HDA18 Affects Cell Fate in Arabidopsis Root Epidermis via Histone Acetylation at Four Kinase Genes

Cui Liu,a,b,1 Lin-Chen Li,a,b,1 Wen-Qian Chen,a,b Xian Chen,c Zhi-Hong Xu,a,b and Shu-Nong Bia,b,2

a Peking University-Yale Joint Research Center of Agricultural and Plant Molecular Biology, State Key Laboratory of Protein and Plant Gene Research, College of Life Sciences, Peking University, Beijing, 100871, China
b The National Center of Plant Gene Research, Beijing, 100871, China
c Department of Biochemistry and Biophysics, School of Medicine, University of North Carolina, Chapel Hill, North Carolina 27599

The differentiation of hair (H) and non-hair (N) cells in the Arabidopsis thaliana root epidermis is dependent on positional relationships with underlying cortical cells. We previously found that histone acetylation relays positional information and that a mutant altered in the histone deacetylase family member HISTONE DEACETYLASE 18 (HDA18) exhibits altered H and N epidermal cell patterning. Here, we report that HDA18 has in vitro histone deacetylase activity and that both mutation and overexpression of HDA18 led to cells at the N position having H fate. The HDA18 protein physically interacted with histones related to a specific group of kinase genes, which are demonstrated in this study to be components of a positional information relay system. Both down- and upregulation of HDA18 increased transcription of the targeted kinase genes. Interestingly, the acetylation levels of histone 3 lysine 9 (H3K9), histone 3 lysine 14 (H3K14) and histone 3 lysine 18 (H3K18) at the kinase genes were differentially affected by down- or upregulation of HDA18, which explains why the transcription levels of the four HDA18-target kinase genes increased in all lines with altered HDA18 expression. Our results reveal the surprisingly complex mechanism by which HDA18 affects cellular patterning in Arabidopsis root epidermis.

INTRODUCTION

How cells are arranged in a particular spatial order is fundamental to the development of multicellular organisms. The single-layered Arabidopsis thaliana root epidermis consists of two types of cells, hair (H) and non-hair (N) cells, in an arrangement that depends on their spatial relationships with underlying cortical cells. Cells residing over the intercellular spaces between cortical cells (the H position) differentiate into H cells, while those directly over cortical cells (the N position) differentiate into N cells (Dolan et al., 1994). This well-characterized position-dependent cellular differentiation serves as a model system for understanding pattern formation in plants (Schiefelbein et al., 2009). Position-dependent cellular differentiation is known to be regulated by a hierarchical regulatory system consisting of at least three levels. The first level is a GL2-centered transcription factor network (TFN) that includes transcription factor genes such as GLABRA2 (GL2), WEREWOLF (WER), CAPRICE/TRIPTYCHON/ENHANCER OF TRY AND CPC1 (CPC/TRY/ETC1), TRANSPARENT TESTAGLABRA (TTG), and GLABRA3/ENHANCER OF GLABRA3 (GL3/EGL3). Referred to as pattern genes, these factors determine the fates of cells located at the N and H positions in root epidermis. Additional players in this fate specification include MYB23 (Tominaga et al., 2007; Kang et al., 2009; Schiefelbein et al., 2009), GL2 EXPRESSION MODULATOR (GEM) (Caro et al., 2007), and ADENOSINE DIMETHYL TRANSFERASE 1A (DIM1A) (Wieckowski and Schiefelbein, 2012). The second level of regulation comprises the plasma membrane-localized receptor-like kinases, such as SCRAMBLED (SCM) and BRASSINOSTEROID INSENSITIVE 1 (BRI1), that sense the N and H positions (Kwak et al., 2005; Kwak and Schiefelbein, 2007, 2008; Kuppusamy et al., 2009). The third level concerns the proper differentiation of cortical cells, where positional information presumably originates, in which JACKDAW (JKD) is involved (Hassan et al., 2010). However, some key questions remain unanswered, including how positional information sensed in the plasma membrane is transduced to the nucleus where pattern genes function.

Previously, we found that the application of trichostatin A (TSA), a specific inhibitor of histone deacetylase (HDAC), alters cellular patterning in the Arabidopsis root epidermis (i.e., confers H fate to cells at the N position) by affecting the expression of pattern genes (Xu et al., 2005). This finding suggests that histone acetylation is involved in relaying positional information during cellular patterning. Further supporting this, cells at the N position are also converted to H fate in a mutant containing defective HDA18 (Xu et al., 2005). Arabidopsis HDA18 contains an HDAC domain and was therefore annotated as a member of the HDAC family (Figure 1A; see Supplemental Figure 1 online; Pandey et al., 2002). Although HDA18 is closely grouped with HDA5 and HDA15 in Class II of the RPD3/HDA1 subfamily (Pandey et al., 2002), it differs in function from HDA5 and HDA15, as no abnormal cellular patterning in the root epidermis was observed in mutants for the latter two genes (Xu et al., 2005). Alinsug et al. (2009) reported the presence of multiple conserved domains in the HDA18 protein with various predicted biological functions, based on similar domains in yeast and mammalian cells (Yang and Seto, 2008). However, none of these functions have been experimentally verified in HDA18.
Here, we report that \textit{HDA18} encodes a protein with HDAC activity. Either reducing or increasing the expression of \textit{HDA18} resulted in conversion of cells at the N position to H fate. Unexpectedly, we found that the \textit{HDA18} protein did not directly bind to and regulate the transcription of pattern genes, but instead it directly bound to and affected the transcriptional regulation of other types of genes, including several kinase genes. These data demonstrate that \textit{HDA18} affects cellular patterning by regulating the transcription of a group of kinase genes through histone acetylation.

**RESULTS**

\textbf{HDA18 Encodes a Protein with HDAC Activity}

\textit{HDA18} is located on chromosome 5. The genomic sequence contains 3202 bp, and the coding sequence contains 2049 bp, including eight exons. Analysis of data at AREX (Birnbaum et al., 2003; Brady et al., 2007; http://www.arexdb.org) indicated that \textit{HDA18} is expressed at low levels, with no tissue preference. These results are consistent with previous in situ hybridization observations (Xu et al., 2005). Because of the similarity between the \textit{hda18} mutant phenotype and the effects of the HDAC inhibitor TSA on cellular patterning of the root epidermis, we tested recombinant \textit{HDA18} protein for HDAC activity. The recombinant protein had significant HDAC activity, which was concentration dependent and inhibited by TSA (Figures 1B and 1C; for detailed data, see Supplemental Figure 1 online). An in-gel assay, using hyperacetylated histones extracted from HeLa cells as substrates and commercially available histone-specific (but site nonspecific) antibodies as indicators, revealed that the recombinant protein deacetylated all four core histones (Figure 1C), suggesting that the HDAC domain of \textit{HDA18} does not have preferential activity on any of the core histones.
Transcriptome analysis of enhanced green fluorescent protein (EGFP)-labeled HDA18 (see Supplemental Figure 2 online) in onion (*Allium cepa*) epidermis revealed that the HDA18 protein was localized to both the nucleus and cytoplasm (Figure 1D), which is consistent with bioinformatic predictions (Alinsug et al., 2009). This result was further verified by observation of EGFP localization in stable transgenic Arabidopsis lines containing the same construct for EGFP-labeled HDA18 (Figure 1E; see Supplemental Figure 2 online).

**Both Down- and Upregulation of HDA18 Convert Some N Cells to H Fate**

To understand further the role of HDA18 in cellular patterning, we analyzed the phenotypes of a T-DNA insertion mutant (*hda18-2*), an RNA interference (RNAi) line (*HDA18 RNAi*), an overexpression (OE) line driven by the 3SS promoter P<sub>3SS</sub>: HDA18 (HDA18 OE/3SS), and an OE line driven by the promoter of the WEREWOLF gene P<sub>WER</sub>:HDA18-GUS (HDA18 OE/WER; see Supplemental Figure 2 online). The *hda18-2* mutant and HDA18 RNAi line exhibited conversion of some cells at N positions to H fate, similar to the previously described *hda18-1* mutant line (Salk_006938) (Xu et al., 2005). Unexpectedly, however, the two HDA18 OE lines also displayed this phenotype (Figure 2A). The number of cells at N positions that were converted to H fate significantly increased in both mutants and overexpressing lines based on statistics analysis compared with wild-type plants (see Supplemental Table 1 online). Introduction of an N cell-specific reporter, the GL2 promoter driving green fluorescent protein (GFP) expression in the *hda18-2* mutant, enabled us to identify cell fate patterns (Figure 2B, asterisk; see Supplemental Figure 3 online), further indicating the conversion of cells at the N position to H fate.

We attempted to rescue the mutant phenotype by complementation. However, possibly because of the low native expression level of HDA18, all transgenic lines were found to overexpress the gene and thus exhibited the corresponding phenotype (see Supplemental Figure 4 and Supplemental Table 1 online).

To test whether the effect of HDA18 could be enhanced by HDA5 and HDA15, single mutants that do not have altered cellular patterning in the root epidermis (Xu et al., 2005), we introduced artificial microRNA constructs targeting HDA5 and HDA15 into the *hda18-2* mutant. We also introduced artificial microRNA constructs targeting HDA5 and HDA18 into the *hda15* mutant (Salk_004027). No enhanced phenotypes were observed in transgenic lines in which all three targeted genes were downregulated (see Supplemental Figure 4 online). These results suggest that the role of HDA18 in the production of the mutant phenotype is independent of HDA5 and HDA15, its two most closely related members of the Class II RPD3/HDA1 subfamily (Alinsug et al., 2009).

**HDA18 Does Not Affect Cellular Patterning through Direct Regulation of Pattern Genes**

To test whether altered HDA18 expression affected the GL2-centered TFN, we examined the expression of five representative pattern genes (*CPC, WER, GL2, TTG, and GL3*) and related genes (EGL3, GEM, and SCM) in *hda18-2*, HDA18 RNAi, and HDA18 OE/3SS. We did not further analyze *hda18-1* or HDA18 OE/WER lines at the molecular level because the former is a weak allele and the latter has a similar phenotype to the HDA18 OE/3SS line, with no obvious differential expression of HDA18 in the H and N position (see Supplemental Figure 2 online). We found that the expression of CPC was significantly downregulated in all three lines (Figure 3A). Expressions of TTG and GL3 were upregulated in the mutant line, while those of WER GL2, EGL3, GEM, and SCM were not changed significantly (Figure 3A). These results reveal that the
pattern of gene expression was affected differentially by altered levels of HDA18 expression.

We previously determined that the histone acetylation status of pattern genes was altered upon treatment with the HDAC inhibitor TSA (Xu et al., 2005), and we confirmed here that HDA18 has in vitro HDAC activity. We therefore examined whether HDA18 expression affects the histone acetylation status of pattern genes. Using the previously identified DNA fragments that displayed altered levels of histone acetylation in response to TSA treatment (Xu et al., 2005), we found that upon down- or upregulation of HDA18 expression, the acetylation levels of H3 and H4 increased to some extent in three representative pattern genes, CPC, WER, and GL2. The increases in acetylation of H3 at CPC and WER were statistically significant (P < 0.05) in the HDA18 RNAi line, while those of H3 and H4 at GL2 were statistically significant (P < 0.05) in hda18-2 and HDA18 OE/35S lines (Figures 3B and 3C). These data reveal that although the downregulation of HDA18 indeed increased histone acetylation, consistent with the previously observed TSA effects, the increased histone acetylation status of the HDA18 OE/35S line could not be directly explained by HDA18 functioning as an HDAC.

Figure 3. Representative Pattern Gene Expression Levels and Histone Acetylation Status of CPC, WER, and GL2 in Lines with Altered HDA18 Expression.

(A) Expression levels of pattern genes were altered in root tips of hda18-2 mutant, RNAi, and OE lines. Data show mean ± SD from four to seven independent real-time PCR experiments, each with three replicates (*P < 0.05 and **P < 0.01; Student’s t test). Col, Columbia.

(B) and (C) Histone acetylation status of H3 and H4, examined by ChIP-PCR with AcH3 and AcH4 antibodies, at CPC, WER, and GL2 sequences in root tips of hda18-2 mutant, RNAi, and OE lines. Data show mean ± SD from three independent experiments, each with three replicates (*P < 0.05 and **P < 0.01; Student’s t test).

(D) HDA18 protein does not bind pattern genes based on ChIP-PCR analysis of regions shown in orange. PR, promoter region; TR, transcribed region.
To clarify further if HDA18 is involved in the transcriptional regulation of pattern genes, we examined whether the HDA18 protein directly binds to chromatin, thus altering pattern gene-related histone acetylation, using an antibody against HDA18 (see Supplemental Figure 5 online). Surprisingly, none of the DNA fragments tested were enriched in this chromatin immunoprecipitation (ChIP) experiment (Figure 3D). Because the primers used in the ChIP-PCR assay covered only limited areas of chromatin, we performed a ChIP-chip screen to search for possible binding sites at the genome level (see Supplemental Figure 5 online). Among the 286 enriched DNA fragments (representing putative HDA18 protein binding sites), none was related to any of the pattern genes (see Supplemental Data Set 1 online).

Taken together, we conclude that although altered HDA18 expression affects the cellular patterning of the root epidermis, this effect does not appear to be due to the direct transcriptional regulation of pattern genes.

Identification of HDA18 Target Genes

As HDA18 did not directly regulate the expression of pattern genes, we explored how altered expression of HDA18 was linked to cellular patterning. We searched among the 286 DNA fragments identified in the HDA18 ChIP-chip experiment for genes with annotated functions potentially related to cellular patterning of the root epidermis and found that 13 of these fragments encoded kinases, in addition to nine encoding transcription factors, eight encoding chromatin modification factors, four functioning in root development, and one encoding a phosphatase (see Supplemental Data Set 1 online). These data suggest that HDA18 can directly bind to genes, as is common for HDAC proteins, and may affect cellular patterning via these target genes.

Because both SCM and BRI1 are plasma membrane–localized receptor-like kinases, we reasoned that there must be some downstream components that transduce the positional information sensed by the receptors. The preferential enrichment of kinase genes in the HDA18 ChIP-chip data suggested that HDA18 might function in the relay of positional information by regulating the transcription of these kinase genes. To test this possibility, we first verified that HDA18 binds to the 20 candidate DNA fragments, including all 13 putative kinase genes, by performing ChIP-PCR. We found that 15 candidates were enriched, whereas five were not (Figure 4A).

Both Down- and Upregulation of HDA18 Increase Expression of Some Targeted Kinase Genes

To examine whether HDA18 is involved in the transcriptional regulation of the targeted genes, we examined the expression of the verified HDA18-bound genes in hda18-2, HDA18 OE/35S, and TSA-treated wild-type plants. Among the 15 genes that were tested, two showed changes in expression that were correlated with HDA18 expression level (At1G19485 and At1G79000), five showed upregulation to various extents regardless of HDA18 expression levels in all lines (At3G27560, At4G26270, At4G31170, At4G31230, and At5G49470), and the remaining eight showed no significant changes in their expression levels that could be correlated with HDA18 expression (Figure 4B).

We then analyzed the mutant phenotypes of all 15 HDA18-targeted genes (see Supplemental Figure 6 online). We found that mutations in eight of the 15 genes led to the conversion of some cells at the N position to H fate (Figure 5A; see Supplemental Tables 2 and 3 online). Among these eight genes, six were kinases, one was a WD-40 gene, and one was a basic HELIX-LOOP-HELIX (bHLH) gene (Figure 5A; see Supplemental Data Set 1 online). Mutations in At5G49470 and At5G53890, both bound by HDA18 and annotated as kinase genes, did not induce cell fate conversion phenotypes in the root (see Supplemental Data Set 1 and Supplemental Table 3 online), indicating that these HDA18-targeted genes may either not be involved in the patterning process or may be involved in a redundant manner.

Although mutations of At1G18890 and At5G53890 produced the cellular patterning phenotype, the transcription levels of these genes were not significantly affected by that of HDA18. We therefore focused our further investigations on the remaining kinase genes (i.e., At3G27560, At4G26270, At4G31170, and At4G31230). First, we verified the phenotype by introducing the cell type–specific reporter P<sub>dr5</sub>GFP into the corresponding mutants. We found that GFP expression patterns were altered in the kinase mutants (Figure 5B; see Supplemental Figure 6 online), consistent with the phenotypes revealed by paraffin sectioning (Figure 5A).

We next examined the histone acetylation status of the four kinase genes in hda18-2, HDA18 RNAi, and HDA18 OE/35S at the verified HDA18 binding sites. The levels of H3 acetylation were significantly increased at At4G26270 in all three lines, at At4G31170 in HDA18 RNAi and HDA18 OE/35S, and At4G31230 in hda18-2 and HDA18 RNAi (Figure 4C). H4 acetylation was significantly increased at At3G27560 in HDA18 RNAi and HDA18 OE/35S (Figure 4D).

Taken together, these data indicate that HDA18 binds to and is involved in the transcriptional regulation of some genes, including At3G27560, At4G26270, At4G31170, and At4G31230.

HDA18-Targeted Kinase Genes Mediate the Conversion of Cells at the N Position to H Fate by either Down- or Upregulating mRNA Levels

We next explored how the cell conversion phenotype could result from both the upregulation of target kinase genes (caused by altered HDA18 expression) and the downregulation of these same genes (caused by the loss-of-function mutations). We chose the straightforward approach of constructing OE transgenic lines for these kinase genes to determine whether increased expression of these genes might produce a similar phenotype as loss-of-function mutations. OE lines for each of the four HDA18-targeted kinase genes, At3G27560, At4G26270, At4G31170, and At4G31230 (see Supplemental Figure 6 and Supplemental Table 3 online), indeed caused some cells at the N position to convert to H fate (Figure 5). These results demonstrate that both down- and upregulation of kinase gene expression could result in this phenotype, indicating that homeostasis of expression of the kinase genes is required for cellular patterning in the Arabidopsis root epidermis and implicating these kinase genes as components relaying positional information during this process.
Figure 4. HDA18 Protein Binds and Affects Transcription of Certain Kinase Genes by Changing Their Histone Acetylation Status.

(A) ChIP-PCR verification of binding of HDA18 protein to putative targets identified by ChIP-chip. The genes marked with asterisks were false positives. The numbers listed to the right indicate the sites identified in the ChIP-chip analysis (for detailed information, see Supplemental Data Set 1 online).

(B) Expression levels of HDA18-targeted genes in root tips with altered HDA18 expression, showing upregulation of four kinase genes (highlighted with frames) regardless of increased or decreased expression of HDA18. Data show mean ± SD from three to four independent experiments, each with three replicates (*P < 0.05 and **P < 0.01; Student's t test). Col, Columbia.

(C) and (D) Histone acetylation status of H3 and H4 correspond to altered HDA18 expression, examined by ChIP-PCR with AcH3 and AcH4 antibodies at the identified binding sites of selected kinase genes. Data show mean ± SD from five independent experiments, each with three replicates (*P < 0.05 and **P < 0.01; Student's t test).
Down- and Upregulation of HDA18 Increase Kinase Gene Transcription by Altering H3 Acetylation at Lysine-9 (Lys-9), Lys-14, and Lys-18 in Distinct Patterns

It is intriguing that both the down- and upregulation of HDA18 resulted in the cell conversion phenotype (Figure 2A). To address the underlying mechanisms of this, we examined the efficiency of enrichment of the HDA18 protein on the kinase genes. Figure 6B shows that as expected, the enrichment of HDA18 protein on the DNA of all four kinase genes was significantly reduced in the lines with reduced expression of the HDA18 gene. However, unexpectedly, the HDA18 enrichment level was similar to that of the wild type in the lines with increased HDA18 expression. These observations suggest that the phenotype of the upregulated HDA18 expression lines cannot simply be explained by decreased target binding by the HDA18 protein.

Figure 5. Identification of Kinase Genes as Components Involved in Cellular Patterning of the Root Epidermis.

(A) Cross sections of root tips of mutants of verified HDA18 target genes at the ends of root caps, showing cells with H fate at N positions (arrows). Col, Columbia.

(B) P_{glc}:GFP expression in roots of mutants (at3g27560, at4g26270, at4g31170, and at4g31230) and the wild type (Col). Asterisks represent the cells at N positions converted to H fate (no GFP signal detected).

(C) Cross sections of root tips of OE lines of selected HDA18 target kinase genes at the ends of root caps, showing cells with H fate at N positions (arrows).
Next, we analyzed the histone acetylation status of specific amino acid residues in the lines with altered HDA18 expression. As indicated in Figure 4, the overall histone acetylation at the kinase genes increased to various levels. As more significantly increased acetylation levels were observed in H3 than in H4, we chose H3 for further analysis. Among the seven known Lys residues available for acetylation in the H3 N-terminal tail, acetylated Lys-9, Lys-14, Lys-18, and Lys-23 are responsible for promoting transcription (Berger, 2007; Chen and Tian, 2007; Choi and Howe, 2009). Therefore, we examined the acetylation levels at Lys-9, Lys-14, Lys-18, and Lys-23 of H3 at the four kinase genes in the hda18-2 mutant, the RNAi line (HDA18 RNAi), and the OE line (HDA18 OE/35S).
Figures 6C to 6F show that although there were some variations, the acetylation levels at the H3 Lys residues changed in similar patterns: Except for At4G31230, the acetylation levels of H3K9 at the kinase genes were significantly enhanced under reduced levels of HDA18 but were not significantly changed with increased HDA18 expression (Figure 6C). The acetylation levels of H3K14 in all four kinase genes were significantly enhanced under both reduced and increased HDA18 levels (Figure 6D). In contrast with H3K9, the acetylation levels of H3K18 in all four kinase genes were significantly enhanced under increased HDA18 levels but not under decreased HDA18 levels, except in At4G31170 (Figure 6E). The H3K23 acetylation levels were all enhanced to some extent whether HDA18 was down- or upregulated (Figure 6F). The above data suggest that the down- and upregulation of HDA18 expression (i.e., the reduced or increased levels of HDA18 protein) affect the acetylation of the four detected H3 Lys residues differentially.

**DISCUSSION**

**HDA18 Protein Has HDAC Activity and Is Involved in Transcriptional Regulation**

HDA18 was previously identified as a member of the HDAC gene family based on sequence annotation. Here, we demonstrated that this protein does indeed have HDAC activity. Based on our ChIP-chip, ChIP-PCR, transcription, and mutant phenotype analysis of HDA18-targeted genes, we demonstrated that HDA18 plays a regulatory role in the transcription of its target kinase genes. The role of HDA18 in the regulation of other targeted genes remains to be examined.

In our previous work, we reported the involvement of HDA18 in cellular patterning of the root epidermis (Xu et al., 2005). Here we not only confirmed this observation, but also found that down- and upregulation of HDA18 expression resulted in similar phenotypes. With the observation that HDA18 affects cellular patterning through the function of target kinase genes, not known pattern genes, the results of this study reveal the complexity of the mechanisms for relaying positional information between plasma membrane–located receptor-like kinases, such as SCM and BRI1, and the GL2-centered TFN, consisting of nucleus-localized transcriptional factors. In addition, our findings present opportunities to decipher this complicated signaling network.

**Four Kinase Genes Are Involved in Positional Information Signaling during Cellular Patterning of Arabidopsis Root Epidermis**

We found that four kinase genes regulated by HDA18 (i.e., At4G26270, At3G27560, At4G31170, and At4G31230) are involved in the relay of positional information for cellular patterning in the root epidermis. It is likely that these kinases are downstream components in transmitting the positional information received by SCM or BRI1. Detailed root gene expression data provided by AREX LITE (Birnbaum et al., 2003; Brady et al., 2007; http://www.arexdb.org) revealed further expression information of the four genes in H and N cells. While the expression level of At4G31230 was quite low, those of the other three genes were at a comparable range to that of SCM (see Supplemental Table 4 online). These data are consistent with the roles of the four HDA18 targeted genes, which affect epidermal cell fate determination.

Information is limited regarding the functions of these kinase genes. Whereas At4G26270 is annotated as phosphofructokinase 3, and the cytoplasmic localization and tissue preferential expression patterns of this gene have been reported (Mustroph et al., 2007), the other three genes have only annotation information. At3G27560 is annotated as an ATN1-like kinase (Tregear et al., 1996; Heazlewood et al., 2004; Rudrabhatla et al., 2006), At4G31170 has STY-like kinase characteristics (Rudrabhatla et al., 2006), and At4G31230 belongs to the 1.4.1 (receptor-like cytoplasmic kinase IX) family (Kerk et al., 2003).

To understand the relationship between these kinase genes and pattern genes, we examined pattern gene expression in various transgenic lines, with both down- and upregulated kinase genes. The results were complex, and it was difficult to establish a simple causal relationship fitting the current model of the GL2-centered TFN for the expression of kinase genes and pattern genes (see Supplemental Figure 7 online). According to the current model of the GL2-centered TFN, which is well established based on mutant analysis, changes in the expression levels of pattern genes are considered to be key criteria for evaluating the potential involvement of other genes in cellular patterning of the root epidermis (Wieckowski and Schiefelbein, 2012). However, changes in the expression of pattern genes are not absolutely related to cellular patterning phenotypes. For example, pattern gene expression was significantly altered in the scr mutant, but no cellular patterning phenotype was observed (see Supplemental Figure 8 online). To explain the phenotypic changes in cellular patterning that resulted from altered kinase gene expression, three possibilities should be considered: The first is the homeostasis of the GL2-centered TFN, including the differential expression of the genes in H and N cells; the second is the complexity of a multifactor positional information signaling network, in which the kinase genes are integrated in various ways, with varying levels of expression of each gene affecting the operation of the network; and the third is that the kinase genes may influence genes involved in H cell differentiation downstream of the GL2-centered TFN. Clearly, our findings present tremendous challenges as well as opportunities for future investigations.

**Complicated Mechanisms Underlying the Regulation of Transcription of the Kinase Genes by HDA18**

Our findings that the four kinase genes are involved in positional information signaling explain why altered HDA18 expression converts cells at the N position to H fate. However, it is intriguing that down- and upregulated HDA18 expression affect acetylation related to the four kinase genes at H3K9, Lys-14, and Lys-18 differentially. As shown in the proposed model in Figure 7, these site-specific differential changes of acetylation levels can explain why both down- and upregulation of HDA18 result in similar changes of target gene transcription levels, thereby leading to a similar cellular patterning phenotype.
We hypothesize that HDA18 interacts with H3 associated with the four kinase genes at the region centered at H3K14, along with one or more hypothetical component(s), as a complex. This structure could maintain relatively low acetylation levels of H3K9, Lys-14, and Lys-18 because of the HDAC activity of HDA18 (Figure 7A). In downregulated HDA18 lines, the quantity of HDA18 protein is reduced, as shown in Figure 7B. Without HDA18, H3K9 and Lys-14 would not be deacetylated, which would result in increased acetylation as found in Figures 6C and 6D. The lack of significant enhancement of H3K18 acetylation levels suggests that other components may be involved in H3K18 deacetylation. Alternatively the HDA18-deficient structure may interfere with the efficiency of putative acetyltransferase functions. In upregulated HDA18 lines, the quantity of HDA18 protein is increased, possibly leading to the formation of an abnormal structure (Figure 7C). While HDA18 covers H3K9 in this structure, although perhaps not as efficiently as in the wild type, the additional HDA18 may make the hypothetical complex crowded and leave H3K14 and K18 untouched by HDA18 protein. This scenario is consistent with the enhanced acetylation levels of H3K14 and K18 detected in the upregulated HDA18 line (Figures 6D and 6E). This working model can successfully explain why both down- and upregulation of HDA18 resulted in upregulation of the kinase genes and, therefore, the cell conversion phenotype.

In conclusion, this study revealed the mechanism of HDA18’s role as an HDAC that affects cellular patterning in Arabidopsis root epidermis. We demonstrated the HDAC activity of HDA18, identified its target genes, among which four kinase genes were demonstrated to be components of a positional information

---

**Figure 7.** Model of Possible Mechanism for HDA18 Regulation of Transcription of the Four Kinase Genes.

The HDA18 target kinase genes function between the membrane-localized receptor-like kinases, such as SCM (orange rectangles) and BRI1 (open circles), and the pattern genes in the GL2-centered TFN (open rectangles).

**(A)** In the wild type, the HDA18 protein, perhaps with other unknown components, binds to the region containing H3K9 through Lys-23 of the H3 related to the four target kinase genes and maintains the acetylation of these residues at the proper levels for balanced transcription of the kinase genes.

**(B)** In the hda18 mutant, the quantity of HDA18 protein is reduced and the region containing H3K9 through K23 of the H3 related to the four kinase genes cannot be properly covered. The acetylation levels are therefore increased (green circles), which results in increased transcription of the four kinase genes (red waves). The latter disturbs the previously balanced expression of the pattern genes and results in the cell conversion phenotype.

**(C)** In the HDA18 OE line, surplus HDA18 protein may interfere with the interaction of HDA18 with the unknown components and lead to an abnormal structure, leaving H3K14 and H3K18 unbound by HDA18. This would result in increased acetylation at those sites, which results in increased transcription of the four kinase genes. The latter disturbs the previously balanced expression of pattern genes and results in the cell conversion phenotype similar to that seen in the hda18 mutants.
relay system, and demonstrated that HDA18 affects cellular patterning by regulating transcription of its target kinase genes through histone acetylation. Furthermore, we solved the puzzle of how both down- and upregulation of HDA18 expression converted N cells to H fate by discovering that under both situations, altered levels of HDA18 led to increased kinase gene transcription by altering H3 acetylation at Lys-9, Lys-14, and Lys-18 in distinct patterns. These findings not only present an opportunity for understanding how positional information is relayed during cellular patterning but also provide a case study for elucidating the underlying mechanism of the phenomenon that up- and downregulation of same gene cause the same phenotype.

**METHODS**

**Plant Materials**

All Arabidopsis thaliana kinase mutant seeds were obtained from the ABRC and are listed in Supplemental Table 2 online. SALK mutant line CS847004 is designated as hda18-2 herein, whereas hda18-1 represents the previously described SALK_006938 mutant line (Xu et al., 2005). The PGL2::GFP marker line was described previously (Lin and Schiefelbein, 2001). Plants were grown under the same conditions described previously (Xu et al., 2005).

**Generation of Recombinant HDA18 and HDAC Activity Assay**

A recombinant HDA18 protein was constructed with the HDAC domain of the HDA18 sequence at the C terminus and a maltose binding protein tag at the N terminus (see Supplemental Figures 5 and 9 online). The in vitro HDAC activity assays were conducted according to Xu et al. (2005) and Rundlett et al. (1996). TSA was purchased from Sigma-Aldrich (catalog number T8552).

**Construction of Transgenic Plants and Characterization of Phenotypes**

HDA18 OE construct was produced by cloning HDA18 coding sequence into pCAMBIA binary vector, driven by the cauliflower mosaic virus 3SS promoter (MaV3SS) (HDA18 OE/SSS) or 4-kb WER promoter fragment (Lee and Schiefelbein, 1999; Kwak and Schiefelbein, 2007) (HDA18 OE/ WER). HDA18 RNAi silencing was performed by cloning HDA18 coding region 1294 to 2026 into pCAMBIA vector in antisense/sense directions, respectively, to generate small hairpin RNA under the CaMV35S promoter.

**PCR was performed to identify T-DNA insertion location in selfed transgenic plants (Liu et al., 1995). To ensure that the phenotypes of the transgenic plants did not result from the interruption of other genes due to T-DNA insertion, we examined the insertion sites of our transgenic plants (see Supplemental Table 5 online). After verification, seeds collected from T1 plants were cultivated and processed to paraffin section phenotype inspection and other experiments.**

**Real-Time PCR Analysis and ChIP**

Examination of expression levels in root tips of plants with various genetic backgrounds was conducted with real-time PCR according to Xu et al. (2005). ChIP was also conducted according to Xu et al. (2005). The HDA18 antibody was raised in mouse (for detailed information, see Supplemental Figure 5 and Supplemental Table 6 online). Antibodies used for examining histone acetylation status by ChIP are listed in Supplemental Table 7 online. Primers used are listed in Supplemental Data Set 2 online.

**Accession Numbers**

Sequence data from this article can be found in The Arabidopsis Information Resource (http://www.arabidopsis.org/) or GenBank/EMBL data libraries under the following accession numbers: HDA18 (At5G61070), HDA5 (At5G61060), HDA15 (At3G18520), CPC (At2G46410), WER (At5G14750), GL2 (At1G79840), TIG (At5G24520), GL3 (At5G41315), EGL3 (At1G63650), GEM (At2G22475), SCR (At1G11130), and SGR (At3G54220); accession numbers of HDA18 target genes are list in Supplemental Table 2 online.

**Supplemental Data**

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

**Supplemental Figure 1.** HDA18 Has an HDAC Domain and Therefore Has Concentration-Dependent and TSA-Inhibited Histone Deacetylase Activity.

**Supplemental Figure 2.** Construction and Analysis of Different HDA18 Transgenic Lines.

**Supplemental Figure 3.** Introducing the PGL2::GFP Transcriptional Reporters into hda18 (CS847004) Mutant by Genetic Crosses.

**Supplemental Figure 4.** The Phenotype of the Transgenic Lines in Which the hda18 Mutant Is Rescued Is Similar to HDA18 OE, and the Phenotype of Transgenic Lines Containing Knocked Down HDA5/ HDA15/HDA18 Is Similar to That of hda18.
Supplemental Figure 5. ChIP-Chip Assays to Search for DNA Fragments Bound by HDA18.

Supplemental Figure 6. Expression of Kinase Genes Is Reduced in Mutants and Elevated in Overexpression Lines.

Supplemental Figure 7. Kinase Genes Affect Expression of Pattern Genes in Arabidopsis Root Epidermis.

Supplemental Figure 8. SCR Affects Expression of Pattern Genes but Not Cellular Patterning.

Supplemental Figure 9. Purification of mMBP-HDA18 to Perform in Vitro HDAC Activity Assays.

Supplemental Table 1. Root-Hair and Non-Hair Cell Specification in the Root Epidermis of Wild-Type, hda18, RNAi; HDA18 OE, and Rescue Lines.

Supplemental Table 2. Mutant Screening to Test Participation of HDA18 and Its Target Genes in Cellular Patterning of Arabidopsis Root Epidermis.

Supplemental Table 3. Root-Hair and Non-Hair Cell Specification in the Root Epidermis of the Wild Type, Mutants, and Overexpression Lines of Some HDA18 Targeted Genes.


Supplemental Table 5. Genome Positions of T-DNA Inserts in Transgenic Plants.

Supplemental Table 6. Procedure for Generation of the HDA18 Antibody.

Supplemental Table 7. Antibodies Used in the Experiments.

Supplemental Data Set 1. HDA18 Binding DNA Fragments by ChIP-Chip and ChIP-PCR–Verified DNA Fragments.

Supplemental Data Set 2. Primers Used in the Experiments.

ACKNOWLEDGMENTS

We thank John Schiefelbein (University of Michigan) and Philip Benfey (Duke University) for their advice on this project and discussions of the article. We also thank them for kindly providing the marker line used in this study. We thank Martin Hulskamp (University of Kiel) for discussions of the article. We thank Xiao-Dong Su, Jian-Guo Ji, and their students Cong Liu and Hai Pu (College of Life Sciences, PKU) for their help in generating and analyzing HDA18 recombinant protein and U-Jia Qu, Yu-Xian Zhu, and Jin-Dong Zhao of the College of Life Sciences for kindly sharing their equipment. We thank Min-Ping Qian and Ming-Hua Deng and their students Lin Wan and Quan Wang (School of Mathematical Sciences, PKU) for their help in analyzing ChIP-chip data. This work was supported by grants from the National Natural Science Foundation (30393114 and 30570901) and the Ministry of Science and Technology of People’s Republic of China (2003CB715906; to S.-N.B.).

AUTHOR CONTRIBUTIONS

C.L., L.-C.L., and S.-N.B. designed the experiments. C.L. and L.-C.L. performed most of the experiments, analyzed the data, and prepared the figures. W.-Q.C. performed some experiments. S.-N.B., X.C., and Z.-H.X. wrote the article. All authors contributed to analyzing the article.

Received November 2, 2012; revised December 22, 2012; accepted January 15, 2013; published January 29, 2013.

REFERENCES


HDA18 Affects Cell Fate in Arabidopsis Root Epidermis via Histone Acetylation at Four Kinase Genes
Cui Liu, Lin-Chen Li, Wen-Qian Chen, Xian Chen, Zhi-Hong Xu and Shu-Nong Bai
Plant Cell; originally published online January 29, 2013;
DOI 10.1105/tpc.112.107045

This information is current as of June 29, 2017

Supplemental Data /content/suppl/2013/01/23/tpc.112.107045.DC1.html
eTOCs Sign up for eTOCs at:
http://www.plantcell.org/cgi/alerts/ctmain
CiteTrack Alerts Sign up for CiteTrack Alerts at:
http://www.plantcell.org/cgi/alerts/ctmain
Subscription Information Subscription Information for The Plant Cell and Plant Physiology is available at:
http://www.aspb.org/publications/subscriptions.cfm

© American Society of Plant Biologists
ADVANCING THE SCIENCE OF PLANT BIOLOGY