The transcription factor BELLRINGER modulates phyllotaxis by regulating the expression of a pectin methylesterase in Arabidopsis

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SUMMARY

Plant leaves and flowers are positioned along the stem in a regular pattern. This pattern, which is referred to as phyllotaxis, is generated through the precise emergence of lateral organs and is controlled by gradients of the plant hormone auxin. This pattern is actively maintained during stem growth through controlled cell proliferation and elongation. The formation of new organs is known to depend on changes in cell wall chemistry, in particular the demethylesterification of homogalacturonans, one of the main pectic components. Here we report a dual function for the homeodomain transcription factor BELLRINGER (BLR) in the establishment and maintenance of the phyllotactic pattern in Arabidopsis. BLR is required for the establishment of normal phyllotaxis through the exclusion of pectin methylesterase PME5 expression from the meristem dome and for the maintenance of phyllotaxis through the activation of PME5 in the elongating stem. These results provide new insights into the role of pectin demethylesterification in organ initiation and cell elongation and identify an important component of the regulation mechanism involved.

KEY WORDS: Cell wall, Pectins, Pectin methylesterase (PME), Shoot apical meristem, Phyllotaxis, Arabidopsis

INTRODUCTION

The multitude of shapes adopted by multicellular organisms are controlled by complex networks of regulatory genes. How these regulatory networks are translated into the local changes in tissue growth that underlie morphogenesis remains a central question in developmental biology.

Plants are useful models with which to study organogenesis as new organs are formed throughout their lives, in contrast to animals in which organogenesis is restricted to embryogenesis. The shoot apical meristem (SAM), which gives rise to all aerial organs of the plant, has a dual function: maintaining a pool of undifferentiated cells, and initiating new lateral organs according to a specific temporal and spatial pattern, known as phyllotaxis (Carraro et al., 2006). Beyond the meristem, the phyllotactic pattern is actively maintained during stem growth. This process requires the restriction of the CUC2 transcription factor to the boundary domain, which involves miR164 (Peaucelle et al., 2007; Sieber et al., 2007).

The homeodomain transcription factors belonging to the KNOX and BEL groups play key roles in both meristem maintenance and organ patterning (Carraro et al., 2006; Smith et al., 2004). The KNOX and BEL transcription factors, which can form various heterodimers, regulate the expression of different sets of downstream effectors. BELLRINGER (BLR; also known as PENNYWISE, REPLUMLESS or VAAMANA) (Byrne et al., 2003; Kanrar et al., 2006; Roeder et al., 2003; Smith and Hake, 2003) is one of the members of the BEL group expressed in the meristem. The blr mutant was first described for its abnormal phyllotaxis, but also presents other developmental defects (Byrne et al., 2003; Kanrar et al., 2006; Kanrar et al., 2008; Roeder et al., 2003; Smith and Hake, 2003). BLR also shows complex genetic interactions with other BEL and KNOX genes (Smith and Hake, 2003; Smith et al., 2004; Ragni et al., 2008; Rutjens et al., 2009; Ung et al., 2011) and directly represses the flower organ identity gene AGAMOUS during flower development (Bao et al., 2004).

The initiation of new lateral organs depends on the local accumulation of the phytohormone auxin (Bayer et al., 2009; Reinhardt et al., 2000; Reinhardt et al., 2003). The auxin distribution within the meristem is highly dynamic and is the result of passive diffusion and active cell-to-cell transport involving the efflux carrier PIN1 and various influx carriers (Bainbridge et al., 2008). In several mathematical models, auxin patterning is autoregulated through feedback loops linking auxin flux or auxin accumulation (Jonsson et al., 2006; Smith et al., 2006; Stoma et al., 2008) to the polar intracellular localisation of PIN1. At the position of the auxin maximum a new organ primordium is initiated. The developing organ is thought to act as an auxin sink, which leads to the redistribution of the auxin and to the emergence of a new maximum at the position of the future primordium. In parallel to auxin patterning, the chemical modification of a cell wall component – the demethylesterification of the pectic polysaccharide homogalacturonan (HG) – also plays a key role in triggering primordia formation (Peaucelle et al., 2008).

Pectins, which represent ~35% of the dry weight in dicotyledonous species, are complex polysaccharides rich in galacturonic acid (Caffall and Mohnen, 2009; Mohnen, 2008). HG, one of the main pectic constituents, is a linear homopolymer of α-(1-4)-linked D-galacturonic acids, which can be methylesterified at...
the C-6 carboxyl residue. HG is synthesized from nucleotide sugars by a variety of glycosyl transferases (Lerouxel et al., 2006) in the Golgi apparatus and secreted in a highly methylsterified form into the cell wall (Sterling et al., 2001). Subsequently, its structure can be altered by the activity of cell wall-based enzymes. For example, the degree of methylsterification can be modified by pectin methylsterases (PMEs, EC 3.1.1.11), the activity of which is in turn regulated by proteinaceous PME inhibitors (PMEs) (Pelloux et al., 2007). Both PMEs and PMEsIs are members of large gene families (66 and 69 members, respectively, in Arabidopsis).

The similarity of the defects in phyllotaxis observed in the Arabidopsis blr mutant and following ectopic pectin demethylsterification prompted us to investigate the link between these two factors. Here, we report that ectopic primordia formation in the floral meristem of blr is the result of meristem-specific changes in the PME-mediated methylsterification status of HG as a result of the ectopic expression of one member of the PME family, PME5. The ectopic primordia formation was reversed in the blr/pme5 double mutant, confirming unequivocally the role of PME5 in this process. Furthermore, we show that, in the blr mutant, the downregulation of PME5 expression in the internode leads to a defect in internode elongation that is associated with reduced cell expansion. In addition to identifying part of the regulatory network that controls the methylsterification status of HG in the stem, our results further confirm the crucial role of the demethylsterification of HG in the regulation of cell elongation.

MATERIALS AND METHODS

Plant material and growth conditions

The blr-6 mutant was identified, based on its phenotype, in the Versailles T-DNA insertion collection (WS ecotype). Tests for allelism were carried out by crossing plants homozygous for pny-42016 (Smith and Hake, 2003) with plants homozygous for blr-6. F1 plants displayed the blr mutant phenotype, showing that blr-6 and pny-42016 are allelic. The right and left flanking sequences of the T-DNA insertion site were amplified by PCR in the blr/pme5 mutant using the T-DNA-specific primer Tag5 (5'-CTACAAATTGCCTTTTCTTATCGAC-3') and the gene-specific primers pm-04 (Smith and Hake, 2003) and Tag3 (5'-CTGTACACAGACGTTGCCGCAATAA-3') and pmny-3, respectively (Smith and Hake, 2003). Sequencing of the PCR products showed that the T-DNA was inserted in the first intron, at position 1262 to 1271 relative to the initiation codon.

pme5-1 and pme5-2 mutants were isolated from the Versailles T-DNA insertion collection (WS ecotype). The left flanking sequence of the T-DNA insertion site was amplified by PCR using Tag5 and the At5g47500 gene-specific primers 5'-CTTGAGCCGCTCCCATGCTA-3' and 5'-GCATCACAATCAAGATTGCC-3' for lines FLAG_175B12 and FLAG_232E12, respectively. PCR products were sequenced and the site of insertion confirmed.

Plant growth in controlled chambers under short-day or long-day conditions was as described previously (Deveaux et al., 2003).

Electron microscopy and phyllotactic pattern measurement

Scanning electron microscopy, confocal microscopy, epidermal cell length measurement and phyllotactic pattern measurement have been described previously (Peaucelle et al., 2008). For each experiment, phyllotaxis measurements were performed on a minimum of five plants and meristematic phyllotaxis measurements on a minimum of ten plants. Cell lengths were measured on at least three internodes from at least five different plants. The Kolmogorov-Smirnov (K-S) test was performed.

Fourier transform infrared (FTIR) microscopy

Ten 12 μm slices from ten meristems of ten different wild-type and blr-6 plants were obtained by Vibratome sectioning of dissected dried inflorescences embedded in 5% low-melting-point agarose. For each meristem slice, ten FTIR spectra were collected from the central zone of the meristem. Spectra were baseline and area-normalised as described (Mouille et al., 2003). Statistical analyses were performed as described (Mouille et al., 2003).

PME activity measurements

PME activity was assayed using the alcohol oxidase-coupled assay on cell wall-enriched total protein extracts as described (Klavons and Bennet, 1986). Protein concentration in extracts was measured according to Bradford (Bradford, 1976) using a protein assay kit (Bio-Rad, Marne-la-Coquette, France). Data are the mean of four to six independent replicates. Data were statistically analysed by the Mann-Whitney test (Statisca, Softist, Saint-Ouen-l’Aumône, France).

Real-time quantitative PCR (RT-qPCR)

Following RNA extraction from floral buds and cDNA synthesis, A5g09760, A3g19730, At5g47500, At4g33220 and At3g49220 transcripts were quantified by RT-qPCR using the following specific primers (5′ to 3′): A5g09760, GGAGGGCCATGGAAGAGATTA and AGCGAGACTGGAAGACAGATG; A3g19730, AATAAAGCAGAGCTCGAGATG and ATTCGAACAGCTAGTGAACAGG; At5g47500, ATGCCGCGTTCTGCATGATGAAAGCAGATG; A4g33220, CCGAAGAAGTGTCAACCAAC and AAGGCGCCAGCAAGATGTCG; At4g39220, CATCGGCCTAGGTTCTTCGC and AATCCCGCAAGAGGACACAC; UBG5 (At3g62250) was used as reference (GAGCTTCTCATCCTCC and CCACAGGTGCTTC). Reactions were performed in a Roche LightCycler using the FastStart DNA MasterPLUS SYBR Green I Kit (Roche). Data are the mean of four to six replicates. These data were exported into ReQuant (Roche), which provides efficiency-corrected normalised quantification results. For each candidate gene, the expression in blr-6 is given relative to that in the wild type, which was set at 1.

β-glucuronidase (GUS) staining and imaging

A 1 kb region of the At5g47500 promoter was amplified using Phusion Hot Start F-Taq Polymerase (Finnzyme, Saint Quentin en Yvelines, France). The PCR product was cloned into the pGEM-T Easy vector (Promega, Charbonnières-les-Bains, France), sequenced and subcloned into the binary vector pBI101.3 upstream of the GUS coding sequence (Clontech, Saint-Germain-en-Laye, France). Plant transformation, using Agrobacterium tumefaciens strain LBA4404, was performed by the floral dip method (Clough and Bent, 1998). Transformsants were selected on 80 μg/ml kanamycin. GUS staining was carried out as described (Sessions et al., 1999), with 10 mM K3Fe(CN)6 and 10 mM K4Fe(CN)6, to limit stain diffusion. Plant samples were destained in 75% ethanol and digital images were taken with a Coolpix 995 camera (Nikon, Champigny sur Marne, France).

A 4.9 kb stretch of KNAT1 (BP) promoter sequence upstream of the translation initiation site was amplified from wild-type WS Arabidopsis using primers 5′-GCCGCCCCTTGGGTTTATTGAGATG-3′ and 5′-AATGTTACCCAGATGAGATG TATTT-3′ and cloned as a NotI-Spal fragment upstream of the ALCR sequence in the pLP999 vector that also contains an AlcA:GFP cassette (Deveaux et al., 2003). Plant transformation and selection were as previously described (Deveaux et al., 2003).

Immunolabelling of pectins

Immunolabelling of demethylsterified HG was conducted on transverse sections of meristems using 2F4 antibodies (Liners et al., 1989). All immunolabelling experiments were carried out using a buffer containing 0.5 mM CaCl2 and milk as previously described (Peaucelle et al., 2008).

In situ hybridisation

An antisense probe of the full-length ORF of PME5 was synthesised in vitro and labelled by DIG-UTP using a gel-purified PCR product that included the T7 RNA polymerase binding site as template. Tissue fixation, embedding, sectioning and in situ hybridisation were as described (Laufs et al., 1998), with the following changes: after dehydration of the tissues by ethanol, an additional pre-hybridisation step was performed (2 hours at 45°C in 50% formamide, 5× SSC, 100 μg/ml tRNA, 50 μg/ml heparin, 0.1% Tween 20). Hybridisation was overnight at 45°C using
normal phyllotactic pattern. In conclusion, the pattern of organ
initiation in the *Arabidopsis blr-6* mutant presents two defects: higher
variability in the positioning of successive primordia within a
normal phyllotactic pattern and ectopic primordia formation.

**RESULTS**

**Altered phyllotaxis in the *Arabidopsis blr-6* mutant**

We identified *blr-6*, a new allele of the *BLR* gene in the wild-type
WS background (see Materials and methods). The *blr-6* mutant is
caracterised by the production of ectopic flowers at the shoot apex
and by a high proportion of short internodes (Fig. 1A,B). To
caracterise the phyllotactic defect, we studied the pattern of organ
initiation in wild-type and *blr-6* SAMs by measuring the angles
between successive primordia (Fig. 1B). As shown in Fig. 1C,D,
the divergence angle distribution was significantly different
between *blr-6* and the wild type (*P*<2.8×10⁻⁵, K-S test). In *blr-6*,
the divergence angle showed a bimodal distribution with peaks at
120-149° and 240-279°. The distribution of the angles around 137°
was similar to that of the wild type but with a higher variability
(s.d.=16 versus s.d.=16 in wild type). The primordia with angles of
240-279° can be considered ectopic as they do not follow the
normal phyllotactic pattern. In conclusion, the pattern of organ

**Increased pectin demethylesterification in the SAM of *blr-6***

To investigate whether the ectopic primordia of the *blr-6* mutant
could be related to changes in cell wall composition within the
SAM, Fourier transform infrared (FTIR) microspectroscopy was
carried out on a 50 μm × 50 μm region delimiting the central
meristem dome on a 12 μm transverse section through the shoot
apex (Fig. 2A,B). We compared wild-type and *blr-6* FTIR spectra
using a *t*-test for each wave number. Only two wave numbers
(1720 cm⁻¹ and 1780 cm⁻¹), which correspond to ester bonds,
showed significant differences in absorbance (higher in wild type
than in *blr-6*). Esters are mainly found in cell wall pectin. These
results suggest a lower degree of HG esterification in the *blr-6*
meristem in the absence of other changes in cell wall composition
detectable with this sensitive technique.

To confirm the changes in pectin structure in the SAM of the *blr-
6* mutant, pectic epitopes were immunolocalised on successive
transverse sections of the meristem with monoclonal antibody 2F4,
which specifically labels demethylesterified HG (Liners et al.,
2003). Washing was as described previously, except that a first washing
step (0.1× SSC, 0.5% SDS, 30 minutes at 45°C) and a second washing
step (2× SSC, 50% formamide, 60 minutes at 45°C) were included.
PMEs was further analysed by RT-qPCR (Fig. 3A). PMEs expressed in the SAM. The expression of five meristem-expressed (http://bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi) to identify PMEs expression of PME genes, we first exploited microarray databases floral buds of the

To investigate whether higher pectin demethylesterification in the To explore whether a reduction in PME5 expression also could affect primordia positioning. We first isolated two mutants, pme5-1 (175B12) and pme5-2 (232E12), which carry T-DNA insertions in the first and third exon, respectively (see Fig. S1A in the supplementary material). Both mutants can be considered null as no PME5 transcripts are detected in floral buds by RT-qPCR (see Fig. S1B in the supplementary material). The absence of PME5 transcripts in the pme5-1 mutant was further confirmed by in situ hybridisation (see Fig. S1C in the supplementary material). PME assays (using standard conditions, see Materials and methods) on cell wall-enriched protein extracts from flower buds showed that total PME activity was ~60% of that of the control in both pme5-1 and pme5-2 lines (Fig. 4A and see Fig. S1D in the supplementary material).

We next compared the phyllotaxis of wild-type and pme5-1 meristems. Interestingly, pme5-1 differed significantly from the wild type in the divergence angle distribution in the meristem (P=0.011, P=0.009 and P=0.0089 by K-S test in three independent experiments) and with a smaller standard deviation (pme5, s.d.=10.1, 7.4, 9.0; wild type, s.d.16, 15, 19).

As a control, the statistical test failed to distinguish between the distributions of the three biological repeats for the wild-type samples (P=0.70, P=0.70 and P=0.71 for experiment 1 versus 2, 1 versus 3, and 2 versus 3, respectively) (Fig. 4B,C). The reduced PME activity in pme5-1 therefore correlates with a reduced variability in primordia positioning in the meristem.

**pme5-1 complements the ectopic primordia phenotype of blr-6**

We next investigated the relationship between the altered phyllotaxis, the increased pectin demethylase activity and the ectopic expression of PME5 in the blr-6 meristem. We first assayed total PME activity in floral buds. The activity was 3-fold higher in the blr-6 mutant than in the wild type (Fig. 4A), which should suggest post-transcriptional or post-translational control of PME activity.

Next, we generated and analysed a blr-6/pme5-1 double mutant. In the double mutant, PME activity was greatly reduced compared with blr-6, indicating that the ectopic expression of PME5 explains most of the increased PME activity in blr-6 (Fig. 4A). Interestingly, the divergence angle distribution in the meristems of the double mutant was indistinguishable from that of pme5-1 (P=0.3, P=0.78, P=0.45 by K-S test in three independent experiments) and significantly different from that of blr-6 (P<1×10^{-6}, P<1×10^{-4}, P=0.001 by K-S test in three independent experiments) (Fig. 4C-E).

To confirm that the phyllotactic pattern observed in blr-6/pme5-1 is due to the absence of PME5 activity, we ectopically expressed PME5 under the control of the constitutive 35S promoter in the double mutant. Double mutants expressing 35S::PME5 indeed
showed a higher PME activity than that of blr-6/pme5-1 (Fig. 4A) and a phyllotaxis in the meristem that was indistinguishable from that of the blr-6 mutant (Fig. 4D,F).

Together, these results indicate that the increased PME activity and the abnormal phyllotactic pattern in the meristem in blr-6 are solely the result of the ectopic expression of PME5. Strikingly, as discussed below, the disordered post-meristematic phyllotaxis phenotype observed in blr-6 was not rescued in blr-6/pme5-1 (see Fig. S2 in the supplementary material). We show that this can be explained by an independent role for PME5 in the regulation of internode length.

**Expression of PME5 is downregulated in the internodes of blr-6**

To investigate the potential role of PME5 in regulating internode length and the post-meristematic maintenance of phyllotaxis, we first analysed the activity of the PME5 promoter in wild-type and blr-6 mutant backgrounds using PME5 promoter::GUS transreportants. The PME5 promoter was active in wild-type but not in blr-6 internodes (Fig. 5). This suggests that, in the internode, BLR acts as an activator of PME5 transcription, in contrast to the meristem, where BLR appears to act as a repressor. In the context of the blr-6 mutant, the post-meristematic phyllotaxis phenotype (i.e. short internodes) might thus be related to the lack of PME5 expression in the internode.

**pme5-1 does not complement the post-meristematic phyllotaxis phenotype of blr-6**

To analyse the post-meristematic modifications of phyllotaxis, we first compared the internode length of blr-6, pme5-1 and blr-6/pme5-1 mutants with that of the wild type. No significant differences were detected between wild-type and pme5-1 plants for this parameter (Fig. 6A; \(P=0.139, P=0.131, P=0.611\) by K-S test in three independent experiments). By contrast, blr-6 and blr-6/pme5-1 plants presented a phenotype of large variability in internode length and, notably, a high frequency of shorter internodes (Fig. 6B,C; \(P<0.001\) by K-S test in three independent experiments). Similar results were obtained for the variability in the divergence angles of the siliques along the stem (see Fig. S3A-C in the supplementary material).

The observed decrease in internode length (Fig. 6B,C) was related to a decreased length of epidermal cells, as shown in blr-6 and blr-6/pme5-1 mutants. For example, the average cell length in the blr-6 mutant was about one-sixth that of the wild type (5.3±5.1 \(\mu\m m\) versus 32±14 \(\mu\m m\)), whereas no such differences were observed for the pme5-1 single mutant compared with the wild type (Fig. 7A-C).

**Expression of PME5 in the internodes of blr-6 partially rescues the post-meristematic maintenance of phyllotaxis**

Next, we investigated whether PME5 expression in the internode could restore post-meristematic maintenance and cell elongation in the blr-6 mutant. We used the promoter of KNAT1, which shows the same expression pattern as PME5 in the internodes (Fig. 5A,C). Internode length and cell length within short internodes were measured in blr-6 expressing PME5 under the control of the KNAT1 promoter. The expression of PME5 in blr-6 internodes rescued the post-meristematic phenotype, as shown by the increase in internode length compared with blr-6 (Fig. 6D) and the rescue of the defects in post-meristematic phyllotaxis (see Fig. S3D in the supplementary material). The observed increase in internode length was related to an increased cell length (Fig. 7D; \(P=0.11, P=0.19\),
$P=0.22$, K-S test in three independent experiments). This confirms that, in blr-6, the post-meristematic defect in phyllotaxis is due to reduced PME5 expression in the internodes.

To investigate whether the ectopic PME activity in the meristem could be indirectly responsible for the reduced internode elongation and altered post-meristematic phyllotaxis, we expressed PME5 under the control of the meristem-specific UFO-derived promoter. Similar internode and cell lengths as well as divergence angles at the post-meristematic levels were observed in UFO::PME5 lines and wild-type plants (see Fig. S4 in the supplementary material), confirming that internode elongation is not affected by ectopic PME5 expression in the meristem. These results show that the altered post-meristematic phyllotaxis in blr-6 is a result of the downregulation of PME5 in the internode rather than of ectopic PME5 expression in the meristem.

We conclude that, in wild-type plants, PME5 plays a dual role in controlling phyllotaxis at the meristematic and post-meristematic level. This involves organ-specific regulation of the expression of PME5 by BLR.

**DISCUSSION**

BLR was previously shown to be required for the maintenance of meristem identity in the SAM. BLR transcripts are present in the meristem and are downregulated in incipient primordia (Byrne et al., 2003). In loss-of-function blr mutants, such as blr-6 used in this study, phyllotaxis is perturbed, with an increased variability in the divergence angles and ectopic primordia (Byrne et al., 2003; Smith et al., 2003). BLR forms heterodimers with the KNOX TALE homeodomain protein STM and acts in combination with two other BEL1-like homeodomain proteins, PNF and ATH1 (Belles-Boix et al., 2003).
al., 2006; Mele et al., 2003; Rutjens et al., 2009). The positive determination of cells in the initium by local accumulation of PME5 expression and phyllotaxis negatively by the loss of meristem identity, as a result of derepression of PME5. Primordia patterning is based on the positive determination of cells in the initium by local accumulation of the phytohormone auxin (Bayer et al., 2009; Reinhardt et al., 2000; Reinhardt et al., 2003; Yu et al., 2009). This might impinge on PME5 expression directly or indirectly, possibly via BLR.

Here, we provided insight into the mechanism underlying the allocation of meristem cells to the developing primordium. We provide evidence that BLR represses, directly or indirectly, the expression of PME5 in the meristem. In the blr-6 mutant, the altered phyllotaxis in the meristem can be explained entirely by the ectopic PME5 expression in the meristem dome, as shown by the complete restoration of meristem phyllotaxis in a blr-6/pme5-1 double mutant. These observations support a scenario in which the demethylsterification of HG in the cell wall is a critical step in the loss of meristem identity and in the allocation of the cell to a primordium. The maintenance of meristem identity during cell division requires the inhibition of PME activity, at least partly through inhibition of the accumulation of the PME5 transcript by BLR. This is consistent with the observation that PME13 overexpression completely prevents primordia formation (Peaucelle et al., 2008). At the meristem periphery, the observed downregulation of BLR expression (Byrne et al., 2003) is likely to cause PME5 transcript accumulation. Demethylsterification of HG in the newly deposited cell wall is sufficient for the recruitment of the cell into the primordium, as shown by the formation of ectopic primordia upon ectopic PME5 expression. In this scenario, it is interesting to note that the primordium fate is determined negatively by the loss of meristem identity, as a result of derepression of PME5. Primordia patterning is based on the positive determination of cells in the initium by local accumulation of the phytohormone auxin (Bayer et al., 2009; Reinhardt et al., 2000; Reinhardt et al., 2003; Yu et al., 2009). This might impinge on PME5 expression directly or indirectly, possibly via BLR.

It should also be noted that pme5-1 rescues the altered phyllotactic pattern in the blr-6 meristem but not the altered distribution of flowers and siliques in the mature inflorescence. This defect reflects changes in the post-meristematic elongation of the internodes, as revealed by the decreased length of internode epidermal cells in blr-6. Since the promoter activity of PME5 was repressed in the internode of blr-6 mutants, this suggests that, depending on the tissue, BLR can either act as an inhibitor or activator of PME5 expression (Fig. 8). This hypothesis is in accordance with the reported expression of BLR in stems (Byrne et al., 2003). The constitutive, or inducible, expression of PME5 in the internodes complemented the blr-6 phenotype, which confirms the role of the pectin methylesterification status in the control of internode cell elongation. Such a role of PME-mediated changes in cell elongation is in accordance with previous data obtained on hypocotyls (Pelletier et al., 2010). However, the absence of a post-meristematic phenotype in the pme5-1 single mutant could be related to potential redundancy within the large PME gene family.

How does demethylsterification of HG lead to primordia formation? This chemical change is expected to cause dramatic changes in the physicochemical properties of the polymer, but also removes the protection against hydrolysis by the pectin-hydrolysing enzymes pectate lyase and polygalacturonase. Cleavage of HG reduces its viscosity and presumably leads to an increase in the porosity of the cell wall, which in turn may facilitate the access of other cell wall-loosening agents, such as expansins, to their substrates (Fleming et al., 1997; Reinhardt et al., 1998). We recently investigated the role of PME5-mediated HG demethylsterification...
in the mechanical properties of the meristem. Using micro-indentation we demonstrated that HG demethylesterification does not lead to the predicted stiffening of the pectic matrix but rather to a local reduction of cell wall rigidity (Peaucelle et al., 2011). This is likely to be related to the mode of action of PME isoforms (blockwise versus non-blockwise) that could generate substrates for pectin-degrading enzymes. Our data, together with data presented in previous work (Peaucelle et al., 2008), suggest that BLR-controlled HG demethylesterification could be one of the key elements controlling the mechanical changes that underlie organ formation. In this respect, it is likely that changes in pectin structure could act synergistically with the regulation of the microtubule cytoskeleton and changes in PIN polarity, affecting auxin transport through mechanical stresses and thus triggering morphogenesis at the shoot apex (Hamant et al., 2008; Heisler et al., 2010). Our results could pave the way to adding novel components to the current model for phyllotaxis through integrating PIN1, the regulation of cell wall structure and cell mechanics.

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References

Fig. 8. The opposing effects of BLR on the expression of PMES in the wild-type meristem and internode and the impact on the establishment and maintenance of the phyllotactic pattern. BLR acts, directly or indirectly, to regulate PMES transcription in a tissue-specific manner. BLR represses PMES expression in the meristem, leading to demethylesterification of pectins that is restricted to primordia, thus influencing the establishment of the phyllotactic pattern. By contrast, BLR activates PMES expression in the internode, promoting cell elongation and the post-meristematic maintenance of phyllotaxis. The tissue-specific regulation of PMES expression by BLR thus directs regular phyllotaxy patterning.


