Arabidopsis PEN3/PDR8, an ATP Binding Cassette Transporter, Contributes to Nonhost Resistance to Inappropriate Pathogens That Enter by Direct Penetration

Mónica Stein, Jan Dittgen, Clara Sánchez-Rodríguez, Bi-Huei Hou, Antonio Molina, Paul Schulze-Lefert, Volker Lipka, and Shauna Somerville

INTRODUCTION

Nonhost resistance is the type of nonspecific resistance that an entire plant species exhibits against all genotypes within a pathogen species (Thordal-Christensen, 2003). Although until recently little was known about the biochemical defenses that contribute to nonhost resistance, cytological descriptions suggested that a majority of inappropriate fungal pathogens were unable to breach the plant cell wall and infiltrate host cells (Yun et al., 2003; Zimmererli et al., 2004). However, some variation in penetration efficiency exists among different host and fungal pathogen combinations (Mellersh and Heath, 2003). These studies also showed that plants respond actively to attack by inappropriate pathogens and do not rely solely on preformed and constitutive barriers for protection against inappropriate pathogens (Meyer and Heath, 1988; Zimmererli et al., 2004). Furthermore, it appears that operationally, nonhost resistance can be divided into penetration resistance, barriers limiting entry of the pathogen into cells, and postpenetration resistance, mechanisms that act intracellularly if penetration resistance is overcome (Fernandez and Heath, 1991; Huitema et al., 2003; Mellersh and Heath, 2003; Yun et al., 2003; Zimmererli et al., 2004; Lipka et al., 2005).

Both surveys of mutants with defects in various defense functions and screens for mutants specifically compromised in nonhost resistance have identified a diverse group of genes that contribute to nonhost resistance. Among the mutants with defects in the salicylic acid (SA) signal transduction pathway, nonhost resistance was diminished in eds1 mutants and transgenic plants with the bacterial NahG gene relative to wild-type plants (Parker et al., 1996; Mellersh and Heath, 2003; Yun et al., 2003; Zimmererli et al., 2004). Using virus-induced gene silencing, the chaperone and chaperone-like proteins HSP70, HSP90, and SGT1, which are thought to stabilize resistance (R) proteins and act upstream of EDS1, were shown to contribute to nonhost resistance in Nicotiana benthamiana (Peart et al., 2002; Kanzaki et al., 2003). Mutants with defects in the ethylene/jasmonate (ET/JA) signal transduction pathways exhibited wild-type levels of nonhost resistance in Arabidopsis thaliana, even though there is evidence from microarray studies that this pathway is preferentially induced after inoculation of plants with some inappropriate pathogens (Huitema et al., 2003; Zimmererli et al., 2004). These data suggest that the ET/JA pathway and components of the SA pathway might be involved in nonhost resistance.
pathway acting downstream of eds1 play no role or only a limited role in nonhost resistance. Alternatively, it is possible that these pathways contribute to resistance to inappropriate pathogens only after the other defenses have been defeated (Jones and Takemoto, 2004). Because EDS1 contributes to basal resistance (Parker et al., 1996), defenses that act to limit the growth of appropriate pathogens even in compatible interactions, it seems likely that there is some overlap between basal resistance and nonhost resistance.

Additional host components, for which no clear role in basal resistance has been demonstrated to date, contribute to nonhost resistance. NHO1, a glycerol kinase, is required for nonhost resistance in Arabidopsis to a bacterial pathogen of bean (Phaseolus vulgaris), Pseudomonas syringae pv phaseolicola (Kang et al., 2003). In physiological studies using inhibitors, the actin cytoskeleton was shown to be required for nonhost resistance against barley (Hordeum vulgare) and wheat (Triticum aestivum) powdery mildews in pea (Pisum sativum) and Arabidopsis, respectively (Kobayashi et al., 1997; Yun et al., 2003). These genes do not fit into a single pathway or process, but their identification does suggest that diverse processes contribute to nonhost resistance. This is consistent with an early model of nonhost resistance in which it was proposed that this form of resistance consists of several barriers operating in parallel to limit pathogen colonization (Heath, 2000).

To identify the components required for nonhost resistance, we screened for Arabidopsis mutants allowing increased penetration by the barley powdery mildew Blumeria graminis f. sp. hordei, assuming that such mutants would carry defects in those components of nonhost resistance that limit pathogen entry into host cells. The syntaxin PEN1 (=SYP121) and the glycosyl hydrolase PEN2 were recovered from this and related screens (Collins et al., 2003; Lipka et al., 2005). Here, we describe a third mutant isolated from this screen and show that PEN3 encodes the putative ATP binding cassette (ABC) transporter PDR8. Subcellular localization of PEN3 in the plasma membrane and extensive gene interaction studies lead us to speculate that PEN3 mediates the targeted export of toxins to penetration sites.

RESULTS

don3 Lacks Penetration Resistance to Three Inappropriate Pathogens

We conducted a screen for the loss of resistance to inappropriate pathogens by screening for Arabidopsis mutants that allowed B. g. hordei to form haustoria within epidermal cells at a higher frequency than on wild-type plants. Haustoria, which are fungal feeding structures encased in a specialized host membrane within epidermal cells, are produced once the fungal germings have successfully breached the host cell wall. The few B. g. hordei haustoria that formed in Arabidopsis were rapidly encased in callose and could be recognized by their distinctive oval shape in inoculated leaves stained with the callose stain aniline blue (Figure 1E, inset). Nine pen mutants were recovered from ~12,000 M2 plants from ethyl methanesulfonate–mutagenized seeds. Mapping experiments and crosses among the mutants were used to place the pen mutants in complementation groups. When the identities of the PEN genes became known, allelism among the various mutants was confirmed by sequencing the appropriate gene (i.e., PEN1, PEN2, or PEN3), pen1–4 (Collins et al., 2003), pen2–3 (Lipka et al., 2005), pen3–1, and pen3–2 were recovered from this screen. pen3–1, like the pen1 and pen2 mutants, supported a higher frequency of fungal penetration (Figure 1A). Another feature of the phenotype conferred by pen3 was that callose deposition lining the entire periphery of invaded epidermal cells was more common than in wild-type plants (Figures 1D and 1E). Compared with wild-type plants, pen3–1 plants also allowed increased frequency of formation of elongating secondary hyphae, an indication that the underlying haustoria were functional (Figures 1A to 1C). Secondary hyphae are the hyphae that emerge from the conidium after the first haustorium is established. Germ tube growth is supported by reserves in the conidium, whereas the emergence and growth of secondary hyphae are thought to be dependent on nutrients acquired from the host via the haustorium (Masri and Ellingboe, 1966; Ellingboe, 1972). Therefore, pen3–1 mutants were partially compromised not only in penetration resistance against B. g. hordei but also in a mechanism restricting haustorium function. Loss of PEN3 function does not allow B. g. hordei to complete its life cycle and form asexual conidia on Arabidopsis as it does on barley, suggesting that additional factors contribute to nonhost resistance to B. g. hordei in Arabidopsis.

To determine whether increased pathogen entry was limited to interactions with B. g. hordei, pen3–1 plants were inoculated with two other inappropriate pathogens, Erysiphe pisi (tribe Erysiphaceae), the powdery mildew pathogenic on pea, belongs to a tribe distinct from Erysiphe cichoracearum (tribe Golovinomyce- teae) and B. g. hordei (tribe Blumerieae) (Saenz and Taylor, 1999; Braun et al., 2002). Similar to B. g. hordei, E. pisi was able to initiate the formation of elongating secondary hyphae at a higher frequency on pen3–1 than on wild-type plants (Figure 5D). Likewise, Phytophthora infestans, which is a hemibiotrophic oomycete pathogen and the causal agent of late blight in potato (Solanum tuberosum), formed invasive hyphae, which were encased in callose (Figure 1I, inset), more often in pen3–1 mutants than in wild-type plants (Figure 1H). Inoculation with P. infestans elicited little callose deposition in wild-type plants, whereas dramatic callose deposition was observed in pen3–1 epidermal cells (Figures 1H and 1I). When it occurred, penetration by P. infestans into Arabidopsis epidermal cells was often accompanied by local cell death at sites of infection (Huitema et al., 2003).

Although the wild type appeared healthy where droplets of P. infestans zoospores had been applied (Figure 1F), pen3–1 exhibited macroscopic cell death (Figure 1G), consistent with the idea that a greater proportion of oomycete individuals had penetrated into host cells and elicited cell death. Thus, pen3–1 had a diminished capacity to restrict pathogen entry by three different inappropriate pathogens.

PEN3 Encodes a PDR-Like ABC Transporter

Mapping populations were generated by crossing pen3–1 and pen3–2 to Landsberg erecta (Ler). Mutant plants identified in the F2 generation were used for bulk segregant mapping (Lukowitz
et al., 2000). In both crosses, PEN3 mapped to the bottom of chromosome 1 between markers nga280 and ciw1. These two markers were used to identify additional recombinants in this genetic interval from ∼3600 F2 plants. In this manner, the interval containing PEN3 was delimited to a region encompassed by BAC F23H11. Nineteen T-DNA mutant populations with insertions in 1 of 15 genes in this interval were screened for the phenotype conferred by pen after inoculation with B. g. hordei (Ecker, 2002). Two of these T-DNA populations (SALK__110926 and SALK_000578) segregated plants with a penetration-deficient phenotype. These mutants had predicted insertions in a PDR-like ABC transporter (At1g59870). Both pen3-1 and pen3-2 carried single nucleotide substitutions at nucleotides 1419 and 3335, respectively, from the A of the ATG initiation codon of the genomic sequence for this gene (Figure 2A). Two T-DNA alleles, pen3-3 (SALK_110926) and pen3-4 (SALK_000578), had insertions near the 5’ end of the coding region (Figure 2A). The PEN3 gene had previously been annotated as PDR8 based on its homology with yeast PDR transporters (van den Brule and Smart, 2002). It encodes a 4.3-kb cDNA and is predicted to encode a 1469–amino acid protein with 13 transmembrane domains (Figure 2B). Arabidopsis has 15 PDR family members, which are highly similar at the amino acid level (van den Brule and Smart, 2002). An alignment of these members showed that the point mutations in pen3-1 and pen3-2 occurred in highly conserved regions of the nucleotide binding folds (Figure 2C). The nucleotide binding folds are thought to mediate ATP binding and consist of a Walker A motif followed by an ABC signature motif and a Walker B motif (van den Brule and Smart, 2002). The mutation in pen3-1 converted a Gly to an Asp in the ABC signature motif of the first nucleotide binding fold, whereas the mutation in pen3-2 converted a Gly to a Ser in the Walker A motif of the second nucleotide binding fold. PEN3 transcript was detected in pen3-1 and pen3-2 but not in the T-DNA mutants pen3-3 and pen3-4 (data not shown). Given that all four pen3 alleles have identical phenotypes, we assume that proteins encoded by pen3-1 and pen3-2 are nonfunctional, at least in nonhost resistance.

Figure 1. pen3 Nonhost Resistance Phenotypes.

(A) Mean of the frequency of B. g. hordei penetration (left) and hyphal elongation (right) on Arabidopsis at 2 DAI, expressed as a percentage of total germinated spores. Wild-type controls are represented in red, pen1-4 plants in blue, pen2-3 plants in yellow, and pen3-1 plants in green. Asterisks denote statistically significant differences between mutants and the wild type by Student’s t test (** P < 0.0001, * P < 0.001). (B) and (D) B. g. hordei inoculation on Columbia-0 (Col-0). Conidia (sp; arrowhead) germinate and produce appressoria but seldom are able to penetrate and establish functional haustoria (B). Papillae (p; arrowhead), callose-rich cell wall appositions, form at penetration sites whether or not the powdery mildew pathogen is able to successfully breach the cell wall and form a haustorium (D). Papillae were used as markers for attempted penetration sites. (C) and (E) B. g. hordei inoculation on pen3-1. A higher proportion of conidia are able to penetrate, establish haustoria, and form elongating secondary hyphae (hy) on pen3 plants relative to Col-0 (C) and inset). Haustorial formation (ha) is associated with callose deposition, encompassing the entire invaded host epidermal cell (ep; arrowhead) (E) and inset). (F) to (I) Response to P. infestans inoculation. Cell death (dc; arrow) is evident macroscopically after inoculation of pen3 (G) but not in Col-0 (F). A small amount of callose is deposited in Col-0 (H), whereas widespread callose deposition and occasional intracellular hyphae (hy; arrowhead) are observed in pen3 (I) and inset). In (B) and (C), samples were stained with trypan blue at 2 DAI and visualized by bright-field microscopy. In (D), (E), (H), and (I), samples were stained with aniline blue at 2 DAI to detect callose and visualized by fluorescence microscopy. Bars = 30 μm.
The Arabidopsis PDR family of ABC transporters has been studied via RNA gel blotting and RT-PCR to determine in which plant organs these transporters are expressed (van den Brule and Smart, 2002). In addition, publicly available databases provide microarray expression profiles of different Arabidopsis organs, tissues, and environmental treatments (Rhee et al., 2003; Zimmermann et al., 2004). These resources showed that PEN3 was expressed in all tissues, but most highly in leaves. Most other PDR family members were expressed at low levels and in specific plant organs (see Supplemental Table 1 online) (Rhee et al., 2003). In leaves, PEN3 transcript accumulated to levels comparable to those of metabolic housekeeping genes, such as cytosolic glyceraldehyde-3-phosphate, and 1 to 2 orders of magnitude higher than the other PDR family members (see Supplemental Table 1 online) (Shih et al., 1991). The gene encoding PDR7, the ABC transporter most similar to PEN3 in sequence (90% amino acid similarity), was expressed primarily in roots (see Supplemental Table 1 online), and T-DNA insertion mutations in PDR7 (SALK_134725 and SALK_008761) did not exhibit the penetration-deficient phenotype (data not shown). These microarray data, together with RNA gel blot analyses, indicate that PEN3 is highly and ubiquitously expressed in plant tissues. These data further suggest that there is limited functional redundancy among the PDR genes and PEN3.

Publicly available expression data were mined to determine whether PEN3 expression was modified after pathogen attack (see Supplemental Tables 2 and 3 online) (Zimmermann et al., 2004). Induction was modest after inoculation with virulent pathogens (e.g., E. cichoracearum, Agrobacterium tumefaciens, and the necrotroph Plectosphaerella cucumerina), inappropriate pathogens (e.g., B. g. hordei, P. infestans), and nonspecific elicitors (e.g., chitin fragments, flg22 peptide) but dramatic after inoculation with avirulent bacteria and the phloem-feeding aphid Myzus persicae (see Supplemental Table 2 online) (Glombitza et al., 2004; Zimmermann et al., 2004; De Vos et al., 2005; Ramonell et al., 2005). Induction by the flg22 peptide, a synthetic version of a conserved region of flagellin, was abolished in plants lacking FLS2, a receptor-like kinase required for flagellin perception (see Supplemental Table 2 online) (Gomez-Gomez and Boller, 2000). Exposure to methyl jasmonate, ozone, and the herbicides primisulfuron and prosulfuron also induced PEN3 expression (see Supplemental Table 2 online) (Glombitza et al., 2004; Zimmermann et al., 2004). Abiotic factors such as heat shock treatments downregulated the expression of PEN3 (see Supplemental Table 2 online) (Busch et al., 2005). Thus, PEN3 expression is altered by pathogens and a subset of abiotic stresses.

**Figure 2.** Molecular Identity of PEN3 and of the pen3 Alleles.

**A** PEN3 gene structure indicating exons (gray boxes) and introns (black lines connecting exons). The genomic sequence of PEN3 is 6.1 kb. Sequencing of the pen3-1 and pen3-2 alleles revealed single nucleotide changes (asterisks) that result in amino acid substitutions. Two T-DNA alleles (black arrowheads) carry insertions early in the gene.

**B** Predicted architecture of the PEN3 protein. PEN3 is predicted to have 1469 amino acids. The amino acid changes in pen3-1 and pen3-2 occur in the ABC signature motif and the Walker A motif of the first and second nucleotide binding folds (NBF), respectively.

**C** Alignment of amino acids of the two nucleotide binding folds of the 15 members of the Arabidopsis PDR family and of tobacco PDR1. Mutations in pen3-1 and pen3-2 result in changing highly conserved Gly (boldface, underlined G) to larger amino acids, Asp and Ser, respectively. Both changes occur in pockets thought to mediate ATP binding.
Resistance to *E. cichoracearum* and Cell Death in *pen3* Are SA-Dependent

To examine the possibility that *pen3-1* plants were also defective in basal resistance to virulent pathogens, they were infected with the *Arabidopsis* powdery mildew, *E. cichoracearum*. Surprisingly, *pen3-1* plants underwent chlorosis and cell death after *E. cichoracearum* infection (Figure 3A). Closer inspection indicated that cell death was fungus-associated and did not spread extensively beyond areas of fungal colonization (Figures 3C and 3E). By 5 d after inoculation (DAI), *E. cichoracearum* hyphae had elongated on wild-type leaves, leaving a trail of callose-containing papillae at each penetration site (Figure 3B). By contrast, hyphal elongation on *pen3-1* plants was accompanied by extensive callose deposition, preceding the death of penetrated cells (Figures 3C and 3E). By 7 DAI, extensive conidiation was observed on wild-type plants, whereas colonies that formed on *pen3-1* were stunted, lacked conidiophores, and were overlaid with patches of dead cells (Figure 3E).

Additionally, *pen3* plants were inoculated with the broad host range necrotrophs *Botrytis cinerea* and *P. cucumerina* (Berrocal-Lobo et al., 2002); *pen3-1* and *pen3-2* mutants were more susceptible to *P. cucumerina* than wild-type plants (Figure 4). Leaf tissue damage and fresh weight reduction caused by this fungus were greater in *pen3* mutants than in wild-type plants and similar to the damage observed in the highly susceptible *agb1-1* mutant, which is impaired in the β-subunit of *Arabidopsis* heterotrimeric G protein (Figure 4A) (Llorente et al., 2005). Resistance of *pen3-1* plants to *B. cinerea* did not differ from that of wild-type plants (data not shown).

Cell death in response to pathogen attack is often associated with the activation of the SA defense pathway (Greenberg and Yao, 2004). Similarly, chlorosis is associated with high levels of ET production (Schaller and Keiber, 2001). Double mutants were generated between *pen3-1* and mutants affecting the SA and ET/JA signal transduction pathways to determine whether these defense signaling pathways were necessary for the pathogen-induced chlorosis and necrosis phenotype. Transgenic NahG plants, as well as mutants lacking a functional SA pathway, such as *eds1*, *pad4*, and *sid2*, suppressed the cell death and resistance phenotypes of *pen3-1*, allowing *E. cichoracearum* to conidiate (Figure 3F). The effect of

![Figure 3](image-url)  
**Figure 3.** *pen3-1* Mutants Are Resistant to *E. cichoracearum* and Become Chlorotic after *E. cichoracearum* Infection.  

(A) Single leaves at 7 DAI with the *Arabidopsis* powdery mildew, *E. cichoracearum*. Col-0 (left) supports good fungal conidiation, which is evident by eye as the whitish powdery appearance of inoculated leaves. Col-0 does not develop lesions, whereas *pen3-1* (right) undergoes chlorosis and cell death.  

(B) and (C) On Col-0, *E. cichoracearum* infection elicits discrete callose deposits at papillae (p) (B), whereas penetration attempts on *pen3-1* plants elicit widespread callose deposition and cell death (dc) (C). Leaves were stained with aniline blue at 5 DAI. Bars = 100 μm.  

(D) and (E) Lesions (dc) can be observed in *pen3-1* (E) but not in Col-0 (D) under conidiophores (cp) and hyphae. Leaves were stained with trypan blue at 7 DAI. Bars = 100 μm.  

(F) Double mutant analysis to evaluate the role of the SA and ET/JA signal transduction pathways on resistance to *E. cichoracearum* in *pen3-1* plants. On double mutants with *pen3-1* and mutants or transgenic plants with blocks in the SA pathway (e.g., *eds1-1*, *NahG*, *pad4-1*, *sid2-1*), powdery mildew growth and conidiation exceed those observed in wild-type plants. The double mutant *pen3-1* *sgt1b-1* and the triple mutant *pen3-1* *sgt1b-1* *rar1-10* support an intermediate level of powdery mildew conidiation that is slightly less than that observed on the wild type. Mutations in the ET pathway genes (e.g., *Etr1-1*), the JA pathway genes (e.g., *col1-1*, *jar1-1*), and in *rar1-10* were not able to suppress the chlorotic and necrotic phenotype that develops on *pen3-1* mutants after infection with the *Arabidopsis* powdery mildew. Plants were photographed at 7 DAI.  

(G) Double mutant analysis of the effect of *pen1-1* and *pen2-3* on *pen3-1*-associated resistance to *E. cichoracearum*. Plants were photographed at 6 DAI unless indicated otherwise.  

(H) Double mutant analysis of the effect of the SA signal transduction pathway (*eds1-1*, *NahG*, *sid2-1*) and of the JA signal transduction pathway (*col1-1*, *jar1-1*) on light-induced chlorosis of *pen3-1* plants. Plants were 4 weeks old when the photograph was taken.
Figure 4. pen3 Mutants Are More Susceptible to the Broad Host Range, Necrotrophic Pathogen P. cucumerina.

(A) pen3 and pen2 are highly susceptible to P. cucumerina. Plants were inoculated with a suspension of $2 \times 10^6$ spores/mL and scored at 7 DAI.
* Significantly different from Col-0 using Student’s t test ($P < 0.05$).

(B) The susceptibility of P. cucumerina to the pen3-1 mutant does not depend on the SA signal transduction pathway. Plants were inoculated with a suspension of $1 \times 10^6$ spores/mL and scored at 10 DAI.
* Significantly different from pen3-1 using Student’s t test ($P < 0.05$).

The susceptibility of plants was scored by fresh weight reduction (mean ± SD). At least 30 plants per genotype were inoculated with each pathogen, and the experiment was repeated four times. The highly susceptible agb1-1 mutant was used as a positive control for disease development. FW, fresh weight.

two other SA-related mutants, rar1 and sgt1b, on resistance to E. cichoracearum in pen3-1 was also investigated. Mutations in RAR1 did not affect the occurrence of cell death in inoculated pen3-1 (Figure 3F). However, in pen3-1 sgt1b double mutants, conidiation was observed initially but chlorosis and cell death were delayed to ~10 DAI (data not shown). Triple pen3-1 sgt1b rar1 mutants resembled pen3-1 sgt1b double mutants. Mutations that affect the ET/JA pathway, such as jar1, cot1, and Etr1, did not alter the pen3-1 cell death phenotype. Thus, pen3-1 resistance to the Arabidopsis powdery mildew is SA-dependent and ET/JA-independent.

Disease development after P. cucumerina infection was modestly enhanced in the SA-deficient lines sid2-1 and NahG, as reported previously (Berrocal-Lobo et al., 2002), although to a lesser extent than in pen3-1 (Figure 4B). The enhanced susceptibility to P. cucumerina observed in pen3 mutants was further enhanced in pen3-1 sid2-1 or pen3-1 NahG double mutant lines, suggesting that PEN3 acts additively with the SA pathway to limit P. cucumerina infections.

We considered the possibility that a propensity to become chlorotic and necrotic could indirectly result in increased pathogen entry. To address this question, a set of 34 Arabidopsis mutants that are resistant to the powdery mildew pathogen were examined for pen3-like phenotypes (see Supplemental Table 4 online) (Greenberg and Ausubel, 1993; Frye and Innes, 1998; Rate et al., 1999; Clough et al., 2000; Petersen et al., 2000; Vogel and Somerville, 2000; Clarke et al., 2001; Mach et al., 2001; Rate and Greenberg, 2001; Maleck et al., 2002; Vogel et al., 2002, 2004; Liang et al., 2003). This collection included published cpr, acd, agd, and pmr mutants as well as a set of mil (for mildew-induced lesion) mutants (M. Nishimura, J. Vogel, and S. Somerville, unpublished data). Only one of these mutants, mil9, exhibited both increased penetration by B. g. hordei and resistance to E. cichoracearum (see Supplemental Table 4 online). The PEN3 gene from mil9 contained a point mutation at nucleotide 3985, which is predicted to change a Trp codon (TGG) to a stop codon (TGA). Thus, mutants prone to chlorosis and cell death do not commonly allow increased invasion by inappropriate pathogens.

Unlike pen3, pen1 and pen2 were not resistant to E. cichoracearum and did not become chlorotic upon infection (Collins et al., 2003; Lipka et al., 2005). As shown by the more rapid appearance of visible symptoms, pen2 was more susceptible to E. cichoracearum than the wild type, indicating that PEN2 is important for both basal and nonhost resistance (Figure 3G). The pen1 mutation was not able to suppress the E. cichoracearum-induced cell death of pen3-1 (Figure 3G). In a pen2-3 pen3-1 double mutant, however, cell death was delayed and resistance was compromised relative to the pen3-1 mutant (Figure 3G). Although some conidiation occurred, pen2-3 pen3-1 leaves underwent cell death and chlorosis at ~10 DAI (Figure 3G, data not shown). Thus, pen3 resistance to E. cichoracearum plants is partially dependent on PEN2. In addition, pen2, but not pen1, was more susceptible to P. cucumerina than the wild type, but to a lesser degree than pen3-1 and pen3-2 (Figure 4A). The double mutants pen3-1 pen1-1 and pen3-1 pen2-3 resembled the pen3 single mutants in their susceptibility to P. cucumerina (Figure 4A) (Lipka et al., 2005).

E. cichoracearum infection was not the only stress capable of inducing chlorosis and cell death in pen3-1 plants. Although pen3-1 plants were indistinguishable from wild-type plants up to 4 weeks after germination, eventually they became chlorotic and senesced earlier than wild-type plants (data not shown). This
phenotype was exacerbated by growth in continuous high light (24 h at 900 μE m⁻² s⁻¹) (Figure 3H). High light–induced chlorosis and senescence were suppressed by mutations in the SA pathway but not by those in the ET/JA pathway (Figure 3H). Thus, the SA pathway appears to be necessary for heightened sensitivity to abiotic stress in pen3-1 plants as well.

**Effects of SA and ET/JA Pathway Mutations on Residual Nonhost Resistance in pen3**

None of the mutations in the SA and ET/JA pathways tested reversed the loss of penetration resistance to *B. g. hordei* (Figure 5). However, plants carrying the NahG transgene and plants carrying mutations in *EDS1* were slightly compromised in their ability to restrict *B. g. hordei* entry into epidermal cells relative to wild-type plants (Figure 5) (Zimmerer et al., 2004). Microscopic inspection of the invasion and growth of *B. g. hordei* on double and single mutants revealed that the frequencies of fungal penetration on *pen3-1 NahG* and *pen3-1 eds1-1* were higher than those on the single mutants (Figure 5A). Colonies growing on these double mutant combinations were typically twice the average size than those growing on the single mutants (Figure 5B). This increase in growth was accompanied by an increase in hyphal branching (Figure 5C). Conidiation by *B. g. hordei* was not observed. *E. pisi* epiphytic growth was increased on *eds1* and *pen3-1* mutants compared with wild-type plants (Figure 5D). A cumulative effect was seen on *pen3-1 eds1-1* double mutants, on which *E. pisi* conidia recovered from *Arabidopsis* double mutants were able to successfully infect pea and cause disease (data not shown).

**Expression Profiling of pen3-1 Plants**

We compared the transcript profiles of wild-type and *pen3-1* plants at 1 DAI with *E. cichoracearum* or *B. g. hordei* using full-genome Affymetrix microarrays. Of the 22,810 probe sets (genes) on the microarray, 4240 exhibited some change in expression in this experiment. When considering the trends observed in the expression patterns of these genes, two main clusters were observed: genes induced by and genes repressed by pathogen attack (see Supplemental Figure 1 online). As described previously (Zimmerer et al., 2004), *B. g. hordei* elicited a more dramatic response than *E. cichoracearum*. Transcripts with increased levels after inoculation with the fungal pathogens included defense-related transcripts primarily, whereas transcripts with reduced levels consisted in large part of transcripts encoding photosynthetic and metabolic components (Zimmerer et al., 2004). It is possible that plants respond more dramatically to *B. g. hordei* because it cannot evade or suppress basal defenses as efficiently as the host powdery mildew, *E. cichoracearum*. In addition, responses to inoculation were more drastic in *pen3-1* than in the wild type. Included among these genes were several SA-associated genes (Table 1). These included genes of the SA pathway, such as *PAD4*, *SID2*, *EDS1*, and *EDS5*, as well as downstream SA pathway markers, such as *PR-4*, *PR-5*, chitinases, and glucanases (Shah, 2003). This hyperactivation of SA defenses, together with the double mutant analysis, suggests that the basis for the resistance to *E. cichoracearum* observed in *pen3-1* plants is an enhanced activation of the SA pathway.

A single transcript (At3g30720) was highly upregulated in *pen3-1*–independent infection status (*P* = 1.7 × 10⁻⁸). This observation was confirmed by semiquantitative RT-PCR using independent samples (data not shown). In addition, the expression of this gene did not change very much upon inoculation with pathogens in either *pen3* or the wild type (i.e., Col-0 uninoculated, 78 intensity units [average of four replicates]; Col-0 + *E. cichoracearum*, 99; Col-0 + *B. g. hordei*, 74; *pen3-1* uninoculated, 1082; *pen3-1* + *E. cichoracearum*, 916; *pen3-1* + *B. g. hordei*, 978). No other gene exhibited this expression pattern. This gene is predicted to encode a 59–amino acid polypeptide with no significant homology with any known protein. ESTs have been found for this transcript, and array data show that this transcript responds to high CO₂ and is constitutively upregulated in the ET-insensitive *Etr1* mutant (Zimmermann et al., 2004). Unlike *pen3-1*, *Etr1* mutants resemble wild-type plants in their ability to restrict the entry of *B. g. hordei* into epidermal cells, and *Etr1* plants are susceptible to *E. cichoracearum* (data not shown). Thus, high levels of expression of this uncharacterized gene are not sufficient to account for the mutant phenotypes of *pen3-1*.

Of the PDR genes, only three, including PEN3, changed expression after inoculation with pathogens (see Supplemental Table 3 online) (Nishimura et al., 2003). Although *PDR4* was repressed after infection, *PDR12* was induced, and its induction was dramatically enhanced in *B. g. hordei*–induced *pen3-1* plants.

**Localization of PEN3 to Penetration Sites after Pathogen Attack**

In plants, ABC transporters have been localized to the tonoplast, mitochondria, chloroplasts, and plasma membrane (Kushnr et al., 2001; Möller et al., 2001; Goodman et al., 2004; Pighin et al., 2004). Recently, proteomic studies of different organelles have placed PEN3 in the plasma membrane, mitochondria, and chloroplasts (Brugiere et al., 2004; Kleffmann et al., 2004; Nühse et al., 2004). Given its high abundance, PEN3 is likely a common contaminant in organelle preparations and unlikely to be localized in all three subcellular structures. To localize PEN3, a translational fusion to green fluorescent protein (GFP) was made, transformed into *pen3-1* plants, and shown to complement the phenotypes conferred by the *pen3-1* mutant (data not shown). PEN3-GFP was localized to the plasma membrane; no GFP signal was associated with chloroplasts (Figure 6A). After inoculation with *B. g. hordei*, PEN3-GFP accumulated to high levels in regions of the plasma membrane just under fungal appressoria, in the shape of compact disks surrounded by diffuse halos approximately the size of papillae (Figures 6B to 6D). Occasionally, this disk of PEN3-GFP signal was surrounded by a concentric circle of intense PEN3-GFP label within the diffuse halo (Figure 6B). Closer inspection of PEN3-GFP fluorescence at attempted entry sites revealed a three-dimensional bubble-like shape, presumably reflecting the invagination of the plant plasma membrane by the growing fungal penetration peg and newly developing haustorium.
A funnel-like structure, which resembled a hollow tube and extended into the plant cell, was sometimes observed at penetration sites at later stages (Figures 6G and 6H). Localization of PEN3-GFP after *E. cichoracearum* infection was similar to that observed after inoculation with *B. g. hordei*. PEN3-GFP accumulated in compact disks beneath appressoria, as well as in diffuse halos around this domain, and in bubble-like structures (Figures 6I to 6K). When *E. cichoracearum* haustoria were formed, the PEN3-GFP marker was also observed partially surrounding the haustorium (Figure 6L).

**Figure 5.** Combined Mutations in PEN3 and EDS1 or Introduction of the NahG Transgene Compromise Nonhost Resistance to *B. g. hordei* and *E. pisi.*

(A) Mean of the frequency of *B. g. hordei* penetration on Arabidopsis, expressed as a percentage of total germinated spores. Wassilewskija (Ws) is the wild-type control for *eds1-1*; Ler *sgt1b-1 rar1-10* is the control for double mutants with *sgt1b-1* and *rar1-10*; and Col-0 is the wild-type control for *npr1-1*, *sid2-1*, *pad4-1*, *jar1-1*, and NahG. Eight leaves per genotype were stained with aniline blue at 2 DAI, and the occurrence of callose-encased haustoria was monitored as a measure of penetration efficiency. *a* Significantly different from the wild type; *b* significantly different from *pen3* using Student’s t test (*P* < 0.001).

(B) Average hyphal length of *B. g. hordei* colonies growing on different mutants. Leaves were stained with trypan blue at 10 DAI, and hyphal lengths per colony were measured from photographs using ImageJ software. A minimum of 10 colonies were measured for hyphal length. This experiment was repeated twice. *c* Significantly different from the corresponding value for *pen3* using Student’s t test (*P* < 0.001).

(C) Examples of *B. g. hordei* colonies growing on different lines. Infected leaves were stained with trypan blue at 10 DAI. Bars = 30 μm.

(D) *E. pisi* growth on Col-0 leaves and the indicated mutant genotypes at 7 DAI. Light microscopic images were taken after visualization of fungal structures using Coomassie Brilliant Blue. Bars = 200 μm. The inset shows a close-up view of *E. pisi* conidiophores on the *pen3-1 eds1-1* double mutant. Bar = 50 μm.

(E) Cryogenic scanning electron micrograph of *E. pisi* growth on *pen3-1 eds1-1* at 7 DAI. The inset shows an *E. pisi* conidiophore. Bars = 50 μm.

(Figures 6E and 6F). A funnel-like structure, which resembled a hollow tube and extended into the plant cell, was sometimes observed at penetration sites at later stages (Figures 6G and 6H). Localization of PEN3-GFP after *E. cichoracearum* infection was similar to that observed after inoculation with *B. g. hordei*. PEN3-GFP accumulated in compact disks beneath appressoria, as well as in diffuse halos around this domain, and in bubble-like structures (Figures 6I to 6K). When *E. cichoracearum* haustoria were formed, the PEN3-GFP marker was also observed partially surrounding the haustorium (Figure 6L).
**Table 1.** Examples of SA-Induced or SA Pathway–Associated Genes That Are Hyperinduced in pen3-1 Mutants after Inoculation with Either the Arabidopsis or the Barley Powdery Mildew

<table>
<thead>
<tr>
<th>Locus</th>
<th>Gene Description</th>
<th>Col-0 Ec</th>
<th>Col-0 Bgh</th>
<th>pen3 Unin</th>
<th>pen3 Ec</th>
<th>pen3 Bgh</th>
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<tbody>
<tr>
<td>At1g65690</td>
<td>Harpin-induced protein–related</td>
<td>3.04</td>
<td>6.67</td>
<td>1.35</td>
<td>7.42</td>
<td>17.87</td>
</tr>
<tr>
<td>At1g74710</td>
<td>Isochorismate synthase1 (ICS1 = SID2)</td>
<td>2.23</td>
<td>5.67</td>
<td>1.15</td>
<td>4.13</td>
<td>10.14</td>
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<tr>
<td>At1g75040</td>
<td>Pathogenesis-related protein5 (PR-5)</td>
<td>4.89</td>
<td>9.18</td>
<td>2.55</td>
<td>12.81</td>
<td>26.13</td>
</tr>
<tr>
<td>At2g43570</td>
<td>Chitinase, putative similar to chitinase class IV</td>
<td>2.88</td>
<td>7.50</td>
<td>1.59</td>
<td>8.24</td>
<td>24.39</td>
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<tr>
<td>At2g43590</td>
<td>Chitinase, putative similar to basic endo chitinase CHB4</td>
<td>1.11</td>
<td>1.48</td>
<td>1.12</td>
<td>2.59</td>
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<tr>
<td>At2g46400</td>
<td>WRKY family transcription factor</td>
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<td>4.80</td>
<td>1.52</td>
<td>3.63</td>
<td>8.42</td>
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<td>At3g04720</td>
<td>Pathogenesis-related protein4 (PR4)</td>
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<td>1.58</td>
<td>1.00</td>
<td>2.24</td>
<td>4.46</td>
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<tr>
<td>At3g12500</td>
<td>Basic endochitinase</td>
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<td>1.14</td>
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<td>8.39</td>
</tr>
<tr>
<td>At3g48090</td>
<td>Disease resistance protein, lipase-like (EDS1)</td>
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<td>3.49</td>
<td>1.34</td>
<td>3.50</td>
<td>4.11</td>
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<tr>
<td>At3g50480</td>
<td>Broad-spectrum mildew resistance RPW8</td>
<td>2.61</td>
<td>4.97</td>
<td>1.52</td>
<td>5.35</td>
<td>11.19</td>
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<tr>
<td>At3g52430</td>
<td>Phytoalexin-deficient4 (PAD4)</td>
<td>3.20</td>
<td>5.48</td>
<td>1.42</td>
<td>5.02</td>
<td>9.75</td>
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<tr>
<td>At3g57240</td>
<td>β-1,3-Glucanase (BG3)</td>
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<td>1.78</td>
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<td>At4g01700</td>
<td>Chitinase, putative similar to peanut type II chitinase</td>
<td>3.79</td>
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<tr>
<td>At4g39030</td>
<td>Enhanced disease susceptibility5</td>
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<td>L-Ascorbate oxidase</td>
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<td>Lipase class 3 family protein</td>
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<td>Bax inhibitor1 putative</td>
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<td>2.23</td>
<td>1.15</td>
<td>2.13</td>
<td>3.19</td>
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</table>

Ec, 1 DAI with Erysiphe cichoracearum; Bgh, 1 DAI with Blumeria graminis f. sp hordei; Unin, uninoculated. Based on the analysis of variance with a Benjamini and Hochberg multiple text correction, the P values for these genes were <0.0008 for the factor genotype and for the factor infection. Values shown indicate average fold induction relative to uninoculated Col-0 (n = 4).

**DISCUSSION**

Like pen1 and pen2, the pen3 mutant allowed increased entry into epidermal cells and haustorium formation by the inappropriate pathogen B. g. hordei (Collins et al., 2003; Lipka et al., 2005). In addition, pen3 supported increased hyphal elongation by the inappropriate fungus, indicating that a higher proportion of haustoria remained functional long enough to support the establishment and growth of secondary hyphae (Figure 1).

Nonhost resistance to B. g. hordei was also slightly compromised in the eds1 mutant and in NahG transgenic plants, as shown for B. g. tritici, the powdery mildew pathogenic on wheat (Figure 5) (Yun et al., 2003; Zimmerli et al., 2004). Double mutants of pen3-1 and eds1 allowed additional penetration and growth by two separate inappropriate biotrophic pathogens, B. g. hordei and E. pisi, and the necrotroph P. cucumerina, than either mutant alone (Figures 4 and 5). Furthermore, E. pisi was able to reproduce asexually on plants with both pen3-1 and eds1-1 mutations (Figures 5D and 5E). Although EDS1 and NahG affect the functioning of the SA pathway, they both have additional poorly characterized but SA-independent effects on resistance (Feyes et al., 2001; Heck et al., 2003; van Wees and Glazebrook, 2003). Because sid2 and its double mutant with pen3 did not implicate the SA pathway in nonhost resistance, it seems likely that the SA-independent responses of EDS1 and NahG contribute to nonhost resistance. Furthermore, double mutant combinations of pen3 and eds1 or NahG exhibited additive rather than epistatic interactions, suggesting that PEN3 operates independently of EDS1 and NahG in nonhost resistance. Therefore, it appears that only two barriers, penetration resistance (e.g., PEN2 or PEN3) and postpenetration or basal resistance (e.g., EDS1 or PAD4), are sufficient to limit E. pisi invasion, growth, and asexual reproduction on Arabidopsis (Lipka et al., 2005). However, an additional barrier(s) appears to limit B. g. hordei infections of Arabidopsis.

Unexpectedly, pen3 mutants were more resistant to the Arabidopsis powdery mildew pathogen. This resistance was associated with the development of chlorosis and necrosis later in the infection sequence (Figure 3). A survey of 34 Arabidopsis mutants that exhibited chlorosis and necrosis upon pathogen infection showed that these phenotypes are not commonly associated with a lack of nonhost resistance (see Supplemental Table 4 online). Both double mutant analysis and microarray expression profiling suggested that the SA pathway was hyperactivated in pen3 plants relative to wild-type plants and that this was responsible for the chlorotic and E. cichoracearum–resistant phenotypes of pen3 (Table 1, Figure 3). SGT1b has a role in cell death signaling in addition to its role in modulating R protein levels, which is consistent with the attenuation of chlorosis and cell death observed in pen3 sgt1b double mutants (Figure 3) (Holt et al., 2005). Because powdery mildews are obligate biotrophs that grow only on living host tissue, the necrosis and chlorosis are likely responsible for the resistance to E. cichoracearum in pen3 plants.

PEN3 encodes a putative PDR-like ABC transporter previously designated PDR8. The Arabidopsis PDR gene family comprises 15 members, of which PEN3 is the most widely and highly
expressed. Although other ABC transporter families in plants are well characterized and their members have been implicated in the transport of auxin, lipids, pigments, and chlorophyll precursors, the PDR family is less well studied (Martinoia et al., 2002). Among the plant PDR subgroup of ABC transporters, studies of two Nicotiana species transporters, N. plumbaginifolia PDR1/ABC1 and tobacco (Nicotiana tabacum) PDR1, which are most similar in sequence to the Arabidopsis PDR12, suggest that they may function in the export of toxic secondary plant metabolites and/or in the detoxification of pathogen toxins. Similar to PEN3, the expression of N. tabacum PDR1 and N. plumbaginifolia PDR1 is induced by defense-related signals such as pathogen elicitors and methyl jasmonate, and N. plumbaginifolia PDR1 is also induced by the phytoalexin sclareol (Jasinski et al., 2001; Sasabe et al., 2002). Arabidopsis does not produce sclareol; however, PDR12 is induced by fungal pathogens, and plants carrying a T-DNA insertion in PDR12 are reportedly more sensitive to exogenous sclareol and to lead (see Supplemental Table 3 online) (Campbell et al., 2003; Lee et al., 2005). Given the broad range of compounds and small peptides that can be transported by ABC transporters, these studies of tobacco PDR transporters cannot be used to suggest a candidate substrate for PEN3. A single gene, encoding a small unknown protein, was strongly upregulated in the pen3 mutant independent of infection status. In yeast, an ABC transporter is responsible for exporting the 38-amino acid mating factor A (Kuchler et al., 1989). Thus, it is possible that the small unknown protein is a substrate for PEN3. Alternatively, this gene could be a novel marker for the stress experienced by pen3 plants. In spite of the expression responses, loss of PDR12 function in Arabidopsis or PDR1 function in N. plumbaginifolia did not lead to increased susceptibility to several fungal and bacterial pathogens (Campbell et al., 2003; Stukkens et al., 2005). However, N. plumbaginifolia plants lacking PDR1 were highly susceptible to the necrotroph B. cinerea (Stukkens et al., 2005). With this result and the cloning of PEN3, PDR-type ABC transporters have been implicated in defense, adding a new role to the diverse repertoire of the PDR-like ABC transporter family.

ABC transporters have been shown to require phosphorylation for activity or regulation (Kolling, 2002). A recent study of phosphorylated plasma membrane proteins identified PEN3 as a target of flagellin-induced phosphorylation (Nühse et al., 2004), supporting the idea that PEN3 functions in nonhost resistance and defenses elicited by nonspecific elicitors such as flagellin. Consistent with this idea, PEN3 expression was 2.5-fold higher in fig22 peptide–treated seedlings compared with control seedlings, and
Localization of PEN3 to the plasma membrane and its accumulation at penetration sites support the idea that PEN3 exports defense compounds in a focal manner at attempted invasion sites (Figure 6). PEN1 (=SYP121 syntaxin), the barley PEN1 homolog ROR2, and the barley MLO protein also localize in a similar pattern to the plasma membrane after powdery mildew infection (Assaad et al., 2004; Bhat et al., 2005). In addition, PEN2-GFP localizes to peroxisomes that accumulate near sites of invasion (Lipka et al., 2005). This marshaling of defense components at sites of attempted pathogen invasion illustrates the importance of subcellular dynamics in plant responses to pathogens.

pen3 and pen2 mutants have similar phenotypes that are not observed in pen1 mutants. For example, only pen2 and pen3 plants were more susceptible to the inappropriate pathogen P. infestans (Figures 1G and 1I) and the necrotroph P. cucumerina (Figure 4) (Lipka et al., 2005). However, pen3 mutants differed from pen2 mutants by their resistance to the Arabidopsis powdery mildew (Figure 3A). Mutations in PEN2 partially suppressed cell death and chlorosis in E. cichoracearum–infected pen3 mutants, suggesting that PEN2 and PEN3 functions might be interdependent. We propose a biochemical model for the role of PEN3 in penetration resistance (Figure 7A) in which PEN2 converts a nontoxic substrate to a toxic product, which is then exported either directly or after further modification to the apoplast by PEN3, poisoning the fungal penetration peg as it attempts to cross the cell wall. This model predicts that the substrate(s) normally exported by PEN3 accumulates to higher levels intracellularly in E. cichoracearum–infected pen3 plants than in pen3 plants inoculated with B. g. hordei, because E. cichoracearum continues to grow and repeatedly penetrate the epidermis, providing a greater stimulus for the production of PEN3 substrate(s) (Figure 7B). Based on the double mutant analysis (Figure 3) and microarray data (Table 1), it seems likely that the PEN3 substrate(s) spuriously activates the SA pathway. Because pen3 but not pen2 mutants develop chlorotic and necrotic patches with E. cichoracearum infections, we further propose that another enzyme(s), acting in parallel with PEN2, generates a related toxin(s) that is also exported by PEN3. To date, one phytoalexin, camalexin, has been identified in Arabidopsis (Tsuij et al., 1992). However, it is unlikely that this compound is solely responsible for the phenotypes conferred by pen3, because phytoalexin-deficient3 (pad3) and pad4 mutants lack the phenotype conferred by pen (data not shown). A postpenetration role for PEN3 can be explained by suggesting that PEN3 exports toxin(s) to the extrahaustorial matrix, poisoning the haustorium, thereby limiting the initiation and growth of secondary hyphae. This suggestion is supported by the localization of PEN3 protein to haustorial complexes (Figure 6). Highlight stress presumably leads to the accumulation of toxic materials that would normally be exported by PEN3. The data supporting this model are incomplete as yet, and it is also possible that the loss of PEN2 attenuates the activation of the SA pathway in pen3 mutants or that PEN3 exports a fungal toxin or a fungal suppressor of defenses.

Plants are resistant to most pathogens in their environment and succumb to only a small number of highly adapted pathogen species. Collectively, the isolation of the pen1, pen2, and pen3 mutants highlights the importance of defenses operating at the cell periphery. Only a subset of pathogens are able to overcome

Figure 7. Model for a Role for PEN3 in Penetration Resistance.

(A) We hypothesize that the PEN3 ABC transporter exports toxic secondary metabolites or other toxic materials (X and Y) to the apoplast at sites of attempted invasion. We speculate that the barley and pea powdery mildews are sensitive to these toxins, whereas the Arabidopsis powdery mildew is either less sensitive to this toxin or fails to fully activate this defense mechanism. Because some ABC transporters can transport a variety of related compounds, we assume that PEN3 exports a family of chemically related compounds, which may have varying toxicity. The glycosyl hydrolase PEN2 may activate one of these toxins (Y) by hydrolysis of a nontoxic precursor metabolite (Y–G). We assume that other enzymes activate related toxins (X).

(B) In the pen3 mutant, the sustained intracellular accumulation of PEN2-activated and related toxin(s) in interactions with the Arabidopsis powdery mildew leads to the activation of the SA pathway and the development of chlorosis and necrosis.

G, conidium; CW, cell wall; PM, plasma membrane.
these defenses and attempt to colonize plants when additional defenses, operating intracellularly, come into play. For some inappropriate pathogens, only a limited number of barriers limit growth and asexual reproduction, suggesting that nonhost resistance may not be as complex as originally thought and that these defenses from nonhost plants can be introduced into host plants to provide stable, broad host range resistance to difficult pathogens.

**METHODS**

**Growth Conditions and Inoculations**

Arabidopsis thaliana and squash (Cucurbita maxima, Hybrid Kuta; Park Seed, Greenwood, SC) were grown in growth chambers at 22°C with a 14-h photoperiod of ~125 µE·m⁻²·s⁻¹ in the 400- to 700-nm range. Host powdery mildew (Erysiphe cichoracearum UCSC1) was cultured on squash for 10 to 12 d and then applied to Arabidopsis using settling towers (Vogel and Somerville, 2000). Barley powdery mildew (Blumeria graminis f. sp hordei CR3) was grown on barley (Hordeum vulgare) line Algerian-S (CI-16138) and inoculated onto Arabidopsis using the methods described by Zimmerli et al. (2004). Phytophthora infestans isolate 1306 (A1 mating type; provided by H. Judelson, University of California, Riverside) was maintained and prepared for inoculations as described by Zimmerli et al. (2004). Plants to be infected with Erysiphe pisi were grown in growth chambers at 20 to 23°C with a 12-h photoperiod and a light intensity of ~150 µE·m⁻²·s⁻¹ on a turf substrate mix (Stender Substrate; Wesel-Schermbeck) containing 0.001% Confidor WG70 (Bayer). Three-week-old plants were inoculated with E. pisi (Birmingham Isolate) using a settling tower (Lipka et al., 2005). For the growth of Plectosphaerella cucumerina and Botrytis cinerea, seeds were surface-sterilized, sown on square, 12.5 × 12.5-cm Petri dishes containing Murashige and Skoog basal salt mixture medium with 0.8% phytagel (Sigma-Aldrich), transferred to a phytocambium, and grown as described previously (Berrocal-Lobo et al., 2002; Berrocal-Lobo and Molina, 2004; Llorente et al., 2005). For high-light treatments, plants were germinated and grown at 22°C under a continuous light regime of ~900 µE·m⁻²·s⁻¹ in the 400- to 700-nm range.

**Cytology and Quantification of Fungal Growth**

For penetration assays, 3-week-old Arabidopsis plants were inoculated with B. g. hordei and leaf samples were taken at 2 DAI. For P. infestans assays, 2-week-old Arabidopsis plants were sprayed with P. infestans zoospore suspensions and leaves were sampled at 2 DAI (Zimmerli et al., 2000). The deposition of callus was visualized by staining with aniline blue (Vogel and Somerville, 2000). For E. cichoracearum infections, 3-week-old Arabidopsis plants were inoculated as described above, and phenotypes were monitored visually at 4, 5, 6, 7, and 10 DAI.

To quantify fungal growth, eight Arabidopsis leaves per genotype were stained with aniline blue as described by Adam and Somerville (1996), with 250 mg of trypan blue added per milliliter. Haustoria, which become encased in callus in incompatible interactions, were visualized with aniline blue staining. Secondary hyphal elongation was quantified in nonoverlapping fields of view at ~200 magnification, avoiding the edge and midvein regions of the leaf. Numbers were expressed as percentages of total germinated conidia and were assessed for differences between mutant and the wild type with Student’s t test. Fungal growth, the occurrence of lesions, and the accumulation of autofluorescent compounds were assessed as described by Vogel and Somerville (2000). To quantify hyphal length per colony, B. g. hordei-inoculated leaves were harvested at 10 DAI, cleared, and stained with trypan blue (Vogel and Somerville, 2000). At least 10 individual colonies were photographed under bright-field illumination at ~200 magnification with a Leica D500 digital camera attached to a Leica Leitz DMRB compound microscope. Hyphal lengths were measured using ImageJ software (version 1.30) (Abramoff et al., 2004; http://rsb.info.nih.gov/ij/).

Leaves infected with E. pisi were fixed and cleared in ethanol/acetic acid (3:1). Epiphytic fungal growth was visualized by staining of fungal structures with an ethanolic solution containing 0.6% Coomassie Brilliant Blue R 250 (Lipka et al., 2005). Cryogenic scanning electron microscopy of E. pisi–infected plants was performed as described by Sturaro et al. (2005).

**Assays of P. cucumerina disease development**

were done by spraying 10-d-old plants with a spore suspension (at either 1 × 10⁶ or 2 × 10⁶ spores/mL, 1.5 mL/plate). Mock inoculations were done by spraying the plants with sterile water. After inoculation, plants were kept under the growth conditions described above; 10 d later, the percentage reduction of plant fresh weight caused by the fungal infection was calculated as described (Berrocal-Lobo and Molina, 2004). Inoculations of wild-type plants and pen3-1 mutants with B. cinerea were performed as described previously (Llorente et al., 2005), and the percentage of decayed plants was determined at different days after inoculation. The highly susceptible agb1-1 mutant was included in these experiments as a control for disease development (Llorente et al., 2005). At least 30 plants per genotype were inoculated with each pathogen, and the experiment was repeated four times. Differences between genotypes were identified using Student’s t test.

**Mapping and Cloning**

Rough mapping markers, PCR conditions, and DNA preparation were as described previously (Lukowitz et al., 2000). Briefly, F2 populations of a mutant crossed to Arabidopsis Ler were sown in 96-well flats and then moved to a greenhouse. Plants were inoculated with B. g. hordei, as described above, at ~3 weeks after germination when they had at least four true leaves. At 2 DAI, the third or fourth true leaf from each plant was harvested. Leaves were stained individually, mounted, and examined at ×50 magnification as described below. Tissue was harvested from plants with mutant phenotypes for DNA preparation and bulk segregant PCR (Lukowitz et al., 2000). Key individuals were retested for their pen3 phenotype in the F3 generation. New markers within the mapping interval were generated using the CEREON database of Col-0 and Ler polymorphisms (Jander et al., 2002) and the Whitehead Institute online primer design software, Primer3 (Rozen and Skaletsky, 2000; http://frodo.wi.mit.edu/cgi-bin/primer3/primer3_www.cgi). All available T-DNA insertion lines for genes in a small interval on chromosome 1 were identified from the Salk Institute Genomic Analysis Laboratory’s T-DNA project (http://signal.salk.edu/cgi-bin/tdnaexpress) (Ecker, 2002). Two SALK lines, SALK_110926 (pen3-3) and SALK_000578 (pen3-4), with insertions in the At1g59870 gene segregated pen3 phenotypes. The At1g59870 gene was sequenced from the pen3-1, pen3-2, and mil9 mutant lines on an ABI 310 Sequencer (Applied Biosystems).

Alignments of PDR family members were made using DNASTar MEGALIGN software with the ClustalW method and default parameters. Microarray data mining was done using the web tool GENEVESTIGATOR (Zimmermann et al., 2004).

**Double Mutant Construction**

The mutant alleles used for the construction of double mutants with pen3-1 were col1-1 (Col-6 background [Feys et al., 1994]), npr1-1 (Cao et al.,...
1994), sid2-1 (Nawrath and Métraux, 1999), pad4-1 (Glazebrook and Ausubel, 1994), eds1-1 (W-s-0 background [Parker et al., 1996], Etr1-1 (Bleecker et al., 1988), jar1-1 (Staswick et al., 1992), eed1 (Frey and Innes, 1998), sgt1b-1 (Ler background [Pearl et al., 2002]), rar1-10 (Ler background [Muskett et al., 2002], NahG (Lawton et al., 1995), pen1-1 (Collins et al., 2003), and pen2-3 (Lipka et al., 2005). All of the mutant lines, unless noted otherwise, were in the Col-0 background. We generated the double mutants by standard genetic crosses, following the mutations with cleaved-amplified polymorphic sequence (CAPS) markers. When the mutation did not lead to a change in a restriction site, we generated derived CAPS markers using the dCAPS web tool (Neef et al., 1998). The Etr1-1 (Hua and Meyerowitz, 1998), NahG (Morris et al., 2000), rar1-10 (Muskett et al., 2002), sgt1b (Austin et al., 2002), coi1-1 (Xie et al., 1998), pad4-1 (Nishimura et al., 2003), and npy1-1 (Nishimura et al., 2003) primers have been described previously. See Supplemental Table 5 online for a listing of primers used in genotyping mutations.

Expression Profiling

Samples of Col-0 and pen3-1 rosettes were collected from uninfected plants, plants infected with E. cichoracearum, or plants inoculated with B. g. hordei at 1 DAI. Each sample represented a pool of the rosettes from 16 plants grown in one pot under the growth conditions outlined above and inoculated as described above. Four pots (each pot a biological replicate) were grown for each treatment × genotype combination for a total of 24 pots. Total RNA was extracted from the plants using the Trizol method (Chomczynski and Sacchi, 1987) (Gibco BRL) and purified (Qiagen; RNeasy) essentially as described (Ramonell et al., 2002). Biotinylated complementary RNA (20 μg) was prepared as described (Hernan et al., 2003). The resulting complementary RNA was used to hybridize ATH1 Arabidopsis GeneChips (Affymetrix) using the manufacturer’s protocols. The array images were analyzed with Affymetrix Microarray Suite 5.0 with the target intensity set to 500. The expression levels of the genes were analyzed with GeneSpring 4.2 software (Silicon Genetics), and the chip-to-chip signal variation was minimized by normalizing signal intensities to the averaged intensity values of uninoculated Col-0 using the expression levels of the top 50th percentile of probe sets. Differentially expressed genes were identified using two-way analysis of variance and a Benjamini and Hochberg multiple testing correction (GeneSpring 4.2). Genes were considered differentially expressed at P ≤ 0.001.

PEN3-GFP Localization

To create a PEN3 fusion to GFP, a 3’ fragment encoding the C terminus (nucleotides 4380 to 5681 of the unsnipped transcript) of PEN3 was amplified by PCR using primers containing a C-terminal adaptor to keep the protein sequence in-frame with GFP in the vector pEGAD (Cutler et al., 2000). The primer sequences were 5’-CCGGGTACCGGACACTGGAAA-GAACCTGTGTC-3’ and 5’-AGCGGTCGACGCTTCAACATGGGAACTC-CTTGATATC-3’. The 35S promoter was removed from pEGAD using SacI, before ligating the PCR-amplified and KpnI-BamHI-digested C-terminal PEN3 fragment in-frame with eGFP. BAC F23H11 was ordered from the ABRC and digested with KpnI, yielding a 10-kb genomic fragment containing the PEN3 gene as well as 2132 nucleotides upstream of the start codon and 2542 nucleotides downstream of the stop codon. This fragment was gel-purified and digested using DraII. The resulting digest was cloned into the pEGAD vector containing the PEN3 sequences encoding the C terminus fused with eGFP and digested with KpnI and DraII, to give the full genomic piece fused in-frame to GFP. The vector was transformed into Agrobacterium tumefaciens (strain GV3101), and flowering pen3-1 plants were dipped into A. tumefaciens—containing infiltration medium as described (Cutler et al., 2000). T1 seeds were surface-disinfected and plated on Murashige and Skoog agar plates containing 50 μg kanamycin/mL (Murashige and Skoog, 1962). Two-week-old healthy seedlings were screened for GFP fluorescence with a Leica dissecting microscope equipped with an epifluorescence filter set. GFP-expressing seedlings were transferred to soil and inoculated with E. cichoracearum or B. g. hordei 2 weeks later. Single inoculated leaves from T1 plants were mounted on microscope cover slips in a 0.01 mg/mL propidium iodide solution in water (Ramonell et al., 2005). Imaging was done using a Nikon inverted fluorescence microscope equipped with a Bio-Rad MRC 1024 confocal head. Images were processed using the software ImageJ.

Accession Numbers

Microarray data sets were deposited in the Gene Expression Omnibus (http://www.ncbi.nlm.nih.gov/geo/; Barrett et al., 2005) under accession number GSE3220. The Arabidopsis Genome Initiative locus identifier for PEN3/PDR8 is At1g59870.

Supplemental Data

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

Supplemental Table 1. Expression of the 12 Members of the Arabidopsis PDR Family in Various Tissues.

Supplemental Table 2. PEN3 Transcript Levels Are Increased under Different Biotic and Abiotic Stresses.

Supplemental Table 3. Changes in Transcript Levels of PDR Family Members upon Powdery Mildew Infection in Wild-Type and pen3-1 Plants.

Supplemental Table 4. Host and Nonhost Resistance Phenotypes of Mutants Resistant to E. cichoracearum.

Supplemental Table 5. Primer Combinations Used to Genotype Mutations by PCR.

Supplemental Figure 1. Transcript Profiling of pen3-1 and Col-0 after Inoculation with the Arabidopsis and barley powdery mildew pathogens.

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REFERENCES


**NOTE ADDED IN PROOF**

Kobae et al. (2006) report that *pdr8*/*pen3* mutants are compromised in nonhost resistance to *Phytophthora infestans* but show increased resistance to *Pseudomonas syringae pv tomato* DC3000.
Arabidopsis PEN3/PDR8, an ATP Binding Cassette Transporter, Contributes to Nonhost Resistance to Inappropriate Pathogens That Enter by Direct Penetration
Mónica Stein, Jan Dittgen, Clara Sánchez-Rodríguez, Bi-Huei Hou, Antonio Molina, Paul Schulze-Lefert, Volker Lipka and Shauna Somerville
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Supplemental Data /content/suppl/2006/02/10/tpc.105.038372.DC1.html
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