Role of the Arabidopsis PIN6 Auxin Transporter in Auxin Homeostasis and Auxin-Mediated Development

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Abstract

Plant-speciﬁc PIN-formed (PIN) eﬄux transporters for the plant hormone auxin are required for tissue-speciﬁc directional auxin transport and cellular auxin homeostasis. The Arabidopsis PIN protein family has been shown to play important roles in developmental processes such as embryogenesis, organogenesis, vascular tissue differentiation, root meristem patterning and tropic growth. Here we analyzed roles of the less characterised Arabidopsis PIN6 auxin transporter. PIN6 is auxin-inducible and is expressed during multiple auxin-regulated developmental processes. Loss of pin6 function interfered with primary root growth and lateral root development. Misexpression of PIN6 aﬀected auxin transport and interfered with auxin homeostasis in other growth processes such as shoot apical dominance, lateral root primordia development, adventitious root formation, root hair outgrowth and root waving. These changes in auxin-regulated growth correlated with a reduction in total auxin transport as well as with an altered activity of DRS-GUS auxin response reporter. Overall, the data indicate that PIN6 regulates auxin homeostasis during plant development.

Introduction

The plant hormone auxin is involved in embryogenesis, organogenesis, vascular tissue differentiation, and hypocotyl and root elongation, as well as growth responses to environmental stimuli. Auxin is synthesized in the shoot, leaf tips as well as in the root apex, and transported to other parts of the plant. Auxin signaling requires the interplay of auxin biosynthesis, conjugation, transport and perception, and can be modiﬁed through complex interactions with other hormones (see reviews by [1,2,3]). Auxin moves in a polar manner from cell to cell or through the phloem from source to sink tissues. The basipetal auxin ﬂow occurs from the shoot apex to the base and contributes to maintaining apical dominance. In roots, auxin moves both acropetally through the central stele and basipetally through the peridermis and outer cortex near the root tip [4,5]. Polar cell-to-cell auxin transport is mediated by carrier proteins of the AUX1 (Auxin resistant 1), LAX (like-AUX1), PGP (Phospho-glycoprotein) and PIN (pin-formed) families [3]. While AUX1, LAX and certain PGP-type proteins are involved in auxin import [6,7,8], there are other PGP-type and PIN proteins that mediate auxin export from the cell [6,9].

The Arabidopsis genome encodes eight PIN proteins and their sequences diﬀer mainly in the central hydrophilic region. PIN proteins 1, 2, 3, 4 and 7 contain a large hydrophilic loop, PIN6 contains a partially reduced loop, while PIN5 and PIN9 lack the central hydrophilic domain [9,10,11]. Accordingly, phylogenetic analysis in Arabidopsis indicated that the PIN family can be divided into two subclasses, the plasma membrane (PM) localized PIN1-type (PIN1, 2, 3, 4, 7) and the endoplasmic reticulum (ER) localized PIN5-type (PIN5, 6, 9) [10,12] that appear functionally distinct. The asymmetric localization of the plasma membrane-localized PIN proteins determines the direction of inter-cellular auxin ﬂow [13].

PIN proteins function to coordinate vascular tissue differentiation and regeneration [14,15], meristem maintenance and patterning in roots [16,17,18] as well as organ development in general [19,20]. The loss-of-function pin1 mutant shows the most...
extensive phenotype as it grows a pin-shaped floral stem inflorescence devoid of floral organs due to lower auxin transport [14,21]. Mutations in pin2 (or ethylene insensitive root 1; eir1) reduced root waving, and the PGP1 and PGP19 phosphoglyco-protein (PGP, auxin transporters [22,23]) as well as the reduced root waving, and the shoot growth as well as reproductive development.

Dependent growth and development processes such as root and genes have functions linked to organogenesis (PIN1), pattern effects on shoot apical dominance and branching, the emergence characterized auxin-associated phenotypes are dose-dependent Arabidopsis stamens and nectary production, its function in recently shown to have a function in the development of cytosol and play an important role in the control of the ER-proteins mediate auxin exchange between the ER lumen and WAG2 PINOID related protein-serine/threonine kinases, which are critical factors in PIN membrane polarity establishment, also affect root waving [24,25,26,27]. However, whether there are particular roles for specific PIN proteins in root waving is not well documented or understood.

The phenotypes associated with the loss-of-function of PIN1, and to lesser extent PIN2, 3, 4 and 7 can be phenocopied by some synthetic auxin transport inhibitors [9,28,29,30]. The best characterized auxin-associated phenotypes are dose-dependent effects on shoot apical dominance and branching, the emergence of root hairs, primary root elongation, lateral root initiation and emergence as well as responses to gravity [31,32,33,34,35]. The PIN genes have functions linked to organogenesis (PIN1), pattern formation during embryogenesis (PIN1, PIN4 and PIN7) and phototropic responses as well as various forms of tropism (PIN2 and PIN3) [16,28,30,36,37]. The ER localised PIN5 and PIN8 proteins mediate auxin exchange between the ER lumen and cytosol and play an important role in the control of the ER-resident auxin metabolism [10,38,39]. PIN6 is the last member of this developmentally important gene family and despite being recently shown to have a function in the development of Arabidopsis stamens and nectary production, its function in mediating auxin growth processes remains functionally uncharacterised [40].

Here we show that PIN6 is a crucial component of auxin transport and auxin homeostasis and contributes to auxin-dependent growth and development processes such as root and shoot growth as well as reproductive development.

Materials and Methods

Plant Growth Conditions and Transgene Selection

Seeds were cold-stratified in the dark for 3 days and grown at 21°C under a 16 hour photoperiod (150 μmol quanta m⁻² s⁻¹ irradiance), unless otherwise stated. Sterilised seeds were grown on Murashige and Skoog (MS) media (4.4 g/L MS salts and vitamins, 1% sucrose, 0.8% agar). Transgenic Arabidopsis (Col-O) lines harbouring pMDC32::PIN6 or TPIN6::FiLUC were selected on MS media containing 50 μg/mL hygromycin (Invitrogen) or 50 mg/L BASTA (Sigma-Aldrich), respectively.

Mutants Used in this Study

All germplasm were in the Arabidopsis thaliana ecotype Columbia (Col-0) background. Germplasm used in this study include TDNA insertion lines [Salk_046393 (pin6-2), Salk_092831 (pin6-4), GABI-KAT_430B01 (pin6-5) and GK711CO9 (pin6-6)].

Construction of PIN6 Overexpression, Promoter-reporter Gene as Well as RNA Silencing Constructs and Selection of Representative Transgenic Lines

A PIN6 overexpression vector was created by PCR amplifying a PIN6 (AT1G77110) genomic fragment (~400 bp 5’UTR, 3554 bp gene and+119 bp 3’UTR) using high fidelity Platinum Pf Taq Polymerase and primers (Table S1) according to the manufacturer’s instructions (Invitrogen). The PIN6 genomic product was cloned into the pMDC32 overexpression vector [41] using Gateway® Technology to create pMDC35::PIN6. A PIN6 promoter sequence (~705 bp) thought to contain most of the upstream regulatory domain was amplified using DNAzyme Polymerase and primers (Table S1), according to instructions (FINNZYMES). The promoter fragment was cloned into ZERO Blunt® TOPO® (INVITROGEN) intermediate vector creating TOPO::PIN6. The PIN6 promoter was subsequently cloned into pTm35::FiLUC (digested with XbaI/NcoI to remove the minimal CaMV 333 promoter) creating pTPIN6::FiLUC. A promoter-GUS reporter fusion was created by amplifying a much larger upstream region (~3763 bp; primers listed in Table S1) of the PIN6 promoter fragment and cloning the amplicon into pMDC182 [41] using Gateway® Technology (Invitrogen) to create pMDC-PIN6::GUS. pPIN6::GUS, pTm35enh::FiLUC and pTm35::FiLUC were prepared as previously described [20,42].

Binary constructs were transferred into Agrobacterium strain LBA4404 and transformed into Arabidopsis thaliana (Col-0) using conventional techniques [43]. Selection criteria for choosing representative transgenic lines were based upon: 1) a consensus in the promoter’s tissue specific reporter gene expression pattern, 2) strength of reporter gene activity levels in leaf tissues, and 3) a consistent 3:1 Mendelian segregation of selectable marker genes. Representative lines are indicated for pTPIN6::FiLUC (Fig S1A), pMDC-PIN6::GUS (Fig S2B, 2C) and pPIN6::GUS [20].

Root Waving Phenotyping

Surface sterilised seeds were sown onto the surface of agar plates (1.5% agar supplemented with modified Hoagland solution, 1% sucrose, 0.5% MES; pH = 5.7) and cold stratified for 3 days. The plates were then placed vertical in a controlled growth chamber with setting defined above. The position of the root tip was marked daily to derive root elongation rates and 10 DAG plates were scanned enabling measurements of root length, wave length (distance between 2 successive crests) and wave amplitude (orthogonal distance between wave crest and root axis) using the ImageJ software. These measurements were used to calculate root spatial and temporal waving frequencies. Root length measurements correspond to developed lengths (determined by following the paths of each root, including along waves) of at least 12 seedlings per line in three successive experiments.

Auxin Transport Assays

Pulse chase auxin transport experiments were performed as described [44]. Four to twelve independent basal inflorescence stem sections, mean length 30 mm, were cut from 30-day-old plants. Inverted sections were pulsed for 60 min by immersion in 20 μL 400 nM 3H-IAA (1 mCi.ml⁻¹; Amersham Biosciences, UK), rinsed with 400 nM unlabelled IAA and chased with 20 μL unlabelled 400 nM IAA (150 min). Stem sections were cut into 3 mm long sections which were extracted into Ecolite scintillant overnight and radioactivity in each segment was analyzed by scintillation counting.

Auxin Root Growth Assays

One component of auxin homeostasis is the conjugation of IAA to different moieties, including linkage to amino acids like IAA-Alanine (IAA-Ala). This type of auxin is compartmentalized in the ER and therefore a sensitivity test to IAA-Ala can reveal the extent to which auxin homeostasis has been perturbed [45]. Seedlings were transferred 3 days after germination to MS agar containing media supplemented with IAA (10, 50 and 100 nM) or IAA-Alanine (10, 20, 30 μM) and relative elongation rate was determined as percentage of the control treatment (EtOH). Experiments were performed twice with similar results.
PIN6 Auxin Transporter in Arabidopsis

Plant Phenotyping

Non-destructive measurements of plant growth were performed using a plant image capture and analysis system (Scanalyzer 3D, LemnaTec, Würselen, Germany; http://www.lemnatec.de/scanalyzer_gh.htm). For root apical meristem (RAM) size measurements, 7 DAG roots were stained with propidium iodide and visualised by confocal microscopy. Root meristem size was defined as the distance from the quiescent centre to the first cells displaying elongation. For stage distribution of lateral root development, 15–20 roots from 9-day-old seedlings were processed. Lateral root primordium density was analyzed as previously described [46]. Experiments were performed twice, with a similar phenotypic outcome.

Chlorophyll Assays

Chlorophyll measurements were performed as previously described with the following modifications: pigments were extracted in 80% acetone, and absorbance was measured at 647, 664 and 750nm [47,48,49].

Real Time Quantitative PCR

Total RNA extraction, first strand cDNA synthesis and quantification of relative transcript levels were performed as previously described [50]. Cyclophilin (At2g29960) was used to normalise for biological variation in cDNA loading and primer sequences are listed in Table S1. Three technical replicates were performed and the results shown are representative of two independent experiments.

β-glucuronidase and Luciferase Reporter Gene Assays

β-Glucuronidase and luciferase assays were performed as previously described [51,52,53].

Results

PIN6 Exhibits Tissue and Organ Specific Expression Patterns

The tissue specific regulation of the PIN6 promoter (−3763 bp, −1794 bp or −705 bp) was investigated in detail using β-glucuronidase and firefly luciferase as reporters of gene expression. A large number of PIN6 promoter-reporter transgenic lines were generated (Figs. S1 and S2), and detailed analyses are shown for several lines. In young seedlings, PIN6 reporter expression was weak in the primary root, hypocotyl, shoot apex as well as cotyledons (Fig. S1B). Basal levels of PIN6 expression were also observed in specific tissue types observed from mature plants, when compared to the constitutive CaMV 35S promoter (Fig. S1C). The PIN6-reporter lines enabled 20-fold lower leaf reporter activities when compared to the strong CaMV 35S-reporter lines (Fig. S1A and S2B). These experimental findings were consistent with anatomical gene expression analysis performed using Genevestigator, which confirms that PIN6 is lowly expressed in most seedling tissues (Fig. S2A). Furthermore, in silico analysis of published microarray data showed that during development mRNA expression levels of the ER-targeted subclade of PIN transporters (PIN5 and PIN6) as well as PIN6, are generally less abundant than those of the PM targeted PIN transporters PIN1, 2, 7, 3 and 4 (Fig. S2D). Interestingly, the chromatin modification mark of histone H3 lysine 27 trimethylation (H3K27) that is associated with low levels of gene expression [54], was enriched surrounding the promoter and/or gene coding regions of the most weakly expressed PIN genes (PIN8, 5, 6, 1 and 2) (Fig. S2E).

The expression of PIN6 is not only developmentally regulated, but also specific of particular tissues in a cell-type specific manner (Fig. 1 and S2). During germination weak PIN6::GUS staining was observed in the embryos from fresh seeds and became considerably stronger in dried seed embryos (Fig. 1A, B). GUS activity was observed near the shoot meristem, root tip (RAM) and root vasculature (Fig. 1B to D). In general, there was a noticeable decline in PIN6 reporter expression during seedling development. Later during seedling development, PIN6 promoter activity was very low in the main root meristem and vasculature (Fig. 1P and Q). PIN6, was however, expressed during lateral root initiation, becoming restricted to the margins of the developing primordium later during lateral root development (Fig. 1F to J) as shown previously [20]. After lateral root emergence, PIN6 promoter activity was strongest in the outer cell layers of the lateral root meristem (Fig. 1K). Most, interestingly, the floral stem tissues showed higher reporter activity levels (Fig. S2B with S2C), which is consistent with an obvious spike in PIN6 mRNA levels observed in floral buds during a PIN developmental expression profile (Fig. S2D) [55]. Finally, the PIN6 promoter enabled reporter expression in flowers (Fig. S1D), in particularly the nectaries and the floral organ boundaries of the anthers (Fig. 1L to N).

We next investigated the effect of auxin on PIN6 promoter activity. Auxin stimulation (10 µM 2,4-D) induced PIN6::GUS staining in the shoot apical meristem (Fig. 1T), the root stele (including pericycle and endodermis) near the hypocotyl (Fig. 1U), and RAM (Fig. 1V). In lateral root primordia the induction of PIN6::GUS activity by auxin treatment was less obvious (Fig. 1W and 1X). This is in line with the presence of auxin response elements in the PIN6 promoter, including AS1-like (TGACG; −91 bp, −839 bp), AuxRE (TGTCCT; −1292 bp, −993 bp) and NDE (CATATG; 1262 bp) [56,57,58]. In summary, the PIN6 promoter activity is observed specifically in different developmental processes and can be induced by auxin.

Loss-of Pin6 Function Affects Root Growth

We identified homozygous pin6 mutants for three T-DNA insertion alleles (SALK_092831, GABI-KAT_430B01 and GK711C09 referred herein as pin6-4, pin6-5 and pin6-6, respectively) (Fig. 2A). PIN6 mRNA levels were not reduced in pin6-4, but partially reduced in pin6-5 suggesting a weak loss-of-function allele (Fig. S3A). pin6-6 represents a stronger loss-of-function mutant as PIN6 transcripts were not observed flanking the intronic-T-DNA insertion (Fig. S3B), although PIN6 transcript levels were still observed in a region upstream from the TDNA insertion using primers that span the third intron (Fig. S3C and D). A portion of the PIN6 protein including the hydrophilic loop may still be translated in pin6-6, however the removal of at least 22 amino acids form the 3’ end of the PIN6 protein could perhaps only partially disrupt protein function.

The hypocotyl and primary root lengths of pin6 mutant alleles were similar to wild type with a slight reduction of root length in the pin6-6 allele (Data not shown). Compared to WT, the weaker pin6-4 and pin6-5 mutant alleles as well as as well as the stronger pin6-6 allele all showed a similar number of primordia at all seven stages of lateral root primordia development and primordium density was similar to wild type (Data not shown).

The recently reported pin6-2 allele represents a complete loss-of-function allele of PIN6 [40]. Root growth was significantly enhanced in this line (Fig. 2B). When the number of lateral root primordia was calculated, we found that there was no difference when compared to WT. However, a shift in the developmental stages of the different lateral root primordia was observed with less primordia in the early stages and more primordia and emerged
Figure 1. Regulation of PIN6 expression during plant development. Representative transgenic reporter lines harbouring −1794 bp (pPIN6::GUS; A–N) of the PIN6 promoter fused to GUS. GUS activity was observed early during germination in fresh seeds (A), dried seeds (B), the root apical meristem of seedlings (C; 1DAG), regions of asymmetric root growth (D; 2 DAG) and in the SAM (E; 3 DAG). The PIN6 promoter enabled GUS expression during lateral root initiation (F), at the boundaries of developing root primordia (G to J) and in the lateral RAM (K), floral organ boundaries (L, M) and anthers (N). Scale bars for G–K are similar to F. O to X) Auxin up regulates PIN6 promoter activity. Scale bars for P–S and U–X are similar to O. Auxin treatment (2 hrs) of pPIN6::GUS transgenic lines with 10 μM 2,4-D (T–X) induces GUS expression in the SAM (T) and root (U and V), but not in the lateral root primordia (W and X). Controls (O–S) were treated with ethanol only. Epidermis (Ep), cortex (Co), endodermis (En) and Pericycle (Pe).

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lateral roots in the later stages (Fig. 2C and D), indicating a faster lateral root development.

In conclusion, the data reveal that the complete loss of $\text{pin6}$ function interferes with auxin regulated growth processes in the root, in particularly lateral root development.

**PIN6 Overexpression Results in Stunted Growth and Reduces Apical Dominance**

To understand whether mis- or overexpression of $\text{PIN6}$ could interfere with auxin related growth processes, we created PIN6 over-expressor lines using the strong 35S promoter (Fig. 3A). Representative transgenic lines displaying increased $\text{PIN6}$ transcript abundance were selected (Fig. 3B) and the three highest overexpressing lines (PIN6-OE) lines #1, #18 and/or #14 were used for subsequent analyses. Overexpression of $\text{PIN6}$ resulted in a compact rosette phenotype (Fig. 3C) and reduced leaf area (Fig. 3D). The relative leaf area expansion rate of $\text{PIN6}$-OE plants was less during the first four weeks of growth when compared to wild type (Fig. S4A). PIN6-OE leaf tissues appeared dark green and accordingly the chlorophyll content was higher on a fresh weight basis than in wild type and a reduction in the chlorophyll a/b ratio was observed (Fig. 3E). PIN6-OE lines flowered 5 to 10 days later, however the number of rosette leaves at the emergence of the floral bolt was not significantly different from wild type (Fig. S4B and S4C). Floral development of PIN6-OE lines appeared stunted when compared to wild type (Fig. 3F). PIN6-OE lines showed one or two additional rosette and cauline branches (Fig. S4D and S4E). The overall floral stem height of PIN6-OE lines was considerably smaller when compared to wild type (Fig. 3G) and there was a significant increase (~10 fold) in the number of reproductive siliques along the entire length of the primary floral stem (Fig. 3H). These observations suggest that rosette development, chlorophyll content, fecundity and shoot apical dominance are affected by $\text{PIN6}$ overexpression.

**PIN6 Overexpression Affects Root Waving, Lateral Root Development and Root Hair Outgrowth**

PIN6-OE interfered also with root growth and development (Fig. 4). The most obvious phenotypes were a pronounced root-waving phenotype (Fig. 4A and B) and a significant reduction in root length (Fig. 4C), which translated into much lower root biomass (Fig. 4D). All roots showed waves of similar amplitude (Fig. 4E), but instead of the regular, loose waves exhibited by wild type roots, $\text{PIN6}$-OE roots displayed much tighter waves (Fig. 4F), occurring at significantly greater frequency, in both spatial and temporal terms (Fig. 5A and B). Clearly, misexpression of $\text{PIN6}$ altered the root oscillatory elongation patterns.

Another striking feature was the absence of root hair outgrowths (Fig. 4G). Confocal microscopy of the zone of cell differentiation showed that trichoblast outgrowths were absent (Fig. 4H), but a cross-section of the root showed the expected pattern of trichoblast (H cells) and atrichoblast (N cells) cells in PIN6-OE lines (Fig. 4I). Since root hair growth is proportional to internal auxin levels in the root hair cell [59], the data reveal that overexpression of $\text{PIN6}$ might interfere with auxin availability in these cells.

Next we examined lateral and adventitious root development, both known to involve auxin signalling and homeostasis [34,60]. PIN6-OE seedlings produced fewer lateral roots (Fig. 5C). As observed for the primary root, lateral roots were shorter than in wild type (Fig. 5D). Stage distribution of lateral root development

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**Figure 2. Characterisation of $\text{pin6}$ mutant alleles.** A) Schematic diagram of the PIN6 genomic DNA fragment showing exon/intron structure (ATG and TGA refer to translation start and stop codons, respectively). PIN6 T-DNA insertions and primer positions (See Table S1 for sequences) are marked by grey arrows. The Salk_046393 ($\text{pin6}$-2), Salk_092831 ($\text{pin6}$-4), GABI-KAT_430B01 ($\text{pin6}$-5) and GK711C09 ($\text{pin6}$-6) T-DNA insertions interrupt intron 2, exon 6, exon 3 and intron 6, respectively. B) Primary root length at 9 DAG (n = 25). (C) The development stage distributions of lateral root primordia that have initiated (I–VII) or emerged (Em) were quantified at 9 DAG (n = 10). D) The density (number of primordia per cm of primary root) of lateral root primordia in early (I–IV) and later (V–Em) stages of development, as well as the total number of primordia (n = 10). Similar results were observed in separate experiments. Homogeneity groups according to Student’s t test (p<0.05) are denoted with same letters. Error bars represent standard error. doi:10.1371/journal.pone.0070069.g002
Figure 3. PIN6 overexpression affects leaf pigmentation, shoot development and silique number. A) PIN6 overexpression binary cassette (pMDC32::PIN6). B) PIN6 mRNA abundance in leaf tissues from four representative lines and normalised to wild type (WT). C) Developing rosettes (4 weeks) from wild type and PIN6-OE lines. D) Rosette leaf area was reduced throughout vegetative development. E) Chlorophyll content was increased in mature leaf tissues (µg/g fresh weight). Average ± SE (n = 8 plants). F) Floral architecture is modified in overexpression lines. G) Floral stem length is reduced in overexpression lines (n = 2–8 plants ± SE). (H) PIN6 overexpression enhances the production of siliques (n = 8 plants ± SE). These results are representative of 2–3 independent experiments. When necessary homogeneity groups according to Student’s t test (p < 0.05) are denoted with same letters. Error bars represent standard error. doi:10.1371/journal.pone.0070069.g003
Figure 4. PIN6 overexpression affects organ development and waving in roots. A) Root architecture of wild type and PIN6-OE (OE#33 and OE#1) seedlings (10 DAG). B) Close up of PIN6-OE#1 waving roots. C) PIN6-OE lines show a reduction in root elongation (10 DAG). D) Root biomass of plants growing in soil was quantified 4 weeks after germination. Average ± SE (n = 12). E) and F) Wave amplitude and wave length, respectively, for primary roots. Error bars show standard error (n = 9 to 133) from a single experiment representative of three independent experiments. G) Root hair
outgrowth (4 DAG) is disrupted by PIN6 overexpression, when compared to wild type. H) Confocal micrographs show the development of trichoblast cells (PIN6-OE#1) or emergence of root hairs in WT. White arrows indicate root hair cells and PIN6-OE#1 is representative of multiple lines examined. I) Cross section of the primary root from wild type and PIN6-OE#14, respectively showing the position of a H (hair) cell in between to two N (no-hair) cells. Similar results were obtained for PIN6-OE#1. J) Development stage distribution of lateral root primordia initiated (I-VI) as well as emerged (Em) (9 DAG; n = 15) representative of multiple experiments. K) Primordium density of lateral root initiation (In) and emergence (Em) per cm of root length (8 DAG; n = 20). O) and P) Cellular patterning of root primordium at different developmental stages from initiation to emergence in PIN6 OE#1 and wild type (WT). All scale bars represent 10 μm and images are representative of multiple primordia examined. When necessary homogeneity groups according to Student’s t test (p<0.05) are denoted with same letters. Error bars represent standard error.

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Figure 5. PIN6 overexpression perturbs ethylene signalling. A) to B) Root waving was quantified in terms of number of root waves per mm (spatial waving frequency) and number of waves formed per day (temporal waving frequency), in A) and B) respectively (n = 9 to 133±SE). Misexpression of PIN6 reduces lateral root emergence (C), perturbs root elongation (D), enhances adventitious root formation (E) and has not effect upon adventitious root length (F). Average±SE (n = 9–26). For some experiments, seedlings were germinated on media containing concentrations of the ethylene precursor, ACC. G) PIN6-OE lines show a reduction in root elongation as well as reduced sensitivity to ACC. H) to K) Responses of PIN6-OE to ACC show that the root waves became distorted, indicating altered gravitropism and sensitivity to ethylene compared to wild type. When necessary homogeneity groups according to Student’s t test (p<0.05) are denoted with same letters. Error bars represent standard error.

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between the first and second cauline nodes) was significantly reduced in PIN6-OE lines when compared to wild type (Fig. 6A). In contrast, the PIN1 overexpression line [9] showed a significant increase in total auxin transport (Fig. 6A). In PIN6-OE plants, the basipetal wave of radioactively labelled auxin showed a slight increase in auxin transport in the stem segments closest to the 3H-IAA source (6–15 mm), but a significant decrease in the more distal segments (18–30 mm) (Fig. 6B). The PIN1-OE line displayed a basipetal wave similar to that of wild type (Fig. 6B).

The decrease in basipetal auxin transport through the PIN6-OE stem could explain the observed defect in apical dominance in the PIN6 overexpressing plants (Fig. 3).

A relative root growth assay showed that the PIN6-OE seedlings were less sensitive to IAA and IAA-alanine (Fig. 6C and D). High concentrations were used for the IAA-alanine conjugate because it needs to be hydrolysed (in the ER) first to IAA before it can inhibit root length [45]. An auxin inducible DR5::GUS reporter system [63] showed that when compared to wild type, stronger DR5 activity was observed in the PIN6-OE root tips and cotyledons during the early stages of germination (Fig. 6E, F, H and I). The application of 200 nM 1-naphthaleneacetic acid (NAA) promoted strong GUS staining in the cortex and epidermis of wild type roots (Fig. 6K to M), but not in PIN6-OE roots (Fig. 6N to P), which showed stronger DR5 activity only in the tips of the emerged lateral roots (Fig. 6K to P). This shows that overexpression of PIN6 interferes with the generation of DR5 auxin activity maxima in the roots. A stronger auxin response maximum in PIN6 overexpressing roots and root growth resistance to IAA and IAA-alanine suggest that PIN6 overexpression might interfere with accumulation of auxin in elongating epidermal and cortical cells.

In conclusion, analysis of PIN6 overexpression revealed a role of PIN6 in regulating auxin transport and auxin homeostasis.

**Discussion**

**PIN6 Promoter Activity is Regulated in a Tissue-specific and Auxin Dependent Manner**

In general, PIN6 expression was relatively low throughout plant development and only detected in particular tissues during specific stages of growth. For instance, in mature embryos, PIN6 was expressed in the root tip and root vasculature, whereas PIN6 expression in these tissues was relatively low in seedlings. Here, PIN6 expression was associated with the margins of the lateral root primordia as shown previously [20] and accumulated asymmetrically during root growth. PIN6 expression levels were generally stronger in meristematic tissues and at the boundaries of root and floral organs (Fig. 1). The low expression levels of PIN6 are in accordance with the presence of the epigenetic mark H3K27m3 that was enriched surrounding the PIN6 promoter and gene regions. H3K27m3 has been shown to reduce gene expression levels and could contribute to the low PIN6 transcript levels (Figure S2). Auxin induced PIN6::GUS expression in the shoot meristem, inner root tissues of the stele (including the pericycle), endodermis and root apical meristem (Fig. 1). Consistent with these observations a number of auxin response elements were identified within the PIN6 promoter. Therefore, although PIN6 is relatively weakly expressed in most tissues, the PIN6 promoter is responsive to developmental cues in a tissue-specific and auxin-dependent manner.

The most important outstanding question concerns the subcellular localization of PIN6. PIN proteins with longer central hydrophilic loop have been shown to be localized at the PM, whereas so-called shorter PINs with reduced hydrophilic loop are localized to the ER [12]. PIN6 in terms of protein topology
Figure 6. PIN6 perturbs inter-cellular auxin homeostasis in the stem, roots and cotyledons. A) Total transport of $^3$H-IAA through an inflorescence stem section. Total auxin transport was calculated by adding the radioactivity determined for each 3mm segment isolated from a 30mm stem section. Average ± SE (n = 4–12 independent stem sections). B) Auxin transport profile showing movement of $^3$H-IAA through the inflorescence stem segments 3 hours after loading labelled auxin. PIN1-OE refers to a PIN1 overexpressing line. The auxin transport results presented are representative of at least three independent experiments. C) and D) Root growth assays indicate that PIN6-OE#1 is less sensitive to IAA and IAA-alanine when compared to WT (Student’s t test *p < 0.05, n = 30 plants, Error bars represent standard deviation). E) to P) PIN6 overexpression enhances auxin accumulation in specific tissues. Histochemical GUS staining of DR5::GUS activity in germinating seeds (E, H), 3 day old seedlings (F, I) and mature primary root tips (G, J). K) to P) GUS staining of auxin treated (200 nM NAA) root tissues from WT (Fig. 5K to 5M) and PIN6-OE#14 (Fig. 5N to 5P) harboring the DR5::GUS reporter. Where appropriate, asterisks indicate a statistically significant difference (Student’s t test p < 0.05).

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represents an intermediate type of PIN proteins with middle-sized hydrophilic loop and thus it is difficult to envision how this type of PIN protein will be localized. The transient expression of PIN6-GFP in tobacco cells suggests an intracellular, non-PM localization of PIN6 [10]. In accordance, the PIN6 gain-of-function analysis showing effects on auxin homeostasis and largely distinct effects on auxin transport as compared to PIN1 gain-of-function [Fig. 6A and B] support a scenario that PIN6 is playing a role distinct from PM-localized PIN proteins. Nonetheless, the definitive answer to the in vivo subcellular localization of PIN6 awaits future characterisation.

The Loss of PIN6 Function Affects Lateral Root Development

None of the identified pin6 mutants in this study affected auxin regulated root growth. Accordingly, PIN6 mRNA levels were not or only slightly reduced in the pin6-4 and pin6-5 mutants. The pin6-6 T-DNA insertion is predicted to remove at least 22 amino acids from the 3’ end of the PIN6 protein. Although full PIN6 transcripts, (flanking the T-DNA insertion) were not detected, the observed transcripts in a region upstream to the T-DNA insertion together with a lack of root phenotype suggest that these 22 last amino acids do not contribute significantly to the functionality of the protein. In contrast, the complete loss of PIN6 activity in pin6-2 allele [40] did affect root growth and lateral root development. Less primordia in the early stages, together with a higher proportion of primordia in the later developmental stages, suggest a faster development of lateral roots in absence of PIN6. Accordingly, PIN6 promoter activity was recorded throughout all the different stages of lateral root organogenesis. Together, the data indicate that auxin regulated root growth, in particular lateral root development requires PIN6 activity.

PIN6 Overexpression Alters Auxin Homeostasis and Plant Development

Misexpression of PIN6 using the CaMV 35S promoter showed that PIN6 also interferes with other growth processes that require correct distribution of auxin. In photosynthetic tissues, the overexpression of PIN6 increased leaf chlorophyll content, promoted a compact rosette, reduced floral stem height and enhanced the emergence of seed nurturing siliques [Fig. 3]. In the root, PIN6 overexpression promoted adventitious root formation and root waving, while also perturbing root elongation, lateral primordia development as well as inhibiting the emergence of trichoblast hair cells (Fig. 4). Auxin has been shown to promote adventitious root formation and while the RNA interference of OsPIN1 significantly inhibited adventitious root development in rice [60,64], the overexpression of AtPIN6 promoted the formation of adventitious roots (Fig. 5). The root-wave phenotype has been well characterised in the main Arabidopsis root [25,61] being linked with distortion of polar auxin transport. Waving of lateral roots has been linked to light/dark cycles [65], while waving of adventitious roots has not yet been reported. The very pronounced waving of lateral and adventitious roots compared to the main root, and accumulation of auxin in the root wave crests, indicate altered auxin gradients and homeostasis interfering with the endogenous root tropisms. As noted above pin2 mutations reduced root waving [27], while to date the overexpression of PIN proteins has not enhanced root waving, revealing this is likely to be specific to PIN6.

Overexpression of PIN6 in lateral root primordia also indicated that misexpression of PIN6 interferes with primordia development. In PIN6 overexpressing lines, more primordia in the early and less primordia in the later stages of development were observed. This was consistent with a perturbation in the cellular patterning of root primordia caused by PIN6 overexpression (Fig. 4) and contrasts nicely with the pin6 loss-of-function phenotype, where a faster development was observed (Fig. 2). The overexpression of PIN6 affected the auxin response maximum in developing primordia, indicating that altered auxin homeostasis induced by the overexpression of PIN6 can interfere with lateral root development.

The tubular outgrowth of a root epidermal cell that produces a root hair can be divided into three stages, 1) fate determination to become a hair (H) or nonhair cell (N), 2) hair initiation, and 3) hair elongation [66]. Auxin is a potent stimulator of trichoblast initiation and elongation but appears to have much less effect upon cell fate–determining process [66,67]. The overexpression of PIN6 perturbed the outgrowth of the root hair cell, however did not affect fate determination as sections from the PIN6-OE primary root showed potential H and N cells, typical of wild type roots (Fig. 4). The perturbation of polar auxin efflux through the overexpression of other long- and short-looped PINs as well as PIN proteins [59,68] was also shown to affect root hair development. It seems likely that PIN6 overexpression reduces the level of auxin in the trichoblast cell. This would be consistent with the hypothesis that auxin efflux inhibits, and auxin influx enhances, the outgrowth of the root hair cell [69].

Evidence that PIN6 misexpression modulates auxin homeostasis during growth and development was also provided by the altered DR5 auxin response activity in roots overexpressing PIN6 and the failure of auxin to induce DR5::GUS activity in the outer cell layers of the root, leading to different GUS expression patterns (Fig. 1 and 6). Consistent with these observations our root growth assays confirmed a lower sensitivity to auxin conjugates when compared to wild type (Fig. 6). Given that PIN6 might localize to the ER, where enzymes involved in IAA metabolism are compartmentalized [70] it could be involved in regulating cellular auxin homeostasis, presumably by compartmentalizing auxin between the ER and the cytosol and thereby fine-tune the cellular free IAA levels.

PIN6 was shown to function as an auxin (IAA) transporter in tobacco Bright Yellow-2 cell lines [9]. Here we show that overexpression of PIN6 reduces total auxin transport through the Arabidopsis inflorescence stem (Fig. 6). The slight increase in the basipetal wave of radioactively labelled auxin nearest the 3H-IAA source relative to the significant decrease in the more distal segments, perhaps reflects a role for PIN6 as a regulator of intercellular movement of auxin efflux in vivo. For example, PIN6 could transport auxin in the opposite direction or in a non-polar manner, alternatively it might sequester auxin intracellularly by transporting auxin into ER thus limiting its availability for intercellular transport. Future experiments should address how PIN6 overexpression affects auxin transport activity.

PIN6 Misexpression Affects Ethylene Responses

Auxin and ethylene synergistically interact to coordinate root elongation with both hormones inhibiting the elongation of cells leaving the RAM [71,72,73,74] (Fig. 5). Ethylene induced inhibition of root growth was reduced by PIN6 misexpression as the root length in the PIN6-OE lines was less sensitive to ACC than in wild type, for both primary and lateral roots (Fig. 5). Interestingly, the reduction in root length appeared to be caused by early inhibitory effects of PIN6 in the first 10 days of growth, as the relative elongation rate thereafter was similar between overexpression and wild type lines (data not shown). Ethylene was shown to reduce temporal wave frequency significantly on nutrient-supplemented agar [61]; so did ACC here in both wild
type and PIN6 overexpressing lines (Fig. 5). The misexpression of PIN6 however caused waves to become distorted, asymmetric and irregular, with the trajectory of root elongation showing strong deviations from the vertical. Therefore, the overexpression of PIN6 reduces the sensitivity of the root to ethylene.

Ethylene regulates root growth by stimulating auxin biosynthesis and basipetal auxin transport toward the elongation zone, where it activates a local auxin response leading to inhibition of cell elongation [73,74]. In mutants affected in basipetal auxin transport, ethylene cannot activate the auxin response or inhibit root elongation [74]. Given that PIN6 overexpression lines have some resistance to ethylene (Fig. 5) it is possible that the misexpression of PIN6 interferes with basipetal auxin transport. Consistently, a strong auxin response maximum at the root tip in PIN6 overexpressors (Fig. 1 and 6), resembles auxin accumulation pattern in pin2/ai1-1 mutants reported to have defects in basipetal auxin flow in the root [17]. Collectively, these data demonstrate that the misexpression of PIN6 can perturb auxin transport dependent ethylene regulation of root growth.

Conclusion

The pin6 loss-of-function and misexpression lines demonstrated that PIN6 in Arabidopsis plays important developmental and physiological roles. We demonstrated that PIN6 expression can be regulated by auxin and developmental cues and that PIN6 modifies auxin transport resulting in altered auxin dependent processes, especially those required for root growth and reproductive development.

Supporting Information

Figure S1 Regulation of PIN6:luciferase expression during development. A) Luciferase activity spectrum for multiple independent PIN6 transgenic lines harbouring pTPIN6::FLUC promoter:luciferase fusion were analysed for luciferase activity and are presented in the order of increasing activity along the X-axis. Select lines chosen for further analysis of PIN6::FLUC regulation after germination are displayed. The luciferase activity of mature leaf tissues (at least 2 leaves/plant) from independent transgenic lines (T0 plants) were measured using the in vivo leaf disk assay (at least 2 leaf discs/leaf, B) to D) Regulation of the PIN6 promoter during seedling development. In vivo bioluminescence was assayed in seedlings (B; 9 DAG), plantlets (C; 20 DAG) and flowering tissues (D; 45 DAG) from transgenic lines harbouring PIN6 (pTPIN6::FLUC) or CaMV 35S (pT35enh:FLUC) promoters. E) False colour images obtained using the Image J software: the threshold was adjusted such that black indicates no luminescence, blue reflects low levels of luminescence and white reflects higher levels of luminescence. (PDF)

Figure S2 Characterisation of PIN6 expression patterns. A) PIN6 anatomical mRNA expression levels in wild type Columbia-O tissues. Genevestigator was used to generate an Arabidopsis PIN6 anatomical mRNA expression levels in wild type Columbia-O tissues. Genevestigator was used to generate an Arabidopsis PIN6 anatomical mRNA expression levels in wild type Columbia-O tissues. Genevestigator was used to generate an Arabidopsis PIN6 anatomical mRNA expression levels in wild type Columbia-O tissues. Genevestigator was used to generate an Arabidopsis PIN6 anatomical mRNA expression levels in wild type Columbia-O tissues. Genevestigator was used to generate an Arabidopsis PIN6 anatomical mRNA expression levels in wild type Columbia-O tissues. Genevestigator was used to generate an Arabidopsis PIN6 anatomical mRNA expression levels in wild type Columbia-O tissues. Genevestigator was used to generate an Arabidopsis PIN6 anatomical mRNA expression levels in wild type Columbia-O tissues. 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Genevestigator was used to generate published microarray data and report expression levels in germinating seeds, young seedlings, mature rosettes, floral bolts as well as young immature and older mature flowers. E) Summary of PIN expression, chromatin modifications and localisation. Genevestigator expression levels were qualitatively scored as strong (++++), medium (+++) and weak (+++) and H3K27 trimethylation marks associated with repressive PIN gene expression were scored as absent (no) or present (yes) (http://www.mcmdb.ucla.edu/Research/Jacobsen/). Subcellular targeting of the PIN genes to the plasma membrane (PM) or endoplasmic reticulum (ER) are shown. (PDF)

Figure S3 Characterisation of additional pin6 mutant allelics. A) End-point PCR was used to quantify PIN6 expression levels in 10 day old seedling tissues from TDNA insertion and overexpression lines. Mutant pin6-5 showed slightly reduced PIN6 mRNA levels, while OE#1 showed increased PIN6 transcript levels. B) to D) RT-PCR was used to measure PIN6 mRNA abundance in pin6-6 seedling (10 DAG) and/or flowering tissues. PCR amplicons either flanked (B) or positioned before the Gk_711C09 TDNA insertion (C). D) ACTIN was used as a control to quantify cDNA. (PDF)

Figure S4 PIN6 overexpression affects floral development. A) Relative rosette expansion rate of PIN6-OE#1 compared to wild type. The asterisk indicates the onset of floral bolt emergence. Relative growth rate = Log{Area (T2)} – Log{Area (T1)}/(T2 – T1). The average±SE (n = 8) are given. B) and C) Days to flowering and number of leaves at the onset of flowering, respectively. ND = not determined. D) and E) The number of rosette and cauline branches, respectively. The number of rosette branches excludes the main primary floral bolt and only cauline branches emerging from the primary floral stem were scored. The average±SE (n = 7–8) are given. Statistically significant data are indicated by a star (t-tests, 2 tailed, unpaired, P<0.05). Similar data were observed in multiple experiments under a range of experimental conditions. (PDF)

Table S1 Primers used to quantify transcript abundance and construct binary vectors. The target gene, primer name, sequence and direction of primer annealing are displayed. (PDF)

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Author Contributions

Conceived and designed the experiments: CIC MV KY JF. Performed the experiments: CJC IRS PM KY JM SS. Contributed reagents/materials/analysis tools: AJC IRS PM KY JM SS. Wrote the paper: CIC MV.
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