Running Title:

Characterization of the Arabidopsis RabE small GTPase

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TITLE

Subcellular localization and functional analysis of the Arabidopsis GTPase RabE

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FOOTNOTES

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ABSTRACT

Membrane trafficking plays a fundamental role in eukaryotic cell biology. Of the numerous known or predicted protein components of the plant cell trafficking system, only a relatively small subset has been characterized with respect to their biological role in plant growth, development, and response to stresses. In this study, we investigated the subcellular localization and function of an Arabidopsis thaliana small GTPase belonging to the RabE family. RabE proteins are phylogenetically related to well-characterized regulators of polarized vesicle transport from the Golgi apparatus to the plasma membrane in animal and yeast cells. The RabE family of GTPases has also been proposed to be a putative host target of AvrPto, an effector protein produced by the plant pathogen Pseudomonas syringae, based on yeast two-hybrid analysis. We generated transgenic Arabidopsis plants that constitutively expressed one of the five RabE proteins (RabE1d) fused to GFP. GFP-RabE1d and endogenous RabE proteins were found to be associated with the Golgi apparatus and the plasma membrane in Arabidopsis leaf cells. RabE down-regulation, due to cosuppression in transgenic plants, resulted in drastically altered leaf morphology and reduced plant size, providing experimental evidence for an important role of RabE GTPases in regulating plant growth. RabE down-regulation did not affect plant susceptibility to pathogenic P. syringae bacteria; conversely, expression of the constitutively active RabE1d-Q74L enhanced plant defenses, conferring resistance to P. syringae infection.
INTRODUCTION

Eukaryotic cells are compartmentalized by membranes that surround organelles having specific functions. Communication and transport between these membrane-bound compartments are vital to the cell and are accomplished through complex and tightly regulated pathways. Trafficking pathways and their players have been extensively described in yeast and mammalian cells, but are still poorly characterized in plants (Lippincott-Schwartz et al., 2000; Jurgens, 2004). The main effectors and regulators of these pathways appear to be shared between all eukaryotes. Among these, Rabs are a group of small monomeric GTPases that act as molecular switches to mediate vesicle transport between membrane-bound cellular compartments (Segev, 2001). Rab GTPases participate in vesicle budding from a donor compartment, transport along the cytoskeleton toward a target compartment, and, eventually, tethering and fusion of the vesicles with the target membrane. Like other small GTPases, Rabs alternate between a GTP-bound active form and a GDP-bound inactive form. Their functional specificity is determined, in part, by their unique subcellular distribution (Stenmark and Olkkonen, 2001; Zerial and McBride, 2001). The *A. thaliana* genome encodes 57 Rab proteins, divided into eight subfamilies (RabA to RabH) based on sequence similarities (Rutherford and Moore, 2002; Vernoud et al., 2003). Recent studies have indicated that members of various plant Rab subfamilies participate in secretion and recycling of cell wall components (Nielsen et al., 2008), apical growth of pollen tubes (de Graaf et al., 2005; Cheung and de Vries, 2008; Cheung and Wu, 2008) and root hair (Preuss et al., 2004; Preuss et al., 2006), formation of the phragmoplast in dividing cells (Chow et al., 2008), endocytosis (Ueda et al., 2004), and potentially osmotic stress tolerance (Mazel et al., 2004).

Fungal and bacterial infections in plants are often associated with activation (or suppression) of extracellular defense responses, including secretion of defense-related proteins and antimicrobial phytoalexins into the apoplast, and formation of callose-rich cell wall appositions, known as papillae (Snyder and Nicholson, 1990; Snyder et al., 1991; Brown et al., 1995; Soylu et al., 2005; Field et al., 2006). Deployment of such defenses is expected to be dependent on vesicle trafficking and secretion (Huckelhoven, 2007; Lipka et al., 2007; Robatzek, 2007). Delivery of innate immune receptors to the plasma membrane and ligand-induced immune receptor endocytosis also play a role in plant response to pathogen-derived elicitors.
Activation and integrity of the secretory pathway have been shown to be critical for resistance against potential pathogens (Collins et al., 2003; Assaad et al., 2004; Wang et al., 2005; Kalde et al., 2007). However, successful pathogens have evolved virulence effectors that inactivate vesicle traffic-associated regulators (Nomura et al., 2006; Robatzek, 2007). Detailed molecular mechanisms underlying vesicle trafficking leading to defense, and the specific cargos transported by these vesicles, have yet to be elucidated.

*Pseudomonas syringae* pv. *tomato* strain DC3000 (*Pst* DC3000) is a Gram-negative bacterium that causes bacterial speck of tomato and *A. thaliana*. Like other Gram-negative bacterial pathogens of plants and animals, *Pst* DC3000 delivers virulence effector proteins directly into the host cell via the type III secretion system (TTSS) (Buttner and Bonas, 2003; Alfano and Collmer, 2004; He et al., 2004). These proteins, collectively called TTSS effectors, alter host cellular processes to ultimately favor pathogen growth and promote disease. To carry out virulence functions, bacterial effectors of plant and animal pathogens interact with and often biochemically modify key regulatory components of basic host cellular functions. A major virulence activity of TTSS effectors of *Pseudomonas syringae* seems to be suppression of host defenses (Nomura et al., 2005; Abramovitch et al., 2006; Desveaux et al., 2006; Bray Speth et al., 2007; Block et al., 2008). For example, the *Pst* DC3000 TTSS effector AvrPto compromises Arabidopsis basal defenses and MAPK signaling, and promotes Arabidopsis susceptibility to non-pathogenic bacteria such as TTSS-defective mutants and nonhost pathogens such as *P. syringae* pv. *phaseolicola* (Hauck et al., 2003; He et al., 2006). Subsequent studies show that AvrPto physically interacts with the flagellin receptor FLS2 (Xiang et al., 2008) and with its signaling partner BAK1 (Chinchilla et al., 2007; Shan et al., 2008). These results suggest that AvrPto could directly interfere with microbe-associated molecular pattern (MAMP) signaling, thereby blocking downstream plant basal defense responses.

A previous yeast-two-hybrid (Y2H) screening of a tomato cDNA library for AvrPto-interacting proteins yielded two small GTPases, named Api2 and Api3 (Bogdanove and Martin, 2000), which are similar to the mammalian protein Rab8 (Huber et al., 1993). Rab8 and its yeast orthologues, Ypt2 of *Saccharomyces pombe* (Craighead et al., 1993) and Sec4p of *Saccharomyces cerevisiae* (Goud et al., 1988), are extensively characterized regulators of polarized vesicle transport from the trans-Golgi network (TGN) to specific regions of the plasma membrane (PM). The closest homologues of Rab8 in Arabidopsis are the five members of the
RabE family of GTPases (Rutherford and Moore, 2002; Vernoud et al., 2003; Supplemental Fig. S1). As described in the Results section, we independently isolated a RabE GTPase in a Y2H screen for AvrPto-interacting Arabidopsis proteins.

The identification of Rab GTPases as AvrPto interactors in both tomato and Arabidopsis suggested that, as part of its virulence mechanism, this effector may perturb intracellular vesicle trafficking in the plant (Bogdanove and Martin, 2000). Interestingly, small GTPases regulating cytoskeleton dynamics and membrane trafficking are among the most common host targets of TTSS effectors produced by bacterial pathogens of animals (Harrison et al., 2004; Machner and Isberg, 2006; Murata et al., 2006; Rzomp et al., 2006; Smith et al., 2007). The biological role of tomato Api2 and Api3 and Arabidopsis RabE GTPases in plant development and defense is unknown. Localization and function of RabE proteins have only recently begun to be investigated. Arabidopsis yellow fluorescent protein (YFP)-RabE1d, transiently expressed in heterologous tobacco epidermal cells, was detected in the Golgi apparatus and in the cytoplasm, and functional analyses indicated that this protein participates in promoting post-Golgi secretory trafficking (Zheng et al., 2005). To gain further insights into the RabE GTPases subcellular localization in native Arabidopsis cells and their function in growth, development, and/or defense at the whole plant level, we generated transgenic plants constitutively expressing GFP-fused wild-type RabE1d and RabE1d-Q74L (predicted to be preferentially GTP-bound, and therefore in an active state) and examined these plants for morphological and developmental phenotypes, and response to \textit{P. syringae} infection.
RESULTS

Identification of Arabidopsis RabE proteins as Y2H interactors of AvrPto

We conducted a Y2H screening of two separate Arabidopsis cDNA libraries, using AvrPto as bait. Several AvrPto-interacting Arabidopsis proteins were identified, including a member of the RabE family of small GTPases (At5g59840), a putative cytoplasmic kinase (At4g11890), an auxin signaling repressor, IAA7 (At3g23050), two hypothetical proteins (At3g26600, At5g16840), and several putatively chloroplast- or mitochondria-targeted proteins. The interaction with the small GTPase RabE was particularly interesting because RabE was predicted to be membrane-localized, as is AvrPto (Shan et al., 2000; He et al., 2006), and, as mentioned above, because screening of a tomato cDNA library had also yielded two AvrPto-interacting proteins homologous to Rab8 (Bogdanove and Martin, 2000), the mammalian counterpart of Arabidopsis RabE.

To characterize the specificity of the AvrPto-RabE interaction, we investigated whether AvrPto interacts with other members of the RabE family and with other Rab proteins. Of the other Arabidopsis Rab protein families (i.e., RabA-D, F, G), we cloned and expressed in yeast RabA1a, B1b, C1, D2a, F2a, and G3a; none of these representatives interacted with AvrPto in the Y2H system (Fig. 1A). Of the five RabE genes, all but RabE1c were successfully cloned and expressed in yeast. All four RabE proteins tested (RabE1a, b, d, and e) interacted with AvrPto (Fig. 1B). Thus, it appears that AvrPto interacts specifically with the Arabidopsis RabE family of GTPases.

Small GTPases normally cycle between the active GTP-bound, and the inactive GDP-bound states. Mutation of highly conserved residues can be used to alter the nucleotide binding and hydrolysis activities of Rab proteins (Nielsen et al., 2008) (Supplemental Fig. S1). The mutant forms RabE1d-S29N (predicted to be GDP-bound) and RabE1d-Q74L (predicted to be GTP-bound) were engineered. In the Y2H system, AvrPto interacted only with wild-type RabE1d or with GTP-restricted RabE1d-Q74L, but not with GDP-restricted RabE1d-S29N (Fig. 1C), suggesting that AvrPto preferably binds to the active form.
**RabE gene expression in Arabidopsis leaves**

Analysis of the Arabidopsis genome showed that 44 of the 57 Rab genes reside in duplicated regions. Of the five RabE genes, RabE1d and E1e appear to be derived from a major duplication event between chromosomes III and V, and the same holds true for RabE1b and E1c (Rutherford and Moore, 2002) (Fig. 2A). The high degree of sequence identity among the five RabE proteins, equal to or higher than 86%, suggests functional redundancy. However, members of a gene family could be preferentially expressed in different tissues, at specific developmental stages, or in response to stresses. We used the Genevestigator Gene Atlas Tool (Zimmermann et al., 2004) to investigate whether this is the case with the five RabE genes. The in silico analysis revealed that all five genes are expressed in all Arabidopsis tissues and developmental stages. RabE1d and E1e (encoding 94% identical proteins) are the only two gene family members whose expression is much lower in pollen than in all other tissues. Based on publicly available microarray data (Genevestigator; Zimmermann et al., 2004), RabE1d appeared to be the most highly expressed RabE gene in Arabidopsis Col-0 rosette leaves, followed by RabE1c. The RabE1a, E1e and E1b genes had the lowest expression levels (Fig. 2B). We conducted reverse transcription (RT)-polymerase chain reaction (PCR) analysis on rosette leaves total RNA, and confirmed a high expression level for RabE1d (Fig. 2C).

To investigate potential up- or down-regulation of the RabE family members in response to pathogens or other stresses, we analyzed the expression patterns of the RabE genes with the AtGenExpress Visualization Tool (http://jsp.weigelworld.org/expviz/expviz.jsp) (Schmid et al., 2005), across several publicly available microarray datasets. None of the five genes appeared to be significantly (more than 2.5-fold) up- or down-regulated in response to pathogens or elicitors. In the absence of any expression-based indication on whether the five RabE proteins have redundant or distinct functions, we chose the highly expressed RabE1d (At5g03520) for further study.

RabE1d is associated with not only the Golgi apparatus, but also the plasma membrane in Arabidopsis leaf cells

All Rab proteins are normally present in cells in two pools, one cytoplasmic, and the other membrane-associated (Novick and Brennwald, 1993). Nucleotide-binding state and interaction with accessory proteins determine whether a Rab is in the cytosol or the membrane, at
any given time. A hallmark feature of Rab proteins is that they localize to the specific membrane compartments in which they function. It was previously reported that Arabidopsis RabE1d, when transiently and heterologously expressed in tobacco epidermal cells as a fusion with YFP, was detected in the Golgi apparatus and in the cytoplasm (Zheng et al., 2005). To determine RabE localization in native Arabidopsis cells, we created stable transgenic plants that express RabE1d fused with enhanced green fluorescent protein (GFP), under the control of the CaMV 35S promoter. By convention, GFP was fused to the N-terminus of RabE1d to preserve the C-terminal CAAX geranylgeranylation site that is critical for membrane association and function (Calero et al., 2003) (Supplemental Fig. S1). Several independent transgenic lines were analyzed by confocal laser scanning microscopy (CLSM). GFP fluorescence was observed not only in intracellular punctate structures consistent with the Golgi apparatus, as detected in heterologous tobacco cells (Zheng et al., 2005), but also prominently at the cell periphery (Fig. 3A-E).

Leaf epidermal cells typically contain a very large vacuole that accounts for most of the cell volume. Fluorescence detected at the cell periphery may represent the plasma membrane (PM), the vacuolar membrane (tonoplast), or the thin layer of cytoplasm that is between the PM and the tonoplast. To more precisely determine whether GFP-RabE1d was also localized at the PM, we stained live leaf tissue with the lipophylic dye FM4-64 (Fischer-Parton et al., 2000; Bolte et al., 2004). FM4-64 produces a bright red fluorescence in membranes but not in aqueous solutions and is rapidly incorporated into the PM. It is often used in microscopy as an endocytic tracker, because it is retained in the portions of PM that are internalized by endocytosis (Ueda et al., 2001). Within the first 15 to 30 minutes after incorporation (depending on the system used), FM4-64 selectively stains the PM. CLSM analysis revealed a precise overlap of GFP-RabE1d fluorescence with FM4-64 fluorescence immediately after staining, indicating that RabE1d is associated with the plasma membrane (Fig. 3D).

To investigate whether the punctate structures labeled by GFP-RabE1d correspond to the Golgi apparatus, we examined co-localization with rat sialyl transferase, a Golgi marker protein (Wee et al., 1998) fused to DsRed (ST-RFP). ST-RFP was transiently expressed in the GFP-RabE1d transgenic leaves via particle bombardment. Observation of cells co-expressing GFP-RabE1d and ST-RFP revealed overlapping fluorescence signals, confirming RabE1d association with the Golgi apparatus (Fig. 3E). Taken together, our analysis of GFP-RabE1d localization revealed that, in the native Arabidopsis leaf cells, membrane-associated RabE1d is found not
only in the Golgi apparatus, as previously reported in heterologous tobacco cells, but also in the PM.

**Endogenous RabE proteins co-fractionate with PM and Golgi markers**

GFP-RabE1d expression in the transgenic plants was driven by the CaMV 35S constitutive promoter. To exclude the possibility that the observed RabE localization reflects patterns of only the transgenically expressed protein, we conducted additional analyses to determine the localization of endogenous RabE in transgenic as well as wild-type Arabidopsis plants. We performed subcellular membrane fractionation by centrifugation of clarified plant extracts on sucrose step gradients (Zeng and Keegstra, 2008). This method allowed separation of the PM from fractions containing lighter membranes (Golgi, tonoplast). Western blot analysis with an anti-RabE polyclonal antibody that reacts with all RabE family members revealed that the bulk of membrane-associated endogenous RabE proteins, as well as transgenically expressed GFP-RabE1d, were in the same fraction as the PM marker H⁺-ATPase (Morseth et al., 1998). A lower amount of endogenous RabE, as well as GFP-RabE1d, co-fractionated with xylosyl transferase (XT1), a Golgi apparatus resident protein (Faik et al., 2002; Cavalier and Keegstra, 2006; Zeng and Keegstra, 2008) (Fig. 3F and G). A tonoplast marker, gamma-tonoplast integral protein (γTIP), was found predominantly in the same fraction as the Golgi marker. Independent membrane fractionation experiments yielded similar results, although minor differences in protein levels and distribution among fractions were occasionally observed across western blots, as a result of inter-experiment variability. Overall, the membrane fractionation experiments complemented the live-cell imaging results; together, they indicate that endogenous and ectopically expressed RabE proteins are not only localized at the Golgi apparatus, but the majority of membrane-associated RabE is in the PM in Arabidopsis leaf cells.

**GTP-restricted RabE1d-Q74L displays altered subcellular localization**

We also produced transgenic plants expressing RabE1d-Q74L, which is predicted to be constitutively active, as a GFP fusion. Unlike wild-type GFP-RabE1d, the GFP-RabE1d-Q74L fusion was not detected in intracellular punctate structures (i.e., Golgi), but was primarily found at the cell periphery (Fig. 4A). PM staining with FM4-64 revealed that the bulk of GFP-RabE1d-
Q74L fluorescence did not overlap with the PM, but was most likely localized in the tonoplast (Fig. 4B). We obtained from ABRC (Arabidopsis Biological Resource Center, Ohio State University) Arabidopsis transgenic lines expressing various endomembrane markers fused to GFP (Cutler et al., 2000). Comparison of GFP-RabE1d-Q74L fluorescence to that of either a PM-localized channel protein (line Q8) or a tonoplast marker (line Q5) revealed a localization pattern similar to that of the tonoplast, both in intact and plasmolyzed leaf tissues (Supplemental Fig. S3. Plasmolysis in line Q8 resulted in the characteristic Hechtian strands (Oparka, 1994), typical of plasma membrane retracting from the cell wall; in mesophyll cells, the chloroplasts were clearly located on the inside of the GFP-labeled PM (Fig. 5). In contrast, plasmolyzed cells expressing GFP-RabE1d-Q74L did not display Hechtian strands and chloroplasts in the mesophyll cells were distinctly on the outside of the GFP-labeled membrane (Fig. 5), further supporting RabE1d-Q74L localization in the tonoplast.

**Challenge with *P. syringae* bacteria promotes focal accumulation of GFP-RabE1d**

To investigate whether intracellular distribution of the RabE1d protein was perturbed in the presence of bacteria, we performed microscopic observation of transgenic GFP-RabE1d plants challenged with various strains of *Pst* DC3000. Leaves were syringe-inoculated with bacteria at 1x10^8 CFUs/ml, and analyzed by CLSM 5 to 6 hours post-inoculation. We observed that bacterial inoculation caused polarized GFP-RabE1d accumulation in mesophyll cells (Fig. 6A). Interestingly, whereas such a phenomenon was restricted to a few sparse cells in leaves challenged with wild-type virulent *Pst* DC3000 (Fig. 6D) or with the non-pathogenic TTSS-defective mutant *hrpA* (Fig. 6C), focal accumulation of GFP-RabE1d was widespread in leaves inoculated with the avirulent strain *Pst* DC3000 (*avrRpt2*) (Fig. 6E). These results suggest that the GFP-RabE1d subcellular localization is dynamic and can respond to bacterial infection, especially in a gene-for-gene interaction.

**RabE1d cosuppression in transgenic plants resulted in altered plant growth and morphology**

A large percentage of GFP-RabE1d transgenic Arabidopsis plants generated in this study showed cosuppression of the transgene and of endogenous RabE, as demonstrated by western blot analysis (Fig. 7A). Severe reduction of the endogenous RabE protein level in transgenic
plants invariably correlated with a distinct morphological phenotype (Fig. 7B and C). Rosette leaves developed normally for the first 3 weeks, when Arabidopsis development is usually slower, and plants were indistinguishable from Col-0. In the following two weeks, when Arabidopsis size increases more rapidly, the leaves of RabE-cosuppressed plants did not fully elongate (Fig. 7D); midribs remained short, while the leaf lamina continued to expand, producing a characteristic wavy phenotype. Mature (6- to 7-week-old) RabE-cosuppressed plants were significantly smaller than wild-type and had short midribs and petioles. RabE-cosuppressed plants flowered at the same time as wild-type Arabidopsis, although their stems were much shorter than wild-type, and the plants produced fertile seeds. The progeny of selected silenced lines (B8, B11, and B13) maintained silencing and had the same phenotype as the parental plants.

Expression of the RabE gene family was analyzed by RT-PCR in the cosuppressed lines and compared to expression in wild-type plants. The RT-PCR demonstrated that not all RabE gene family members are equally affected by cosuppression. RabE1d and RabE1e were knocked-down most severely, followed by RabE1b and RabE1c. RabE1a showed only slight down-regulation (Fig. 7E). Given the high degree of sequence similarity among small GTPases of the Arabidopsis Rab superfamily, we tested whether other closely related Rabs were affected by silencing. The closest relatives of the RabE clade in Arabidopsis are the four RabD proteins (RabD1, D2a, D2b, and D2c). RabD was previously characterized asa regulator of the early secretory pathway, being involved in transport from the endoplasmic reticulum to the Golgi (Batoko et al., 2000; Zheng et al., 2005). RT-PCR revealed that transcripts of all four RabD genes were present at similar levels in RabE1d-silenced plants and in wild-type Arabidopsis (Fig. 7E). Silencing in the transgenic plants is therefore specific and limited to the RabE genes, primarily RabE1d and E1e.

**RabE-cosuppressed plants are not compromised in resistance to Pst DC3000**

We performed pathogenesis assays with Pst DC3000 to establish whether the partially RabE-cosuppressed plants are impaired in their defenses against P. syringae. Pst DC3000 consistently caused disease symptoms and multiplied on RabE-cosuppressed plants, reaching similar population levels as on wild-type Arabidopsis (Supplemental Fig. S2). In several instances, however, we observed that older (6- to 7-week-old) or environmentally stressed RabE-
cosuppressed plants displayed some degree of basal resistance, possibly due to stress caused by RabE down-regulation (Supplemental Fig. S2). We did not observe a consistent and reproducible difference between wild-type Col-0 plants and RabE-cosuppressed plants in the multiplication of Pst DC3000 (avrRpt2), or a TTSS-defective mutant of Pst DC3000, the hrpA- mutant (Supplemental Fig. S2).

**Transgenic expression of RabE1d-Q74L confers resistance against Pst DC3000**

GFP-RabE-Q74L plants did not exhibit significant alterations in growth and development, other than appearance of minute sparse indentations in mature rosette leaves, about two weeks prior to bolting. The origin and significance of these indentations is unclear; however, we have been unable to show, using Trypan Blue staining, that they develop as a consequence of cell death.

Although transgenic expression of constitutively active GFP-RabE1d-Q74L did not globally affect plant growth or development (as did RabE cosuppression), it had a remarkable effect on plant responses to P. syringae infection. Upon challenge with Pst DC3000, the GFP-RabE1d-Q74L-expressing plants displayed a considerable degree of resistance, reflected by bacterial multiplication being consistently restricted 10- to 100-fold, compared to multiplication on wild-type Arabidopsis (Fig. 8A). This observation was consistent across several experiments on different transgenic lines. Visible disease symptoms, namely chlorosis and necrosis, were also markedly reduced (Fig. 8B). This enhanced resistance phenotype apparently requires the constitutively active form of RabE1d, as transgenic expression of GFP-RabE1d did not result in enhanced resistance (Supplemental Fig. S2).

**Constitutive secretion of extracellular proteins in GFP-RabE1d-Q74L-expressing plants**

Up-regulation of the secretory pathway was recently demonstrated in systemic acquired resistance (SAR) (Wang et al., 2005), and plants undergoing SAR accumulate secreted proteins in the apoplast, including antimicrobial polypeptides (Uknes et al., 1992). Because RabE proteins are predicted to be involved in regulating secretory vesicle trafficking, the enhanced resistance to Pst DC3000 in GFP-RabE1d-Q74L-expressing plants could be caused by constitutive stimulation of defense-associated secretion. To test this possibility, Arabidopsis wild-type and GFP-RabE1d-Q74L-expressing plants were sprayed with benzothiadiazole (BTH), a synthetic
activator known to trigger SAR in plants (Lawton et al., 1996), or with water, as a control. Three days later, total protein secretion in the apoplast and secretion of the extracellular defense protein PR1 (Pathogenesis-Related protein 1) were monitored. Intercellular wash fluid (IWF) collected from water-treated GFP-RabE1d-Q74L-expressing plants contained PR1 and several unknown proteins that were absent from the water-treated Arabidopsis wild-type IWF, indicating a constitutive activation of secretory and defense pathways. BTH application resulted in similar levels of secreted PR1 and several other proteins in the apoplast of both wild-type and transgenic plants (Fig. 8C). Interestingly, some protein bands were exclusively detected in the IWF of water- and BTH-treated RabE1d-Q74L-expressing plants, but not in the BTH-treated wild-type plant IWF (indicated by arrowheads in Fig. 8C). These unique extracellular proteins associated with expression of RabE1d-Q74L suggest that other secretory pathways, in addition to the SAR pathway, are activated in these plants.

DISCUSSION

Plant RabE GTPases are predicted to be involved in mediating secretory vesicle traffic from the Golgi to the PM. They could therefore play fundamental roles in secretion of extracellular matrix molecules, thereby influencing plant growth and development, as well as in secretion of extracellular defense molecules in response to pathogen infections. RabE proteins from both tomato (Bogdanove and Martin, 2000) and Arabidopsis (this study) interact with a pathogen effector protein, AvrPto, in Y2H assays. Because a number of studies have implicated vesicle trafficking in pathogen defenses (Collins et al., 2003; Assaad et al., 2004; Wang et al., 2005; Nomura et al., 2006; Kalde et al., 2007), physical interaction between AvrPto and RabE GTPases could indicate a potential role of RabE GTPases in plant defense. However, to date only one report has documented subcellular localization of Arabidopsis GFP-RabE1d transiently expressed in heterologous tobacco epidermal cells (Zheng et al., 2005). Subcellular localization of RabE GTPases in native Arabidopsis cells and the biological role of RabE GTPases in regulating plant growth or defense at the whole-plant level remained unknown.

Using a combination of confocal microscopy and cell membrane fractionation on transgenic plants expressing GFP-RabE1d and on wild-type plants, we show that RabE proteins are not only localized in the Golgi, as reported by Zheng and colleagues (2005), but also that a prominent fraction is associated with the PM of Arabidopsis leaf cells. Because a hallmark
feature of Rab proteins is that they localize to the specific membrane compartments in which they function, association of RabE with both the Golgi and the PM provides strong support for a role in mediating traffic of secretory vesicles from the Golgi to the PM (i.e., instead of other post-Golgi target membranes), as previously suggested by Zheng et al. (2005).

Interestingly, the RabE-Q74L protein expressed in Arabidopsis as a GFP fusion displayed an unanticipated localization pattern. The bulk of fluorescent protein was localized at the vacuolar membrane, and we could not detect by CLSM fluorescence in the Golgi or in the PM, the predicted destination of the active form of RabE. After delivery of vesicles to the target membrane, Rab proteins are usually recycled back to the cytoplasm and then incorporated again into the donor membrane for multiple rounds of vesicle transport. Such recycling is dependent on hydrolysis of GTP into GDP because inactivated GDP-bound Rabs are extracted from the target membrane by accessory proteins that mediate their recycling (Segev, 2001). The Q74L mutation is predicted to inactivate the GTP hydrolysis activity of RabE. Presumably, RabE-Q74L cannot be dephosphorylated and, thus, cannot be recycled to the cytoplasm. It is possible that a default non-specific endocytosis pathway such as that observed for the FM4-64 dye (Ueda et al., 2001) could carry the GTP-bound RabE-Q74L protein from its target location, the PM, to the tonoplast, where it accumulates.

Analysis of RabE-cosuppressed plants clearly indicates that RabE GTPases play a role in plant growth, as evidenced by dwarf plant sizes and altered leaf morphology in RabE-cosuppressed plants. Rosette leaves of RabE-cosuppressed lines developed relatively normally for the first 3 weeks, when Arabidopsis development is usually slower. However, when Arabidopsis size increases more rapidly, in the 4th and 5th weeks, the leaves of RabE-cosuppressed plants were not able to fully elongate; leaf midribs and petioles remained short, yielding characteristically wavy leaves. Inflorescences emerged at the same time as in wild-type, but the overall stature of the RabE-cosuppressed plants remained much shorter. These observations lead us to suggest that RabE-mediated vesicle traffic from the Golgi to the PM is required for rapid elongation of certain tissues (e.g., leaf midribs and stems) associated with rapid plant growth. The dwarf phenotype of RabE-cosuppressed plants was likely caused by simultaneous down-regulation of more than one RabE gene, as suggested by reduced expression of RabEld and Ele and, to a lesser extent, RabE1a, E1b, and E1c (Fig. 6E). Consistent with this speculation, knock-out mutants of RabEld, caused by T-DNA insertions, did not exhibit any
defect in growth and development (data not shown). Notably, cosuppression did not affect the expression of RabD genes, the closest homologues of RabE genes and, therefore, the observed phenotypes can be ascribed to partial silencing of multiple RabE gene family members.

Besides our interest in determining the subcellular localization of RabE GTPases in native Arabidopsis cells and a possible role of RabE GTPases in growth and development at the whole plant level, another major motivation for this work was to investigate a potential role of RabE GTPases in plant defense. Bogdanove and Martin (2000) first identified RabE GTPases as AvrPto interactors in tomato and discussed the possibility that these GTPases could be virulence targets of AvrPto. In an independent Y2H screen for AvrPto-interacting Arabidopsis proteins, we also isolated a RabE GTPase. We found that AvrPto interacted with all tested members of the RabE family, but not with members of other Rab families of Arabidopsis (Fig. 1). Moreover, AvrPto interacted with a RabE mutant (RabE1d-Q74L) predicted to be GTP-bound, but not with a RabE mutant (RabE1d-S29N) predicted to be GDP-bound. Finally, we found that the majority of membrane-associated RabE1d is localized at the PM, where AvrPto is known to be located in tomato and Arabidopsis cells (Shan et al., 2000; He et al., 2006). Despite the intriguing specificity in Y2H assays and the apparent co-localization of AvrPto and RabE1d to the same host membrane, we have been unable to detect AvrPto-RabE1d interaction using in vivo co-immunoprecipitation or in vitro pull-down methods. Physical interaction of AvrPto with confirmed virulence targets FLS2 and BAK1 was demonstrated using both in vitro and in vivo methods (Shan et al., 2008; Xiang et al., 2008). Our results, thus, suggest that RabE proteins may not be host targets of AvrPto. Alternatively, RabE GTPases may interact with AvrPto in the plant cell only transiently and/or require special conditions.

Interestingly, GFP-RabE1d plants challenged with the avirulent strain Pst DC3000 (avrRpt2) manifested dramatic focal accumulation of GFP-RabE1d in mesophyll cells (Fig. 5). GFP-RabE1d focal accumulation was limited to a few sporadic cells when plants were inoculated with wild-type virulent Pst DC3000 (i.e., in a susceptible interaction) or with the hrpA\textsuperscript{-} mutant (which activates plant basal defenses). Polarized accumulation of RabE GTPase during a gene-for-gene interaction could be part of the host cell response to direct defense-associated vesicle trafficking toward invading pathogens. If so, the GFP-RabE1d fusion may be a useful cellular marker for future study of vesicle trafficking in the gene-for-gene response in Arabidopsis. Accumulation of other vesicle traffic-associated regulators (such as t-SNAREs and
v-SNAREs) at the site of pathogen penetration has also been observed in fungal infections (Assaad et al., 2004; Huckelhoven, 2007; Kwon et al., 2008).

RabE cosuppression in Arabidopsis, under the conditions reported in this study, did not result in increased susceptibility to *P. syringae* bacterial strains. RabE proteins, therefore, may not be required for establishing defenses against this pathogen. Alternatively, partial down-regulation of RabE proteins may be insufficient to confer a discernable defense phenotype. A complete knockout of all five RabE genes would be necessary to resolve this question. However, the dwarf phenotype of partially RabE-cosuppressed plants suggests it is unlikely that completely RabE-deficient plants would be viable and/or suitable for bacterial infection assays.

Transgenic expression of the RabE1d-Q74L variant, on the other hand, conferred in Arabidopsis a significant degree of resistance to *Pst* DC3000. It remains to be determined whether this resistance is caused by a direct effect of RabE1d-Q74L, due to enhancement of defense-related vesicle traffic, or rather is triggered by an indirect effect, due to overall perturbation of cellular vesicle traffic. We found that the IWF collected from water-treated GFP-RabE1d-Q74L plants contained PR1 and several unknown proteins that were absent from the IWF of water-treated wild-type Arabidopsis, indicating constitutive activation of secretory and defense pathways in these plants. BTH application resulted in similar levels of secreted PR1 and other proteins in the apoplastic space of both wild-type and RabE1d-Q74L transgenic plants (Fig. 8C). However, some of these extracellular proteins are detected only in the IWF of water- and BTH-treated RabE1d-Q74L-expressing plants, but not in the IWF of BTH-treated wild-type plants. These unique extracellular proteins associated with expression of RabE1d-Q74L suggest activation of other secretory pathways in these plants in addition to the SAR pathway. Interestingly, activation of SAR and resistance to *Pst* DC3000 in the GFP-RabE1d-Q74L transgenic plants did not correlate with a dwarf phenotype, a common phenotype of Arabidopsis mutants that are constitutively resistant to pathogens (Lorrain et al., 2003). Further analysis of the RabE-Q74L transgenic plants may provide novel insights in plant defense, and indicate possible avenues for engineering resistance in crops.

**METHODS**

**Yeast two-hybrid assay**
We identified Arabidopsis proteins that interacted with AvrPto of *Pst* DC3000 by using the Matchmaker LexA-based yeast two-hybrid system (Clontech Laboratories Inc., Palo Alto, CA). Two Arabidopsis cDNA libraries, constructed from infected and uninfected *Landsberg erecta* plants (kindly provided by J. Jones), were screened. The *avrPto* coding sequence was amplified from *Pst* DC3000 genomic DNA by PCR (sense primer: 5'-GCGAATTCGGAAACATGGGAATATGTGTC-3'; antisense primer: 5'-GCCTCGAGATTGCCAGTTACGGA-3') and cloned into pNLexA, to serve as bait in the yeast two-hybrid screen.

**RabE cloning and mutagenesis**

We amplified the *RabE1d* (At5g03520) coding sequence from Arabidopsis Col-0 cDNA using the rabE-5' and rabE-3' primers (Table S1), containing the *Eco*RI and *Bam*HI restriction sites, respectively. The PCR product was ligated into a TOPO vector (pCR2.1, Invitrogen) and sequenced. Single nucleotide changes were introduced in the *RabE1d* sequence by two-step overlapping PCR, to generate the *RabE1d*-S29N and *RabE1d*-Q74L mutant derivatives. *RabE1d*-S29N was obtained through a G→A substitution; in the first PCR step, two overlapping *RabE1d* fragments were amplified using the primer combinations rabE-5'/S29N-rev and rabE-3'/S29N-for (Table S1). The products were purified from agarose gel, mixed, and used as template for a second PCR amplification step, with the rabE-5' and rabE-3' primers. The presence of an overlapping region allowed annealing of the two gene fragments and amplification of the full-length coding sequence. A similar procedure was used for introducing the Q74L mutation, through an A→T substitution. In this case, the following primer combinations were used in the first PCR step: rabE-5'/Q74L-rev and rabE-3'/Q74L-for (Table S1). *RabE1d*-S29N and *RabE1d*-Q74L amplification products were introduced in a TOPO vector by TA-cloning and sequenced.

**GFP-RabE1d transgenic plants**

*RabE1d* and the mutant variant *RabE1d*-Q74L were subcloned in the *Eco*RI and *Bam*HI sites of the binary expression vector pEGAD (Cutler et al., 2000), downstream of the enhanced green fluorescent protein (GFP) sequence, to create translational fusions. The binary vector was introduced in *Agrobacterium tumefaciens* strain GV3850 via triparental mating for plant transformation. Arabidopsis Col-0 *glabrous* (Col-0 *gl1*) plants were transformed using the floral
dip method (Clough and Bent, 1998). Transgenic plants were selected based on resistance to the herbicide Basta (glufosinate). A solution containing 0.012% glufosinate (Finale concentrate, AgrEvo Environmental Health) and 0.025% Silwet L-77 was sprayed on 2-week-old seedlings growing in soil. Surviving T1 plants were screened for GFP fluorescence with a Zeiss Axiophot microscope, and expression of the correct size GFP-RabE fusion proteins was verified by western blot with an anti-RabE polyclonal antibody (described below).

**Protein extraction and immunoblotting**

Total proteins were extracted as follows: approximately 20 mg (fresh weight) of fresh or frozen leaf tissue were ground with a pestle in a microfuge tube in the presence of 100 μl of 1× SDS-PAGE loading buffer [90 mM Tris-HCl, pH 8.0, 100 mM DTT, 3% SDS, 22.5% sucrose, 10 μl/ml Protease Inhibitor Cocktail for plant cell extracts (Sigma), bromophenol blue (to saturation)]. Extracts were immediately heated at 80°C for 10 min and then frozen at -20°C. Before loading, extracts were thawed at room temperature and centrifuged at 20,000×g for 2 min, to pellet debris. An equal volume of each sample was used for SDS-PAGE electrophoresis. Total proteins were separated on precast gradient gels (4 to 20%, ISC BioExpress), then transferred onto Immobilon-P membrane (Millipore, MA) using a semi-dry transfer apparatus (SEMI PHOR, Hoefer Scientific Instruments, San Francisco, CA). Protein detection was carried out with the following primary antibodies: anti-RabE (raised in chicken against recombinant RabE protein expressed in *E. coli*, Cocalico Biological, Inc.), anti-XT1 (Faik et al., 2002; Cavalier and Keegstra, 2006), anti-PM ATPase (Morsomme et al., 1998), and anti-γTIP (gift of Dr. N. Raikhel).

**Cell membrane fractionation**

Leaves were harvested and weighed immediately prior to extraction. Leaf tissue (2.5 g) was ground with a cold mortar and pestle in the presence 5 ml of ice-cold extraction buffer [50 mM HEPES, pH 7.5, 100 mM KCl, 10 mM EDTA, 1 mM DTT, and 10 μl/ml Protease Inhibitor Cocktail for plant cell extracts (Sigma)] containing 34% sucrose (w/v). The extract was homogenized with a Polytron immersion blender (3 pulses of 10 s each), filtered through a single layer of Miracloth, and centrifuged for 10 min at 10,000×g, to remove most unbroken
chloroplasts and nuclei. The supernatant was adjusted to 40% sucrose in about 10 ml final volume (concentration was determined with a refractometer), and layered on a 5 ml cushion of 50% sucrose, in clear ultracentrifugation tubes. The homogenate was subsequently layered with 10 ml of 34% sucrose, 8 ml of 25% sucrose and 8 mL of 18% sucrose (w/v). All sucrose solutions were prepared in the same buffer used for extraction. Gradients were centrifuged at 100,000×g for 3 h, at 4°C, in an SW28 rotor (Beckman). After centrifugation, the membrane-containing interphases were collected and diluted with sucrose-free extraction buffer, and membranes were collected by ultracentrifugation (1 h at 100,000 ×g). Membrane pellets were resuspended in equal volumes of SDS-PAGE loading buffer and heated at 80°C for 10 min. Equal volumes were loaded on SDS-PAGE gels. Protein electrophoresis and western blot were performed as described above.

Confocal microscope analysis and imaging

Pieces of leaves were sampled randomly and mounted in water. Imaging was performed using an LSM510 META inverted confocal laser scanning microscope (Zeiss), and either a 20× or a 40× oil immersion objective. For GFP-RabE fluorescence analysis, the 488-nm excitation line of an argon ion laser was used, with a 505 to 530 nm band-pass filter, in the single-track facility of the microscope. Images were processed with the LSM Image Browser Version 3.1 (Zeiss) and with the Adobe Photoshop Elements Version 5.0 software (Adobe Systems Inc.). For FM4-64 staining, detached Arabidopsis leaves were submerged in 8.2 µM FM4-64 (Molecular Probes, Leiden, The Netherlands) in water for 15 min. Leaves were rinsed in distilled water and observed immediately. For imaging GFP-RabE1d and FM4-64 fluorescence, the 488-nm excitation line was used; GFP fluorescence was collected with a 505 to 530 nm band-pass filter, and FM4-64 fluorescence was collected with a 615-nm long-pass filter.

Biolistic transformation

ST-RFP transient expression in Arabidopsis leaves was achieved by biolistic transformation. The binary vector bearing rat sialyl transferase fused to DsRed (ST-RFP) was a gift of Dr. F. Brandizzi (Saint-Jore et al., 2002). Gold particles (1.0 μm, Bio-Rad) were coated with the ST-RFP plasmid DNA as described by Zhang et al. (Zhang et al., 2001). Arabidopsis
leaves were harvested and arranged on MS agar plates (4.3 g/l MS salts, 0.8% agar, pH 5.7). The DNA-coated particles were delivered into the lower leaf epidermis with a particle gun (Dupont), using 1100 psi rupture discs under a vacuum of 25 in Hg. After bombardment, leaves were incubated in the sealed plates at room temperature and fluorescence was observed 24 h post transformation. For co-imaging GFP-RabE1d and ST-RFP, the argon ion laser excitation lines of 488 nm (for GFP) and 543 nm (for DsRed) were used. GFP fluorescence was collected with a 505 to 530 nm band-pass filter, and DsRed fluorescence was collected with a 615-nm long-pass filter.

**Plant growth and bacterial multiplication assay**

Arabidopsis plants were grown in soil, in growth chambers, under a 12 h dark/12 h light cycle. The light intensity averaged 100 µE m\(^{-2}\) sec\(^{-1}\), and the temperature was kept constant at 20°C. *Pst* DC3000 bacteria were cultured in low-salt LB medium (10g/l Tryptone, 5g/l Yeast Extract, 5g/l NaCl), supplemented with 100 µg/ml rifampicin. For multiplication assays in plants, bacterial liquid cultures were incubated at 30°C to the mid- to late-logarithmic phase. Bacteria were collected by centrifugation and resuspended in sterile water with the addition of 0.004% Silwet L-77 (OSI Specialties, Friendship, WV). Titer of the bacterial inoculum was 1x10\(^5\) colony-forming units (CFUs)/ml, unless otherwise indicated. Arabidopsis leaves were inoculated by syringe-infiltration, and bacteria enumeration in leaves was conducted as previously described (Katagiri et al., 2002).

**RNA extraction and RT-PCR analysis**

Total RNA was extracted from 100 mg of Arabidopsis leaf tissue with the RNeasy Plant Mini Kit (QIAGEN), according to the manufacturer’s specifications. RNA concentration in samples was determined with a NanoDrop ND-1000 Spectrophotometer (NanoDrop, Wilmington, DE). RNA reverse transcription and target gene amplification (RT-PCR) were performed using the RNA LA PCR Kit (AMV), Ver. 1.1 (TaKaRa, Japan). Reverse transcription reaction mixture was prepared according to the manufacturer’s protocol (5 mM MgCl\(_2\), 1x RNA PCR Buffer, 1 mM dNTP mixture, 1 unit/µl RNase Inhibitor, 0.25 units/µl AMV Reverse Transcriptase, 0.125 µM Oligo-dT Adaptor Primer, RNase-free water and 1 µg total RNA). For
amplification of the *RabE* and *RabD* transcripts, a single RT reaction was carried out in a total volume of 50 µl and incubated in a thermal cycler for 30 min at 45°C, followed by 5 min at 99°C and 5 min at 5°C. Five microliters of reverse-transcribed cDNA were used as template in each of ten PCR reactions with gene-specific primer pairs designed to amplify the five *RabE* gene family members, the four *RabD* genes, and the *Actin8* gene as a control. Primer sequences are listed in Table S2. Each PCR reaction contained 2.5 mM MgCl2, 1×LA PCR Buffer II, 0.2 µM forward primer and 0.2 µM reverse primer, sterilized distilled water, and 5 µl of the RT reaction described above, in a final volume of 25 µl. The reactions were placed in a thermal cycler and amplification was performed under the following conditions: 94°C, 2 min (1 cycle), 94°C, 30 s, 54°C, 30 s, 72°C, 1 min (22 or 25 cycles), 72°C, 1 min (1 cycle), 4°C. Ten microliters of the PCR reactions were loaded on a 1% agarose gel. Gels were photographed with a Bio-Rad Gel Documentation System, and band intensity was analyzed with the Quantity One software (Bio-Rad).

**BTH treatment**

Benzothiadiazole (BTH; Actigard) was prepared at a final concentration of 300 µM in water and sprayed onto potted GFP-RabE1d-Q74L and Col-0 gl1 Arabidopsis plants. A separate set of plants was sprayed with water as a control. Plants were covered with a tight-fitting clear plastic dome and assayed for responses 3 d after BTH application.

**Intercellular wash fluid (IWF) collection and analysis**

BTH-treated and control plants were harvested 3 d after treatment. Whole plants were vacuum-infiltrated for 2 min with distilled water containing 0.002% Silwet L-77 (OSI Specialties, Friendship, WV). The plants were placed in conical centrifuge tubes (Nalgene) containing a mesh septum placed about 2 cm above the bottom. IWF was collected by centrifuging the infiltrated plants at 400 ×g for 20 min, at 4°C. The IWF volume was measured with a micropipette and the appropriate volume of 5×SDS-PAGE loading buffer was immediately added. Samples were heated at 85°C for 5 min, then frozen or loaded on acrylamide gel.
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FIGURE LEGENDS

Figure 1: Arabidopsis RabE proteins interact with *P. syringae* AvrPto in the yeast two-hybrid system. Interaction is visualized by development of blue color on media containing X-Gal. Negative control (−) = pNLexA (bait) and pB42AD (prey) vectors; positive control (+) = pLexA-A53 and pB42AD-T. A, AvrPto (in pNLexA) interacts with Arabidopsis RabE1d, but not with other members of the Rab superfamily (in pB42AD). B, AvrPto (in pNLexA) interacts with all four tested Arabidopsis RabE proteins (in pB42AD). Yeast expressing AvrPto in pNLexA and RabD2a in pB42AD is shown as negative control. C, AvrPto (in pB42AD) interacts with RabE1d or RabE1d-Q74L, but not with RabE1d-S29N. For this experiment only, wild-type RabE1d and the mutated RabE1d proteins were cloned in the bait vector pGILDA and modified by replacing the two C-terminal conserved cysteine residues—sites of geranylgeranylation (Figure S1)—with glycine and serine to prevent prenylation and membrane association.

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Figure 3: GFP-RabE1d localization in Arabidopsis leaf cells. Confocal microscope images of the leaf epidermis of transgenic Arabidopsis plants expressing GFP-RabE1d. A, projection along the Z-axis of several optical planes intersecting the leaf epidermal cell layer. GFP-RabE1d is visible in intracellular punctate structures and at the cell periphery. B, single focal plane intersecting a stomate and the cortical layer of epidermal cells.
Arrowheads point at intracellular punctate structures. C, single focal plane intersecting epidermal cells. The same pattern of distribution of GFP-RabE1d was observed in at least five independent transgenic lines. Scale bars = 50 μm. D and E, Confocal microscope images illustrating GFP-RabE1d co-localization with the FM4-64 dye at the plasma membrane (A) and with sialyl transferase (ST-RFP) at the Golgi apparatus (B). D, single focal plane crossing adjacent epidermal cells (40x oil immersion objective, 4x zoom). Left, GFP-RabE1d fluorescence, green; center, FM4-64 fluorescence, red; right, merged image, in which the yellow color results from the overlap of red and green. E, single focal plane crossing the cytoplasm of a cell (40x oil immersion objective, 4x zoom). Left, GFP-RabE1d fluorescence, green; center, ST-RFP fluorescence, red; right, merged image, in which the yellow color results from the overlap of red and green. Arrowheads point at some of the co-labeled Golgi stacks in the merged image. Scale bars = 10 μm. F and G, Western blots of cellular membrane fractions separated by ultracentrifugation on a sucrose step gradient. Two different samples are shown: transgenic Arabidopsis overexpressing GFP-RabE1d (F), and nontransgenic Arabidopsis Col-0 gl1 (G). Lanes 1 through 4 represent the 4 membrane fractions collected at the interfaces between layers of different sucrose concentration: 18-25% (1), 25-34% (2), 34-40% (3) and 40-50% (4). Equal volumes of each fraction were loaded on SDS-PAGE gel. PM-ATPase is a plasma membrane marker, XT1 is a trans-Golgi resident protein, and g-TIP is a marker for the tonoplast. GFP-RabE1d and endogenous RabE proteins were detected with a polyclonal anti-RabE antibody (courtesy of Dr. K. Nomura).

**Figure 4.** Intracellular localization of the mutant GFP- RabE1d-Q74L protein.

A, Confocal microscope image of a representative Arabidopsis leaf expressing GFP-RabE1d-Q74L. Projection along the Z-axis of several focal planes crossing the epidermal cell layer. Several independent transgenic lines were analyzed with similar results. B, GFP-RabE1d-Q74L is mostly localized in the tonoplast. Leaves were stained with FM4-64, to visualize the plasma membrane, and immediately observed. The image represents a single focal plane (40x oil-immersion objective). Top, GFP fluorescence; middle, FM4-64 fluorescence (asterisks indicate autofluorescent chloroplasts in the mesophyll layer, below the epidermis); bottom, merged image. Arrowheads indicate where the tonoplast is most clearly distinct from the plasma membrane. Invaginations and formation of membranous structures are typical of the highly
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**Figure 6.** Focal accumulation of GFP-RabE1d in response to bacteria. Leaves of transgenic GFP-RabE1d Arabidopsis were syringe-inoculated with various strains of *Pst* DC3000 at a density of 1x10⁸ CFUs/ml. Confocal microscope observation 6 h post inoculation revealed focal accumulation of the fluorescent GFP-RabE1d in mesophyll cells (A, scale bar = 50 μm). Such accumulation is limited to a few cells in response to virulent and non-pathogenic bacteria, whereas it is widespread in response to avirulent bacteria, which trigger gene-for-gene resistance. B, no bacteria; C, *Pst* DC3000 *hrpA* mutant bacteria, non pathogenic; D, wild-type *Pst* DC3000, virulent; E, *Pst* DC3000 (*avrRpt2*), avirulent. Three independent transgenic lines (A1, A5, and A14) yielded similar results. B-E, all panels represent Z-stacks of the same number of optical planes intersecting the leaf mesophyll (arrowheads indicate some of the points of accumulation, scale bar = 200 μm). A second, independent set of images is represented in Supplemental Figure S4.

**Figure 7.** *RabE* cosuppression adversely affects Arabidopsis plant size and leaf morphology. A, Western blot (with anti-RabE antibody) illustrating how *RabE*-cosuppressed plants (lane 3) have a considerably lower amount of endogenous RabE protein, compared to both wild-type (lane 1) and GFP-RabE1d-overexpressors (lane 2). B, *RabE*-cosuppressed plants (top and bottom right) have smaller size and altered morphology, compared to wild-type Arabidopsis (top left), and to *RabE1d*-overexpressing plants (bottom left). C, Enlarged picture of the *RabE*--
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