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AtMyb41 Regulates Transcriptional and Metabolic Responses to Osmotic Stress in Arabidopsis [W][OA]

Felix Lippold¹, Diego H. Sanchez, Magdalena Musialak, Armin Schlereth, Wolf-Ruediger Scheible, Dirk K. Hincha, and Michael K. Udvardi*¹


Myb transcription factors have been implicated in a wide variety of plant-specific processes, including secondary metabolism, cell shape determination, cell differentiation, and stress responses. Very recently, AtMyb41 from Arabidopsis (Arabidopsis thaliana) was described as a gene transcriptionally regulated in response to salinity, desiccation, cold, and abscisic acid. The corresponding transcription factor was suggested to control stress responses linked to cell wall modifications. In this work, we have characterized AtMyb41 further by subjecting independent AtMyb41-overexpressing lines to detailed transcriptome and metabolome analysis. Our molecular data indicate that AtMyb41 is involved in distinct cellular processes, including control of primary metabolism and negative regulation of short-term transcriptional responses to osmotic stress.

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tailed transcriptome and metabolome analysis. Our molecular data indicate that AtMyb41 is involved in distinct cellular processes, including control of primary metabolism and negative regulation of short-term transcriptional responses to osmotic stress.

RESULTS

AtMyb41 Expression Is Induced by Salt and Osmotic Stress in an ABA-Dependent Manner

We identified AtMyb41 in a screen for salt shock- and osmotic shock-inducible TFs in 9-d-old Arabidopsis seedlings grown in sterile liquid culture using a high-throughput quantitative real-time reverse transcription (RT)-PCR resource for almost all known Arabidopsis TFs (Czechowski et al., 2004). AtMyb41 transcript levels in seedlings increased reproducibly after 3 h of 100 mM NaCl or 200 mM mannitol treatment (Fig. 1A). Subsequent analysis of the kinetics of AtMyb41 induction revealed a rapid increase in transcript levels within 1 h of NaCl addition, as described previously (Cominelli et al., 2008), but under our experimental conditions AtMyb41 peaked between 2 and 3 h and subsequently declined to basal, non-stressed control levels (Fig. 1A). Induction of AtMyb41 transcription was partially blocked in the aba2 mutant with reduced capacity to synthesize ABA (Fig. 1B). Similar results were obtained for a set of known stress marker genes, including AtRd29b and AtRab18, confirming an ABA-dependent regulation (Fig. 1B). NaCl induction of AtMyb41 expression was also observed in 4-week-old hydroponically grown plants acclimated to 50 mM NaCl (Fig. 1C), implicating AtMyb41 in long-term adjustment of plant cells to moderate osmotic stress in addition to more dramatic, short-term responses to osmotic shock (Fig. 1A). In line with a previous report (Cominelli et al., 2008), we observed that AtMyb41 expression was up-regulated by drought, cold, and ABA treatments (data not shown).

Ectopic Overexpression of AtMyb41 Retards Arabidopsis Growth

To investigate the role of AtMyb41 in plant response to stress, transgenic Arabidopsis lines were created using the constitutive promoter Cauliflower mosaic experiments are shown separately, with error bars representing s.e.m from three biological replicates. Ctrl, Control. B, Expression of AtMyb41 (left) and stress marker genes (right) after 3 h of 100 mM NaCl treatment in 9-d-old aba2 mutant and wild-type seedlings. Data represent means ± s.e.m of three independent replicates. Black bars represent salt-stressed wild type (Wt) versus control wild type (Wt Ctrl); gray bars represent control aba2 versus control wild type; dotted black bars represent salt-stressed aba2 versus control wild type; striped gray bars represent salt-stressed aba2 versus control aba2. C, Expression of AtMyb41 (left) and stress marker genes (right) in hydroponically grown 4-week-old plants. Plants were treated with increasing salt concentrations, reaching 50 mM NaCl in the final week. Data represent means ± s.e.m of three independent replicates. The Arabidopsis Genome Initiative codes of the genes are provided in Supplemental Table S4.

Figure 1. A, Expression of AtMyb41 in 9-d-old seedlings after 3 h of treatment with 100 mM NaCl or 200 mM mannitol (left panel); data represent means ± s.d. of three independent replicates and after 24 h of treatment with 100 mM NaCl (right panel; data from two independent
virus-35S to drive AtMyb41 expression. In the T3 generation, eight kanamycin-resistant lines were identified and AtMyb41 overexpression was confirmed by quantitative real-time RT-PCR in four of five putative single-insertion lines (Fig. 2A). Growth was not affected significantly in seedlings of AtMyb41 overexpressors (data not shown). However, prolonged overexpression of AtMyb41 inhibited growth (Fig. 2, B and C), albeit to a much lower extent than described previously for independent AtMyb41 transgenic lines (Cominelli et al., 2008). Despite the mild dwarf phenotype, no significant differences in relative growth rate were observed between AtMyb41 overexpressors and wild-type plants in vitro on salt-containing plates, in long-term salt acclimation experiments performed in hydroponic culture, or in soil-grown salt- or drought-stressed plants (data not shown).

**AtMyb41 Overexpression Deregulates a Subset of Salt-Induced Genes**

Rapid induction of AtMyb41 expression in response to osmotic and salt stress indicated a possible role for AtMyb41 in immediate/early responses of seedlings to osmotic stress. To identify potential targets of AtMyb41 action as a step toward defining its physiological role, transcriptome analysis of the two most highly overexpressing AtMyb41 lines, lines 1 and 7, was performed using the Affymetrix GeneChip Arabidopsis ATH1 Genome Array. Three independent experiments were performed with seedlings of the transgenic lines and wild-type plants grown in vitro under control conditions and after treatment with 100 mM NaCl for 3 h. For a global overview, gene expression data were analyzed first via unsupervised principal component analysis, which demonstrated good reproducibility between independent experiments (Fig. 3A). Principal component 1 (PC1), representing 37% of the variance within the data set, separated the transgenic lines from wild-type seedlings, while PC2, encompassing 19% of the variance, separated stressed plants from controls (Fig. 3A). To assess differential expression among the genotypes and the treatments, data were further analyzed by a significance-based comparison applying a false discovery rate (FDR)-corrected false positive rate (type I error) of 5% (FDR < 0.05; Benjamini and Hochberg, 1995) and a threshold >1.5-fold change (log2 scale). Comparisons were made between genotypes for a given treatment or between treatments for a given genotype (Supplemental Table S1). Genes differentially expressed between genotypes and/or treatments were clustered with the K-means method, revealing five groups with broad differential patterns of expression (Fig. 3B). Clusters A and B represented salt-induced and salt-repressed genes, respectively, regardless of the genotype, many of which are known to be stress responsive like AtRd29a, AtCor15a, and AtKin1 (Supplemental Table S1). The other three clusters included genotype-specific genes. We found transcripts induced (cluster C) or repressed (cluster D) in the transgensics (cluster D) in the transgenics that did not respond to salt treatment, indicating stress-unrelated roles for AtMyb41 or reflecting pleiotropic effects of AtMyb41 overexpression. Most interesting, cluster E contained genes that were salt induced in the wild type but not in AtMyb41-overexpressing plants, indicating a possible role for AtMyb41 in feedback repression of these genes. This cluster contained a number of known stress-responsive genes, including some late embryogenesis abundant genes, AtDreb2a and AtNcd3.

![Figure 2](https://via.placeholder.com/150)

**Figure 2.** A. Analysis of transgene expression in AtMyb41-overexpressing lines using quantitative real-time RT-PCR. B. Growth of AtMyb41-overexpressing plants compared with wild-type plants, as estimated by shoot biomass. Data represent means ± so of 45 plants from eight independent replicates, harvested before bolting. FW, fresh weight; WT, wild type. C. AtMyb41-overexpressing plants from lines 1 and 7 compared with wild-type (WT) plants at 4 and 5 weeks after sowing.
Figure 3. A, Principal component analysis of the transcriptomic profiles obtained from three independent biological replicates of each genotype and treatment. The first two principal components are shown, which constitute the major variation of the data set. Ctrl, Control; Wt, wild type. B, K-means clustering of the genes declared to be changed (FDR $P<0.05$, >1.5-fold changed in log$_2$ scale) in AtMyb41 overexpressors versus the wild type and treatment versus control. Cluster A, Salt-induced genes; cluster B, salt-repressed genes; cluster C, genes up-regulated in the transgenic lines; cluster D, genes down-regulated in the transgenic lines; cluster E, salt-induced genes in the wild type but not in the transgenic lines. C, PageMan statistical overrepresentation analysis of genes significantly changed in expression due to AtMyb41 overexpression (genes only responding to salt stress were excluded). D, Comparison of microarray and quantitative real-time RT-PCR (qRT-PCR) data (data represent means ± so of two overexpressing lines under control conditions in three independent experiments) of selected genes found significantly changed in the transcriptomic profiles. The Arabidopsis Genome Initiative codes of the genes are provided in Supplemental Table S4.
Quantitative real-time RT-PCR was used to confirm the results of the microarray studies for the most strongly up- and down-regulated genes (Fig. 3D). All of the genes tested were confirmed to be either induced or repressed in AtMyb41 overexpressors compared with the wild type. In many cases, the magnitude of changes calculated from quantitative real-time RT-PCR data were greater than from array data, as expected, but the correlation between technologies was remarkably good (linear regression $r^2 = 0.8937$).

**AtMyb41 Overexpression Alters Primary Metabolism in Seedlings**

Metabolite profiling of seedlings, using gas chromatography coupled to electron impact ionization-time of flight-mass spectrometry (GC/El-TOF-MS), was carried out to determine the extent to which AtMyb41-induced changes in gene expression altered plant metabolism. A total of 92 mass spectral tags (MSTs; Desbrosses et al., 2005) were recognized, and 60 of these were ascribed to known chemical compounds (Supplemental Table S2). Data were analyzed first using unsupervised independent component analysis (ICA), which revealed marked differences between genotypes (transgenic versus wild type) but not between the treatments (control versus NaCl; Fig. 4A). Further statistical analysis using ANOVA also demonstrated significant changes in metabolite pools between genotypes but only minor changes between treatments. Sugars, amino acids, and some organic acids were changed in the AtMyb41 overexpressors relative to wild-type seedlings (Table I). Differences due to NaCl treatment were small, and only six metabolites, mostly sugars, accumulated in wild-type and transgenic lines in response to salt shock (Table II). Similar results in other plant species implicate glycolysis and Suc metabolism in evolutionarily conserved responses to short-term osmotic stress (Sanchez et al., 2008b). Only Glc and Gal accumulated under short-term osmotic stress in the wild type and constitutively in AtMyb41 overexpressors (Tables I and II). Taken together, these results point to a role of AtMyb41 in the control of primary metabolism.

**Long-Term Effects of Myb41 Overexpression in Plants**

Given the effects of AtMyb41 overexpression on long-term plant growth (Fig. 2, B and C), it was of interest to us to investigate the molecular consequences of AtMyb41 overexpression in older plants. Rosettes from AtMyb41 transgenics and wild-type plants, subjected to control and various stress treatments, were profiled at the metabolome level. A total of 91 MSTs were recognized, but only 54 were found in both seedlings and mature plants. Seventy MSTs of rosettes of mature plants were ascribed to known chemical compounds (Supplemental Table S3). Changes in metabolite profiles following salt, drought, cold, and ABA treatments were revealed by unsupervised ICA, but surprisingly, no clear separation was observed between genotypes for these treatments (Fig. 4B). A significance-based analysis (ANOVA) demonstrated that the pool sizes of only two metabolites were statistically different in the shoots of transgenic compared with wild-type plants: myo-inositol and galactinol (Fig. 5). Myo-inositol levels were significantly lower in control and cold-treated AtMyb41 overexpressors than in wild-type plants, and galactinol was lower in the transgenic lines not only under these two conditions but also under salt-stress conditions. Raffinose levels also tended to be lower in the transgenic lines than in the wild type under control and stress conditions, although differences were not significant at $P < 0.01$ (Fig. 5). Note that myo-inositol levels were also lower in seedlings of AtMyb41 overexpressors than in wild-type controls (Table I).
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Table 1. Significantly changed metabolites due to AtMyb41 overexpression in lines 1 and 7 (ANOVA P < 0.01)

<table>
<thead>
<tr>
<th>Type</th>
<th>Metabolite</th>
<th>Lines 1 and 7 Control/Wild-Type Control</th>
<th>Lines 1 and 7 NaCl/Wild-Type NaCl</th>
</tr>
</thead>
<tbody>
<tr>
<td>Amino acids</td>
<td>Pyroglutamic acid</td>
<td>5.40</td>
<td>5.68</td>
</tr>
<tr>
<td></td>
<td>Ala</td>
<td>5.16</td>
<td>5.40</td>
</tr>
<tr>
<td></td>
<td>Glu</td>
<td>3.87</td>
<td>4.16</td>
</tr>
<tr>
<td></td>
<td>Asp</td>
<td>2.97</td>
<td>3.06</td>
</tr>
<tr>
<td></td>
<td>Phe</td>
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<td>2.50</td>
</tr>
<tr>
<td></td>
<td>Thr</td>
<td>2.22</td>
<td>2.53</td>
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<tr>
<td></td>
<td>Gly</td>
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<td>2.58</td>
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<tr>
<td></td>
<td>Se</td>
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<tr>
<td></td>
<td>[Orn lactam]</td>
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<td>0.75</td>
</tr>
<tr>
<td>Sugars</td>
<td>Maltose</td>
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<td></td>
<td>Xyl</td>
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<tr>
<td></td>
<td>Rha</td>
<td>1.81</td>
<td>3.68</td>
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<tr>
<td></td>
<td>1,6-Anhydro-β-D-Glc</td>
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<td></td>
<td>Glc-6-P</td>
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</tr>
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<td>Gal</td>
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<tr>
<td></td>
<td>Glc</td>
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<td>1.77</td>
</tr>
<tr>
<td></td>
<td>Myo-inositol</td>
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<td>0.84</td>
</tr>
<tr>
<td></td>
<td>[2-NH 2-deoxy Glc]</td>
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<td>0.74</td>
</tr>
<tr>
<td>Organic acids</td>
<td>Gluconic acid</td>
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<td></td>
<td>Citric acid</td>
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<td></td>
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<td></td>
<td>Malic acid</td>
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<tr>
<td></td>
<td>Glyceric acid</td>
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<td></td>
<td>[Glycerophosphoglycerol]</td>
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<td>1.51</td>
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<tr>
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<td></td>
<td>A302001</td>
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<td></td>
<td>A199004</td>
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<td>A147001</td>
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<td>0.83</td>
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<td></td>
<td>A126003</td>
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<td>0.23</td>
</tr>
<tr>
<td></td>
<td>A237006</td>
<td>0.13</td>
<td>0.31</td>
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</table>

To test if the genes that were differentially expressed in Myb41 overexpressor compared with wild-type seedlings were also differentially expressed in adult plants of these genetic backgrounds, we measured expression of AtMyb41-responsive genes (Fig. 3D) in greenhouse-grown plants. A comparison between seedlings and adult plants grown under control, non-stress conditions revealed that only AtAP3 was differentially expressed between rosettes of AtMyb41 overexpressors and those of the wild type (Fig. 6A). Transcripts of several genes were barely detected, and subsequent analysis of seedlings revealed that some of these genes were predominantly expressed in roots, explaining the lack of expression in mature rosettes (Supplemental Fig. S1). However, differences between transgenic and wild-type plants in the expression of some of these genes were observed when adult plants were exposed to abiotic stress, suggesting that AtMyb41 overexpression alters stress signaling pathways not only in seedlings but also in mature rosettes (Fig. 6, B–E).

**DISCUSSION**

Although many TFs of the Myb family are expected to be involved in stress responses, few have been characterized functionally. Recently, AtMyb41 was implicated in stress-induced cell wall expansion and
Table II. Significantly changed metabolites in seedlings under salt shock, regardless of the genotype (ANOVA P < 0.05)

To aid comprehension, metabolite pool sizes were averaged for both overexpressors. Data represent means of three independent experiments and are expressed as ratios of the 100 mM NaCl treatment to controls. The unknown is an unidentified metabolite that has been detected before and is denoted by Gal Metabolite Database code (Kopka et al., 2005).

<table>
<thead>
<tr>
<th>Type</th>
<th>Metabolite</th>
<th>Wild-Type NaCl/Control</th>
<th>Lines 1 and 7 NaCl/Control</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sugars</td>
<td>Suc</td>
<td>1.76</td>
<td>1.70</td>
</tr>
<tr>
<td></td>
<td>Glc</td>
<td>1.37</td>
<td>1.87</td>
</tr>
<tr>
<td></td>
<td>Gal</td>
<td>1.40</td>
<td>1.87</td>
</tr>
<tr>
<td></td>
<td>Fru</td>
<td>1.39</td>
<td>1.62</td>
</tr>
<tr>
<td>Unknown</td>
<td>A1990904</td>
<td>1.19</td>
<td>1.89</td>
</tr>
</tbody>
</table>

modification in Arabidopsis, based on the dual observations that AtMyb41 transcript levels could not be detected under normal growth conditions but accumulated under stress and that overexpression of AtMyb41 resulted in abnormal morphology with severely inhibited cell and whole plant growth (Cominelli et al., 2008). Using quantitative real-time RT-PCR, we were able to detect AtMyb41 transcripts under non-stress conditions not only in seedlings but also in shoots and roots of mature plants. We showed that AtMyb41 was induced by osmotic stress in an ABA-dependent manner, similar to known ABA-responsive genes like AtAII1, AtRab18, AtRi29b, and AtAla1, suggesting that AtMyb41 may be part of the AREB regulon (Fujita et al., 2005). Consistent with this idea, putative ABRE cis elements are present in the promoter region of AtMyb41, together with myc recognition sites (Supplemental Fig. S2). A gain-of-function approach was used to shed light on possible molecular and physiological roles of AtMyb41. Constitutive overexpression of AtMyb41 in Arabidopsis inhibited plant growth, but to a much lower extent than described previously for similar transgenic plants (compare figure 2C with figure 2F in Cominelli et al., 2008).

Transcriptome analysis revealed a subset of genes that were induced by salt treatment in wild-type seedlings that failed to be induced in AtMyb41 overexpressors (Fig. 3B). Clearly, AtMyb41 overexpression interfered with the response of these genes, suggesting that this Myb TF may act as a transcriptional repressor. Among these transcripts were a number of known stress-responsive genes, including six late embryogenesis abundant-like proteins that are crucial in seed development and stress responses (Hundertmark and Hincha, 2008), AtDreb2a encoding a key TF involved in stress signaling (Sakuma et al., 2006), and AtNcd3 encoding a key enzyme of ABA biosynthesis with a major role under stress (Iuchi et al., 2001). Noteworthy, AtBgl1, which encodes a β-glucosidase involved in the activation of conjugated ABA pools (Lee et al., 2006), was more expressed in the AtMyb41 overexpressors than in the wild type under both stress and nonstress conditions (Supplemental Table S1). Transcriptional changes in AtNcd3 and AtBgl1 indicate that a disturbance in ABA metabolism may have been responsible for the deregulation of stress-related genes in the AtMyb41 overexpressors, but further work will be required to test this hypothesis.

Interestingly, 10 Myb TFs were differentially expressed in AtMyb41 overexpressors compared with the wild type (Fig. 3C). Eight of these, AtMyb71, AtMyb121, AtMyb9, AtMyb52, AtMyb49, AtMyb64, AtMyb102, and AtMyb93, were responsive to salt treatment in the wild type but not in the transgenic lines, while expression of AtMyb40 and AtMyb74 was repressed in the AtMyb41 overexpressors under nonstress conditions (Supplemental Table S1). Phylogenetic analysis of the protein sequences revealed that the majority of these TFs are closely related (Kranz et al., 1998), and a survey of publicly available transcriptomic data suggested that they are similarly transcriptionally regulated, particularly in the case of osmotic and salt stresses (Supplemental Fig. S3). Of the 10 Myb TFs, only AtMyb102 has been characterized in any detail: AtMyb102 transcripts accumulated rapidly following osmotic stress and wounding and contain a 5’ untranslated region with a crucial role in posttranscriptional regulation (Denekamp and Smeekens, 2003). Taken together, these results point to the existence of a network of interregulated Myb TFs that orchestrates transcriptional reprogramming in Arabidopsis to mount appropriate responses to abiotic stress.

Transcriptomic analysis identified a set of well-known stress-responsive genes that are part of the overall response to stress, such as AtRd29a, AtCor15a, and AtKin1 (Ma et al., 2006), which were apparently not deregulated by AtMyb41 overexpression. Thus, AtMyb41 controls some but not all of the signaling pathways responding to salt shock in seedlings. In addition, transcriptome analysis also revealed a subset of transcripts that were either up- or down-regulated in AtMyb41 overexpressors relative to the wild type, which were not responsive to salt treatment in any genotype (Fig. 3B; Supplemental Table S1). Altered expression of these genes in transgenic lines may have been a pleiotropic effect of prolonged, high-level AtMyb41 expression. However, it may also reflect physiological roles of AtMyb41 not necessarily linked to osmotic stress. For example, AtMyb41 may be involved in sulfur homeostasis, because its expression increased under low sulfur and in the sulfate transporter sultr1;2 mutant (sel1-10; Maruyama-Nakashita et al., 2003). In our data set, this transporter was up-regulated in the AtMyb41-overexpressing seedlings, while AtSultr3;4 was down-regulated under salt treatment in the transgenic lines but not in the wild type (Supplemental Table S1). These results support the hypothesis that AtMyb41 may be involved in the regulation of nutrient homeostasis.

Metabolomic analysis revealed strong differences between seedlings of AtMyb41 overexpressors and the wild type, indicated by constitutive changes in the level of primary metabolites including amino acids,
Organic acids, and sugars (Tables I and II). Some of the AtMyb41-induced metabolic changes, such as the increase in amino acids and organic acids, have been observed under various abiotic stress conditions (Guy et al., 2008; Sanchez et al., 2008b). It is unlikely that the altered metabolic phenotype of AtMyb41 overexpressor seedlings was a result of changes in growth rate, as reduced plant size was evident only later in plant development. Almost all of the major metabolic changes were observed in seedlings but not in adult plants of the AtMyb41 transgenic lines, which indicates some form of developmental control of AtMyb41 function. The potential involvement of Myb TFs in the control of primary metabolism is an interesting area for further research, since, to the best of our knowledge, this family of TFs has so far only been shown to be involved in the control of secondary metabolism (Borevitz et al., 2000; Xie et al., 2006).

Consistent with the changes in metabolite levels, transcript levels of genes encoding a variety of enzymes involved in central metabolism were affected in the AtMyb41 overexpressors, including β-amylase (AtBmy1), pyruvate kinase (AtPK), phosphoglycerate/biphosphoglycerate mutase (AtBpm), Suc-P synthase (AtSprs2f), Ala-glyoxylate aminotransferase (AtAg1), Gln synthetase (AtGln-1;4), and Tyr aminotransferase (AtTaf3). Furthermore, transcripts for several transporters, including sulfate (AtSultr1;2 and AtSultr3;4), nitrate (AtNr12;4), sugar, and amino acid transporters were differentially regulated (Supplemental Table S1).

Despite the negative impact of AtMyb41 overexpression on the growth of adult plants (Fig. 2), these lines showed few differences in metabolite levels compared with wild-type controls under nonstressed or stressed conditions at this developmental stage. Only myoinositol and galactinol levels were significantly lower in adult AtMyb41 overexpressors compared with wild-type controls, and raffinose levels showed a similar trend (Fig. 5). Note that the raffinose biosynthetic pathway, which includes all of these three compounds, has been linked to osmotic and cold stresses in Arabidopsis (Taï et al., 2002; Zuther et al., 2004). Two galactinol synthase genes (AtGols2 and AtGols4) were deregulated in the AtMyb41-overexpressing seedlings (Supplemental Table S1), suggesting the involvement of AtMyb41 in transcriptional control of this metabolic pathway. Taken together, this indicates that at least some of the stress-related roles of AtMyb41 in seedlings are conserved at later stages of plant development. Consistent with this idea, some of the transcripts that were differentially expressed between wild-type and transgenic seedlings were also differentially regulated under stress conditions in adult plants (Fig. 6).

**Figure 5.** Metabolites significantly changed in shoots of mature AtMyb41-overexpressing plants grown in soil under different stress conditions. Data represent means ± so of eight independent biological replicates. Asterisks highlight statistically significant difference between the wild type (Wt) and transgenics within each treatment at P < 0.01 (ANOVA).
Cominelli et al. (2008) identified numerous genes that were either up- or down-regulated in AtMyb41 overexpressors compared with the wild type under nonstress conditions. We retested 20 of these by real-time quantitative RT-PCR but found few that were regulated in the same way in our AtMyb41 overexpressors (Supplemental Fig. S4A). Although some of these genes were regulated in the wild type by abiotic stress (salt, drought, cold) or ABA, most were regulated in the same way in our AtMyb41 overexpressors (Supplemental Fig. S4, B–E). Therefore, few if any of these genes appear to be controlled by AtMyb41. The discrepancies between our results and those of Cominelli et al. (2008) may be explained, in part, by differences in the magnitude of the effects of AtMyb41 overexpression in the different transgenic lines. The AtMyb41 overexpressors of Cominelli et al. (2008) were highly stunted, while those in this study were only moderately affected in growth, and only at later stages of development. Differences in plant culture and treatment conditions may also account for some of the differences observed between the two studies. It should also be pointed out that the results of Cominelli et al. (2008) lack internal consistency: some of their results on cell wall-related gene transcripts obtained by RT-PCR were not confirmed by their microarray experiments, undermining their conclusion that changes in the expression of such genes in the AtMyb41 overexpressors may account for the growth defects of their transgenic lines. In fact, no causal relationship between cell wall-related genes and...
the dwarf phenotype of their AtMyb41 overexpressors was proven (Cominelli et al., 2008).

Whatever the explanation for the growth defect in AtMyb41 overexpressors, it seems unlikely that it was caused by constitutive activation of stress pathways by AtMyb41, as none of the stress-related metabolites identified in previous studies, including amino acids, organic acids, sugars, and polyols (Sanchez et al., 2008b), were altered in mature, nonstressed transgenic plants compared with the wild-type controls (Fig. 4). In contrast to previous results (Cominelli et al., 2008), we observed no increase in the sensitivity of growth to salt and drought stresses of AtMyb41-overexpressing plants compared with wild-type controls, which is perhaps not surprising given the multigenic nature of abiotic stress tolerance. Again, differences between these two studies in this regard may be related to differences in the severity of the growth defects exhibited by the two sets of AtMyb41 overexpressors, with the dramatic dwarf phenotype observed by Cominelli et al. (2008) reflecting marked pleiotropic effects that would confound any interpretation of the physiological roles of AtMyb41.

In summary, we demonstrated the involvement of the ABA-regulated AtMyb41 TF in the control of distinct cellular processes in Arabidopsis seedlings, including negative regulation of short-term transcriptional responses to osmotic stress and associated changes in primary metabolism.

MATERIALS AND METHODS

Plant Material, Growth, and Experimental Conditions

Arabidopsis (Arabidopsis thaliana) lines overexpressing AtMyb41 were obtained using the PyA4h2610 cDNA clone from the ORFeome collection (Gong et al., 2004). Through the Gateway system (Invitrogen), the At4g28110 open reading frame was cloned into PMDC 32 ( Curtis and Grosnicklaus, 2003), where the expression is driven by the constitutive Cauliflower mosaic virus-35S promoter. Plants were transformed and selected with kanamycin for at least three generations.

For in vitro culture, approximately 100 seedlings were grown at 22°C in sterile liquid medium in Erlenmeyer flasks on a shaker under constant fluorescent light (approximately 50 μm2 s−1 m−2) in the flask; Scheible et al., 2004). Seven days after sowing, the medium was changed, and on day 9, NaCl or mannitol was added at a final concentration of 100 or 200 mM, respectively. Whole seedlings were harvested after 1, 2, 3, 6, 12, 18, and 24 h. Each experiment consisted of sample sets with at least three biological replicates (i.e. independent flasks). For hydroponic culture, seeds were sown in 0.5-mL plastic tubes filled with half-strength Hoagland medium (Hoagland and Arnon, 1938) including 0.8% agar. After 1 week, tubes were cut open at the bottom and transferred to a 2-L box filled with nutrient solution without agar and grown at 20°C and 12 h of light/12 h of darkness. The salt acclimation experiment was performed by increasing NaCl concentration weekly in three steps, from 0 to 10 mM, 25 mM, and 50 mM NaCl, with fresh nutrient solution each week. Medium was also changed every week for control plants. For greenhouse culture, plants were grown in soil (type GS90 + vermiculite; Einheitserde) using 10-cm pots under 20°C/18°C day/night temperatures with a long-day (16 h) photoperiod (minimum 200 μm2 s−1 m−2). Salt and drought stress treatments were performed on 1-week-old plants, watering with a 50 mM NaCl solution or withholding irrigation for 2 weeks, respectively. For cold stress, 3-week-old plants were transferred to a 4°C growth chamber with a 16-h photoperiod at 90 μm2 s−1 m−2. ABA-treated plants were sprayed with 100 μM ABA solution 24 h before harvest. For each condition, rosette leaves were harvested before bolting in eight biological replicates consisting of pools of five plants each.

Gene Expression Analysis

For the Affymetrix GeneChip Arabidopsis ATH1 Genome Array experiments, RNA extraction was performed from seedling material grown in vitro from three independent experiments in pools of three biological replicates each (i.e. independent flasks). Total RNA was isolated using the hot borate method (Wan and Wilkins, 1994), and quality and quantity were assessed with a Bioanalyzer 2100 using RNA 6000 NanoChips (Agilent Technologies) and a NanoDrop ND-1000 spectrophotometer (NanoDrop Technologies), respectively. RNA was labeled with the Message Amplify-Biotin Enhanced kit following the manufacturer’s instructions (Ambion). Hybridization and scanning were performed at ATLAS Biolabs. For quantitative real-time RT-PCR analysis, total RNA was treated with TURBO DNAse (Ambion) and first-strand cDNA was synthesized with an oligo(dT) primer and SuperScript III reverse transcriptase (Invitrogen). Real-time PCR was performed using the 2xSYBR Green PCR Mastermix and an ABI Prism 7900HT Sequence Detection System (Applied Biosystems). Primer design, reaction conditions, cycling and dissociation curve parameters, DNA contamination, and 3′ to 5′ ratio checks were performed as described by Czechowski et al. (2005) without spike-in controls in a reaction volume of 10 μL. Amplification efficiency was assessed with the LineRegPCR program (Ramakers et al., 2003). Analysis of expression data was performed as described previously by Czechowski et al., 2004, 2005 using the geometric mean of three housekeeping genes for normalization (Vandesompele et al., 2002). The housekeeping genes were At1s39d (At2g28390), At1g33440, and At1g33200, selected among the most stably expressed genes in Arabidopsis (Czechowski et al., 2005). A list of the primers used is available in Supplemental Table S5.

Metabolite Analysis

Metabolomic analysis was performed essentially as described by Sanchez et al. (2008a). In brief, plant material (60 mg) was extracted with chloroform/methanol, and the polar fraction was prepared by liquid partitioning into water, derivatized, and injected in a GC/EL-TOF-MS system (Wagner et al., 2003). Peak height representing arbitrary mass spectral ion currents was normalized with the sample fresh weight and ribitol content for internal standardization, and the resulting metabolomic profiles were analyzed using the TagFinder software (Luukemann et al., 2008). A series of discrete metabolic features were obtained after filtering for those represented by three or more intercorrelated mass fragments within the whole data set. Metabolites were identified using the NIST05 software (www.nist.gov/srd/mlslist.htm) and the mass spectral and retention time index collection of the Golm Metabolome Database (Kopka et al., 2003). Mass spectral matching was manually supervised and accepted with thresholds of match > 650 (maximum 1,000) and retention time index < 1.0%. Data Analysis and Statistics

K-means clustering, principal component analysis, and ICA were used as clustering algorithms to analyze profiling data in a non-supervised approach, using the Institute for Genomic Research multiple experiment viewer software (TMEV_3.1), the pcaMethods package for the R programming language (www.bioconductor.org/packages/2.1/bioc/html/pcaMethods.html), and the MetaGeneAlyse Web page (http://metagenalyse.mpimp-golm.mpg.de).

Microarray raw data were analyzed using the bioconductor software package for R (Gentleman et al., 2004). Data quality was assessed with the affy (Gautier et al., 2004) and AffyPLM packages, and expression estimates were obtained with the Robust Multi-Array algorithm (Irizarry et al., 2003). Genes assigned as present (P < 0.05) using the MA55 present/absent algorithm were statistically tested for differential expression using mixed models with the LIMMA biocomparator package (Smyth, 2004). P values describing control versus treatment and genotype comparisons were corrected for multiple testing using the FDR correction (Benjamini and Hochberg, 1995). Metabolomic data were log_{10} transformed prior to statistical analysis, performed with ANOVA using the TMEV_3.1 software.

Supplemental Data

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

Supplemental Figure S1. Root-shoot expression ratio of selected genes identified in the microarray analysis as differentially expressed in AtMyb41-overexpressing seedlings.
Supplemental Figure S2. cis-Regulatory elements in the putative promoter region of AtMYB41 identified from the PLACE database (www.dma.afrc.go.jp/PLACE).

Supplemental Figure S3. Coexpression analysis of the 10 Myb TEs using the Genevestigator database (www.genevestigator.ethz.ch).

Supplemental Figure S4. Comparison of the expression of the genes most highly regulated by AtMYB41 overexpression in the study of Cominelli et al. (2008) with the expression in the independent transgenic lines (1 and 7) described in our study.

Supplemental Table S1. Transcriptomic profile data from seedlings.

Supplemental Table S2. Metabolic profile data from seedlings.

Supplemental Table S3. Metabolic profile data from rosettes.

Supplemental Table S4. Arabidopsis Genome Initiative codes of all of the genes described.

Supplemental Table S5. List of primers used for quantitative real-time RT-PCR.

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