Differential Effects of Prenylation and S-Acylation on Type I and II ROPS Membrane Interaction and Function\textsuperscript{1,W,OA}

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Prenylation primarily by geranylgeranylation is required for membrane attachment and function of type I Rho of Plants (ROPs) and Gy proteins, while type II ROPs are attached to the plasma membrane by S-acylation. Yet, it is not known how prenylation affects ROP membrane interaction dynamics and what are the functional redundancy and specificity of type I and type II ROPs. Here, we have used the expression of ROPs in mammalian cells together with geranylgeranylation and CaaX prenylation-deficient mutants to answer these questions. Our results show that the mechanism of type II ROP S-acylation and membrane attachment is unique to plants and likely responsible for the viability of plants in the absence of CaaX prenylation activity. The prenylation of ROPs determines their steady-state distribution between the plasma membrane and the cytosol but has little effect on membrane interaction dynamics. In addition, the prenyl group type has only minor effects on ROP function. Phenotypic analysis of the CaaX prenylation-deficient pluripetala mutant epidermal cells revealed that type I ROPs affect cell structure primarily on the adaxial side, while type II ROPs are functional and induce a novel cell division phenotype in this genetic background. Taken together, our studies show how prenyl and S-acyl lipid modifications affect ROP subcellular distribution, membrane interaction dynamics, and function.

Protein prenylation involves the covalent attachment of the C15 and C20 isoprenoids farnesylphosphate (FFP) and geranylgeranyldiphosphate (GGPP) to Cys residues in the C-terminal CaaX box or in C-terminal double Cys motifs of Rab small G proteins. Prenylation is required for membrane targeting and function of diverse protein groups, many of which have key regulatory functions (Maurer-Stroh et al., 2003, 2007; Magee and Seabra, 2005; Crowell and Huizinga, 2009; Sorek et al., 2009). Prenylation of CaaX box proteins is catalyzed by two distinct prenyltransferases: protein farnesyltransferase (PFT) and protein geranylgeranyltransferase-I (PGGT-I; Maurer-Stroh et al., 2003). PFT and PGGT-I are heterodimeric proteins composed of a common \(\alpha\)-subunit and distinct substrate-specific \(\beta\)-subunits (Maurer-Stroh et al., 2003). Both PFT and PGGT-I are conserved in plants (Yalovsky et al., 1997; Caldelari et al., 2001). PFT and PGGT-I recognize a conserved C-terminal sequence known as the CaaX box, in which C is a Cys, a usually represents an aliphatic amino acid, and X is usually Ser, Met, Cys, Ala, Gln, or Leu. If X is a Leu, the protein is geranylgeranylated by PGGT-I. If X is another amino acid, the protein is preferentially farnesylated by PFT (Reiss et al., 1991; Seabra et al., 1991; Maurer-Stroh et al., 2003; Reid et al., 2004). The presence of an Arg/Lys-rich polybasic domain proximal to the CaaX box greatly increases substrate affinity of PGGT-I (James et al., 1995; Caldelari et al., 2001). PFT and PGGT-I recognize a conserved C-terminal sequence known as the CaaX box, in which C is a Cys, a usually represents an aliphatic amino acid, and X is usually Ser, Met, Cys, Ala, Gln, or Leu. If X is a Leu, the protein is geranylgeranylated by PGGT-I. If X is another amino acid, the protein is preferentially farnesylated by PFT (Reiss et al., 1991; Seabra et al., 1991; Maurer-Stroh et al., 2003; Reid et al., 2004). The presence of an Arg/Lys-rich polybasic domain proximal to the CaaX box greatly increases substrate affinity of PGGT-I (James et al., 1995; Caldelari et al., 2001).
Reid et al., 2004). PFT can prenylate most PGGT-I substrates but cannot use GGPP as a prenyl group donor (Reid et al., 2004). Mutations in the PGGT-I β-subunit gene (Cdc43/Calc) are lethal in the budding yeast Saccharomyces cerevisiae (Trueblood et al., 1993). Knockout of the PGGT-I β-subunit gene in mouse leads to inhibition of K-Ras-induced cell proliferation and inhibition of lung tumor formation. Surprisingly, leads to inhibition of K-Ras-induced cell proliferation and inhibition of lung tumor formation. Surprisingly, some mouse pggt-I mutants also show increased drought tolerance due to enhanced stomatal closure (Cutler et al., 1996; Pei et al., 1998; Allen et al., 2002). Corresponding to the mild phenotype of era1 (Pei et al., 2000), the shared PFT and PGGT-I α-subunit mutant, plants display severe growth and developmental alterations characterized by even more pronounced SAM expansion compared with era1, strongly retarded growth rate, and almost complete sterility (Running et al., 1998; Bonetta et al., 2000; Yalovsky et al., 2000; Ziegelhoffer et al., 2000; Fowler, 2010). The normal-looking pavement cells, root hairs, and fertility of pggt-1b mutant plants suggested that when ROPs are farnesylated (ROPs-F) instead of geranylgeranylated (ROPs-GG), their activity is not affected much, and their interaction dynamics with the plasma membrane, the mild phenotype of era1 pggt-1b double mutants are likewise inseparable from plp (Johnson et al., 2005). Corresponding to the mild phenotype of pggt-1b, only a minor mislocalization of the Gγ-subunit AGG1 was observed in the pggt-1b background, while plp mutant plants showed accumulation of AGG1 in the soluble fraction (Zeng et al., 2007). Taken together, these data suggested that in Arabidopsis, PFT function could almost fully compensate for the loss of PGGT-I activity. However, it remained to be demonstrated that PGGT-I substrate proteins are indeed only farnesylated in the pggt-1b background.

Rho of Plants (ROPs)/RACs are implicated in the regulation of diverse signaling cascades (Nibau et al., 2006; Yalovsky et al., 2008; Yang, 2008). For clarity, the ROP nomenclature will be used in this work. ROPs have been subdivided into two major subgroups designated type I and type II based on the amino acid sequences of their C-terminal hypervariable domains (Winge et al., 1997) and into three clades based on their nucleotide sequences (Fowler, 2010). Whereas type I ROPs terminate with a canonical prenylation CaaL box motif and are prenylated by PGGT-I, type II ROPs do not have a functional CaaX box prenylation motif and instead contain a plant-specific motif called the GC-CG box and are only S-acylated (Lavy et al., 2002; Lavy and Yalovsky, 2006; Sorek et al., 2007, 2009). An unrooted phylogram of 150 ROP coding sequences shows that type I ROP genes are divided into two clades, designated clades I and 3, whereas type II ROP genes constitute a single clade, designated clade 2 (Fowler, 2010). Clade 1 includes all four moss (Physcomitrella patens) and two lycophyte (Selaginella moellendorfii) ROP genes and is represented in Arabidopsis by AtROP7 and AtROP8. Clade 3 includes most well-studied type I ROPs, namely AtROP1, AtROP2, AtROP4, and AtROP6, and also AtROP3 and AtROP5. In Arabidopsis, clade 2 is presented by AtROP9, AtROP10, and AtROP11 (Fowler, 2010). For clarity, given the focus of this study on the differential effects of C-terminal prenylation and S-acylation on ROP function, we will mostly refer to the division of ROPs into type I and type II based on their amino acid sequences.

Recently, we demonstrated that the Arabidopsis type I ROP, AtROP6 (ROP6), is transiently S-acylated on two G-domain Cys residues and that S-acylation affects membrane dynamics and function in the regulation of cell polarity (Sorek et al., 2010). The two S-acylated Cys residues are highly conserved; therefore, it is likely that other ROPs undergo similar activation-dependent S-acylation. The type I ROPs ROP2, ROP4, and ROP6 have been implicated in the regulation of pavement cell growth (Fu et al., 2002, 2005; Yang, 2008). ROP2 is also involved in root hair growth (Jones, 2002). ROP1, ROP3, and ROP5 are pollen specific, and the function of ROP1 in the regulation of pollen tube elongation has been studied in great detail (Yang and Fu, 2007; Yang, 2008). The normal-looking pavement cells, root hairs, and fertility of pggt-1b mutant plants suggested that when ROPs are farnesylated (ROPs-F) instead of geranylgeranylated (ROPs-GG), their activity is not affected much, if at all. Since ROPs function primarily at the plasma membrane, the mild phenotype of pggt-1b mutants suggests that subcellular distribution of ROPs-GG and ROPs-F could be similar. Alternatively, if similar to AGG1, a greater fraction of ROPs accumulates in the soluble fraction of the pggt-1b mutant relative to wild-type plants, and the question arises whether the type of prenyl group affects the steady-state protein distribution between the plasma membrane and cytoplasm or the interaction dynamics with the plasma membrane. We have recently shown that the transient S-acylation of the G-domain affects the stability of ROPs association with the plasma membrane and its partitioning into lipid rafts but not the steady-state distribution of the protein between the membrane and cytoplasm (Sorek et al., 2010). Hence, the contribution of prenylation and S-acylation to ROP function could be examined by studying ROP subcellular distribution, prenylation and S-acylation status, the resulting alterations in plasma membrane interaction dynamics, and the effects on cell polarity in both wild-type and pggt-1b mutant plants.

Because type II ROPs are attached to the plasma membrane by S-acylation of hypervariable domain...
GC-CG box Cys residues (Lavy et al., 2002; Lavy and Yalovsky, 2006), their function should not be compromised in the CaaX prenylation-deficient mutant \textit{plp} and they might be responsible for the viability of this mutant. In yeast, ROP10 remained in the soluble fraction, while ROP9 was recruited to the plasma membrane and endomembrane by a farnesylation-dependent mechanism (Lavy et al., 2002), suggesting that the \textit{S}-acylation mechanism of these proteins is plant specific. Thus, plants likely represent a special case where recruitment of some Rho GTPases to the plasma membrane takes place by a prenylation-independent mechanism. Previously, we showed that \textit{plp} abaxial epidermis pavement cells have smaller lobes (Running et al., 2004), likely due to absent or only residual type I ROP function. The existence of lobes in the cells, however, indicates that cell polarity is maintained by other factors, possibly a redundant function of type II ROPs. The viability of the \textit{plp} mutant plants provided us with an unprecedented opportunity to examine the redundancy and specificity of type I and type II ROP function in Arabidopsis.

In this study, we examined the specificity of type II ROP membrane attachment to plants by expressing type I and type II ROPs in mammalian cells and examining their localization and function. To explore the cross-specificity between PFT and PGGT-I, we directly analyzed the in vivo subcellular distribution and lipid modifications in wild-type PGGT-IB and \textit{pggt-Ib} mutant plants of two protein substrates of PGGT-I: AGG1 (Zeng et al., 2007) and ROP6 (Sorek et al., 2007). To further define the function of prenylation and C-terminal \textit{S}-acylation in ROP function, we examined the adaxial and abaxial pavement cell morphology in \textit{plp} and the subcellular localization and function of the type II ROP AtROP11 in \textit{plp}. We found how the type of prenyl lipid moiety affects the steady-state and membrane interaction dynamics of ROP6 and its function in the regulation of cell polarity as well as the specificity and redundancy between type I and type II ROPs.

RESULTS

Expression of Type I and Type II ROPs in Mammalian Cells

A representative from either subgroup of ROPs was expressed in NIH3T3 mammalian cells to examine the specificity of type II ROP C-terminal \textit{S}-acylation to plants and the functional conservation of type I ROPs. Both the wild-type GFP-ROP6 and its constitutively active form GFP-rop6\textsuperscript{CA} were localized in the plasma membrane (Fig. 1, A and B). In the plasma membrane, GFP-rop6\textsuperscript{CA} was associated with lamellipodia enriched with phaloidine-labeled actin (Fig. 1, E–G, arrowheads in G). Interestingly, GFP-rop6\textsuperscript{CA} induced intercellular cell junctions in these fibroblast cells, where it was found to colocalize with \textit{β}-catenin, a marker of cell-cell junctions (Fig. 1, H–J; note the yellow label in J, which corresponds to the colocalized proteins). Similar to activated mammalian Rac proteins, GFP-rop6\textsuperscript{CA} induced the formation of membrane ruffles (Fig. 1H, arrowheads; Supplemental Movie S1). In contrast to GFP-ROP6 and GFP-rop6\textsuperscript{CA}, the dominant negative mutant GFP-rop6\textsuperscript{DN} accumulated in aggregates inside the cells and was not detected at the plasma membrane (Fig. 1C). Different from either form of ROP6, the type II ROP, GFP-ROP9, was dispersed throughout the cytoplasm. Taken together, the data presented in Figure 1 indicated that ROP6 was recruited to the plasma membrane by prenylation and was able to interact with Rac effectors and induce signaling that led to the formation of lamellipodia, membrane ruffles, and cell-cell junctions. Membrane recruitment of ROP6 also depended on the ability of the protein to bind GTP and/or exchange nucleotides.

RPs and AGG1 Show Reduced Association with the Plasma Membrane in the \textit{pggt-Ib} Mutant Background

It has been previously demonstrated that nonprenylated rop6\textsuperscript{C196S} and agg1\textsuperscript{I95S} mutants, in which the prenyl acceptor Cys residues were converted to Ser, accumulated in the soluble fraction (Sorek et al., 2007, Zeng et al., 2007). Furthermore, in \textit{pggt-Ib}, AGG1 partially lost its association with the plasma membrane (Zeng et al., 2007). Confocal fluorescent images of leaf epidermis pavement cells show that, similarly, when expressed in \textit{pggt-Ib} plants, a constitutively active His\textsubscript{6}-GFP-rop6\textsuperscript{CA} (rop6\textsuperscript{CA}) was found in the plasma membrane, cytoplasm, and nuclei, while in wild-type PGG-IB plants, it was only detected in the membrane (Fig. 2A; Supplemental Movies S2 and S3). The plasma membrane localization of ROP6 in wild-type PGG-IB plants has been demonstrated previously (Sorek et al., 2007, 2010) and verified in this work by plasmolysis (Supplemental Fig. S1). Similar analyses were carried out with three independent transgenic lines for each genotype, and the results were the same. Supplemental Movies S2 and S3 show that in wild-type PGG-IB plants, no movement of rop6\textsuperscript{CA} through the cytoplasm could be detected (Supplemental Movie S2). In contrast, movement of rop6\textsuperscript{CA} through the cytoplasm was detected in \textit{pggt-Ib} plants (Supplemental Movie S3).

Membrane flotation on Suc density gradients followed by immunoblot analysis was used to complement the fluorescence data (Fig. 2B). Quantification of

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In the Suc gradients, the membrane fraction accumulated in fraction 3 from the top. In accord with previous reports (Sorek et al., 2007, 2010), protein immunoblots probed with anti-ROP6 antibodies showed that GFP-rop6CA was exclusively localized in the plasma membrane in wild-type PGGT-IB plants. However, in pggt-Ib, it was detected in both membrane and soluble fractions (Fig. 2B; Supplemental Fig. S2). Immunoblots decorated with anti-GFP antibodies showed that a larger fraction of yellow fluorescent protein (YFP)-AGG1 was localized in the plasma membrane in wild-type PGGT-IB plants and that the amount of protein in the soluble fraction slightly increased in pggt-Ib (Fig. 2B; Supplemental Fig. S2), in line with previous findings (Zeng et al., 2007). Using the same anti-ROP6 antibodies, endogenous ROPs were only detected in the membrane fraction of wild-type PGGT-IB plants and in both membrane and soluble fractions in pggt-Ib protein extracts (Fig. 2B; Supplemental Fig. S2). The overall lower level of ROPs in the pggt-Ib background likely reflects the reduced stability of proteins. Thus, the loss of PGGT-I function similarly affected the subcellular distribution of recombinant GFP-rop6CA and endogenous ROPs, leading to partial accumulation in the soluble fraction. Our previous findings showed that ROP6 is primarily geranylgeranylated and that in the pggt-Ib background a larger fraction of AGG1 is detected in the cytoplasm (Sorek et al., 2007; Zeng et al., 2007). These previous findings together with the data in Figure 2 suggested that PGGT-I is the primary enzyme responsible for membrane targeting of both type I ROPs and AGG1. The data further suggested that in pggt-Ib, ROPs and AGG1 are either not prenylated or farnesylated by PFT, leading to a partial loss of membrane targeting/interaction and to accumulation in the soluble fraction.

In Vitro Prenylation of ROP6

In vitro prenylation assays were carried out to assess the efficiency of ROP6 prenylation by PGGT-I and PFT (Fig. 3). Recombinant PGGT-I and PFT were expressed in baculovirus-infected insect cells (Caldelari et al., 2001), and ROP6 was expressed in Escherichia coli (Lavy et al., 2007). The purity of the recombinant proteins was verified with Coomassie Brilliant Blue-stained gels (Fig. 3A). ROP6 was prenylated more effectively by PGGT-I than by PFT, both qualitatively (Fig. 3B) and quantitatively, as determined by scintillation counting of [3H]GGPP- or [3H]FPP-labeled protein bands that were extracted from gels (Fig. 3, C and D). Comparison of the kinetic parameters shows that the $K_m$ of PGGT-I toward ROP6 is approximately 10-fold lower than the $K_m$ of PFT (0.16 versus 1.41 $\mu$M). The $k_{cat}$ of ROP6 geranylgeranylation by PGGT-I is approximately 40-fold higher than the $k_{cat}$ of its farnesylation by PFT (28.9 versus 0.71 min$^{-1}$). This is in line with the report that prenylation of AGG1 and AGG2 by PGGT-I is more efficient than by PFT (Zeng et al., 2007). These data suggest that, in vivo, ROPs and G$_{y}$-subunits are prenylated by PGGT-I, but in its absence...
they are farnesylated by PFT. To examine this hypothesis, we purified recombinant rop6CA and AGG1 from transgenic Arabidopsis plants and analyzed their modifying lipid moieties by gas chromatography-mass spectrometry (GC-MS).

**Lipid Analysis of rop6CA and AGG1 in Vivo**

Recombinant rop6CA and AGG1 were expressed in wild-type (ecotype Columbia [Col-0]) and pggt-Ib Arabidopsis plants. The proteins were purified from the membrane fraction (wild-type pggt-Ib) or from both the membrane and soluble fractions (pggt-Ib) using NH4SO4 precipitations, ion-exchange chromatography, and nickel-nitrilotriacetic acid (Ni-NTA) metal chelate chromatography. Lipids were released from the purified proteins as described previously (Farnsworth et al., 1990; Sorek et al., 2007) and in “Materials and Methods.”

Hydrogenation, which is used in the lipid preparation procedure, reduces the prenyl double bounds, converting farnesyl and geranylgeranyl to 2,6,10-trimethyldodecane and 2,6,10,14-tetramethyldodecane, respectively. For simplicity, we will refer to 2,6,10-trimethyldodecane as farnesyl (C15) and to 2,6,10,14-tetramethyldodecane as geranylgeranyl (C20). Hydrogenation, which is carried out in the presence of ethanol and formic acid, also releases the acyl groups from proteins and promotes the formation of ethyl palmitate and ethyl stearate derivatives, which in turn can be efficiently analyzed by GC-MS (Sorek et al., 2007, 2010).

In wild-type pggt-Ib plants, rop6CA was primarily geranylgeranylated (Fig. 4A; Supplemental Fig. S3), confirming earlier findings (Sorek et al., 2007). rop6CA, which was purified from the pggt-Ib membrane fraction, was farnesylated but not geranylgeranylated.
confirming the prediction that in the absence of PGGT-I, PFT prenylates ROP proteins. Interestingly, rop6CA purified from the soluble fraction of pggt-Ib mutant plants was also farnesylated (Fig. 4A; Supplemental Fig. S3), indicating that the accumulation of ROPs in the soluble fraction was not due to their inefficient prenylation. This suggests either that targeting of the farnesylated rop6CA to the membrane is less efficient or that its interaction with the membrane is less stable.

Similar to rop6CA, AGG1 was only geranylgeranylated in wild-type plants and farnesylated in pggt-Ib mutants (Fig. 4C). Like rop6CA, AGG1 isolated from the soluble fraction of pggt-Ib plants was farnesylated (Fig. 4C). The results with rop6CA and AGG1, which are unrelated proteins, confirm that PGGT-I is the only CaaX geranylgeranyltransferase in Arabidopsis and that PFT can farnesylate diverse PGGT-I substrates.

Taken together, due to the higher affinity of PGGT-I compared with PFT toward type I ROPs and AGG1, they are preferentially geranylgeranylated. However, the affinity of PFT toward type I ROP and AGG1 is sufficient for prenylating these proteins in the absence of PGGT-I function and thus for partially maintaining their attachment to the plasma membrane and function.

In wild-type PGGT-IB plants, rop6CA was also S-acylated by palmitic (C16:0) and stearic (C18:0) acids (Fig. 4B; Supplemental Fig. S3), confirming our previous results (Sorek et al., 2007). S-Acylation was unaltered in the pggt-Ib mutant (Fig. 4B). Furthermore, in pggt-Ib plants, the membrane-associated rop6CA partitioned into detergent-resistant membranes that could be lipid rafts (data not shown), similar to its partitioning in wild-type PGGT-IB plants (Sorek et al., 2007). Surprisingly, rop6CA purified from the soluble fraction of pggt-Ib plants was also S-acylated (Fig. 4B). Because S-acylation likely takes place when ROP6 is localized in the plasma membrane, these results suggested that geranylgeranylation is required for stable steady-state plasma membrane localization. Neither the membrane-bound nor the soluble AGG1 proteins were S-acylated (Supplemental Fig. S4), in line with our previous results (Zeng et al., 2007).

**Effect of the Prenyl Group on the Membrane Interaction Dynamics of ROP6**

We have previously shown that the S-acylation of ROP6 is transient, occurs in the membrane, and depends on the activation status of the protein (Sorek et al., 2007, 2010). Thus, the farnesylated rop6CA must first be targeted to the membrane to become S-acylated. Therefore, geranylgeranylation may affect either the steady-state distribution of ROPs between the plasma membrane and cytoplasm or the interaction dynamics of ROPs with the plasma membrane. To examine whether the type of the prenyl group affects the dynamics of the interactions of ROP proteins with the membrane, we used florescence recovery after photobleaching (FRAP) beam-size analysis (Henis et al., 2006). This technique enabled us to measure the dynamics of ROP6 and rop6CA interactions with the plasma membrane of living cells.

The method employs FRAP with two different laser beam sizes, both small enough that diffusion in the cytoplasm is instantaneous and does not contribute to the measurement. FRAP beam-size analysis (I llenberger et al., 2003; Henis et al., 2006) explores the membrane interaction mode of proteins capable of both lateral diffusion in the membrane and exchange between membrane-associated and cytoplasmic pools. Typical...
FRAP experiments are depicted in Figure 5A. Quantitative results on multiple cells using two different sizes of a Gaussian laser beam are shown in Figure 5, B and C. Two beam sizes were generated by focusing the Gaussian laser beam through a 63× objective (smaller Gaussian radius $\omega$) or a 40× objective (larger $\omega$), and the characteristic fluorescence recovery time ($\tau$) values were determined with each. The ratio between the illuminated areas, $\omega^2(40\times)/\omega^2(63\times)$, was 2.28. When FRAP occurs by lateral diffusion, the ratio between the $\tau$ values measured with the two beam sizes, $\tau(40\times)/\tau(63\times)$, should equal the ratio between the illuminated areas; on the other hand, a $\tau$ ratio of 1 is indicative of recovery by exchange, which is a chemical relaxation process whose rate is independent of the beam size (Henis et al., 2006).

The fluorescence recovery mobile fraction values were high in all cases (0.93 or greater; Fig. 5A). Wild-type ROP6 exhibited a $\tau(40\times)/\tau(63\times)$ ratio of 2.0, close to but smaller than the 2.28 ratio typical of lateral diffusion (Fig. 5, B and C); this suggests that although the lateral diffusion of wild-type ROP6 is faster than its exchange and has a higher contribution to the FRAP, the exchange is not negligible and also contributes to the recovery (Niv et al., 2002; Illenberger et al., 2003; Rotblat et al., 2004; Henis et al., 2006). The constitutively active rop6CA mutant recovered with a $\tau(40\times)/\tau(63\times)$ ratio of 2.3, suggesting recovery by pure lateral diffusion (Fig. 5, B and C). The $\tau$ ratio of rop6CA in the pggt-Ib background was 1.9. Thus, although exchange contributed to the recovery, the lateral diffusion was faster and had a higher contribution to the FRAP (Fig. 5, B and C).

Thus, it appears that geranylgeranylation primarily affects the steady-state distribution of ROPs between the plasma membrane and cytoplasm and has only a minor effect on the association dynamics of ROPs with the membrane (Fig. 5). This, together with the subtle phenotype of the pggt-Ib mutant, suggests that the type of prenyl group has relatively small effects on ROP signaling. ROPs have been implicated in the regulation of cell polarity (Yang and Fu, 2007; Yalovsky et al., 2008), and their roles in the regulation of the structure of leaf epidermis pavement cells are well documented (Fu et al., 2002, 2005; Bloch et al., 2005). As the changes in epidermal cell morphology are simple to observe and quantify, we took advantage of this system to determine the effect of the prenyl group type on ROP signaling.

**Effect of Prenyl Group Type on ROP-Regulated Cell Polarity**

Images of typical leaf epidermis pavement cells are shown in Figure 6A. Differences in cell structure between nontransgenic wild-type (WT) and rop6CA (6CA) cells and between His6-GFP-ROP6 (6WT) and rop6CA (6CA) cells are apparent. Cells of wild-type and ROP6 plants have many lobes, while the cells of the rop6CA-expressing plants are more rectangular and have fewer and shallower lobes. Yet, the differences in the epidermal pavement cell structures between the wild type and pggt-Ib (gg-b), between the wild-type and ROP6, and between rop6CA and rop6CA pggt-Ib double mutants are more difficult to observe without quantification.

To quantify the differences in pavement cell structure, we used two ImageJ-based generated values called skeleton end points and circularity (Le et al., 2006) with modifications as described. The skeleton parameter turns the cell structure into lines and counts the number of end points. A single line with two end points would represent a cell without lobes. Thus, the minimal value of skeleton end points is always 2. The circularity parameter is defined by $(4\pi \text{ area})/(\text{perimeter}^2)$. Thus, for a circle, $(4\pi \pi^2)/(2\pi)^2 = 1$. For a given cell, circularity would have a value between 0 and 1. The circularity of a rectangular cell without lobes (similar to that of rop6CA) would be closer to 1, whereas that of a cell with many deep and narrow lobes would be closer to 0. For clarity, the skeleton end points and circularity parameters were converted to “normalized skeleton” and “normalized circularity,” respectively. Normalized skeleton $= (X - 2)/14$, where $X$ is the number of skeleton end points. The maximal number of skeleton end points that we counted was 15 ($n \geq 500$ cells). We assume that in rare cases, this number could be higher. Thus, normalized skeleton $= 1$ in a cell with 16 skeleton end points and 0 in a cell without lobes. Normalized circularity $= 1 -$ circularity. A plot of skeleton end point versus circularity shows an almost direct linear relationship between the two parameters (Supplemental Fig. S3C). Because normalized skeleton and normalized circularity also have the same scale and direction, they can be averaged. We designated average polarity score (APS) = normalized skeleton + normalized circularity/2 (Fig. 6B).

APS was calculated for 35 abaxial epidermal cells of seven different 14-d plants (examination of adaxial epidermal cells showed that their polarity was not different from that of abaxial cells). Wild-type cells had an average APS of 0.75 (Fig. 6B). ROP6 (6WT) pavement cells had an average APS of 0.68 and were significantly different from wild-type nontransgenic plants ($P \leq 0.01$, ANOVA). The pggt-Ib (gg-b) pavement cells had an average APS of 0.69 and were significantly different from wild-type cells ($P \leq 0.01$, ANOVA) but not from ROP6 cells. The rop6CA (6CA) cells had an average APS of 0.17, indicating a large reduction in cell polarity. The rop6CA pggt-Ib (6CA gg-b) double mutant cells had an average APS of 0.27, significantly different from 0.17 ($P \leq 0.01$, ANOVA). Thus, the analysis of cell structure shows that the lack of geranylgeranylation has significant but small effects on ROP-regulated cell polarity. Next, we examined cell polarity and type II ROP function in plp mutant plants that lack both PFT and PGGT-I function.

**Function of Type II ROPs in plp**

Images of adaxial and abaxial leaf epidermis in the wild type and plp are shown in Figure 7, A to D, and
The line and the solid line correspond to FRAP by pure lateral diffusion or
(Student’s cells when comparing values measured with the same objective
cells from wild-type plants or between 6CA in wild-type versus
objectives. The curves obtained with either 40
brane dynamics in wild-type (WT) and
(6WT), His6-GFP-rop6CA (6CA) in the wild type, or
measurements
the
m
v
3
3
v
m
2
values of His6-GFP-ROP6 (6WT) and His6-GFP-rop6CA (6CA) in
plants. A, Typical FRAP
pggt-Ib
pggt-Ib
plp
plp
8D). In addition, the
plp
abaxial pavement cells have a
reduced density of stomata in plp abaxial epidermis. In
wild-type abaxial epidermis, there are on average 60
stomata per 185 mm², whereas in plp, there are around
2,500 μm² in wild-type cells (Fig. 8D). Another notable difference is the
reduced density of stomata in plp abaxial epidermis. In
wild-type abaxial epidermis, there are on average 60
stomata per 185 mm², whereas in plp, there are around
2,500 μm² (P ≤ 0.005, Student’s t test). Similar variability in the cell sizes and stomata density
was also observed in the plp adaxial epidermis (Fig. 7, A and B). Hence, in addition to cell growth, plp is also
affected in cell division. Since type II ROPs are likely functional in plp, they may be responsible for the
viability of the mutant plants. In addition, it could be that the phenotype of plp plants also results from an
imbalance between the activities of type I and type II ROPs. The following series of experiments addressed
these hypotheses.

A constitutively active GFP-rop11CA (rop11CA) mutant (Bloch et al., 2005) was expressed in plp to examine the function of type II ROPs in a CaaX prenylation-
deficient background (Fig. 7, E–H). In plp as in wild-
type plants (Bloch et al., 2005), rop11CA was localized
in the plasma membrane (Fig. 7, F–H), confirming that
targeting and association of type II ROPs with the
membrane are unaffected in the absence of prenyla-
tion. Abaxial cells expressing the rop11CA mutant were
rectangular or cubical (Fig. 7E) and were different in
their morphology compared with abaxial plp pave-

Figure 5. FRAP beam analysis of GFP-ROP6 and GFP-rop6CA membrane dynamics in wild-type (WT) and pggt-Ib plants. A, Typical FRAP curves obtained with either 40× or 63× objectives for His6-GFP-ROP6 (6WT), His6-GFP-rop6CA (6CA) in the wild type, or pggt-Ib (gg-b) leaf epidermis pavement cells. The solid lines show the best fit of a nonlinear regression analysis to the lateral diffusion equation (Petersen et al., 1986). The τ and mobile fraction (Rf) values derived for each specific curve are shown. B, Average τ values obtained with 40× (dark gray bars; τ = 1.17 μm) and 63× (light gray bars; τ = 0.77 μm) objectives. The ω²(40×)/ω²(63×) ratio was 2.28. Bars are means of 35 measurements ± se. No significant differences were obtained between the τ values of His6-GFP-ROP6 (6WT) and His6-GFP-rop6CA (6CA) in cells from wild-type plants or between 6CA in wild-type versus pggt-Ib cells when comparing values measured with the same objective (Student’s t test). C, Ratios of the τ values shown in A. The dashed line and the solid line correspond to FRAP by pure lateral diffusion or pure exchange, respectively. The τ ratios, beam-size ratio, and their se were calculated from the experimentally measured τ and ω² values using bootstrap analysis. This analysis showed that the τ ratios of wild-type ROP6 in cells from wild-type plants (6WT) and of rop6CA in cells from pggt-Ib plants (6CA × gg-b) differed significantly from the 2.28 beam-size ratio predicted for FRAP by lateral diffusion (* P ≤ 0.02, bootstrap analysis).
ment cells (Fig. 7D). In addition, rop11CA induced ectopic symmetric and asymmetric cell divisions resulting in many developing stomata. We have not observed this phenotype when either ROP11 or other activated ROP mutants were expressed in the wild-type background (Lavy et al., 2002; Bloch et al., 2005; Sorek et al., 2007, 2010). Hence, the ectopic cell divisions resulted from expression of the activated ROP in the plp background. The functionality of type II ROPs in plp suggests that they may indeed substitute in part for the loss of type I ROP function, facilitating the viability of this mutant. These results also revealed a function for ROPs in the regulation of cell division and suggest that the GFP-rop11CA gain-of-function phenotype is balanced by the function of other prenylated proteins, possibly type I ROPs.

DISCUSSION

The function of ROP GTPases depends on C-terminal stable prenylation or S-acylation and on activation-dependent transient S-acylation in the G-domain. The association of GFP-rop6CA with actin enriched lamellipodia, and its capability to induce membrane ruffles and cell-cell junctions (Fig. 1) resembles the activities of mammalian Rac (Jaffe and Hall, 2005) and its GEF Tiam1 (Hordijk et al., 1997; Uhlenbrock et al., 2004). Hence, it is likely that ROP6 can interact with Rac effectors. Despite the differences in the insert domains of ROPs and mammalian Racs (Berken and Wittinghofer, 2008), Rac/ROP-interacting proteins contain domains such as the Cdc42 Rac-interacting binding domain (Wu et al., 2001), which is conserved in eukaryotes. Therefore, although most of the mammalian Rac effector proteins do not exist in plants, ROPs could presumably interact with some of them.Because type I ROPs are prenylated, they can be recruited to the plasma membrane, depending on their ability to bind GTP, and become active. The recruitment of wild-type ROP6 to the plasma membrane of...
NIH3T3 cells indicates that it could interact with and be activated by the mammalian RhoGEFs, as would be expected from in vitro studies (Berken et al., 2005; Basu et al., 2008). Type II ROPs are almost identical to type I ROPs in the catalytic G domain, but the mechanism of their recruitment to the plasma membrane is plant specific, and hence they remain inactive. In the future, elucidation of the Rac effectors that interact and are activated by type I ROPs could be used as a basis for an evolution-based structure-function analysis of the Rho GTPase signaling module.

The analysis of prenylation and S-acylation in vivo demonstrated how each of these modifications affects the steady-state distribution of ROPs in the cell, their membrane interaction dynamics, and function. Recently, we have demonstrated that transient S-acylation of G-domain Cys residues is required for ROP membrane dynamics and signaling in cell polarity (Sorek et al., 2010). In this work, we show that the type of prenyl group affects the steady-state distribution of ROPs between the plasma membrane and the cytoplasm, but only to a limited extent are ROP membrane dynamics and signaling affected in cell polarity. Owing to their recruitment to the plasma membrane by S-acylation, type II ROPs remain functional in the plp CaaX protein prenylation-deficient mutant and may partially suppress the loss of type I ROP function in the regulation of cell polarity, revealing both unique and partial functional redundancy of the two ROP subgroups. The analysis of protein prenylation by GC-MS (Fig. 4) shows that although the $k_{cat}$ of PGGT-I toward ROP6 is 40 times higher than the $k_{cat}$ of PFT (Fig. 3), in vivo, PFT can substitute PGGT-I. The GC-MS analysis also shows that ROP6 and AGG1 purified from the soluble fraction of pggt-ib were farnesylated (Fig. 4, A and C). This indicates that the accumulation of the Caal box containing PGGT-I protein substrates in the soluble fraction in pggt-Ib mutant plants is not the result of inefficient prenylation by PFT. The surprising identification of farnesylated and S-acylated forms of rop6 CA in the soluble fractions indicates that the combination of farnesylation in the hypervariable domain and polyene group(s) in the G-domain does not ensure stable steady-state association with the plasma membrane. The functionality of farnesylated ROP forms may explain the relatively subtle phenotype of the pggt-ib mutant plants (Johnson et al., 2005; Zeng et al., 2007). Yet, under some growth conditions, the requirement for efficient prenylation and stable interaction with the plasma membrane could become critical, explaining why PFT and PGGT-I have been conserved in plants.

The reduced steady-state association of ROPs with the plasma membrane in pggt-ib (Fig. 2; Supplemental Movie S3) resulted in a minor decrease in the $t_{1/2}$ ratio of rop6 CA from 2.3 in wild-type cells to 1.9 in pggt-ib (Fig. 5). The lateral diffusion always has a higher contribution to the measured FRAP at the smaller beam size ($63\times$), where diffusion occurs faster relative to exchange (Henis et al., 2006). Hence, comparison of the $t_{1/2}$ values could highlight differences in the lateral diffusion of the protein in the membrane under different conditions or genetic backgrounds. The $t_{1/2}$ values measured for rop6 CA in the wild type and in pggt-ib were essentially similar (Fig. 5B). This indicates that the lateral mobility rop6 CA in the plasma membrane of cells from wild-type and pggt-ib cells is similar. Taken together, the FRAP beam-size analysis indicates that the type of prenyl group

Figure 8. Polarity, cell area, and stomata density in wild-type Col-0 (W) and plp leaf epidermis. Error bars correspond to se. In A to C, letters above the bars correspond to significant differences as determined by Tukey-Kramer ANOVA ($P \leq 0.01$). Statistical analysis in D and E was carried out with Student’s t test.
has only minor effects on the membrane interaction dynamics of ROPs.

ROPs undergo transient S-acylation by palmitic and/or stearic acids and consequential partitioning into detergent-resistant membranes that could be lipid rafts (Sorek et al., 2007, 2010). It was shown that S-acylation takes place on two highly conserved G-domain Cys residues, Cys-21 and Cys-156. The \( \tau(40 \times 1/\tau(63 \times) \) ratio of a rop6\(^{CA} \) C21S/C156S double mutant (rop6\(^{CA} \) C21S/C156S) exhibited a highly significant shift to 1.4 (Sorek et al., 2010), suggesting that this mutation slowed down its lateral diffusion and elevated the exchange rate, resulting in a higher contribution of exchange to the FRAP. Furthermore, over-expression of the rop6\(^{CA} \) C21S/C156S had only small effects on cell polarity (Sorek et al., 2010), indicating that S-acylation, partitioning into lipid rafts, and stable association with the plasma membrane are required for the regulation of cell polarity by ROPs. Prenylation is required for initial targeting of type I ROPs to the membrane (Sorek et al., 2007), presumably for their interaction with RhoGDI (Boulter and Garcia-Mata, 2010) and for the steady-state distribution of ROPs between the plasma membrane and cytoplasm. Once in the membrane, ROP function is modulated by activation-dependent transient S-acylation that likely affects protein conformation (Sorek et al., 2010). rop6\(^{CA} \) was S-acylated in pggt-ib; therefore, its membrane interaction dynamics was between wild-type and mutant backgrounds. The minor effects on ROP function in pggt-ib could be explained by the overall reduction in the levels of ROPs at the plasma membrane. The lower levels of ROPs in pggt-ib may be due to the degradation of mislocated ROPs that accumulated in the cytoplasm, as been shown for Rho proteins in yeast and mammalian cells (Boulter et al., 2010). It was shown that RhoGDI protects prenylated Rho proteins from degradation (Boulter et al., 2010). Both geranylgeranylated and farnesylated Rho were shown to interact with RhoGDI (Michaelson et al., 2001), however, based on structural considerations, ROPs-F are expected to have lower affinity to RhoGDI compared to RhoGDI (Hoffman et al., 2000; Scheffzek et al., 2000; Grizot et al., 2001). The degree of identity between type I and type II ROPs in the catalytic G-domain is above 90%. Hence, it is likely that they can interact with a similar set of effectors. Yet, the changes in cell structure in incomplete male sterility and the few lobes and indentations that are formed on the adaxial pavement cells. The degree of identity between type I and type II ROPs in the catalytic G-domain is above 90%. Hence, it is likely that they can interact with a similar set of effector molecules. Yet, the changes in cell structure in plp indicate that type I and type II ROPs may be targeted to different domains in the plasma membrane or that they are differentially expressed. Microarray data from Genevestigator (Hruz et al., 2008) indicate that the type I ROPs (ROP2, ROP4, and ROP6) and all three type II ROPs are expressed at low levels in early and mature leaves (Supplemental Fig. S6). Expression, however, could be confined to different cell types.

Prenylation is required for Rho interaction with RhoGDI under physiological conditions (Hoffman et al., 2000; Scheffzek et al., 2000; Grizot et al., 2001), and palmitoylation (S-acylation) was suggested to function as a RhoGDI displacement factor (Michaelson et al., 2001). Possibly, therefore, type II ROPs do not interact with RhoGDI. Since type I ROPs cannot be prenylated in plp, they are unlikely to interact with RhoGDI, a fact that may facilitate their instability. It
has been demonstrated that RhoGDIs are involved in the regulation of ROP function and cell polarity in tip growth. In tobacco (*Nicotiana tabacum*) pollen tubes, RhoGDI was shown to facilitate recycling of ROPs to the growing tip (Klahre et al., 2006). In Arabidopsis, a loss-of-function mutant in the RhoGDI SCN1 gene developed root hairs with multiple tips in which ROP2 was mislocalized. Hence, in addition to differential expression, the ability of ROPs to interact with RhoGDI may affect cell polarity in *plp*. Future studies will have to address whether type II ROPs interact with RhoGDI and how they regulate cell polarity.

The differences in cell structure on the adaxial and abaxial sides of *plp* leaves suggest that cell growth on both side of the leaf is regulated by partially non-overlapping mechanisms. The stronger change in cell polarity on the adaxial side may reflect a greater contribution of type I ROP to cell growth on this side of the leaf. Alternatively, ROPs may interact with different pathways to control cell growth on the adaxial and abaxial leaf sides. Interestingly, mutants of the ROP effector ICR1 have altered epidermal cell morphology on the adaxial epidermis (Lavy et al., 2007). Adaxial/abaxial leaf polarity is set up early during leaf development by a signal coming from the SAM, and mutations in transcriptional regulators of adaxial/abaxial cell identity or disruption of their expression lead to the development of radialized leaves instead of flat laminas (Efroni et al., 2010). It has recently been reported that loss of all YABBY gene activities led to reduced functions of type I

Molecular Cloning

The ROP cDNAs were ligated to the Clontech mammalian expression vector pLPcx that was modified as follows. A cDNA of the improved, higher fluorescence Venus version of YFP (Nagai et al., 2002) was inserted between Xhol and HindIII of the pLPcx multiple cloning site. A linker of Gly-Ther-Ser-Gly was added downstream to the YFP. The ROP cDNAs were ligated in-frame to YFP between EcoRI and Csl.

Protein Expression in *Escherichia coli* and Baculovirus-Infected Insect Cells

*E. coli* DH5α was used for DNA propagation. For protein expression in *E. coli*, His6-ROP6 (pSY186; Sorek et al., 2007) was transformed into *E. coli* BL21 CodonPlus DE3 RIL cells (Strategene). Cells were grown to an optical density at 600 nm of 0.6, and then protein expression was induced by adding 2 μM isopropyl-b-D-thiogalactopyranoside and growth at 25°C for 2 h. Protein extraction and purification on Ni-NTA columns was performed according to the manufacturer’s instructions (Qiagen).

Protein Immunoblots

Protein preparations were performed essentially as described (Calderari et al., 2001). Typical reactions contained 0.5 pmol (0.01 μM) of purified PGGT-I or PFT, 0.8 μM all-trans [3H]GGPP or [3H]FP (30 Ci mmol−1; American Radiolabeled Chemicals), 0.2 μM ROP6, 50 μM HEPES-KOH, pH 7.8, 5 μM MgCl2, 50 μM ZnCl2, 2.5 μM dithiothreitol, and 0.3% [v/v] Nonidet P-40 in a total volume of 25 μL. Protein concentrations were determined using the bicinechonic acid kit (Pierce) and by absorption at 280 nm. All ingredients except the enzyme were mixed and kept on ice. The enzyme was then added, and each mix was incubated at 30°C for 30 min. Reactions were carried out in triplicate and terminated by adding SDS-PAGE denaturing buffer. Equal amounts of proteins were resolved by SDS-PAGE. A lane with a nonmodified ROP6 protein was run next to each reaction. The gels were briefly stained with Coomassie Brilliant Blue; gel slices harboring the radiolabeled proteins were identified according to the stained protein bands, excised from the gels, cut into pieces, and incubated in scintillation liquid for 48 h, followed by measuring the radioactivity in a scintillation counter.

Protein Immunoblot Analysis

Anti-ROP6 antibodies (Sigma R9529, lot 106K4831) were used at a dilution of 1:3,000 together with blotting-grade horseradish peroxidase-conjugated goat anti-rabbit IgG (Bio-Rad). Anti-GFP monoclonal antibodies (Covance) were used at a dilution of 1:1,000 followed by horseradish peroxidase-conjugated goat anti-mouse IgG (Bio-Rad). Detection was with EZ-ECL (Biological Industries). Quantification of protein bands was done with ImageJ (http://rsbweb.nih.gov/ij/).

Protein Extraction and Purification from Plants

To prepare protein extracts containing His6-GFP-rop6 or YFP-AGG1, 15 g of rosette leaves from 2-week-old transgenic plants was harvested and batch frozen in liquid N2. Proteins were extracted from the frozen leaves by grinding with a pestle and mortar in 3× volumes (45 mL) of plant extraction buffer (50 mM NaH2PO4, pH 7.6, 2 mM MgCl2 [only in extraction ROP6], 300 mM NaCl, 10% glycerol, 2 mM β-mercaptoethanol, and plant protease inhibitor mixture [Sigma]). To precipitate insoluble material, homogenates were centrifuged at

MATERIALS AND METHODS

Plant Material

Wild-type Col-0 and pggt-1b, plp, and plp GFP-rop11CA mutants and transgenic Arabidopsis (*Arabidopsis thaliana*) plants were grown in 5-cm pots on soil (Marom Golan mix) and irrigated from below. Plants were grown under long-day conditions (16-h-light/8-h-dark cycle) at 21°C. The light intensity was 100 μE m−2 s−1. Analyses of transgenic plants were carried out with three independent transgenic lines for each genotype.
Membrane Flotation on Suc Step Gradients

For protein preparation, 100 mg of liquid N₂-frozen tissue was ground to powder with pestle and mortar. Total proteins (soluble and insoluble) were extracted by adding 1 mL of extraction buffer (50 mM HEPES-KOH, pH 7.5, 10 mM EDTA, 5 mM EGTA, 10% Suc, 1 mg mL⁻¹ phenylmethylsulfonyl fluoride, and protease inhibitor cocktail [Roche Diagnostics]) into 10 mL of 1% Triton X-100 in water. The mixture was overlaid with 7 mL of 65% Suc and then 3 mL of 10% Suc in TE buffer. The dialyzed fractions were collected, and the YFP-AGG1 was purified over a 0.5-mL bed-volume DEAE-cellulose column, using a NaCl step gradient, according to the manufacturer’s instructions (Qiagen). Typically, 500 μg of purified protein was obtained.

AGG1 was purified from extracts using the following procedure. First, YFP-AGG1 was precipitated in the 20% to 40% NH₄SO₄ fraction. Samples were dialyzed against 50 mM NaH₂PO₄, pH 6.0, 2 mM β-mercaptoethanol, and 0.2% Tween 20. The dialyzed fractions were collected, and the YFP-AGG1 was purified over a 0.5-mL bed-volume DEAE-cellulose column, using a NaCl step gradient, according to the manufacturer’s instructions (Qiagen). Typical, 500 μg of purified protein was eluted with the 200 mM NaCl fraction.

Calculation of APS

Calculation of APS is based on measuring skeleton end points and circularity using ImageJ (Ie et al., 2006). Cell structures were copied using ImageJ. The images were then filled and copied into a new blank image, which was then analyzed with the skeleton and circularity functions. APS was calculated with the following equation: APS = normalized skeleton + normalized circularity/2, where normalized skeleton = (sketchend points) – 2/14 and normalized circularity = 1 – measured circularity.

FRAP Beam-Size Analysis

FRAP studies (Axelrod et al., 1976; Koppel et al., 1976) were carried out essentially as described previously (Illenberger et al., 2003; Henis et al., 2006; Eisenberg et al., 2008). FRAP measurements were carried out at 22°C on the abaxial side of caiulin leaves taken from 2-week-old plants. The monitoring argon ion laser beam (488 nm, 1.2 μW) was focused through the microscope (AxioImager.D1; Carl Zeiss MicroImaging) to a spot with a Gaussian radius of 0.77 ± 0.03 μm (63/1.4 numerical aperture oil-immersion objective) or 1.17 ± 0.05 μm (40/1.2 numerical aperture water-immersion objective). FRAP experiments were conducted with each beam size as described (Illenberger et al., 2003; Henis et al., 2006), measuring 35 cells for each beam size. The ratio between the illuminated areas [a(40×)/a(63×)] was 2.28 ± 0.17 (n = 59).

After a brief measurement at the monitoring intensity, a 5-mW pulse (4–6 or 10–20 ms for the 63× and 40× objectives, respectively) bleached 50% to 70% of the fluorescence in the spot. Fluorescence recovery was measured using a 488 nm, 5-mW Argon laser for monitoring beam. The apparent characteristic τ and the mobile fraction were derived from the FRAP curves by nonlinear regression analysis, fitting to a lateral diffusion process with a single τ value. The significance of differences between τ values measured with the same laser beam size was evaluated by Student’s t test. To compare ratio measurements [r(40×)/r(63×)] and [a(40×)/a(63×)], we employed bootstrap analysis, which is preferable for comparison between ratio values (Efron and Tibshirani, 1993). The r(40×) and r(63×) values were resampled with replacement using Excel, and average values from each group of resampled data [r(40×)mean and (63×)mean] were derived. For each beam size, 1,000 averaged samples were generated, followed by calculation of the bootstrap ratio, dividing r(40×)mean by r(63×)mean.
by \(7(63 \times 2^{30})\). To evaluate whether the \(r\) ratios thus obtained differ significantly from the beam-size ratio calculated by the same method \([a(63 \times 2^{30})\omega(63 \times 2^{30})]\), the set of the \(r\) bootstrap ratios was divided by the set of beam area bootstrap ratios, and the \(P\) value was derived from the spread of the resulting histogram around 1.

Mammalian Tissue Culture and Transfections

NIH3T3 cells were cultured in Dulbecco’s modified Eagle’s medium supplemented with 10% fetal calf serum in a 37°C/5% CO\(_2\) incubator. Transfection into NIH3T3 cells was carried out with TransIT reagent (Mirus) using the manufacturer’s instructions.

Immunostaining and Microscopy of Mammalian Cells

Cells were permeabilized with 3% paraformaldehyde and 0.5% Triton X-100 for 2 min and then mixed with 3% paraformaldehyde for an additional 30 min. Cells were washed with phosphate-buffered saline prior to immunostaining. Actin was stained with tetramethyl rhodamine isothiocyanate-phalloidin (Sigma P1951) and \(\beta\)-catenin with a polyclonal antibody (Sigma C2206) and a secondary antibody conjugated to Alexa 555 (Molecular Probes). Images were acquired with an IX81 Olympus microscope equipped with Hamamatsu’s ORca C4742-80-12AG CCD camera.

Supplemental Data

The following materials are available in the online version of this article.

Supplemental Figure S1. GFP-ROP6 is localized to the plasma membrane.

Supplemental Figure S2. Quantification of the immunoblots from Figure 1B.

Supplemental Figure S3. MS spectra of prenyl and acyl lipids.

Supplemental Figure S4. Control GC chromatograms of AGGI S-acylation.

Supplemental Figure S5. Quantification of pavement cell polarity.

Supplemental Figure S6. ROP gene expression microarray data.

Supplemental Movie S1. GFP-rop6CA-induced membrane ruffles.

Supplemental Movie S2. His6-GFP-rop6CA in Col-0 cells.

Supplemental Movie S3. His6-GFP-rop6CA in pggt-1b cells.

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LITERATURE CITED


Prenylation Protein Membrane Dynamics and Function

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