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Research Article

Expression of *AtWRI1* and *AtDGAT1* during soybean embryo development influences oil and carbohydrate metabolism

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SUMMARY

Soybean oil is one of the most consumed vegetable oils worldwide. Genetic improvement of its concentration in seeds has been historically pursued due to its direct association with its market value. Engineering attempts aiming to increase soybean seed oil presented different degrees of success that varied with the genetic design and the specific variety considered. Understanding the embryo's responses to the genetic modifications introduced, is a critical step to successful approaches. In this work the metabolic and transcriptional responses to *AtWRI1* and *AtDGAT1* expression in soybean seeds were evaluated. *AtWRI1* is a master regulator of fatty acid (FA) biosynthesis, and *AtDGAT1* encodes an enzyme catalyzing the final and rate limiting step of triacylglycerides biosynthesis. The events expressing these genes in the embryo did not show an increase in total FA content, but they responded with changes in the oil and carbohydrate composition. Transcriptomic studies revealed a down-regulation of genes putatively encoding for oil body packaging proteins, and a strong induction of genes annotated as lipases and FA biosynthesis inhibitors. Novel putative *AtWRI1* targets, presenting an AW-box in the upstream region of the genes, were identified by comparison with an event that harbors only *AtWRI1*. Lastly, targeted metabolomics analysis showed that carbon from

sugar phosphates could be used for FA competing pathways, such as starch and cell wall polysaccharides, contributing to the restriction in oil accumulation. These results allowed the identification of key cellular processes that need to be considered to break the embryo's natural restriction to uncontrolled seed lipid increase.

INTRODUCTION

Soybean (*Glycine max* [L.] Merr.) is the largest feedstock for protein and the second largest source of vegetable oil in the world with an estimated 2020/2021 production of over 363 million metric tons (USDA: www.nass.usda.gov). Commodity soybean seeds accumulate close to 40% protein and 20% oil. Soybean protein is primarily used as feed and food, while its oil is broadly incorporated into food, feed, and industrial products (Clemente and Cahoon, 2009). The demand for soybean oil is projected to continue to increase in the next ten years (Dohlman *et al.*, 2021). Soybean seed oil is composed almost exclusively of triacylglycerols (TAGs), which contains three acyl groups from five dominant common fatty acids: palmitic acid, stearic acid, oleic acid, linoleic acid, and linolenic acid (Clemente and Cahoon, 2009). Optimizing carbon flux towards fatty acid (FA) synthesis, incrementing nutritional properties and expanding end-use functionality products have been among the foci of soybean breeding and genetics improvement programs.

TAG biosynthesis is conserved among plant species: it involves *de novo* FA biosynthesis in plastids and TAG assembly in the endoplasmic reticulum (ER) (Bates, 2016; Xu and Shanklin, 2016). *De novo* FA biosynthesis is initiated with the carboxylation of acetyl-CoA by the heteromeric acetyl-CoA carboxylase (pACC). The product of this reaction, malonyl-CoA, is the substrate for consecutive rounds of two carbon additions catalyzed by the FA synthase complex. The growing acyl chains are esterified to an acyl carrier protein (ACP) and proceed up to FA chain length of 18 carbons with either no or one unsaturation. The acyl groups are subsequently cleaved from ACP by acyl-ACP thioesterases and released as free FAs. The FAs are activated to CoA esters by long chain acyl CoA synthases (LACS) located about the outer plastid envelope, and transported to the ER. Then, the newly synthesized acyl-CoA mixes with other recycled FA and can be used in four identified acylation reactions. The acyl-receptors include: (1) lysophosphatidylcholine (lyso-PC) generating phosphatidylcholine (PC) by the lyso-PC acyltransferase (LPCAT); (2) glycerol-3-phosphate generating lysophosphatidic acid (lyso-PA) by the glycerol-3-phosphate acyltransferase (GPAT); (3) lyso-PA through a

second round of acylation producing phosphatidic acid (PA) by the lyso-PA acyltransferase (LPAAT); and (4) diacylglycerol (DAG) generating TAG by the DAG acyltransferase (DGAT). Using ^{14}C -pulse labeling of cultured soybean embryos, it was estimated that approximately 57% of newly synthesized FAs were directly esterified to the sn-1 or sn-2 position of PC (Bates *et al.*, 2009). PC acyl chains can be desaturated, exchanged with other FA from the acyl-CoA pool (aka PC editing) and/or transacylated to the sn-3 position of the DAG, as another path for generating TAGs catalyzed by the phosphatidylcholine:diacylglycerol acyltransferase (PDAT) (Vanhercke *et al.*, 2013; Zhang *et al.*, 2009). The DAG backbone for TAG biosynthesis could potentially be derived from two consecutive acylations of glycerol-3-phosphate and posterior dephosphorylation of the PA (Kennedy pathway), or derived from the interconversion of PC:DAG. In soybean embryos, the DAG pool used for TAG synthesis was shown to be mostly derived from PC backbone (Bates *et al.*, 2009). Each step across the TAG biosynthetic pathway can be targeted for optimization as a way to boost oil accumulation, however, determination of rate limiting steps, along the pathway, remains a challenge (Bates, 2016).

Recent metabolic engineering efforts aiming to enhance seed oil have focused on both increasing the synthesis of FAs (PUSH) and their incorporation into TAGs (PULL). The most studied “PUSH” approach utilizes the overexpression of a global regulator of lipid biosynthesis *WRINKLED1* (*WRI1*). *WRI1* is a member of the APETALA2/ethylene responsive element-binding protein (AP2/EREBP) transcription factor family (Baud *et al.*, 2007; Cernac and Benning, 2004; Focks and Benning, 1998). In Arabidopsis, AtWRI1 protein participates in the transcriptional regulation of glycolytic and FA biosynthetic genes by binding to a consensus motif, AW-Box ‘CnTnG(n)7CG’, in the upstream region of the target genes (Baud *et al.*, 2009; Chen *et al.*, 2018; Maeo *et al.*, 2009). In many cases, overexpression of *WRI1*, by either constitutive or tissue specific promoters, resulted in increased lipid accumulation in seeds and vegetative tissues in various plant species, including Arabidopsis, maize, rice, camelina, and soybean (An and Suh, 2015; Cernac and Benning, 2004; Chen *et al.*, 2020; Guo *et al.*, 2020; Liu *et al.*, 2010; Shen *et al.*, 2010; Sun *et al.*, 2017). Analyses of downstream regulation of various *WRI1* homologs showed that they shared regulation partners (Grimberg *et al.*, 2015). The “PULL” strategies investigated, include the overexpression of *DGAT* which also resulted in higher accumulation of oil, and showed a synergistic effect when stacked with *WRI1* expression cassette. For example, transient co-expression of Arabidopsis *WRI1* and *DGAT1* genes in *Nicotiana benthamiana* leaves resulted in TAG levels five-fold higher than that observed from transient expression of individual genes (Vanhercke *et al.*, 2013). Higher oil levels were also observed in seeds when AtWRI1 and AtDGAT1 were overexpressed in Arabidopsis under seed-specific promoters (van Erp *et al.*, 2014).

Two *WRI1* homologs, *GmWRI1a* (Glyma.15G221600) and *GmWRI1b* (Glyma.08G227700), are best characterized in soybean. Both genes have been successfully overexpressed in soybean, rendering seeds with increased total seed oil, changes in FA composition, and yield (Chen *et al.*, 2018; Guo *et al.*, 2020). *GmWRI1a* and *GmWRI1b* bind directly to AW-box elements and regulate FA production, elongation, desaturation, and export from plastid (Chen *et al.*, 2018; Guo *et al.*, 2020; Maeo *et al.*, 2009). Soybean events harboring these transgenic alleles also showed an increase in seed yield without affecting the protein level. Introducing a transgenic *AtWRI1* into soybean, however, did not translate to an increase in the total oil but rather a doubling of the palmitate percentage in the oil, likely due to an induction of a specific homolog of an acyl-acyl carrier protein thioesterases (*FATB*) gene (Vogel *et al.*, 2019). The contrasting observations in soybean events carrying an ectopic *GmWRI1* expression allele and *AtWRI1* cassette, in regards to seed oil accumulation highlights the need to gain insight on the underlying biology leading to these differing phenotypic outcomes.

The introduction of other *DGAT* variants into soybean has also led to an increase in seed TAG levels. For example, introducing a transgenic *DGAT2A* allele from the oil-accumulating fungus *Umbelopsis ramanniana* or *DGAT1* from *Sesamum indicum* L. in soybean during seed development led to 1.5% and 1.75% increase in total oil content, respectively (Lardizabal *et al.*, 2008; Wang *et al.*, 2014). Expression of *DGAT* appears to enhance carbon flux towards oil since the increase in total oil was associated with reduced soluble carbohydrate content in mature seeds (Roesler *et al.*, 2016). Despite the evidence of *DGAT* improving oil content and its synergy with *WRI1* observed in other species, there have been no communicated investigations into the metabolic and transcriptomic changes that occur during seed development in soybean events carrying a transgene stack of *AtDGAT* and *AtWRI1*.

The work described herein communicates the research outcomes on embryo transcriptomic and metabolic responses to the stable co-expression of *AtWRI1* and *AtDGAT1* in soybean. The data highlighted the induction of processes at both transcription and post transcriptional levels that offset the positive flux towards in FA and TAG accumulation, triggered by *AtWRI1* and *AtDGAT1* transgene stack. In addition, we identified competing end-products, which may contribute to the restricted oil biosynthesis. Employing transcriptomic and metabolic analyses, we observed that gene expression could explain the steady state levels of metabolites associated with sucrose metabolism and those associated with the initial steps of glycolysis, but not the levels of glycolytic intermediates downstream of triose phosphates. Furthermore, using transcriptomics datasets gathered on soybean events carrying either *AtWRI1/AtDGAT1* stack or *AtWRI1* alone

(Vogel *et al.*, 2019), we catalogued the putative targets for AtWRI1 in soybean. The identification of embryo's responses and adaptations to *AtWRI1* and *AtDGAT1* expression allows guidance for further engineering approaches aimed at increase oil content in soybean.

RESULTS

***Arabidopsis WRI1* and *DGAT1* were successfully expressed in soybean**

In order to evaluate whether the expression of *AtWRI1* and *AtDGAT1* could direct carbon flow towards lipid accumulation, three independent soybean events, hereafter designated as WD-1, WD-2, and WD-3, were characterized. The two expression cassettes were regulated by the seed-specific beta-conglycinin promoter (Allen *et al.*, 1989) and cloned into a T-DNA element (Figure S1). Integration of the T-DNA element in the genome of the selected events was confirmed by Southern blot analysis. The results showed that events WD-2 and -3 carry a single transgenic locus, while WD-1 harbors two (Figure S2). The selected events were carried down to homozygosity. The homozygous lineages were evaluated under field conditions in 2018, 2019 and 2020, as well controlled greenhouse environments.

Mature seeds of transgenic WD presented different FA and carbohydrate composition

To assess whether the expression of the *AtWRI1* and *AtDGAT1* transgenic alleles altered seed reserve accumulation, the composition of the mature seeds was determined from plants grown under both greenhouse and field conditions (Figure 1). WD-3 displayed the same lipid content and FA composition as the WT (data not shown), and, therefore, was not included for further analyses. Under greenhouse conditions, the transgenic events WD-1 and -2 showed no significant differences with the WT regarding total FA and protein contents at maturity (Figure 1a). However, their FA composition was significantly affected. An increase in the levels of palmitic and linoleic acids, and a decrease in stearic and oleic acids were observed in the transgenic events (Figure 1a). Similar results of total FA content and composition in mature seeds were obtained when these events were grown under field environments, but with a reduced accumulation of linolenic acid (Figure 1b). The presence of a *DGAT1* transgenic allele was expected to enhance the assembly of TAGs, however, no difference in TAG content was observed between the transgenic events and WT plants (Figure 1c). Quantification of carbohydrates in mature seeds, harvested under greenhouse conditions, revealed an increase in the total content of soluble sugars and sugar alcohols in the transgenic events.

Specifically, WD-1 and-2 events had higher levels of tetraols, pentitols, and raffinose relative to the control (Figures 1d and 1e). Interestingly, the only soluble sugar with decreased levels in the transgenics was maltose. In addition, starch content at maturity was significantly higher than WT in WD-2 (Figure 1f). The levels of the matrix polysaccharides, hemicelluloses, and crystalline cellulose, were determined by the quantification of individual monosaccharides after hydrolysis. WT and transgenic events presented a similar profile of hemicellulose subunit, with only WD-2 showing a significant decrease in rhamnose, galactose, and total hemicellulose (Figure 1g). Finally, no significant change in the levels of crystalline cellulose was observed (Figure 1h). These data demonstrated that the expression of *AtWRI1* and *AtDGAT1* affected mature seed carbon partition, especially the composition of FA and soluble sugars.

Seed yield and germination were decreased in WD events

The transgenic events grown under field conditions in 2018, 2019, and 2020 did not show a significant difference in agronomic parameters, days to flowering and to maturity (Table S1). However, a roughly 15-25% decrease in yield per square meter was observed, without a significant change in 100 seed weight (Table S1). Mature seeds collected from the field showed a mild wrinkled-seed off-type, that was markedly enhanced in seeds collected from the greenhouse (Figure S3). To evaluate if the differences in seed composition and phenotype affected seed viability, germination assays were performed in the field (Table S1). The results were consistent in each field trial, showing reduced germination in the transgenic events compared to the WT (Table S1). These data show that both changes in the biomass composition and agronomic parameters were affected by the expression of *AtWRT1* and *AtDGAT* genes in soybean.

Starch and hemicellulose accumulation competed with FA synthesis in WD events during seed filling

To identify earlier processes altered by *AtWRI1* and *AtDGAT1* expression, and responsible for the changes that ultimately give rise to the mature seed composition, we monitored the storage of the different biomass components in immature embryos, across six developmental stages under controlled greenhouse conditions. The selected points (21 to 36 days after pollination, DAP) span a period of linear reserve accumulation in the embryo (Figure S4). The results showed that the embryo's DW did not differ among WT and transgenic events at the developmental points after 27 DAP (Figure 2a). However, the production of protein and FA was reduced in the transgenic events at nearly all developmental points (Figure 2b and 2c), despite showing

similar synthesis rates of protein and FA (Figure S4) and reaching similar concentrations at maturity (Figure 1a). The reduction in stearic and oleic acids, as well as the increase of palmitic and linoleic acids in the WD-1 and -2 events, observed at maturity were detected at the immature stages as well (Figure 3). At some developmental stages, linolenic acid was higher, following the same trend as observed in mature seeds from the greenhouse (Figures 1a and 3). In addition, the transgenic embryos had a 3-fold increase in the starch accumulation rate (Figure S4), doubling WT levels in the last stages evaluated (Figure 2d). Interestingly, the resulting ratio of FA accumulation rate to starch accumulation rate was 3.48, 0.93, and 0.89 in the WT, WD-1, and WD-2, respectively. Therefore, besides the well-known competition for carbon with protein accumulation, FA synthesis in WD events was also competing with a higher rate of starch production (Figure S4), which likely impacted final FA concentration.

Given the observed changes in the rates of starch accumulation in the WD-1 and -2 events, we subsequently monitored for alterations in levels of cell wall polysaccharides (Figure S5). Two additional time points were added at later stages for this analysis. The results revealed an increase in the content of glucose in the matrix polysaccharides, probably derived from the hemicellulose xyloglucan and amorphous cellulose. The rates of glucose accumulation as hemicelluloses in WD-1 and -2 were 1.50 and 1.25 times higher than the WT, respectively (Figure S6). Besides, the level of total hemicelluloses in the WD events was increased relative WT until 33 DAP, after which they were not significantly different from the WT, and ,at maturity, WD-2 showed a significant decrease (Figure 1g). The levels of crystalline cellulose during development, was significantly increased only in event WD-2. These results highlight that; besides starch, the production of cell wall polysaccharides was also competing for carbon with FA synthesis in WD events.

***AtWRI1* and *AtDGAT1* expression increased during the development in WD events**

To assess changes in the transcriptome during seed development in the WD-1 and-2 events, an RNAseq analysis was performed in immature embryos of both transgenic events grown under greenhouse conditions. Despite both expression cassettes were regulated by the same β -conglycinin promoter (Figure S1), which in its native genomic context, is active starting at 14 days after flowering (DAF) and peaks at approximately 44 DAF (Figure S7), the expression of *AtWRI1* was approximately 10 times higher than *AtDGAT1* (Figures 4a and 4d). The *GmWRI1* homologs (Glyma.08G227700 and Glyma.15G221600) were down-regulated in the embryos of transgenic events during development (Figures 4b and 4c). The *GmDAGT1* gene calls were only slight

changed in their expression pattern (Figures 4e to 4n), suggestive that AtWRI1 is not regulating their transcription as it is for other lipid related genes (Figure 5).

Gene calls annotated for function in glycolysis and FA metabolism were enriched among the differentially expressed genes in the WD events during seed development

DEGs were identified from each time point in which the transcriptome was assessed via RNAseq analysis, for each transgenic event (Table S2). Common DEGs among the events were selected for further analysis, discarding those that presented opposite behavior (Table S2). With 969 native genes being differentially expressed, 30 DAP represented the stage with most DEGs (Table S2). Among the 134 gene calls differentially expressed across all four developmental stages and both transgenic events, only 12 were down-regulated (Figure S8).

To assign association with metabolic pathways and biological processes to the gene calls over-represented in the total pool of DEGs, an enrichment analysis was performed with both KEGG pathways and Gene Ontology (GO) terms databases. The outcome of this enrichment analysis revealed the categories of FA biosynthesis, FA metabolism, and glycolysis/gluconeogenesis were among the top enriched pathways across all stages (Figure 5a), indicating that AtWRI1 is capable of activating the expression of its known targets in the genome of soybean. In accordance with the KEGG pathway enrichment, GO terms of lipid biosynthesis, carbohydrate metabolism, and generation of precursor metabolites and energy processes were identified as the top enriched biological processes (BP). For molecular functions (MF), the enriched GO term with the highest gene count was catalytic activities (Figure 5b). Interestingly, the membrane was the only enriched GO term for cellular compartments (CC) and this is in alignment with the enriched GO terms of transport in BP and transporter activity in MF (Figure 5b).

Annotated gene calls assigned to *de novo* FA synthesis were up-regulated while those for oil body structural proteins down-regulated in WD events during seed development.

To evaluate what specific steps in lipid biosynthesis were affected by *AtWRI1* and *AtDGAT1* co-expression, we investigated the processes that takes place in the chloroplast and the ER (Figure 6). One or more genes involved in each step of the plastidic *de novo* FA synthesis pathway were up-regulated in two or more developmental stages, including subunits of the ACC and the FA synthase complex (Figure 6). Moreover, gene

calls annotated to function in ER FA elongation and desaturation, such as ketoacyl-CoA synthase and reductase, were also induced in the transgenic events (Figure 6). In addition to *AtDGAT1* expression, only one enzyme from TAG biosynthesis, a putative glycerol 3-phosphate acyltransferase, was found in the DEG list (Figure 6). Finally, genes encoding putative oleosins and caleosins, structural proteins required for oil body (OB) stabilization, were down-regulated up to 10 times in the transgenic events (Figure 6). Therefore, despite the induction of FA synthesis genes and the expression of *AtDGAT1*, the reduced expression of the lipid droplet packaging proteins may limit oil accumulation.

Putative AtWRI1 targets were identified

Many of the WRI1 targets described in the literature were found to be induced in WD events grown under greenhouse conditions, including genes encoding subunits of the plastid pyruvate kinase (PK), pyruvate dehydrogenase (PDH) and pACC, and versions of the ketoacyl-ACP synthase I, hydroxyacyl-ACP dehydrase, and enoyl-ACP reductase (Figure 6). To complement the list of *AtWRI1* putative targets and evaluate transcript behavior under field conditions, we enlarged the RNA-seq study and analyzed the transcriptome of immature seeds collected from the field at R5, R5/6, and R6 stages of development (equivalent to 24, 30 and 38 DAP, respectively). The biologicals utilized in this analysis were WT, WD-1 event along with an event, designated here as W-1, previously described (Vogel *et al.*, 2019). W-1 only carries the *AtWRI1* cassette, which will allow for the discrimination between the indirect changes in gene expression due to the presence of *AtDGAT1* from those directly related to the expression of *AtWRI1*. Compared to the greenhouse RNA-seq experiments, substantially fewer DEGs were identified in the field (Table S2). *AtWRI1* expression was detected in field samples (Figure S9a), however, the down-regulation of *GmWRI1* homologs was less evident than under greenhouse conditions (Figures S9b and S9c). The expression of *AtDGAT1* and *GmDGAT1* homologs in the field, on the other hand, are consistent with the greenhouse analyses, reaching comparable expression levels for most of the homologs (Figures S9d to S9n). Comparisons between the DEGs identified from the field and the greenhouse for WD-1, revealed 25 and 212 common DEGs at R5-24 DAP and R5/6-30 DAP stages, respectively (Figure S10a). Furthermore, in the field experiment, among WD-1 and W-1 DEGs, we identified 531 common ones along the development (Figure S10b). Including data with a higher degree of variability, such as the samples from plants grown in the field, allows a more robust identification of true targets.

To identify putative targets of *AtWRI1*, we vetted calls using three criteria: (1) genes up-regulated in at least one stage in the field W-1 and WD-1 events and at least one stage in the greenhouse WD-1 and -2 events; (2)

genes with the AW-box motif in their 2 kb upstream sequence; and (3) genes whose expression correlates with the expression of *AtWRI1* with a Pearson correlation coefficient higher than 0.85 (Zaborowski and Walther, 2020). This vetting process identified 82 genes, including transcription factors, kinase receptors, transporters, genes related to lipid and central metabolism, and some with unknown function (Table S3). Among the vetted gene calls with annotated functions associated with FA metabolism that have not been previously identified as *AtWRI1* targets, were some putatively encoding for FA amide hydrolases, a long chain acyl-CoA synthetase, and monoacylglycerol and GDSL-motif lipases (Table 1). Interestingly, besides PK and PDH regulation, other central metabolism genes were detected as putative *AtWRI1* targets, including genes annotated as glucose 6-phosphate/phosphate translocator, UDP-glucose pyrophosphorylase, fructose biphosphate aldolase, plastidic glyceraldehyde 3-phosphate dehydrogenase, and plastidic malate dehydrogenase (Table 1). Some gene calls that are not directly assigned function in lipid metabolism or carbon or energy supply were also identified. These include a putative actin subunit, abscisic acid, jasmonates, ethylene, and auxin associated genes (Table 1), potentially linking the *AtWRI1* regulon beyond the FA metabolism and glycolysis in developing soybean seeds.

Among vetted *AtWRI1* targets, we identified one putative acyl-acyl carrier protein thioesterase (*GmFATB*, Glyma.04g151600) in the transgenic events in all the stages, which likely accounts for the observed significant increase in palmitic and decrease in stearic and oleic acid levels during seed development and at maturity (Figures 1, 3, and 6). Gene calls with functional annotations that would negatively affect oil accumulation were also found to be potential targets of *AtWRI1*. For example, genes putatively encoding lipolytic enzymes, such as GDSL esterase/lipases, α/β hydrolases, and monoacylglycerol lipases (MAGL), were identified as putative *AtWRI1* targets and were highly up-regulated in the transgenic events (Table 1). Particularly, three gene calls, annotated as GDSL esterase/lipase motif type II (homolog to At1G53920), Glyma.09G074000, Glyma.15G182900, and Glyma.15G183000, were expressed up to 64 times higher than in the WT, pattern conserved along with development (Table 1). In addition to these potential *AtWRI1* targets, other genes annotated as lipases and lipid transfer proteins lacking an AW-motif in their sequence, also resulted induced in different stages of development (Figure S11). Lastly, the up-regulation of two putative genes encoding soybean biotin/lipoyl attachment domain-containing (BADCD) proteins (Glyma.11G233700 and Glyma.18G023300) during development, proposed to act as pACC inhibitors (Salie *et al.*, 2016), was observed (Figure 6). The differential regulation of these gene calls may have contributed to the lack of an observed oil content increase in the transgenic events.

Gene calls with functional annotation in carbohydrate metabolism were differentially regulated

To assess if the observed differences in carbohydrate metabolism were governed by transcriptional or post-transcriptional mechanisms we analyzed the transcript levels in gene calls annotated for functionality in central metabolism during development. The results reveal that transcripts linked with sucrose metabolism were affected in the embryos of the transgenic events. The expression of a gene encoding a putative sucrose 6-phosphate synthase was down-regulated, while genes encoding putative degradative enzymes, such as a neutral invertase and two sucrose synthases, were up-regulated (Figure 7). Changes in expression of gene calls associated with sucrose metabolism was accompanied with the down regulation of a gene encoding a putative cell wall/vacuolar invertase inhibitor and the up-regulation of two genes encoding putative sucrose transporters, especially at the latest stages (Figure 7). The WD events displayed an induction in transcripts assigned function to almost all glycolytic enzymes, with the exception of three genes putatively encoding two phosphofructokinase enzymes and an NADP-dependent glyceraldehyde 3-phosphate dehydrogenase that were down-regulated (Figure 7). These results suggested an overall increase in carbon flux towards precursors for FA synthesis and energy.

We also analyzed expression levels of genes putatively functioning within pathways competing with FA synthesis, such as starch and cell wall production. Unexpectedly, the expression of two putative genes encoding ADP-glucose pyrophosphorylase regulatory subunits were down-regulated in the WD events along the selected developmental timepoints. This enzyme catalyzes the first and rate limiting step in starch biosynthesis. While, an up-regulation of a gene encoding a phosphoglucomutase, an enzyme that transforms glucose 6-phosphate into glucose 1-phosphate, the starch biosynthesis substrate (Figure 7), was also observed. Assuming transcript changes, would correlate with post-translations enzymatic activities, these two opposing key enzymes, coupled with complex pattern of transient starch accumulation, highlights that the seed centric phenotypic outcomes observed in the WD events is likely governed at a transcriptional and post-transcriptional manner. Differences in hemicellulose content also cannot be explained solely at transcript level. Among many of the gene calls functionally annotated as enzymes involved in cell wall metabolism, we could identify DEGs encoding two probable glycosyltransferases (exostosin family proteins) with putative functions in cell wall biosynthesis, four xyloglucan endotransglucosylase/hydrolase, three pectin methylesterases, and six plant invertase/pectin methylesterase inhibitor superfamily. The transcriptome changes among these gene calls could not fully explain the phenotypic characteristics observed in the

transgenic events, again suggesting that post-transcriptional regulations influence soybean's adaptation to the expression of *AtWRI1* and *AtDGAT1* during maturation.

Metabolic profile of WD events during reproductive stage of development under greenhouse conditions.

To gain insight on the potential post-transcriptional regulations that are influencing the observed seed phenotypic outcomes in the WD events a metabolic profiling of the developing embryos was carried out targeting the same four developmental stages selected for the transcriptomics analysis. Here a total of 101 intermediates of central metabolism were quantified, including amino acids, sugars, sugar alcohols, organic acids, and phosphorylated compounds (Table S4). Principal component analysis of the data at each developmental stage showed a clear separation between the metabolomic profiles of WD-1 and -2 and the WT, with the number of metabolites with significantly different levels increasing at later stages (Figure S12). At each time point, the top fifteen metabolites with significantly different levels compared to the WT were identified. Among the main differences observed in the transgenic events, included many sugars and sugar phosphates, TCA intermediates, and amino acids such as Glu, Gly and Lys (Figure S12).

Among the changes observed in the various sugar metabolites, the levels of sucrose and sucrose 6-phosphate were reduced in the WD events, while many of the intermediates of the preparatory phase of glycolysis were increased (Figure 7). The precursors of starch biosynthesis, on the other hand, including glucose 1-phosphate (quantified together with mannose 1-phosphate) and ADP-glucose, accumulated to higher levels in the transgenic events (Figure 7). The increase in ADP-glucose, despite the observed downregulation of the gene putatively encoding the ADP-glucose pyrophosphorylase larger subunit (Figure 7), is consistent with the larger amount of starch during development (Figure 2d). How these changes in levels of sugars and sugars phosphates control the flux of carbon towards the different end products: TAG, starch or the cell wall matrix, is unknown. However, the results taken together clearly show post-transcriptional regulatory processes are contributing to the observed distinctive seed composition phenotypes of the WD events.

DISCUSSION

The identification of novel genetic variation leading to improved yield, protection of yield and/or quality of the harvest requires a better understanding of a plant's metabolism and adaptability to perturbations. Progress in this space is a continuous improvement process through a build-test-learn cycle. The expression of

AtWRI1 and/or *AtDGAT1* has been widely used as an approach to increase carbon flux towards oil accumulation, with varied levels of success (Baud *et al.*, 2009; Guo *et al.*, 2020; Jako *et al.*, 2001; Li *et al.*, 2015; Roesler *et al.*, 2016; Vanhercke *et al.*, 2013). In soybean, seed specific ectopic expression of *GmWRI1a* (Glyma.15G221600) in a 'Williams 82' background, showed an increase in total oil, namely changes in oleic and linoleic acids (Chen *et al.*, 2018). In contrast, the expression of *AtWRI1* under the control of conglycinin promoter in Thorne background, led to negligible changes in total seed oil content, but palmitate levels increased by approximately 20% (Vogel *et al.*, 2019). Therefore, it seems that the effect of transgenic *AtWRI1* expression on oil content and profile have a strong dependence on the genetic design, promoter, isoform, tissue, variety, and/or species used. In this work, we analyzed specifically Thorne embryos and their response to the localized expression of *AtWRI1* and *AtDGAT1* during seed development.

***AtWri1* and *AtDGAT1* were expressed at different levels in Thorne embryos**

The two events selected for deeper characterizations that expressed *AtWRI1* and *AtDGAT1*, WD-1 and WD-2, shared a similar degree of cellular changes at both the transcriptome and metabolome level. The two gene stack was successfully co-expressed in the events, with relatively high transcript accumulation across the reproductive stages analyzed (Figures 4 and S9). *AtWRI1* transcripts, however, reached higher levels than the ones of *AtDGAT1* (Figures 4 and S9). Multi-gene engineering strategies that rely on multiple copies of the same promoter are often associated with sub-optimal co-expression levels, which can result from DNA instability or transgene silencing (Shockey *et al.*, 2015). Furthermore, the lower levels of *AtDGAT1* expression could contribute to the similarity in the phenotype of the WD events with events that expressed only *AtWRI1* (Vogel *et al.*, 2019).

Multiple processes restricted uncontrolled FA increase to maintain cellular lipid homeostasis

The analysis of the WD events showed that the introduction of *AtWRI1* and *AtDGAT1* into Thorne genome provoked changes in the seed composition over development. Protein and total FA contents were lower in the WD events in early seed maturation (Figure 2), but reached WT levels at maturity (Figure 1). In addition, despite the attempt to pull more FA into TAG biosynthesis by the simultaneous co-expression of *AtWRI1* and *AtDGAT1*, TAG levels were not enhanced in the transgenic events (Figure 1). Nearly all the steps of glycolysis and *de novo* FA synthesis were up-regulated (Figure 6), suggesting that other downstream regulatory mechanisms are limiting the "PUSH and PULL" efforts. We identified four processes that were affected in the

transgenic events and that are able to restrict oil accumulation. Firstly, WD-1 and WD-2 events displayed an up-regulation of the transcripts annotated as BADC (Figure 6). These proteins were first described as long-term irreversible inhibitors of the pACC in the presence of excess FA, and consequently FA synthesis inhibitors (Salie *et al.*, 2016; Liu *et al.*, 2019). A contrasting role of BADC on pACC was recently suggested (Shivaiah *et al.*, 2020), where these proteins may facilitate the assembly of its intermediary subcomplexes. The regulatory role of this protein over the activity of pACC needs further investigation to fully address its potential as a bottleneck. Secondly, the WD events displayed altered expression of multiple genes putatively encoding lipases (Figure S11). We identified 16 differentially expressed genes putatively encoding proteins with lipolytic activities, 15 of which were up-regulated in at least one stage of development in both WD-1 and -2 events (Figure S11). Particularly, the expression of three of these genes putatively encoding GDSL-motif lipases, Glyma.09G074000, Glyma.15G182900, and Glyma.15G183000, were induced from 4 to 64 times at the developmental stages evaluated. Monitoring accumulation of vegetative lipids in tobacco leaves, Grimberg *et al.*, 2015, postulated the development of a futile cycle of FA synthesis and degradation when transiently expressing different *WRI1* homologs in *Nicotiana benthamiana*. It was suggested that boosting TAG levels in a cell, may trigger the up-regulation of gene calls with FA degradation function, thereby acting like a cellular rheostat to limit oil accumulation. Thirdly, the strong repression of putative OB proteins, such as oleosins and caleosins (Figure 6), suggests that TAG packaging is altered in WD events, which, ultimately, may affect the oil accumulation capacity of the embryo. In accordance with our results, a recent study, where *GmOLE1* (Glyma.20G196600) was overexpressed, suggested that soybean oil content is limited by oleosin expression level (Zhang *et al.*, 2019). Finally, it cannot be excluded that the down-regulation of the endogenous *WRI1* homologs in the transgenic events impacted oil enhancement through the reduction of the expression of specific targets not recognized by *AtWRI1* (Figures 4 and S9). It has been previously shown that the ability of the upstream region of *WRI1* to initiate transcription *in planta* is negatively affected by the presence of *WRI1* proteins (Snell *et al.*, 2019). This conserved negative autoregulatory mechanism of *WRI1* expression is a result of downstream actions of *WRI1*, as this protein is unable to bind to its upstream region (Snell *et al.*, 2019). This negative loop can explain the downregulation of the *GmWRI1* homologs when *AtWRI1* is strongly expressed (Figure 4). Altogether, these results indicate that soybean embryos respond to *AtWRI1* and *AtDGAT1* expression by triggering mechanisms, at many levels, to restrict uncontrolled FA increase and maintain cellular lipid homeostasis.

FA composition was altered in mature seed of the transgenic events, showing higher levels of palmitic and linoleic acid and reductions in stearic and oleic acid, evident from early maturation (Figures 1 and 3). These changes may arise, partially, as a consequence of the up-regulation, at all the studied points of development, of one *FATB* homolog (Glyma.04g151600), putatively encoding an acyl-acyl carrier protein thioesterase (Figure 6). An accumulation of palmitate in *Arabidopsis* seeds has been reported in lines overexpressing *AtFATB1* (Dörmann *et al.*, 2000). However, contrasting results have been reported in Chen *et al.*, 2018, where an up-regulation of seven *GmFATB* homologs (including Glyma.04g151600) with no increase in palmitate levels were reported in *GmWRI1a* overexpressing seeds. Further studies will be needed to corroborate the impact of each *GmFATB* homolog in seed FA composition.

The embryos expressing *AtWRI1* and *AtDGAT1* also responded with an alteration of their carbohydrate metabolism (Figures 1, 2, and S5). An increase in the levels of sugar and sugar phosphates was observed in the WD events along the reproductive stages monitored (Figure 7), with the exception of sucrose, sucrose 6-phosphate, and trehalose 6-phosphate. Increased expression of genes encoding sucrose degradative enzymes, such as invertase and sucrose synthase, coupled with a downregulation of invertase inhibitor and sucrose biosynthesis genes, likely explains the lower levels of sucrose and higher content of hexoses and hexose phosphates observed in the embryos (Figure 7). Trehalose 6-phosphate, a signal of cellular sucrose status, can regulate FA biosynthesis by stabilizing WRI1 protein, avoiding its phosphorylation by SnRK1 and posterior degradation by the proteasome (Zhai *et al.*, 2018). Conversely, when the cellular sucrose content is low, levels of trehalose 6-phosphate decrease, WRI1 becomes phosphorylated and is degraded, with the result of reducing energy-consuming pathways (Zhai *et al.*, 2018). Even though *AtWRI1* targets were induced, the reduction in trehalose 6-phosphate levels, may have increased *AtWRI1* turnover, which in turn, may have lessened the degree of up-regulation of its target gene calls in the soybean genome. The alteration of the embryo's hexose metabolic status during development also affected the rate of accumulation of starch and hemicelluloses (Figures S4 and S6), which was not fully accompanied by changes in the expression of genes involved in these biosynthetic pathways. These data further support the notion that post transcriptional processes such as metabolic regulation and carbon re-distribution may also have contributed to the restriction in oil accumulation in the events.

Interestingly, there are some similarities between the *Arabidopsis* embryos' responses to a complete loss of *WRI1* (*Atwri1* mutants) (Focks and Benning, 1998) and outcomes observed in soybean co-expressing *AtWRI1*

and *AtDGAT1*. Except for the extremely low oil accumulation in the *Atwri1*, the *Arabidopsis* mutant and the WD events share some similar physiological and biochemical responses, including a wrinkled seed phenotype, reduced germination, higher starch accumulation, higher glucose and fructose (except sucrose), and a deficient conversion of sucrose into FA (Focks and Benning, 1998). Therefore, perturbations in lipid homeostasis, in both directions, led to similar embryo adaptations.

AtWRI1 potential targets were identified

The systematic prediction of AtWRI1 potential targets in the soybean genotype Thorne, by a comparative analysis of gene calls up-regulated in WD-1, WD-2, versus the W-1 events, revealed a high correlation with the expression of *AtWRI1*, and the presence of an AW-box in their upstream sequence (Table S3). The gene calls identified through this process include those functionally annotated for late glycolytic and FA biosynthetic genes, which is consistent with previous reports (Fei *et al.*, 2020). Among the putative targets with central metabolism functions, gene calls with an AW-box footprint in their up-stream region included a putative glucose 6-phosphate/phosphate translocator (*GPT2*), UDP-glucose pyrophosphorylase (*UGP2*), and plastidic malate dehydrogenase (Table 1). *GPT2* is responsible for the transport of glucose 6-phosphate into the plastids where it can be used as a carbon source for starch and FA biosynthesis or for NADPH generation via the oxidative pentose phosphate pathway (Kunz *et al.*, 2010; Niewiadomski *et al.*, 2005). In addition to having a central role in carbon partitioning between cytosol and plastids, *GPT2* transcript abundance correlates with the levels of glucose and its induction by the sugar-sensing pathway was proposed as a mechanism to regulate cellular sugar homeostasis (Kunz *et al.*, 2010). The regulation of *GPT2* by AtWRI1 may provide another mechanism by which AtWRI1 can direct carbohydrates towards FA synthesis. Similarly, the induction of *UGP2* by AtWRI1 could direct UDP-glucose -the product of sucrose synthase, and other AtWRI1 known target (Fei *et al.*, 2020)- towards the production of glucose 1-phosphate and glucose 6-phosphate impacting both glycolysis and FA biosynthesis (Figure 7). However, in soybean embryos co-expressing *AtWRI1* and *AtDGAT1*, UDP-glucose carbons were directed towards cell wall polysaccharides, and glucose 1-phosphate apparently shunted to starch biosynthesis (Figure 7). Finally, plastidic malate dehydrogenase was found to contribute to the production of carbon precursor and NADPH for *de novo* FA synthesis in developing maize (Alonso *et al.*, 2010; Cocuron *et al.*, 2019) and pennycress embryos (Tsogtbaatar *et al.*, 2020), as well as in the maintenance of the energy homeostasis in developing *Arabidopsis thaliana* seeds (Selinski *et al.*, 2014).

Given these outcomes, it is probable that WRI1 governs additional processes to ensure the cellular environment and carbon flux for FA synthesis.

In addition to the identification of *FATB* and *BADC* gene calls that were previously proposed as AtWRI1 targets (Liu *et al.*, 2019; Vogel *et al.*, 2019) four putative lipolytic genes were highlighted in the present study (Figure S11). These include, a MAGL and three GDSL-motif lipases (Figure S11). As it was suggested for BADC FA inhibition (Liu *et al.*, 2019), coordinated regulation of oil biosynthetic and degradative genes by WRI1 help maintain cellular homeostasis of lipids.

Additional putative AtWRI1 targets identified in soybean included hormone-related genes annotated to encode for auxin-responsive GH3 family proteins and an auxin response factor protein (Table 1). *AtGH3.3*, a gene involved in auxin degradation, was found up-regulated in *wri1* Arabidopsis mutants, and AtWRI1 protein was proven to recognize and bind to the AW-box in *AtGH3.3* promoter (Kong *et al.*, 2017). A role for AtWRI1 in root auxin homeostasis was suggested (Kong *et al.*, 2017), however remains to be studied if that function is occurring in embryos.

Novel strategies for oil improvement in soybean

The findings of this study can guide future genetic strategies aiming to improve oil content in soybean seeds. First, the beta-conglycinin promoter may not be ideal for this effort, as it allows some degree of expression in roots (Figure S7). As mentioned above, AtWRI1 affects auxin responses in roots (Kong *et al.*, 2017) and therefore, root architecture, which may explain the reduced yield in WD events (Table 1). Secondly, if oil levels are to be enhanced, it will require sufficient availability of OB packaging proteins to support an increased TAG biosynthesis. Thirdly, editing of the AW-box or targeted down-regulation of the undesired FA synthesis inhibitors and lipolytic targets of AtWRI1 may also need to be considered in order to protect the increased accumulation of oil. Finally, genetic approaches to reduce the flow of hexose phosphates to competing pathways, such as starch and cell wall polysaccharides, should be evaluated.

METHODS

Vectors construction and plant transformation

AtDGAT1 (GenBank accession NP_179535.1) and *AtWR1* (GenBank accession NP_191000) sequences were codon optimized for soybean expression and synthesized by GenScript, Piscataway, NJ. Both genes were under the control of the soybean seed-specific beta-conglycinin promoter (Allen *et al.*, 1989), fused to the tobacco etch virus translational enhancer element (Carrington and Freed, 1990), and terminated with the 35S cauliflower mosaic virus polyadenylation signal (Figure S1). The two gene cassettes were assembled into a final binary vector, referred as pPTN1248, which harbors a *bar* gene (Thompson *et al.*, 1987) under control of the *Agrobacterium* Pnos promoter for herbicide selection (Figure S1). pPTN1248 was mobilized into *A. tumefaciens* strain EHA101 (Hood *et al.*, 1986) via triparental mating. The transformations were performed on the soybean variety Thorne using the procedures previously described (Xing *et al.*, 2000; Zhang *et al.*, 1999). The identification of transformed plants was carried out by monitoring the expression of the *bar* gene via leaf painting technique (Zhang *et al.*, 1999). Genomic DNA isolated following a modified CTAB method (Springer, 2010) was used for PCR genotyping in all generations of the transgenic plants. Synthetic *AtWR1* gene was amplified with the primer set 5'-GTCTATCTCGGTGCTTACGACTCT-3' and 5'-CCTGAGGTGGTTCCTCTACATACTG-3'. Amplification of *AtDGAT1* was carried out with the primer set 5'-GATCGCTGTAACTCTAGGCTGA-3' and 5'-AGCAGTAGAACATACAGAGCCACAC-3'. The PCR reactions were conducted with GoTaq Green Master Mix, following the manufacturer's instructions (Promega Corporation, Madison, WI). The number of transgenic allele integrations was determined by Southern blot hybridization. For that, genomic DNA was isolated from young leaves according to the protocol described by Dellaporta *et al.*, 1983. Ten micrograms of the genomic DNA were digested with the restriction enzyme *Sall*, which has a single restriction site within the T-DNA at the *bar* ORF. Then, DNA fragments were separated by electrophoresis on 0.8 % agarose gels, blotted and UV crossed linked to a nylon membrane (Bio-Rad cat #162-0196, Hercules, CA). Membranes were hybridized with a labeled probe generated by amplification of a sequence of either *AtWR1* or *AtDGAT1* by the random primer labelling technique using dCT³²P (Prime-It II Cat # 300385; Stratagene, La Jolla, CA) as previously described (Eckert *et al.*, 2006). For homozygous plant identification, genotyping was performed for 24 or 48 plants, for single or double insertion events, respectively, along different generations of soybean in the field.

Field growing conditions and germination and yield analyses

Field trials were conducted on homozygous transgenic events and lineages of T4, and T5 generations of transgenic plants in crop seasons 2018, 2019 and 2020. The soybean variety Thorne was used as a control for

all cropping seasons. In 2018, three independent events of Thorne transformation with pPTN1248, namely 970-1 (WD-1), 970-2 (WD-2), and 978-3 (WD-3) were evaluated, while in 2019 and 2020, only the WD-1 event was analyzed. In 2019, the transgenic event 917-17 (W-1) which expressed the single gene *AtWR1* (Vogel *et al.*, 2019) was also included in the field trial. All evaluations were conducted in completely randomized plots in three replicates. Each plot consisted of four 10 ft rows in a four-row plot design (30 inches row to row) in which two border rows were the WT Thorne. Data were collected from the plants in the inner two rows. Either two or three plots per event or lineage were planted each year depending on the seed availability. One hundred seeds were sown in each row. After sowing for two weeks, a total number of plants were counted and germination rates were calculated based on the initial number of seeds sown (200 seeds per plot). Observations were performed for phenology according to a soybean guideline (Pedersen *et al.*, 2004). At harvest, total seed weight per plot and one hundred seed weights were recorded.

Greenhouse growing conditions and sample collection

The seeds were planted in 30 by 26 cm plastic pots (Nursery supplies Inc., Orange, CA, USA) containing Baccto, Horticultural sphagnum peat, and perlite (Michigan peat company, Houston, TX, USA). After planting, the pots were placed in a greenhouse at 30° and 25° C, day and night, respectively, with a photo-period of 16 h. The light intensity was maintained at around 450 $\mu\text{mol.m}^{-2}.\text{s}^{-1}$. The transgenic events, WD-1, WD-2, and the control WT were separated in the greenhouse by pollen screens to avoid cross-pollination between genotypes. After the first 45 days, the plants were fertilized every 2 weeks with 6 g of 15-5-15 fertilizer (Everris NA Inc., Dublin, OH, USA). Open flowers were tagged every day in order to identify the correct developmental stage. Samples for biomass, metabolomic and transcriptomic analysis were collected at different points of development (21, 24, 27, 30, 33, 36, 42, and 48 averaged DAP) and at maturity. Samples from each developmental stage corresponded to three DAP that once averaged matches the given timepoint. For example, the 21 DAP samples were collected from 20, 21 and 22 DAP pods, and 24 DAP samples were collected from 23, 24 and 25 DAP pods, etc. The collected immature seeds were peeled to remove the seed coat and endosperm and frozen under liquid N₂. At least four replicates were collected for each time point and genotype, and each replicate consisted of one embryo, with the exception of 21 and 24 DAP, where three embryos were used instead. For the mature stage, four seeds were ground for each replicate and four replicates were analyzed. Finally, the samples for biomass and metabolomics were freeze dried in a

lyophilizer (Labconco Freezone 12 plus Freeze Dryer) for three days prior to analysis while samples for transcriptomic were kept at -80°C.

Biomass extraction and quantification

Seven mature seeds collected from two plants from the field (2018) were pooled as one biological replicate and three replicates were used to determine the total fatty acid, fatty acid compositions and TAG. The seeds were grounded using a coffee grinder and ~200 mg of the seed powder was used for lipid extraction, using chloroform and methanol method (Bligh and Dyer, 1959). For each tube, 10 mg of triheptadecanoin was used as a standard reference for calculation of total lipid. The lipid phase was collected and divided into two parts for total lipid and TAG analyses, then dried at 50°C under nitrogen. TAG was purified using the Supelco Supelclean LC-Si SPE column and dried under nitrogen at 50°C. Both total lipid and total TAG fractions were then methylated using methanol/sulfuric acid 2.5 % for 45 min at 90°C. FAMES were isolated and analyzed on a 6890N gas chromatography-flame ionization detector (Agilent Technologies, Santa Clara, CA) fitted with a 30 m x 250 µm HP-INOWAX column (Cat # 19091N-133; Agilent Technologies).

Immature embryos (21 to 36 DAP) and mature seeds collected under greenhouse conditions were analyzed according to their biomass content. FA and proteins, and starch were sequentially extracted and quantified as previously described (Cocuron *et al.*, 2014) with minor modifications. Briefly, 5 mg of dried grounded embryos, supplemented with 100 µg of glyceryl triheptadecanoate as internal standard, were subjected to three consecutive rounds of FA extractions using 1ml hexane/isopropanol (2:1). The dried pooled FA supernatant was methylated using methanol/sulfuric acid 2.5% for 120 min at 80 °C. FAMES were then analyzed using an Agilent Technologies 6890N network GC system coupled to a single-quadrupole 5975B VLMSD mass spectrometer and injector 7683B series (Santa Clara, CA, USA). The oven's initial temperature was set to 120 °C and held for 0.5 min after being raised to 120 °C at 100 °C/min to reach a final temperature of 245 °C which was held for 4.25 min. FAME derivatives were quantified using the known internal standard concentration. Proteins were extracted from the residual pellet after FA extraction by three rounds of 1 ml of extraction buffer [20 mM Tris-HCl, pH 7.5, 150 mM NaCl and 1% (w/v) SDS]. The supernatants were combined and total protein content was quantified using the DC Protein Assay kit from Bio-Rad and bovine serum albumin (BSA) as a standard. Finally, starch extraction was performed on the pellets after protein extraction by digestion with 10 µL of amyloglucosidase from the Megazyme International Ireland Ltd Total

Starch Assay Kit for 1,5 h at 55°C. Glucose content was then quantified using the colorimetric method from the Total Starch Assay Kit (Megazyme International Ireland). For all pairwise multiple comparison procedures Fisher LSD method or Student-Newman-Keuls method was used as parametric or non-parametric test, respectively using Sigmaplot 12.3. GraphPad Prism 9 software was used for slope statistics.

Carbohydrate quantification

Soluble sugars, hemicellulose and cellulose from mature soybean seed and immature embryos (24, 30, 33,36, 42, and 48 DAP) were quantified as described in Moretti et al., 2020.

RNA extraction of greenhouse collected samples and sequencing

Immature embryos of the same greenhouse grown plants as the biomass and metabolomics analyses were used to collect RNA for the transcriptomics analysis. For each of the three genotypes of WD-1, WD-2, and WT, RNA was extracted at four timepoints of 24, 27, 30, and 33 DAP. For each replicate, one immature embryo was flash-frozen with liquid nitrogen and ground with pestle and mortar into fine powder from which RNA was isolated and cleaned using the Macherey-Nagel NucleoSpin RNA Plant Mini kit (MACHEREY-NAGEL Inc.). RNA samples were submitted for sequencing via the Illumina NovaSeq 6000 platform with 150bp paired-end reads at the Genomics Shared Resource of the Ohio State University Comprehensive Cancer Center.

Field-grown sample collection, RNA extraction, and sequencing

Immature seeds from WD-1, W-1, and WT grown in the field (2019) were collected at R5, R5/6, and R6 developmental stages (Pedersen *et al.*, 2004). Stages R5 and R5/6 are equivalent to the 24 DAP and 30 DAP timepoints in the greenhouse, respectively. For each biological replicate four seeds from one plant were bulked, and three plants were used as a different replicate. RNA extraction was performed using the QIAGEN RNEasy Kit (QIAGEN, INC.). The quality of the RNA was evaluated by 1% agarose gels and its concentration was quantified by Nanodrop. The RNA was cleaned from any DNA contamination by DNase treatment using the Turbo DNA free kit (Invitrogen, INC.). The sequencing of RNA was performed via Illumina NovaSeq 6000 by the University of Nebraska Medical Center.

Sequence alignment and differential expression analysis

Illumina-associated adapter sequences were trimmed by the sequencing service. Sequence alignment and differential expression analysis were conducted using the kallisto/sleuth pipeline. Reads of all sequenced samples were assessed for quality control using the FastQC program (version 0.11.5). High-quality reads were loaded to kallisto (version 0.43.1) available as a graphic user interface on Cyverse (www.cyverse.org) with bootstrap value set at 100 and k-mer length at 31. *AtWR1* and *AtDGAT* sequences used in the transformation vector were added to the *G. max* cDNA database corresponding to the Wm82.a2.v1 genome retrieved from Ensembl (<http://plants.ensembl.org>). This cDNA library served as the transcriptome reference for pseudo-alignment and read quantification. Results from kallisto were used as input for differential expression analysis at gene level via the sleuth package (version 0.30.0) in R (version 3.6.3). Pairwise comparisons between WD-1, WD-2, and W-1 versus WT plants were conducted at each of the timepoints. Beta values from the Wald test were used as estimators of \log_2 fold-change (\log_2FC) values. Differentially expressed genes (DEG) had likelihood ratio test-derived FDR-adjusted p-values (greenhouse data) or p-values (field data) below 0.05 and fold change of 2 (or $|\log_2FC| \geq 1$). Due to high variation in field data, unadjusted p-values, rather than adjusted p-values, were used as a less stringent cutoff.

Gene set enrichment analysis

Common DEGs found in both pairwise comparisons between WD-1 versus WT and WD-2 versus WT were used for gene enrichment analysis at each timepoint. Gene Ontology (GO) analysis was conducted via AgriGOv2 (<http://bioinfo.cau.edu.cn>) and KEGG pathway via DAVID (<http://david.ncifcrf.gov>). Significantly enriched KEGG and GO terms had FDR-adjusted p-values below 0.05. Detailed annotation of DEG was obtained from SoyBase (<http://soybase.org>) and Phytozome v12.0 (<http://www.phytozome.net>).

Gene co-expression analysis

Greenhouse RNA-seq data were used to calculate correlation with *AtWR1*. Each gene has twelve data points for three genotypes and four time points. The mean values of three replicates on the same time point were used. The Pearson correlation was calculated between *AtWR1* and other 49661 expressed genes with the R function `cor()`. These expressed genes have a total of TPM > 0.

Targeted metabolomics

For targeted metabolomics analysis four time points (24, 27, 30 and 33 DAP, four replicates each) collected under greenhouse conditions at a consistent hour of the morning were studied. Intracellular metabolites were extracted from 5 mg of ground freeze-dried soybean embryos using boiling water, and following the procedure described by Cocuron *et al.*, 2014 and De Souza *et al.*, 2015. Sugars, sugar alcohols, amino acids, organic acids, and phosphorylated compounds were measured using an UHPLC 1290 Infinity II from Agilent Technologies (Santa Clara, CA, USA) coupled with a linear triple-quadrupole/ion trap mass spectrometer QTRAP 6500+ (AB Sciex Instruments, Framingham, MA, USA) using the methodologies previously described (Cocuron *et al.*, 2014). The quantification was accomplished using i) [$U-^{13}C_6$] glucose, [$U-^{13}C_4$] fumarate, and [$U-^{13}C_2$] glycine as internal standards for each type of metabolites to account for any loss of material during sample preparation; ii) unlabeled external standard mix run in parallel to the samples with known concentrations of the different metabolites. All measurements lie within the linear range of the analytical method. Principal component analysis, ANOVA, and Fisher LSD analysis were performed in log transformed data using the free web-based statistical software MetaboAnalyst 5.0 ($p < 0.05$) (Pang *et al.*, 2021).

Accession numbers

The RNA-seq discussed in this publication have been deposited in NCBI's Gene Expression Omnibus (Edgar *et al.*, 2002) and are accessible through GEO Series accession number GSE186058 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE186058>).

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflict of interest.

AUTHOR CONTRIBUTIONS

A.P.A, L.M., and T.E.C. conceived and designed the project. H.N., M.G., and T.Q. designed and generated the transgenic events. T.Q. grew and analyzed the transgenic events in the field. A.M., A.R., and C.L.A. grew the plants under greenhouse conditions, collected the samples and performed the biomass, metabolomic and carbohydrate analysis. T.Q., T.H., and K.V. performed the RNA extraction from the field and greenhouse samples. T.H., Y.S., and C.Z. processed the RNAseq data. C.L.A., T.Q., T.H., and C.Z. contributed to data analysis, interpretation and drafted the manuscript. C.L.A., T.Q., T.H., C.Z., A.P.A, L.M., and T.E.C. reviewed and edited the document. All authors critically revised and agreed to the published version of the manuscript.

SHORT SUPPORTING MATERIALS LEGENDS

Table S1. Soybean field trials in 2018, 2019, and 2020 crop seasons in Nebraska fields.

Table S2. Total number of differential expressed genes for each transgenic event at each developmental stage.

Table S3. Complete list of putative *AtWRI1* targets.

Table S4. Metabolite concentrations.

Figure S1. T-DNA of plasmid pPTN1248 harboring a soybean codon-optimized *AtWRI1* transcription factor and *AtDGAT1* from Arabidopsis under control of the beta-conglycinin promoter.

Figure S2. Southern blot analysis of the transgenic soybean events expressing *AtWRI1* and *AtDGAT1*.

Figure S3. Wrinkled-seed phenotype.

Figure S4. DW, protein, FA and starch accumulation rates.

Figure S5. Accumulation of cell wall polysaccharides during development.

Figure S6. Rate of glucose accumulation as hemicelluloses in WD events.

Figure S7. Beta-conglycinin promoter pattern of expression.

Figure S8. DEGs in transgenic soybeans grown under greenhouse conditions.

Figure S9. Expression of *WRI1* and *DGAT1* from Arabidopsis and soybean in transgenic soybean grown under field conditions.

Figure S10. Differentially expressed genes in the field experiment and comparison with the greenhouse results.

Figure S11. Changes in lipid transfer protein and lipid degradation enzyme expression in WD events between 24 and 33 DAP under greenhouse conditions.

Figure S12. Principal component analysis and top fifteen changes in metabolites.

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FIGURE LEGENDS

Figure 1. Mature seed composition of soybean. Results from soybean grown under greenhouse conditions (a, d, e, f, g, and h) or in Nebraska fields in 2018 (b and c) are shown. With the exception of the FA composition that was expressed as a percentage of the total FA (a and b), all the other variables measured were expressed in % (mg/100mg DW). C16:0, C18:0, C18:1, C18:2, C18:3 correspond to palmitic, stearic, oleic, linoleic and linolenic acids, respectively. For all pairwise multiple comparison procedures, the Fisher LSD or Student-Newman-Keuls method was used as parametric or non-parametric tests, respectively. Error bars are the standard deviation of three or more biological replicates and the presence of an asterisk denotes a significant difference with the WT ($p < 0.05$). FA: Fatty acid. TAG: triacylglycerides. DW: Dry weight. WD-1 and -2: independent transgenic events expressing *AtWR1* and *AtDGAT1*.

Figure 2. DW, protein, FA, and starch accumulation during development. Results from soybean grown under greenhouse conditions. The embryo's DW (a), the content of FA (b), protein (c) and starch (d) are shown in % (mg /100mg DW). For all pairwise multiple comparison procedures Fisher LSD method or Student-Newman-Keuls method was used as parametric or non-parametric test,

respectively. Error bars are the standard deviation of four biological replicates and the presence of an asterisk denotes a significant difference with the WT ($p < 0.05$). DW: Dry weight. DAP: days after pollination. WD-1 and -2: independent transgenic events expressing *AtWRI1* and *AtDGAT1*.

Figure 3. Fatty acid composition during development. The content of each FA is expressed in relation to the total content of FA at each time point. C16:0, C18:0, C18:1, C18:2, C18:3 correspond to palmitic, stearic, oleic, linoleic and linolenic acids, respectively. For all pairwise multiple comparison procedures Fisher LSD method or Student-Newman-Keuls method was used as parametric or non-parametric test, respectively. Error bars are the standard deviation of four biological replicates and the presence of an asterisk denotes a significant difference with the WT ($p < 0.05$). FA: Fatty acid. DAP: days after pollination. WD-1 and -2: independent transgenic events expressing *AtWRI1* and *AtDGAT1*.

Figure 4. Expression of *WRI1* and *DGAT1* from *Arabidopsis* and soybean in the transgenic events grown under greenhouse conditions. The expression of the transgenes and endogenous versions are shown at four developmental points: 24, 27, 30, and 33 DAP. Error bars are the standard deviation of three biological replicates and the presence of an asterisk denotes a significant difference with the WT ($FDR < 0.05$). TPM, transcripts per million. DAP: days after pollination. WD-1 and -2: independent transgenic events expressing *AtWRI1* and *AtDGAT1*.

Figure 5. KEGG pathway enrichment and GO functional classification of differentially expressed genes in WD events grown in a greenhouse. Statistically significantly enriched ($FDR < 0.05$) KEGG pathways in (a) and Gene Ontology terms in (b) are shown for the DEGs identified at each developmental stage. Three GO categories are presented, including Biological Processes (BP), Cellular Compartment (CC), and Molecular Function (MF). The gene count represents the number of non-unique DEGs enriched in a pathway. The absence of a dot indicates the pathway was not significantly enriched in that developmental stage. Gene ratio was calculated as the number of DEGs involved in a pathway divided by the total number of soybean genes in the pathway. Enriched GO terms resulting from AgriGOv2 were consolidated into fewer non-redundant GO terms using Revigo (<http://revigo.irb.hr>) for visualization purposes in (B) ($FDR < 0.05$). DAP: days after pollination. TCA: tricarboxylic acid cycle.

Figure 6. Alteration of lipid biosynthesis in WD embryos between 24 and 33 DAP. Red and blue circles were used to account for significantly increased or decreased levels of each FA at each stage, respectively ($n=4$, $p < 0.05$). Red and blue boxes were used to show the significantly up- or down- regulated expression of each enzyme at each stage under greenhouse conditions, respectively ($n=3$, $p < 0.05$, $|\log_2(\text{Fold Change})| \geq 1$). The symbol # next to the corresponding enzyme number denotes the presence of the AW-box motif in the promoter of the enzyme's gene. ACP, plastidic acyl carrier protein; FAS, fatty acid synthase; pACC, heteromeric acetyl CoA carboxylase, biotin carboxylase subunit: (1.1) Glyma.05G221100 and (1.2) Glyma.08G027600, biotin carboxyl carrier protein: (2.1) Glyma.13G057400, (2.2) Glyma.18G265300 and (2.3) Glyma.19G028800, carboxyltransferase alpha subunit: (3.1) Glyma.18G195700, (3.2) Glyma.18G195900 and (3.3) Glyma.18G196000; BADCL, biotin/lipoyl attachment domain-containing protein: (4.1) Glyma.11G233700# and (4.2) Glyma.18G023300#; ACP, acyl carrier protein: (5.1) Glyma.13G214600#, (5.2) Glyma.15G098500 and (5.3) Glyma.20G230100; MCMT, malonyl-CoA: ACP malonyltransferase: (6) Glyma.11G164500; KASIII, ketoacyl-ACP synthase III: (7.1) Glyma.09G277400, (7.2) Glyma.15G003100 and (7.3) Glyma.18G211400#; KAR, ketoacyl-ACP reductase: (8.1) Glyma.11G248000 and (8.2) Glyma.18G009200; HAD, hydroxyacyl-ACP dehydrase: (9.1) Glyma.08G179900# and (9.2) Glyma.15G052500; ER, enoyl-ACP

reductase: (10.1) Glyma.08G345900#, (10.2) Glyma.12G027300, and (10.3) Glyma.18G156100; KASI, ketoacyl-ACP synthase I: (11.1) Glyma.05G129600#, (11.2) Glyma.08G024700# and (11.3) Glyma.08G084300#; SAD, stearoyl-ACP desaturase; FATA, fatty acyl thioesterase A; FATB, fatty acyl thioesterase B: (12) Glyma.04G151600#; pLACS, plastidic long-chain acyl- CoA synthetase: (13) Glyma.06G112900#; ACBP, acyl CoA binding protein: (14.1) Glyma.13G152900 and (14.2) Glyma.11G014900; ACCc, homomeric acetyl CoA carboxylase; FAE, fatty acid elongase; KCS, ketoacyl-CoA synthase: (15.1) Glyma.06G012500#, (15.2) Glyma.04G149300# and (15.3) Glyma.06G214800#; KCR, ketoacyl-CoA reductase: (16) Glyma.11G245600; DHAP, dihydroxyacetone phosphate; G3PDH, glycerol 3 phosphate dehydrogenase: (17.1) Glyma.19G053500, (17.2) Glyma.02G186600 and (17.3) Glyma.10G107100#; GPAT, glycerol-3-phosphate acyltransferase: (18) Glyma.20G070400; Lyso-PA, lysophosphatidic acid; LPAAT, 2-lysophosphatidic acid acyltransferase; PA, phosphatidic acid; PAP, phosphatidate phosphatase; DAG, diacylglycerol; TAG, triacylglycerol; DGAT, acyl-CoA: diacylglycerol acyltransferase; PDAT, phospholipid:diacylglycerol acyltransferase; PC, phosphatidylcholine; LPCAT, lysophosphatidylcholine acyltransferase; PLA, phospholipase A; erLACS, ER long-chain acyl- CoA synthetase: (19) Glyma.10G010800#; ACOS, acyl-CoA synthase: (20) Glyma.08G329700; FFA, free fatty acid; AtDGAT, transgen expressed (21); Oleosin: (22.1) Glyma.05G004300 and (22.2) Glyma.19G004800; and Caleosins: (23.1) Glyma.10G189900, (23.2) Glyma.20G200900, (23.3) Glyma.20G201000. DAP: days after pollination.

Figure 7. Carbon partitioning in WD embryos between 24 and 33 DAP. Metabolites and end products: red and blue circles were used to account for significantly increased or decreased levels of each metabolite at each stage, respectively ($n=4$, $p<0.05$) and a grey circle reflects data not measured. The contents of Glc1P are shown with an asterisk (*) as were determined together with the levels of mannose 1-phosphate. Sucrose6P, sucrose 6-phosphate; Trehalose6P, trehalose 6-phosphate; Glc, glucose; Fru, fructose; Glc6P, glucose 6-phosphate; Glc1P, glucose 1-phosphate; Fru6P, fructose 6-phosphate; Fru1,6BP, fructose 1,6-bisphosphate; UDP-Glc, UDP-glucose; ADP-Glc, ADP-glucose; 6PG, 6-phosphogluconate; Pentoses5P, pentoses 5-phosphate; DHAP, dihydroxyacetone phosphate; GAP, glyceraldehyde 3 phosphate; 1,3BPG, 1,3-bisphosphoglycerate; 2 and 3PG, 2-and 3-phosphoglycerate; PEP, phosphoenolpyruvate and PYR, pyruvate. Enzyme expression: red and blue boxes were used to show the significantly up- or down-regulated expression of each enzyme at each stage under greenhouse conditions, respectively ($n=3$, $p<0.05$). The enzyme names correspond to the specific homolog isoforms in Arabidopsis. The symbol # denotes the presence of the AW-box motive in the promoter of the enzyme's gene. INV, neutral invertase (1) Glyma.04G005700; C/VIF2, cell wall/vacuolar inhibitor of fructosidase 2 (2) Glyma.04G214000; SPS3F, sucrose phosphate synthase 3F (3) Glyma.18G108100; SuSy4, sucrose synthase 4 (4.1) Glyma.09G073600 and (4.2) Glyma.13G114000#; UGP2, UDP-glucose pyrophosphorylase 2 (5) Glyma.13G152500#; PGM2, phosphoglucomutase (6) Glyma.08G044100; APL2, ADP-glucose pyrophosphorylase large subunit (7) Glyma.14G072500#; HXK1, hexokinase 1 (8) Glyma.07G015100; PGI1, phosphoglucose isomerase 1 (9) Glyma.06G094300; G6PD2, glucose 6 phosphate dehydrogenase 2 (10.1) Glyma.02G096800 and (10.2) Glyma.18G284600; 6PGDH, 6-phosphogluconate dehydrogenase (11) Glyma.05G214000; PFK2, phosphofructokinase 2 (12) Glyma.07G269500#; PFK3, phosphofructokinase 3 (13) Glyma.13G353400#; PFK5, phosphofructokinase 5 (14.1) Glyma.08G280700 and (14.2) Glyma.18G145500; PFPβ1, pyrophosphate: fructose 6-phosphate 1-phosphotransferase (15) Glyma.18G135100; FBA3, fructose bisphosphate aldolase 3 (16.1) Glyma.10G268500 and (16.2) Glyma.20G122500#; GAPCP1, glyceraldehyde-3-phosphate dehydrogenase of plastid 1 (17) Glyma.03G092700#; GAPC1, glyceraldehyde 3 phosphate dehydrogenase C subunit 1 (18) Glyma.11G247600; ALDH11A3, NADP-dependent glyceraldehyde 3-phosphate dehydrogenase (19) Glyma.02G202500; ENO1, enolase 1 (20.1) Glyma.04G144300 and (20.2) Glyma.06G208200#; PK, pyruvate kinase family protein (21)

Glyma.19G190100;PKP α 1, plastidial pyruvate kinase 1 subunit alpha (22) Glyma.20G211200; PKP β 1, plastidial pyruvate kinase 1 subunit beta (23.1) Glyma.09G126300, (23.2) Glyma.10G227800#, (23.3) Glyma.16G173100#; PDH-E1 α , E1a component of pyruvate dehydrogenase complex (24.1) Glyma.03G261000#, (24.2) Glyma.16G018300, (24.3) Glyma.19G260000; PDH-E1 β , E1b component of pyruvate dehydrogenase complex (25.1) Glyma.05G141000, (25.2) Glyma.08G096300, (25.3) Glyma.14G092100, (25.4) Glyma.17G231400#; PDH-E2, E2 component of pyruvate dehydrogenase complex (26.1) Glyma.10G215400#, (26.2) Glyma.20G176300, (26.3) Glyma.01G081900#, (26.4) Glyma.20G114500# and PDH-E3, E3 component of pyruvate dehydrogenase complex (27.1) Glyma.15G143100, (27.2) Glyma.07G241600, (27.3) Glyma.17G032300.

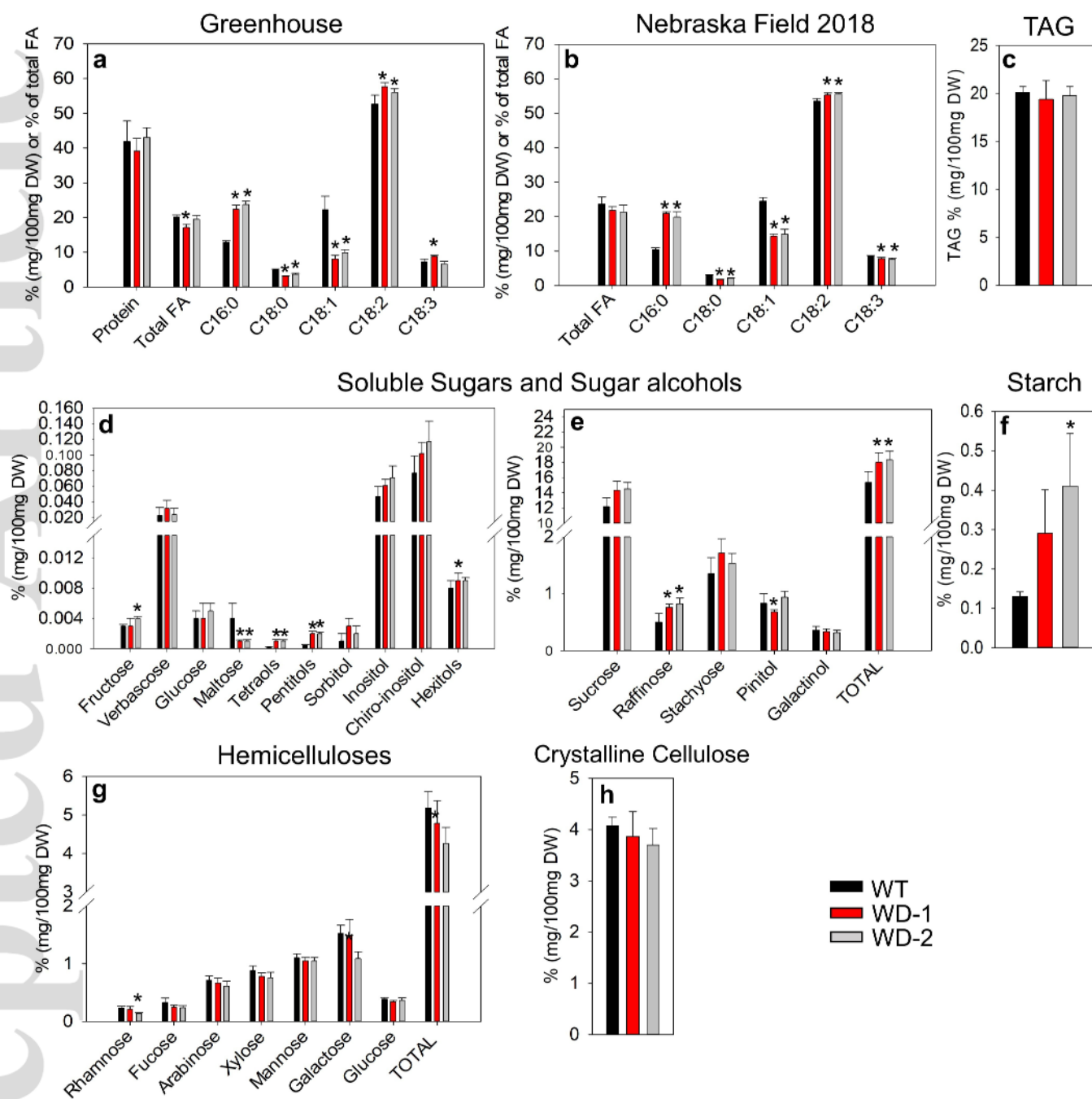
TABLES

Table 1. Putative WRI1 targets.

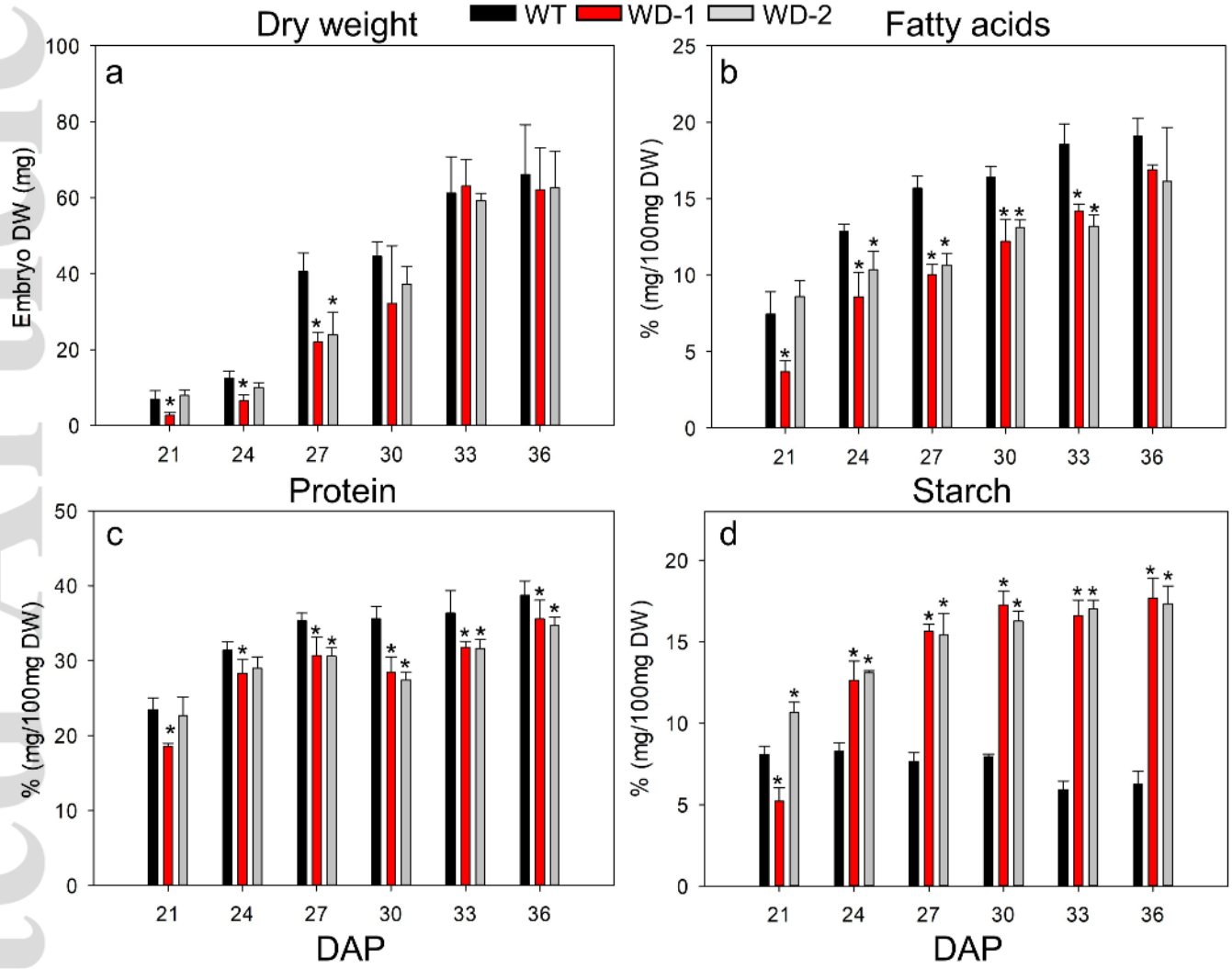
Line	log ₂ FC_ Greenhouse												log ₂ FC_Field						PCC	Top Arabidopsis BLASTP Hit	ATH hit Annotations																	
	WD	WD	WD	WD	WD	WD	WD	WD	WD	WD	WD	WD	WD	WD	WD	WD	WD	WD				WD	WD	WD														
	-1	-2	-1	-2	-1	-2	-1	-2	-1	-2	-1	-2	-1	-2	-1	-2	-1	-2				-1	-2	-1														
geneID	24 DAP	27 DAP	30 DAP	33 DAP	R5	R5/6	R6	R5	R6	R5/6	R5	R6	R5/6	R6	AW site	ATWR11	AT5G52920	AT3G56130	AT5G64440	AT5G43940	AT2G34590	AT5G46290	AT1G62640	AT1G80280	AT2G01140	AT2G22230	AT3G25860	AT1G61800	AT5G13710	AT2G26640	AT5G17310	AT1G79530	AT3G12110	AT2G26640	AT5G64440	AT3G56130	AT1G34430	AT3G28345
Glyma.16G173100	1.5	1.3	2.1	2.1	2.4	2.1	2.3	2.2	1.7	2.1	2.0	2.1	2.0	2.1	526	0.99	Pyruvate kinase beta subunit 1																					
Glyma.18G023300	1.2	1.1	1.9	2.1	1.8	2.0	1.9	1.4	1.7	1.7	1.6	1.7	1.6	1.7	913	0.99	Biotin/lipoyl attachment domain-containing protein																					
Glyma.05G195500	4.4	4.5	4.1	4.7	4.5	4.8	4.7	4.3	2.5	4.0	2.5	4.0	2.5	4.0	1089	0.98	Fatty acid amide hydrolase																					
Glyma.03G168700	1.4	1.2	1.4	1.7	1.3	1.4	1.8	1.1	1.7	1.7	1.9	1.7	1.9	1.7	1896	0.98	Alcohol dehydrogenase 2																					
Glyma.17G231400	1.3	1.1	1.8	2.0	1.7	1.7	1.8	1.1	1.8	1.8	1.9	1.8	1.9	1.8	1608	0.97	Pyruvate dehydrogenase 1b																					
Glyma.08G024700	2.0	2.1			4.9	1.6	3.5	2.7	4.8	4.8	1.8	4.8	1.8	1.8	1876	0.97	Ketoacyl-ACP Synthase I																					
Glyma.18G211400	1.2		1.8	1.8	1.8	1.7	1.8	1.2	1.6	1.6	1.6	1.6	1.6	1.6	2	0.96	Ketoacyl-ACP synthase III																					
Glyma.07G033000	1.0		1.2	1.2	1.6	1.3	1.4		2.4	2.4	2.2	2.4	2.2	2.2	1587	0.96	Alpha/beta-hydrolases																					
Glyma.20G122500	1.1	1.1	1.5	1.6	1.3	1.4	1.8	1.2	1.7	1.7	1.6	1.7	1.6	1.7	586	0.96	Fructose biphosphate aldolase 3																					
Glyma.08G179900	1.4	1.1	1.9	1.9	2.1	2.2	2.3	1.6	1.7	1.7	1.7	1.7	1.7	1.7	306	0.96	Hydroxyacyl-ACP dehydrase																					
Glyma.01G081900	3.1	2.6	5.0	4.9	5.0	4.8	6.0	5.3	1.7	4.0	1.8	4.0	1.8	4.1	1552	0.95	Pyruvate dehydrogenase E2																					
Glyma.17G015500	1.9	1.6	2.9	2.8	2.9	2.8	3.2	2.2	1.1	3.9	1.1	3.9	1.1	4.1	244	0.95	Glucose 6 phosphate/phosphate translocator 2																					
Glyma.15G276300			1.6	1.8	1.4	1.6	1.6	1.1	1.2	1.2	1.2	1.2	1.2	1.2	405	0.95	Sterol methyltransferase 1																					
Glyma.06G214800	1.3	1.1	1.7	1.6	1.8	1.7			3.0	3.0	3.0	3.0	3.0	3.0	1890	0.95	Ketoacyl-CoA synthase 11																					
Glyma.13G152500	1.0		1.3	1.5	1.1	1.3	1.5	1.2	1.6	1.6	1.5	1.6	1.5	1.5	1971	0.95	UDP-glucose pyrophosphorylase 2																					
Glyma.03G092700			1.2	1.3	1.3	1.5	1.4	1.1	1.4	1.4	1.6	1.4	1.6	1.6	58	0.94	Glyceraldehyde-3-phosphate dehydrogenase 1																					
Glyma.05G000900	1.1		1.9	1.8	1.7	1.6	1.8	1.2	1.7	1.7	1.6	1.7	1.6	1.6	1613	0.94	Actin 11																					
Glyma.04G149300	1.6	1.4	2.3	2.3	2.7	3.1			2.9	2.9	2.7	2.9	2.7	2.7	104	0.94	Ketoacyl-CoA synthase 11																					
Glyma.08G003100	3.8	3.9	3.5	4.3	3.9	4.3	4.6	4.6	1.6	3.6	3.0	3.6	3.0	4.7	936	0.94	Fatty acid amide hydrolase																					
Glyma.11G233700			1.1	1.3	1.0	1.2	1.3		1.2	1.2	1.5	1.2	1.5	1.5	800	0.93	Biotin/lipoyl attachment domain-containing protein																					
Glyma.10G215400	1.1		1.8	1.7	2.0	1.9	1.8	1.2	1.6	1.6	1.6	1.6	1.6	1.6	121	0.93	Pyruvate dehydrogenase E2																					
Glyma.12G135300	3.6	3.3	3.9	4.1	4.2	4.4	4.2	3.8	1.7	5.0	2.2	5.0	2.2	4.9	1921	0.92	ABC transporter																					

Glyma.01G190600	1.4	1.3	1.2	1.3	1.8	1.7	1.8	2.4	1.8	1909	0.92	AT2G14960	Auxin-responsive GH3 family protein
Glyma.04G151600	1.2	1.3	1.5	2.0	1.6	2.0	2.2	2.2	2.3	163	0.92	AT1G08510	Acyl-ACP thioesterase B
Glyma.20G114500	1.2	2.0	2.0	1.7	2.0	1.7	2.0	1.1	1.6	1736	0.92	AT3G25860	Pyruvate dehydrogenase E2
Glyma.15G178400	1.0	1.3	1.7	1.7	1.4	1.4	1.4	1.3	1.6	1895	0.92	AT1G54100	Aldehyde dehydrogenase 7B4
Glyma.08G164600	1.5	1.5	2.2	2.1	2.5	2.7	3.1	2.0	2.9	1834	0.91	AT3G04940	Cysteine synthase D1
Glyma.15G182900	4.7	5.4	5.8	7.1	5.1	6.3	5.7	5.8	3.5	95	0.91	AT1G53920	GDSL-motif lipase 5
Glyma.05G026300	1.0		1.2	1.0	1.3	1.2	1.4		1.0	437	0.90	AT3G47520	NAD dependent malate dehydrogenase
Glyma.06G112900			1.2	1.0	1.4	1.3	1.4		1.1	1379	0.90	AT1G77590	Long chain acyl-CoA synthetase 9
Glyma.15G183000	1.5	1.7	3.1	3.9	2.7	3.8	3.5	3.5	3.9	75	0.90	AT1G53920	GDSL-motif lipase 5
Glyma.07G268100	1.0		1.2	1.4	1.2	1.2	1.3		1.3	1981	0.90	AT5G47670	LEC1-LIKE, NF-YB6,nuclear factor Y,
Glyma.06G087100	1.4	1.0	1.6	1.9	1.4	1.7	2.1	1.6	2.3	495	0.89	AT5G11650	Monoacylglycerol lipase
Glyma.19G206100	3.1	2.6	2.9	3.3	3.0	3.3	3.8	3.6	2.2	211	0.89	AT5G62000	Auxin response factor 2
Glyma.13G223800	2.4	2.4	2.8	2.5	2.4	1.9	2.2	1.3	2.5	687	0.89	AT1G69850	Nitrate transporter, ABA importer transporter 1
Glyma.09G074000	5.2	5.9	5.3	6.7	5.1	6.4	5.8	6.4	4.4	1936	0.89	AT1G53920	GDSL-motif lipase 5
Glyma.08G159500	1.0		1.9	1.5	2.0	2.0	2.2	1.8	1.7	1814	0.88	AT1G05590	Beta-hexosaminidase 2
Glyma.06G312200			1.3	1.5	2.0	2.4	2.0	2.3	1.1	483	0.87	AT1G65440	Global transcription factor group B1
Glyma.07G027000	1.2		1.7	2.3	1.5				2.2	785	0.87	AT1G80580	Ethylene-responsive transcription factor
Glyma.01G198700	1.3		2.0	1.8	1.6	1.8	1.8	1.2	1.4	124	0.86	AT4G17810	C2H2 domain regulatory protein

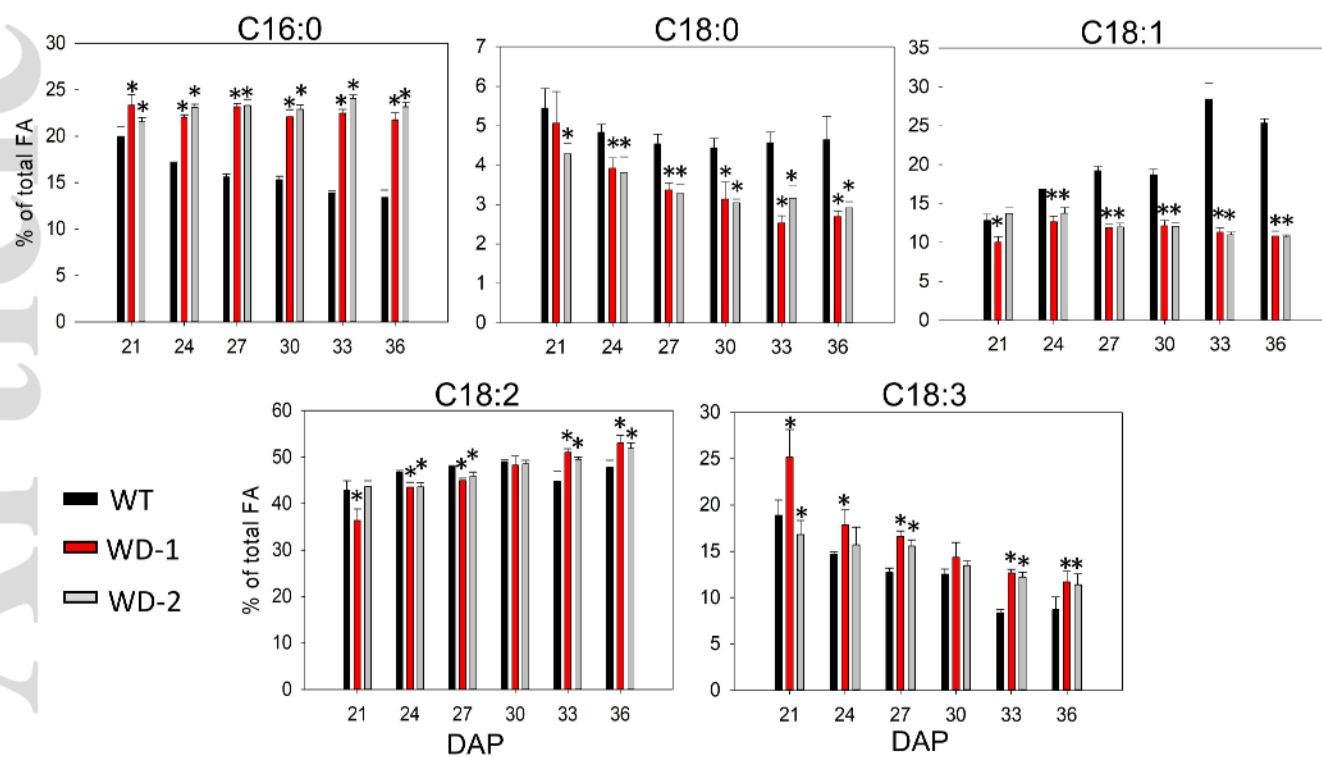
Only genes with a significantly different expression and a $|\log_2(\text{Fold Change})| \geq 1$ with respect to the WT were included. PCC, Pearson correlation coefficient. DAP: days after pollination. WD-1 and -2: independent transgenic events expressing *AtWRI1* and *ATDGATI1*. W-1 event expressing only *AtWRI1* (Vogel *et al.*, 2019)



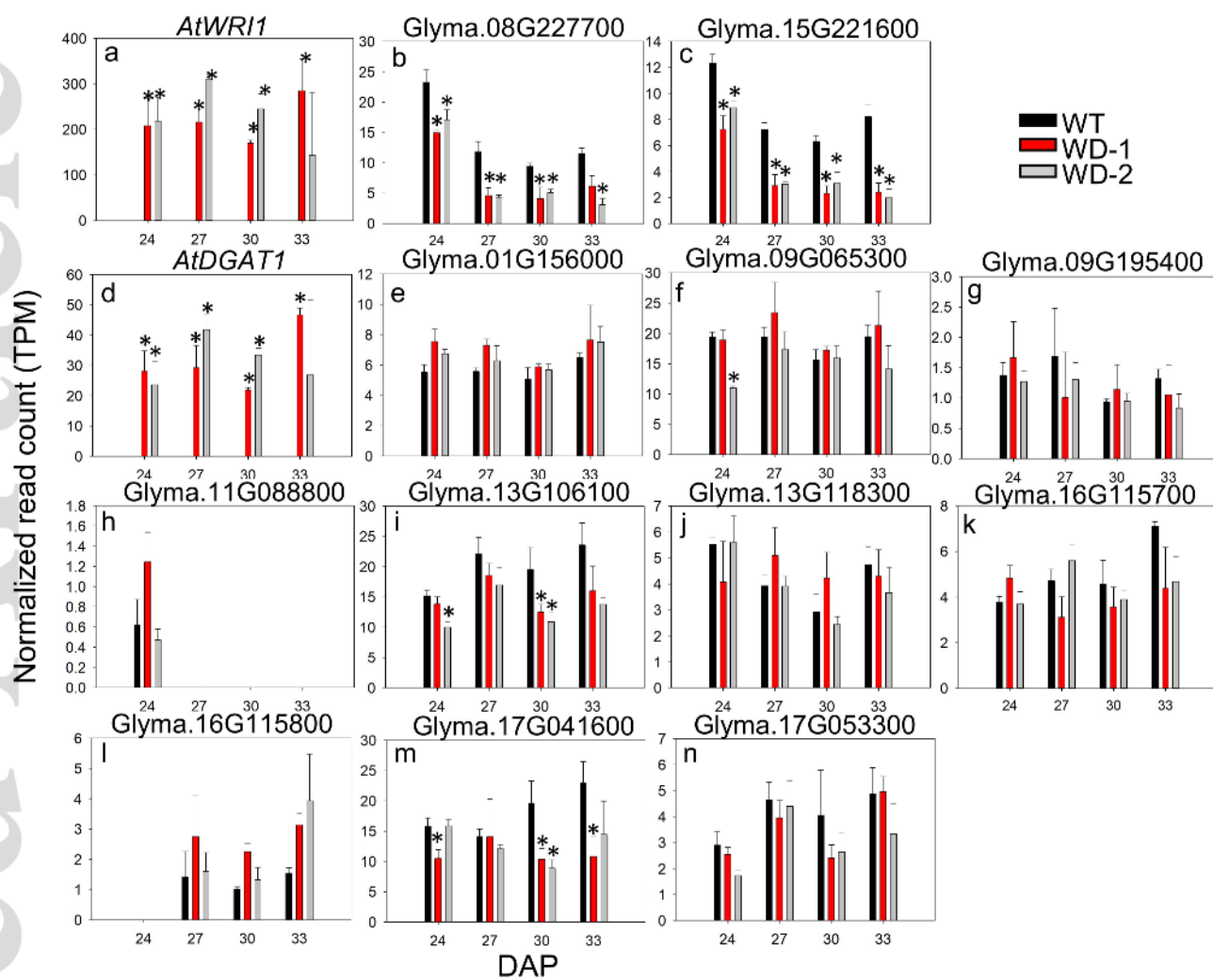
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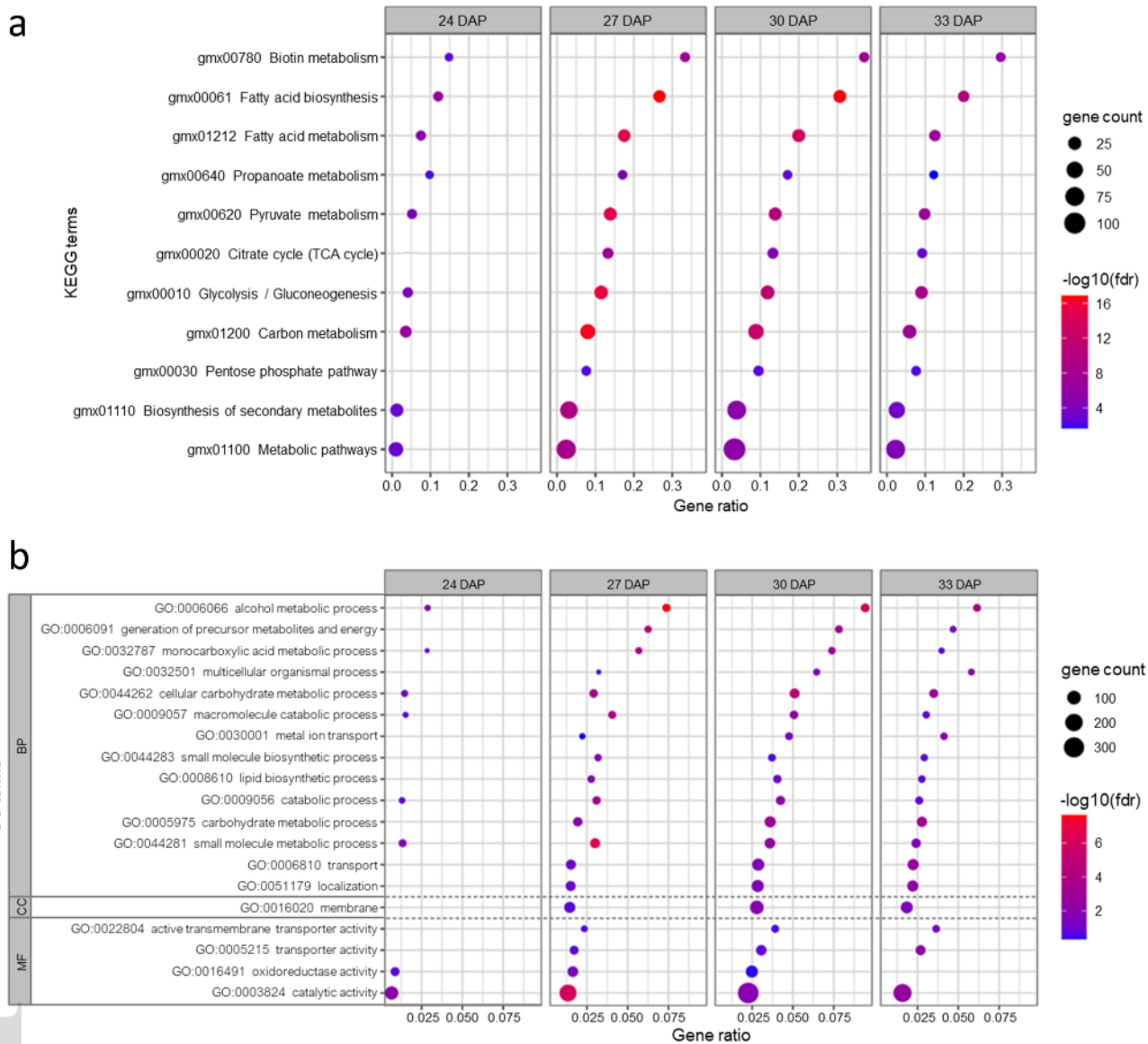
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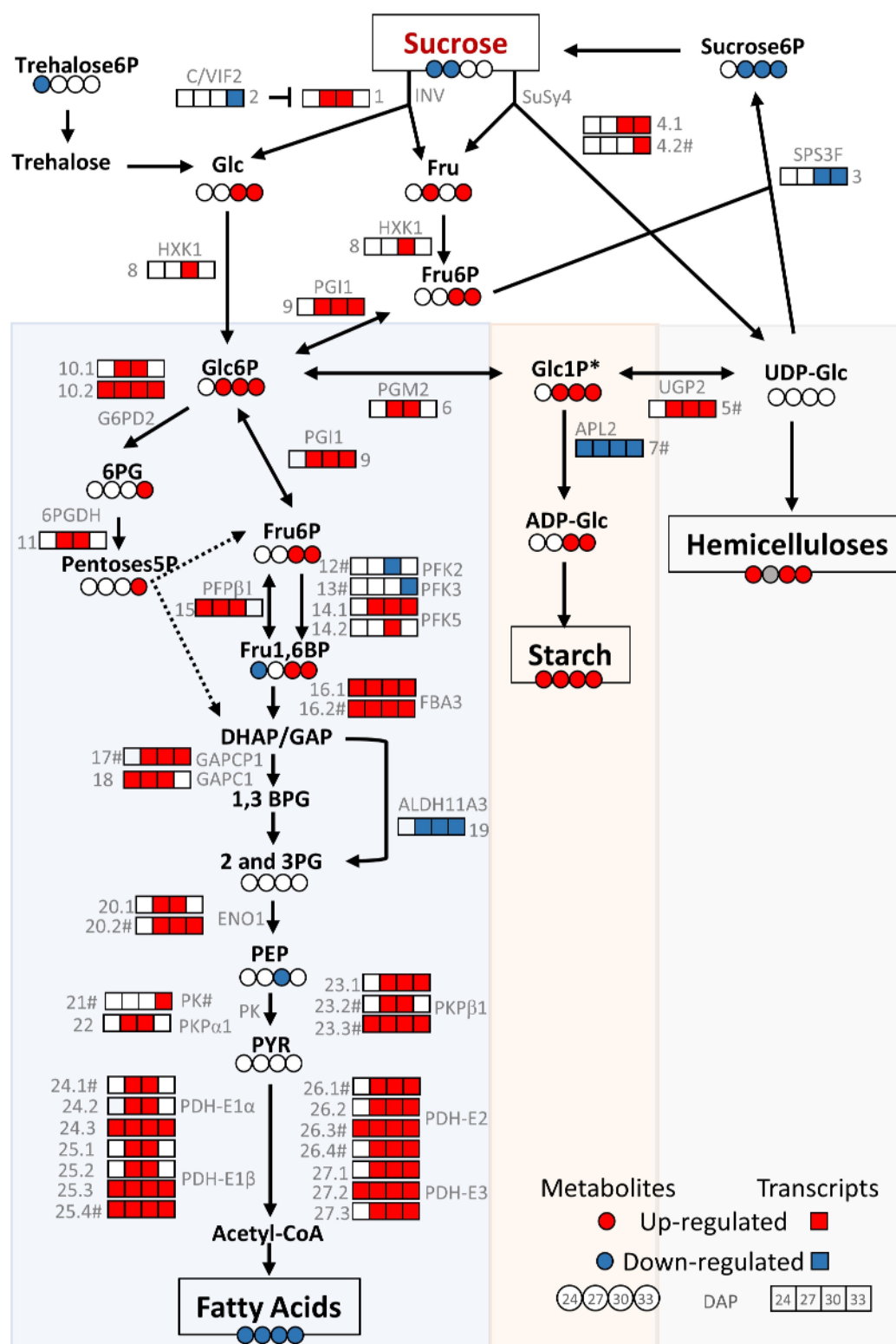
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