RESEARCH PAPER

CEP5 and XIP1/CEPR1 regulate lateral root initiation in Arabidopsis

Ianto Roberts1,2,*, Stephanie Smith3,*, Elisabeth Stes1,2,4,5, Bert De Rybel1,2, An Staes4,5, Brigitte van de Cotte1,2, Maria Fransiska Njo1,2, Lise Dedeyne1,2, Hans Demo1,5, Julien Lavenus1,2,†, Dominique Audenaert1,2, Kris Gevaert4,5, Tom Beeckman1,2,‡ and Ive De Smet1,2,3,6,‡,§

1 Department of Plant Systems Biology, VIB, B-9052 Ghent, Belgium
2 Department of Plant Biotechnology and Genetics, Ghent University, B-9052 Ghent, Belgium
3 Division of Plant and Crop Sciences, School of Biosciences, University of Nottingham, Loughborough LE12 5RD, UK
4 Medical Biotechnology Center, VIB, B-9000 Ghent, Belgium
5 Department of Biochemistry, Ghent University, B-9000 Ghent, Belgium
6 Centre for Plant Integrative Biology, University of Nottingham, Loughborough LE12 5RD, UK

* These authors contributed equally to this work.
† Present address: Institute of Plant Sciences, University of Bern, Alterbergrain 21, 3013 Bern, Switzerland
‡ These authors contributed equally to this work.
§ Correspondence: ive.desmet@psb.vib-ugent.be

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Abstract

Roots explore the soil for water and nutrients through the continuous production of lateral roots. Lateral roots are formed at regular distances in a steadily elongating organ, but how future sites for lateral root formation become established is not yet understood. Here, we identified C-TERMINALLY ENCODED PEPTIDE 5 (CEP5) as a novel, auxin-repressed and phloem pole-expressed signal assisting in the formation of lateral roots. In addition, based on genetic and expression data, we found evidence for the involvement of its proposed receptor, XYLEM INTERMIXED WITH PHLOEM 1 (XIP1)/CEP RECEPTOR 1 (CEPR1), during the process of lateral root initiation. In conclusion, we report here on the existence of a peptide ligand–receptor kinase interaction that impacts lateral root initiation. Our results represent an important step towards the understanding of the cellular communication implicated in the early phases of lateral root formation.

Key words: Arabidopsis, CEP5, lateral root initiation, post-translationally modified peptide, receptor kinase, XIP1.

Introduction

Co-ordinated positioning and development of lateral roots is central to shape root system architecture, allowing plants to adapt their below-ground organs for optimal soil exploration (De Smet, 2012; Smith and De Smet, 2012; Kong et al., 2014; Tian et al., 2014). Lateral root primordia are formed from approximately three pairs of xylem pole pericycle (XPP) cells arranged in neighboring cell files that undergo asymmetric cell division and subsequently form a new organ (Dubrovsky et al., 2001; Kurup et al., 2005; De Smet et al., 2006, 2007; Péret et al., 2009; Lavenus et al., 2013). In the basal meristem, close to the primary root tip and before any asymmetric cell division, a periodic transcriptional mechanism specifies pre-branch sites that are competent to form lateral roots in a regular pattern (De Smet et al., 2007; Moreno-Risueno et al., 2010; Van Norman et al., 2013; Xuan et al., 2015, 2016).
Several plant hormones have been shown to affect root architecture, among which auxin has been shown to act as a central role (Lau et al., 2008; Vanneste and Friml, 2009). In addition, a number of transcription factors and miRNAs have been shown to affect lateral root development (Satbhai et al., 2015). However, several recent studies are beginning to reveal the importance of different classes of small signalling peptides during the process of lateral root development (Ohyama et al., 2008; Delay et al., 2013; Fernandez et al., 2013, 2015; Kumpf et al., 2013; Araya et al., 2014; Bergonci et al., 2014; Czyzewicz et al., 2015). However, in Arabidopsis, very few small signalling peptides have been linked to a receptor (Murphy et al., 2012; Czyzewicz et al., 2013), and very few receptors involved in lateral root development have been identified (De Smet et al., 2008, 2009; Kumpf et al., 2013; Wierzb and Tax, 2013; Araya et al., 2014; Cho et al., 2014; Tabata et al., 2014). Recently, the leucine-rich repeat (LRR) receptor kinases XYLEM INTERMIXED WITH PHLOEM 1 (XIP1)/C-TERMINALLY ENCODED PEPTIDE (CEP) RECEPTOR 1 (CEPR1; At5g49660) and CEPR2 (At1g72180) were proposed to act as receptors for CEPI and other members of the CEP family (Tabata et al., 2014). Both XIP1/CEPR1 and CEPR2 contain a short secretory signal peptide sequence, an N-terminal extracellular LRR receptor domain with 21 LRR repeats, a single helical transmembrane region, and a C-terminal cytoplasmic serine/threonine kinase domain. It was previously shown that a loss-of-function xip1 mutant displays anthocyanin accumulation in the leaves, xylem-like lignification of phloem in inflorescence stems, disrupted xylem vessel formation, phloem cells sometimes located adjacent to xylem cells, and shorter inflorescence stems (Bryan et al., 2012), and that the cepr1 cepr2 double mutant displays a pleiotropic phenotype, including pale green leaves, smaller rosette leaves, shorter floral stems, anthocyanin accumulation, enhanced lateral root elongation, decreased expression of nitrate transporters, and reduced nitrate uptake activity (Tabata et al., 2014). Interestingly, the Medicago truncatula compact root architecture (cra2) mutant is also affected in its root system architecture, and CRA2 was shown to be closely related to XIP1 (Huault et al., 2014). The post-translationally modified CEP family members contain an N-terminal signal peptide sequence and a C-terminal conserved CEP domain from which the mature 15 amino acid peptide is processed (Ohyama et al., 2008; Delay et al., 2013; Roberts et al., 2013; Tabata et al., 2014). Some members of the CEP family have already been shown to regulate lateral root development (Ohyama et al., 2008; Delay et al., 2013; Mohd-Radzman et al., 2015), but in this work we functionally characterized C-TERMINALLY ENCODED PEPTIDES (CEP5; At5g66815) in the context of lateral root initiation. Furthermore, we explored the involvement of XIP1/CEPR1 in lateral root initiation, and could show that CEP5 and XIP1 are co-expressed during early stages of lateral root initiation, and that both affect this process.

### Materials and methods

#### Plant materials

The following transgenic lines and mutants were described previously: pCEP5::GFP-YFP, CEP5<sup>OM</sup> and CEP5<sup>BMM</sup> (Roberts et al., 2013), xipl-1 and pXIP1::GUS (Bryan et al., 2012).

#### Plant growth and treatment conditions

Unless otherwise noted, seedlings were grown at 21°C under continuous light (110 μE m<sup>-2</sup> s<sup>-1</sup>) photosynthetically active radiation, supplied by cool-white fluorescent tungsten tubes, Osram) on square Petri plates (12×12 cm) containing 50 ml of solid half-strength Murashige and Skoog (MS) growth medium supplemented with sucrose (per litre: 2.15 g of MS salts, 0.1 g of myo-inositol, 0.5 g of MES, 10 g of sucrose, and 8 g of plant tissue culture agar; pH adjusted to 5.7 with KOH). For peptide treatments, medium was supplemented with CEP5<sup>Pro</sup> (DFRPTTPGHSPIGIGH), CEP5<sup>Hyp</sup> (DFR[HYP]TT[HYP]GH[HYP]GIGH), or mCEP5<sup>Hyp</sup> (DFL[HYP]HT[HYP]GHV[HYP]GISH) peptide to a concentration as indicated in the text and/or figure legends. Synthetic peptides (CEP5<sup>OM</sup>, CEP5<sup>Hyp</sup>, and mCEP5<sup>Hyp</sup>) were obtained from GenScript (www.genscript.com/peptide-services.html?src=home), and were supplemented to growth medium with concentrations as indicated in the text and/or figure legends. For auxin treatments, medium was supplemented with indole-3-acetic acid (IAA) or 1-naphthaleneacetic acid (NAA) to a concentration as indicated in the text and/or figure legends.

#### Transcriptome profiling data

The naxillin treatment transcriptome data from De Rybel et al. (2012) can be searched in the Lateral Root Initiation EFP Browser (bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi?dataSource=Lateral_Root_Initiation) (Winter et al., 2007).

#### Primary and lateral root phenotyping

At the indicated time, images of plates with seedlings were taken and roots were measured using ImageJ (https://imagej.nih.gov/ij/index.html) or FIJI software (Schindelin et al., 2012). For detailed staging of lateral roots, samples were cleared as described previously (Malamy and Benfey, 1997) and analysed by differential interference contrast microscopy (Olympus BX53).

#### Histochemical GUS assays

For GUS (β-glucuronidase) assays, plants were put overnight in 90% aceton, then transferred to a GUS-solution (1 mM X-Gluc, 0.5% (v/v) dimethylformamide (DMF), 0.5% (v/v) Triton X-100, 1 mM EDTA (pH 8), 0.5 mM potassium ferricyanide [K₃Fe(CN)₆], 0.5 mM potassium ferrocyanide [K₄Fe(CN)₆], 500 mM phosphate buffer (pH 7)) and incubated at 37°C for GUS staining, and finally washed in 500 mM phosphate buffer (pH 7). For microscopic analysis, samples were cleared with 90% lactic acid or as described previously (Malamy and Benfey, 1997). Samples were analysed by differential interference contrast microscopy (Olympus BX53) and stereomicroscopy (Leica MZ16). For anatomical analysis (microtome transversal sectioning) of GUS-stained roots, stained samples were processed as described previously (De Smet et al., 2004).

#### Real-time qRT–PCR analyses

For the analysis of CEP5 expression, RNA was extracted by first performing an RNA extraction with TRI Reagent® from Sigma-Aldrich according to the manufacturer’s protocol, followed by an extra RNA extraction procedure with the Plant RNAeasy Mini kit from Qiagen according to the manufacturer’s protocol to clean up...
the RNA further. Next, 1 µg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit from BIORAD according to the manufacturer’s protocol. The real-time quantitative reverse transcription–PCR (qRT–PCR) was carried out on the LightCycler 480 from Roche Applied Science with the LightCycler 480 SYBR Green I Master Mix from Roche Applied Science. The expression of CEP5 (CCATGGACGAACCCTAAAG and TGCCATCATCGTCTTGCTAT) was determined using at least three biological repeats and the reference genes EEF-1α (CTGGAGTTTGGAGCTGGTAT and CCAAGGTTGAA AGCAAGAGA) and At2g21770 (GGACCTCTCTTTGTATCA TTTTGC and CAACCCCTTCTTACCTCACAAC).

SRM analysis of the CEP5 peptide

For SRM (selected reaction monitoring) experiments, the CEP5 peptide containing an isoleucine residue with heavy, stable isotopes, NH2-DFRP<hydroxy>TTP<hydroxy>GHSP<hydroxy>G1(13C6, 15N)GH-COOH, was in-house synthesized by Fmoc [N-(9-fluorenyl)methoxycarbonyl] chemistry on a 433A peptide synthesizer (Applied Biosystems, Framingham, MA, USA). Frozen 5-day-old 35S::CEP5 seedlings were ground to a fine powder in liquid N2 and proteins were extracted in 50 mM triethylammonium bicarbonate (TEAB) buffer containing 8 M urea and the suggested amounts of protease and phosphatase inhibitors according to the manufacturer’s instructions (cOmplete protease inhibitor cocktail tablet and PhosStop phosphatase inhibitor cocktail tablet, Roche). After determining the protein concentration using the Bradford assay and diluting the protein extract in 50 mM TEAB buffer, a total of 500 µg of protein material was filtered over a 3kDa cut-off filter (Pall Nanosep® centrifugal devices, Sigma-Aldrich) to retain only peptides with masses <3 kDa in the filtrate. This peptide mixture was spiked with 10 pmol of the synthetic heavy CEP5 peptide and vacuum dried. Next, the sample was re-dissolved in 2% acetonitrile (ACN) with 0.1% trifluoroacetic acid (TFA) and used for SRM analysis. SRM analysis was performed on an Ultimate 3000 RSLC nano HPLC system (Thermo Fisher Scientific, Bremen, Germany) coupled to a TSQ Vantage (Thermo Fisher Scientific). The nano-LC system was configured with a trapping column [made in-house, 75 µm ID×150 mm, 3 µm beads, C18 Reprosil-HD (Dr. Maisch GmbH, Ammerbuch-Entringen, Germany)] and an analytical column [made in-house, 100 µm internal diameter (ID)×20 mm, 5 µm beads, C18 Reprosil-HD (Dr. Maisch GmbH)]. The loading solvent consisted of 0.1% TFA in 2:98 ACN:H2O, and the nano-LC was run with 0.1% formic acid as nano-LC solvent A and 0.1% formic acid in 80:20 ACN:H2O as nano-LC solvent B. The needle voltage in the nano-ESI source was set at 1300 V and the capillary temperature at 275 °C. A 5 µl aliquot of each sample was injected using a full loop injection. Injection was at 10 µl min⁻¹ in loading solvent. After loading, the trapping column was flushed for 4 min in order to pre-concentrate the components while removing buffer components, before it was put in-line with the analytical column. Compounds were eluted at 300 nl min⁻¹ with an ACN gradient of 30 min from 2% to 35% of nano-LC solvent B. The column was washed with 90% of nano-LC solvent B for 1 min and equilibrated with nano-LC solvent A for 9.5 min before analysis of the next sample. A dwell time of 120 ms for each transition was applied. Seven transitions were monitored for both the heavy and the light form of the CEP5 peptide, with the doubly charged precursor as the first mass filter. Data analysis was performed through the Skyline software (MacLean et al., 2010).

Results and Discussion

Focused transcript profiling data identifies CEP5 as a putative regulator of lateral root development

Since the plant hormone auxin is a major regulator of primary root growth and lateral root development (Overvoorde et al., 2010; Lavenus et al., 2013), several transcript profiling studies based on auxin treatments have been performed in order to identify the molecular players involved (Himinen et al., 2004; Vanneste et al., 2005; De Smet et al., 2008). However, because of the pleiotropic effects caused by exogenous auxin application, such data sets risk compromising the spatiotemporal resolution required when looking for components specific for a single developmental process. To circumvent this, we searched for putative novel early lateral root formation regulators by screening a data set obtained through a highly focused transcript profiling analysis on seedlings treated with the synthetic molecule naxillin. Naxillin specifically induces an auxin response in the basal meristem associated with lateral root initiation through enhancing indole-3-butyric acid (IBA) to IAA conversion in the root cap (De Rybel et al., 2012). Driven by the recurrent programmed cell death of the outermost lateral root cap cells, a periodic input of the converted auxin into the main root contributes to a fine-tuned mechanism that results in an evenly spaced lateral root distribution pattern (Xuan et al., 2016). Importantly, through its local activity, naxillin does not display the typical pleiotropic effects of exogenous application of auxin or auxin-like molecules (De Rybel et al., 2012). In order to identify novel putative early lateral root formation regulators, seedlings were grown for 72 h on growth medium supplemented with the polar auxin transport inhibitor N-1-naphthylphthalamic acid (NPA), which prevents lateral root initiation, followed by 2010; Lavenus et al., 2013), several transcript profiling studies

Fig. 1. Auxin effect on CEP5 expression. (A) CEP5 expression in 7-day-old roots following the indicated hours of auxin (1 µM IAA) treatment in liquid medium. (B) CEP5 expression in 5-day-old root tips of野生型 (including the basal meristem) following 2 h of auxin (NAA) treatment at the indicated concentrations. CEP5 levels were analysed through real-time qRT–PCR. Graphs show the average ±SE of three biological replicates. *P<0.05 according to Student’s t-test compared with 0 µM NAA or IAA.
by a transfer to growth medium supplemented with naxillin to trigger the priming event synchronously in the basal meristem. In a genome-wide transcript profiling analysis, we identified CEP5 (At5g66815) as differentially early up-regulated between non-treated and naxillin-treated seedling roots (De Rybel et al., 2012) [data not shown; see Lateral Root Initiation eFP Browser (Winter et al., 2007)]. The CEP5 gene encodes a small protein of 105 amino acids and contains a conserved 15 amino acid C-terminal CEP domain that gives rise to a small signalling peptide (Ohyama et al., 2008; Roberts et al., 2013; Tabata et al., 2014).

CEP5 expression is regulated by auxin

Since CEP5 is transcriptionally regulated following naxillin treatment, we subsequently checked if CEP5 expression is also auxin regulated. Treatment of wild-type roots with different concentrations of the synthetic auxin NAA or with IAA revealed that CEP5 expression was down-regulated by auxin (Fig. 1A, B). These results suggested that CEP5 expression is (directly or indirectly) regulated by auxin.

CEP5 expression is associated with early stages of lateral root development

Based on its naxillin-regulated expression profile, CEP5 represents a candidate peptide to be involved in the early developmental steps toward lateral root development. Using a pCEP5::NLS:GFP::GUS reporter line (Roberts et al., 2013), we observed regularly spaced patches of CEP5 expression associated with lateral root primordia, confirming its potential involvement in this process (Fig. 2A–C). We did not detect CEP5 expression in the primary root stem cell niche; however, CEP5 was expressed in the basal meristem (Fig. 2D). The latter is important in the context of lateral root initiation as this region is defined as part of the oscillation zone where pre-branch sites are established by the input of auxin derived from the lateral root cap (De Smet et al., 2007; Moreno-Risueno et al., 2010; Xuan et al., 2016). Tissue-specific analyses showed that both in the basal meristem and during early stages of lateral root development, CEP5 was predominantly expressed in the phloem pole-associated pericycle (PPP) cells, but also—although more weakly—in the adjacent phloem (Fig. 2E–G; Supplementary Fig. S1; Supplementary Movie S1 at JXB online). This CEP5 expression is associated with early stages of lateral root development

Fig. 2. CEP5 expression in the Arabidopsis root. Representative pictures for CEP5 expression (monitored through GUS expression in a pCEP5::NLS:GFP::GUS transgenic line) in the root: (A) in a complete seedling (overstained for illustrative reasons), (B) in a part of the root from the seedling depicted in (A), (C) at the site of a lateral root primordium, (D) at the root apex, (E) in the basal meristem on a transverse section, (F) at a site of lateral root formation with the lateral root primordium pointing to the right (outlined with the dotted red line), and (G) on a transverse section through a lateral root primordium (outlined with the dotted red line). Seedlings are 5–6 d after germination. *, Lateral root primordium; arrowheads in (F) separate individual cells; P, phloem; X, xylem; Pe, pericycle; En, endodermis; C, cortex; b.m., basal meristem.
expression pattern does not overlap with the well-documented sites of high auxin response in the primary root or during lateral root initiation, which in Arabidopsis occurs in XPP cells (De Smet et al., 2007). To check whether the expression pattern of CEP5 is perturbed under conditions of altered auxin response in the XPP cells, the \( pCEP5::\text{NLS:GFP:GUS} \) reporter line was grown on NPA. Under these conditions, we did not observe any change in the \( CEP5 \) expression pattern (such as radial expansion) compared with control conditions (Supplementary Fig. S1). Taken together, \( CEP5 \) is negatively regulated by auxin and specifically expressed in the PPP cells that are closely associated with the lateral root development process, suggesting a negative correlation with auxin activity. However, what the specific cellular threshold is, is at the moment not known.

**Altering CEP5 expression levels affects root architecture**

Given the spatial (appearing in common regions of the root, although not in the same cells) and temporal (being induced at the same time points) correlation of \( CEP5 \) expression with lateral root initiation and development, we assessed if \( CEP5 \) loss of function affected this process. A *Cauliflower mosaic virus* (CaMV) 35S promoter-driven \( CEP5 \) RNAi knockdown line (\( CEP5\text{RNAi} \)) (Roberts et al., 2013) displayed a significant difference in primary root length compared with the control (Fig. 3A, B). In addition, detailed analyses of lateral root initiation in this \( CEP5\text{RNAi} \) line revealed an increased number of stage I and II lateral root primordia compared with the control (Fig. 3C; Supplementary Fig. S2). Additionally, in a root bending assay (Péret et al., 2012), the \( CEP5\text{RNAi} \) line progressed faster through lateral root developmental stages than the wild type (Fig. 3D). These loss-of-function data, together with the \( CEP5 \) expression pattern, indicate that \( CEP5 \) plays a role in early lateral root initiation events.

Next, we analysed a line with CaMV 35S promoter-driven constitutive overexpression of \( CEP5 \) (\( CEP5\text{OE} \)) (Roberts et al., 2013), which displayed shorter primary roots (similar to other independent \( CEP5\text{OE} \) lines) as compared with the wild type (Fig. 4A, B; Supplementary Fig. S2). Furthermore, the
CEP5 give rise to CEP5pHyp

CEP5 has a conserved C-terminal CEP domain, containing three proline residues and a predicted N-terminal signal peptide cleavage site that undergoes proteolytic processing to form a mature CEP5 peptide of 15 amino acids (CEP5p) (Roberts et al., 2013; Tabata et al., 2014). However, small signalling peptides are often post-translationally modified, thereby modulating—amongst others—the ability and specificity of peptides in binding to their targets (Murphy et al., 2012). In this context, it was previously shown that members of the CEP family give rise to a peptide containing hydroxyproline (Hyp) residues (Tabata et al., 2014). To confirm that a 15 amino acid CEP5 peptide with three Hyp residues (CEP5pHyp) (Fig. 5A) is indeed present in seedlings overexpressing CEP5, we performed SRM on a CEP5OE line. SRM is a mass spectrometry technique that allows detection and quantification of specific (low abundant) peptides in total protein preparations (Picotti and Aebersold, 2012). Indeed, in the CEP5OE proteome spiked with a chemically synthesized version of CEP5pHyp containing an isoleucine residue with heavy, stable isotopes, transitions for both the heavy, spiked-in CEP5pHyp and the light, naturally occurring CEP5Hyp peptide could be detected (Fig. 5B–E). These results supported that a CEP5 peptide with three Hyp residues can be present in planta.

Synthetic CEP5 peptide affects root architecture

Based on previous studies (Tabata et al., 2014) and the above-described results, a synthetic CEP5pHyp peptide was generated for further analysis of CEP5 function (Fig. 5A). To assess the activity of synthesized CEP5pHyp, we first analysed its effect on primary root growth, which has previously been shown to be a straightforward, although possibly non-specific, assay to test the activity of small post-translationally modified (CEP) peptides (Delay et al., 2013). Indeed, seedlings grown in the presence of CEP5pHyp (also at low concentrations) displayed shorter roots compared with the mock-treated control and compared with a synthetic variant with four randomly positioned, but not very unlikely amino acid substitutions based on a BLOSUM62 substitution matrix within the 15 amino acid CEP5 peptide sequence, while retaining the Hyp residues at the same positions (mCEP5pHyp) (Figs 5A, 6A, B; Supplementary Fig. S4). Next, we addressed the effect of synthetic CEP5pHyp on lateral root formation. Seedlings grown in the presence of different low concentrations of CEP5pHyp displayed a decreased total lateral root density, which is mainly due to a significant reduction in lateral root initiation events (Fig. 6C; Supplementary Fig. S3). Conversely, this did not occur in mCEP5pHyp-treated seedlings (Supplementary...
When lateral root initiation occurred, we occasionally observed regions of ectopic and/or aberrant pericycle cell divisions (observed in 10 out of 149 lateral root primordia of eight CEP5pPro-treated seedlings, while this did not occur in the untreated wild type), resulting in malformed lateral root primordia or closely spaced primordia in CEP5pPro/Hyp-treated seedlings, which differed from regularly spaced lateral roots in the wild type (Fig. 6D–F). Taken together, the similarities in primary and lateral root phenotypes between CEP5p treatment and CEP5OE indicate that the chemically synthesized CEP5pHyp has the same bioactivity as the overexpressed CEP5. These results further support a role for CEP5pHyp in lateral root initiation.

The proposed CEP family receptor XIP1/CEPR1 regulates lateral root initiation

Recently XIP1/CEPR1 and CEPR2 were proposed to be the receptors for CEP peptides, including CEP5 (Tabata et al., 2014). However, a role in lateral root initiation for XIP1/CEPR1 and/or CEPR2 was not yet explored. Therefore, we performed detailed analyses of a previously described pXIP1::GUS line (Bryan et al., 2012) and we showed that XIP1/CEPR1 is expressed in the root from the basal meristem onward (Fig. 7A), a pattern that overlaps with CEP5 expression (Fig. 2D). Furthermore, tissue-specific analyses showed that XIP1/CEPR1 is expressed in the phloem pole pericycle and in the adjacent phloem (Fig. 7B), confirming the overlap with CEP5 expression (Fig. 2E), and is excluded from early stages of lateral root development (Fig. 7C), similarly to CEP5 (Fig. 2C). This expression pattern combined with the results from Tabata et al. (2014) suggested that XIP1/CEPR1 could be a receptor for CEP5 in the root and therefore might take part in lateral root initiation. To explore this further, we assessed lateral root stages and density of the previously described xip1-1 mutant (Bryan et al., 2012). This revealed a reduced total lateral root density in xip1-1 in comparison with the control, which seemed mainly due to a reduction in stage I and II lateral root primordia and—in part—to fewer emerged lateral roots (Fig. 8A; Supplementary Fig. S3), suggesting that XIP1 is a positive regulator of lateral root initiation and development.

To evaluate further an interaction between CEP5 and XIP1, we explored to what extent xip1-1 is (in)sensitive to CEP5pHyp...
treatment. This revealed that, compared with the control, xip1-1 is less or not sensitive to CEP5pHyp with respect to primary root growth (Fig. 8B) or number of emerged lateral roots, respectively (Fig. 8C). These data—together with the biochemical evidence from Tabata et al. (2014)—support that CEP5 and XIP1 are a peptide ligand–receptor kinase pair in the context of lateral and primary root development. However, in general, the mutant phenotypes of the genes encoding the peptide ligand and its receptor are very similar (Butenko et al., 2009; Murphy et al., 2012; Czyzewicz et al., 2013; Kumpf et al., 2013). However, in our case, the xip1-1 root architecture phenotype is similar to that of CEP5OE or CEP5pHyp-treated seedlings and opposite to that of CEP5RNAi lines (Figs 4, 6), possibly suggesting that CEP5 negatively regulates XIP1 activity (e.g. by acting as an antagonist) in the context of lateral root initiation. In this context, the fact that CEP5pHyp had no strong impact on xip1-1 can also be interpreted as no further CEP5-mediated inhibitory effect if XIP1 is already absent (and hence fully inhibited). Alternatively, CEP5 does not exclusively act via the XIP1 receptor (or close homologues) in regulating root architecture. Furthermore, the observed lateral root phenotypes can be obtained through various mechanisms (e.g. the effect on lateral root initiation can impact development of nearby lateral root primordia), and further analyses will be required to unravel fully the developmental and biochemical mechanisms underlying CEP5 and XIP1 action.

Conclusion

Previously, a role for CEPs in regulating aspects of root architecture, namely nitrate-dependent lateral root elongation, was proposed. Specifically, CEPs might act as root-derived ascending N-demand signals to the shoot, where their perception by CEPRs leads to the production of a putative shoot-derived descending signal that up-regulates nitrate...
transporter genes in the roots (Ohyama et al., 2008; Delay et al., 2013; Tabata et al., 2014; Mohd-Radzman et al., 2015). Here, we provide evidence that CEP5 may also act (probably together with XIP1/CEPR1) during lateral root initiation. Our gain-of-function and knock-down data suggest CEP5 to be part of a lateral root inhibitory mechanism. Faster lateral root development was observed in the CEP5RNAi line, while overexpression or treatment with the peptide resulted in fewer lateral root initiation events. The observed clustering of lateral roots in later developmental stages in the gain-of-function condition might be a secondary effect. Slowing down lateral root development can interfere with the timely development of auxin sources and therefore retard the draining of auxin from the main root. In turn, this might lead to higher auxin levels in the neighbourhood of existing primordia and induce ectopic and/or irregularly patterned primordia. Finally, it is intriguing that a phloem-derived signal downstream of CEP5 and XIP1/CEPR1 has such an impact on lateral root initiation and development at the xylem pole (Fig. 9). So far, no mutants have been reported to show lateral root initiation at the phloem poles in Arabidopsis (and so far we have also not observed this in loss- or gain-of-function CEP5 or XIP1 lines) arguing for a strong and complex lateral root inhibition mechanism in this part of the root pericycle. Earlier, a cell cycle inhibitory mechanism, based on the pericycle-specific expression of KIP-RELATED PROTEIN2 (KRP2), a cyclin-dependent kinase inhibitor, has been proposed as essential to allow, spatially and temporally, for lateral root initiation by repressing cell division activity in the entire pericycle except for sites of lateral root initiation (Himanen et al., 2002). In the future, it will be interesting to reveal if there is any direct interaction of CEP5-dependent signalling with the control of cell cycle regulation with respect to lateral root initiation. Additionally, it will be exciting to explore alternative mechanisms on how the phloem-expressed CEP5 affects lateral root initiation in the xylem pole pericycle cells.
At the moment, however, it is not yet possible to visualize CEP5 peptide reliably in planta in order to evaluate possible movement to other cells and/or tissues.

Supplementary data

Supplementary data are available at JXB online.

Figure S1. CEP5 expression on a transverse section of the pCEP5::NLS:GFP:GUS line.

Figure S2. Analyses of CEP5RN and CEP5OE lines.

Figure S3. Lateral root phenotypes upon CEP5 perturbation and in xip1-1.

Figure S4. Bioactivity of CEP5pHp at lower concentrations in the primary root length assay.

Movie S1. 3D reconstruction of pCEP5::NLS:GFP:GUS in the Arabidopsis root.

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