Transcriptional Regulation of Arabidopsis LEAFY COTYLEDON2 Involves RLE, a cis-Element That Regulates Trimethylation of Histone H3 at Lysine-27

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INTRODUCTION

In eukaryotes, complex developmental programs require tightly regulated expression of a specific set of genes at both spatial and temporal levels. Chromatin state dynamics and transcription factors are involved in the underlying molecular mechanisms (Beisel and Paro, 2011). Recent research has emphasized the importance of histone posttranslational modifications, such as acetylation, methylation, ubiquitination, or phosphorylation, in these regulatory processes (Berger, 2007; Kouzarides, 2007; Zhang et al., 2007a; Lee et al., 2010). In plants, genome-wide chromatin and transcriptomic analyses have confirmed the correlation existing between histone posttranslational modifications and transcriptional activity (Pfluger and Wagner, 2007; Roudier et al., 2009, 2011; Lauria and Rossi, 2011). For instance, Histone H3 Lys (residues 4, 9, 27, and 36) methylations are strongly associated with the transcriptional regulation of plant genes (Li et al., 2008; Liu et al., 2010; Lafos et al., 2011; Zheng and Chen, 2011). H3K4me3 and H3K36me2/me3 are predominantly linked with active chromatin, whereas H3K9me1/me2 and H3K27me3 modifications are considered to be repressive. More specifically, dynamic regulation of H3K27me3 marking has been shown to play a crucial role in the developmental regulation of gene expression in eukaryotes, including plants (Kouzarides, 2007; Zhang et al., 2007a; Schatlowski et al., 2008; Bouyer et al., 2011; Zheng and Chen, 2011). H3K27me3 is extensively distributed over the transcribed and promoter regions of genes. It extends over large intergenic regions in animals, whereas the distribution seems to be more gene centered in plants (Turck et al., 2007; Zhang et al., 2007b; Schatlowski et al., 2008).

H3K27me3 deposition is catalyzed by Polycomb-group (PcG) proteins with a SET [for Su(var)3-9, Enhancer-of-zeste, Trithorax] domain that belong to Polycomb Repressive Complex2 (PRC2) (Schuettengruber and Cavalli, 2009; Simon and Kingston, 2009; Morey and Helin, 2010; Margueron and Reinberg, 2011). On this line, it has been recently shown that PRC2 activity is necessary for H3K27me3 deposition in plants (Schubert et al., 2006; Bouyer et al., 2011). PcG proteins were first identified in Drosophila melanogaster and are evolutionary conserved among higher eukaryotes, including plants (Ringrose et al., 2004; Hennig and Derkacheva, 2009; Chen et al., 2010; Sawarkar and Paro, 2010; Margueron and Reinberg, 2011; Zheng and Chen, 2011). The PRC2 complex is composed of four core proteins, including ENHANCER OF ZESTE [E(Z)]; a PcG protein with a SET domain and methyltransferase activity], EXTRA SEX COMBS (ESC; a WD40 domain protein), SUPPRESSOR OF ZESTE-12 (a zinc finger protein), and NUCLEOSOME REMODELING FACTOR55. PcG proteins act in establishing and maintaining inactive chromatin states at numerous target genes throughout development (Francis and Kingston, 2001; Schwartz et al., 2006; Schwartz and Pirrotta, 2008; Müller and Verrijzer, 2009; Köhler and Hennig, 2010; Margueron and Reinberg, 2011).

Recruitment of PRC2 at a specific locus likely relies on multiple mechanisms (Margueron and Reinberg, 2011). Genomic
domains named Polycomb Repressive Element (PRE) have been described mainly in Drosophila (Ringrose and Paro, 2007; Schuettengruber et al., 2007). PRE domains are characterized by short DNA motifs that include binding sites for regulatory proteins like PLEIOHOMEOtic (PHO), ZESTE (Z), and GAGA factors (GAFs) (Schuettengruber and Cavalli, 2009). PHO and GAFs would be directly involved in recruiting PRC2. Recently, PRE-like elements have also been identified in mice and humans (Sing et al., 2009; Woo et al., 2010). Nevertheless, our understanding of PRC2 recruitment is still scarce, and no PRE elements have been identified in plants to date (Schatlowski et al., 2008; Morey and Helin, 2010; Sawarkar and Paro, 2010; Smith and Shilatifard, 2010; Enderle et al., 2011; Marguero and Reinberg, 2011).

In Arabidopsis thaliana, the three E(Z) homologs, namely MEDEA (MEA) and the two partially redundant proteins CURLY LEAF (CLF) and SWINGER (SWN), act throughout plant development (Kyosue et al., 1999; Luo et al., 1999; Pien and Grossniklaus, 2007; Hennig and Derkacheva, 2009; Köhler and Hennig, 2010; Rodrigues et al., 2010; Zheng and Chen, 2011). MEA predominantly represses the MADS box gene PHERES1 and MEA itself in the endosperm (Baroux et al., 2006; Gehring et al., 2006; Jullien et al., 2006). CLF and SWN are required for the repression of floral homeotic genes, such as AGAMOUS (AG) or SHOOTMERISTEMLESS (STM) (Goodrich et al., 1997; Katz et al., 2004; Schubert et al., 2006; Farrona et al., 2008). PRC2 activity also represses the transcription of the master regulators of seed development during vegetative and/or endosperm development (Makarevich et al., 2006; Bouyer et al., 2011). These master regulators include LEAFY COTYLEDON1 (LEC1), a protein homologous to the HAP3 subunits of the CAAT Box binding Factors, and three B3-domain transcription factors, namely, ABA INSENSITIVE3 (ABI3), FUSCA3 (FUS3), and LEC2 (Braybrook and Harada, 2008; Santos-Mendoza et al., 2008). These AFL (for ABI3, FUS3, and LEC) regulatory proteins control a network of local and redundant gene regulations (Santos Mendoza et al., 2005; To et al., 2006). Among these regulators, LEC2 is specifically expressed in embryos within a short temporal window, from 4 d after pollination (DAP) to 14 DAP, peaking at 10 DAP, and is not expressed in any other tissues (Stone et al., 2001; Kroj et al., 2003). The ectopic expression of LEC2 in transgenic plants triggers the formation of somatic embryos as well as other organ-like structures and confers embryonic characteristics to seedlings (Stone et al., 2001).

Consistent with the involvement of proteins with a SET domain, other reports have confirmed that the expression of LEC2 is controlled, in a developmental manner, by PcG complexes. It has been shown recently that FERTILIZATION INDEPENDENT ENDOSPERM, the Arabidopsis ESC homolog of the PRC2 complex, negatively regulates the expression LEC2 and other AFL genes (Bouyer et al., 2011). PRC1-like ring finger proteins also repressed the expression of the AFL genes (Chen et al., 2010). In addition, PICKLE (PKL), a chromatin remodeler of the CHD3 family, and a closely related homolog (PKR2) are also involved in this regulation (Ogas et al., 1999; Zhang et al., 2008; Aichinger et al., 2009). PKL promotes indirectly H3K27me3 deposition at different loci, including LEC2, in vegetative tissues, through the induction of PcG gene expression (e.g., SWN or EMBRYONIC FLOWER2) (Aichinger et al., 2009, 2011). Other mechanisms involved in the regulation of LEC2 expression have been identified (Zhang and Ogas, 2009). For example, the inhibition of histone deacetylase activity triggers LEC2 expression upon germination (Tanaka et al., 2008). ASIL1 (for Arabidopsis 6b-interacting protein 1-like 1), a plant-specific trihelix factor, represses LEC2 during both germination and early maturation phase (Gao et al., 2009).

Besides the large amount of data accumulated regarding the regulation of LEC2 expression, the DNA cis-elements involved in the specific expression of LEC2 during seed development are unknown. More specifically, the means by which the LEC2 locus is marked by H3K27me3 during vegetative development remain to be determined. In this work, we identified and functionally characterized three cis-regulatory elements involved in the developmental regulation of LEC2 expression. Two of them were found to be essential for the transcriptional activation of LEC2. The first one presents some similarities with CarG regulatory elements recognized by MADS box transcription factors. The second one is similar to a GAF’s box and bound by plant BASIC PENTACYSTEINE (BPC) proteins, both in yeast and in vitro. The third element, which we named Repressive LEC2 Element (RLE), is 50 bp long and is necessary for the repression and H3K27 trimethylation of LEC2 in vegetative tissues. Remarkably, the RLE cis-element was also sufficient to regulate the activity of an unrelated promoter (PFSH4) and to promote H3K27me3 mark deposition in transgenic plants. Therefore, RLE acts as a functional homolog of the PRE element found in Drosophila. Taken together, the data presented here shed new light on the regulation of LEC2, a master regulator of seed development and bring important new insights into the regulation of H3K27me3 deposition and, thus, PRC2 recruitment in plants.

RESULTS

Identification of the cis-Regulatory Elements That Control the Specific Expression of LEC2

It has been previously shown that the 2.5-kb sequence located upstream of the LEC2 open reading frame recapitulates the embryo-specific pattern of LEC2 expression when fused to the β-glucuronidase (GUS) reporter gene (Stone et al., 2001; Kroj et al., 2003). Here, it was shown that a 500-bp-long fragment, hereafter denoted as PLEC2, was sufficient to faithfully confer a similar expression pattern (Figure 1A). In addition, the expression of the LEC2 cDNA under the control of PLEC2 fully complemented the lec2-4 mutation (see Supplemental Figure 1 online).

To gain further insight into the cis-regulatory elements necessary for LEC2 expression during embryogenesis, a series of 5′-end deletions was performed on PLEC2, and the resulting DNA fragments were fused to the GUS reporter gene to test their respective transcriptional activity in transgenic plants (Figure 2A). The analysis of GUS activity identified a region between −447 and −400 bp upstream of the first codon that is necessary for the expression of LEC2 in the embryo. Deletions every 5 bp narrowed this region down to a 5-bp motif (CATAT; between −447 and −442 bp). This 5-bp regulatory sequence showed
no similarity to any known consensus cis-regulatory element described in public databases.

In parallel, a series of 3'-end deletions of \( P_{LEC2} \) was performed and fused to a minimal 35S promoter carrying a transcription start site derived from the cauliflower mosaic virus that was placed upstream of the GUS reporter gene (Debeaujon et al., 2003). Analysis of the GUS activity in transgenic plants indicated that the 50-bp region upstream of the first codon, which corresponds to the 5' untranslated region of \( LEC2 \), was required for the activity of \( P_{LEC2} \) in this context (Figure 2B). Surprisingly, further deletion of 150 bp resulted in the recovery of GUS expression. In fact, the promoter fragment extending from \(-500\) to \(-250\) bp was sufficient to confer ubiquitous GUS expression throughout plant and seed development. This analysis suggested that the 50-bp domain comprised between \(-200\) and \(-150\) bp contained sufficient information to repress the transcriptional activity of \( P_{LEC2} \) (Figure 2B).

**LEC2 Expression Relies on a CT-Rich Element Bound by BPC Proteins**

In silico analysis of the 50-bp sequence located upstream of the first codon revealed a GAGA box motif (inverted CT repeats; Figure 3A) previously found in different plant promoters (Meister et al., 2004; Monfared et al., 2011; Wanke et al., 2011). The conversion by site-directed mutagenesis of CT to CA repeats (mCA) did not affect the transcriptional activity of \( P_{LEC2} \) in planta, whereas changing CT to AT repeats (mAT) fully abolished the activity of \( P_{LEC2} \) (Figure 3A). Previous analyses have shown the positive effect of adding CT repeats on promoter activity (Pauli et al., 2004). Here, the addition of three CT repeats to the GAGA box led to the ectopic activation of \( P_{LEC2} \) in pollen grains (see Supplemental Figure 2 online). These data indicated that the GAGA box made of eight C-T (or A) dinucleotide repeats is essential for the correct expression of \( LEC2 \).
In plants, GAGA motifs are bound by BPC proteins (Meister et al., 2004; Monfared et al., 2011; Wanke et al., 2011). In Arabidopsis, the BPC family contains seven members grouped into three classes. The accumulation of BPC mRNA in embryos shown in the databases (http://bbc.botany.utoronto.ca/efp/cgi-bin/efpWeb.cgi) was confirmed by RT-PCR experiments (Figure 3B). All BPC genes but BPC5 (which likely is a pseudogene) (Meister et al., 2004; Monfared et al., 2011) were expressed in 10-d-old embryos.

Then, the ability of BPC proteins to interact with \( P_{\text{LEC2}} \) was tested in yeast one-hybrid experiments (Figure 3C). A strong interaction was detected for the three BPCs of class I (BPC1, 2, and 3), whereas a weak interaction was detected for BPC proteins that belong to class II (BPC4) and III (BPC7). To define the ability of BPC to bind directly to the GAGA motif found in \( P_{\text{LEC2}} \), in vitro electrophoretic mobility shift assays (EMSAs) were performed with recombinant BPC2 (class I) and BPC4 (class II) proteins. Both proteins BPC2 and BPC4 proteins were able to interact with the poly-CT double-stranded probe (Figure 3D). Competition experiments with wild-type and mutated (m47) probes demonstrated the specificity of these interactions. Finally, the accumulation of \( LEC2 \) mRNA was measured in seeds of available \( bpc \) mutants (i.e., \( bpc1 \), \( bpc2 \), and \( bpc3 \) single or the corresponding multiple mutants). No significant differences were observed in comparison to wild-type seed mRNA level (see Supplemental Figure 3 online).

Taken together, these results showed that \( LEC2 \) expression relies on a GAGA box and that BPC proteins are probably involved in the transcriptional regulation of \( LEC2 \). Further analyses of additional \( bpc \) mutants are required to determine which of the BPC proteins are involved. Interestingly, the functional analysis of a modified \( LEC2 \) promoter, active in vegetative tissues (see the results presented below), strongly supported the role of the BPC proteins in the control of \( LEC2 \) expression.

**Characterization of a cis-Regulatory Element (RLE) That Restricts \( LEC2 \) Expression to the Embryo**

To further characterize the domain located between 200 and 150 bp upstream of the first codon (Figure 2B), a new series of deletions fused to the 35S minimal promoter upstream of the GUS reporter gene was constructed and tested in transgenic plants (Figure 4). This experiment suggested that at least the sequences between -185/-178 and -168/-160bp were necessary to repress \( P_{\text{LEC2}} \) transcriptional activity in seed and vegetative tissues, respectively (Figure 4A). To supplement this deletion analysis, mutagenesis experiments were performed using the entire \( P_{\text{LEC2}} \) promoter. The 50-bp element associated with the repression activity was replaced by a random 50-bp nucleotide sequence, with no similarity within the Arabidopsis genome, providing the \( P_{\text{LEC2rand}} \) promoter. In comparison to the embryo-specific GUS staining observed with \( P_{\text{LEC2}} \)-GUS lines (Figure 1A), the \( P_{\text{LEC2rand}} \) GUS lines showed ectopic expression in leaves, stems, flowers, pollen, siliques, and seed coat (Figures 1B and 4B). Similar results were obtained in the Columbia-0 background (see Supplemental Figure 4 online), and these results confirmed the role of the repressive element in the developmental regulation of \( LEC2 \) expression. Thus, we named this element \( RLE \). In addition, site-directed mutagenesis was performed to support and refine the structure of the repressive cis-regulatory element. Some of the mutations (m1 and m3) did not modify the pattern of GUS activity, whereas other mutations (m2 and m4) led to the ectopic activity of GUS in pollen (Figure 4B).

Taken together, these results indicated that the 50-bp element located between −150 and −200 bp upstream of the first codon has a negative effect on the transcriptional activity of \( P_{\text{LEC2}} \) in plants. In addition, they suggested that \( RLE \) likely contains different functional motifs that are necessary to confer this repressive activity.

Finally, to test if the BPC proteins are involved in the ectopic activity of \( P_{\text{LEC2}} \) when \( RLE \) is mutated, \( P_{\text{LEC2rand}} \)-GUS was introduced into the triple \( bpc1 \) \( bpc2 \) \( bpc3 \) mutant by transformation. In this genetic background, GUS activity was completely lost in siliques and seed integument and was strongly down-regulated in leaves and cotyledons, in comparison to the wild type (Figure 1C). These results strongly suggested that class I BPCs were involved in the regulation of \( LEC2 \) expression.

**The RLE Element Identified in \( P_{\text{LEC2}} \) Is Necessary for H3K27me3 Deposition**

Previous reports have shown that PRC2, which catalyzes H3K27 trimethylation, is involved in the transcriptional repression of
LEC2 in seedlings (Makarevich et al., 2006; Chen et al., 2010; Bouyer et al., 2011). To determine if the RLE element identified in PLEC2 was involved in this chromatin-based regulatory process, H3K27me3 enrichment was investigated by chromatin immunoprecipitation (ChIP) and subsequently analyzed by quantitative PCR. The H3K27me3 mark was detected over the LEC2 locus, in the promoter and more strongly right downstream of the first codon. These results are consistent with the data obtained by genome-wide analyses (Zhang et al., 2007b; Roudier et al., 2011).

Then, the level of H3K27me3 at the PLEC2:GUS and PLEC2:rand:GUS loci was investigated in 10-d-old seedlings of transgenic plants. The distribution of H3K27me3 at the PLEC2:GUS loci was similar to the pattern found at the endogenous LEC2 locus.
Importantly, the level of H3K27me3 over the PLEC2rand\(\text{GUS}\) locus was significantly lower than over PLEC2\(\text{GUS}\) locus (at \(P < 0.002\), according to a Student's unpaired \(t\) test). The level was between 45- and 85-fold lower, depending on the probes considered (Figure 5B). The analyses were performed using several (\(n > 10\)) independent transgenic lines for each construct. Therefore, the result indicated that the difference between PLEC2rand\(\text{GUS}\) and PLEC2\(\text{GUS}\) loci was strictly dependent on the presence of \(\text{RLE cis-element}\), independent of the transgene insertion sites within the genome. These observations therefore demonstrated that H3K27me3 enrichment over \(\text{LEC2}\) depends on the \(\text{RLE} \) sequence. Taken together, these data and the ectopic \(\text{GUS}\) activity detected in the PLEC2rand\(\text{GUS}\) transgenic plants (Figure 1B) strongly suggest that the \(\text{RLE} \) cis-element is a major determinant of PRC2-mediated repression of \(\text{LEC2}\) outside of embryogenesis (Figure 1B).

Insertion of \(\text{RLE} \) in pF3H, an Unrelated Promoter, Is Sufficient to Repress Its Transcriptional Activity in Seed and Can Trigger H3K27me3 Deposition

The repressive function and the role of \(\text{RLE} \) in the initiation of H3K27me3 marking were tested by a gain-of-function experiment with an unrelated promoter. The \(\text{RLE} \) sequence or a mutated version (random) were introduced at similar position (i.e., 150 bp upstream of the first codon) into the promoter of the FLAVONONE 3-HYDROXYLASE \(\text{(F3H)}\) gene to generate \(\text{PF3H}^{\text{rle}}\):\(\text{GUS}\) and \(\text{PF3H}^{\text{rand}}\):\(\text{GUS}\) constructs, respectively. The \(\text{F3H} \) promoter was chosen for two reasons. First the \(\text{cis}\)-regulating elements that control its activity have been described, and no motifs were located at the insertion site (Hartmann et al., 2005). Furthermore, no H3K27me3 was detectable in ChIP-quantitative PCR analyses (Figure 5C), in agreement with previous analyses (Zhang et al., 2007b). Similar analyses were performed to establish the H3K27me3 landscape at the \(\text{PF3H}^{\text{rle}}\):\(\text{GUS}\) and \(\text{PF3H}^{\text{rand}}\):\(\text{GUS}\) loci in transgenic seedlings. It revealed a weak enrichment of H3K27me3 at \(\text{PF3H}^{\text{rle}}\):\(\text{GUS}\) loci when compared with \(\text{PF3H}^{\text{rand}}\):\(\text{GUS}\) (Figure 5D).

The effect of \(\text{RLE} \) insertion on \(\text{PF3H} \) transcriptional activity was investigated. The endogenous \(\text{F3H} \) promoter was fused to the \(\text{GUS} \) reporter gene (\(\text{PF3H}\)\(\text{GUS}\)) and introduced into Arabidopsis as a control. GUS activity was analyzed in transgenic plants carrying one of the three different constructs, namely, \(\text{PF3H}^{\text{rle}}\):\(\text{GUS}\) and \(\text{PF3H}^{\text{rand}}\):\(\text{GUS}\). For each construct, 24 independent transformants were analyzed. Whereas a strong GUS activity was detected in seeds of 19 transgenic lines carrying \(\text{PF3H}\)\(\text{GUS}\) and 17 \(\text{PF3H}^{\text{rand}}\):\(\text{GUS}\) lines, it was undetectable in seeds of the 14 \(\text{PF3H}^{\text{rle}}\):\(\text{GUS}\) transgenic lines showing GUS activities in other tissues (Figure 6). These results demonstrated that the insertion of \(\text{RLE} \) is sufficient to repress \(\text{PF3H} \) transcriptional activity in the seed (embryo and seed coat). On the contrary, similar GUS activity was found in vegetative tissues for the three constructs, suggesting that H3K27me3 marking was not sufficient to fully inhibit gene expression in these tissues. Taken together, these observations demonstrate that the \(\text{RLE} \) cis-element is sufficient to trigger H3K27me3 deposition and control transcriptional activity in a developmentally regulated manner.
DISCUSSION

Both a CArG and a CT-Rich Activating cis-Element Are Essential for PLEC2 Activity

The molecular and functional dissection of the LEC2 promoter in planta revealed two essential activating sequences that are necessary for embryo-specific expression (Figure 7). The first cis-regulatory element is made of five nucleotides (5’-CATAT-3’) and located 447 bp upstream of the translational start codon. This very short motif did not present any obvious similarities with known cis-regulatory sequences. Nevertheless, when a wider frame is considered (i.e., GATATTAAGG), a similarity was found with the consensus CArG motif [i.e., CCA(T/A)GG] (Riechmann and Meyerowitz, 1997). The CArG motifs are known to be recognized by MADS box proteins, a family of transcription factors that control multiple developmental processes, ranging from root to floral or embryo development (Becker and Theissen, 2003).

Figure 5. ChIP-PCR Analysis of H3K27me3 Enrichment over the Endogenous and Transgenic LEC2 and F3H Loci.

The H3K27me3 enrichments in 10-d-old seedlings at LEC2 (A), PLEC2:GUS (B), F3H (C), and PF3H:GUS (D) loci are presented. The enrichment is expressed relative to chromatin input (%input). All the experiments were repeated at least twice on a pool of five independent transgenic lines. ACT7 and FWA genes were used as negative and positive controls, respectively. Bars denote SE, and n = not detectable. For (A) and (C), the positions of the primers used (thick lines), RLE element (black box), introns (thin line), and exons (dark boxes) are indicated on the top. For (B) and (D), the positions of the primers (thick lines), LEC2 promoter (striped box), RLE element (dark box), and GUS coding sequence (white box) are indicated on the top. The numbers above the histogram bars represent the ratio of the H3K27me3 enrichment when comparing constructs with and without the RLE element (i.e., PLEC2 with PLEC2Rand [B] and PF3H:RLE with PF3HRand [D]). The asterisks indicate that the difference (with or without RLE) is significant at P < 0.002 according to Student’s unpaired t test.
Interestingly, the AGAMOUS-like15 (AGL15) MADS box protein preferentially binds CArG motifs with longer A/T-rich region, such as C(A/T-rich)$_7$G and C(A/T-rich)$_7$GG sequences (Tang and Perry, 2003; Hill et al., 2008; Zheng et al., 2009). This later motif is similar to the CArG sequence found in $P_{LEC2}$ [i.e., C(A/T)$_7$GG]. In addition, genetic and genome-wide ChIP analyses have demonstrated that $LEC2$ is a direct target of AGL15 (Zheng et al., 2009). Taken together, these results strongly suggested that the C(A/T-rich)$_7$GG motif found in $P_{LEC2}$ is one of the AGL15 binding sites involved in the regulation of $LEC2$ expression. Furthermore, AGL15 can interact with histone deacetylase HDA19 (Hill et al., 2008) and thus could be involved in histone deacetylase recruitment at the $LEC2$ locus.

The second cis-regulatory element essential for $LEC2$ expression is a CT-rich domain (containing eight CT repeats) located in the 5'-untranslated region of $LEC2$ (Figure 3A). This domain displays strong similarities with GAGA elements (inverted CT repeats). Consistent with functional data previously obtained (Meister et al., 2004; Kooiker et al., 2005), the results presented here demonstrated that the CT-rich element of $P_{LEC2}$ is bound by BPC proteins (preferentially of class I), both in yeast and in vitro. The quantitative differences in DNA binding observed between the BPC in vitro and yeast (Figures 3C and 3D) may be related to the target sequences used [i.e., the entire 500-bp-long promoter for the one-hybrid experiment and a short repetition of three CT motifs, $3 \times (CT)_b$, in vitro] (see Supplemental Table 1 online). It has been shown that, in vitro, BPC1 binding was affected by modification of the stretch of purine residues (i.e., by introducing any pyrimidine residue) (Kooiker et al., 2005). Our results suggested that, in planta, the replacement of cytosine by adenine residues strongly affected $P_{LEC2}$ activity (Figure 3A). This suggested that the strong base pairing between complementary C-G nucleotides is important for the function of the CT element. Interestingly, the addition of three extra CT repeats was sufficient to trigger ectopic $P_{LEC2}$:GUS activity in pollen grains (see Supplemental Figure 2 online). This result was consistent with evidence indicating that CT repeats have an enhancer effect on promoter activity (Pauli et al., 2004). The three additional CT repeats inserted in $P_{LEC2}$ may increase transcriptional activation, up to the threshold of detection of GUS activity, in pollen. A second nonexclusive possibility is that the addition of these repeats increased the affinity for another BPC protein expressed in pollen. This later hypothesis is supported by the fact that the promoter of $BPC2$, $BPC3$, $BPC4$, and $BPC7$ are all active in pollen (Monfared et al., 2011).

The BPC mRNAs of class I ($BPC1$, $2$, and $3$) together with $BPC4$ (class II) were the most abundant in embryo (Figure 3). Other BPC mRNAs were also detected (with the exception of $BPC5$) but at very low levels. These expression profiles together with the results of DNA binding assays suggested that BPC factors are likely to regulate $LEC2$ through binding to the GAGA cis-element found in $P_{LEC2}$. Consistent with this hypothesis, the ectopic GUS activity driven by $P_{LEC2}$:GUS was fully abolished in silique and seeds integuments and was strongly affected in leaves and cotyledons of the triple class I mutant (Figure 1C).

Altogether, these results suggested that BPC proteins that belong to class II or III act redundantly with class I BPCs to activate $LEC2$ expression through its specific GAGA cis-regulatory motif. This hypothesis is in agreement with the high genetic redundancy recently reported for BPCs (Monfared et al., 2011). Moreover, it has been shown that BPCs of group II can form homodimers or heterodimers with group I BPCs (Wanke et al., 2011). Therefore, obtaining new bpc single and multiple mutants of the different classes will be necessary to unravel which of the BPC proteins are involved in the regulation of $LEC2$ expression.

**RLE Is Sufficient to Repress Transcriptional Activity and Is Necessary to Trigger H3K27me3 Deposition**

The molecular and functional dissection of $P_{LEC2}$ presented here has identified a new and negative regulatory cis-element (RLE) involved in restricting the expression of $LEC2$ to the seed (Figure 7). This 50-bp-long cis-acting sequence located 150 bp
upstream of the \textit{LEC2} first codon is required for repressing \textit{LEC2} expression in leaves, stems, flowers, pollen, seed coat, and siliques (Figures 1 and 2B). Additional experiments (i.e., deletions of 10 bp and site-directed mutagenesis approaches) confirmed these observations and suggested that \textit{RLE} is made of different functional stretches of nucleotides that are necessary to confer this repressive activity (Figure 4B).

Remarkably, the presence of \textit{RLE} in \textit{PLEC2}:\textit{GUS} is sufficient to trigger H3K27me3 deposition in transgenic seedlings (Figures 5C and 5D). In addition, some \textit{PREs} have been found in the proximal promoter of target genes in \textit{Drosophila} (Morey and Helin, 2010; Enderle et al., 2011), as \textit{RLE} in \textit{LEC2}. Last, it has been demonstrated recently that H3K27me3 deposition is abolished in \textit{fie} mutant lacking PRC2 activity (Bouyer et al., 2011). These results suggest that the \textit{RLE} element functions as \textit{Drosophila PRE}. Nevertheless, the weak effect of \textit{RLE} on H3K27me3 deposition at \textit{pF3H} suggests that it may not be sufficient in any genomic contexts. \textit{PREs} contain a few short transcription factor binding sites, including a GAGA box (Hagstrom et al., 1997; Horard et al., 2000). Similarly, \textit{RLE} is associated with a \textit{CT}-rich element in \textit{PLEC2}. In addition, some other plant promoters that are regulated by PcG also display \textit{CT}-rich elements and are regulated by BPC proteins. For instance, \textit{SEEDSTICK} and \textit{INNER NO OUTER (INO)} are two targets of BPC1 and BPC2, respectively (Villanueva et al., 1999; Meister et al., 2004; Kooiker et al., 2005). Both loci are associated with strong H3K27me3 enrichment (Zhang et al., 2007b; Roudier et al., 2011). GA repeats can be found in the

\textbf{RLE Functions as PREs Identified in \textit{Drosophila}}

It has been shown that PcG complexes that control the H3K27me3 level are involved in the transcriptional repression of \textit{LEC2} in seedlings (Madejovich et al., 2006; Chen et al., 2010; Bouyer et al., 2011). Our results demonstrated that the \textit{RLE} element found in \textit{PLEC2} is sufficient to initiate H3K27me3 deposition at the \textit{LEC2} locus. In addition, some \textit{PREs} have been found in the proximal promoter of target genes in \textit{Drosophila} (Morey and Helin, 2010; Enderle et al., 2011), as \textit{RLE} in \textit{LEC2}. Last, it has been demonstrated recently that H3K27me3 deposition is abolished in \textit{fie} mutant lacking PRC2 activity (Bouyer et al., 2011). These results suggest that the \textit{RLE} element functions as \textit{Drosophila PRE}. Nevertheless, the weak effect of \textit{RLE} on H3K27me3 deposition at \textit{pF3H} suggests that it may not be sufficient in any genomic contexts.

\textbf{PREs} contain a few short transcription factor binding sites, including a GAGA box (Hagstrom et al., 1997; Horard et al., 2000). Similarly, \textit{RLE} is associated with a \textit{CT}-rich element in \textit{PLEC2}. In addition, some other plant promoters that are regulated by PcG also display \textit{CT}-rich elements and are regulated by BPC proteins. For instance, \textit{SEEDSTICK} and \textit{INNER NO OUTER (INO)} are two targets of BPC1 and BPC2, respectively (Villanueva et al., 1999; Meister et al., 2004; Kooiker et al., 2005). Both loci are associated with strong H3K27me3 enrichment (Zhang et al., 2007b; Roudier et al., 2011). GA repeats can be found in the
regulatory sequences of many other PcG targets, such as AG, FLOWERING LOCUS C (FLC), and STM (Schatowski et al., 2008). In Drosophila, the GAGA factors were shown to be involved in the regulation of gene expression in relation with chromatin packaging (Adkins et al., 2006; Nakayama et al., 2007). Therefore, it is very tempting to speculate that there is an interaction between BPC and PcG silencing in plants. The availability of new and multiple bpc mutants will give the opportunity to further investigate this hypothesis, by looking at the chromatin landscape, at different loci containing both type of elements, such as LEC2, but also INO, STM, FLC, or STM.

No sequences showing similarity with RLE were detected genome-wide. This is not surprising considering that PREs are made of different short transcription factor binding sites. These motifs are usually small, degenerate, and difficult to detect by simple DNA sequence comparison (Ward and Bussemaker, 2008; Badis et al., 2009; Moyroud et al., 2011). Additional functional analyses, similar to those presented in this report, will be necessary to establish a model allowing a more systematic identification of putative RLE elements in plant genomes.

Sequence analysis of \( P_{\text{LEC2}} \) revealed the presence of three transposable elements (Figure 7). The transcription start site and the GAGA box are included in a class II transposable element sequence of the MuDR superfamily (Lisch, 2002). The CARG motif is located at the beginning of a HELITRON element (Kapitonov and Jurka, 2007; Yang and Bennetzen, 2009), which is itself juxtaposed with another MuDR sequence. Finally, RLE is flanked by the two MuDR sequences. It can be reasonably speculated that insertion of these transposable elements likely shaped the specific expression pattern of LEC2. It has been shown that transposons can be involved in transcriptional regulation of nearby genes, including PRE, although the precise mechanisms remain unknown and seem to be rather gene specific (Valenzuela and Kamakaka, 2006; Weil and Martienssen, 2008; Comet et al., 2010). However, the hypothesis that transposons have a role in the developmental regulation of LEC2 expression results from a combination of activating and repressive mechanisms involving histone H3 methylation. This regulation involves at least three distinct cis-regulatory elements located within the proximal \( P_{\text{LEC2}} \) promoter, including repressive RLE element. Remarkably, RLE is sufficient to initiate H3K27me3 deposition and to repress transcription in a developmentally regulated manner. This study provides important new insights into the mechanism by which PRC2 might be recruited at specific target loci and paves the way for a more comprehensive understanding of PcG-mediated gene silencing in plants.

**METHODS**

**Plant Material and Growth Conditions**

Arabidopsis thaliana, accession Wassilewskija, was used for plant transformation. The mutant lines bpc1 (SALK_072966.43.30.x), bpc2 (SALK_090810C), and bpc3 (N89719) were obtained from the Nottingham Arabidopsis Stock Centre (Scholl et al., 2000) and have all been described by Monfared et al. (2011). Plants were grown, transformed, and selected as previously described (Harsoeot et al., 2010).

**Constructs and Plant Transformation**

All the primers used in this work are described in Supplemental Table 1 online. For 5' end deletions of the LEC2 promoter (\( P_{\text{LEC2}} \)) genomic DNA was PCR amplified with the Phusion DNA polymerase (Finnzymes) using primers carrying B1 and B2 GATEWAY recombination sites (Invitrogen). PCR products were cloned by BP recombination (according to the manufacturer’s recommendations) into the entry vector pDONR207 and then LR recombined into the destination vector pBII101R1R2 for plant transformation (Baudry et al., 2004). Modified CT repeat constructs were performed similarly using 3' primers as follows: AttB2mCA, AttB2mAT, and AttB2m-3CT.

The 3' end deletion series constructs were PCR amplified using 5' and 3' oligonucleotides carrying KpnI and Xhol restriction sites, respectively. The 5' primer used was P500KpnI, and the 3' primers were P250Xhol, P200Xhol, P190Xhol, P180Xhol, P170Xhol, P160Xhol, P150Xhol, P140Xhol, and P500Xhol. PCR products were digested with KnpI-Xhol and cloned into KnpI-Xhol-digested pBS35sminGUS (Debeaujon et al., 2003). \( P_{\text{LEC2}} \) fragments fused to the minimum 35S promoter and the UidA reporter gene were transferred into pCAMBIA1300 linearized by HindIII-KpnI digestion and ligated with T4 DNA ligase (New England Biolabs).

For the \( P_{\text{LEC2}}\text{and} \) construct, the fragment P500-200 was amplified with the Phusion DNA polymerase using the 5' primer P500KpnI and the 3' primer P200andXhol. The sequence (5'-CTTAAAGACATTGCAAACCTGGAACAGTGCAGACAACTCGATATCGCGCCGCTG)' was randomly chosen, and in silico analysis was performed to ensure that no known cis-regulatory elements were found in the sequence. The PCR product was digested with KpnI-Xhol and cloned into KpnI-Xhol-digested pBS35sminGUS (Debeaujon et al., 2003). The minimum 35S promoter was discarded after Xhol-Ncol digestion of the p200and-pBS35sminGUS and replaced by the PCR amplified fragment between −150 and the translational start site, with P150Khol and PATGncol 5' and 3' primers, respectively. The F3H promoter sequence was PCR amplified with Phusion DNA polymerase and primers AttB1PF3H and AttB2PF3H carrying B1 and B2 GATEWAY recombination sites. \( P_{\text{PF3H}} \) and \( P_{\text{PF3H}}\text{and} \) were amplified with three successive PCRs using AttB1PF3H/PF3Hrev1, AttB1PF3H/PF3Hrev2, and AttB1PF3H/AttB2PF3H and were cloned using the approach described for wild-type PF3H. All these promoter fragments were recombined in the entry vector pDONR207 and then LR recombined into pBII101R1R2 for plant transformation, as described above.

**One-Hybrid Assays**

Reporter constructs containing the different promoters were made in the pHis-i plasmid (Clontech), which carries the URA3 selection marker and the minimal HIS3 promoter upstream of the HIS3 reporter gene (Li and Herskowitz, 1993). The 500-bp-long LEC2 promoter (\( P_{\text{LEC2}} \)) was PCR amplified with the Phusion DNA polymerase with P5000KpnI and PATGncol 5' and 3' primers, respectively, and blunt cloned into pHis-i digested with SmaI. The control (−500 to −250 fragment of the LEC2 promoter) was cloned using the same method with 5' primer P500KpnI and the 3' primer P250LEC2 (see Supplemental Table 1 online). LEC2 and BPCs cDNAs were amplified with the Phusion DNA polymerase using primers carrying B1 and B2 GATEWAY recombination sites. PCR products were BP recombined according to the manufacturer’s (Invitrogen) recommendations into pDONR207 and then LR recombined into pDEST22 vector that allows fusion with the GAL4-activating domain, pHis-i constructs.
were stably transformed into the EGY 48 yeast (Saccharomyces cerevisiae) strain and selected on SD-Uracil medium prior to transformation with pDEST22 vectors for protein expression. The interactions were tested on SD-Uracil-Trp-His medium. To increase the stringency of the test, various concentrations of 3-aminotriazol were used, from 5 to 50 mM.

EMSA Experiments

The cDNAs obtained for one-hybrid experiments were introduced into pDEST15 (Invitrogen), which produces an N-terminal glutathione S-transferase tag fusion. BPCs proteins were produced in Escherichia coli and purified with the Glutathione Sepharose 4B system (Amersham Biosciences) according to the manufacturer’s instructions. One hundred nanograms of both forward and reverse primers (EMSCACT/mAT forw and rev) were boiled for 5 min and annealed at room temperature. Double-stranded probes were 32P labeled after Klenow treatment (Invitrogen). Binding conditions have been previously described (Koolker et al., 2005).

Histochemical GUS Assays

Arabidopsis tissues were immersed in GUS staining solution (100 mM sodium phosphate buffer, pH 7.2, 10 mM EDTA, 0.1% Triton, and 1 mM X-Gluc) and then placed under vacuum for 1 h. After incubation at 37°C overnight, the staining solution was removed and samples were cleared by sequential changes of 75 and 95% (v/v) ethanol.

ChIP Experiments

The experiments were performed as previously described (Gendrel et al., 2002). Briefly, all the experiments have been duplicated and performed using pools of five independent transformants. Relative enrichment was measured by comparison between input and ChIP value. ACT7 was used as a negative control (H3K27me3 modification is barely detectable over the ACT7 locus), and FWA was used as a positive control for H3K27me3 enrichment (Roudier et al., 2011). Primers used in this analysis are described in Supplemental Table 1 online.

Analysis of Gene Expression

RNA extractions were performed using the total mammalian RNA kit (Sigma-Aldrich) according to the manufacturer’s instructions. cdnas were synthesized using the SuperScriptII first-strand synthesis system for (Sigma-Aldrich) according to the manufacturer’s instructions. cDNAs were purified with the Glutathione Sepharose 4B system (Amersham Biosciences) according to the manufacturer’s instructions. One hundred nanograms of both forward and reverse primers (EMSCACT/mAT forw and rev) were boiled for 5 min and annealed at room temperature. Double-stranded probes were 32P labeled after Klenow treatment (Invitrogen). Binding conditions have been previously described (Koolker et al., 2005).

Accession Numbers

Sequence and mutant data from this article can be found in the GenBank/EMBL data libraries or the Arabidopsis Genome Initiative database under the following accession numbers: bpc1 (SALK_072966.43.30), bpc2 (SALK_090810C), bpc3 (N89719), BPC1 (At2g01930), BPC2 (At1g4688), BPC3 (At1g68120), BPC4 (At2g21240), BPC5 (At4g38910), BPC6 (At5g2520), BPC7 (At2g35530), LEC2 (At1g23030), ACT7 (At5g99810), FWA-5 (At4g25530), and EF1a (At5g60390).

Supplemental Data

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

Supplemental Figure 1. Complementation of the lec2-4 Mutation by PLEC2::LEC2.

Supplemental Figure 2. Activation of PLEC2 in Pollen by Adding 3CT Repeats in the GAF Box of PLEC2.

Supplemental Figure 3. LEC2 Expression Is Not Modified in bpc Mutants.

Supplemental Figure 4. Expression Patterns of PLEC2::GUS and PLEC2:GUS in the Col-0 Ecotype Background.

Supplemental Table 1. List of Primers Used in This Study.

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AUTHOR CONTRIBUTIONS

N.B., B.D., and C.D. performed the experiments. All the authors designed the research, analyzed data, and wrote the article.

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REFERENCES


Transcriptional Regulation of Arabidopsis LEAFY COTYLEDON2 Involves RLE, a cis-Element That Regulates Trimethylation of Histone H3 at Lysine-27
Nathalie Berger, Bertrand Dubreucq, François Roudier, Christian Dubos and Loïc Lepiniec
Plant Cell 2011;23;4065-4078; originally published online November 11, 2011;
DOI 10.1105/tpc.111.087866

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References This article cites 99 articles, 32 of which can be accessed free at:
/content/23/11/4065.full.html#ref-list-1
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