

Chapter 8

Auxin on the Road Navigated by Cellular PIN Polarity

Pawel Baster and Jiří Friml

Abstract The generation of asymmetry, at both cellular and tissue level, is one of the most essential capabilities of all eukaryotic organisms. It mediates basically all multicellular development ranging from embryogenesis and de novo organ formation till responses to various environmental stimuli. In plants, the awe-inspiring number of such processes is regulated by phytohormone auxin and its directional, cell-to-cell transport. The mediators of this transport, PIN auxin transporters, are asymmetrically localized at the plasma membrane, and this polar localization determines the directionality of intercellular auxin flow. Thus, auxin transport contributes crucially to the generation of local auxin gradients or maxima, which instruct given cell to change its developmental program. Here, we introduce and discuss the molecular components and cellular mechanisms regulating the generation and maintenance of cellular PIN polarity, as the general hallmarks of cell polarity in plants.

1 Introduction

The emergence of multicellularity during the evolution of species had its inevitable repercussions. Efficient intercellular communication was one of such. In other words, to achieve a mutual goal, neighboring cells (single elements of the system) needed to perceive and transduce externally or internally generated signals. As a result, the multicellular organism, as a whole, should be able to translate these

P. Baster • J. Friml (✉)

Department of Plant Systems Biology, VIB, 9052 Gent, Belgium

Department of Plant Biotechnology and Genetics, Ghent University, 9052 Gent, Belgium

Institute of Science and Technology Austria (IST Austria), 3400 Klosterneuburg, Austria

e-mail: Jiri.FRIML@ist.ac.at

signals into a developmental response. This basic necessity for efficient internal communication underlies the origin of the small signaling molecules, termed hormones, present in both plants and animals (Alberts et al. 2007). While the essential role of hormones in cell-to-cell communication is evident in both cases, the response of the organism into which the hormonal signal is translated, diverge between two kingdoms. In animal species, solutions based on a modulation of behavior were primarily promoted (Davies 2004). In contrast, plants, due to the sessile nature of their lifestyle, developed a remarkable repertoire of mechanisms which allow them, through fine-tuning of metabolism or body shaping, to adjust and survive in ever changing and often adverse environments (Tanaka et al. 2006). These mechanisms are facilitated not only by intercellular communication but also by tightly regulated cell division, morphogenesis, and differentiation. Importantly, most, if not all of them, are based on cell polarization and repolarization which guide tissue and organ patterning and thus underpin basic shape and functionality of an organism. The phenomenon of cell polarity can be reflected in various aspects like disproportional growth or asymmetrical distribution of the cellular components. The term itself, however, is much broader and in largest sense applies to the generation of any asymmetry in relation to an axis (Sauer and Friml 2004; Geldner 2009).

Despite its complexity, plant development, with its remarkable polarization-based flexibility, is coordinated most prominently by a single phytohormone—auxin—which serves itself as a polarizing cue (Chap. 14; Berleth and Sachs 2001; Sauer et al. 2006; Leyser 2011). Moreover, generation of local auxin accumulations (gradients) plays an essential role in plethora of crucial events during plant development, like embryogenesis (Chap. 9; Friml et al. 2003; Schlereth et al. 2010), organogenesis (Chaps. 10 and 11; Benková et al. 2003), phyllotaxis (Reinhardt et al. 2003), root meristem organization (Sabatini et al. 1999; Friml et al. 2002a), root stem cell differentiation (Ding and Friml 2010), or vascular tissue patterning (Scarpella et al. 2006). Although essentially all plant tissues possess the capacity for auxin biosynthesis (Mano and Nemoto 2012; Ljung 2013) and metabolism (Ludwig-Müller 2011; Ruiz Rosquete et al. 2012), it is the directional auxin transport that most significantly contributes for establishing of auxin gradients across plant tissues (Tanaka et al. 2006). The existence of such a cell-to-cell transport of auxin (see Chap. 5), which is the unique feature among other phytohormones, was predicted in the mid-1970s by so-called chemiosmotic model (Rubery and Shelldrake 1974; Raven 1975). This model postulated an auxin efflux from the cell, facilitated by polarly localized exporters, as a critical step during intercellular auxin translocation. These predictions were spectacularly confirmed by characterization of the broad spectrum of developmental phenotypes caused by mutations in the *PIN-FORMED* (*PIN*) genes (Gälweiler et al. 1998; Luschnig et al. 1998; Okada et al. 1991). Basically all different phenotypes found in various *pin* mutants could be mimicked by treatments with auxin transport inhibitors (Vieten et al. 2007). Transport assays from both plant and heterologous systems, provided later, shown that PIN proteins indeed mediate auxin export from the cells (Petrášek et al. 2006). The intercellular auxin transport, beside of PINs, rely on the

coordinated activity of two other transporter families. These are AUXIN RESISTANT1/LIKE AUX1 (AUX1/LAX) and MULTIDRUG RESISTANCE/PHOSPHOGLYCOPROTEIN/ATP-BINDING CASSETTE OF B-TYPE (MDR/PGP/ABCB) proteins, facilitating influx and efflux of auxin from the cell, respectively (Bennett et al. 1996; Noh et al. 2001; Kramer 2004; Yang et al. 2006; Mravec et al. 2008; Swarup et al. 2008; Verrier et al. 2008). Despite the fact that multiple components are involved, a critical control of the directionality of auxin flux is attributed to the efflux activity of the PIN transporters at their highly defined, polar, subcellular domains (Wiśniewska et al. 2006; Blakeslee et al. 2007; Titapiwatanakun et al. 2009). PIN family consist of eight members, most of which (PIN1, 2, 3, 4, 6, and 7) dependent on the tissue or developmental context exhibit plasma membrane (PM) localization restricted mainly to the apical (shootward; shoot-apex-facing) or basal (rootward; root-apex-facing) side of the cell (Zažímalová et al. 2007). Notably, also AUX/LAXs and ABCBs, which serve as an additional source of auxin for PIN-mediated transport (Geisler et al. 2005; Mravec et al. 2008; Christie et al. 2011; Kubeš et al. 2012), in some cases display asymmetric distribution (Swarup et al. 2001; Panikashvili et al. 2007; McFarlane et al. 2010).

Although some similarities can be found (Geldner 2009), in general, the mechanisms underlying cell polarity in plants differ from those characterized in animals (Tepass et al. 2001; Humbert et al. 2006; Wells et al. 2006; Chen et al. 2010). It seems that in both animal and plant systems the delivery of protein to the place of action by subcellular trafficking is equally important (Dudu et al. 2004; Altschuler et al. 2008; Geldner 2009; Shivas et al. 2010). On the other hand, the most prominent trafficking-based determinants of polarity found in animals, like CRUMBS, SCRIBBLE, and PAR complexes, are missing in plant genomes (Geldner 2009). Additionally, counterparts of so-called tight junctions which in animals serve as diffusion barriers, dividing PM of epithelial cells into apical and baso-lateral, polar domains (Giepmans and van Ijzendoorn 2009), are missing in majority of plant cell types. A similar structure is present in plants in form of 'Casparian Strip', belts of specialized cell wall material generating an extracellular diffusion barrier, found exclusively in endodermis (Roppolo et al. 2011). Polar trafficking pathways described in plants cells appear to be more complex than those found in animals. Besides apical and basal PM domains, characteristic for animal epidermal cells, also outer- and inner-lateral domains, with corresponding polar cargos, can be found in similar cell types in plants (Miwa et al. 2007; Langowski et al. 2010; Takano et al. 2010). What is more, the differences are reflected not only on the cellular but also on the tissue level. Plants in contrast to animals cannot use the mechanism of invasive, cell-migration-based tissue patterning due to the presence of the rigid extracellular matrix, cell wall, encapsulating plant cells and making them immobile (Dettmer and Friml 2011).

Considering the aforementioned differences it is not surprising that alternative, to animal, solutions were promoted by evolution in plant kingdom. In this chapter, these plant-specific mechanisms for cellular polarization are discussed. The polarity of cellular components is mainly considered in context of PIN proteins, due to their

essential role in auxin-mediated plant development. Moreover, in case of PIN family enough molecular components and polarity generating/maintaining signals are described for drawing a comprehensive and interesting overview. First, subcellular trafficking machinery relevant for PIN polarity is characterized. Next, cell structure and cargo-related determinants for PIN targeting and maintenance at the polar domain are presented. Finally, the feedback mechanisms for PIN polarization are discussed. It should be taken into account that such a categorization, due to frequently redundant nature of the biological processes, is largely subjective and serves mainly for presentation purposes.

2 Long Journey with Unsure Destination: Trafficking for PIN Polarization

Polar localization of PIN auxin transporters, restricted to the specific side of the cell relies, among other mechanisms, on the function of complicated network, encompassing multiple bypassing and interconnected pathways collectively referred to as ‘intracellular trafficking’ (Paul and Frigerio 2007; Bassham et al. 2008; Robinson et al. 2008; Irani and Russinova 2009; Žárský et al. 2009). Auxin transporters, subjected to intracellular trafficking, originate from de novo synthesis and are delivered to the PM through so-called anterograde route. This mode of intracellular transport generally involves sequential steps including protein folding in endoplasmic reticulum (ER), translocation through the cis- and trans-cisternae of the Golgi Apparatus (GA) with final arrival to the cell surface (Vitale and Denecke 1999; Matheson et al. 2006).

2.1 Constitutive PIN Cycling for Rapid Repolarizations

Contrary to the usually presented rather static snapshot pictures, the polar localization of PIN proteins is in reality very dynamic. Once delivered to the cell surface, PINs undergo continuous shuttling between PM and intracellular compartments by rounds of internalization (endocytosis) and polar recycling (exocytosis). These processes are jointly referred to as ‘constitutive endocytic cycling’ (Geldner et al. 2001; Dhonukshe et al. 2007; Kleine-Vehn et al. 2011). It is not entirely clear to which extent the initial secretion of de novo synthesized PINs to the PM occurs in polar fashion (Langowski and Friml, unpublished) or whether the endocytic cycling is generating the polar distribution following apolar secretion (Dhonukshe et al. 2008a).

Nevertheless, the first station reached by internalized PINs on their endocytic trafficking route from the PM is early endosome (EE). This subcellular compartment is critical as it is the intersection between secretory and endocytic routes and,

in plants, originates from and associates with trans-Golgi network (TGN) (Dettmer et al. 2006; Lam et al. 2007; Viotti et al. 2010). Thus, sorting of vesicular cargo for various subcellular destinations occurs at EE/TGN (Liu et al. 2002; Dettmer et al. 2006). Once destined for recycling, PINs are translocated from EE/TGN to the hypothetical compartment called recycling endosome (RE), where they fall under the control of ADP-Ribosylation Factor GTPase (ARF-GTPase) machinery. ARF-GTPases, by recruitment of vesicle coat proteins and organizing cytoskeleton at membrane surfaces, control vesicle trafficking. Their spatiotemporal activity is determined by the antagonistic activity of ARF guanine nucleotide exchange factors (ARF-GEFs) and ARF-GTPase activating proteins (ARF-GAPs), which are activating and deactivating ARF-GTPase complex, respectively (D'Souza-Schorey and Chavrier 2006). GNOM, a protein belonging to the golgi-associated, brefeldin-A resistant guanine nucleotide exchange factor (GBF) class of ARF-GEFs, most prominently controls the polar recycling of PINs to the PM (Fig. 8.1; Geldner et al. 2003). This protein, and more specifically its Sec7 domain, is a target of fungal toxin brefeldin A (BFA), which by inhibiting GNOM-mediated exocytosis, causes reversible intracellular accumulation of constitutively endocytosed proteins and aggregation of TGN into so-called BFA compartments or BFA bodies. This effect serves as a tool to visualize the constitutive cycling of PM proteins (Geldner et al. 2001). Interestingly, GNOM controls preferentially PIN recycling to the basal side of the cell, whereas pathway by which PINs are targeted to the apical domain is, most likely, additionally controlled by uncharacterized, BFA-insensitive ARF-GEF (Kleine-Vehn et al. 2008a, b).

Besides ARF-GTPases, also RabA1B, a member of small Rab-GTPase family and INTERACTOR OF CONSTITUTIVE ACTIVE ROP1 (ICR1), an effector of RHO OF PLANTS1 (ROP1) RAC-GTPase, were recently associated with defective PIN recycling (Fig. 8.1; Hazak et al. 2010; Feraru et al. 2012). Importantly, genetic interference with ICR1 results with severely disturbed polarity of PIN1 and PIN2, as well as various developmental defects (Hazak et al. 2010). Moreover, ICR1 was shown to interact with Sec3A (Lavy et al. 2007), one of the exocyst complex (EC) components. EC is known to participate in the extensive fusion of exocytic vesicles at specific sites of PM during so-called polarized exocytosis. Polarized exocytosis is controlled, among others, by Rho GTPases (Žárský et al. 2009). Interestingly, another subunit of the EC, Exo70, influences polar auxin transport through the regulation PIN1 and PIN2 recycling (Drdová et al. 2013).

The fundamental role of the cellular scaffolding and cytoskeleton for intracellular PIN trafficking should be also underlined here. PIN constitutive cycling seems to depend mainly on actin filaments since pharmacological interference with the integrity of this component abolishes internalization and recycling of PINs. On the other hand, microtubules are essential for both PIN trafficking in dividing cells as well as for maintenance of the general polarity of the cell (Geldner et al. 2001; Friml et al. 2002b; Petrášek and Schwarzerová 2009; Dhonukshe et al. 2008b; Boutté et al. 2006; Kleine-Vehn et al. 2006, 2008b, c; Kleine-Vehn and Friml 2008). The components of cytoskeleton not only serve as an orientation cues,

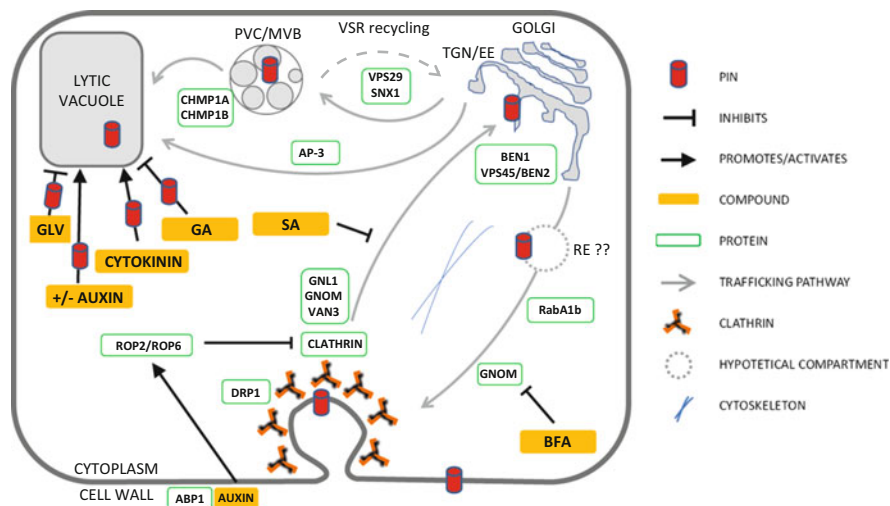


Fig. 8.1 Intracellular trafficking for polarization of PINs. Auxin, when extracellularly bound to ABP1, rapidly inhibits clathrin-mediated PIN endocytosis through mutually exclusive ROP2/ROP6 signaling. Formation of the PIN-containing, clathrin-coated vesicles, in case of cell plate formation, requires the function of DRP1. Internalization of cargo vesicles from the plasma membrane is mediated by Rab5 GTPase ARA7, ARF-GEFs GNOM, GNL1, and ARF-GAP VAN3, inhibited by SA and proceeds along cytoskeletal cell scaffold. Early endocytic trafficking of PINs requires function of VPS45 BEN2 and ARF-GEF BEN1. PIN recycling depends on RabA1b GTPase and GNOM, a target of BFA-mediated inhibition of exocytosis. PIN vacuolar targeting route passing through PVC/MVB includes the regulation by retromer complex components VPS29 and SNX1, as well as ESCRT components CHMP1A and CHMP1B. PVC/MVB-bypassing route for regulating vacuolar function is mediated by AP-3 complex. Cytokinin and long-term, above- or below-optimal auxin levels reduce the membrane abundance of PINs by promoting their turnover. In contrast, vacuolar targeting of PINs is inhibited by GA and GLV peptides

according to which PINs polarize (Heisler et al. 2010), but also provide guidance for vesicle trafficking (Voigt et al. 2005) (Fig. 8.1).

The functional significance of an energy-demanding process such as constitutive cycling still remains unclear. Evidently, this process provides the means for fast and de novo synthesis-independent repositioning of PIN auxin transporters, in response to internal and external cues. It, thus, allows developmental flexibility conditioned by rapid redirection of auxin fluxes within tissues (Michniewicz et al. 2007a; Vanneste and Friml 2009). Another, attractive scenario highlights a possible analogy between auxin efflux and neurotransmitter release. In this scenario, PIN transporters localized at the surface of constitutively cycling intracellular vesicles would mediate uptake of auxin from the cytosol into these vesicles and after their arrival and fusion with the PM, auxin would be released from the cell, similarly to the synaptic release of neurotransmitters (Friml and Palme 2002; Baluška et al. 2003). Such a hypothesis was to some extent supported by experiments based on auxin immunolocalization and manipulation of secretory pathway using phospholipase

D ζ 2 mutant (Schlicht et al. 2006; Mancuso et al. 2007). The validation of the ‘neurotransmitter’ hypothesis would provide a connection between the effect of established inhibitors of auxin transport on both vesicle trafficking and on PIN-dependent auxin transport (Geldner et al. 2001; Dhonukshe et al. 2008b). Finally, auxin transporters were proposed to have an additional function, similar to known, dual function receptor/transporters (Hertel 1983; Foti et al. 2004; Holler and Dikic 2004). In this scenario, endocytic cycling, analogously to the situation in animals, would serve as a way to transduce the signal and to regenerate receptors during ligand-dependent endocytosis. It is important to note that all the interpretations for functionality of constitutive cycling in the process of auxin transport are not mutually exclusive, but the latter two (‘neurotransmitter’ and transporter/receptor) remain rather speculative.

On the other hand, changes in PIN polarity have been observed in courses of many developmental processes including embryogenesis (Friml et al. 2003), organogenesis (Benková et al. 2003; Reinhardt et al. 2003), fruit development (Sorefan et al. 2009), vascular tissue formation and regeneration (Scarpella et al. 2006; Balla et al. 2011), as well as in response to light (Ding et al. 2011) or gravity (Kleine-Vehn et al. 2010; Rakusova et al. 2011). Such a dynamic translocation of polar cargos from one cell side to another via recycling endosomes is called transcytosis (Tuma and Hubbard 2003; Kleine-Vehn et al. 2008a, b) and it appears that plants evolved to utilize this mechanism to adjust their development in response to different cues via redirecting of PIN-dependent auxin fluxes.

2.2 *Early Endocytic Processes for PIN Polarization*

The first step of endocytic recycling is the internalization from the PM. The most prominent route of PIN internalization occurs through the creation of the membrane curvature from which upon scission the intracellular vesicle is formed, during clathrin-mediated endocytosis (CME) (Fig. 8.1). Clathrin is a self-assembling protein, recruited to the membranes where it contributes to membrane deformation and serves as a vesicular coat constituent (Chen et al. 2011). The fundamental role of CME in PIN trafficking and thus its essential contribution to generation of intrinsic polar localization of PINs is well characterized. It was demonstrated by pharmacological and genetic interference with the clathrin function (Dhonukshe et al. 2007; Kitakura et al. 2011). The notion that auxin efflux carriers from the PIN family are cargos of CME was further supported by identification of DYNAMIN-RELATED PROTEIN 1 (DRP1) as associated with PIN1 and important for its endocytosis (Fig. 8.1; Mravec et al. 2011). In plants, the precise function of the dynamin superfamily, represented among others by DRP1, is not well characterized. It is speculated that these proteins might regulate membrane dynamics by modulation of its scission and tubulation (Praefcke and McMahon 2004; Heymann and Hinshaw 2009). Importantly, proteins belonging to this family were previously implicated in plant CME (Konopka et al. 2008; Fujimoto et al. 2010) and

interference with DRP1 function results in altered distribution of PIN1 in dividing cells which eventually leads to a range of developmental phenotypes related to defective auxin transport (Mravec et al. 2011).

Interestingly, ARF-GEF GNOM, function of which is typically associated with recycling to the PM, was also implicated in the regulation of endocytosis, based on its partial localization at the PM and PIN endocytosis defects observed in *gnom* knock-down mutants (Fig. 8.1; Naramoto et al. 2010). In addition, another GBF subfamily member GNOM LIKE1 (GNL1) and ARF-GAP—VASCULAR NETWORK DEFECTIVE 3 (VAN3)—have been functionally associated with PM and endocytic processes, corroborating the notion that ARF GTPase machinery is involved in endocytosis (Fig. 8.1; Teh and Moore 2007; Naramoto et al. 2010).

Following internalization from the PM, the early endocytic trafficking of PINs has been shown to rely on the BFA-VISUALIZED ENDOCYTIC TRAFFICKING DEFECTIVE1/HOPM INTERACTOR7 (BEN1/MIN7/BIG5) ARF-GEF, belonging to BFA-inhibited guanine nucleotide exchange protein (BIG) subfamily (Fig. 8.1; Tanaka et al. 2009). PIN internalization is regulated also by Rab5/ARA7, a member of Rab GTPase family (Fig. 8.1; Dhonukshe et al. 2008a) and an universal component of membrane fusion in eukaryotes—VACUOLAR PROTEIN SORTING45 (VPS45/BEN2) (Fig. 8.1; Tanaka et al. 2013). Genetic interference with all aforementioned components regulating endocytosis or early endocytic trafficking leads, besides perturbations in PIN trafficking and polarity, to significant developmental aberrations like embryogenesis and organogenesis defects, reduced growth and apical dominance, leaf venation pattern discontinuity, and root meristem disorganization. These observation links early endocytic processes to PIN polarity and auxin-mediated development.

2.3 Late Endocytic Trafficking for PIN Abundance at the Cell Surface

Certain proportion of internalized PINs, based on signals which are not fully understood, is targeted for the late endocytic pathway. This mode of transport originates generally at EE/TGN, where proteins are sorted, proceeds through late endosomes (LE), prevacuolar compartments/multivesicular bodies (PVC/MVB) and terminates at the final destination of membrane proteins—the lytic vacuole. This subcellular route eventually results with protein degradation. Vacuolar targeting defines additional mechanism, by which polar localization of PINs and specifically the aspect of their membrane abundance can be controlled (Müller et al. 2007; Scheuring et al. 2011). As mentioned above, plant trafficking machinery encompasses multiple bypassing, often unidirectional transport routes. Accordingly, PINs can be retrieved from late endocytic pathway and thus avoid degradation. This is accomplished by the Retromer Complex (RC) capacity for retrieval of certain trafficking components like VACUOLAR SORTING RECEPTORS (VSR)

from PVC to EE/TGN (Arighi et al. 2004; Seaman 2005). Both the core component of this complex—VACUOLAR PROTEIN SORTING29 (VPS29) and its prominent interactor—SORTIN NEXIN1 (SNX1) were shown to control the rate of PINs progression toward the vacuole (Fig. 8.1; Kleine-Vehn et al. 2008c; Nodzyński et al. 2013). Such a mechanism is in agreement with widely accepted and evolutionary conserved function of RC (Arighi et al. 2004; Seaman 2005; Shimada et al. 2006). Notably, a more unorthodox function, related more directly to PIN polarity, has been also proposed for RC at the level of early endocytic recycling (Jaillais et al. 2006, 2007).

The significance of the final steps during late endocytic trafficking of PIN proteins for their polar localization and abundance is not to be underestimated. The endosomal-sorting complexes required for transport (ESCRT) machinery, controlling the formation of internal vesicles within PVC/MVB, which upon fusion are released into vacuolar lumen, appears to play important role for PIN polarization (Winter and Hauser 2006; Wollert et al. 2009; Scheuring et al. 2011). Interfering with the function of CHARGED MULTIVESICULAR BODY PROTEIN/CHROMATIN MODIFYING PROTEIN 1A and 1B (CHMP1A/CHMP1B), components of ESCRT machinery, leads to severe developmental defects including seedling lethality. These phenotypes were associated with inaccurately generated auxin distribution correlated with the ectopic (PVC/MVB and vacuolar membranes) PIN localization (Fig. 8.1; Spitzer et al. 2009). Also an alternative, PVC-bypassing, late endocytic pathway, dependent on the ADAPTOR PROTEIN (AP) Complex 3 subunits β and δ , generally regulates vacuolar function and thus PIN degradation rate, although it does not affect PIN polarity or abundance at the PM (Fig. 8.1; Feraru et al. 2010; Zwiewka et al. 2011).

3 Where to Go and Why to Stay? Cues and Cellular Requirements for Pin Polarity

3.1 *Cargo-Based Determinants for Polar PIN Localization*

One of the most important initial findings concerning the determination of PIN polarity was derived from the ectopic PIN expression in particular cell types. The PIN2 promoter-driven expression of PIN1 targeted this protein predominantly to the basal side of root epidermal cells contrasting to the native apical PIN2 localization in the same cells. Consecutive introduction of the fluorescent tag into certain place within central hydrophilic loop of PIN1 was sufficient to cause basal-to-apical switch in PIN1 localization. This was a clear indication that some determinants of polar PIN localization are encoded intrinsically in PIN amino acid sequence (Wiśniewska et al. 2006). This sequence-based instruction turned out to be the phosphorylation status of specific serine residues located within PIN central hydrophilic loop (Huang et al. 2010; Zhang et al. 2010). Current model postulates that

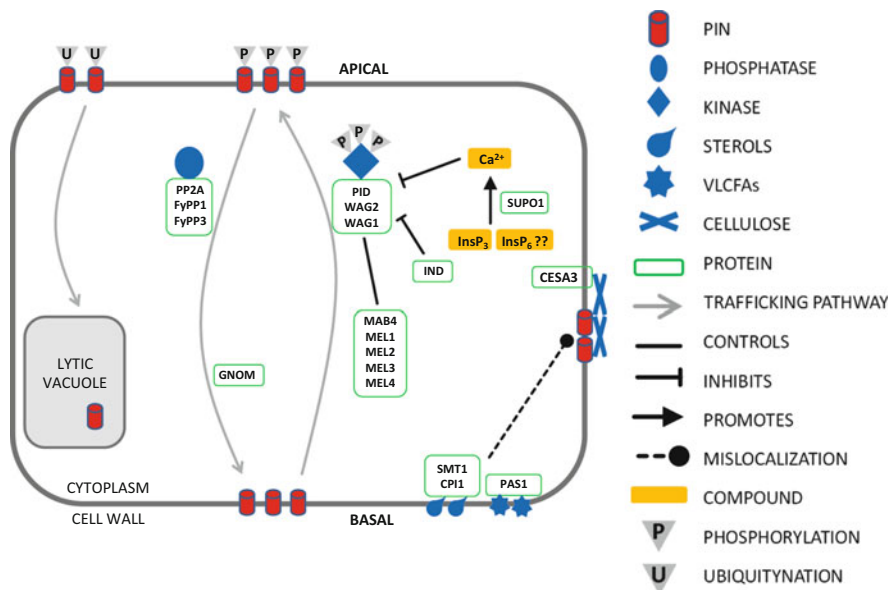


Fig. 8.2 Posttranslational modifications and cellular requirements for polarization of PINs. PINs dephosphorylated by PP2A, FyPP1, or FyPP3 phosphatases are preferentially recruited to the basal, GNOM-dependent, BFA-sensitive pathway, whereas phosphorylation by PID, WAG1, or WAG2 kinases targets PINs into apical cell site independently of GNOM function. The transcription of PID kinase is controlled by IND transcription factor. The activity of the kinases is influenced also by MAB4, its homologs MELs and by InsP_3 (or alternatively InsP_6) that regulate cellular Ca^{2+} levels with the assistance of SUPO1. The polar localization of PINs depends on the sterol and VLCFA composition of the membrane controlled by SMT1, CPI1, and PAS1, respectively. Membrane abundance of PINs, regulated by their vacuolar targeting, depends on the ubiquitination status of the protein. Cellulose content of the cell wall regulated by CESA3 contributes to the maintenance of PIN polarity

dephosphorylated PINs are preferentially recruited to the basal, GNOM-dependent and BFA-sensitive pathway, whereas phosphorylation targets PINs into the apical cell side, independently of GNOM function (Fig. 8.2; Friml et al. 2004; Michniewicz et al. 2007b; Kleine-Vehn et al. 2009).

Readjustments of PIN phosphorylation status rely on the antagonistic activity of protein kinases and phosphatases. AGC3 protein kinases PINOID (PID) and its homologs WAVY ROOT GROWTH1/2 (WAG1/WAG2) (Benjamins et al. 2001; Friml et al. 2004; Santner and Watson 2006; Dhonukshe et al. 2010) phosphorylate, while PROTEIN PHOSPHATASE2A (PP2A) (Muday and DeLong 2001; Michniewicz et al. 2007b; Ballesteros et al. 2013) dephosphorylate PINs (Fig. 8.2). Along with PID and WAG proteins, also other kinases such as D6 protein kinase (Zourelidou et al. 2009) or CDPK-RELATED KINASE5 (Rigó et al. 2013) can phosphorylate PIN proteins and regulate their function, but their exact role is less clear. On the other hand, phosphatase subunit PP2AA interacts with another Ser/Thr protein phosphatase, FyPP1, to form functional holoenzyme. FyPP1 and its

close homolog FyPP3 were reported to interact with and directly dephosphorylate PINs (Fig. 8.2; Dai et al. 2012). Importantly, fluctuations of PIN phosphorylation status both above and below certain native threshold lead eventually to severe developmental aberrations like defective embryogenesis and patterning of shoot apical meristem and root (Christensen et al. 2000; Benjamins et al. 2001; Friml et al. 2004; Michniewicz et al. 2007b; Dhonukshe et al. 2010; Li et al. 2011; Dai et al. 2012).

Given the crucial role of PID-mediated PIN phosphorylation in PIN polarity, it is important to highlight that the regulation of PID activity, on various levels, has also impact on polar PIN localization and thus on auxin fluxes. Calcium (Ca^{2+}), which is one of the most ubiquitous secondary messengers in eukaryotes, appears to be the prominent part of such a system for the regulation of PID kinase activity (Fig. 8.2). Early experiments in animal and yeast systems have associated the appearance of cytosolic Ca^{2+} with the phospholipase C (PLC)-generated inositol trisphosphate (InsP_3). PLC signaling is known to be important for various biological processes including cell division and differentiation (Michell 2008). The plant field has followed this paradigm upon an observation that InsP_3 is able to trigger the release of Ca^{2+} from the cellular storage compartments (Blatt et al. 1990; Gilroy et al. 1990; Krinke et al. 2007; Tang et al. 2007). Controversially, up to date no unambiguous InsP_3 -activated Ca^{2+} channel could be identified in plants (Testerink and Munnik 2011). Interestingly, there are indications that InsP_6 can function as a signaling molecule, triggering Ca^{2+} release with a much higher potency than InsP_3 (Lemtiri-Chlieh et al. 2003). Moreover, InsP_3 when microinjected into plant can be rapidly converted into InsP_6 (Munnik and Testerink 2009), explaining the earlier observations of InsP_3 being able to release Ca^{2+} . PID kinase was shown to be regulated by both phospholipid and Ca^{2+} signaling. Some PID interactors bind Ca^{2+} (Benjamins et al. 2003; Zegzouti et al. 2006). Moreover, *suppressor of PIN1 overexpression-1* (*supo-1*) mutant encoding ALTERED EXPRESSION OF APX2 8/FIERY1/HIGH EXPRESSION OF OSMOTICALLY RESPONSIVE GENES2/ROTUNDA1 (ALX8/FRY1/HOS2/RON1/SAL1) inositol polyphosphate 1-phosphatase also with 3'(2'),5'-bisphosphate nucleotidase activity exhibits aberrant PIN polarization presumably as a result of changed PID activity. It was proposed that this effect is a result of altered content of cytosolic Ca^{2+} in a mutant due to disturbed InsP_3 metabolism (Fig. 8.2; Zhang et al. 2011a). Although in light of recent findings, an alternative explanation, in which InsP_6 would be the signal activating Ca^{2+} cascade, seems more plausible (Munnik and Nielsen 2011).

Another mode of PID activity regulation applies to its transcription. INDEHISCENT (IND), a basic helix–loop–helix transcription factor through negative regulation of PID and WAG2 expression influences polar localization of PIN1 and PIN3 proteins (Fig. 8.2). Interestingly, in this case local auxin minimum, which is required for valve margin formation in *Arabidopsis* fruit, is not properly established. Consequently, abnormal fruits which fail to open and thus do not disperse seeds are observed in *ind* mutant (Sorefan et al. 2009). Another regulator of PID activity is ENHANCER OF PINOID/MACCHI-BOU4 (ENP/MAB4) (Trembl et al. 2005; Furutani et al. 2007) and its close homologs MAB4/ENP/

NPY1-LIKEs (MEL1, MEL2, MEL3, and MEL4) that are known to influence polar PIN localization (Fig. 8.2; Furutani et al. 2011). MAB4 encodes NON-PHOTOTROPIC HYPOCOTYL3-like (NPH3)-like protein, which associates with light activated kinase PHOTOTROPIN1 (PHOT1), a blue-light receptor (Motchoulski and Liscum 1999). NPH3 has been shown to modulate PIN2 trafficking in root phototropism (Wan et al. 2012).

Regulation of PID activity provides also an entry point for various external signals, such as light or gravity, to which plants are able to dynamically respond by modulation of their growth. For example, during hypocotyl gravitropic response, PIN3 and PIN7 polarize to the bottom side of gravity-sensing endodermal cells and mediate the differential auxin accumulation at the lower side of hypocotyl for asymmetric bending and growth (Rakusova et al. 2011). Accordingly, blue-light-dependent signaling cascade causes polarization of PIN3 away from the light during phototropic response in hypocotyl endodermal cells. This coincides with an establishment of auxin maximum at the shaded side of an organ (Ding et al. 2011). Importantly, in both cases PIN repolarization is initiated by differential recruitment into GNOM-mediated trafficking pathway and depends on the PID-mediated phosphorylation status of the PIN protein (Ding et al. 2011; Rakusova et al. 2011).

Beside PIN phosphorylation, another posttranslational protein modification appears to be instructive for PIN localization. The destabilization of PINs from the PM and their sorting for vacuolar delivery was associated with the linking of the polyubiquitin chains to specific lysine residues within PIN2 central hydrophilic loop (Fig. 8.2; Leitner et al. 2012). Moreover, PIN2 degradation was shown to be dependent on the 26S proteasome, the universal proteolysis complex of eukaryotic organisms, which targets ubiquitinated, typically soluble proteins (Sieberer et al. 2000; Abas et al. 2006). Although recent data clearly show that ubiquitination is a crucial part of PIN abundance control (Abas et al. 2006; Leitner et al. 2012), it remains unclear how proteasome activity can contribute to the degradation of PM proteins such as PINs, which were shown to be targeted to the lytic vacuoles (Kleine-Vehn et al. 2008c; Laxmi et al. 2008; Shirakawa et al. 2009; Marhavý et al. 2011; Baster et al. 2013).

3.2 *Cell Structural Determinants of PIN Polarity Maintenance*

The cues and mechanisms described in the previous paragraph dealt mainly with targeting of PINs to their respective polar domains but not with their maintenance there. As mentioned before, crucial polarity trafficking components as well as ‘tight junctions’, which in animals limit migration of the surface proteins between polar domains of epithelial cells, are absent in the plant kingdom. On the other hand, plant cells are surrounded by cell wall, a structure absent in animal cells. It appears that in

order to preserve abundance and asymmetry of proteins within fluid PM, in comparison to animals, plants developed both overlapping and alternative mechanisms. The migration of transmembrane proteins within the lipid bilayer can serve as an example of polarity regulation mechanism which is common for plants and animals. Interestingly, certain fraction of membrane localized PINs, as reported previously, appears to be surprisingly stagnant (Dhonukshe et al. 2008a; Men et al. 2008; Kleine-Vehn et al. 2011). This phenomenon was proposed to be linked with processes that actually immobilize this fraction of PINs within specific structures at the PM, called clusters, which have been detected by super-resolution microscopy approaches (Kleine-Vehn et al. 2011). The nature of these highly immobile structures is not entirely clear; however, their appearance might be related to specific sterol and lipid composition of the PM (Kleine-Vehn et al. 2011; Men et al. 2008; Roudier et al. 2010; Carland et al. 2010; Martinière et al. 2012). In fact, the *sterol methyl transferase 1 (smt1)* mutant, function of which is required for appropriate synthesis and composition of major membrane sterols (Diener et al. 2000), is characterized by defective polar auxin transport correlating with mislocalization of PIN1 and PIN3 proteins (Fig. 8.2; Willemsen et al. 2003). Similarly, the improper reestablishment of PIN2 polarity following cytokinesis as a consequence of defective PIN2 endocytosis was reported for sterol biosynthesis, *cyclopropylsterol isomerase1-1 (cpi1-1)* mutant (Fig. 8.2; Men et al. 2008). The involvement of sterols in polar distribution of PIN proteins is additionally supported by the fact that the internalized PIN2 co-localizes with the sterol marker filipin and a prolonged disruption of membrane sterols by filipin treatments reduces the heterogeneity and polar localization of PIN2 in the PM (Grebe et al. 2003; Kleine-Vehn et al. 2006, 2011).

Apart from sterols, some other molecular components that physically scaffold structure of the membrane appear very important for maintaining PIN polarity. Sphingolipids, membrane constituents and signaling molecules (Dickson et al. 2006), were shown to influence cell polarity (Hoekstra et al. 2003; Nyasae et al. 2003). The immunophilin-like protein PASSTICINO1 (PAS1) (Bach et al. 2008; Roudier et al. 2010) is involved in the biosynthesis and metabolism of very-long-chain fatty acids (VLCFAs), one of the composites of sphingolipids. In case of *pas1* mutant, patterning defects at the cellular level were attributed to altered auxin distribution during key events in plant life. Disturbed formation of auxin gradients was associated with abnormal PM distribution of PIN1 protein due to defective VLCFA synthesis (Fig. 8.2; Roudier et al. 2010). Additionally, PIN1 abundance in its polar domain was shown to be stabilized by interaction with PGP1/PGP19 ABCB transporters (Titapiwatanakun et al. 2009). Notably, the efflux activity of these ABCB transporters at the PM is positively regulated by PID, most likely through direct phosphorylation. In this case, another immunophilin—TWISTED DWARF (TWD) by interaction with PID appears to decrease ABCB activity at the cell surface (Bouchard et al. 2006; Henrichs et al. 2012; Wang et al. 2012, 2013).

Finally, recent reports suggest that not only structure of the PM but also the integrity of the cell wall is required for maintenance of PIN polarity. Such a notion

was suggested upon characterization of *regulator of PIN polarity3* (*repp3*) mutant (Feraru et al. 2011), exhibiting defects in localization of ectopically expressed PIN1. The mutation responsible for *repp* mutant phenotype was found in the gene coding for CELLULOSE SYNTHASE CATALYTIC SUBUNIT3/CONSTITUTIVE EXPRESSION OF VSP1/ISOXABEN RESISTANT1/ECTOPIC LIGNIN1 (CESA3/CEV1/IXR1/ELI1). CESA3 is a part of the enzymatic complex required for synthesis of 1,4 glucans, molecules which are able to associate to form cellulose microfibrils and thus scaffold cell wall (Fig. 8.2; Richmond and Somerville 2000; Ellis and Turner 2001; Scheible et al. 2001; Caño-Delgado et al. 2003; Desprez et al. 2007). Additionally, pharmacologically induced cell wall degradation or inhibition of the cell wall biosynthesis resulted in similar phenotypes as in case of *repp3* mutant. Interestingly, plasmolysis-based experiments forcing detachment of the polar domain from the cell wall suggested that the mechanisms immobilizing PIN-containing PM clusters might relate to cellulose-based connections between the polar domain and the cell wall (Feraru et al. 2011; Martinière et al. 2012).

4 Transport in Loops: Hormonal Feedback Regulations of PIN Polarity

4.1 Auxin Feedback on PIN-Dependent Auxin Transport

Polar distribution of PIN auxin transporters can be regulated through plethora of controlling mechanisms with various molecular players involved. Intriguingly, another layer of complexity for auxin-driven plant development emerges from the self-organizing abilities of auxin transport. Already early experiments implied that auxin-induced changes could instruct capacity and directionality of auxin flow and thus auxin would have the ability to shape its own transport (Sachs 1981, 1991). Indeed, the effect of auxin on PIN amounts and PIN localization and thus existence of multiple feedback mechanisms at various levels has been validated experimentally. One of such mechanisms is a well-characterized nucleus-based SCF^{TIR1/AFB}-dependent auxin signaling (Dharmasiri and Estelle 2004; Dharmasiri et al. 2005a, b; Kepinski and Leyser 2005; Chapman and Estelle 2009), involved in the regulation of PIN transcription (Peer et al. 2004; Vieten et al. 2005; Heisler et al. 2005; Scarpella et al. 2006). SCF^{TIR1/AFB}-dependent auxin signaling appears to have a double role in transport feedback, controlling both PIN transcription and abundance at the PM by promoting, upon prolonged auxin exposure, PIN vacuolar targeting for degradation (Baster et al. 2013). The gravitropic response of the roots serve as an example of the process facilitated by such a dual mechanism in which fluctuations of auxin above or below certain physiological threshold through (SCF^{TIR1/AFB})-dependent signaling mediate PIN degradation (Fig. 8.1; Abas et al. 2006; Kleine-Vehn et al. 2008c; Baster et al. 2013). In addition, this transcriptional signaling is

also required to feedback on PIN polarity and thus directionality of auxin transport in both root- and shoot-based model systems (Sauer et al. 2006; Balla et al. 2011).

The auxin feedback loop which has recently drawn considerable amount of attention, due to its proposed contribution to the polarization of auxin transporters, is the non-transcriptional auxin effect on PIN endocytosis. Indeed auxin, rapidly upon application, inhibits PIN internalization and promotes the retention of PINs at the PM correlating with increased auxin efflux capacity (Paciorek et al. 2005). Although the mechanism is still largely elusive, it was proposed that auxin, when extracellularly bound to AUXIN-BINDING PROTEIN1 (ABP1), executes this inhibitory function through dynamic activation of mutually exclusive RHO OF PLANTS2 and 6 (ROP2/ROP6) pathways downstream of ABP1 (Fig. 8.1). This mechanism is functionally important in developmental processes like patterning of the leaf epidermis or root gravitropism (Robert et al. 2010; Xu et al. 2010; Nagawa et al. 2012; Chen et al. 2012; Lin et al. 2012).

Additional complexity of the system, which depends on auxin-mediated feedback and regulates plant development, emerges from the fact that some of its elements are interconnected. For example CME, activity of which was shown to be nonuniform throughout the root meristem, directly influences auxin-responsive gene expression. Such a mechanism is based on the positive autoregulatory feedback mediated by BREVIS RADIX (BRX). This plant-specific transcription factor, through auxin-regulated PM-to-nucleus transfer and subsequent transcriptional activation of certain auxin response factor targets, controls the cell elongation and proliferation in the root tip. Therefore, the differential pattern of endocytosis splits the transcriptional auxin signaling within the root meristem and might thus provide additional positional information to interpret auxin gradients (Mouchel et al. 2004; Santuari et al. 2011).

Notably, the experimental approaches aiming to explain the principles of auxin feedback-mediated plant development are more and more prominently supported by computational models. For example, recently proposed 'extracellular receptor-based polarization' (ERP) model integrates transcription-based intracellular feedback mechanisms with a competitive utilization of auxin receptors in the cell exterior for the spatial regulation of PIN internalization (Wabnik et al. 2010, 2011). Given the fact that during various developmental processes, PINs can behave differentially, polarizing either toward or away from the auxin source (Grieneisen et al. 2007; Blilou et al. 2005; Benjamins and Scheres 2008; Kleine-Vehn et al. 2008b), it is worth mentioning that ERP model proposes mechanistic principles explaining these contrasting self-organizing properties of auxin transport (Wabnik et al. 2010, 2011). However, it remains to be seen whether this largely theoretical model corresponds to the biological reality. This question will be solved only after the molecular mechanism underlying the polarization of PINs and auxin transport will be elucidated.

4.2 Other Hormonal Regulations of PIN-Dependent Auxin Transport

It seems that not only auxin can shape the capacity and directionality of its transport. Other hormones, by influencing the PM stability of PIN auxin transporters, can be also integrated into the PIN-dependent auxin distribution network. Most of the plant hormones have been shown to regulate transcription of numerous genes downstream of their corresponding signaling pathways, thus many of them directly or indirectly influence also the transcription of *PIN* genes. Such an effect is well characterized in case of cytokinin and ethylene, both of which have also multiple developmental functions (Swarup et al. 2007; Růžička et al. 2007, 2009; Dello Ioio et al. 2008; Zhang et al. 2011b; Bishopp et al. 2011; Liu et al. 2013).

Other hormones prominently modulate PIN activity by posttranscriptional regulation. For example, a stabilization of PINs at the PM by interference with their endocytosis was observed when plants were subjected to pharmacologically or genetically induced accumulation of the plant hormone salicylic acid (SA) (Fig. 8.1; Du et al. 2013). In contrast, gibberellic acid (GA) deficiency, observed in GA biosynthesis mutants, promotes degradation of PIN proteins, whereas treatment with GA increases PIN protein stability by inhibiting PIN vacuolar trafficking. This mechanism appears to be important for correct gravitropic response of the root (Fig. 8.1; Willige et al. 2011; Löffke et al. 2013). The stabilization of PIN2 at the membrane resulting in the perturbations in root gravitropism could be also observed in both *Arabidopsis* plants overexpressing *GOLVEN* (*GLV*) genes encoding for small secretory peptides of ROOT GROWTH FACTOR (RGF) family as well as upon exogenous applications of such compounds (Fig. 8.1; Matsuzaki et al. 2010; Whitford et al. 2012). In contrast to these stabilizing effects, cytokinin promotes vacuolar trafficking of PINs thus destabilizing them from the PM. Functionality of this mechanism was demonstrated during lateral root organogenesis (Fig. 8.1; Marhavý et al. 2011). These frequent observations on the effects of various signaling pathways converging at the regulation of PIN-dependent auxin distribution network are in line with the model that PIN-mediated asymmetric auxin distribution functions as a versatile mechanism integrating multiple internal and external signals (Vanneste and Friml 2009).

5 Conclusions and Perspectives

In recent years, there has been a significant advance achieved in our understanding of the basic rules governing generation, maintenance, and refining of the cellular polarity in plants. It becomes clear how polar protein localization at the subcellular scale can underpin basic functionality of an organism and instruct its development. In particular, the studying of asymmetric distribution displayed by PIN auxin transporters allowed us to deepen the knowledge about polarity. At the same

time, it provided excellent means to comprehend auxin transport machinery and its contribution, by establishment of asymmetric auxin distribution, to the regulation of various developmental processes. An important open question remains: to which extent cellular mechanisms and molecular components of the PIN polar targeting machinery can be translated into proteins localized at different polar domains in plants. Another important aspect is the evolution of auxin transport machinery and thus mechanisms governing polarity generation in more ancient plant species. For this, the examination of evolutionary older than Angiosperms plant species like moss or algae, which is rapidly gaining popularity in the plant field, will hopefully significantly contribute to our understanding of the polarity phenomenon in the close future.

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