Deciphering Transcriptional and Metabolic Networks Associated with Lysine Metabolism during Arabidopsis Seed Development[1][C][W][OA]

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In order to elucidate transcriptional and metabolic networks associated with lysine (Lys) metabolism, we utilized developing Arabidopsis (*Arabidopsis thaliana*) seeds as a system in which Lys synthesis could be stimulated developmentally without application of chemicals and coupled this to a T-DNA insertion knockout mutation impaired in Lys catabolism. This seed-specific metabolic perturbation stimulated Lys accumulation starting from the initiation of storage reserve accumulation. Our results revealed that the response of seed metabolism to the inducible alteration of Lys metabolism was relatively minor; however, that which was observable operated in a modular manner. They also demonstrated that Lys metabolism is strongly associated with the operation of the tricarboxylic acid cycle while largely disconnected from other metabolic networks. In contrast, the inducible alteration of Lys metabolism was strongly associated with gene networks, stimulating the expression of hundreds of genes controlling anabolic processes that are associated with plant performance and vigor while suppressing a small number of genes associated with plant stress interactions. The most pronounced effect of the developmentally inducible alteration of Lys metabolism was an induction of expression of a large set of genes encoding ribosomal proteins as well as genes encoding translation initiation and elongation factors, all of which are associated with protein synthesis. With respect to metabolic regulation, the inducible alteration of Lys metabolism was primarily associated with altered expression of genes belonging to networks of amino acids and sugar metabolism. The combined data are discussed within the context of network interactions both between and within metabolic and transcriptional control systems.

Metabolism is one of the most important and best recognized networks within biological systems. However, advances in the understanding of metabolic regulation still suffer from insufficient research concerning the modular operation of such networks. Furthermore, elucidation of metabolic regulation within the context of the entire system, including transcriptional, translational and posttranslational mechanisms, is rarely attempted (Sweetlove et al., 2008). Instead, to date, studies on metabolic regulation have mostly been limited to regulatory interactions within the metabolic pathways themselves. These studies have revealed, among other things, that amino acid biosynthesis generally occurs through branched pathways, which are considerably more complex than the nonbranched pathway of glycolysis (Sweetlove and Fernie, 2005; Sweetlove et al., 2008). Of the pathways associated with plant amino acid metabolism, studies of the branched Asp family pathway involved in the synthesis of Lys, Met, Thr, and Ile as well as the conversion of Thr into Gly (Fig. 1) led to a considerable understanding of the intrapathway regulation of the synthesis of these amino acids as well as the interregulation of Asp and Glu metabolism (Karchi et al., 1994; Galili, 2002; Zhu and Galili, 2003, 2004; Joshi et al., 2006; Stepansky et al., 2006; Less and Galili, 2009). Lys metabolism was also shown to be regulated by both the rate of its synthesis and its catabolism via the α-amino adipic acid pathway (Zhu and Galili, 2004; Less and Galili, 2009). In addition, two genes associated with the response of plants to biotic stresses

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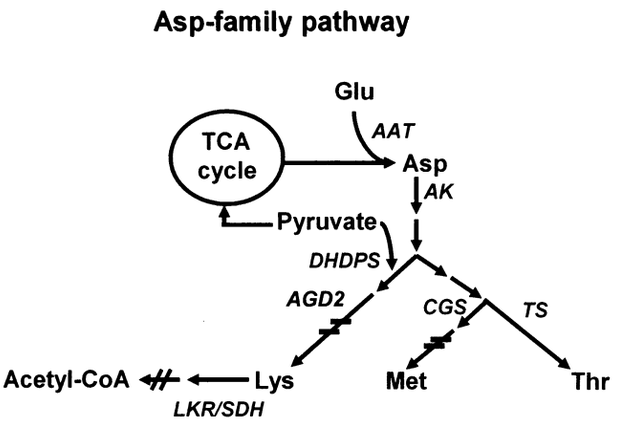

Figure 1. A schematic diagram of the Asp family pathway. Only several enzymes are illustrated. Broken arrows represent several enzymatic steps. Abbreviations not defined in the text: AAT, Asp aminotransferase; AK, Asp kinase; CGS, cystathionine γ-synthase; TS, Thr synthase.

have been shown to encode enzymes of Lys biosynthesis (AGD2) and likely also catabolism (ALD1) into a yet unknown compound, important for pathogen resistance (Song et al., 2004a, 2004b). Notwithstanding the significant complexity of the pathway of Lys metabolism in plants, remarkably little is known concerning the influence of this pathway on genome-wide patterns of gene expression or of its impact on primary metabolism as a whole.

Developing seeds can serve as an excellent system for studying developmentally controlled metabolic regulation within a broad context, including both metabolic and transcriptional parameters alongside their associated networks (Sweetlove and Fernie, 2005). Seed development initiates by embryogenesis and is followed by a period characterized by highly active sugar, amino acid, and lipid metabolism (Weber et al., 2005). During this metabolically active period, developing seeds also induce a massive synthesis of reserve compounds, including storage proteins, starch, and oil, whose relative proportions vary between seeds of different plant species (Weber et al., 2005; Gallardo et al., 2008). Furthermore, the synthesis of seed storage proteins is entirely seed specific, occurring via a strict seed-specific stimulation of expression of a family of genes encoding the different groups of storage proteins (Verdier and Thompson, 2008). In fact, the induction of expression of the storage protein genes is very fast, initiating from nondetectable levels at the initiation of the period of storage reserve accumulation and reaching massive amounts of both storage protein mRNAs and storage proteins themselves in a relatively short time period of up to a few days (Verdier and Thompson, 2008). This renders developing seeds as an excellent developmentally inducible system in which to study metabolic regulation.

We have previously generated transgenic Arabidopsis (*Arabidopsis thaliana*) plants expressing a bacterial feedback-insensitive dihydrodipicolinate synthase (DHDPS) of Lys biosynthesis under a seed-specific storage protein promoter and crossed these transgenic plants with a T-DNA knockout mutant in the *LKR/SDH* (for Lys-ketoglutarate reductase/saccharopine dehydrogenase) gene of Lys catabolism (Zhu and Galili, 2003). This crossed transgenic genotype (termed the "KD" genotype) possesses a highly efficient, developmentally induced accumulation of Lys, initiated at the start of the period of reserve accumulation (Zhu and Galili, 2003). In this study, we have subjected developing seeds of this KD genotype to detailed transcriptomics, metabolomics, and bioinformatics analyses to decipher how Lys metabolism cross-interacts with primary metabolism as well as genome-wide gene expression programs. Our results revealed a strong connection between Lys metabolism and the tricarboxylic acid (TCA) cycle and also shed new light on the modular operation of plant metabolism. They also suggest that Lys metabolism has a relatively small impact on the network of primary metabolism but, in contrast, has surprisingly wide impact on specific genome-wide gene expression networks.

RESULTS

A Seed-Specific Developmentally Inducible System to Decipher Gene Expression and Metabolic Networks Associated with Lys Metabolism

In order to elucidate novel network interactions of Lys metabolism with genome-wide gene expression programs and networks of primary metabolism, we utilized an Arabidopsis mutant (termed KD; Zhu and Galili, 2003) displaying a seed-specific, developmentally induced bacterial feedback-insensitive DHDPS enzyme of Lys biosynthesis in addition to a T-DNA knockout mutation in the *LKR/SDH* gene affected in Lys catabolism (Zhu and Galili, 2003). Maturing seeds of the wild-type and KD genotypes showed comparable morphologies across seed development (Fig. 2A) as well as efficient developmental induction of the bacterial DHDPS from negligible levels at approximately 10 d after flowering (DAF) to high expression levels during the later stages of seed maturation (Fig. 2B). Metabolic analysis also showed a developmentally inducible accumulation of Lys from approximately 10 DAF to mature dry seeds (Fig. 2C), proving the functionality of our genetic system in altering the flux of Lys metabolism.

Effect of the Developmentally Inducible Alteration of Lys Metabolism on Primary Metabolism during Seed Maturation

To study the effect of altered Lys metabolism on networks of primary metabolism, maturing seeds of the wild-type and KD genotypes were profiled using an established gas chromatography-mass spectrometry (GC-MS) protocol (Roessner et al., 2001), which

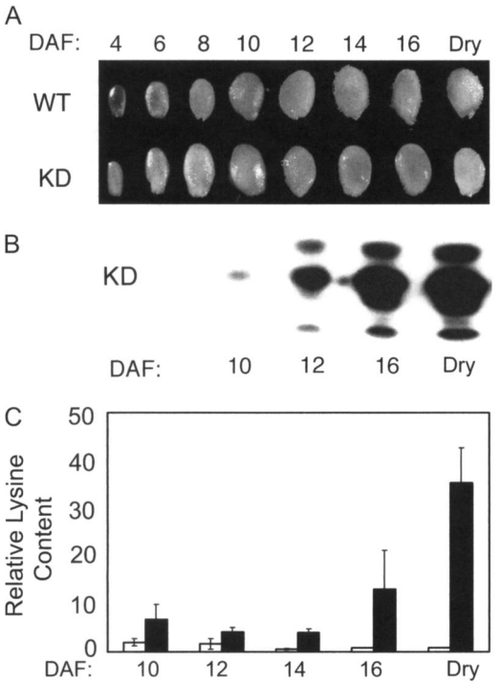

Figure 2. Effects of altered Lys metabolism in the KD genotype on seed maturation and free Lys level. The developmental stages of seed maturation are marked by DAF, while mature dry seeds are designated "Dry." A, Morphology of maturing seeds of the wild-type (WT; top) and KD (bottom) gentotypes. B, Immunoblot analysis with antibacterial DHDPS antibodies showing the level of expression of the bacterial DHPS during seed maturation in the KD genotype. C, Relative Lys level in the wild-type and KD genotypes at different stages of seed maturation. Values represent means of the response of the metabolite, expressed as peak area normalized to the internal standard ribitol as well as to dry weight. The relative metabolite levels of the wild-type and KD genotypes along the different stages of seed maturation in DAF are illustrated by white and black histograms, respectively. Error bars represent SE values of four biological replicates grown together, each derived from 5 mg of isolated lyophilized seeds, bulked from at least 10 plants for each time point. [See online article for color version of this figure.]

allowed us to quantify the relative content of over 70 metabolites (for details, see "Materials and Methods"). Since environmental differences can have a great impact on metabolite content, GC-MS analysis was performed on two independently grown and sampled seed batches. However, although these data confirm the consistency across experiments and the full data set is supplied in Supplemental Tables S1 and S2, here, for the sake of simplicity, we present the analysis of a single experiment. In the case of specific metabolites, we focused on those that were significantly different between the wild-type and KD genotypes in both experiments when assessed by a two-way ANOVA (for details, see "Materials and Methods"; Supplemental Table S3) and that displayed similar patterns of change in both experiments. When analyzing the global trends of changes of metabolites in developing seeds by principal component analysis (PCA), the wild-type and KD genotypes exhibited comparable changes in the metabolic profile, implying a relatively small effect of the genetic manipulations exhibited by KD on primary metabolism (Supplemental Fig. S1). Interestingly, we observed a major switch in metabolism during desiccation in both genotypes (transition from 16 DAF to dry seeds; Supplemental Fig. S1), which is in accordance with our previous report (Fait et al., 2006). These lines of evidence further demonstrate that the KD seeds exhibit mainly a wild-type-like metabolism throughout seed development.

In order to gain a higher resolution of the metabolic changes than that available following global PCA analysis, we next tested the effect of the KD mutation on the levels of the independent metabolites detected by the GC-MS analysis. Surprisingly, as shown in Figure 3, the two-way ANOVA indicated that among the approximately 70 metabolites identified in the GC-MS analysis, the levels of only four metabolites were consistently different between genotypes across seed maturation, implying a relatively minor interaction of Lys metabolism with primary metabolism. Interestingly, three of these metabolites (fumarate, citrate, and 2-oxoglutarate; Fig. 3, A–C) are TCA cycle intermediates, suggesting a strong interaction of Lys metabolism with mitochondrial energy metabolism.

Effect of the Developmentally Inducible Alteration of Lys Metabolism on Metabolic Networks in Seeds

Despite the importance of metabolism in the regulation of plant growth, the structure and dynamics of the metabolic networks in plants have received relatively little attention to date, with only a handful of studies focusing on this aspect (Weckwerth et al., 2004;

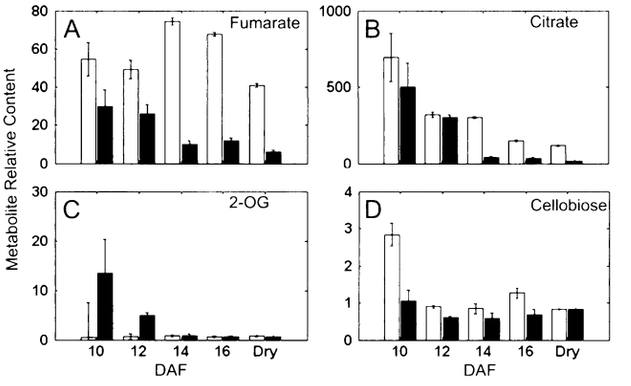

Figure 3. Relative contents of the four metabolites whose levels were altered significantly in maturing seeds of the KD genotype compared with the wild type. Comparable results were obtained in both growing times. The names of the metabolites are given in A to D. The relative metabolite levels in the wild-type and KD genotypes along the different stages of seed maturation in DAF are illustrated by white and black histograms, respectively. Error bars represent SE. Relative values were analyzed as described in the legend of Figure 2.

Schauer et al., 2006, 2008; Sulpice et al., 2009). The mode of interaction between metabolites can provide important insight into the modular behavior of biochemical processes and their regulation (Camacho et al., 2005; Steuer et al., 2006). Therefore, we were interested to study whether the perturbation of Lys metabolism influences the association of individual metabolites and/or of groups of metabolites within developing seeds. Examination of the metabolite correlation networks was performed exactly as described in "Materials and Methods," following the method of Nikiforova et al. (2005). A matrix of Spearman correlation coefficients was independently constructed for each genotype and was subsequently filtered using a common significance threshold of 10^{-9}. A strict threshold was chosen because of the highly synergistic behavior of all metabolites in the analyzed data sets. The obtained adjacency matrix was used to create a so-called community-based network, in which metabolites are represented as nodes and significant correlations are represented as lines (edges) that connect the nodes (detailed in "Materials and Methods"; Newman, 2006). We first built the metabolic network of the wild-type genotype in which we identified the number and composition of groups (communities) of associated metabolites (Fig. 4A, five circles of metabolites having different colors; Table I, columns 1–5). Network analysis emphasized links both between and within the various compound classes of metabolites detected. For example, the amino acids measured in the wild-type genotype split into three separate communities, of which only one consists exclusively of amino acids, although it is important to note that the amino acids in this community are not necessarily synthesized from the same metabolic pathway (Table I). Several sugars and organic acids grouped to the same community (community 5; Table I), while fatty acids grouped to a separate community (community 3; Table I). TCA cycle intermediates, however, were scattered across the different communities, although this may well reflect the complexity of their subcellular compartmentation (Winter et al., 1993; Martinoia and Rentsch, 1994). We next constructed the metabolic network of the KD genotype in the exact same way (Fig. 4B). Interestingly, the wild-type and KD genotypes differed in the metabolites making up each community (Tables I and II; Fig. 4). For example, the amino acids that composed community 2 in the wild type grouped in the KD genotype into two different communities, community 2 and community 4, which consisted not only amino acids but also sugars, sugar phosphates, and organic acids.

In order to highlight both commonalties and diversities in network topologies of the genotypes (Fig. 4, A and B), we also merged the networks of the wild-type and KD genotypes (Fig. 4C). In the resultant union network, different node colors represent the different wild-type communities (as displayed in Fig. 4A), while the graphic grouping of the nodes into different circles represents the different KD communities (Fig. 4B). This graphic reveals considerable scattering of nodes of identical colors across the combined network of Figure 4C, indicating the degree of network perturbation caused by Lys accumulation in the KD mutation during seed development. Although the major structure of metabolite-metabolite associations was conserved in the two genotypes (indeed, a highly significant overlap between the mutant and wild-type networks was confirmed by application of the Fisher exact test at $P = 0.00001$), the KD genotype revealed markedly higher connectivity than the wild-type genotype (see correlation matrices visualized in Fig. 4). Comparative network analysis also suggested that the effect of the KD genotype on the associations between metabolites within the different communities was largely modular. Namely, specific metabolites formed more robust associations by preserving their links, but grouping linked metabolites into different communities in the two genotypes (comparison between Fig. 4, A and B, is shown in Table II). These groups, therefore, can be regarded as basic metabolic modules (Table II; Fig. 4B). As would be expected, some modules contained metabolites belonging to the same biochemical pathway; for example, module 6 contains sugars and sugar alcohols and module 1 contains intermediates in fatty acid biosynthesis (Table II). Surprisingly, among the TCA cycle metabolites, only succinate and 2-oxoglutarate maintained their associations between genotypes, while other TCA cycle intermediates such as γ-aminobutyrate (GABA), citrate, and fumarate did not display modular behavior. This is likely due, at least in part, to the complex subcellular distribution of the GABA, citrate, and fumarate. Within the amino acids, two different modules could be observed: the first included Asn, Ile, and Ser (Table II, module 5), while the second contained Phe, Gly, and Glu (Table II, module 8). Thus, while the KD genotype neither displays a prominent effect on the levels of the different metabolites detected in the GC-MS analysis nor on the global structure of the metabolic network of developing seeds, it does change specific associations between metabolites or modules thereof. Finally, the alteration of Lys content in the KD genotype resulted in the formation of Lys-containing associations. For example, Lys strongly associated with Ala, fatty acids, and Gln in the KD genotype.

Effect of the Developmentally Inducible Alteration of Lys Metabolism on Gene Expression Networks in Developing Seeds

We were also interested in studying the regulatory role of Lys metabolism in the context of the entire system, namely, elucidating the inducible effect of altered Lys metabolism in the KD genotype on networks of gene expression. For this purpose, we performed microarray analysis of developing seeds (stages 14 DAF, 16 DAF, and dry seeds) of the wild-type and KD genotypes using the Affymetrix AtH1 chips. ANOVA of the microarray results indicated that

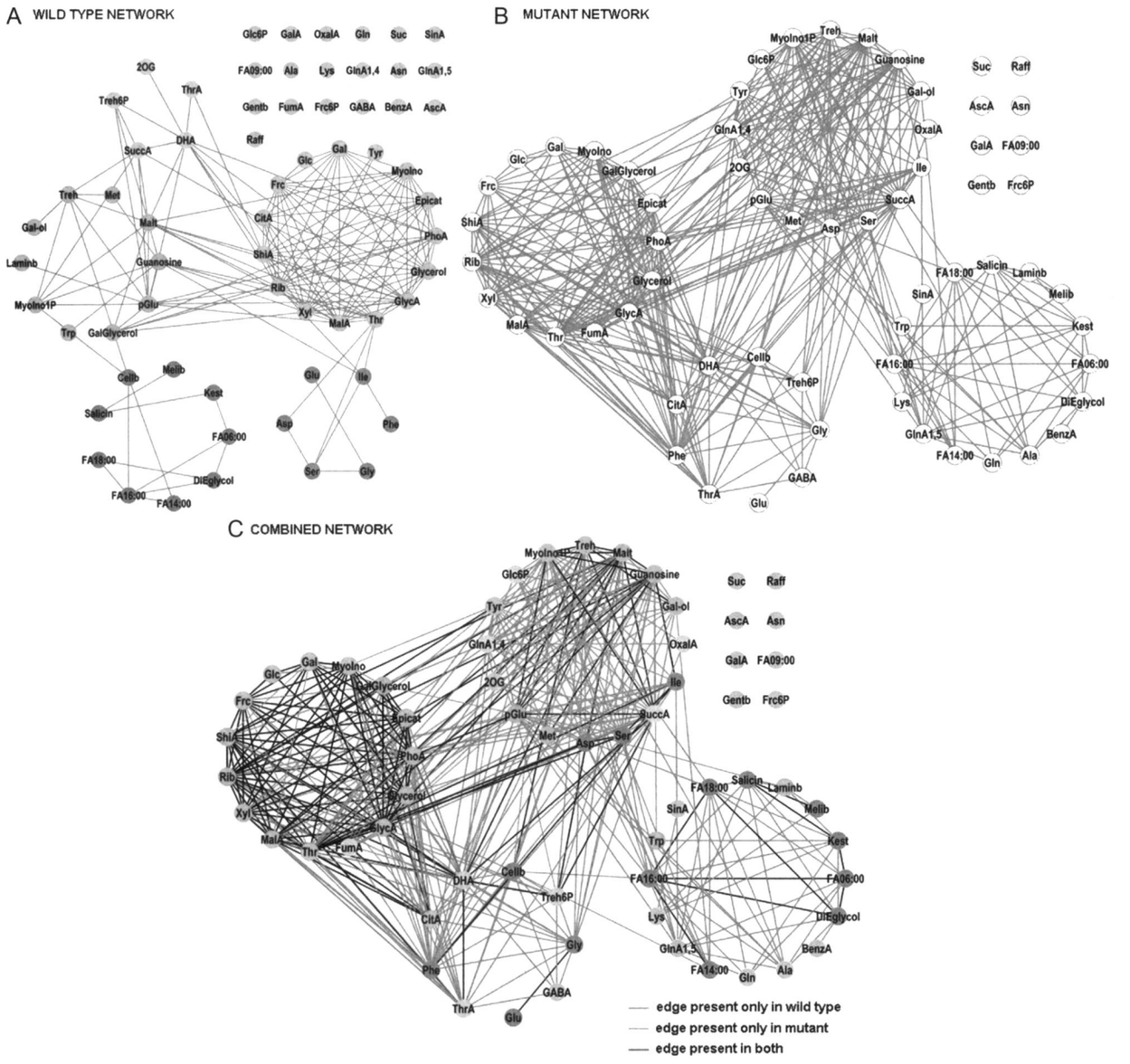

Figure 4. Network interactions between different metabolites during seed maturation in the wild-type and KD genotypes. A and B, Metabolites were grouped into five distinct communities in the wild-type genotype (A) and four distinct communities in the KD genotype (B). C, The merge of the networks visualization based on their coordinated levels during seed maturation of the KD genotype is represented by different colors for the different metabolites, each color representing a defined community in the wild-type genotype metabolic network. The edges (lines) connecting two nodes represent a significant correlation between metabolites: black when it occurs in both genotypes, blue when it occurs in the wild-type genotype and fails in the KD genotype, and red when it occurs in the KD genotype but is absent in the wild-type genotype. Metabolites abbreviations are provided in Supplemental Table S8. [See online article for color version of this figure.]

the expression of approximately 1,400 genes showed a significant and at least 2-fold change between the wild-type and KD genotypes in at least one time point during seed development, with a false discovery rate < 0.05 (Supplemental Table S4). We further identified the genes that were consistently up-regulated (650) and down-regulated (507) across all time points and subjected them to overrepresentation analysis using the tools embedded in the PageMan and MapMan software tools (http://mapman.mpimpgolm.mpg.de/general/ora/ora.shtml; Usadel et al., 2006). For a detailed probe set list and calculated ratios, see Supplemental Table S7. The major effects of the KD mutation included a stimulation of the expression of approximately 300 genes belonging to functional categories associated with anabolic processes and plant

Table I. *Metabolic composition of five communities occurring in the wild-type genotype*

DiEglycerol, Glycerol ethyl derivative; DHA, dehydroascorbic acid dimer; FA 16:00, hexadecanoic acid; FA 18:00, octadecanoic acid; FA 14:00, tetradecanoic acid; FA 06:00; 2-ethyl-hexanoic acid; MyoInt1P, myoinositol-1-P; pGlu, pyroglutamic acid.

Community 1	Community 2	Community 3	Community 4	Community 5
2-Oxoglutarate	Glu	DiEglycerol	Maltose	Gal
Succinate	Asp	FA 06:00	Laminaribiose	Fru
Trehalose-6-P	Ile	FA 14:00	Trehalose	Glc
DHA	Gly	FA 18:00	Galactinol	Rib
Threonate	Ser	FA 16:00	Galactosylglycerol	Xyl
	Phe	Melibiose	MyoInt1P	Tyr
		Kestose	pGlu	Thr
		Salicin	Trp	MyoInt
		Cellobiose	Met	Glycerol
			Guanosine	Glycerate
				Citrate
				Shikimate
				Malate
				Phosphoric acid
				Epicatechin

vigor (Table III; Figs. 5 and 6). Among these are (1) 221 genes associated with protein synthesis (including 149 genes encoding ribosomal proteins and 20 genes encoding translation initiation elongation factors); (2) 25 genes encoding enzymes associated with amino acid metabolism, from which six genes interestingly belong to the Asp family pathway that synthesizes Lys (AT3G25900, HMT-1; AT4G01850, SAM-2; AT2G45440, DHDPS2; AT2G59890, dihydrodipicolinate reductase; AT5G13280, AK-LYS1; AT1G14810, Asp semialdehyde dehydrogenase); (3) 12 genes encoding enzymes associated with nucleotide metabolism; (4) six methyl transferase genes; and (5) 20 genes associated with RNA processing. In addition to stimulating the expression of genes associated with the above processes, the KD genotype also seems to have mixed effects (induction/reduction) on small sets of genes involved in several metabolic processes as well as those associated with

Table II. *Metabolite composition of the four communities occurring in the KD genotype*

Metabolites that are grouped together in both the wild-type and KD genotypes are defined as modules and are shown in modules 1 to 8. DiEglycerol, Glycerol ethyl derivative; DHA, dehydroascorbic acid dimer; FA 16:00, hexadecanoic acid; FA 18:00, octadecanoic acid; FA 14:00, tetradecanoic acid; FA 06:00; 2-ethyl-hexanoic acid; GlnA 1,5, gluconate-1,5-lactone; GlnA 1,4, galactonate-1,4-lactone; MyoInt, myoinositol; pGlu, pyroglutamic acid.

Community 1	Community 2	Community 3	Community 4
Module 1	Module 3	Module 6	Module 7
FA 06:00	Maltose	Gal	Trehalose-6-P
FA 14:00	Trehalose	Fru	DHA
FA 18:00	Galactinol	Glc	Threonate
FA 16:00	pGlu	Rib	Module 8
Melibiose	Met	Xyl	Phe
Kestose	Guanosine	Thr	Gly
Salicin	Module 4	Glycerate	Glu
Module 2	2-Oxoglutarate	Shikimate	Unassigned
Trp	Succinate	Malate	Citrate
Laminaribiose	Module 5	Phosphoric acid	GABA
Unassigned	Asn	Epicatechin	Cellobiose
DiEglycerol	Ile	MyoInt	
Benzoate	Ser	Unassigned	
Sinapate	Unassigned	Galactosylglycerol	
Ala	GlnA 1,4	Fumarate	
Gln	Tyr	Glycerol	
GlnA 1,5	Glc-6-P		
Lys	Maltose		
	MyoInt-6-P		
	Oxalate		

Table III. *Overrepresented categories of down-regulated genes*

Functional categories that are overrepresented in the list of genes that exhibit significant changes in expression levels between the wild-type and KD genotypes and were consistently down-regulated (507) genes at all time points. Overrepresentation analysis was performed by PageMan (see "Materials and Methods"). Only functional categories with more than three genes are shown; the elaborated analysis is available in Supplemental Table S5. CHO, Carbohydrate.

Main Category	Subcategories	No. of Elements	*P*
Major CHO metabolism	Synthesis	10	8.86E-05
	Starch	5	8.80E-04
		5	1.98E-04
Amino acid metabolism	Degradation, Gly	3	8.36E-04
Abiotic stress, heat	–	14	6.55E-05
DNA synthesis chromatin structure	–	8	4.83E-04
RNA regulation of transcription	NIH-like bZIP-related family	3	1.17E-03

RNA transcription and processing, posttranslational modifications, and protein turnover (Tables III and IV; Figs. 5 and 6).

In contrast to the principal stimulatory effect of the KD genotype on genes associated with anabolic processes thought to be related to plant performance, this mutant had an inhibitory effect on the expression of a very small number of genes, particularly those associated with sugar synthesis (10 genes), amino acid degradation (three genes), heat shock stress (14 genes, including a gene encoding a novel heat shock transcription factor [AT3G24520]), DNA synthesis and chromatin structure (eight genes), and transcriptional regulation (three genes). Given the enriched down-regulation of heat shock genes in the KD genotype (Tables III and IV), we decided to focus further on the specific response to biotic and abiotic stress-related transcripts and visualized the KD response using the MapMan tool (Fig. 7). In doing so, we observed a down-regulation of the expression of genes associated with stress; however, it is important to note that only heat stress response genes were signif-

Table IV. *Overrepresented categories of up-regulated genes*

Functional categories that are overrepresented in the list of genes that exhibit significant changes in expression levels between the wild-type and KD genotypes and were consistently up-regulated (650) genes at all time points. Overrepresentation analysis was performed by PageMan (see "Materials and Methods"). Only functional categories with more than three genes are shown; the elaborated analysis is available in Supplemental Table S5.

Main Category	Subcategories	No. of Elements	*P*
Proteins	Synthesis:	221	2.16E-42
	Miscellaneous ribosomal proteins	176	6.46E-149
	BRIX	149	1.70E-156
	Mito/plastid	6	5.32 E-10
	Initiation	3	7.46 E-04
	Elongation	14	1.1.06E-07
	Protein targeting mitochondria	6	1.176E-04
		5	1.26E-03
	Degradation:	18	1.79E-05
	Ubiquitin	14	2.25E-03
	Proteosome	7	7.42 E-04
	E3 ligase	5	1.07E-05
Amino acid metabolism		25	2.81E-07
	Synthesis:	18	2.11E-06
	Asp family	6	2.56E-04
	Glu family	4	2.72E-04
	Arg family	4	1.20E-04
Nucleotide metabolism		12	8.46E-04
	Synthesis:	8	2.44E-06
	Purine	5	4.44E-05
	Pyrimidine	3	2.39E-03
O-Methyl transferases	–	6	5.03E-06
RNA processing	–	17	5.23E-04
RNA regulation of transcription	–	13	1.11E-03
Signaling	–	13	1.11E-03

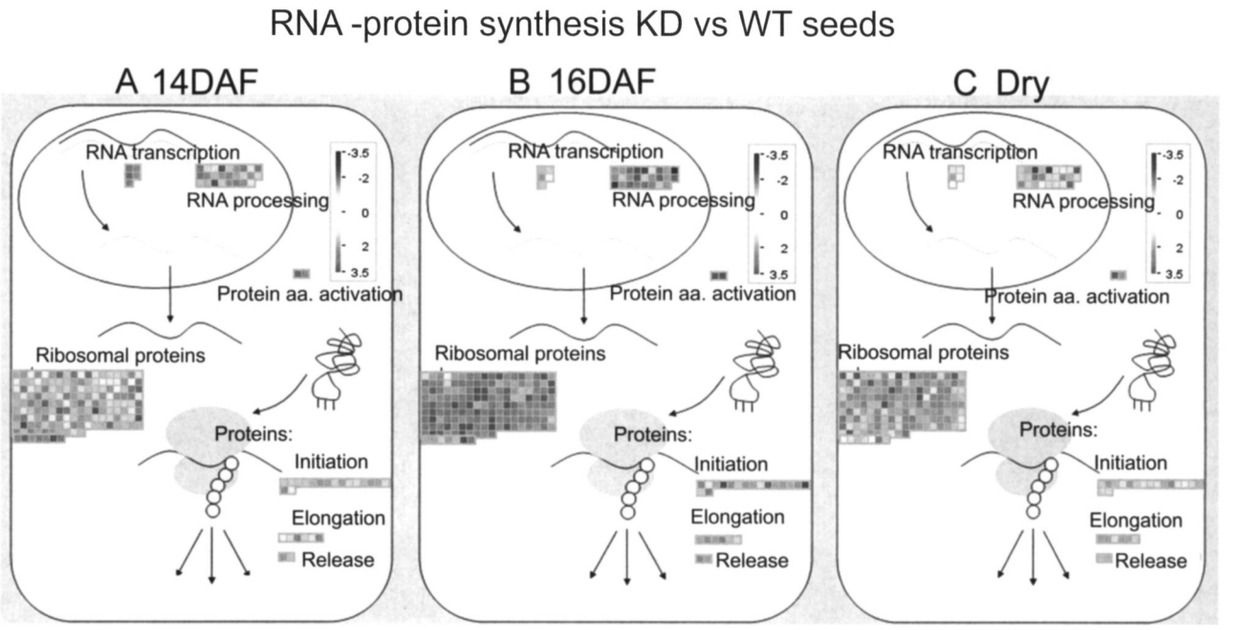

Figure 5. MapMan RNA-protein synthesis overview maps showing differences in transcript levels between the wild-type (WT) and KD genotypes in 14-DAF (A), 16-DAF (B), and dry (C) seeds. Average transcript levels were calculated from two independent replicates of Affymetrix AtH1 GeneChips, and fold changes were calculated from the normalized gene expression data of the KD versus wild-type genotypes in 14-DAF, 16-DAF, and dry seeds. The resulting file was loaded into the MapMan Image Annotator module to generate the RNA-protein synthesis overview map (Supplemental Table S7). The normalized expression levels (in $\log_2$) of the genes that exhibit significant changes between the wild-type and KD genotypes are available in Supplemental Table S4. [See online article for color version of this figure.]

icantly overrepresented within the data set (Tables III and IV).

To test if the major reduction in certain TCA cycle intermediates observed in the KD genotype was limited to the metabolic level, we also searched for specific alteration in the expression of genes associated with the TCA cycle. The expression of a number of TCA cycle-associated genes was affected in the KD genotype, of which two particularly interesting cases were the up-regulation of succinate dehydrogenase 2 (AT3G2738) and alternative oxidase 1A (AT3G22370). The former gene product converts succinate to fumarate and in doing so supplies electrons to the mitochondrial electron transport chain. In contrast, the latter is often associated with inhibition of the mitochondrial electron transport chain. However, it is important to note that the in vivo activity of alternative oxidase is most likely not controlled at the transcriptional level but rather at the posttranscriptional level (Day et al., 1994; Oliver et al., 2008; Rasmusson et al., 2009). Thus, taken together, it is apparent from our microarray analysis that the induced stimulation of Lys biosynthesis, coupled with a down-regulation of its degradation, principally stimulates a large number of genes associated with plant vigor while simultaneously suppressing a limited number of genes associated with plant response to stress, particularly heat stress. That said, our examination of whether the KD genotype exhibited a major influence on the proteome of mature dry seeds suggests that the proteomes of the two genotypes were highly comparable (Supplemental Fig. S2).

We also wished to test whether the KD genotype also alters the transcription patterns during seed maturation compared with the wild-type genotype. To address this issue, we clustered the genes that were consistently up-regulated (650) or down-regulated (507) in the KD genotype during seed maturation of both wild-type and KD genotypes (three time points for each genotype; total six time points). Clustering analysis was performed using the Expander tool (see "Materials and Methods") as follows. (1) The six time points were clustered together with the three wild-type time points on the left and the three KD time points on the right, thus generating a single cluster of six points. This connected trend line has no biological relevance but was used in order to enable us to compare both the pattern and the relative intensity of the same genes in wild-type and KD genotypes. (2) The artificial line connecting the dry wild-type seeds to the 14-DAF KD seeds was eliminated, and then we showed the cluster trend lines of the wild-type and KD genotypes separately. As shown in Figure 8, the gene data set grouped into four different clusters (A–D). In each panel, the trend lines of the wild-type and KD genotypes appear on the left and right, respectively. Interestingly, the mRNA expression patterns during seed maturation were quite comparable between the two genotypes. Next, we subjected the genes lists from

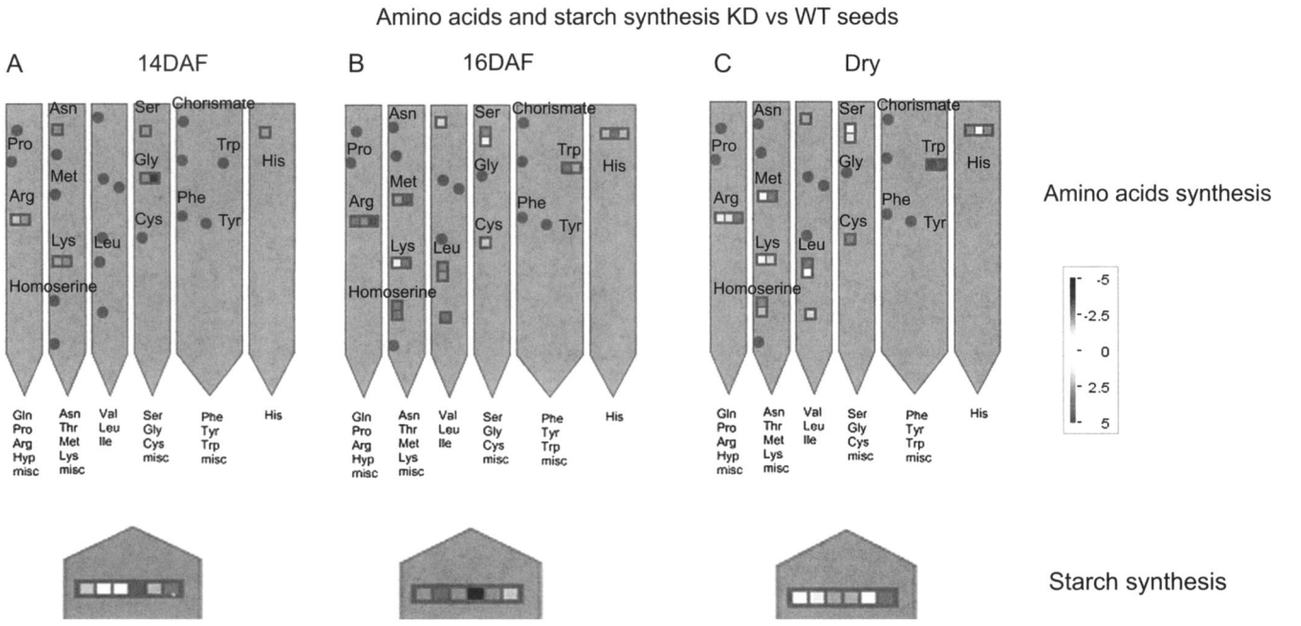

Figure 6. MapMan metabolism overview maps showing differences in transcript levels between the wild-type (WT) and KD genotypes in 14-DAF (A), 16-DAF (B), and dry (C) seeds. Average transcript levels were calculated from two independent replicates of Affymetrix AtH1 GeneChips, and fold changes were calculated from the normalized gene expression data of the KD versus wild-type genotypes in 14-DAF, 16-DAF, and dry seeds. The resulting file was loaded into the MapMan Image Annotator module to generate the metabolism overview map (Supplemental Table S7). The normalized expression levels (in $\log_2$) of the genes that exhibit significant changes between the wild-type and KD genotypes are available in Supplemental Table S4. [See online article for color version of this figure.]

the four different clusters to an overrepresentation analysis using the tools embedded in the PageMan and MapMan softwares (http://mapman.mpimpgolm.mpg.de/general/ora/ora.shtml; Usadel et al., 2006) in order to elucidate the expression pattern of the functional categories identified in Table II.

Genes that were associated with amino acid metabolism, signaling processes, and nucleotide synthesis were overrepresented in cluster 1. Genes associated with protein synthesis, including the ribosomal proteins, were overrepresented in clusters 1 and 4. Genes associated with heat shock were overrepresented in cluster 3. Genes associated with starch degradation were overrepresented in cluster 2 (Fig. 8).

Does the High Lys Accumulation in the KD Genotype Influence the Expression of EF1α, Whose Expression Correlates with Lys Level in Maize High-Lys Opaque Mutants?

Lys is the most limiting essential amino acid in cereal crops; hence, improving its content in seeds represents a major biotechnological challenge (Ufaz and Galili, 2008). Previous studies in maize (*Zea mays*) using a variety of high-Lys, Opaque, and Quality Protein Maize (QPM) genotypes showed a strong correlation between seed Lys content and the expression level of the translation elongation factor EF1α (Habben et al., 1995). Hence, even though distinct methodologies were used to improve Lys content in the Opaque/QPM maize genotypes and in the Arabidopsis KD genotype, it was interesting to test whether the expression of the Arabidopsis EF1α homologs are up-regulated in the high-Lys KD genotype compared with the wild-type genotypes. Notably, expression of the two Arabidopsis EF1α genes (AT1G07940 and AT2G38900) was comparable between the wild-type and KD genotypes, but interestingly, the expression levels of two genes encoding other putative translational elongation factors (AT1G09640 and AT2G31060) were higher in the KD genotype compared with the wild-type genotype (Supplemental Table S4). We also tested the expression levels of nearly 20 Arabidopsis genes, known from the literature to encode Lys-rich proteins, in the wild-type and KD genotypes. We found that the expression levels of all of these genes were not different between the wild-type and KD genotypes (data not shown).

DISCUSSION

Suitability of Maturing Seeds as a Developmentally Inducible System to Study Gene Expression and Metabolic Networks That Interact with Lys Metabolism

In this report, we used maturing Arabidopsis seeds as a developmentally inducible system to alter the

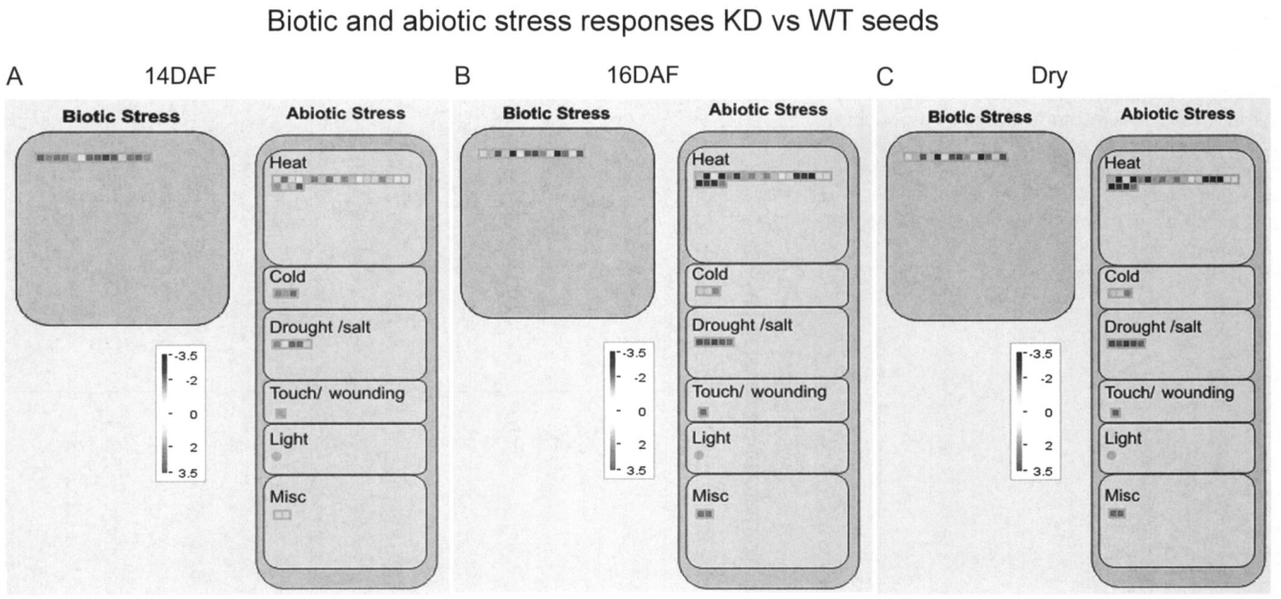

Figure 7. Abiotic and biotic stress response overview maps showing differences in transcript levels between the wild-type (WT) and KD genotypes in 14-DAF (A), 16-DAF (B), and dry (C) seeds. Average transcript levels were calculated from two independent replicates of Affymetrix AtH1 GeneChips, and fold changes were calculated from the normalized gene expression data of the KD versus wild-type genotypes in 14-DAF, 16-DAF, and dry seeds. The resulting file was loaded into the MapMan Image Annotator module to generate the cell response overview map (Supplemental Table S7). The normalized expression levels (in $\log_2$) of the genes that exhibit significant changes between the wild-type and KD genotypes are available in Supplemental Table S4. [See online article for color version of this figure.]

metabolic flux of Lys metabolism as a tool to investigate systems-wide interactions of Lys metabolism with the primary metabolome as well as with genome-wide transcriptional programs. As opposed to chemical-based inducible systems, such as the ethanol- and dexamethasone-inducible systems (Aoyama and Chua, 1997; Junker et al., 2003), maturing seeds offer a chemical-free, rapid, and efficient developmentally inducible system that is based on a promoter of a storage protein gene. Our specific inducible alteration of Lys metabolism was based on a developmentally inducible stimulation of Lys biosynthesis by expressing a bacterial gene encoding feedback-insensitive DHDPS of Lys biosynthesis under the control of the phaseolin storage protein promoter in the background of a T-DNA knockout mutant in the *LKR/SDH* gene of Lys catabolism. The rapid induction of the bacterial DHDPS gene and the inducible accumulation of Lys metabolism across seed maturation are shown in Figure 1, B and C, respectively.

Modularity of the Metabolome Network of Developing Seeds in Response to the Inducible Alteration of Lys Metabolism

Interestingly, the inducible alteration of Lys metabolism in the KD genotype had no major effect on the levels of other primary metabolites, causing only a pronounced reduction in the levels of the TCA cycle intermediates fumarate and citrate. The reason for the major suppressive effect of the KD genotype on the TCA cycle metabolites is yet unknown, but it may be due to a competition of the Lys biosynthesis pathway with the TCA cycle for their common precursor metabolite pyruvate, because pyruvate is also used as a cosubstrate for the DHDPS enzyme of Lys metabolism (Fig. 1). An even more interesting observation was seen in the adjustment of the metabolic network of maturing seeds to the inducible alteration of Lys metabolism, which offers considerable insight into the operation of this network in maturing seeds. Our metabolite network analysis revealed that the altered Lys metabolism generally increases the number of significant correlations between metabolites with respect to the dynamic changes in their levels during seed maturation. In addition, as shown in Tables I and II, the alteration in Lys metabolism also modifies the degree of association between metabolites, resulting in their grouping within slightly different communities as compared with the wild type. However, this reorganization of metabolic associations involved not only single metabolites but also basic metabolic modules that were conserved between the wild-type and KD genotypes (Table II). Examples of the modular organization of the metabolic network in response to the KD mutation included the TCA cycle intermediates 2-oxoglutarate and succinate, but not fumarate, malate, or citrate, in both the wild-type and KD genotypes.

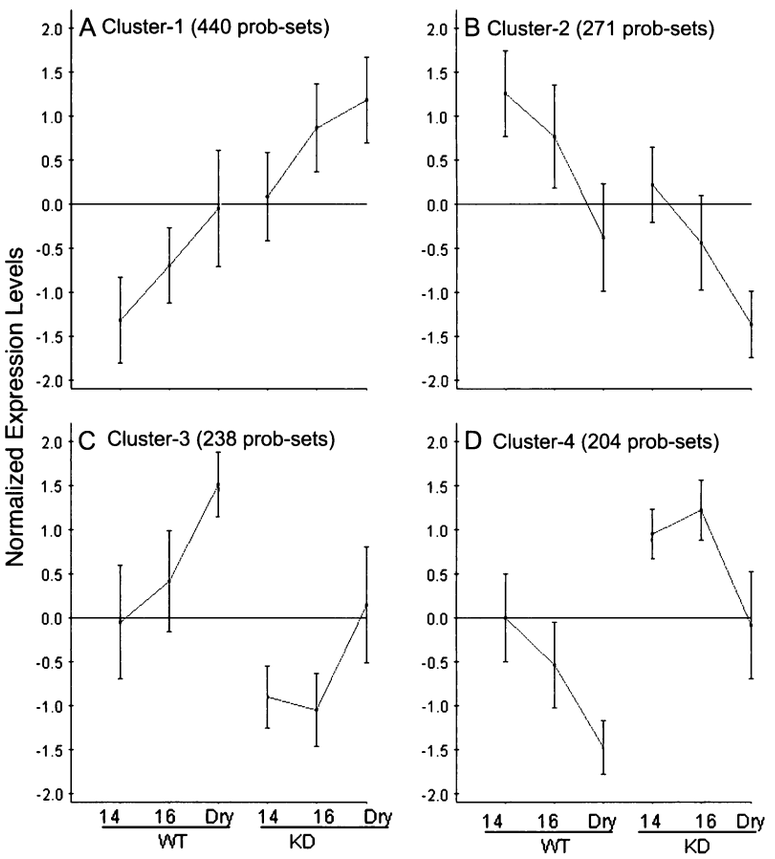

Figure 8. Clustering analysis of genes whose mRNA levels were significantly different between the wild-type (WT) and KD genotypes during seed maturation. Clustering analysis was performed by comparing the average patterns of the normalized expression levels of identical groups of genes in the wild-type and KD genotypes in maturing seeds, as described in "Materials and Methods." Error bars represent SE. Seed maturation stages in DAF are provided at the bottom.

This finding implies a complex modular regulation of different parts of this metabolic cycle and as such supports the contrasting phenotypes observed on perturbing various reactions involved in the TCA cycle in plants (Nunes-Nesi et al., 2005, 2007). The suggestion of such a modular function of the TCA cycle is also not without precedence, with such functional activities being commonly described in microbes (McCammon et al., 2003). Combination of results from these studies should provide the evidence required to initiate further studies on the modularity of metabolic networks in plants.

Interestingly, the KD genotype also displayed a dispersed association of amino acids that were synthesized by different branches of primary metabolic networks (Table II). These results imply that network associations of amino acids are not only due to their function in protein synthesis but also due to their regulatory function in plant metabolism. An interesting example implying such novel associations of amino acids is the observation that in both the wild-type and KD genotypes, trehalose is more strongly associated with Met than with trehalose-6-P (Fig. 4). Other interesting observations are the new association groups that are formed in response to the altered Lys metabolism. Three examples are (1) the association of Met with Ile in the KD genotype (Table II), which may signify an adjusted operation of the newly discovered channeling of Met via Met γ-lyase into Ile (Rébeillé et al., 2006; Joshi and Jander, 2009); (2) the association of Glu with GABA in the KD genotype, which may signify an adjustment of the established conversion of Glu into GABA (Fait et al., 2008); and (3) the association of Gly and Ser in the wild-type genotype but not in the KD genotype, which may imply a modified operation of photorespiration. Thus, our results imply that the metabolic network-association approach, coupled with analysis of the metabolic mutant, may provide a novel insight into rerouting of metabolic pathways that could be further validated by metabolic flux analyses.

Response of the Transcriptome Network of Developing Seeds to the Inducible Alteration of Lys Metabolism

Our results showed that the inducible alteration of Lys metabolism in the KD genotype had a significant effect on gene expression programs in the developing seeds. The most significant effect of the KD genotype included a stimulatory effect on a large array of genes principally controlling anabolic processes that are associated with plant vigor (Table IV), namely processes associated with active plant growth when growth conditions are usually optimal. In addition,

the KD genotype also suppressed the expression of a smaller group of genes principally associated with amino acid degradation and response to stress conditions (particularly heat shock; Table III). Thus, our results imply that the Lys metabolism pathway participates in the regulation of plant growth and response to stress through modulating networks of gene expression. If true, this observation begs the question, how does such a system interaction operate? Active plant growth is principally associated with up-regulated expression of genes encoding enzymes of amino acid biosynthesis, which are particularly necessary for protein synthesis. In contrast, our recent bioinformatics analysis (Less and Galili, 2009) revealed that exposure to various stresses slightly suppresses the expression of some genes encoding biosynthetic enzymes of Lys biosynthesis while significantly stimulating the *LKR/SDH* gene of Lys catabolism. Thus, we hypothesize that changes in either the flux of Lys metabolism and/or the level of Lys itself are recognized by the plant as signal(s) regulating gene expression. This hypothesis is supported by two additional independent lines of evidence: (1) a mutation increasing the resistance of Arabidopsis plants to pathogen infection and also simulating the expression of a number of genes associated with pathogen resistance (termed the *agd2* mutant) has been shown to occur in a gene encoding a transaminase enzyme of Lys biosynthesis (Hudson et al., 2006); and (2) a T-DNA knockout mutation in another Arabidopsis gene (termed the ALD1 gene), which is highly homologous to the AGD2 gene of Lys biosynthesis and was also shown to encode an enzyme that in vitro transaminates Lys into a yet unknown metabolite, was further shown to render Arabidopsis plants more sensitive to pathogens and also to affect the expression of various stress-associated genes in a different manner to that of the AGD2 gene (Song et al., 2004a, 2004b).

Interestingly, as opposed to the major effect of the KD genotype on the global gene expression program, metabolic engineering approaches generating rice Trp-overproducing plants as well as Arabidopsis Phe-overproducing plants resulted in only small effects on global gene expression programs (Dubouzet et al., 2007; Tzin et al., 2009). This illustrates that different amino acid metabolic networks may possess variable interactions with gene expression programs.

CONCLUSION

This report describes the first example, to our knowledge, of an approach to use seeds as a developmentally inducible system to study metabolic regulation in the context of a comprehensive system that includes interactions with transcriptional networks. Our results expose novel metabolic and transcriptional network interactions associated with Lys metabolism and illustrate the modular behavior of these interactions. They additionally demonstrate that Lys metabolism is relatively inert with respect to its general impact on metabolic regulation, which is primarily associated with TCA cycle metabolites. This comparison provides an important advance in the understanding of the regulation of plant metabolism. While much recent experimental and theoretical research effort has been focused on understanding the intra-regulation of plant amino acid metabolism (Hare et al., 1999; Galili, 2002; Curien et al., 2009), attempts to evaluate the role of amino acid metabolism with respect to primary metabolism have rarely been directly assessed. The results presented here are in accordance with general theories of metabolic robustness (Stephanopoulos and Vallino, 1991; Rontein et al., 2002) in that they suggest that, at least under the optimal conditions tested here, the alterations in Lys metabolism exhibited in the KD genotype did not greatly influence metabolite partitioning between the genotypes. Yet, Lys metabolism did display a more pronounced influence in the context of the entire system, affecting the expression of a large set of genes. The increased Lys accumulation in the KD genotype strongly stimulates gene expression programs associated with plant vigor while suppressing a smaller number of genes principally associated with stress (heat shock) response. These results thus support our previous bioinformatics analysis (Less and Galili, 2009) in revealing that the expression of genes encoding biosynthetic enzymes of the Asp family network is principally coregulated with genome-wide genes associated with plant growth, while the expression of genes encoding catabolic enzymes of this network is principally coregulated with stress-associated genes.

MATERIALS AND METHODS

Chemicals

All chemicals were purchased from Sigma-Aldrich Israel with the exception of *N*-methyl-*N*-[trimethylsilyl]trifluoroacetamide (Macherey-Nagel).

Plant Growth and Seed Collection

Arabidopsis (*Arabidopsis thaliana* ecotype Wassilewskija) seeds of the wild-type and KD genotypes (Zhu and Galili, 2003) were germinated on soil and grown for two consecutive rounds in the greenhouse (21°C). Flowers were marked, and at given time intervals following flowering (10 ± 1 to 18 ± 1 DAF), maturing siliques were collected and lyophilized to dryness, and seeds were then dissected from the dried siliques and immediately frozen in liquid nitrogen. Mature seeds were collected at the end of the desiccation period and stored at 4°C. Three thousand to 5,000 seeds were harvested for each extraction.

Extraction, Derivatization, and Analysis of Seed Metabolites Using GC-MS

Collected material was extracted and analyzed by GC-MS using a GC-time of flight protocol optimized for Arabidopsis (Lisec et al., 2006) by adjusting the extraction protocol to seed material as described by Fait et al. (2006). Relative metabolite content was calculated as described by Roessner et al. (2001) following peak identification using TagFinder (Luedemann et al., 2008). Substances were identified by comparison with mass spectral tags represented in our in-house database (Schauer et al., 2005; Erban et al., 2007; Hummel et al., 2007).

Statistical and Network Analyses

Statistical analysis, PCA, and two-way ANOVA were performed on the data sets obtained from metabolite profiling with the software package TMEV (Saeed et al., 2003) using the default weighted covariance-estimation function. Prior to the analysis, data were log transformed and normalized to the median of the entire sample set for each metabolite. This transformation reduces the impact of outliers without affecting the discrimination within the data set. Furthermore, to test statistical significance between specific time points, *t* tests were performed using the algorithm incorporated into Microsoft Excel with Bonferroni correction of the critical *P* value for multiple comparisons. Networks of metabolite correlations were reconstructed based on the method described by Nikiforova et al. (2005). From the entire set of metabolite responses, we first produced a correlation matrix based on the calculation of the Pearson product moment correlation coefficient between each pair of metabolites across the whole developmental period. To this aim, we unified both batches in order to increase the robustness of the analysis and identify those correlations shared by both batches. We then calculated the significance of each correlation coefficient. We set the correlation significance threshold fixed at the level of Spearman correlation coefficient ($P < 10^{-10}$). Next, we visualize the correlation matrix as a graph, wherein each metabolite is a vertex (or node) and each significant correlation between two metabolites is a line between two vertices. The resulting graph was analyzed in the context of its topology. A cumulative degree distribution and network modularity were investigated. The former defines a hierarchy in node connectivity, whereas the latter informs about the presence of highly connected clusters. Newman's algorithm based on matrix eigenvectors was used to detect a community structure (Newman, 2006), leading to partition of the network into communities of vertices characterized by a higher number of ties and higher structural equivalence within the community as compared with the their ties outside the community. These clusters contain metabolites that are structurally equivalent and thus putatively functionally associated. Structural equivalence is a property that can be scaled based on the number and nature of ties between metabolites. A subset of vertices is defined as approaching structural equivalence when they share ties with identical vertices. To emphasize the changes in the structural features of the merged metabolic networks, we visualized the communities built from the wild-type correlation matrix in different colors, while communities built in the mutant are shown as circles. Networks were visualized and merged using the open source bioinformatics software platform for visualizing molecular interaction networks Cytoscape software 2.6.1, and all of the calculations and network analyses were performed using R 2.8.0 software (Gentleman et al., 2004).

RNA Extraction and Microarray Analysis

All experiments analyzing RNA expression levels were carried out using two replicates of seed materials, obtained from two independent seed lots, from plants grown under controlled-environment conditions. Fresh developing seeds at 10, 14, and 16 DAF were harvested, and total RNA was extracted as described previously (Ruuska and Ohlrogge, 2001) as well as for dry seeds, imbibed seeds, and germinating seeds as described above (seed germination). Total RNA was treated with DNAase RQ-1 (Promega), then RNA was amplified using two-cycle Affymetrix labeling using the standard Affymetrix protocol. Hybridization, labeling, scanning, and data extraction were performed according to the standard Affymetrix protocols. Transcriptome analysis was carried out using Partek Genome Suite software (www.partek.com). Preprocessing was carried out using the Robust Microarray Averaging algorithm (Irizarry et al., 2003) Two-way ANOVA was performed. Batch effects between the two duplicate experiments were removed. False discovery rate was applied to correct from multiple comparisons (Hochberg and Benjamini, 1990). Differentially expressed genes were chosen according to false discovery rate < 0.05 and a 2-fold change between genotypes in at least one time point. Overrepresentation/underrepresentation analysis was performed by PageMan (http://mapman.mpimp-golm.mpg.de/general/ora/ora.shtml; Usadel et al., 2006). Visualization of metabolic pathways and other functional categories was performed with the MapMan (Usadel et al., 2005) software tool. Clustering analysis was performed by Expander software (Shamir et al., 2005; http://acgt.cs.tau.ac.il/expander/) using the click algorithm.

Protein Analysis

For two-dimensional isoelectric focusing/SDS-PAGE fractionation, 50 mg of seeds was extracted as described previously (Ruuska and Ohlrogge, 2001), and proteins were then extracted from the phenol phase. Isoelectric focusing/SDS-PAGE was then performed as described previously (Liska et al., 2004) and stained with Coomassie Brilliant Blue.

Microarray data have been deposited to the Gene Expression Omnibus database under series number GSE18112.

Supplemental Data

The following materials are available in the online version of this article.

Supplemental Figure S1. PCA of metabolite profiles of distinct maturation stages of seeds of the wild-type and KD genotypes.

Supplemental Figure S2. Effects of altered Lys metabolism in the KD genotype on the levels and deposition of the 12S cruciferin storage proteins.

Supplemental Table S1. The entire data set of the relative contents of metabolites in growing time 1.

Supplemental Table S2. The entire data set of the relative contents of metabolites in growing time 2.

Supplemental Table S3. The entire data set of the *P* values of the two-way ANOVA of the data sets from the different seed growing times.

Supplemental Table S4. Expression levels of genes whose mRNA levels were significantly different between wild-type and KD genotypes during seed maturation (data presented in $\log_2$ values).

Supplemental Table S5. An elaboration of the overrepresentation analysis of genes whose mRNA levels were significantly different between wild-type and KD genotypes during seed maturation.

Supplemental Table S6. Complete microarray results of expression levels in wild-type and KD seeds during seed maturation (data presented in $\log_2$ values).

Supplemental Table S7. Calculated ratios of transcript levels of KD versus wild-type genes whose mRNA levels were significantly different between wild-type and KD seeds

Supplemental Table S8. Abbreviations of the network metabolites in Figure 4.

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