Subcellular Localization and Functional Analysis of the Arabidopsis GTPase RabE<sup>1[W][OA]</sup>

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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 have been characterized with respect to their biological roles in plant growth, development, and response to stresses. In this study, we investigated the subcellular localization and function of an Arabidopsis (<em>Arabidopsis thaliana</em>) 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 <em>Pseudomonas syringae</em>, based on yeast two-hybrid analysis. We generated transgenic Arabidopsis plants that constitutively expressed one of the five RabE proteins (RabE1d) fused to green fluorescent protein (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 <em>P. syringae</em> bacteria; conversely, expression of the constitutively active RabE1d-Q74L enhanced plant defenses, conferring resistance to <em>P. syringae</em> infection.

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. The main effectors and regulators of these pathways appear to be shared between all eukaryotes. Among these, Rab proteins 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 compart-

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role in plant response to pathogen-derived elicitors (Robatzek et al., 2006). 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 (*Solanum lycopersicum*) and Arabidopsis. 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 *P. 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 mitogen-activated protein kinase signaling and promotes Arabidopsis susceptibility to nonpathogenic bacteria such as TTSS-defective mutants and to 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 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 *Schizosaccharomyces 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 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 “Results,” 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 roles of tomato Api2 and Api3 and Arabidopsis RabE GTPases in plant development and defense are unknown. Localization and function of RabE proteins have only recently begun to be investigated. Arabidopsis yellow fluorescent protein-RabE1d, transiently expressed in heterologous tobacco (*Nicotiana tabacum*) 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 GTPase 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 *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 and 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 to -D, -F, and -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 ecotype Columbia (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)-PCR analysis on rosette leaf 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 data sets. 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 of whether the five RabE proteins have redundant or distinct functions, we chose the highly expressed RabE1d (At5g03520) for further study.

**RabE1d Is Associated Not Only with the Golgi Apparatus But Also with 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 yellow fluorescent protein, 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 GFP under the control of the cauline

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**Figure 1.** Arabidopsis RabE proteins interact with *P. syringae* AvrPto in the Y2H system. Interaction is visualized by development of blue color on medium containing X-Gal. Negative 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 a 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 Cys residues (sites of geranylgeranylation) with Gly and Ser to prevent prenylation and membrane association.
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. 3, A–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 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 min 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 colocalization 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 coexpressing GFP-RabE1d and ST-RFP revealed overlapping fluorescence signals, confirming RabE1d’s 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 reported previously in heterologous tobacco cells, but also in the PM.

Endogenous RabE Proteins Cofractionate with PM and Golgi Markers

GFP-RabE1d expression in the transgenic plants was driven by the cauliflower mosaic virus 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 Suc 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 (Morsomme et al., 1998). A lower amount of endogenous RabE, as well as GFP-RabE1d, cofractionated with xylosyl transferase (XT1), a Golgi apparatus resident protein (Faik et al., 2002; Cavalier and Keegstra, 2006; Zeng and Keegstra, 2008; Fig. 3, F and G). A tonoplast marker, γ-tonoplast transporter, was not detected in the fractions containing the PM or Golgi markers.
integral protein (γ-TIP), 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 interexperiment 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 that 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 the Arabidopsis Biological...
Resource Center Arabidopsis transgenic lines expressing various endomembrane markers fused to GFP (Cutler et al., 2000). Comparison of GFP-RabE1d-Q74L fluorescence with 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 in 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 $1 \times 10^9$ colony-forming units (cfu) mL$^{-1}$ and analyzed by CLSM at 5 to 6 h after 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 nonpathogenic TTSS-defective mutant hpaA$^-$ (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. 7, B and C). Rosette leaves developed normally for the first 3 weeks, when Arabidopsis development is usually slower, and plants were indistinguishable from Col-0 plants. In the following 2 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 plants 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 stems 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 with expression in wild-type plants. 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 as a 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, therefore, is specific and limited to the RabE genes, primarily RabE1d and -E1e.

Figure 5. Localization pattern of GFP-RabE1d-Q74L compared with the localization of a PM marker protein. A, C, and E, Arabidopsis expressing a GFP fusion to the PM integral protein PIP2A (line Q8). B, D, and F, Arabidopsis expressing GFP-RabE1d-Q74L. In C to F, samples were plasmolyzed in 1 M NaCl. Asterisks indicate areas between plasmolyzed cells; Hechtian strands are noticeable in C and E (PM) but not in D and F (RabE-Q74L). Arrowheads indicate chloroplast auto-fluorescence (red); chloroplasts are on the inside of the PM (E), while GFP-RabE1d-Q74L fluorescence is on the cytoplasmic side of the chloroplasts. All images are single focal planes. Bars = 50 μm (A and B), 20 μm (C), and 10 μm (D–F).

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 $1 \times 10^8$ cfu mL$^{-1}$. A, Confocal microscopy observation at 6 h after inoculation revealed focal accumulation of the fluorescent GFP-RabE1d in mesophyll cells. Such accumulation is limited to a few cells in response to virulent and nonpathogenic bacteria, whereas it is widespread in response to avirulent bacteria, which trigger gene-for-gene resistance. Bar = 50 μm. B, No bacteria. C, Pst DC3000 hrpA2 mutant bacteria, nonpathogenic. D, Wild-type Pst DC3000, virulent. E, Pst DC3000 (avrRpt2), avirulent. Three independent transgenic lines (A1, A5, and A14) yielded similar results. For B to 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). A second, independent set of images is shown in Supplemental Figure S4. Bar = 200 μm.
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 the appearance of minute sparse indentations in mature rosette leaves about 2 weeks prior to bolting. The origin and significance of these indentations are 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 with 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 (for 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 (Fig. 8C, arrowheads). 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. Therefore, they could play fundamental roles in the secretion of extracellular matrix molecules, thereby influencing plant growth and development, as well as in the 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
Characterization of the Arabidopsis RabE Small GTPase

protein, AvrPto, in Y2H assays. Because a number of studies have implicated vesicle trafficking in pathogen defense (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 not only that RabE proteins are 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 the traffic of secretory vesicles from the Golgi to the PM (i.e. instead of other post-Golgi target membranes), as suggested previously 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 (Ségev, 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 nonspecific 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 the 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 the 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 RabE1d and -E1g and, to a lesser extent, RabE1a, -E1b, and -E1c (Fig. 6E). Consistent with this speculation, knockout mutants of RabE1d, 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; 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 colocalization of AvrPto and RabE1d to the same host membrane, we have been unable to detect AvrPto-RabE1d interaction using in vivo communoprecipitation 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). Thus, our results 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 may require special conditions.

Interestingly, GFP-RabE1d plants challenged with the avirulent strain Pst DC3000 (avrKpt2) 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 \textit{Pst} DC3000 (i.e. in a susceptible interaction) or with the \textit{hrpA} 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).

\textit{RabE} cosuppression in Arabidopsis, under the conditions reported in this study, did not result in increased susceptibility to \textit{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 discernible defense phenotype. A complete knockout of all five \textit{RabE} genes would be necessary to resolve this question. However, the dwarf phenotype of partially \textit{RabE}-cosuppressed plants suggests that it is unlikely that completely \textit{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 \textit{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 apoplast in 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 the expression of RabE1d–Q74L suggest the activation of other secretory pathways in these plants in addition to the SAR pathway. Interestingly, activation of SAR and resistance to \textit{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 into plant defense and indicate possible avenues for engineering resistance in crops.

\section*{Materials and Methods}

\subsection*{Y2H Assay}

We identified Arabidopsis (\textit{Arabidopsis thaliana}) proteins that interacted with \textit{AvrPto} of \textit{Pseudomonas syringae pv tomato strain DC3000} using the Matchmaker LexA-based \textit{Y2H} system (Clontech Laboratories). Two Arabidopsis cDNA libraries, constructed from infected and uninfected Landsberg erecta plants (kindly provided by J. Jones), were screened. The \textit{AvrPto} coding sequence was amplified from \textit{Pst} DC3000 genomic DNA by PCR (sense primer, 5′-CGGAATTCCGACATTGGAATAATATGTTGC-3′; antisense primer, 5′-GCTCGAGATGCAGCTTTACCA-3′) and cloned into pNLexA to serve as bait in the \textit{Y2H} screen.

\subsection*{RabE Cloning and Mutagenesis}

We amplified the \textit{RabE} \textit{(At5g0520)} coding sequence from Arabidopsis Col-0 cDNA using the rabE-5′ and rabE-3′ primers (Supplemental Table S1), containing the EcoRI and BamHI restriction sites, respectively. The PCR product was ligated into a TOPO vector (pCR2.1; Invitrogen) and sequenced. Single nucleotide changes were introduced in the \textit{RabE} sequence by two-step overlapping PCR, to generate the \textit{RabE1d–S29N} and \textit{RabE1d–Q74L} mutant derivatives. RabE1d–S29N was obtained through a G→A substitution; in the first PCR step, two overlapping \textit{RabE} fragments were amplified using the primer combinations rabE-5′/S29N-rev and rabE-3′/S29N-for (Supplemental 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 allowing annealing of the two gene fragments and amplification of the full-length coding sequence. A similar procedure was used to introduce 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 (Supplemental Table S1). RabE1d–S29N and RabE1d–Q74L amplification products were introduced into pCR2.1-TOPO and sequenced.

\subsection*{GFP-RabE1d Transgenic Plants}

\textit{RabE1d} and the mutant variant \textit{RabE1d–Q74L} were subcloned in the EcoRI and BamHI sites of the binary expression vector pEGAD (Catlier et al., 2000), downstream of the enhanced GFP sequence, to create translational fusions. The binary vector was introduced in \textit{dictyostelium} and \textit{Arabidopsis} bacterial strains. 

\subsection*{Protein Extraction and Immunoblotting}

Total proteins were extracted as follows: approximately 20 mg (fresh weight) of fresh or frozen leaf tissue was ground with a pestle in a microtube in the presence of 100 μl of 1× SDS-PAGE loading buffer (90 μg tris-HCl, pH 8.0, 100 μS dithiothreitol, 3% SDS, 22.5% Suc, 10 μl 3-molal Pro tease Inhibitor Cocktail for plant cell extracts [Sigma], and bromphenol 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 20,000g for 2 min to pellet debris. An equal volume of each sample was used for SDS-PAGE. Total proteins were separated on precast gradient gels (4%–20%; ISC BioExpress), then transferred onto Immobilon-P membranes (Millipore) using a semidyax transfer apparatus (SEMI PHOR; Hoefer Scientific Instruments). Protein detection was carried out with the anti-RabE polyclonal antibody (described below).

\subsection*{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 of 5 ml of...
Characterization of the Arabidopsis RabE Small GTPase

of ice-cold extraction buffer (50 mM HEPES, pH 7.5, 100 mM KCl, 10 mM EDTA, 1 mM dithiothreitol, and 10 μL mL⁻¹ Protease Inhibitor Cocktail for plant cell extracts [Sigma]) containing 34% Suc (w/v). The extract was homogenized with a Polytron immersion blender (three 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% Suc in about a 10-mL final volume (concentration was determined with a refractometer) and layered on a 5-mL cushion of 50% Suc in clear ultracentrifugation tubes. The homogenate was subsequently layered with 10 mL of 34% Suc, 8 mL of 25% Suc, and 8 mL of 18% Suc (w/v). All Suc 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 Suc-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 blotting were performed as described above.

Confocal Microscopy 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. 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). For FM4-64 staining, detached Arabidopsis leaves were submerged in 8.2 μM FM4-64 (Molecular Probes) 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 was a gift of Dr. F. Brandizzi (Saint-Jore et al., 2002). Gold particles (1.0 μm) were harvested and arranged on Murashige and Skoog agar plates (4.3 g L⁻¹ Murashige and Skoog salts, 0.8% agar, pH 5.7). The DNA-coated particles were delivered into the lower leaf epidermis with a particle gun (DuPont), using 1,100-psi rupture discs under a vacuum of 25 in mercury. After bombardment, leaves were incubated on the sealed plates at room temperature, and fluorescence was observed at 24 h after transformation. For 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 μm 2 m⁻² s⁻¹, and the temperature was kept constant at 20°C. Pst DC3000 bacteria were cultured in low-salt Luria-Bertani medium (10 g L⁻¹ tryptone, 5 g L⁻¹ yeast extract, and 5 g L⁻¹ NaCl) supplemented with 100 μg mL⁻¹ 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 0.002% Silwet L-77 (OSI Specialties). The plants were placed in conical centrifuge tubes (Nalgene) containing a mesh septum placed above 2 cm above the bottom. IWF was collected by centrifuging the infiltrated plants at 400g 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 onto an acrylamide gel.

Supplemental Data

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

Supplemental Figure S1. ClustalW alignment of the five Arabidopsis RabE proteins and their closest homologues in other organisms.

Supplemental Figure S2. Bacterial multiplication assays.

Supplemental Figure S3. Localization pattern of GFP-RabE1d-Q74L. The following primers were used for RTPCR in response to bacteria.

Supplemental Table S1. Primers for RabE cloning and mutagenesis.

Supplemental Table S2. Gene-specific primers for RT-PCR.

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Characterization of the Arabidopsis RabE Small GTPase


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