

# The PXY-CLE41 receptor ligand pair defines a multifunctional pathway that controls the rate and orientation of vascular cell division

J. Peter Etchells and Simon R. Turner\*

## SUMMARY

Controlling the orientation of cell division is fundamental to the development of complex body plans. This is particularly apparent in plants, where development is determined by differential growth that results solely from changes in cell expansion and orientation of the cell division plane. Despite the fundamental importance of cell division orientation to plant development, the mechanisms regulating this process remain almost completely unknown. During vascular development, the meristematic cambial cells divide down their long axis in a highly orientated manner to generate clear files of cells. The receptor kinase PXY has previously been shown to be essential for this orientation. Here, we demonstrate that the division plane is determined by the interactions of PXY and its peptide ligand, CLE41. PXY is expressed within dividing meristematic cells of the procambium, whereas CLE41 localises to the adjacent phloem cells. Altering the pattern of CLE41 expression leads to a loss of cell division orientation and a dramatic loss of ordered vascular tissue development. By contrast, increasing phloem-specific expression of CLE41 results in more cell divisions, but the orientation of cell division is retained, leading to both increased and well-ordered vascular development. We demonstrate that PXY signalling is down-regulated by CLE41. This feedback mechanism is crucial in integrating the different roles of PXY signalling in controlling xylem differentiation, regulating the rate of vascular cell division and determining the orientation of cell division. Parallels with animal systems indicate that localised signalling from adjacent cells is a general mechanism for defining the plane of cell division.

**KEY WORDS:** *Arabidopsis*, Vascular development, Cell division

## INTRODUCTION

Orientated cell divisions are an essential part of development in a wide range of multicellular organisms (Müller et al., 2009; Siller and Doe, 2009). This is particularly evident in plants, where even complex and elaborate morphologies are the consequence solely of differential growth. The absence of cell migration in plants means that growth occurs as a consequence of cell expansion and orientation of the cell division plane. Despite the importance of the orientation of cell divisions in plant development, how this process is regulated remains unclear.

In the shoot apical meristem it is well established that signalling via the receptor-like kinase (RLK) CLAVATA 1 (CLV1) is essential to maintain the balance between stem cell division and differentiation (Clark et al., 1997; DeYoung et al., 2006; Fletcher et al., 1999; Schoof et al., 2000). More recently, it has been demonstrated that orientated cell divisions in the apical meristem are an essential part of organ formation (Reddy et al., 2004). Furthermore, the presence of ectopic CLAVATA3/ESR-RELATED (CLE) proteins in roots results in alterations in the normal pattern of highly orientated cell divisions (Fiers et al., 2005). Other signalling components such as POLTERGEIST (POL) and POLTERGEIST LIKE 1 (PLL1), which are phosphatases acting downstream of CLV1 (Song et al., 2006), also influence the position of cell divisions in *Arabidopsis* embryos (Song et al., 2008).

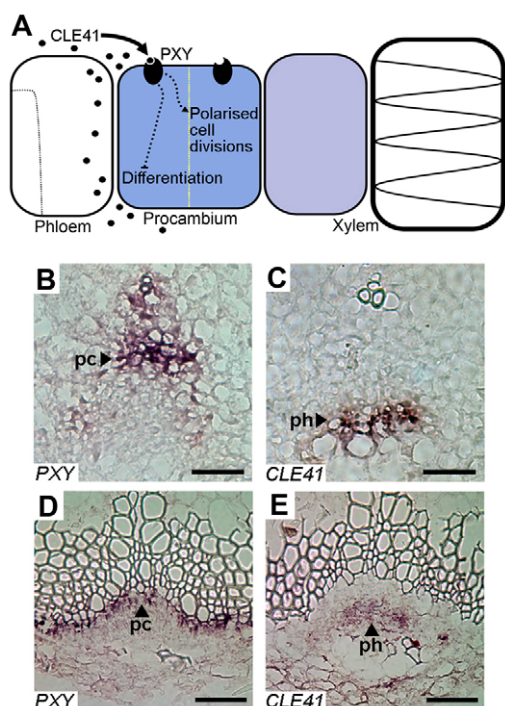
More direct evidence for a role for RLKs in controlling cell division in plant meristems has come from studies of the vascular meristem where the highly ordered nature of vascular development makes it an excellent system for studying the mechanisms that control the orientation of cell division. In contrast to initials in apical meristems, vascular initials are long thin cells, yet they divide down the centre of their long axis and parallel to the outside of the plant (periclinally) in order to generate files of cells along the radial axis that are also aligned along the apical basal axis (Fig. 1A; Fig. 2E; Fig. 4E). This process is disrupted by mutations at the *PHLOEM INTERCALATED WITH XYLEM* (PXY) locus, which encodes an RLK that is essential for ordered, coordinated cell divisions in the *Arabidopsis* procambium (Fisher and Turner, 2007). A more general role for RLKs in the orientation of cell division is supported by the identification of RLKs as being essential for the asymmetric cell division that occurs prior to lateral root initiation (De Smet et al., 2008) and a polarised cell division in Maize stomatal mother cells (Cartwright et al., 2009). Although these studies all illustrate the importance of receptor-like kinases in orientating plant cell divisions, in the absence of information on a ligand, how these kinases function to impart the positional information required to orientate the cell division plane remains unclear.

A short peptide, CLV3/ESR1-LIKE 41 (CLE41) has been shown to repress xylem differentiation in cell culture (Ito et al., 2006). CLE41 has been recently shown to bind to PXY and is thought to act synergistically with CLE6 to regulate the rate of cell division in a PXY-dependent manner (Hirakawa et al., 2008; Whitford et al., 2008). None of these studies, however, addresses how PXY or CLE41 function to orientate the plane of cell division.

A model for PXY function predicts that localised expression of the PXY ligand is essential to generate the spatial information required for oriented cell divisions (Fisher and Turner, 2007) (Fig.

Faculty of Life Sciences, University of Manchester, Manchester M13 9PT, UK

\* Author for correspondence (Simon.Turner@manchester.ac.uk)



**Fig. 1. A model to show how CLE41 and PXY determine the orientation of the cell division plane.** (A) CLE41 is expressed in the phloem and signals to PXY in the procambium, thus providing positional information to the dividing cell, which sets the appropriate division plane (yellow line). (B–E) In situ hybridisation showing PXY expressed in the procambium (B,D) and CLE41 expressed in the phloem (C,E) at the top (B,C) and the base (D,E) of inflorescence stems. pc, procambium; ph, phloem. Scale bars: 25 µm in B,C; 25 µm in D,E.

1A). Here, we demonstrate how CLE41 expression specifically localised in phloem cells is perceived by PXY and used to generate the spatial information essential for regulating the proper orientation of cell division.

PXY signalling clearly has multiple functions in vascular development that include orientating the plane of cell division, repression of xylem differentiation and regulation of the rate of cell division. We are also able to demonstrate that interactions between CLE41 and PXY involve a negative-feedback mechanism that is essential to integrate the different outputs of PXY signalling that are essential for plant vascular tissue development.

## MATERIALS AND METHODS

### Generation of plant stocks

All plant work was carried out in the Columbia ecotype. *Arabidopsis* DNA sequences were obtained from the TAIR database (Swarbreck et al., 2008). Oligonucleotides used are listed in Table S1 in the supplementary material. 35S constructs for *Arabidopsis* transformation were generated by cloning PXY, CLE41 and CLE42 genomic DNA sequences into pK2GW7.0 (Karimi et al., 2002) via pENTR-D-TOPO (Invitrogen). *IRX3::CLE41* was made similarly using p3HSC gateway destination vector (Atanassov et al., 2008). For *SUC2::CLE41*, we used overlapping PCR. The *SUC2* (*SUCROSE-PROTON SYMPORTER 2*) promoter and CLE41 coding sequences were amplified separately with overlapping ends. These products were mixed, annealed and elongated prior to amplification with *SUC2* and CLE41 forward and reverse oligos, respectively. The resulting PCR product was cloned into pTF101.gw1 (Paz et al., 2004) via pENTR-D-TOPO. For tissue

specific expression, promoters known to give xylem (*IRX3*) (Gardiner et al., 2003) or phloem (*SUC2*) (Truernit and Sauer, 1995) specific expression were used. Plasmids were sequenced, then transformed into *Arabidopsis* using floral dip (Clough and Bent, 1998). Phenotypes described are representative of 8 of 10, 11 of 12 and 14 of 15 independent events for plants transformed with 35S::CLE41, *IRX3::CLE41* and *SUC2::CLE41*, respectively. 35S::CLE42 phenotypes were found in ten independent transgenic lines. The *pxy-3* allele (Fisher and Turner, 2007) was used for genetic analysis. Homozygous *pxy-3* plants were identified by PCR. 35S::CLE41 *pxy*, 35S::CLE42 *pxy*, 35S::CLE41 35S::PXY and 35S::CLE42 35S::PXY lines were generated by crossing and were identified in the F2 population. *IRX3::CLE41* 35S::PXY and *SUC2::CLE41* 35S::PXY lines were generated by directly transforming plants carrying the 35S::PXY construct with p*IRX3::CLE41* or p*SUC2::CLE41*. *SUC2::CLE41* and 35S::CLE41 cell counts were carried out on ten independent T2s (2 bundles/plant) and six independent T1s (3 bundles/plant), respectively. Five-week-old plants were used.

### Histology

Analysis of vasculature using thin sections cut from JB4 resin embedded material was carried out as previously described (Pinon et al., 2008). For hand cut sections, tissue was stained with either aqueous 0.02% Toluidine Blue or 0.05 M Aniline Blue in 100 mM phosphate buffer, pH7.2. Vascular tissue was considered to be ordered in stem vascular bundles if the xylem and phloem could be separated by a simple curved line and ordered in the hypocotyl if xylem could be incorporated within an elliptical shape that excluded the phloem.

### Gene expression

qRT-PCR analysis was carried out using the gene-specific primers listed (see Table S1 in the supplementary material) using SYBR Green JumpStart Taq ReadyMix (Sigma) and an ABI Prism 7000 machine (Applied Biosystems) with the standard SYBR Green detection programme. A melting curve was produced at the end of every experiment to ensure that only single products were formed. Gene expression was determined using a version of the comparative threshold cycle (Ct) method. The average amplification efficiency of each target was determined using LinReg (Hardstedt et al., 2005) and samples were normalised to *18S* rRNA and *ACT2*. Results were similar, independent of the control used. All samples were measured in technical triplicates on biological triplicates and in all experiments, controls were within two Cts. Methods for in situ hybridisation analysis using digoxigenin-labelled mRNA probes were carried out as previously described (Narita et al., 2004). Oligos for making probe templates are listed in Table S1 in the supplementary material.

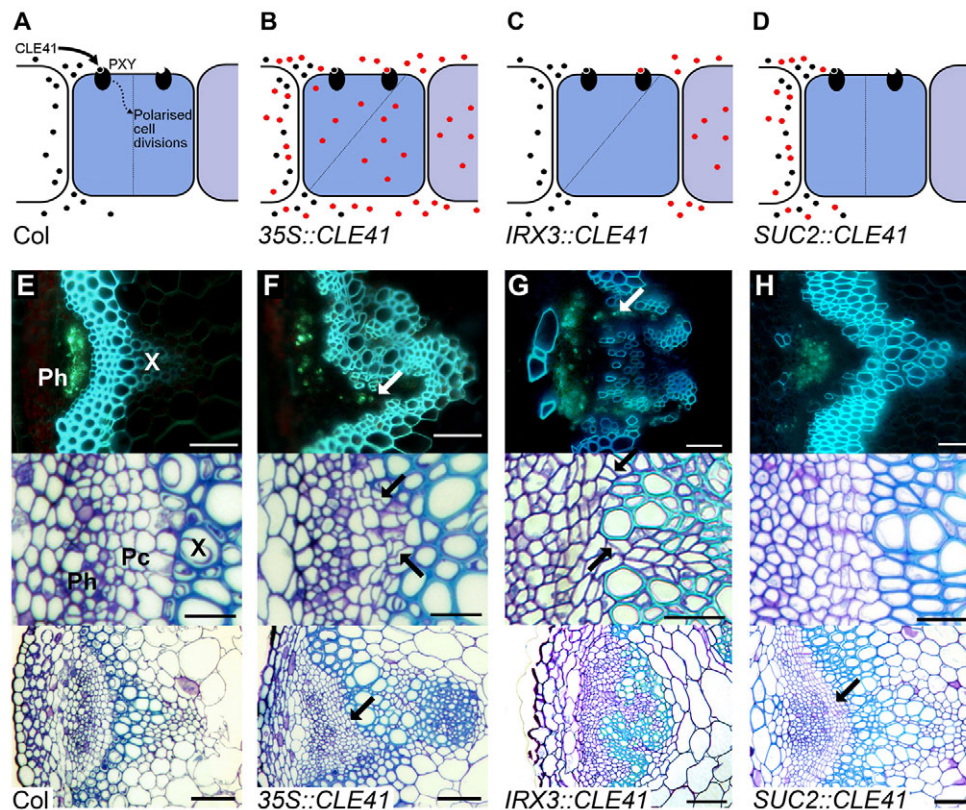
## RESULTS

### Disruption of CLE41 expression alters the plane of vascular cell divisions

Our previous model for PXY function is dependent on the secretion of PXY ligand from cells adjacent to those expressing PXY (Fisher and Turner, 2007) (Fig. 1A). Using in situ hybridisation, we found that CLE41 is expressed throughout the phloem in a domain that is adjacent to dividing cells in the procambium where PXY is expressed in both young (Fig. 1B,C) and old (Fig. 1D,E) inflorescence stems. Thus, PXY and CLE41 are expressed in adjacent, non-overlapping domains and, as such, secretion of CLE41 could impart positional information to adjacent cells expressing PXY (Fig. 1A).

CLE41 RNAi lines have previously been described as having no phenotype (Whitford et al., 2008). We reduced CLE41 expression using RNA silencing by generating plants harbouring an artificial microRNA against CLE41. There are thought to be 83 CLE genes in *Arabidopsis*. These give rise to peptides that have been classified into 13 groups, based on the CLE motif, which corresponds to their known biological functions (Oelkers et al., 2008). CLE41 was identified as a member of the group 5 family of CLE peptides, of





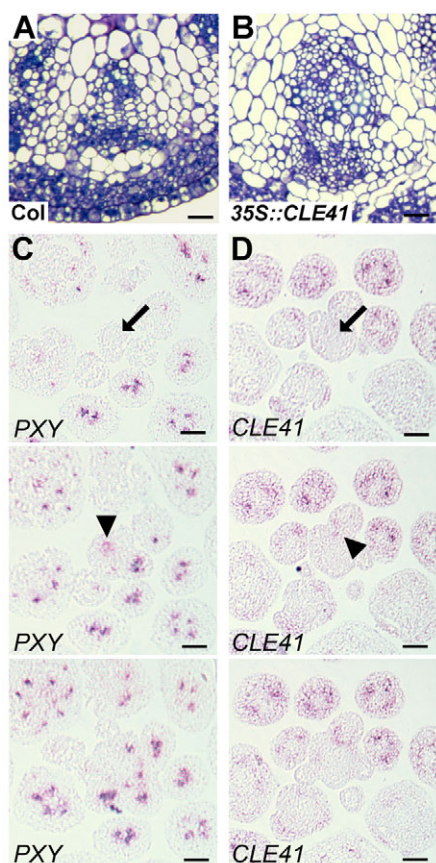
**Fig. 2. Ectopic *CLE41* expression results in disrupted vascular bundles.** (A–D) Diagrammatic representation of vascular cell divisions specified by *CLE41* and *PXY* in wild-type and transgenic lines. Native *CLE41* is represented by black dots, *CLE41* from overexpression in red. In wild type (A), *CLE41* is expressed in the phloem and signals to *PXY* in the procambium, thus providing positional information to the dividing cell, which sets the appropriate division plane (dotted line). In *35S::CLE41* (B) and *IRX3::CLE41* (C) lines, the polar nature of the *CLE41* signal is disrupted, resulting in loss of oriented cell division. *SUC2::CLE41* (D) lines have more ligand than do wild-type lines, but it is expressed in a polar manner such that positional information is maintained and the cell division is oriented. (E–H) Col stems in transverse section (E) compared with *35S::CLE41* (F), *IRX3::CLE41* (G) and *SUC2::CLE41* (H) lines. Phloem sieve plates fluoresce green in Aniline Blue stain (top panel) and are found in a discrete arc in wild-type (E) and *SUC2::CLE41* (H) lines, but are displaced towards the centre of the stem in *35S::CLE41* and *IRX3::CLE41* lines (F,G, white arrows). Procambial cells divide in a highly ordered process (middle panel) in wild type (E) and *SUC2::CLE41* (H) lines compared with *35S::CLE41* (F) and *IRX3::CLE41* (G) lines, where some cell divisions are present at altered orientations (black arrows). A large number of undifferentiated cells are present in *35S::CLE41* and *SUC2::CLE41* lines (F,H, bottom panel, black arrows) compared with wild-type lines (E). Pc, procambium; Ph, phloem; X, xylem. Scale bars: 50 μm in E–H top and bottom panels; 20 μm in E–H middle panels.

which *CLE42* and *CLE44* are the other members in *Arabidopsis* (Ito et al., 2006; Oelkers et al., 2008; Strabala et al., 2006). These three *CLE* genes have previously been identified as encoding tracheary element differentiation inhibitory factor (TDIF) on the basis of their ability to inhibit xylem differentiation (Ito et al., 2006). We crossed our strong *CLE41* knockdown lines to plants carrying a T-DNA insertion disrupting *CLE42*. In all cases, plants appeared as wild type (data not shown). It is probable that redundancy among family members explains the lack of phenotype. We analysed a large number of publicly available array experiments using the Genevestigator Digital Northern tool (Zimmermann et al., 2004). *CLE44* was expressed in array sets rich in vascular tissue, albeit at very low levels (not shown). *CLE41* has been shown to demonstrate synergism with *CLE6*, a member of the group 2 *CLE* peptides, of which there are seven members in *Arabidopsis*. As a result, it might be the case that a knockdown/knockout of ten *CLE* genes (three from group 5 and seven from group 2) is required to observe a phenotype.

To test whether localised *CLE41* expression is important for determining the orientation of cell divisions in the procambium and cambium, we disrupted its highly localised pattern by expressing it

ubiquitously using the *35S* promoter and in its polar opposite location using the well-characterised xylem-specific *IRX3* promoter (Gardiner et al., 2003; Mitsuda et al., 2007). *35S::CLE41* vascular bundles had significantly more cells than wild-type bundles ( $311.6 \pm 15.6$  cells in wild type;  $373.17 \pm 24.3$  in *35S::CLE41*;  $P < 0.05$ ; Fig. 2A,B,E,F), consistent with previous reports that established that *CLE41* overexpression results in increased vascular tissue in the root (Hirakawa et al., 2008). *CLE41* clearly influences the orientation at which procambial cells divide because in contrast to the highly polarised periclinal divisions seen in the wild-type procambium, both *35S::CLE41* and *IRX3::CLE41* lines exhibited cell divisions in a range of different orientations (Fig. 2A–C,E–G). In wild-type stems, highly orientated cell division results in spatially separated xylem and phloem, in which the phloem is restricted to a discrete arc adjacent to the cortex. Disorganised cell divisions in *35S::CLE41* and *IRX3::CLE41* lines result in the phloem expanding towards the centre of the stem and developing in regions where xylem is normally localised (Fig. 2E,F).

Misaligned cell divisions and organisational defects were observed in newly generated vascular tissue at the top of *35S::CLE41* inflorescence stems (Fig. 3A,B), suggesting that polar



**Fig. 3. PXY-CLE41 signalling acts early in vascular development.** (A,B) Transverse sections through wild-type (A) and *35S::CLE41* (B) vascular tissue in recently initiated vascular bundles 5 mm below the shoot apex of 4-week inflorescence stems. (C,D) In situ hybridisation showing that both *PXY* (C) and *CLE41* (D) expression is absent from the apical meristem (top panels, black arrow), appearing just below it as vascular development is initiated (middle panel, arrowheads), and is apparent in several vascular bundles in older tissue (lower panel). Scale bars: 20  $\mu$ m in A,B; 50  $\mu$ m in C,D.

*CLE41* expression is required early in vascular development. In situ hybridisation experiments demonstrated that no *PXY* or *CLE41* expression was observed in apical meristems. Expression was first observed below the apex where vascular development is initiated (Fig. 3C,D), suggesting that PXY/CLE signalling is required both to set up and to maintain organised vascular tissue.

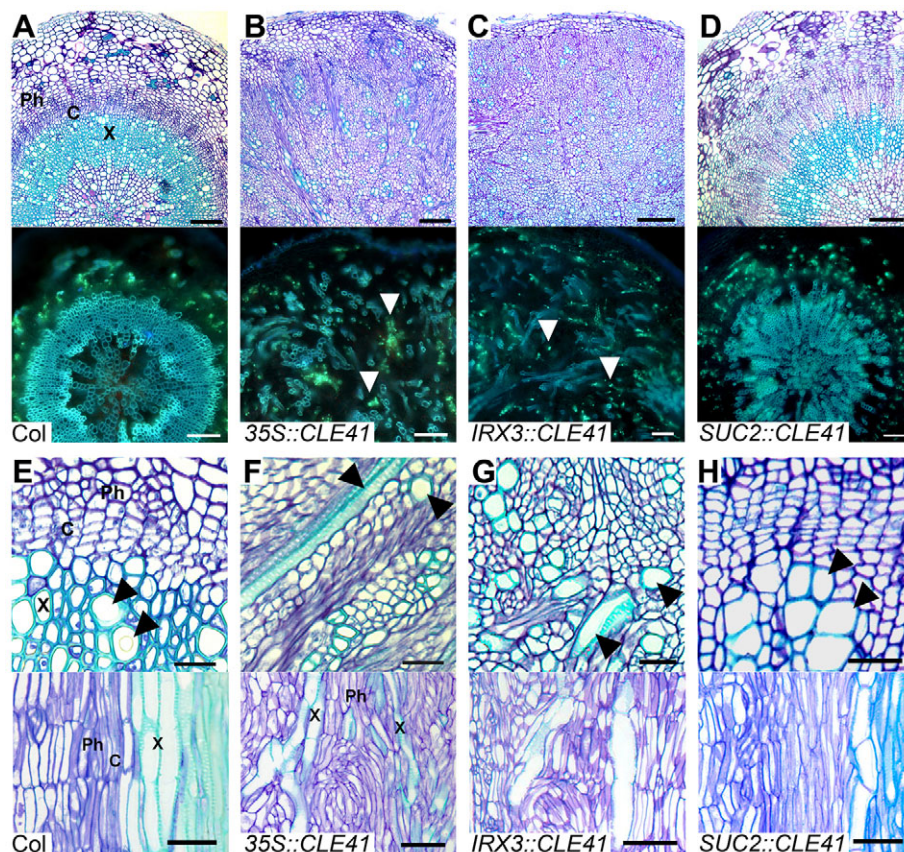
We addressed whether *CLE42*, which is predicted to generate a similar peptide to *CLE41* (Kondo et al., 2006), demonstrated similar function. *35S::CLE42* lines had similar, albeit slightly weaker, phenotypes to *35S::CLE41* in stems (see Fig. S1 in the supplementary material), demonstrating that *CLE41* and *CLE42* have similar functions. For both *35S::CLE41* and *35S::CLE42*, these phenotypes were *PXY*-dependent. *pxy 35S::CLE41* and *pxy 35S::CLE42* plants had identical phenotypes to those of *pxy* single mutants (Fig. 5; see Fig. S1 in the supplementary material). As such, *CLE41* and *CLE42* are epistatic to *pxy*, indicating that *CLE41* and *CLE42* signal through PXY and are dependent on the presence of a functional PXY receptor. These observations are consistent with *CLE41/42* and PXY acting as a ligand-receptor pair, as has been demonstrated previously by studies showing that *CLE41* binds to PXY (Hirakawa et al., 2008).

### CLE41 acts in secondary growth

To address the role of *CLE41* in PXY signalling during secondary growth, we analysed hypocotyls in plants with altered *CLE41* expression (Fig. 4A-C,E-G). Phenotypes were even more dramatic than those observed in inflorescence stems. Altering the *CLE41* expression domain overrides the patterning set up across the whole hypocotyl as it completely lacks organisation. The highly ordered and predictable pattern of vascular tissue seen in the wild-type plants (Fig. 4A,E) is largely lost in *35S::CLE41* and *IRX3::CLE41* plants (Fig. 4B,C,F,G). Some of the cells within the hypocotyl do have a xylem or phloem fate, but these tissues are completely interspersed such that xylem and phloem are no longer separated into recognisable domains. Phloem cell differentiation occurs even in tissue surrounded by xylem and vice-versa, indicating that cambial cells retain the ability to generate xylem and phloem whatever their position within the tissue and that their fate is not reprogrammed dependent on mediolateral position in the stem. Not only is mediolateral patterning disrupted but apical-basal organisation of cells within these hypocotyls is also altered. In wild-type plants, all xylem cells are oriented in a similar manner and run either parallel to the plane of longitudinal sections or at right angles to it in transverse sections (Fig. 4E). This is in striking contrast to *35S::CLE41* and *IRX3::CLE41* plants where xylem vessels are present with dramatically differing orientations, such that cells exhibiting a normal orientation are located adjacent to cells in a perpendicular orientation (Fig. 4F,G). *35S::CLE42* lines had similar, albeit slightly weaker, phenotypes to *35S::CLE41* in hypocotyls (Fig. 5; see Fig. S1 in the supplementary material).

To confirm that the plane of cell division was disrupted by changes to the location of *CLE41* expression and not simply by increasing *CLE41* expression per se, we expressed *CLE41* from the strong phloem-specific and widely used *SUC2* promoter (Truernit and Sauer, 1995) and found that vascular tissue was highly ordered (Fig. 2D; Fig. 4D). The *SUC2::CLE41* construct was clearly functional as, in common with *35S::CLE41* lines (see above), significant increases in vascular cell number were observed ( $358.8 \pm 15.1$  cells per bundle in wild type;  $557.0 \pm 27.6$  in *SUC2::CLE41*;  $P < 0.0001$ ). Our data demonstrate that expression of *CLE41* in or around cells expressing PXY is sufficient to drive vascular cell division but localised expression of *CLE41* in the phloem is essential to maintain properly orientated cell divisions. To confirm that this was indeed the case, and that cell misarrangements were not the consequence of high-level *CLE41* expression for an extended period of time or the result of very different expression levels in different lines, we screened the progeny from five independent transformants for each of the *SUC2*, *IRX3* and *35S* promoter constructs and selected three lines that exhibited comparable *CLE41* expression but were relatively weak overexpressing lines (see Fig. S2A in the supplementary material). When *CLE41* was expressed from the phloem using the *SUC2* promoter, cell divisions were ordered. By contrast, when *CLE41* was expressed either ubiquitously using the *35S* promoter or from the xylem using the *IRX3* promoter, this was not the case and divisions were found that were misoriented (see Fig. S2, arrows, in the supplementary material). The result of the misoriented cell divisions is most clearly seen in the hypocotyl, where *SUC2::CLE41* retains the wild-type orientation, but this is lost in lines using either the *35S* and/or *IRX3* promoter to drive *CLE41* expression. As mentioned above, these lines are weak overexpressers of *CLE41* (see Fig. S2A in the supplementary material) and, consequently, the data clearly demonstrate that the orientation of cell division is dependent on





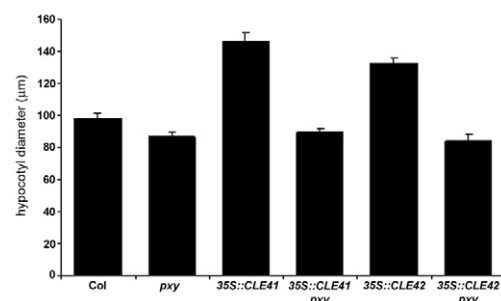
**Fig. 4. Ectopic CLE41 expression results in intercalation of xylem and phloem in hypocotyls.** (A-D) Transverse sections of Toluidine Blue-stained hypocotyls (upper panels) demonstrate that in wild-type (A) and *SUC2::CLE41* (D) hypocotyls, the vascular cylinder is highly ordered with a continuous ring of xylem. Conversely, *35S::CLE41* (B) and *IRX3::CLE41* (C) hypocotyls are disorganised, with cell types interspersed. In sections stained with Aniline Blue (lower panels), wild-type (A) and *SUC2::CLE41* (D) hypocotyls have phloem (fluorescing green) on the outside of the stem surrounding xylem on the inside. In *35S::CLE41* (B) and *IRX3::CLE41* (C) hypocotyls, phloem cells develop towards the centre of the stem (arrowheads) surrounded by xylem. (E-G) Toluidine Blue-stained close-up images show that in wild-type (E) and *SUC2::CLE41* (H) hypocotyls, all xylem cells are running parallel (arrowheads) into the plane of section; however, in *35S::CLE41* (F) and *IRX3::CLE41* (G) hypocotyls, xylem vessels are in a variety of orientations (arrowheads). Xylem cells running parallel to the plane of section demonstrate a lack of order along the apical-basal axis and this is clearly demonstrated in longitudinal section (lower panels). C, cambium; Ph, phloem; X, xylem. Scale bars: 100 µm in A-D; 20 µm in E-H upper panels; 50 µm in E-H lower panels.

*CLE41* localisation and not due to high-level *CLE41* expression. Taken together, these results, for the first time, demonstrate that polarised ligand signalling to an adjacent receptor can set the cell division plane required for coordinated positioning of a cell division.

### A negative-feedback mechanism regulates *PXY* expression

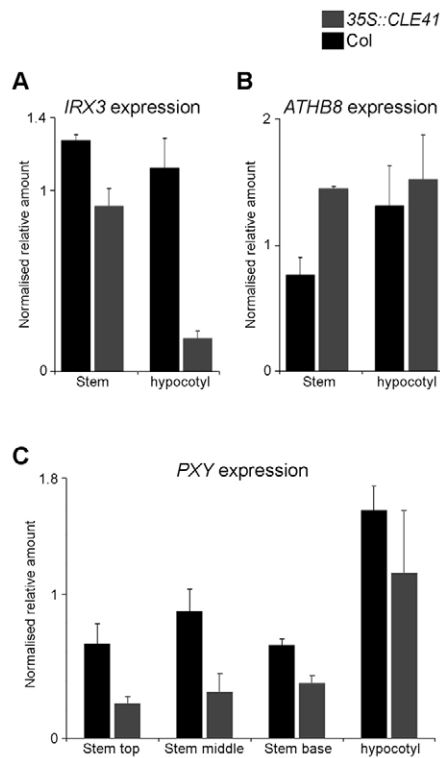
Previously, *PXY* expression has been shown to be higher in *pxy* mutants than wild type (Fisher and Turner, 2007). This suggests that a negative-feedback mechanism could be a feature of *PXY* signalling as *PXY* signalling represses *PXY* expression. To investigate this further, expression of *PXY* was assayed in *35S::CLE41* plants. A reduction in *PXY* expression was observed in the inflorescence stem and hypocotyl consistent with *CLE41* acting to negatively regulate its receptor (Fig. 6), as has been observed with some ligand-receptor interactions in animal systems (Cadigan et al., 1998). We addressed the consequences of relieving *PXY* from negative regulation of *CLE41* by using a *35S::PXY* construct in a *35S::CLE41/42* background. The stems of *35S::CLE41 35S::PXY* and *35S::CLE42 35S::PXY* plants were characterised by dramatic increases in cell number in both the vascular bundle and in the interfascicular region, such that a continuous ring of additional tissue was observed within the stem. New cells were generated between the xylem and phloem in vascular bundles and in the interfascicular region, making the phenotype characteristic of dramatically increased secondary growth (Fig. 7D-G). These results provide strong genetic evidence that *CLE41/42* and *PXY* are a ligand-receptor pair and are sufficient to promote vascular cell division within the procambium and for the induction of secondary growth in the interfascicular region.

Interestingly, the majority of increased cell divisions occurring when both *CLE41/42* and *PXY* were overexpressed were relatively ordered, although aberrant cell divisions were still present (Fig. 7F). How relative order is restored upon ectopic expression of both *PXY* and *CLE41/42* is unclear; however, *35S::PXY* might act to prevent the native receptor from becoming saturated, thus allowing the receptor to perceive a small ligand gradient that might still exist. To test this hypothesis, we made lines harbouring both *IRX3::CLE41* and *35S::PXY* constructs. Consistent with our model (Fig. 1A), we found that vascular organisation was disrupted in *35S::PXY IRX3::CLE41* plants (Fig. 7G,H) but increased secondary growth was also observed, supporting the hypothesis that a signal gradient that is high on the phloem side of the cambium is required for vascular organisation and that overcoming *PXY* negative regulation by *CLE41* can initiate



**Fig. 5. The diameter of plant hypocotyls at senescence.** Error bars are standard error. *t*-tests show that *pxy* is significantly smaller than Col ( $P < 0.005$ ) and that *35S::CLE41* and *35S::CLE42* are significantly larger than Col ( $P < 0.0001$ ). *35S::CLE41 pxy* and *35S::CLE42 pxy* were not significantly different from *pxy*.



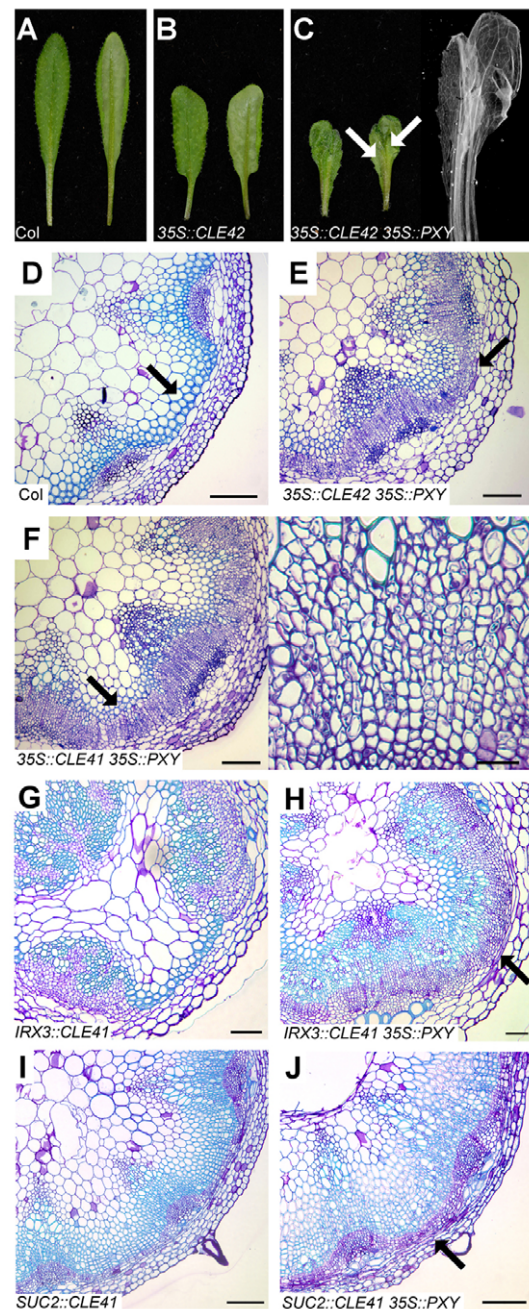


**Fig. 6. Changes in gene expression in 35S::CLE41 compared with wild type, normalised to 18S rRNA. (A–C)** Quantitative RT-PCR was used to assay *IRX3* (A), *ATHB8* (B) and *PXY* (C) expression in stems and hypocotyls of wild-type plants compared with 35S::CLE41. Error bars are standard error.

secondary growth. 35S::PXY SUC2::CLE41 plants also demonstrated enhanced secondary growth (Fig. 7I,J) but, in contrast to 35S::PXY *IRX3*::CLE41, vascular tissue was highly ordered.

An additional phenotype was observed in the leaves of 35S::CLE42 35S::PXY plants. In Col, 35S::CLE42 (Fig. 7A,B) and 35S::PXY (data not shown) plants, leaves have a single midvein; however, in a minority of 35S::CLE42 35S::PXY plants, the leaves appeared to exhibit increased vascular development. This additional vascular tissue develops together with the associated lamina, suggesting development of ectopic midveins (Fig. 7C) reminiscent of plants overexpressing both CLE41 and CLE6 (Whitford et al., 2008). This leaf phenotype adds to the increasing evidence that co-expression of CLE41/42 and PXY is sufficient to drive vascular cell division.

A previously described function of CLE41-derived peptides is repression of tracheary element differentiation in *Zinnia* cell culture (Kondo et al., 2006). *ATHB8*, which is a provascular marker (Baima et al., 1995), has been found to be upregulated in plants treated with CLE41 peptide (Whitford et al., 2008) and, similarly, we observed high *ATHB8* expression in the stems of 35S::CLE41 plants (Fig. 6B). *ATHB8* does not mark cambial cells and, as such, its expression in the hypocotyl was not different from that in the wild type. We used *IRX3* expression as a marker for xylem development as *IRX3* is a subunit of the cellulose synthase complex that acts in secondary cell wall formation and is strongly upregulated as xylem cells differentiate (Taylor et al., 1999). Consistent with the observations of Kondo (Kondo et al., 2006), 35S::CLE41 had reduced *IRX3* expression compared with that of wild type (Fig. 6A), suggesting



**Fig. 7. Ectopic vascular tissue in 35S::PXY 35S::CLE41/42 plants.**

(A–C) Wild-type (A) and 35S::CLE42 (B) leaves have a single midvein, whereas leaves from some 35S::CLE42 35S::PXY (C, arrows) plants have more. (D–F) Vascular and interfascicular tissue (arrow in D) from wild-type (D), 35S::CLE42 35S::PXY (E) and 35S::CLE41 35S::PXY (F) plants. 35S::CLE42 35S::PXY and 35S::CLE41 35S::PXY have more undifferentiated cells than do wild type. (G–J) *IRX3*::CLE41 (G) and *IRX3*::CLE41 35S::PXY (H) have disorganised vascular bundles, but this is not the case in *SUC2*::CLE41 (I) and *SUC2*::CLE41 35S::PXY (J), which have a large number of vascular cells that are highly ordered. Arrows in E, F, H and J point to areas of strong secondary growth. Scale bars: 100  $\mu$ m, except 20  $\mu$ m in F, right-hand panel.

that xylem differentiation was repressed. This is clearly reflected in 35S::PXY 35S::CLE41 and 35S::CLE42 plants (Fig. 7E,F), which had a reduction in xylem differentiation as the additional cells generated in this line appeared to be undifferentiated. However, in

35S::PXY SUC2::CLE41 lines, xylem was well-developed, suggesting that the range of CLE41 is limited as it is unable to repress xylem differentiation when expressed from the phloem. This suggests that phloem-expressed CLE41 does not cross the procambium to act on young developing xylem cells and is consistent with the range of the well-characterised and closely related CLAVATA3 peptide, which is expressed in layers 1 to 3 of the apical meristem (Fletcher et al., 1999) and binds its receptor, CLV1, in layer 3 and a further two cell layers below (Clark et al., 1997).

## DISCUSSION

Genetic analysis presented in this manuscript, together with previous data showing that PXY binds to a dodecapeptide derived from CLE41 and/or CLE44 using photoaffinity labelling (Hirakawa et al., 2008), indicate that CLE41 and CLE42 are ligands for the PXY receptor kinase. Our results show that signalling through PXY/CLE regulates division of vascular cells and that specific localisation of CLE41 in the phloem adjacent to the dividing cells that express PXY is required for properly orientated vascular cell divisions. The disrupted tissue phenotype occurs only when the specific localisation of CLE41 is disrupted (i.e. by using the 35S or IRX3 promoter to drive its expression) and is therefore the result of altering the CLE41 expression domain. Disruption does not occur when expression is increased specifically in the phloem (using the SUC2 promoter), where native CLE41 is expressed. The lines used in this study are directly comparable as the increased cell division output of PXY-CLE41 signalling is similar in 35S::CLE41 lines (which have disorganised vasculature) and SUC2::CLE41 lines (which have organised vasculature). As both lines demonstrate similar increases in cell division, there must be similar levels of signalling through PXY. The difference in the phenotypes is likely to be a consequence of the difference in expression domain. The 'disrupted' phenotype is unlikely to be due to a general increase in cambial or procambial cell division because lines that have previously been described with increases in vascular cell number, such as *acl5* (Hanzawa et al., 2000), *hca* (Pineau et al., 2005), *soc1 ful* (Melzer et al., 2008) or *hca2* (Guo et al., 2009) have highly ordered vascular tissue, clearly demonstrating that this phenotype is not a general symptom of high levels of vascular cell division. Our experiments show an essential role for localised expression of CLE41 in the highly ordered nature of cell divisions in vascular meristems. We demonstrate for the first time in the plant kingdom that polar localisation of a ligand can confer positional information through a receptor, which sets a cell division plane. Our model of CLE41/PXY signalling is reminiscent of the ordered cell division that occurs in the *C. elegans* EMS cells. Orientation of the EMS division is dependent on the position of the neighbouring P2 cell, from which the MOM-2 ligand signals to the MOM-5 receptor in the EMS cell (Schlesinger et al., 1999). This suggests that orientation of cell division based upon signalling from an adjacent cell is a general mechanism that has arisen in a diverse array of multicellular organisms.

The signalling pathway involving CLE41/PXY is multifunctional as, in addition to its previously identified role in repressing xylem development, it plays a central role in regulating the number and orientation of cell divisions in vascular meristems. Just such a signalling mechanism was first proposed four decades ago in classical experiments carried out on castor bean hypocotyls where, prior to cambial development, a piece of interfascicular tissue was removed, rotated 180° and reinserted such that cells at the periphery were now positioned towards the centre of the stem. In successful

grafts, the cambium developed in the expected position but orientation of xylem and phloem generated in the graft was consistent with the original orientation of the tissue, thus at 180° to surrounding tissue. Xylem was therefore on the periphery with phloem towards the centre of the stem (Siebers, 1971). In further experiments using crab apple trees, the signal which orients the cambium was shown to be maintained in tissue that was grafted at 90° to its original orientation in the third growing season (Thair and Steves, 1976). This suggests that the mechanism by which this organisation is set acts early – prior to formation of the cambium – and is set by a short range signal, i.e. from within the graft area (Siebers, 1971), as polarity is retained irrespective of the organisation of surrounding tissue and, therefore, in the absence of any additional positional information. Our data suggest that this polarity is set up by the expression of PXY in nascent vascular initials and CLE41 expression in nascent phloem cells. The grafting experiments described above suggest that once this spatial expression pattern is in place it is sufficient to propagate itself without any additional spatial cues.

Negative regulation of a receptor by a ligand is a mechanism for regulating the ligand-receptor dynamic. Our observation that high levels of CLE41 expression results in suppression of PXY expression are consistent with previous data that show increased PXY expression in *pxy* mutants (Fisher and Turner, 2007). One such example of ligand-mediated repression of receptor expression occurs in early fly wing development, where the Wingless (Wn) ligand is highly expressed at the dorsoventral boundary of imaginal discs and thus forms a gradient that is high at the dorsoventral stripe and low in regions distal to it. Wn negatively regulates its receptor, Frizzled (Fz), where it occurs in high concentrations at the boundary. This negative regulation does not extend to Fz expression further from the boundary where Wn concentration is lower, thus allowing regulation of the Wn morphogen gradient (Cadigan et al., 1998).

We have shown that the PXY-CLE41/42 ligand-receptor pair is essential to regulate the rate of cell division, cell differentiation and the orientation of the cell division (Fig. 1A; see also Fig. S1 in the supplementary material). Given the importance of RLKs in cell division and orientation in other systems, it is possible that similar integration is essential in many other aspects of plant development.

## Acknowledgements

We thank Ilian Atanassov for assistance with *pIRX3::CLE41* and especially Andrew Hudson for assistance with in situ hybridisation. This work was funded by BBSRC (grant BB/E00380X/1).

## Competing interests statement

The authors declare no competing financial interests.

## Supplementary material

Supplementary material for this article is available at <http://dev.biologists.org/lookup/suppl/doi:10.1242/dev.044941/-DC1>

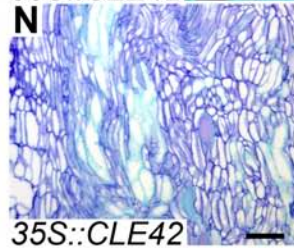
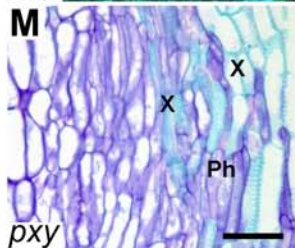
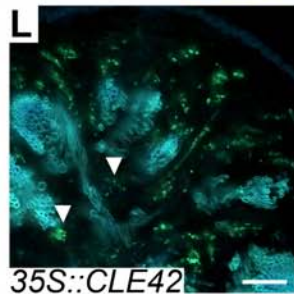
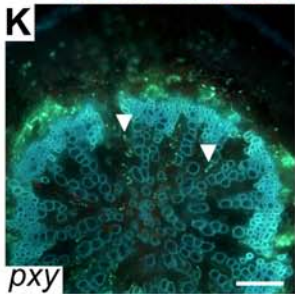
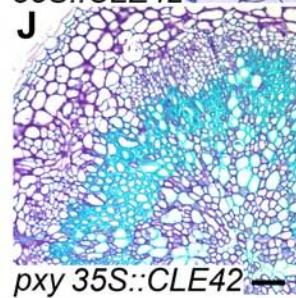
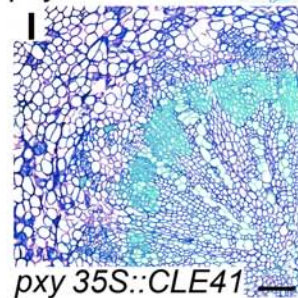
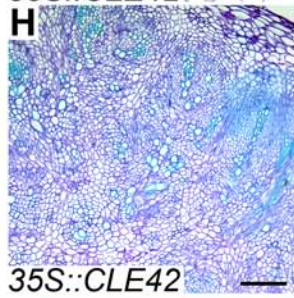
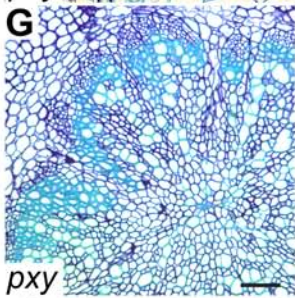
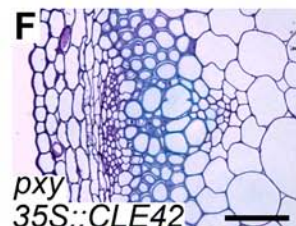
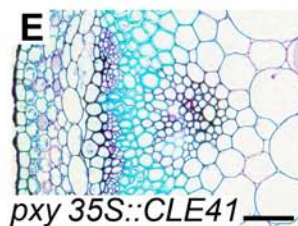
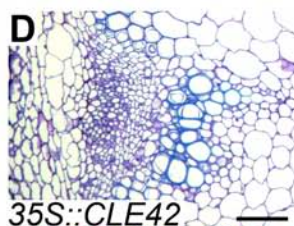
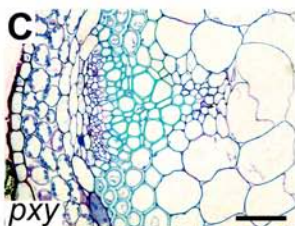
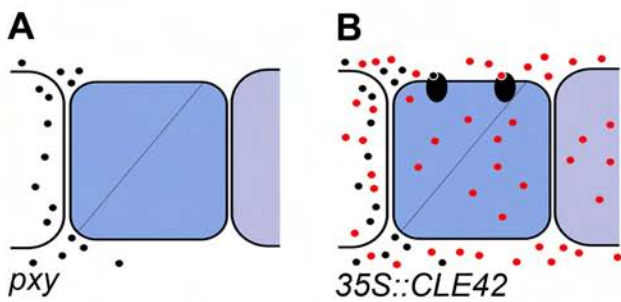
## References

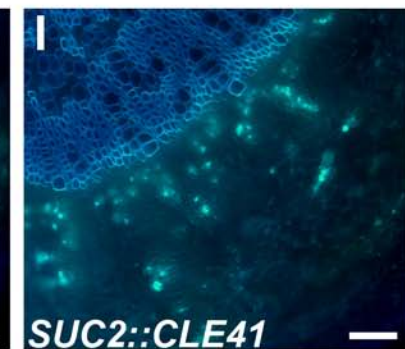
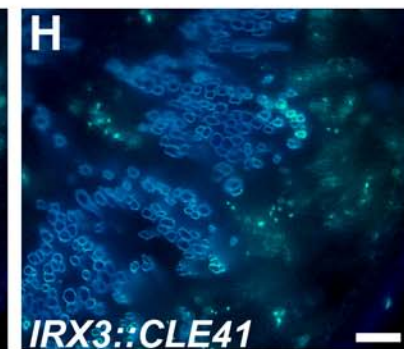
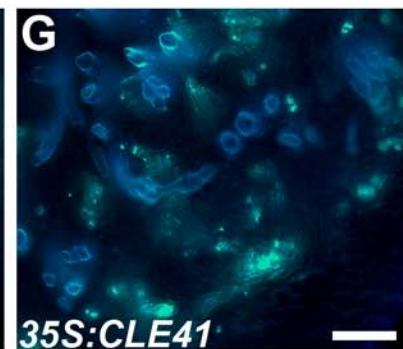
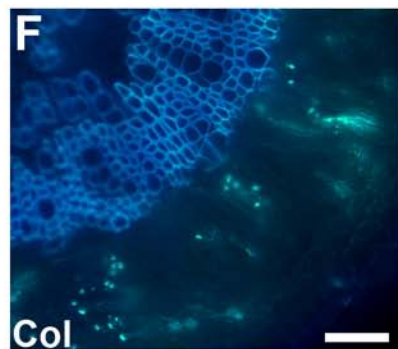
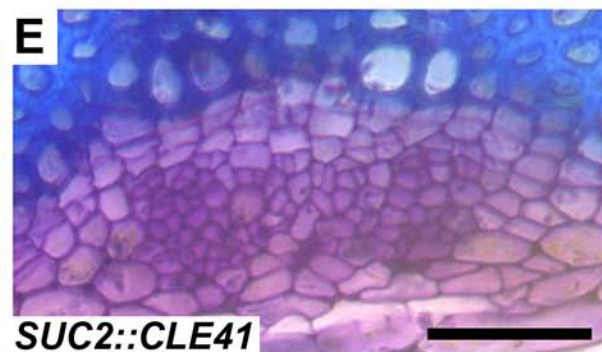
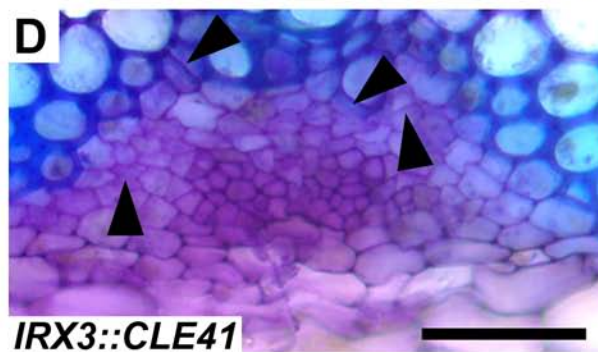
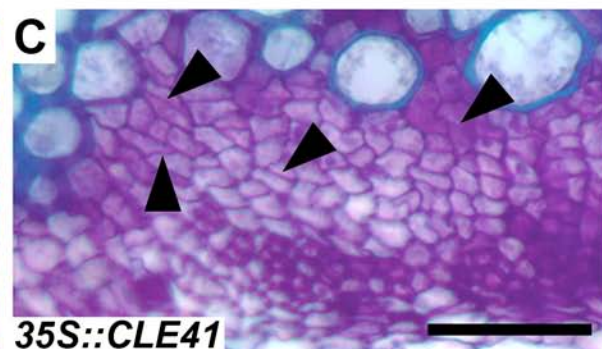
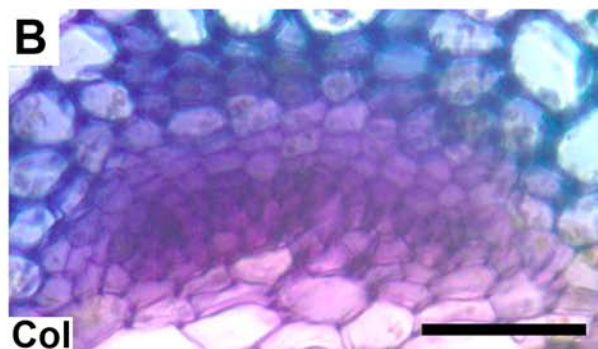
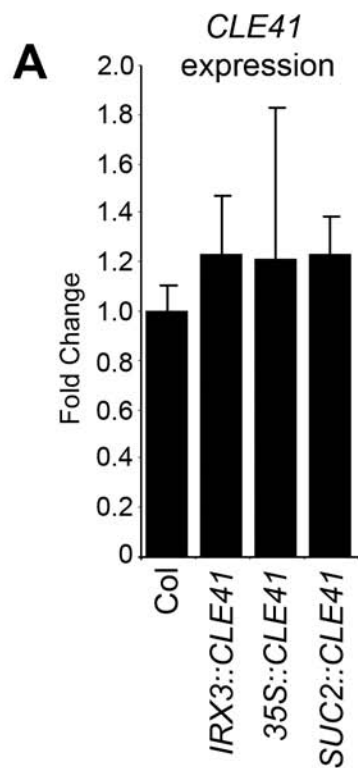
- Atanassov, I. I., Pittman, J. K. and Turner, S. R. (2008). Elucidating the mechanisms of assembly and subunit-interaction of the cellulose synthase complex of *Arabidopsis* secondary cell walls. *J. Biol. Chem.* **284**, 3833–3841.
- Baima, S., Nobili, F., Sessa, G., Lucchetti, S., Ruberti, I. and Morelli, G. (1995). The expression of the Athb-8 homeobox gene is restricted to provascular cells in *Arabidopsis thaliana*. *Development* **121**, 4171–4182.
- Cadigan, K. M., Fish, M. P., Rulifson, E. J. and Nusse, R. (1998). Wingless repression of *Drosophila* frizzled 2 expression shapes the Wingless morphogen gradient in the wing. *Cell* **93**, 767–777.
- Cartwright, H. N., Humphries, J. A. and Smith, L. G. (2009). PAN1: A receptor-like protein that promotes polarization of an asymmetric cell division in maize. *Science* **323**, 649–651.
- Clark, S. E., Williams, R. W. and Meyerowitz, E. M. (1997). The CLAVATA1 gene encodes a putative receptor kinase that controls shoot and floral meristem size in *Arabidopsis*. *Cell* **89**, 575–585.



- Clough, S. J. and Bent, A. F. (1998). Floral dip: a simplified method for Agrobacterium-mediated transformation of *Arabidopsis thaliana*. *Plant Journal* **16**, 735-743.
- De Smet, I., Vassileva, V., De Rybel, B., Levesque, M. P., Grunewald, W., Van Damme, D., Van Noorden, G., Naudts, M., Van Isterdael, G., De Clercq, R. et al. (2008). Receptor-like kinase ACR4 restricts formative cell divisions in the *Arabidopsis* root. *Science* **322**, 594-597.
- DeYoung, B. J., Bickle, K. L., Schrage, K. J., Muskett, P., Patel, K. and Clark, S. E. (2006). The CLAVATA1-related BAM1, BAM2 and BAM3 receptor kinase-like proteins are required for meristem function in *Arabidopsis*. *Plant J.* **45**, 1-16.
- Fiers, M., Golemic, E., Xu, J., van der Geest, L., Heidstra, R., Stiekema, W. and Liu, C.-M. (2005). The 14-amino acid CLV3, CLE19, and CLE40 peptides trigger consumption of the root meristem in *Arabidopsis* through a CLAVATA2-dependent pathway. *Plant Cell* **17**, 2542-2553.
- Fisher, K. and Turner, S. (2007). PXY, a receptor-like kinase essential for maintaining polarity during plant vascular-tissue development. *Curr. Biol.* **17**, 1061-1066.
- Fletcher, L. C., Brand, U., Running, M. P., Simon, R. and Meyerowitz, E. M. (1999). Signaling of cell fate decisions by CLAVATA3 in *Arabidopsis* shoot meristems. *Science* **283**, 1911-1914.
- Gardiner, J. C., Taylor, N. G. and Turner, S. R. (2003). Control of cellulose synthase complex localization in developing xylem. *Plant Cell* **15**, 1740-1748.
- Guo, Y., Qin, G., Gu, H. and Qu, L.-J. (2009). Dof5.6/HCA2, a Dof transcription factor gene, regulates interfascicular cambium formation and vascular tissue development in *Arabidopsis*. *Plant Cell* **21**, 3518-3534.
- Hanzawa, Y., Takahashi, T., Michael, A. J., Burtin, D., Long, D., Pineiro, M., Coupland, G. and Komeda, Y. (2000). ACAULIS5, an *Arabidopsis* gene required for stem elongation, encodes a spermine synthase. *EMBO J.* **19**, 4248-4256.
- Hardstedt, M., Finnegan, C. P., Kirchhof, N., Hyland, K. A., Wijkstrom, M., Murtaugh, M. P. and Hering, B. J. (2005). Post-transplant upregulation of chemokine messenger RNA in non-human primate recipients of intraportal pig islet xenografts. *Xenotransplantation* **12**, 293-302.
- Hirakawa, Y., Shinohara, H., Kondo, Y., Inoue, A., Nakanomyo, I., Ogawa, M., Sawa, S., Ohashi-Ito, K., Matsubayashi, Y. and Fukuda, H. (2008). Non-cell-autonomous control of vascular stem cell fate by a CLE peptide/receptor system. *Proc. Natl. Acad. Sci. USA* **105**, 15208-15213.
- Ito, Y., Nakanomyo, I., Motose, H., Iwamoto, K., Sawa, S., Dohmae, N. and Fukuda, H. (2006). Dodeca-CLE peptides as suppressors of plant stem cell differentiation. *Science* **313**, 842-845.
- Karimi, M., Inze, D. and Depicker, A. (2002). GATEWAY(TM) vectors for Agrobacterium-mediated plant transformation. *Trends Plant Sci.* **7**, 193-195.
- Kondo, T., Sawa, S., Kinoshita, A., Mizuno, S., Kakimoto, T., Fukuda, H. and Sakagami, Y. (2006). A plant peptide encoded by CLV3 identified by in situ MALDI-TOF MS analysis. *Science* **313**, 845-848.
- Melzer, S., Lens, F., Gennen, J., Vanneste, S., Rohde, A. and Beeckman, T. (2008). Flowering-time genes modulate meristem determinacy and growth form in *Arabidopsis thaliana*. *Nat. Genet.* **40**, 1489-1492.
- Mitsuda, N., Iwase, A., Yamamoto, H., Yoshida, M., Seki, M., Shinozaki, K. and Ohme-Takagi, M. (2007). NAC transcription factors, NST1 and NST3, are key regulators of the formation of secondary walls in woody tissues of *Arabidopsis*. *Plant Cell* **19**, 270-280.
- Müller, S., Wright, A. J. and Smith, L. G. (2009). Division plane control in plants: new players in the band. *Trends Cell Biol.* **19**, 180-188.
- Narita, N. N., Moore, S., Horiguchi, G., Kubo, M., Demura, T., Fukuda, H., Goodrich, J. and Tsukaya, H. (2004). Overexpression of a novel small peptide ROTUNDIFOLIA4 decreases cell proliferation and alters leaf shape in *Arabidopsis thaliana*. *Plant J.* **38**, 699-713.
- Oelkers, K., Goffard, N., Weiller, G., Gresshoff, P., Mathesius, U. and Frickey, T. (2008). Bioinformatic analysis of the CLE signaling peptide family. *BMC Plant Biol.* **8**, 1.
- Paz, M., Shou, H., Guo, Z., Zhang, Z., Banerjee, A. and Wang, K. (2004). Assessment of conditions affecting Agrobacterium-mediated soybean transformation using the cotyledonary node explant. *Euphytica* **136**, 167-179.
- Pineau, P., Freydisier, A., Ranocha, P., Jauneau, A., Turner, S., Lemonnier, G., Renou, J.-P., Tarkowski, P., Sandberg, G., Jouanin, L. et al. (2005). *hca*: an *Arabidopsis* mutant exhibiting unusual cambial activity and altered vascular patterning. *Plant J.* **44**, 271-289.
- Pinon, V., Etchells, J. P., Rossignol, P., Collier, S. A., Arroyo, J. M., Martienssen, R. A. and Byrne, M. E. (2008). Three *PIGGYBACK* genes that specifically influence leaf patterning encode ribosomal proteins. *Development* **135**, 1315-1324.
- Reddy, G. V., Heisler, M. G., Ehrhardt, D. W. and Meyerowitz, E. M. (2004). Real-time lineage analysis reveals oriented cell divisions associated with morphogenesis at the shoot apex of *Arabidopsis thaliana*. *Development* **131**, 4225-4237.
- Schlesinger, A., Shelton, C., Maloof, J. N., Meneghini, M. and Bowerman, B. (1999). Wnt pathway components orient a mitotic spindle in the early *Caenorhabditis elegans* embryo without requiring gene transcription in the responding cell. *Genes Dev.* **13**, 2028-2038.
- Schoof, H., Lenhard, M., Haecker, A., Mayer, K. F. X., Jurgens, G. and Laux, T. (2000). The stem cell population of *Arabidopsis* shoot meristems is maintained by a regulatory loop between the CLAVATA and WUSCHEL genes. *Cell* **100**, 635-644.
- Siebers, A. M. (1971). Initiation of radial polarity in the interfascicular cambium of *Ricinus communis* L. *Acta Bot. Neerl.* **20**, 211-220.
- Siller, K. H. and Doe, C. Q. (2009). Spindle orientation during asymmetric cell division. *Nat. Cell Biol.* **11**, 365-374.
- Song, S.-K., Lee, M. M. and Clark, S. E. (2006). POL and PLL1 phosphatases are CLAVATA1 signaling intermediates required for *Arabidopsis* shoot and floral stem cells. *Development* **133**, 4691-4698.
- Song, S. K., Hoffhuis, H. F., Lee, M. M. and Clark, S. E. (2008). Key divisions in the early *Arabidopsis* embryo require POL and PLL1 phosphatases to establish the root stem cell organizer and vascular axis. *Dev. Cell* **15**, 98-109.
- Strabala, T. J., O'Donnell, P. J., Smit, A. M., Ampomah-Dwamena, C., Martin, E. J., Netzler, N., Nieuwenhuizen, N. J., Quinn, B. D., Foote, H. C. C. and Hudson, K. R. (2006). Gain-of-function phenotypes of many CLAVATA3/ESR genes, including four new family members, correlate with tandem variations in the conserved CLAVATA3/ESR domain. *Plant Physiol.* **140**, 1331-1344.
- Swarbreck, D., Wilks, C., Lamesch, P., Berardini, T. Z., Garcia-Hernandez, M., Foerster, H., Li, D., Meyer, T., Muller, R., Ploetz, L. et al. (2008). The *Arabidopsis* information resource (TAIR): gene structure and function annotation. *Nucl. Acids Res.* **36**, D1009-D1014.
- Taylor, N. G., Scheible, W. R., Cutler, S., Somerville, C. R. and Turner, S. R. (1999). The irregular xylem3 locus of *Arabidopsis* encodes a cellulose synthase required for secondary cell wall synthesis. *Plant Cell* **11**, 769-779.
- Thair, B. W. and Steves, T. A. (1976). Response of the vascular cambium to reorientation in patch grafts. *Can. J. Bot.* **54**, 361-373.
- Truernit, E. and Sauer, N. (1995). The promoter of the *Arabidopsis thaliana* SUC2 sucrose-H<sup>+</sup> symporter gene directs expression of  $\beta$ -glucuronidase to the phloem: evidence for phloem loading and unloading by SUC2. *Planta* **196**, 564-570.
- Whitford, R., Fernandez, A., De Groodt, R., Ortega, E. and Hilson, P. (2008). Plant CLE peptides from two distinct functional classes synergistically induce division of vascular cells. *Proc. Natl. Acad. Sci. USA* **105**, 18625-18630.
- Zimmermann, P., Hirsch-Hoffmann, M., Hennig, L. and Gruissem, W. (2004). GENEVESTIGATOR. *Arabidopsis* microarray database and analysis toolbox. *Plant Physiol.* **136**, 2621-2632.









**Table S1. Oligonucleotides used in the generation of plant stocks**

Oligo name	Sequence (5'-3')	Function
<i>CLE41F</i>	CACCATGGCAACATCAAATGAC	<i>CLE41</i> entry clone/ <i>SUC2::CLE41</i> overlap PCR entry clone/in situ hybridization probe
<i>CLE41R</i>	aaaccagatgtgccaaactca	<i>CLE41</i> entry clone/in situ hybridization probe/ <i>CLE41</i> construct genotyping
<i>CLE42F</i>	caccatgagatctctcacatc	<i>CLE41</i> entry clone/ <i>35S::CLE42</i> genotyping
<i>CLE42R</i>	tgaatcaaacaagcaacataacaa	<i>CLE42</i> entry clone
<i>PXY_ORF_f</i>	CACCTTAAATCCACCATTTGTCA	<i>35S::PXY</i> construct
<i>PXY_ORF_r</i>	CCAAGATAATGGACGCCAAC	<i>35S::PXY</i> construct
<i>PXY_SEQ_1F</i>	CGGAACCTCTCTGGTCGTAT PXY	in situ probe
<i>PXY_SEQ_1R</i>	TGATCGGTGAATCTGTTGTTG	<i>PXY</i> in situ probe
<i>SUC2promFtopo</i>	caccaacacatgttgccgagtc	<i>SUC2::CLE41</i> overlap PCR entry clone & genotyping
<i>SUC2pro/CLE41(1)</i>	GTCATTTGATGTTGCCATgaaatttctttgagagggttttg	<i>SUC2::CLE41</i> overlap PCR entry clone
<i>SUC2pro/CLE41(2)</i>	caaaaacctctcaaagaatttcATGGCAACATCAAATGAC	<i>SUC2::CLE41</i> overlap PCR entry clone
<i>CLE41_RTF</i>	CCATGACTCGTCATCAGTCC	qRT-PCR
<i>CLE41_RTR</i>	TTTGGACCACTAGGAACCTCA	qRT-PCR
<i>qATHB8f</i>	ctccgaattccctcagatca	qRT-PCR
<i>qATHB8r</i>	tcgacatgcatattctcca	qRT-PCR
<i>qIRX3f</i>	gcgtgtgcaccatcatcc	qRT-PCR/ <i>IRX3::CLE41</i> genotyping
<i>qIRX3r</i>	tcatccattctttccgccc	qRT-PCR
<i>18s rRNA F</i>	CATCAGCTCGCGTTGACTAC	qRT-PCR control
<i>18s rRNA R</i>	GATCCTTCCGCAGGTTACAC	qRT-PCR control
<i>35S promoter F</i>	cgacaatcccactatcctt	Genotyping
<i>salk_LBa1</i>	TGGTTCACGTAGTGGGCCATCG	Genotyping
<i>pxy-3-f</i>	TTCATCCCCCTTCTCCTTCTTC	Genotyping
<i>pxy-3-r</i>	TTACCGTTTGATCCAAGCTTG	Genotyping