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Cell polarity: ROPing the ends together

Jian Xu and Ben Scheres

Cell polarity plays an important role in plant development, but the mechanisms that first establish polarity cues remain obscure. By contrast, a flurry of information has recently emerged on the elaboration of cell shape from such unknown initial cell-polarity cues. Recent studies suggest that Rho-related GTPases in plants (ROPs), and their effector targets among the ROP-interactive CRIB motif-containing proteins (RICs), mediate two antagonistic pathways that have opposing action on cell polarization. ROP proteins appear to interact directly with upstream regulators of the ARP2/3 complex, which are conserved modulators of the actin cytoskeleton. ROP function is dependent on the class 1 ADP-ribosylation factors (ARFs), which are core components of the vesicle transport machinery that are also involved in the polar localization of PIN-FORMED (PIN) family auxin efflux facilitators.

Addresses

Department of Molecular Genetics, Utrecht University, Padualaan 8, 3584CH Utrecht, The Netherlands

Corresponding author: Scheres, Ben (b.scheres@bio.uu.nl)

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Introduction

Cells can be viewed along three orthogonal axes. When one axis can be clearly distinguished from the others a cell is said to be ‘axialized’. The distribution of subcellular structures and molecules may be asymmetric along one or more particular axes, making one end of the cell different from the others. This often stunning internal asymmetry is known as ‘cell polarity’.

Cell polarity plays important roles in both animal and plant development. For example, in *Caenorhabditis elegans*, *Drosophila melanogaster* and *Arabidopsis thaliana*, the main body axis is defined by the polarity of the single-celled zygote and polar information is used for patterning and cell specification along this axis.

In plants, single-cell systems such as pollen tubes or root hairs have been used to reveal molecular components that

are required for apical–basal cell polarity and polar outgrowth. At the multicellular level, the polar localization of the PIN-FORMED (PIN) family auxin transport facilitators has yielded valuable molecular markers for cell polarization and better understanding of coordinated cell polarity in plant growth and development.

In this review, we can discuss only brief highlights of recent findings that have contributed to our understanding of the mechanisms that control cell polarity in plants. Several recent accounts provide further reading [1–3].

ARFs, ARF-GEFs and vesicle trafficking

ADP-ribosylation factors (ARFs) are core factors for vesicle trafficking. ‘Class 1’ ARF proteins regulate intracellular vesicular trafficking at multiple stages of the secretory and lysosomal/vacuolar transport pathways in mammalian and plant cells [4–8]. In particular, they participate in the formation of transport vesicles and the selection of transmembrane protein cargo from donor compartments in mammalian cells [9,10].

The vesicle transport inhibitor Brefeldin A (BFA) interferes with ARF action in mammalian, fungal, and plant cells [11,12]. BFA treatment compromises specific cell polarization processes such as the establishment of apical–basal polarity in root-hair-bearing epidermal cells (trichoblasts), reflected by root hair position defects and by defects in polar outgrowth [13], indicating that ARF-dependent vesicle trafficking is involved in cell polarity.

Consistent with a potential role for the ARF proteins in the establishment of plant cell polarity, mutations in the *GNOM/EMB30* gene, which encodes a BFA-sensitive guanine nucleotide exchange factor for ARFs (ARF-GEF) [14,15], lead to aberrant cell shape and orientation of cell division [15,16]. *GNOM/EMB30* localizes to endocytic organelles, where it controls the polarized vesicle trafficking of the BFA-sensitive auxin efflux facilitator PIN1 to the basal end of the plasma membrane [17,18]. Weak alleles show auxin-related defects that support a specialized function for the *GNOM* ARF-GEF in polar-auxin transport [19].

Plants have many class 1 ARF proteins [18,20] and *Arabidopsis* ARF1 complements the ARF1 ARF2 yeast double mutant [7], suggesting that class 1 ARF proteins in *Arabidopsis* have canonical cellular functions. Co-localization studies reveal that *Arabidopsis* ARF1 is localized to the Golgi apparatus and endocytic organelles in both onion and *Arabidopsis* cells [21]. Manipulation of *Arabi-*

dopsis ARF1 function influences cytokinesis and polar outgrowth [21^{*}]. Moreover, the position of root hair outgrowth is affected when GTP- and GDP-locked mutants of ARF1 are expressed at early stages of cell differentiation but after they exit mitosis, revealing specific modulation of apical–basal epidermal polarity by ARF1-dependent vesicle trafficking machinery in a distinct phase of plant development [21^{*}].

ROPs and RICs

Targets for ARF-dependent vesicle trafficking are suggested by the observation that BFA inhibits early polar localization of RHO-of-plants proteins (ROPs) at the root hair initiation site [22]. ROPs are homologs of RHO/RAC/CDC42 RHO-family GTPases, which include key regulators of cell polarity in yeast and animals [23]. Among 11 *Arabidopsis* ROP genes [24], *ROP1*, *ROP2* and *ROP4* are essential for pollen tube or root hair outgrowth [21^{*},22,25,26,27^{**}]. Consistent with its role in plant cell polarity, the expression of *ROP2* is highly enriched in the apical plasma membranes of the root meristematic cells [28], and *ROP2* localizes to the future site of root hair formation as well as to the tips of growing root hairs [21^{*},25]. *ROP2* partially co-localizes with the endocytic marker FM4-64 upon BFA treatment, and both polar *ROP2* localization to the hair tip and the activity of *ROP2* in this region requires ARF1 function [21^{*}], supporting the idea that root hair outgrowth involves ARF-dependent polar localization of ROP proteins [22].

A genome-wide search for putative ROP effector targets led to the identification of genes that encode ROP-interactive CRIB (for CDC42/RAC-interactive binding) motif-containing proteins (RICs) [29]. The CRIB motif is required for the specific interaction of RICs with GTP-bound ROPs. RICs share little sequence homology with each other outside of the conserved ROP-interactive domain. The overexpression of *RIC* genes in pollen causes various degrees of growth inhibition in pollen tubes, implying that various RICs have distinct functions.

Like *ROP1*, both *RIC3* and *RIC4* cause depolarized growth. Furthermore, they display *ROP1*-enhanced localization to the tip of pollen tubes, suggesting that these RICs might be targets of *ROP1* [29]. Indeed, *RIC4* promotes F-actin assembly, whereas *RIC3* activates calcium ion signaling that leads to F-actin disassembly. Polar outgrowth defects that are caused by the overexpression or depletion of either *RIC3* or *RIC4* can be rescued by the overproduction or depletion of the other protein. Thus, *ROP1* modulates actin cytoskeletal dynamics and polar outgrowth in pollen tube by coordinating two counteracting downstream pathways that are controlled by the *ROP1* targets *RIC3* and *RIC4* [27^{**}]. Similar ROP-mediated regulatory mechanisms appear to account for the jigsaw-puzzle shape of *Arabidopsis* leaf pavement cells, in which locally activated *ROP2* activates *RIC4*

to promote the assembly of cortical actin microfilaments that are required for the localized outgrowth of lobes [30^{**}]. At the same time, *ROP2* inactivates *RIC1*, promoting the formation of well-ordered cortical microtubules and the microtubule-dependent suppression of *ROP2*–*RIC4* interaction in the indentation zone [30^{**}]. Although the underlying mechanism by which microtubules regulate *ROP*–*RIC4* interaction is not known, these findings suggest a fascinating precisely regulated cross-talk between ROP-mediated signaling pathways, which might serve as a general molecular mechanism for the polar outgrowth of plant cells.

ARP2/3 and its upstream regulatory factors

The inhibitory activity of the potent actin filament-disrupting drug latrunculin B suggests that actin cytoskeletal dynamics play an important role during axis establishment and polar outgrowth [31,32]. Recent genetic studies in *Arabidopsis* demonstrate that the major actin protein *ACTIN2* is essential for both apical–basal root hair polarity and polar outgrowth [33,34], further supporting the importance of the actin cytoskeleton in plant cell polarity.

The seven-subunit actin-related protein (ARP)2/3 complex is a conserved modulator of the actin cytoskeleton. The identification of different subunit homologs in *Arabidopsis* suggests the existence of a functional ARP2/3 complex in plants [3^{*}]. Mutations in genes that encode subunits of the ARP2/3 complex lead to increased F-actin bundling and aberrant actin patches, which misdirect the expansion of various cell types including trichomes, pavement cells, hypocotyl cells and root hair cells [35–40]. These mutations reveal a pivotal role for the ARP2/3 complex and the actin cytoskeleton in controlling polar cell expansion in plants.

In animal cells, the activity of the ARP2/3 complex is regulated by a variety of proteins of the WAVE (for Wiskott–Aldrich syndrome protein family verprolin homologous)/SCAR (for suppressor of cAMP receptor) complex [41–44]. In response to signals from the RHO family small GTPase *Rac1*, alterations in the composition and/or subcellular localization of the WAVE/SCAR complex lead to ARP2/3 activation [41,43]. Putative homologs for proteins of these upstream regulatory complexes were identified recently in *Arabidopsis* and maize [45,46^{**},47–49,50^{**},51–55]. In *brick1* mutants of maize, the failure of lobes to form along the margins of expanding leaf pavement cells is associated with the loss of local enrichments of cortical F-actin that are found at sites of lobe outgrowth in wildtype cells [45]. *Arabidopsis Atscar2|distored3*, *pirogi* (*pir*)/*Atpir*/*Atsra1*, *gnarled*/*Atnap1* and *klunker* mutants have trichome F-actin alterations and trichome morphology defects that are nearly identical to those of Arp2/3 complex mutants and to those of plants that express constitutively active *ROP2* [46^{**},47–49,51,53,56]. Moreover, *PIR*/*AtPIR*/*AtSRA1* directly interacts with *ROP2*

with isoform specificity and with selectivity for active forms of the protein [46^{••}], although *in vivo* interaction and its significance has yet to be investigated. Together, these findings strongly suggest that ROP signaling, the ARP2/3 complex and its upstream regulatory complexes play essential roles in the local modulation of actin cytoskeletal dynamics, which in turn regulate axis establishment and polar outgrowth in plants.

Polar PIN protein localization

Polar transport of auxin plays crucial roles in axis establishment and polar growth during both embryonic and post-embryonic development [2[•],57]. Both the presumptive auxin influx carrier AUX1 and the PIN efflux facilitators display an asymmetrical subcellular localization at the plasma membranes of auxin-transporting cells, which correlates with the presumed direction of auxin flow [58,59]. PIN proteins act redundantly, and their expression and localization undergo dynamic changes in response to developmental regulation [60,61^{••}] or environmental stimuli, such as light or gravity [62], which makes them excellent read-outs for cell polarity.

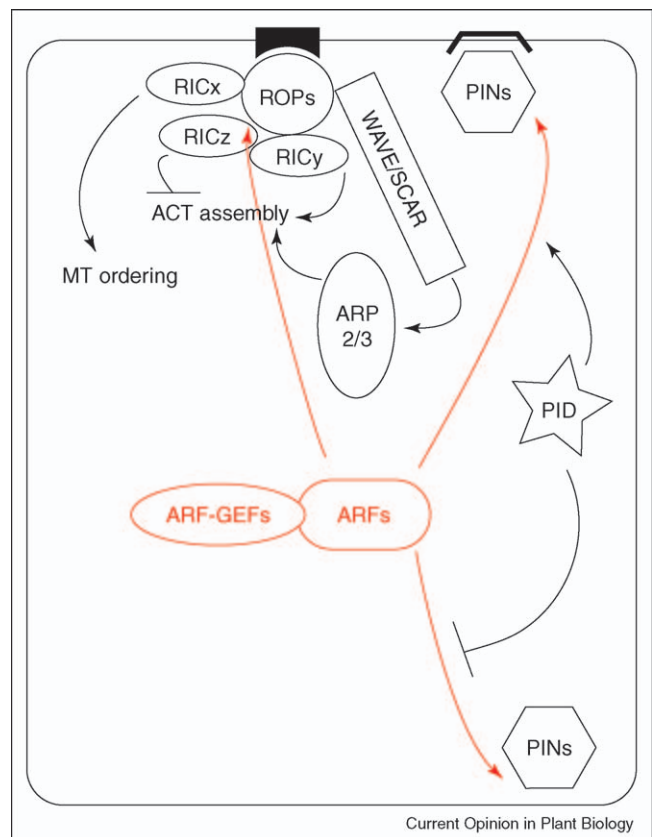
Besides the earlier-mentioned role of vesicle-trafficking machinery in polar PIN protein localization, the serine-threonine kinase PINOID (PID) acts as a major determinant of PIN protein localization [63^{••}]. In cells in which PID is present above a threshold level, PIN proteins are targeted to the apical membrane, whereas low levels of PID activity lead to the basal localization of the PIN proteins. The dependence on kinase activity of the precise switching between two alternative localizations suggests that PID mediates the choice of PIN trafficking or docking to alternative localization cues.

Interestingly, the accumulation of *PID* transcript is strongly and rapidly upregulated by auxin, the early expression of *PID* mRNA in the embryo is dependent on PIN1, and the recycling of PIN proteins from the membrane appears to be auxin dependent [64,65,66[•]], suggesting a tight connection among auxin, polar auxin transport, PINs and PID. Moreover, PID interacts with two calcium-binding proteins TOUCH3 and PID-BINDING PROTEIN 1 (PBP1) [67], supporting a role for calcium ion signaling in a PID-dependent signaling pathway for the control of PIN protein localization. PID protein localization should reveal whether ARF-dependent vesicle-trafficking machinery is involved in the localization or function of PID, for which a mechanism has been proposed that resembles insulin-stimulated GLUT4 transport in mammalian insulin-responsive tissues [68].

Polar PIN protein localization also appears to require sterol function because mutations in the *Arabidopsis* sterol biosynthesis gene *ORC*/*Sterol methyl-transferase 1* (*SMT1*) lead to reduced auxin transport and mis-localization of

PIN proteins [69]. The underlying mechanisms, however, remain to be discovered. The internalization of sterols and PIN2 exhibited similar kinetics and pharmacological sensitivities, raising the possibility that the redistribution of sterols plays a role during the endocytic recycling of PIN proteins [70]. Sterol transport to the plasma membrane is actively mediated by P-glycoproteins (PGP)/multiple drug resistance (MDR) proteins in animal cells [71]. Mutations in *PGP/MDR*-related genes from plants result in the mislocalization of PIN proteins and in defective auxin transport [72–74], suggesting a potential mechanism by which PGP/MDR-related proteins in plants mediate the transport of sterols to distinct membrane domains in response to yet unknown signals, resulting in the polar localization of PIN proteins. Alternatively, PGP/MDR-related proteins might interact with PIN proteins and regulate their localization directly.

Figure 1



Processes contributing to cell polarization. Vesicle trafficking that is mediated by Class 1 ARFs is required for the polar localization of ROP GTPases, which control actin (ACT) assembly through RICs and WAVE/SCAR-ARP2/3 pathways and microtubule (MT) bundling through other RICs. ARF-mediated vesicle trafficking and a specific ARF-GEF regulator of this process also control the localization of PIN proteins, and the polarity of this localization is controlled by the PID kinase, which functions as a binary switch. Polar localization cues for ROP localization or activation and for PIN localization (black bodies) remain unknown. Red arrows: vesicle trafficking control. Black arrows: protein activity control.

In summary, the subcellular localization of PIN proteins is known to rely on targeted vesicle transport, on PID kinase activity, and on the function of sterol and PGP/MDR-related proteins but the initial cues for the polar localization of PIN proteins are as yet unknown.

Conclusions

Many of the components that are involved in polarized growth and polar protein distribution have recently been discovered and are beginning to be connected within pathways that lead from regulators to cytoskeletal elements (Figure 1). Vesicle trafficking plays a central role in polarized growth, but the specific controls of this process during cell polarization need to be identified, for example by studies on regulators of vesicle fusion [75,76]. However, the nature of initial polarity cues remains unknown. Emerging connections between lipid signaling and cell polarity might help in the identification of such cues [77–79]. After that, the challenge will be to find out whether diverse cues regulate the polar activity and localization of diverse proteins in distinct or in related pathways, or whether a very small set of initial polar marks are used by all systems that elaborate plant cell polarity. Can we rope these ends together?

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