA level was not reduced but increased in *pgk3.2* plants compared to WT (Fig. 8A). We postulate that some of the 3-PGA needed for respiration could be provided by plastidial glycolysis and be transported to the cytosol by the triose phosphate transporter (TPT), the main carbon transporter in the AP. To investigate this hypothesis, we interrupted the metabolite communication

between the cytosol and the plastids by generating a double knock-out mutant of *pgk3.2* and TPT (*tpt3*), (Fig. 4A).

The *pgk3.2 tpt3* showed a more dramatic growth phenotype than the single mutants, indicating an additive effect of the mutations (Fig. 8B). Accordingly, the starch level in the AP of *pgk3.2 tpt3* was even higher than in *tpt3* (Fig. 8C). The metabolomics analysis of the *pgk3.2 tpt3* AP indicated that there was a general increase in amino acid content as observed in *pgk3.2* (Fig. 8D and Supplemental Table S5). It is worth mentioning that serine and its derivatives (methionine and *O*-acetyl-serine) also increased, which could indicate an activation of the plastidial phosphorylated pathway of serine biosynthesis. When amino acids increased in both single mutants, an additive effect was always observed in the double mutants. Interestingly, the glyceric and phosphoric acid contents, which decreased dramatically in *pgk3.2,* increased in *tpt3*. In *pgk3.2 tpt3*, these metabolites displayed an intermediate phenotype. Sugar levels (glucose, mannose and fructose) increased in *pgk3.2* but were decrease in *tpt3*, displaying intermediate values in *pgk3.2 tpt3*. Once again when sugar trends were similar in both single mutants, the change became more marked in *pgk3.2 tpt3*. For example, galactinol, *myo*-inositol, xylose and trehalose, which increased in both single mutants were further increased in *pgk3.2 tpt3*. Thus the metabolomics analysis fully corroborated the additive effect of the double mutation.

DISCUSSION

Functions of the PGK isoforms and impact in plant development

The study of the expression patterns of PGK family genes, as well as their intracellular localization provided important information concerning their function in Arabidopsis. Both PGK1 and PGK2 are plastid-localized, while PGK3 is localized in both the cytosol and the nucleus. The nuclear localization of PGK3 corroborates previous findings in peas (Anderson et al., 2004), which could indicate that this enzyme not only participates in metabolism, but also performs additional functions, as previously demonstrated in mammals. *PGK1* is almost exclusively expressed in photosynthetic tissues and *PGK3* is quite uniformly expressed in all organs. The expression studies, along with the results obtained in the metabolomics and photosynthetic analyses of the different lines (i.e. lower levels of starch and photosynthetic activities in *pgk1.1*), clearly indicate that PGK1 is a photosynthetic isoform, whereas PGK3 is the cytosolic glycolytic isoform.

The low values of the maximum quantum efficiency of PSII (Fv/Fm) in *pgk1.1* suggests the existence of a photoinhibition or photosynthetic damage phenomenon. This negative effect could be related to a reduced PGK1 activity in this mutant. PGK consumes most of the ATP required in the Calvin-Benson cycle, so its low activity would limit the regeneration of electron acceptors required for the operation of the photosynthetic electron transport chain. The smaller *pgk1.1* size may be related to their lower photosynthetic capacity and/or damage caused by photoinhibition. The negative effect on mutant growth was observed more clearly under greenhouse conditions, where the light intensity is higher than in growth chambers. In the greenhouse, the greater photosynthetic capacity of the WT and/or its lesser photoinhibition could accentuate the growth differences between the two lines.

pgk3.2 showed the more dramatic reduction in growth of all the single mutants characterized here. This may be related to the mutant incapacity to metabolize

carbohydrates for growth, since the starch and sugar levels in this mutant were higher than in the WT. Thirty-day-old *pgk3.2* displayed symptoms of photoinhibition and a dramatic reduction of *PGK1* expression along with a reduction in the photosynthetic activity. The high levels of carbohydrates could have a negative feed-back effect on the expression of photosynthetic genes (Paul and Pellny, 2003; Smith and Stitt, 2007; Stitt et al., 2010; McCormick and Kruger, 2015) and thus a general inhibition of photosynthesis.

PGK2 was plastid-localized, and is most probably a glycolytic isoform. Yet the high *PGK2* expression in leaves raises the question of additional functions in photosynthetic tissues, especially when compared with the low expression of the plastidial glycolytic isoforms of GAPDH in this organ (Muñoz-Bertomeu et al., 2009). Phylogenetic studies of plant PGKs indicate that photosynthetic and glycolytic isoenzymes have a common origin and come from an ancestral eubacteria gene that duplicated and replaced the pre-existing eukaryotic gene (Brinkmann and Martin, 1996; Archibald and Keeling, 2003). This situation contrasts with that of the GAPDHs, where the glycolytic isoforms have an eukaryotic origin (Petersen et al., 2003) whilst the photosynthetic enzymes are prokaryotic in nature (Shih et al., 1986). The bacterial origin of both glycolytic and photosynthetic PGKs could be relevant to both the enzyme activity and regulation, and could be related with a greater versatility of these enzyme isoforms. While the Arabidopsis genome has five plastidial and two cytoplasmic GAPDH isoforms, the PGK only have one cytosolic and two plastidial isoforms, which indicates a greater degree of specialization in the GAPDH than in the PGK family. A partially redundant function of PGK2 in photosynthesis could explain the high level of gene expression in leaves. However, the *amiRNA-PGK2* lines did not have any effect either on the photosynthetic activity or on the starch content, which renders this hypothesis difficult to prove.

In spite of the possible lethal phenotype of *pgk2.1* (this study, Myouga et al., 2010; Ouibrahim et al., 2014), the *amiRNA-PGK2* lines displayed weaker metabolite changes than the other mutants (Fig. 6). This suggests that either *pgk2.1* is not lethal or that silenced lines have residual levels of PGK2 activity which are sufficient to maintain them. There are other examples of enzymes whose insertional mutants are lethal and whose silenced lines are viable (Cascales-Miñana et al., 2013). This fact reinforces the idea that low transcription levels in amiRNA lines may mask the more dramatic phenotypes observed in knock-out mutants, and, thus, other levels of enzyme posttranscriptional and/or post-translational regulation (regulation by substrates and other interacting proteins, enzyme biosynthesis turnover) may compensate for the low transcription level. Hence, a silencing strategy may be of limited use for metabolic enzymes. In any case, due to the lack of phenotypic complementation of *pgk2.1,* we cannot rule out that other closely linked mutations may be partly responsible for the observed lethal phenotype of this mutant.

PGK1 and PGK3 are transcriptionally co-regulated to adjust metabolism

We found a correlation between PGK gene expression and enzyme activities, which indicates that transcription is an important mechanism of PGK regulation. The importance of transcriptional regulation for PGKs may be related to their bacterial origin and could be different from other metabolic enzymes of eukaryotic origin.

Since *pgk1.1* and *pgk3.2* single mutants displayed reduced growth, we expected this reduction to be even more drastic in the double mutant as both photosynthetic and glycolytic activities were affected. However, contrary to our expectations, *pgk1.1 pgk3.2* was bigger than *pgk3.2*, and displayed an intermediate phenotype between the two single mutants in all measured biochemical and physiological parameters (metabolite contents and photosynthetic activity). These results rule out an additive effect of the double mutation and point rather towards a compensatory effect which could be related to the co-regulated *PGK* expression in the single mutants. Thus, *PGK3* expression is repressed in *pgk1.1* in late development stages. The reduced PGK activity in this mutant compared to earlier stages might therefore be related to *PGK3* repression, at least in part. The repression of genes involved in sugar catabolism has also been observed in mutants with a low starch content, and has been associated with an adaptive response to avoid reserve depletion (Blasing et al., 2005; Smith and Stitt, 2007).

Furthermore, the reduced PGK activity found in the AP of *pgk3.2* adult plants could be due in part to *PGK1* repression. This repression would avoid the accumulation of carbohydrates in *pgk3.2*, which could have an inhibitory effect on the photosynthetic activity, and thus ultimately on growth. Our results indicate that when the glycolysis is limited, the plant tends to readjust the rate of photosynthesis to compensate for the effects caused by accumulation of carbohydrates, and *vice versa*. Therefore, reduced photosynthetic activity in the double mutant in early stages would avoid the accumulation of excess sugars as a result of a diminished glycolytic activity, which has a beneficial effect on the long-term growth of the double mutant as compared to the single mutants.

PGK3 activity is by-passed in *pgk3* metabolism

Since metabolism is a complex and dynamic process, it is difficult to predict the metabolite changes associated with the lack of a certain enzyme activity, especially if the same activity is displayed by different isoforms and in distinct compartments. PGK3 should be the main provider of cytosolic 3-PGA for the downstream reactions of glycolysis, and thus for respiratory activity. Lack of PGK3 activity was associated to an increase in soluble sugar (mainly glucose and fructose) and starch. These increases could be caused by a reduced glycolytic activity which, in turn, slows down plant growth. However, total 3-PGA content, the product of the PGK3 activity, increased in *pgk3.2*. This could indicate that more 3-PGA is generated in *pgk3.2* by other reactions, e,g., through a higher photosynthetic activity. However, this was not always the case, since both photosynthetic activity and PGK1 expression were reduced in the adult *pgk3.2* plants, in which 3-PGA was measured. Another possible route to increase 3-PGA availability is via the plastidial glycolytic pathway which, as the increased *PGK2* expression suggests, could have been more active in the *pgk3.2*. In the WT AP, the triose-phosphates are transported from the plastid to the cytosol through the TPT (Fig. 1). We hypothesized that in *pgk3.2*, PGK2 activity is increased to produce more 3-PGA in the plastid to by-pass the PGK3 reaction, which is then transported to the cytosol through the TPT (Fig. 1). Once in the cytosol, 3-PGA could complete with glycolysis in order to fuel the TCA cycle when necessary. The increased plastidial glycolytic activity hypothesis could also be applicable to heterotrophic plastids. In root plastids, where TPT activity is absent, 3-PGA can be potentially converted into phospho-*enol*-pyruvate (PEP) by phosphoglycerate mutase and enolase (Prabhakar et al., 2010; Flores-Tornero et al., 2017). PEP could be the metabolite transported from the plastid to complete glycolysis in the cytosol. Indeed, it has been postulated that the PEP/Pi translocator acts as a net importer of PEP into the chloroplast, but as a net exporter in root plastids

(Staehr et al., 2014) and probably in plastids from other non-photosynthetic tissues such as embryos (Flores-Tornero et al., 2017).

The drastic phenotype of *pgk3.2 tpt3* would suggest that the TPT activity could, at least in part, alleviate the PGK3 deficiency. In this double mutant, the 3-PGA formed by photosynthesis or plastidial glycolysis in the AP could not be exported to the cytosol and would mainly accumulate as starch as it does in the *tpt3* single mutant. Besides, the measured increases in serine and derivatives (methionine and *O*-acetyl-serine), which were already apparent in *tpt3*, could indicate an activation of the plastidial phosphorylated pathway of serine biosynthesis to divert part of the 3-PGA flux towards serine synthesis.

Since *pgk3.2 tpt3* is a double knock-out mutant that is still viable, there must be other mechanisms able to supply the essential 3-PGA to the cytosol in the mutant AP. These other possible mechanisms could include the inefficient 3-PGA transport through other chloroplast membrane transporters of the phosphate translocator family, such as glucose or xylulose-5-phosphate translocators (Fischer and Weber, 2002) or the involvement of the non-phosphorylating cytosolic GAPDH, which produces 3-PGA from glyceraldehyde-3-phosphate bypassing the PGK3 reaction (Rius et al., 2006). These mechanisms whilst inefficient may be sufficient to maintain the mutants viability.

Evaluation of the metabolomics data from different lines can help to find those changes in metabolite levels which can corroborate the above-postulated hypotheses and establish the connections between different metabolic pathways. Several metabolites changed in the opposite direction in the *pgk3.2* and *tpt3* single mutants, including glucose, fructose and glycerate. As previous mentioned, the accumulation of glucose, fructose and starch in *pgk3.2* may be caused by the impairment of their metabolism via glycolysis. In *tpt3*, the low levels of soluble sugars most likely reflect the inhibition of triose-phosphate transport to the cytosol, and as such a restricted substrate supply in support of their formation. Carbohydrates thus instead accumulate in the form of starch, a phenomenon that was also observed in *pgk3.2 tpt3*. Moreover, glyceric acid decreased in *pgk3.2*, increased in *tpt3* and presented an intermediate value in the double mutant. These reverse changes between *pgk3.2* and *tpt3* could be related to the strategy in *pgk3.2* to redirect the glycolytic flux towards the plastid. Low glyceric acid levels in the AP, could be the result of the conversion of this metabolite into 3-PGA by the plastidial glycerate kinase to be transported to the cytosol through TPT (Fig. 1). Interestingly, the phosphoric acid content also dramatically decreased in the *pgk3.2* AP, but increased in *tpt3*. Given that it correlated with the inorganic phosphate levels, the low phosphoric acid levels in the *pgk3.2* AP may be indicative of the high 3-PGA:Pi exchange rate, which is, by contrast, disrupted in *tpt3*.

CONCLUSIONS

Our results provide new insights into the functions of PGK isoforms and how they are regulated. The expression studies, along with the biochemical and physiological characterization, demonstrate that PGK1 is the photosynthetic isoform, while PGK2 is most probably involved in plastid glycolysis. PGK3 would be the cytosolic glycolytic isoform.

The study of the double mutant supports both the complexity and the plasticity of the primary metabolic network. Here it is emphasized that imbalances of photosynthetic

metabolism tend to be corrected by the regulation of the glycolytic routes and *vice versa*. Therefore, results obtained in this work support that plastidial and cytosolic metabolism are intimately connected, and that regulatory mechanisms exists which tend to maintain the balance between catabolic and anabolic reactions in the central carbon metabolism of plants.

MATERIALS AND METHODS

Plant Material and Growth Conditions

Arabidopsis thaliana seeds (ecotype Columbia-0) were supplied by the European Arabidopsis Stock Center (Scholl et al., 2000). Seeds were sterilized and sown on 0.8% agar plates containing one-fifth-strength Murashige and Skoog (1/5 MS) medium with Gamborg vitamins buffered with 0.9 g/l MES (adjusted to pH 5.7 with Tris). After a 4-day treatment at 4ºC, plates were vertically placed in a growth chamber (IBERCEX, V350, Spain) at 22ºC under a 16 h day/8 h night photoperiod, 100 μmol m^{-2} s^{-1}. To select the transgenic plants, half-strength MS plates supplemented with 0.5% sucrose and appropriate selection markers were used. Some seeds were also grown under greenhouse conditions in pots filled with a (1:1, v/v) mixture of vermiculite and fertilized peat (KEKILA 50/50; kekkilä Iberia, S.L.) irrigated with demineralized water as required. Trays were placed in a cold chamber (4ºC) and were placed under the greenhouse staging after 4 days. Growth conditions consisted of 16h light, 50-70% relative humidity and an average temperature of 24ºC during the daytime and 17ºC during the night. Whenever necessary, these conditions were supplied with artificial light from sodium and mercury vapor lamps. For analyses, 18-30 day-old pre-bolting material from plates or pots was harvested and separated into AP (including leaves and cotyledons) and roots. Unless otherwise stated, the material was sampled at the middle of the light period.

Primers

All primers used in this work are listed in Supplemental Table S6.

Mutant Isolation and Characterization

The mutant alleles of *PGK1* (At3g12780), *PGK2* (At1g56190), *PGK3* (At1g79550) and *TPT* (At5g46110) were identified in the SIGnAL Collection database at the Salk Institute (Alonso et al., 2003); GK_172A12 and GK_908E11 for *PGK1*, SALK_016097 for *PGK2*, SALK_062377 and SALK_066422 for *PGK3* and SALK_09334 for *TPT*. Mutants were identified by PCR genotyping using gene-specific primers and left border primers of the T-DNA insertion (Supplemental Table S6). The T-DNA insertions were confirmed by sequencing the fragment amplified by the T-DNA internal primers and gene specific primers (Supplemental Table S6).

Cloning and Plant Transformation

Standard methods were used to make the gene constructs (Sambrook and Russell, 2001). For gene promoter-GUS fusions, genomic DNA was PCR-amplified using primers At3g12780PromHind3F and At3g12780PromSpeR for the *PGK1* promoter (1508 bp), At1g56190PromNcoIR and At1g56190PromXbaIF for the *PGK2* promoter

(1466 bp), and At1g79550PromSpeIR and At1g79550PromHind3F for the *PGK3* promoter (1284 bp). Plasmid pCAMBIA1303 was used to fuse the promoter fragments to the β-Glucuronidase gene using the sites indicated in the respective primer names.

For promoter-PGK-GFP fusions, PGK cDNAs were PCR-amplified with the following primers: At3g12780GFP-F and At3g12780GFP-R for *PGK1*; At1g56190GFP-F and At1g56190GFP-R for *PGK2*; and At1g79550GFP-F and At1g79550GFP-R for *PGK3*. PCR products were cloned in the pCR8/GW/TOPO plasmid (Invitrogen). These cDNAs were subcloned in the plasmid pMDC83 under the control of the *35S* promoter (Curtis and Grossniklaus, 2003) using the Gateway technology with clonase II (Invitrogen). The pMDC83 plasmids allowed us to clone *PGK* cDNAs in frame with a green fluorescent protein (GFP) cDNA at the C-term position (PGK1-GFP, PGK2-GFP, PGK3-GFP). Promoter regions of PGKs previously cloned in pCAMBIA1303 were PCR-amplified to introduce restriction sites (primers At3g12780PmeIProF and At3g12780PromSpeR introduced *Pme*I and *Spe*I restriction sites into the *PGK1* promoter; primers At1g56190FProPmeI and At1g56190RevProPacI introduced *Pme*I and *Pac*I restriction sites into the PGK*2* promoter; primers At1g79550ProPmeIFo and At1g79550PromSpeIR introduced *Pme*I and *Spe*I restriction sites into the *PGK3* promoter). Subsequently, the *35S* promoters of constructs in pMDC83 were exchanged with the native promoters of *PGKs*, PCR-amplified from pCAMBIA1303 and digested with the appropriate restriction enzymes. These vectors, called *ProPGK:PGKs*, were used for PGKs expression and localization studies, and for the complementation of *PGK1* and *PGK2* mutants. For *pgk3.2* complementation studies, the *Pro35S:PGK3-GFP* construct in pMDC83 was used. Besides, *pgk2.1* was also transformed with a construct carrying a 3718 bp genomic fragment which was PCR-amplified from BAC *F14G9* using primers At1g56190ForGENO and At1g56190RevGENO. This fragment, including 1466 nucleotides upstream of the ATG, was cloned in the pCR8/GW/TOPO plasmid (Invitrogen), and was subsequently subcloned in the plasmid pMDC99 (Curtis and Grossniklaus, 2003) using the Gateway technology with clonase II (Invitrogen).

Artificial microRNA (amiRNAs) were produced to target *PGK1* and *PGK2* using the web microRNA designer (http://wmd2.weigelworld.org/cgi-bin/mirnatools.pl). The amiRNAs were cloned according to the protocol by Rebecca Schwab in Prof. Weigel's laboratory (http://wmd2.weigelworld.org/themes/amiRNA/pics/Cloning_of_artificial_microRNAs.pdf) using primers listed in Supplemental Table S6; then placed in the pCR8/GW/TOPO plasmid (Invitrogen) and finally subcloned in the plasmid pMDC83 behind the *35S* promoter (Curtis and Grossniklaus, 2003). All PCR-derived constructs were verified by DNA sequencing.

Various Arabidopsis WT and mutant lines were transformed with the different constructs by the floral dipping method (Clough and Bent, 1998) with *Agrobacterium tumefaciens* carrying *pSOUP*. For the amiRNA and GUS lines, WT were used. Transformants were selected by antibiotic selection, while homozygous individuals in complementation studies were identified by PCR genotyping using gene-specific primers and left border primers of the T-DNA insertions listed in Supplemental Table S6. At least four independent single insertion homozygous T3 lines were obtained for all different constructs. After characterization by RT-PCR, two different lines were selected for further analyses according to their expression level. We used both syngenic WT lines, as well as WT Columbia 0, as controls for our studies. For amiRNAs, we used the WT used for transformation with the amiRNAs as controls.

RT-PCR and RNA-seq data

RT-PCR was performed as previously described (Cascales-Miñana et al. 2013). Each reaction was performed in triplicate with 1 µL of the first-strand cDNA in a total volume of 25 µL. Data are the mean of three biological samples. The specificity of the PCR amplification was confirmed with a heat dissociation curve (from 60ºC to 95ºC). Efficiency of the PCR reaction was calculated and different internal standards were selected (Czechowski et al., 2005) depending on the efficiency of the primers. Primers used are listed in Supplemental Table S6.

For the gene expression analysis by RNA-seq, 21-day-old WT plants vertically grown on 1/5 MS plates were used. Three independent biological replicates of WT AP and roots were used for the analysis. Total RNA was extracted using NucleoSpin RNA II kit (Macherey-Nagel). Using as starting material 3-15 µg of RNA, a mRNA enrichment was performed with the *MicroPoly(A) Purist kit* (AMBION). To prepare the RNA-Seq library, the *SOLID Total RNA-seq* kit (Life Technologies) was used. After obtaining the library, an equimolar mixture of it was used to perform an emulsion PCR using the automatic system of EZ Beads (Life Technologies). Then, the bead enrichment was performed followed by its deposition in the sequencing wells. The sequencing step was done by SOLID 5500XL equipment of 75 nucleotides using the Exact Call Chemistry. To filtrate the readings depending on their adaptor the Cutadapt v1.8 program was used. FastqQC was employed to evaluate the quality of the reads. Afterward, Tophat2 was employed to perform the mapping against a reference. To visualize and obtain the raw counts, Seqmonk v0.29 was used.

GUS activity assays and GFP microscopy

GUS activity assays were performed as described in Muñoz-Bertomeu et al. (2009). GFP fluorescence was observed under a confocal microscope (Leica TCS-SP). To confirm the nuclear localization of PGK3, root cells were stained with 10 µg/mL Hoechst dye.

Photosynthetic activity measurements

Simultaneous gas exchange and chlorophyll fluorescence measurements were performed as described by Faus et al. (2015). Measurements were taken 2 h after the beginning of the light period to allow full photosynthesis activation.

Metabolite determination and PGK activity assay

The AP and roots of WT, single and double mutants, and silenced lines (two different lines per silenced gene) grown on 1/5 MS plates, were used to determine metabolite content in derivatized methanol extracts by GC-MS using the protocol defined in Lisec et al. (2006). Metabolites were identified in comparison to database entries of authentic standards (Kopka et al., 2005). Chromatograms and mass spectra were evaluated using Chroma TOF 1.0 (LECO) and TagFinder 4.0 software (Luedemann et al., 2008). Material was sampled for metabolite analysis after 4-6 h in the light. 3-PGA was measured as previously described (Flores-Tornero et al., 2017). PGK activity was measured by an enzymatic assay following NADH oxidation associated with the coupled reaction of phosphoglycerate kinase and GAPDH. Frozen AP were ground in liquid nitrogen and resuspended in extraction buffer (50 mM HEPES-KOH, pH 7.4, 1 mM EDTA, 1 mM EGTA, 2 mM Benzamidine, 2 mM E-aminocaproic acid, 0.5 mM phenylmethylsulfonyl fluoride (PMSF), 10% glycerol, 0.1% Triton x-100). The

supernatant was obtained after centrifugation at 15000*g* for 20 min at 4ºC. Reactions were carried out in a medium containing 100 mM HEPES-KOH, 1 mM EDTA, 2 mM $MgSO_4$, 0.3 mM NADH, 6.5 mM 3-PGA, 1 mM ATP and 3.3 Units of GAPDH. Starch was determined by the ENZYTEC starch kit (ATOM) at the end of the light period.

Bioinformatics and Statistics

PGK and *TPT* genes were initially identified in the Arabidopsis Information resource. The percentage of identity between different PGKs was obtained by aligning pair sequences using bl2seq at NCBI (http://blast.ncbi.nlm.nih.gov/Blast.cgi). Amino acid sequences were aligned using the ClustalOmega program [http://www.ebi.ac.uk/Tools/msa/clustalo/; (McWilliam et al., 2013)]. Phylogenetic analyses were performed according to the neighbor-joining method (Saitou and Nei, 1987). Units represent the number of amino acid substitutions per site for one unit. The analysis was performed using the Mega6 tool (Tamura et al., 2013).

Experimental values represent mean values and standard error, *n* represents the number of independent samples. Significant differences as compared to WT were analyzed by Student's t-tests algorithms (two-tailed) using Microsoft Excel. Statistical differences between groups were analyzed with a one-way ANOVA and further post hoc Tukey b (WSD) test with the IBM SPSS Statistics software. The level of significance was fixed at 5% (0.05).

Accession numbers:

Arabidopsis Genome Initiative locus identifiers of Arabidopsis genes used in this article are as follows: At3g12780 (*PGK1*), At1g56190 (*PGK2*), At1g79550 (*PGK3*) and At5g46110 (*TPT*).

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Table 1. Photosynthetic parameters in *PGK* single and double mutants, and in complemented lines. Photosynthetic rate (A_N), effective (PhiPS2) and maximum photochemical yield of Photosystem II (Fv/Fm) in 20- and 30-day-old plants are shown. Each value is the mean (± SE) of 10 independent determinations. For each growth stage different letters indicate significant differences between groups ($P < 0.05$).

			A_N (µmol $m^{-2}s^{-1}$)		PhiPS2		Fv/Fm	
Mutants	20 day-old	WT	7.0 ± 0.348	**a**	0.139 ± 0.004	**ab**	0.769 ± 0.003	**a**
		pgk1.1	4.7 ± 0.332	**b**	0.112 ± 0.004	**c**	0.745 ± 0.008	**b**
		pgk3.2	7.5 ± 0.408	**a**	0.151 ± 0.007	**a**	0.766 ± 0.006	**a**
		pgk1.1 pgk3.2	5.0 ± 0.365	**b**	0.128 ± 0.006	**b**	0.768 ± 0.007	**a**
	30 day-old	WT	9.1 ± 0.295	**a**	0.174 ± 0.004	**a**	0.769 ± 0.002	**a**
		pgk1.1	6.2 ± 0.115	**c**	0.130 ± 0.004	**c**	0.758 ± 0.004	**b**
		pgk3.2	7.5 ± 0.276	**b**	0.160 ± 0.004	**b**	0.752 ± 0.004	**b**
		pgk1.1 pgk3.2	7.0 ± 0.222	**b**	0.140 ± 0.004	**c**	0.777 ± 0.001	**a**
Complemented lines	20 day-old	WT	9.0 ± 0.606	**a**	0.115 ± 0.005	**a**	0.778 ± 0.003	**a**
		pgk1.1	5.1 ± 0.502	**c**	0.077 ± 0.006	**c**	0.748 ± 0.005	**b**
		pgk1.1 ProPGK1:PGK1GFP-L3	7.0 ± 0.257	**b**	0.089 ± 0.004	**bc**	0.753 ± 0.005	**b**
		pgk1.1 ProPGK1:PGK1GFP-L15	7.7 ± 0.494	**ab**	0.101 ± 0.006	**ab**	0.760 ± 0.003	**b**
	30 day-old	WT	8.6 ± 0.128	**a**	0.140 ± 0.004	**a**	0.759 ± 0.007	**a**
		pgk3.2	4.8 ± 0.590	**c**	0.122 ± 0.006	**b**	0.754 ± 0.008	**a**
		pgk3.2 Pro35S:PGK3-GFP-L1	7.2 ± 0.099	**b**	0.141 ± 0.003	**a**	0.761 ± 0.006	**a**
		pgk3.2 Pro35S:PGK3-GFP-L11	7.0 ± 0.236	**b**	0.151 ± 0.080	**a**	0.743 ± 0.152	**a**

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FIGURE LEGENDS.

Figure 1. Schematic representation of the contribution of PGKs in the primary carbon metabolic pathways in photosynthetic cells. Abbreviations: 1,3-BPGA, 1,3-bis-phosphoglycerate; 2-OG, 2-oxoglutarate; 2-PG, 2-phosphoglycolate; 3-PGA, 3-phosphoglycerate; 3-PHP, 3-phosphohydroxypyruvate; 3-PS, 3-phosphoserine; ADPGlu, ADP-glucose; AGPase, ADP-glucose pyrophosphorylase; ALD, aldolase; DHAP- dihydroxyacetone phosphate; ENO, enolase; FBP, fructose 1,6-bisphosphatase; Fru, fructose; Fru-1,6BP, fructose 1,6- bisphosphate; Fru-6P, fructose 6-phosphate; GAP, glyceraldehyde 3-phosphate; GAPDH, glyceraldehyde 3-phosphate dehydrogenase; Glu-1P, glucose 1-phosphate; Glu-6P, glucose 6-phosphate; GLYK, glycerate kinase; HP, hydroxypyruvate; INV, vacuolar invertase; MEX1, maltose translocator; PEP, phosphoenolpyruvate; PFK, phosphofructokinase; PGDH, 3-phosphoglycerate dehydrogenase; PGI, phosphoglucoisomerase; PGK, phosphoglycerate kinase; PGLm, phosphoglycerate mutase; pGluT, glucose translocator; PGM, phosphoglucoisomerase; PGP, 2-phosphoglycolate phosphatase; PPT, phospho*enol*pyruvate translocator; PK, pyruvate kinase; PSAT, 3-phosphoserine aminotransferase; PSP, 3-phosphoserine phosphatase; Ru-5P, ribulose 5-phosphate; RuBP, ribulose 1,5-bisphosphate; SPP, sucrose 6-phosphate phosphatase; SPS, sucrose phosphate synthase; Suc-6P, sucrose 6-phosphate; TCA, tricarboxylic acid cycle; TPI, triose phosphate isomerase; TPT, triose phosphate translocator; UDPGlu, UDP-glucose; UGPase, UDPGlu pyrophosphorylase;. "p" or "c" after the enzyme name denotes plastidial or cytosolic isoform, respectively. Discontinuous arrows represent fluxes between compartments. Hypothetical 3-PGA flux in *pgk3.2* is highlighted in red.

Figure 2. Expression analysis of *PGK* family genes. A and B, RT-PCR analysis of *PGKs* in 18-day-old seedlings grown in a MS 1/5 medium (A) and in adult plants grown under greenhouse conditions (B). C, *GUS* expression under the control of *PGK1, PGK2* and the *PGK3* promoter in different plant organs. Scale Bars = 1 mm (cotyledons, leaves and flowers), 0.1 mm (roots). Values in A and B (mean ± SE; n = 3 independent biological replicates) are normalized to the expression in the Aerial parts (A) or stems (B).

Figure 3. Subcellular localization of PGK isoforms by stable expression of PGK-GFP fusion proteins under the control of PGK native promoters. Bars = 100 µm.

Figure 4. Genomic organization and expression analysis of the *PGK* and *TPT* T-DNA mutant lines. A, Black boxes represent exons and grey lines introns. The T-DNA insertion point in each mutant is shown. B, Detection of the *PGK* and *TPT* transcripts in the aerial parts of 18-day-old seedlings of single and double mutants by RT-PCR analysis. Values (mean ± SE; n = 3 independent biological replicates) are normalized to the expression in the wild-type (WT).

Figure 5. Phenotypical analysis of *PGK* T-DNA mutants and silenced lines grown in MS 1/5 (18-day-old seedlings) or greenhouse conditions (30-day-old plants) as compared to wild-type plants (WT). Seedling aerial part (AP) and root fresh weight (FW) of different lines grown in vertical plates are shown in A and B, respectively. Rosette FW is shown in C. D, picture of a representative individual of each line grown in greenhouse. E, FW of the AP of mutant and the complemented lines grown in

greenhouse. Values are the mean ± SE (n ≥ 36 plants). In (E) data are the mean of two independent transgenic lines. * Significantly different as compared to WT; different letters indicate significant differences between WT, single and double mutants ($P < 0.05$).

Figure 6. Biochemical and molecular analyses of *PGK* mutant and silenced lines (amiRNA lines) as compared to wild-type plants (WT). A, B, and C, starch content, PGK activity and RT-PCR analysis of PGK*s* in the aerial parts (AP) of 20- and 30-day-old plants grown in greenhouse. In B, PGK activity was also measured in 20-day-old roots grown in plates. Values are the mean ± SE ($n \geq 30$ plants). In A and B, data from the silenced lines are the mean of individuals from two independent transgenic lines. * Significantly different as compared to the WT; different letters indicate significant differences between groups ($P < 0.05$).

Figure 7. Most relevant changes in the metabolite content of aerial parts (AP) and roots of 21-day-old *pgk* mutants and silenced lines grown in vertical plates as compared to wild-type (WT). Log^2 values of the relative metabolic contents are presented as a heat-map. *Significant differences between the mutant and the wild type (WT) ($P < 0.05$). Detailed results of the assay are presented in Supplemental Tables S3 and S4.

Figure 8. Phenotypical, biochemical and molecular analyses of *pgk3.2 tpt3* mutant as compared to single mutants (*pgk3.2*, *tpt3*) and wild-type (WT). A, relative 3-PGA content in the aerial parts (AP) of 25-day-old plants grown in greenhouse normalized to the mean content of the WT (34 ± 1 µg g^{-1} fresh weight). B and C, Rosette fresh weight (FW) and starch content of the AP of 25-day-old plants grown in greenhouse. D, most relevant changes in the metabolite content of AP of 19-day-old *pgk*3.2 *tpt3* lines grown in vertical plates as compared to single mutants and wild-type (WT). Log^2 values of the relative metabolic contents are presented as a heat-map. Detailed results of the assay are presented in Supplemental Table S5. * Significantly different as compared to WT; different letters indicate significant differences between groups ($P < 0.05$).

SUPPLEMENTAL MATERIAL

Supplemental Figure S1. Amino acid alignment and cladogram of the Arabidopsis PGK proteins.

Supplemental Figure S2. Expression of GUS under the control of *PGK1* promoter in seedlings and adult plants.

Supplemental Figure S3. Expression of GUS under the control of *PGK2* promoter in seedlings and adult plants.

Supplemental Figure S4. *GUS* Expression under the control of *PGK3* promoter in seedlings and adult plants.

Supplemental Figure S5. Subcellular localization of PGK3 by stable expression of PGK-GFP fusion proteins under the control of *35S* promoter.

Supplemental Figure S6. RT-PCR analysis of the aerial parts of 20-day-old seedlings of *PGK2* (A) and *PGK1* (B) silenced lines grown on vertical plates.

Supplemental Table S1. Genomic localization of *PGK* family T-DNA mutant lines confirmed by sequencing.

Supplemental Table S2. Photosynthetic parameters in wild-type (WT) and two independent amiPGK2 silenced lines (*amiPGK2-H35*, *amiPGK2-H49*).

Supplemental Table S3. Metabolite levels in the aerial parts of 21-day-old *PGK* single (*pgk1.1*, *pgk3.2*) and double (*pgk1.1 pgk3.2*) mutants, silenced (*amiPGK2*) lines, and wild-type (WT).

Supplemental Table S4. Metabolite levels in the roots of 21-day-old *PGK* single (*pgk1.1*, *pgk3.2*) and double (*pgk1.1 pgk3.2*) mutants, silenced (*amiPGK2*) lines, and wild-type (WT).

Supplemental Table S5. Metabolite levels in the aerial parts of 19-day-old *PGK*3 and *TPT* single (*pgk3.2*, *tpt3*) and double (*pgk3.2 tpt3*) mutants, and wild-type (WT) plants.

Supplemental Table S6. List of primers used in this work.

Supplemental Figure S1. Amino acid alignment and cladogram of the Arabidopsis PGK proteins. A, Amino acid alignment of Arabidopsis PGK family proteins using the ClustalOmega program. Asterisks denote the same amino acid between sequences, a colon indicates conserved amino acids. Amino acids that form the ligand binding domain are marked with empty triangles, the ADP binding domain with black triangles, and the catalytic site is marked with grey triangles. B, The phylogenetic tree was constructed from an alignment of the deduced amino acid sequences, as described in Materials and Methods (M&M). Branch length is given under each segment according to the algorism specified in M&M.

Supplemental Figure S2. Expression of GUS under the control of *PGK1* promoter in seedlings and adult plants. Cotyledon (A), Leaves (B), Stomata (C), Hypocotyl (D), Roots (E, F), Caulin leaves (G, H), Rosette leaves (I), Flowers (J), Siliques (K), Roots (L). Bars = 1 mm (A, B, D, G, J, K), 0.5 mm (F, L), 0.2 mm (H,J) and 0.1 mm (C, E).

Supplemental Figure S3. Expression of GUS under the control of *PGK2* promoter in seedlings and adult plants. Cotyledon (A), Leaves (B), Stomata (C), Roots (D), Rosette leaves (E), Flowers (F), Stigma (G), Anthers and stigma (H), Siliques (I) and Roots (J). Bars = 1 mm (A, B, E, F, H, I), 0.5 mm (G), 0.2 mm (D) and 0.1 mm (C, J).

Supplemental Figure S4. *GUS* Expression under the control of *PGK3* promoter in seedlings and adult plants. Cotyledon (A), Leaves (B), Roots (C), Rosette leaves (D, E), Siliques (F), Flowers (G), Anther (H) and Roots (I). Bars = 1 mm (A, B, D, E, F, G), 0.5 mm (H, I) and 0.1 mm (C).

Supplemental Figure S5. Subcellular localization of PGK3 by stable expression of PGK-GFP fusion proteins under the control of *35S* promoter. The nuclear localization of PGK3 was visualized by staining root cells with the Hoechst marker. Bar = 10 µm.

Supplemental Figure S6. RT-PCR analysis of the aerial parts of 20-day-old seedlings of *PGK2* (A) and *PGK1* (B) silenced lines grown on vertical plates.

Supplemental Table S1. Genomic localization of *PGK* family T-DNA mutant lines confirmed by sequencing. Nucleotide numbering is relative to the gene translation start codon.

Supplemental Table S2. Photosynthetic parameters in wild-type (WT) and two independent amiPGK2 silenced lines (*amiPGK2-H35*, *amiPGK2-H49*). Photosynthetic rate (A_N), effective (PhiPS2) and maximum photochemical yield of Photosystem II (Fv/Fm) were determined in 20-day-old plants. Each value is the mean (± SE) of 10 independent determinations. ns, indicates non-significant differences between groups ($P < 0.05$).

Supplemental Table S3. Metabolite levels in the aerial parts of 21-day-old *PGK* single (*pgk1.1*, *pgk3.2*) and double (*pgk1.1 pgk3.2*) mutants, silenced (*amiPGK2*) lines, and wild-type (WT). Data are relative values normalized to the mean response calculated for each WT. Values represent the mean ± SE of six independent determinations for WT and *PGK* mutants, and 12 determinations for *amiPGK2* (corresponding to samples of two independent transgenic plants). Those values that were significantly different to WT are set in bold type, $P < 0.05$. ND, Non detected.

Supplemental Table S4. Metabolite levels in the roots of 21-day-old *PGK* single (*pgk1.1*, *pgk3.2*) and double (*pgk1.1 pgk3.2*) mutants, silenced (*amiPGK2*) lines, and wild-type (WT). Data are relative values normalized to the mean response calculated for each WT. Values represent the mean ± SE of six independent determinations for WT and *PGK* mutants, and 12 determinations for *amiPGK2* (corresponding to samples of two independent transgenic plants). Those values that were significantly different to WT are set in bold type, $P < 0.05$. ND, Non detected.

885 **Supplemental Table S5.** Metabolite levels in the aerial parts of 19-day-old *PGK*3 and
886 *TPT* single (*pgk3.2*, *tpt3*) and double (*pgk3.2 tpt3*) mutants, and wild-type (WT) plants.
887 Data are relative values normalized to the mean response calculated for each WT.
888 Values represent the mean ± SE of six independent determinations. Those values that
889 are significantly different to WT are set in bold type, $P < 0.05$.

890

891 **Supplemental Table S6.** List of primers used in this work.

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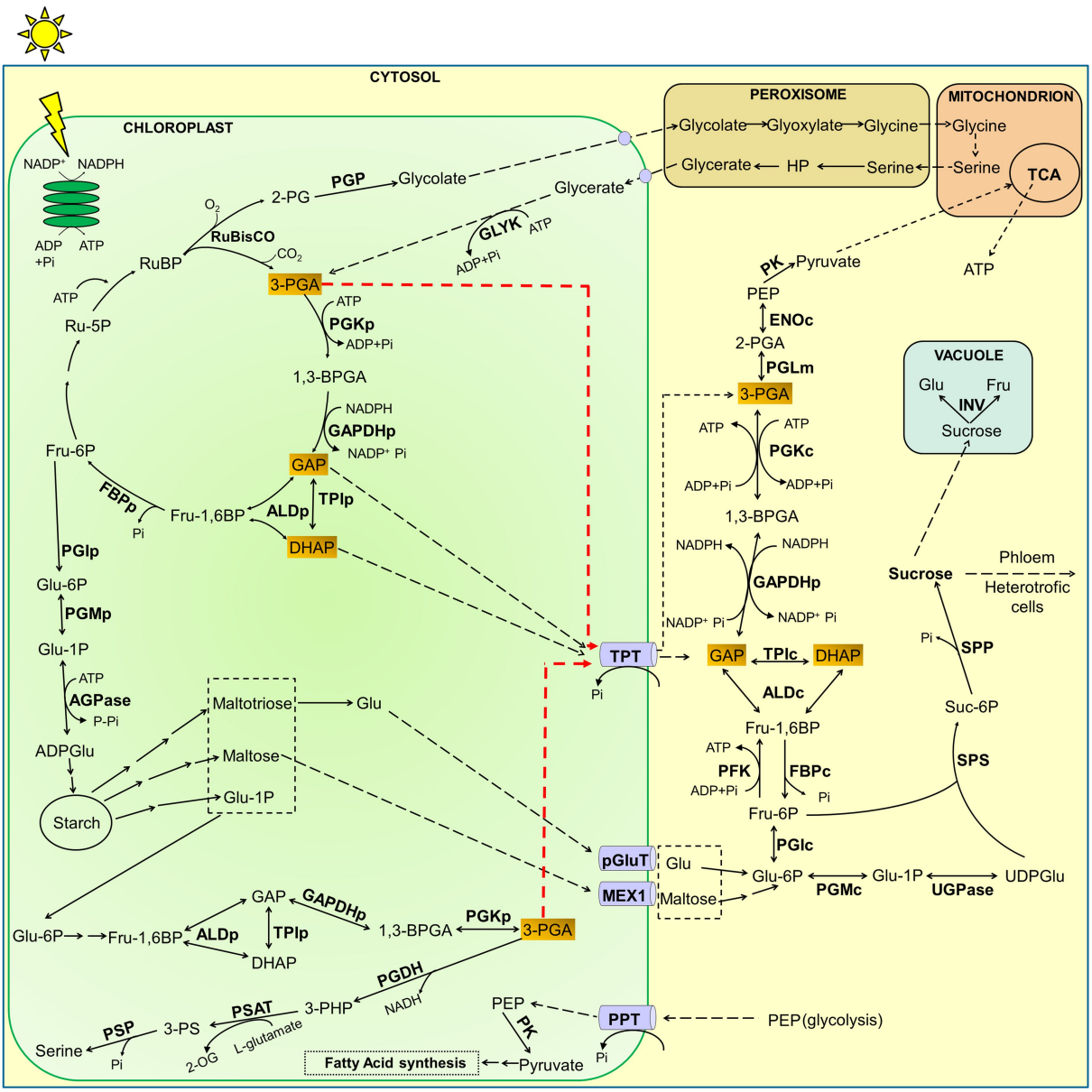
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PGP
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Glycerate
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PGKp
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NADPH
NADP+ Pi
GAP
TPIp
ALDp
DHAP
Fru-1,6BP
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Pi
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Ru-5P
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Glu-6P
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Glu-1P
AGPase
P-Pi
ADPGlu
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Maltotriose
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Glu
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Glycolate
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HP
Serine
TCA
PK
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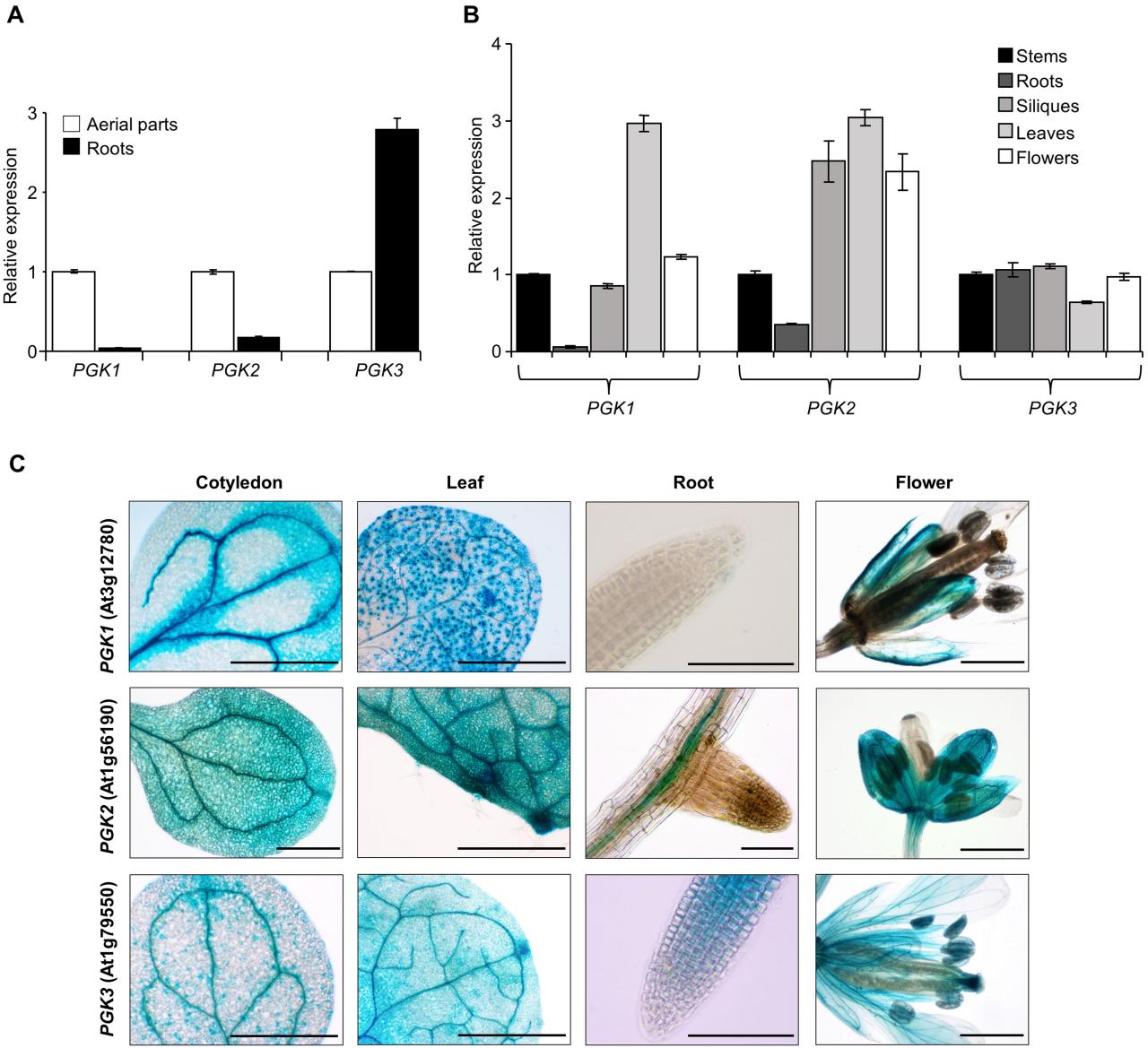
A
Relative expression
Aerial parts
Roots
PGK1
PGK2
PGK3
B
Relative expression
Stems
Roots
Siliques
Leaves
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PGK1
PGK2
PGK3
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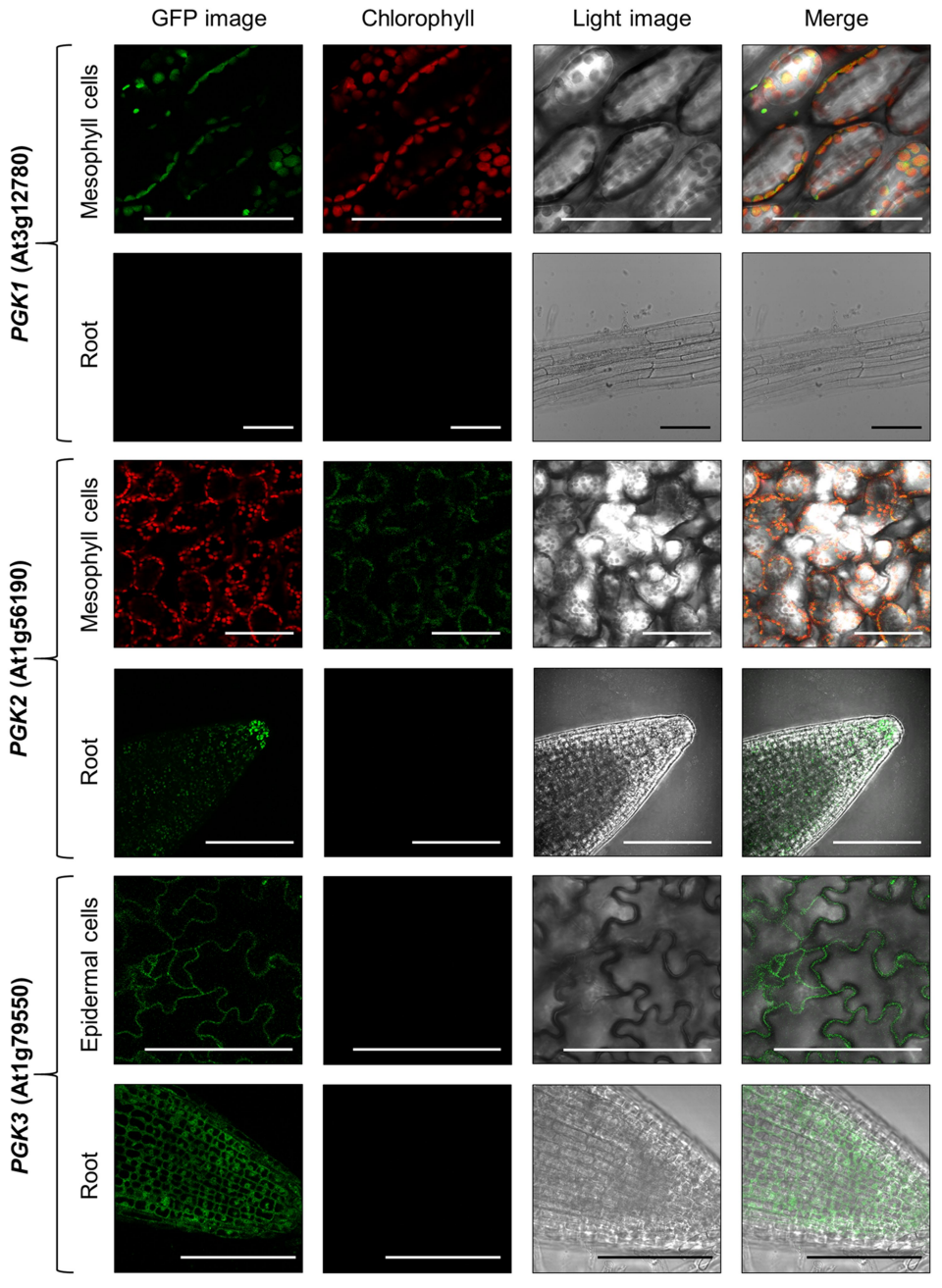
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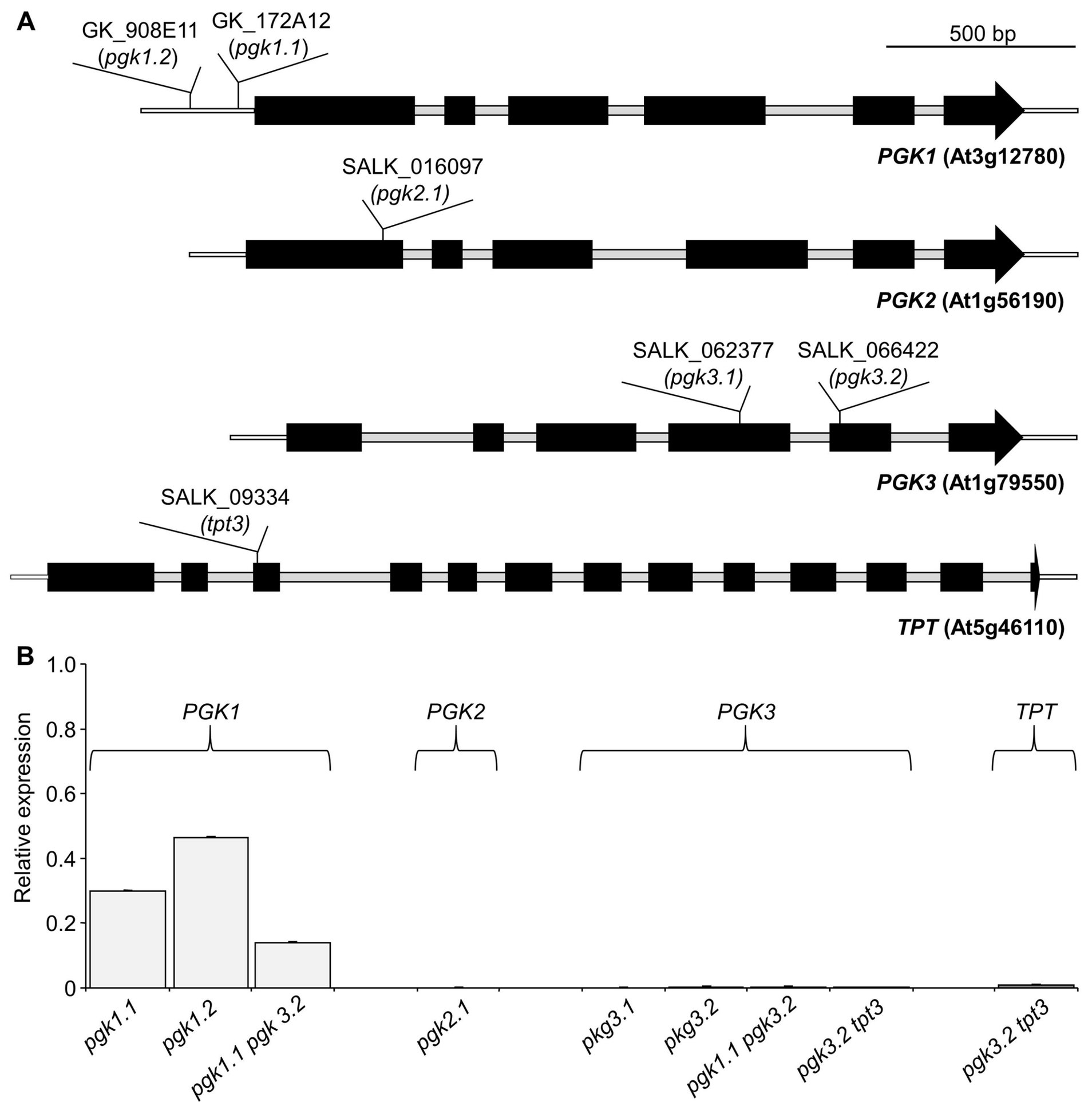
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SALK_09334
(tpt3)
TPT (At5g46110)
B
Relative expression
1.0
0.8
0.6
0.4
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0
PGK1
PGK2
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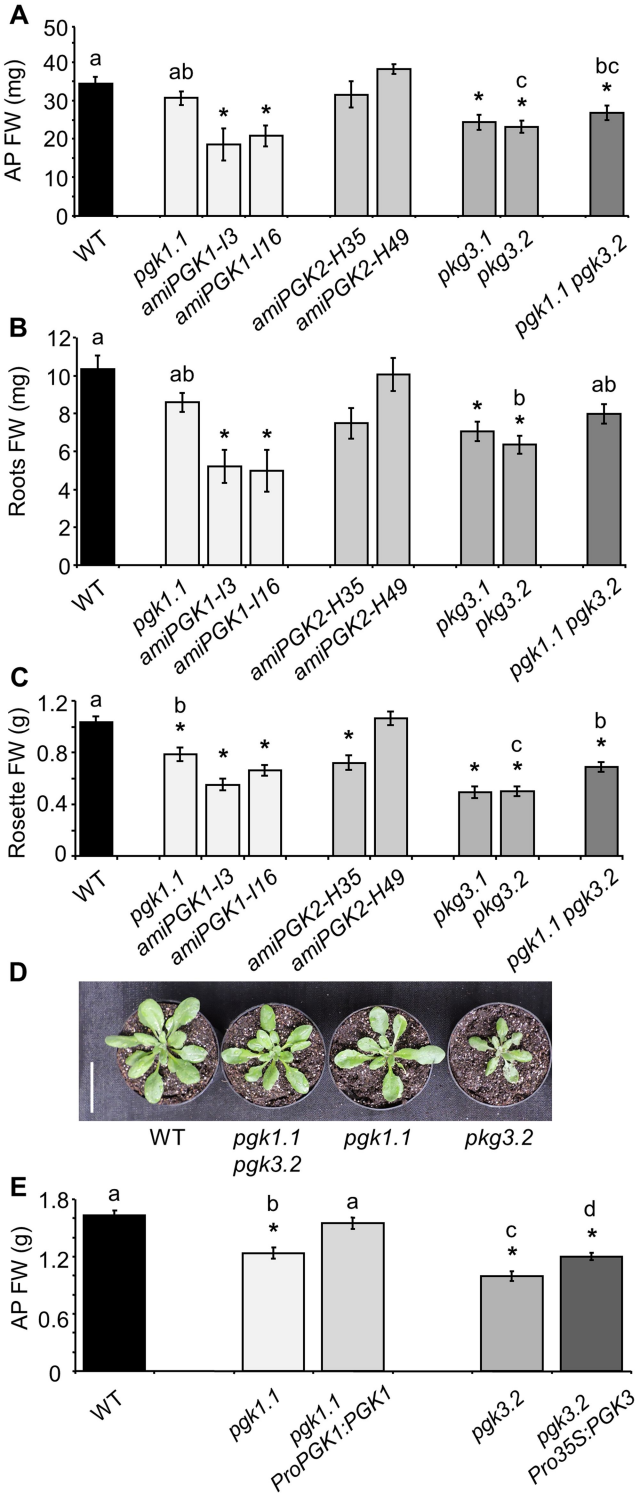
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amiPGK2-H35
amiPGK2-H49
pkg3.1
pkg3.2
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B
Roots FW (mg)
12
10
8
6
4
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b
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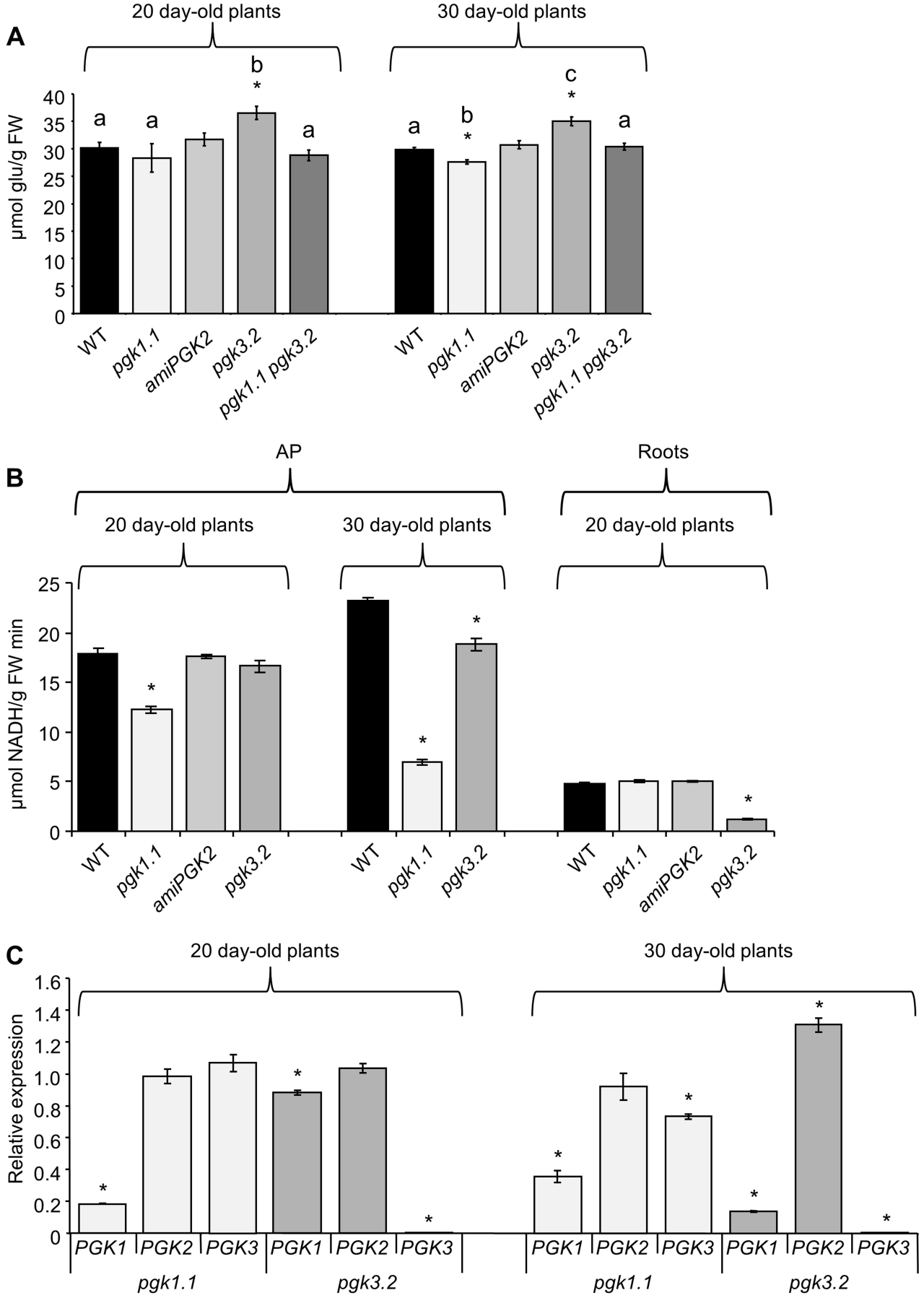
pgk1.1
ProPGK1:PGK1
pgk3.2
pgk3.2
Pro35S:PGK3


A
20 day-old plants
30 day-old plants
µmol glu/g FW
WT
pgk1.1
amiPGK2
pgk3.2
pgk1.1 pgk3.2
B
AP
Roots
20 day-old plants
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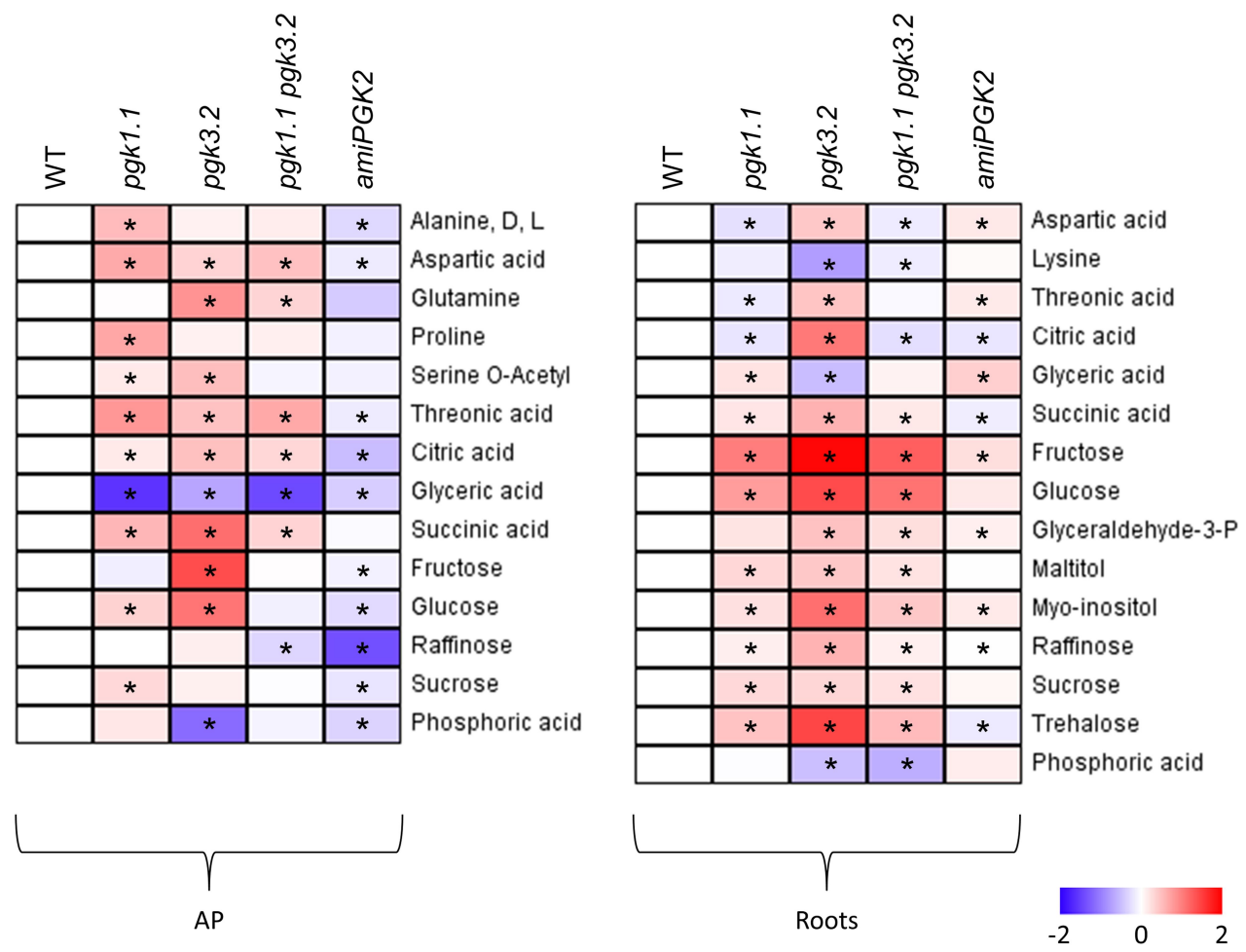
µmol NADH/g FW min
C
Relative expression
PGK1
PGK2
PGK3
pgk1.1
pgk3.2


WT
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pgk3.2
pgk1.1 pgk3.2
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Alanine, D, L
Aspartic acid
Glutamine
Proline
Serine O-Acetyl
Threonic acid
Citric acid
Glyceric acid
Succinic acid
Fructose
Glucose
Raffinose
Sucrose
Phosphoric acid
AP
WT
pgk1.1
pgk3.2
pgk1.1 pgk3.2
amiPGK2
Aspartic acid
Lysine
Threonic acid
Citric acid
Glyceric acid
Succinic acid
Fructose
Glucose
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Sucrose
Trehalose
Phosphoric acid
Roots
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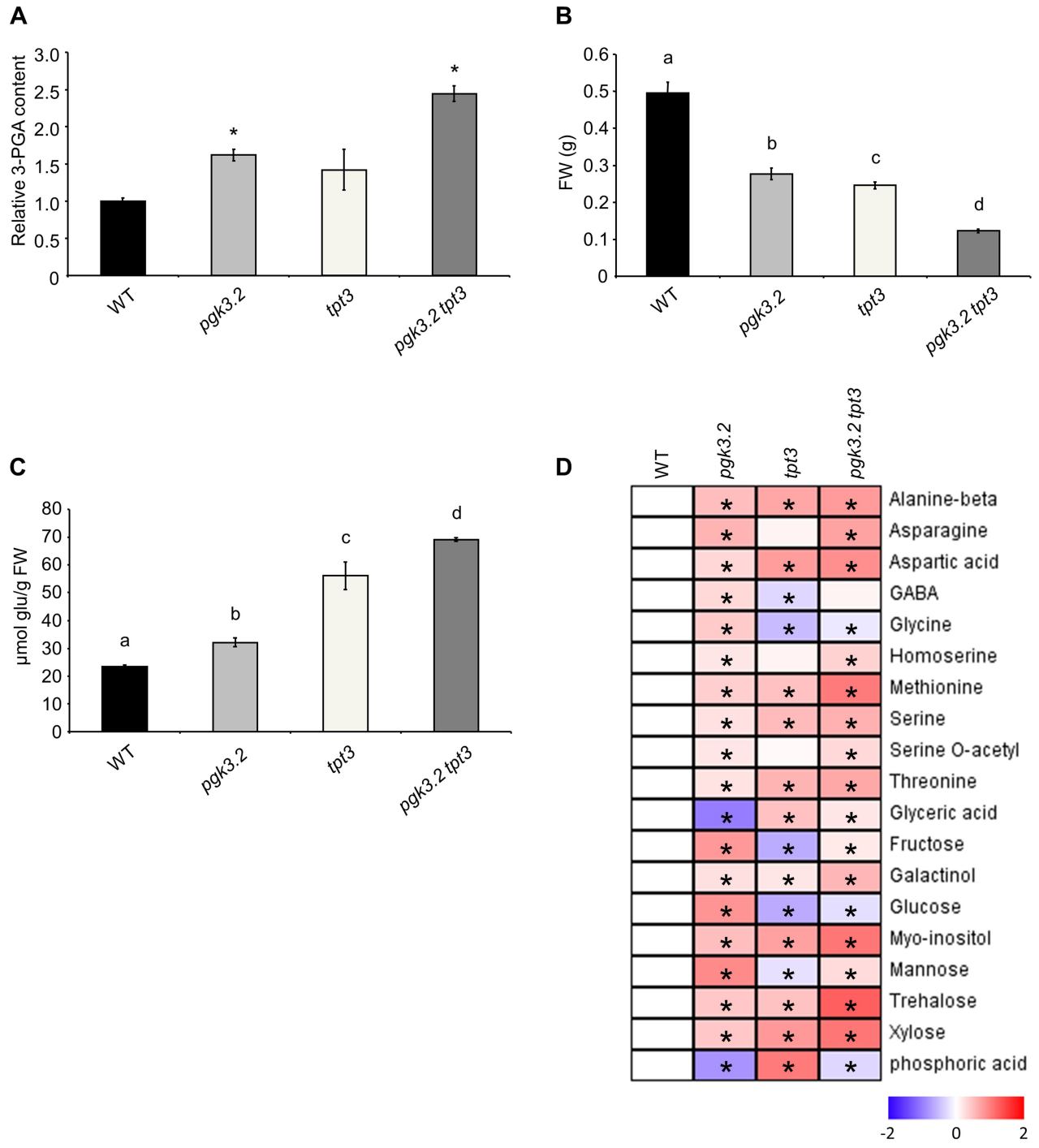
0
2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Relative 3-PGA content
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2.5
2.0
1.5
1.0
0.5
0
*
*
WT
pgk3.2
tpt3
pgk3.2 tpt3
B
FW (g)
0.6
0.5
0.4
0.3
0.2
0.1
0
a
b
c
d
WT
pgk3.2
tpt3
pgk3.2 tpt3
C
µmol glu/g FW
80
70
60
50
40
30
20
10
0
a
b
c
d
WT
pgk3.2
tpt3
pgk3.2 tpt3
D
WT
pgk3.2
tpt3
pgk3.2 tpt3
Alanine-beta
Asparagine
Aspartic acid
GABA
Glycine
Homoserine
Methionine
Serine
Serine O-acetyl
Threonine
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Glucose
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Mannose
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2

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