

Differential Recognition of Highly Divergent Downy Mildew Avirulence Gene Alleles by *RPP1* Resistance Genes from Two *Arabidopsis* Lines

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The perception of downy mildew avirulence (*Arabidopsis thaliana* Recognized [ATR]) gene products by matching *Arabidopsis thaliana* resistance (Recognition of *Peronospora parasitica* [RPP]) gene products triggers localized cell death (a hypersensitive response) in the host plant, and this inhibits pathogen development. The oomycete pathogen, therefore, is under selection pressure to alter the form of these gene products to prevent detection. That the pathogen maintains these genes indicates that they play a positive role in pathogen survival. Despite significant progress in cloning plant RPP genes and characterizing essential plant components of resistance signaling pathways, little progress has been made in identifying the oomycete molecules that trigger them. Concluding a map-based cloning effort, we have identified an avirulence gene, *ATR1^{NdWsB}*, that is detected by *RPP1* from the *Arabidopsis* accession Niederzenz in the cytoplasm of host plant cells. We report the cloning of six highly divergent alleles of *ATR1^{NdWsB}* from eight downy mildew isolates and demonstrate that the *ATR1^{NdWsB}* alleles are differentially recognized by *RPP1* genes from two *Arabidopsis* accessions (Niederzenz and Wassilewskija). *RPP1-Nd* recognizes a single allele of *ATR1^{NdWsB}*; *RPP1-WsB* also detects this allele plus three additional alleles with divergent sequences. The Emco5 isolate expresses an allele of *ATR1^{NdWsB}* that is recognized by *RPP1-WsB*, but the isolate evades detection in planta. Although the Cala2 isolate is recognized by *RPP1-WsA*, the *ATR1^{NdWsB}* allele from Cala2 is not, demonstrating that *RPP1-WsA* detects a novel ATR gene product. Cloning of *ATR1^{NdWsB}* has highlighted the presence of a highly conserved novel amino acid motif in avirulence proteins from three different oomycetes. The presence of the motif in additional secreted proteins from plant pathogenic oomycetes and its similarity to a host-targeting signal from malaria parasites suggest a conserved role in pathogenicity.

INTRODUCTION

Plant-pathogenic oomycetes are responsible for economically and environmentally devastating epidemics, including the 19th century Irish potato famine (*Phytophthora infestans*) and the current sudden oak death (*Phytophthora ramorum*) epidemic in California. The obligate biotrophic oomycete *Hyaloperonospora parasitica* (formerly *Peronospora parasitica* [Constantinescu and Fatehi, 2002]) causes downy mildew of the model plant *Arabidopsis thaliana*. *Arabidopsis* accessions that are resistant

to *H. parasitica* carry Recognition of *Peronospora parasitica* (RPP) resistance genes. RPP proteins perceive avirulence (*Arabidopsis thaliana* Recognized [ATR]) gene products produced by *H. parasitica* isolates and trigger resistance responses. Coevolving populations of *Arabidopsis* and *H. parasitica* have been used to genetically define and clone *Arabidopsis* RPP genes that represent two intracellular classes and an extracellular class of Leu-rich repeat disease resistance genes (Holub et al., 1994; Parker et al., 1997; Botella et al., 1998; McDowell et al., 1998; Bittner-Eddy et al., 2000; van der Biezen et al., 2002; Sinapidou et al., 2004; Tör et al., 2004). Studying the interaction between RPP proteins and their *H. parasitica* targets represents an opportunity to examine the mechanisms underlying host resistance to, and parasite pathogenicity of, a naturally occurring parasite of the model plant *Arabidopsis*. To analyze this interaction in both plant and pathogen, it is necessary to identify the ATR genes complementary to specific RPP genes. These can then be used as tools to investigate their role in pathogenicity and to assess the role and strength of natural selection at the molecular level in host–parasite interactions.

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Few avirulence genes have been cloned from oomycetes or obligate biotrophs (i.e., plant pathogens that cannot be cultured in vitro because their life cycle is entirely dependent on living host tissue). *ATR13* from *H. parasitica* was cloned by isolating an in planta-expressed sequence that cosegregated with and encoded *ATR13* (Allen et al., 2004). By contrast, map-based cloning approaches resulted in the identification of *Avr1b-1* from *Phytophthora sojae* (Shan et al., 2004) and *AvrL567* from *Melampsora lini* (Dodds et al., 2004). All three genes are predicted to encode proteins with N-terminal signal peptides, suggesting that they are secreted from the pathogens. Alleles of *ATR13* and *AvrL567* encode proteins with extreme levels of amino acid polymorphism, which is indicative of diversifying selection and potentially driven by, and driving, the polymorphism seen in the matching resistance proteins (Dodds et al., 2000, 2004; Allen et al., 2004; Rose et al., 2004). Alleles of *Avr1b-1* are also polymorphic, and some virulent *P. sojae* isolates carry avirulence *Avr1b-1* alleles but avoid detection because *Avr1b-1* mRNA fails to accumulate in these isolates (Shan et al., 2004).

Genes at the *RPP1* locus of different Arabidopsis accessions recognize different but overlapping sets of *H. parasitica* isolates (Holub et al., 1994; Botella et al., 1998). In accession Wassilewskija (*Ws-0*), four genes at the *RPP1* locus have been described: *RPP1-WsA* specifies resistance to *H. parasitica* isolates Emoy2, Maks9, Noks1, and Cala2; *RPP1-WsB* detects Emoy2, Maks9, and Noks1; *RPP1-WsC* detects Noks1 alone; and *RPP1-WsD* was not studied (Botella et al., 1998) (Table 1). Botella and coworkers (1998) speculated that, although the *RPP1-Ws* genes may recognize allelic avirulence gene determinants, it was more likely that they detected different avirulence gene products. A single functional *RPP1* gene in accession Niederzenz (*Nd-1*) specifies resistance to the *H. parasitica* isolates Emoy2, Hiks1, and Waco5 but not Maks9 (Gordon, 2002). The overlapping recognition profiles of *RPP1* genes from the two accessions are intriguing; we are interested in elucidating the complex interaction between these genes and their matching *ATR* gene(s).

ATR1Nd, the avirulence gene perceived by the resistance gene *RPP1* carried by the Arabidopsis accession *Nd-1*, segregates as a single dominant locus in an F2 mapping population derived from a cross between *H. parasitica* isolates Emoy2 (avirulent) and Maks9 (virulent). A mapping interval spanning *ATR1Nd* was

defined, and a contig spanning the genetic interval was assembled using clones from a BAC library constructed from isolate Emoy2 (Rehmany et al., 2003). We have used the sequence across the genetic interval to identify *ATR1Nd*, described here, and to analyze a conserved syntenic region in *P. infestans* (Armstrong et al., 2005). *ATR1Nd* is a secreted protein that is recognized in the host cytoplasm and is under intense diversifying selection. As well as a signal peptide, it contains a novel motif conserved in many secreted oomycete proteins. Furthermore, our analysis reveals that (1) *RPP1-Nd* recognizes a single allelic form of *ATR1Nd*; (2) *RPP1-WsB* recognizes highly variable allelic forms of the gene; (3) *RPP1-WsA* does not detect this gene in the *H. parasitica* isolate Cala2; and (4) the isolate Emco5 expresses a form of *ATR1Nd* that *RPP1-WsB* is capable of detecting, but detection does not occur when the pathogen expresses the gene during infection.

RESULTS

A Candidate for *ATR1Nd* Encodes a Polymorphic Secreted Protein

The sequence of the genetic interval containing *ATR1Nd* (Rehmany et al., 2003) was used to identify new genetic markers to refine the interval further. One marker revealed five single nucleotide polymorphisms (SNPs) between Emoy2 and Maks9 that were found to cosegregate with *ATR1Nd* in the F2 mapping population of 311 F2 individuals. Furthermore, the SNPs were within a region that was predicted to be protein-coding by an algorithm differentiating the base composition of coding and noncoding DNA sequences (Fickett, 1982). The predicted protein-coding sequence resided between nucleotides 17,975 and 18,930 (numbers relate to BAC clone 12113). An open reading frame (ORF) starting with ATG was identified (nucleotides 17,977 to 18,909); within this ORF, all five SNPs between the Emoy2 and Maks9 sequences were predicted to result in non-synonymous amino acid substitutions (Figures 1 and 2). The ORF was predicted to encode a protein with a signal peptide ($P = 0.99$; SignalP) (Bendtsen et al., 2004); therefore, the protein would appear to be secreted, exposing it to plant detection mechanisms and consistent with two previously reported

Table 1. Differential Resistance Phenotypes Determined by *RPP1* Loci from *Nd-1* and *Ws-0*

<i>H. parasitica</i> Isolate	<i>Nd-1</i>	<i>Ws-0</i>	Resistance Specified by <i>RPP1-Ws</i> Genes ^a
Emoy2	Resistant ^b	Resistant	<i>RPP1-WsA</i> , <i>RPP1-WsB</i>
Hiks1	Resistant ^b	Resistant	NT
Waco5	Resistant ^b	Resistant	NT
Maks9	Susceptible	Resistant	<i>RPP1-WsA</i> , <i>RPP1-WsB</i>
Noks1 ^c	Susceptible	Resistant	<i>RPP1-WsA</i> , <i>RPP1-WsB</i> , <i>RPP1-WsC</i>
Cala2	Susceptible	Resistant	<i>RPP1-WsA</i>
Emco5	Susceptible	Susceptible	NT
Emwa1	Susceptible	Susceptible	NT

^a Individual *RPP1-Ws* genes are sufficient to provide resistance to the *H. parasitica* isolates shown (Botella et al., 1998). NT, not tested.

^b *RPP1* locus resistance specified by a single gene, *RPP1-Nd* (Gordon, 2002).

^c Noks1 was derived from an oospore of Noco2 (used in Botella et al., 1998), and its interaction phenotype matches that of Noco2 (Holub et al., 1994).

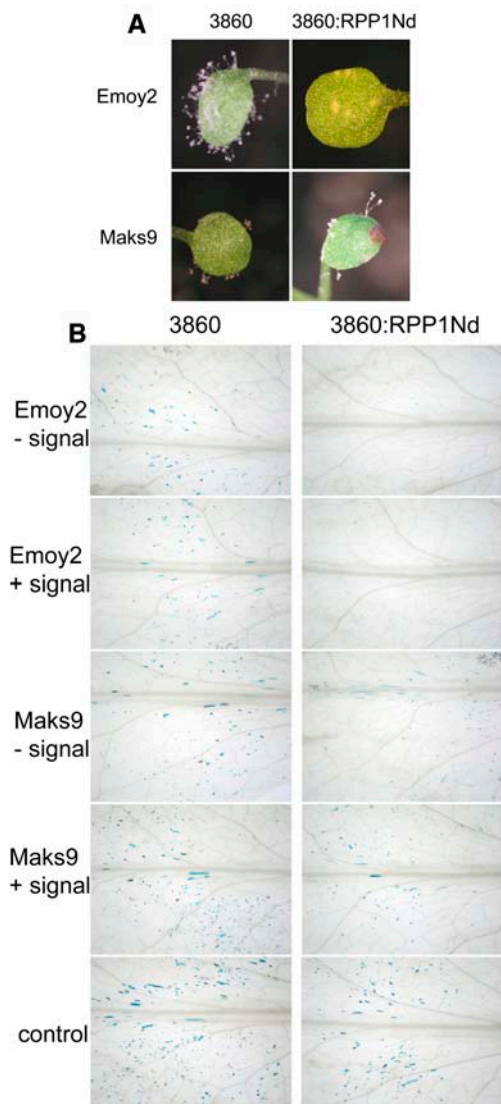


Figure 3. Recognition of *ATR1^{NdWsB}* by RPP1-Nd.

(A) Pathology of Emoy2 and Maks9 on 3860 (susceptible control) and 3860:RPP1Nd (transgenic) lines.

(B) Emoy2 and Maks9 alleles of *ATR1^{NdWsB}* cloned with (+ signal) or truncated for (– signal) sequences encoding predicted signal peptides and cobombarded with GUS into 3860 and 3860:RPP1Nd lines. Sequences were expressed constitutively from the 35S promoter. Control panels show cobombardment of pK2GW7 (empty vector) with GUS. Bar = 0.5 cm.

leaves (3860 and 3860:RPP1Nd) that were cobombarded together in a single shot. For this reason, the numbers of blue-stained cells in each bombarded leaf in an experiment and the ratio between the numbers of blue-stained cells in pairs of leaves that were shot together are listed in Table 2. The ratios provide a clear measure of the differences between responses to different test constructs, allowing for the between-replicate variability. Cobombardment of 3860:RPP1Nd with Maks9 (viru-

lent) ORFs or a control plasmid produced high numbers of blue-stained plant cells; the mean ratios between the numbers of blue-stained cells in pairs of 3860:RPP1Nd and 3860 leaves ranged from 0.70 to 1.05. By contrast, the Emoy2 (avirulent) ORFs resulted in few or pale blue-stained cells (Table 2, Figure 3B). Therefore, coexpression of the candidate avirulent ORF was sufficient to reduce the expression of GUS specifically in plants carrying the *RPP1-Nd* resistance gene. The reduction in blue-stained cells was more pronounced with the Emoy2 construct lacking the predicted signal peptide (the mean ratio between the numbers of blue-stained cells in 3860:RPP1Nd and 3860 leaves was 0.09) (Table 2, Figure 3B). The full-length Emoy2 construct consistently resulted in numerous blue-stained cells (mean ratio, 0.39; Table 2), although they stained less intensely than the controls (Figure 3B). The detection of *ATR1Nd* by RPP1-Nd was clearly apparent from macroscopic comparisons between replicate pairs of leaves (Figure 3B) as well as from the quantitative analysis of the relative numbers of blue-stained cells (Table 2). The sequences encoding *ATR1Nd* alleles from

Table 2. Detection of *ATR1^{NdWsB}* by RPP1-Nd

Test Construct	3860 ^a	3860:RPP1Nd ^a	Ratio 3860:RPP1Nd to 3860
Emoy2 – signal	62	16	0.258
	322 ^b	32 ^b	0.099
	110	5	0.045
	229	10	0.044
	237	1	0.004
			Mean = 0.09
Emoy2 + signal	306	69	0.225
	169	11	0.065
	170	176	1.035
	257 ^b	106 ^b	0.412
	486	111	0.228
			Mean = 0.39
Maks9 – signal	107	57	0.533
	604	213	0.353
	406 ^b	435 ^b	1.071
	192	282	1.469
	560	250	0.446
			Mean = 0.77
Maks9 + signal	593 ^b	348 ^b	0.587
	725	308	0.425
	463	781	1.687
	363	49	0.135
	69	165	2.391
			Mean = 1.05
Control (pK2GW7 empty vector)	276	366	1.326
	73	66	0.904
	68	17	0.250
	56	19	0.339
	707 ^b	477 ^b	0.675
			Mean = 0.70

^a The numbers of blue-stained cells present in each pair of leaves (3860 and 3860:RPP1Nd) after cobombardment with 35S:GUS and a test construct and the ratio between control and test leaves within each replicate are shown.

^b Highlighted leaves were photographed and are shown in Figure 3B.

Noks1, Cala2, Emco5, and Emwa1 were cloned and tested in cobombardment experiments. As predicted, because the isolates are virulent in the presence of *RPP1-Nd*, these alleles did not cause a reduction in blue-stained cells on 3860:RPP1Nd (data not shown).

Recognition of *ATR1Nd* by *RPP1-WsB*

The *RPP1* loci from *Arabidopsis* accessions Nd-1 and Ws-0 determine resistance to different but overlapping sets of *H. parasitica* isolates (Table 1). Whereas a single functional *RPP1* gene in Nd-1 specifies resistance to Emoy2, Hiks1, and Waco5 (Gordon, 2002), three similar genes at the *RPP1* locus in Ws-0 (*RPP1-WsA*, *RPP1-WsB*, and *RPP1-WsC*) specify resistance to Emoy2, Maks9, Noks1, and Cala2 (Botella et al., 1998) (Table 1). Allelism between *RPP1-Nd* and *RPP1-Ws* genes is difficult to determine because of the complexity of *RPP1* loci. Nevertheless, we tested whether *ATR1Nd* alleles are also recognized by *RPP1-Ws* genes. Cobombardment experiments reproducibly indicated that the *ATR1Nd* alleles from Emoy2, Maks9, and Noks1 were recognized by the Ws-0 *Arabidopsis* accession (few blue-stained cells [data not shown]), whereas the Cala2 allele clearly was not (many blue-stained cells [Figure 4A]). Thus, the alleles were considered good candidates for avirulence determinants recognized by *RPP1-WsB*, because *RPP1-WsB* specifies resistance to Emoy2, Maks9, and Noks1 but not to Cala2 (Botella et al., 1998) (Table 1). Therefore, a homozygous transgenic line carrying *RPP1-WsB* (CW84:RPP1WsB [Botella et al., 1998]) was used in cobombardment experiments using a selection of *ATR1Nd* alleles, and the relative numbers of blue-stained cells in each leaf were scored macroscopically (according to Bryan et al., 2000). The recognition of Emoy2, Maks9, and Noks1 was confirmed as well as the lack of recognition of Cala2 (Table 3, Figure 4B). As predicted, the allele from Emwa1 (virulent on Ws-0) was not recognized (many blue-stained cells [Table 3, Figure 4B]). Because products of specific *ATR1Nd* alleles were recognized by *RPP1-WsB*, we renamed the gene *ATR1^{NdWsB}*. This notation is necessary because, although *RPP1-WsA* recognizes an avirulence determinant in Cala2 (Table 1), it does not recognize the Cala2 allele of *ATR1^{NdWsB}* (*ATR1^{NdWsB}-Cala2* does not cause cell death in the Ws-0 accession after cobombardment [Figure 4A]).

RPP1-WsB Recognizes an in Planta-Expressed *ATR1^{NdWsB}* Allele from a Virulent Isolate

The *Arabidopsis* accession Ws-0 is susceptible to the Emco5 isolate, but both the Ws-0 accession (data not shown) and CW84:RPP1WsB (Table 3, Figure 4B) exhibited recognition of *ATR1^{NdWsB}-Emco5* in cobombardment experiments. RNA was extracted from plants 24 h after inoculation with different isolates. First-strand cDNA was produced and used as the template for PCR using a selection of primers. PCR amplification using methylenetetrahydrofolate dehydrogenase (MTD; a conserved *H. parasitica* gene from the *ATR1^{NdWsB}* interval) primers demonstrated the presence of *H. parasitica* RNA in each infection after 24 h (Figure 5). Primers corresponding to *ATR1^{NdWsB}*

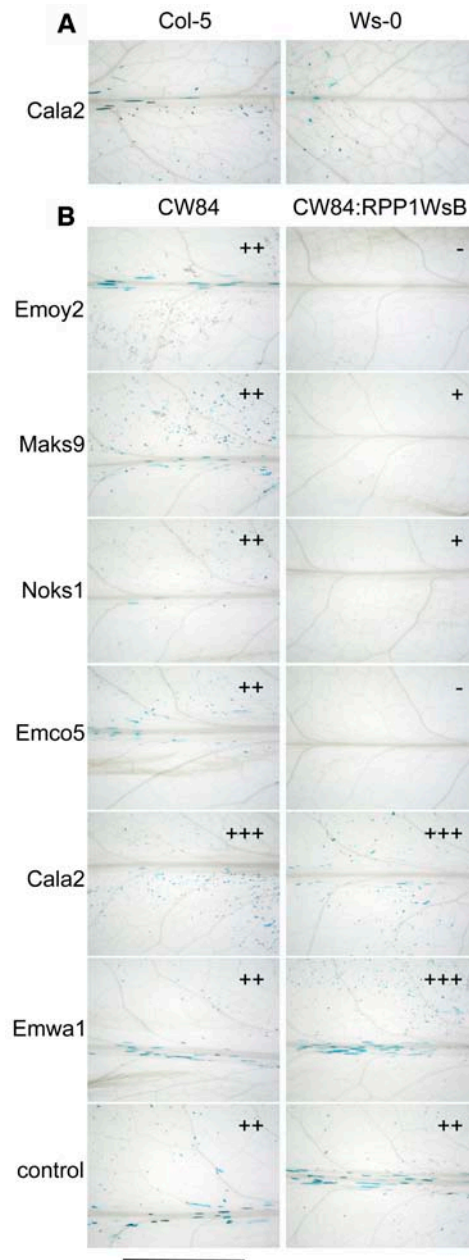


Figure 4. Recognition of *ATR1^{NdWsB}* by *RPP1-WsB*.

(A) Cala2 allele, truncated for the predicted signal peptide, cobombarded with GUS into Col-5 (control) and Ws-0 accessions.

(B) Emoy2, Maks9, Noks1, Emco5, Cala2, and Emwa1 sequences, truncated for the predicted signal peptides, cobombarded with GUS into CW84 (susceptible control) and CW84:RPP1WsB (transgenic) lines (Botella et al., 1998). The relative scores (-, +, ++, and +++) of blue-stained cells illustrate and correspond to those shown in Table 3. Sequences were expressed constitutively from the 35S promoter. Control panels show cobombardment of pK2GW7 (empty vector) with GUS. Bar = 0.5 cm.

Table 3. Detection of *ATR1^{NdWsB}* by RPP1-WsB

Test Construct	CW84 ^a	CW84:RPP1WsB ^a
Emoy2	++	-
	++ ^b	- ^b
	++	-
Maks9	++	+
	++ ^b	+ ^b
	++	+
Noks1	++	-
	++ ^b	+ ^b
	+	-
Emco5	+	+
	++ ^b	- ^b
	++	-
Cala2	++	+
	+++ ^b	+++ ^b
	++	++
Emwa1	++	+
	+++	+
	+++	++
Control (pK2GW7 empty vector)	+	+
	++ ^b	+++ ^b
	++ ^b	++ ^b
	+++	++

^aThe relative numbers of blue-stained cells present in CW84 and CW84:RPP1WsB leaves after cobombardment with 35S:GUS and a test construct, truncated for the predicted signal peptide, are shown. The relative scores (-, +, ++, and +++) of blue-stained cells are illustrated in Figure 4B.

^bHighlighted leaves were photographed and are shown in Figure 4B.

amplified a sequence-verified product from each cDNA preparation, indicating that the gene is expressed in all isolates (Figure 5). PCR amplifications, using an internal *ATR1^{NdWsB}* primer and a primer outside of the *ATR1^{NdWsB}* transcribed region, failed to amplify products, confirming that no contaminating genomic DNA was present (data not shown). Therefore, Emco5 expresses an allele of *ATR1^{NdWsB}* that is recognized by RPP1-WsB, yet the isolate is virulent on Ws-0.

The RXLR Motif

The first 67 amino acids of *ATR1^{NdWsB}* proteins from different *H. parasitica* isolates are relatively conserved compared with the remainder of the proteins (Figure 2). *ATR1^{NdWsB}* lies in a conserved region of synteny with *Avr3a* from *P. infestans*, and *AVR3a* shows homology with *Avr1b-1* from *P. sojae* (Shan et al., 2004; Armstrong et al., 2005). Aligning the amino acid sequences encoded by these three genes revealed no overall sequence conservation (data not shown), but a conserved motif was apparent within 32 amino acids of the predicted signal peptides (Figure 6). The core motif consists of the consensus sequence

RXLR followed by a variable length of amino acids comprising >50% acidic amino acids (Asp [D] and Glu [E]) and concluding with Arg (R). As with *ATR1^{NdWsB}*, most variation between proteins encoded by alleles of *Avr1b-1* occurs beyond the motif (Shan et al., 2004). By searching publicly available sequences of plant pathogenic oomycetes and the sequences of BAC clones spanning the *ATR1^{NdWsB}* interval, we identified eight additional genes from three oomycete species in which a similar motif immediately follows a predicted signal peptide (Figure 6). Among these were secreted *Phytophthora* proteins (Pieterse et al., 1994; Kamoun et al., 1999; Qutob et al., 2002), predicted *Phytophthora* extracellular proteins (PEXs) (Torto et al., 2003) from *P. infestans*, and a predicted secreted protein from a *H. parasitica* BAC sequence linked to *ATR1^{NdWsB}* (12I13.1; Figure 6). Alignment of these sequences with the three avirulence proteins further defined the consensus for the motif as RXLR-X₅₋₂₁-ddEER (uppercase letters denote the consensus amino acid in 10 of 11 sequences; lowercase letters denote the consensus amino acid in more than half of the genes; Figure 6); for simplicity, the term "RXLR motif" is used to describe the sequence. The RXLR motif is also found in >40 diverse (in both size and sequence) secreted *P. infestans* proteins (C. Young, T.D. Kanneganti, J. Win, and S. Kamoun, personal communication) and >100 predicted secreted proteins with weak sequence similarity to *Avr1b-1* from each of the genome sequences of *P. sojae* and *P. ramorum* (B.M. Tyler, unpublished data). Thus, the RXLR motif is found within different oomycete genomes and within avirulence proteins. The *H. parasitica* *ATR13* protein (Allen et al., 2004) represents an alternative form, in which the amino acid residues RXLR are present and preceded by a signal peptide but are not followed by an acidic stretch of amino acids.

Distribution of Sequence Polymorphism in the *ATR1^{NdWsB}* Locus

A sliding-window analysis revealed that the synonymous and nonsynonymous polymorphism is not distributed uniformly across the alleles of *ATR1^{NdWsB}* (Figure 7). Synonymous variation ranges from $\pi = 0.00$ to 0.063, and the central core of the coding region shows no segregating synonymous variation from codon

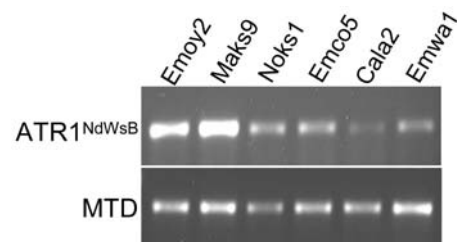


Figure 5. Expression Analysis of *ATR1^{NdWsB}* in Planta at 24 h after Inoculation.

Sequence-verified PCR products separated on agarose gels and amplified from cDNA derived from Emoy2-, Maks9-, Noks1-, Emco5-, Cala2-, or Emwa1-infected seedlings using *ATR1^{NdWsB}*-specific primers. Also shown, PCR products amplified from the same cDNA samples using primers corresponding to a control *H. parasitica* gene (MTD).



Figure 6. The RXLR Motif.

(A) Graphic representation of the sequence alignment shown in **(B)**. The height of each amino acid symbol indicates its frequency at that position (Schneider and Stephens, 1990; Crooks et al., 2004). Amino acids Leu (L) and Arg (R) (red) and acidic amino acids (green) are highlighted.

(B) Alignment of the N-terminal regions of predicted protein sequences of ATR1^{NdWsB} from *H. parasitica* (Hp) isolate Emoy2, AVR3a (Armstrong et al., 2005) from *P. infestans* (Pi), Avr1b-1 (Shan et al., 2004) from *P. sojae* (Ps), secreted Pi proteins MY-20-B-07 (Kamoun et al., 1999), IPI-O1, and IPI-O2 (Pieterse et al., 1994) (IPI-O proteins are identical in this region), a predicted Hp secreted protein from BAC sequence 12I13, putative Pi PEXs from BACs 14M19 (GenBank accession number AC146943) and 34A11 (GenBank accession number AC147544), and secreted Ps proteins 3-9f-HA and 1-6b-ZO (Qutob et al., 2002). Dashes indicate gaps in the alignment. Predicted signal peptides (blue), the RXLR motif (red), acidic amino acids (green), and the RGD tripeptide motif (underlined) are highlighted.

positions 81 to 249 (nucleotides 462 to 968; Figure 7). Non-synonymous variation is lowest in the first one-fifth of the coding region, increases to intermediate levels ($\pi = 0.0451$) in the center of the gene, and is extremely high in the last third of the coding region ($\pi = 0.131$). The region of protein conservation at the 5' end of the coding region corresponds to the signal peptide and the RXLR motif, described above. The five SNPs differentiating the alleles derived from Emoy2 and Maks9, which were used in the mapping study, are located between nucleotides 495 and 795 (Figures 1 and 7).

Recombination at the ATR1^{NdWsB} Locus

Sequence analysis of the ATR1^{NdWsB} alleles revealed that recombination had occurred at this locus in the ancestry of these eight *H. parasitica* isolates. The four-gamete test (Hudson and Kaplan, 1985) detected a minimum of two recombination events between nucleotides 591 and 751 and nucleotides 796 and 949. The recombination event between positions 796 and 949 was also detected by an independent analysis using the GENECONV program (www.math.wustl.edu/~sawyer). Further analysis revealed that the Noks1 allele appears to be a chimera of two other alleles in the sample. Specifically, the first 546 nucleotides of the Noks1 allele are 100% identical to the Cala2 allele (Figure 1). From nucleotide 519 (Figure 1) to the end of the sequenced region, the Noks1 allele is 100% identical to the Emco5 allele. Significantly, the Noks1 and Emco5 alleles are recognized by the RPP1-WsB gene, whereas the Cala2 allele is not. This implies that the recognition specificity of alleles of ATR1^{NdWsB} by RPP1-WsB is confined to the C-terminal portion of the ATR1^{NdWsB} protein.

DISCUSSION

We have successfully used a map-based cloning strategy to clone the avirulence gene detected by the RPP1 resistance gene

from the Arabidopsis accession Nd-1. Using a cobombardment assay, we found only one allelic form of ATR1^{NdWsB} that is recognized by RPP1-Nd. The observation that optimum recognition occurs in the absence of a signal peptide is consistent with cytoplasmic recognition of the avirulence protein. This is

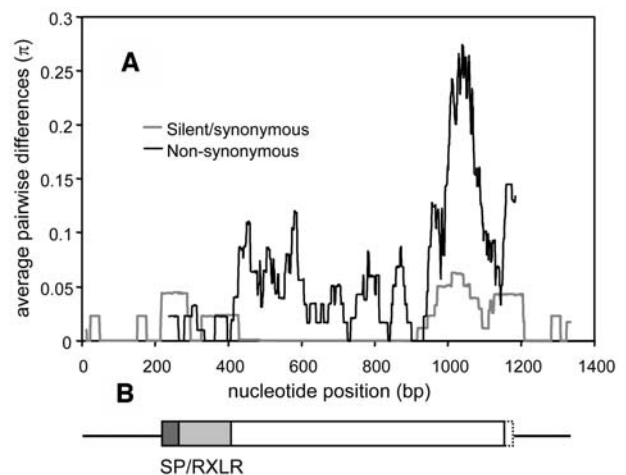


Figure 7. Sliding-Window Analysis.

(A) Average number of pairwise differences between ATR1^{NdWsB} alleles from eight *H. parasitica* isolates. Gray lines represent silent and synonymous variations (in noncoding and coding regions, respectively); black lines represent nonsynonymous variations. Values are midpoints of 25-bp windows.

(B) The ATR1^{NdWsB} coding region (box) and noncoding regions (solid black lines) aligned with **(A)**. The hatched 3' end of the coding region represents the slightly longer coding sequences of the Cala2 and Emwa1 alleles. The regions encoding the signal peptide (SP; dark gray) and the RXLR motif (light gray) are indicated.

reminiscent of the weaker recognition of the full-length compared with the truncated avirulence genes *AVR-Pita* from *Magnaporthe grisea* in rice (*Oryza sativa*) (Jia et al., 2000), *AvrL567* from *M. lini* in flax (*Linum usitatissimum*) (Dodds et al., 2004), and *Avr3a* from *P. infestans* in potato (*Solanum tuberosum*) (Armstrong et al., 2005). This suggests that the signal peptide interferes with the recognition of *ATR1^{NdWsB}*. Perhaps the signal peptide's presence, when expressed inside the plant cell, physically blocks a protein interaction that is required for full recognition; alternatively, the signal peptide may be biologically functional in plant cells, exporting *ATR1^{NdWsB}* and preventing the accumulation of *ATR1^{NdWsB}* in the plant cell. By contrast, the *H. parasitica* *ATR13* protein was recognized equally efficiently with or without its signal peptide (Allen et al., 2004). This finding suggests that the signal peptide does not physically interfere with *ATR13* recognition or that *RPP13* is capable of detecting lower levels of *ATR13*.

In cloning *ATR1^{NdWsB}*, the *H. parasitica* avirulence gene that is perceived by *RPP1* from Nd-1, we also identified *ATR1^{NdWsB}* alleles that are perceived by *RPP1*-WsB from the Ws-0 *RPP1* locus. *RPP1*-WsB recognizes diverse *ATR1^{NdWsB}* protein sequences, only one of which was recognized by *RPP1*-Nd. Surprisingly, although the Ws-0 accession is susceptible when inoculated with the Emco5 isolate, *ATR1^{NdWsB}*-Emco5 is recognized by *RPP1*-WsB in our cobombardment assay. Virulent *P. sojae* isolates that carried avirulence alleles of *Avr1b-1* were virulent because they failed to accumulate *Avr1b-1* mRNA (Shan et al., 2004). By contrast, we have demonstrated that *ATR1^{NdWsB}* is expressed by the Emco5 isolate during infection. Conceivably, Emco5 is virulent on Ws-0 because *ATR1^{NdWsB}* is expressed at low levels, is unstable in vivo, or fails to be taken up by the plant and so remains undetected by *RPP1*-WsB. An exciting alternative is that the Emco5 isolate somehow evades or suppresses either recognition by *RPP1*-WsB or the resistance responses triggered by recognition.

ATR1^{NdWsB}-Cala2 is not recognized by *RPP1*-WsA. Therefore, *RPP1*-WsA recognizes the product of an avirulence gene other than *ATR1^{NdWsB}* in Cala2, consistent with the hypothesis of Botella and coworkers (1998) that different *RPP1*-Ws genes recognize different avirulence determinants.

ATR1^{NdWsB} differs from other known oomycete or obligate biotroph avirulence genes in both size and the level of encoded protein diversity. *ATR1^{NdWsB}*, which is >300 amino acids long, is larger than *ATR13* (187 amino acids [Allen et al., 2004]), *Avr1b-1* (138 amino acids [Shan et al., 2004]), and *AvrL567* (150 amino acids [Dodds et al., 2004]). Furthermore, nearly one-third of the coding positions for *ATR1^{NdWsB}* are polymorphic for two or more amino acid residues. In comparable data sets of allelic variation in avirulence proteins from oomycetes, we observed 10.6% variable amino acid positions among six isolates of *H. parasitica* at *ATR13* and 13% variable amino acid positions among six isolates of *P. sojae* at *Avr1b-1* (Allen et al., 2004; Shan et al., 2004).

The RXLR Motif

Cloning of *ATR1^{NdWsB}* has broader implications. *ATR1^{NdWsB}*, avirulence proteins from *P. sojae* and *P. infestans*, and numerous secreted oomycete proteins share a highly conserved motif that

we term the RXLR motif. In *ATR1^{NdWsB}*, the RXLR motif is encoded by a region of the gene exhibiting the least nonsynonymous variation. The position of the RXLR residues of the motif in IPI-O proteins is intriguing because it overlaps the RGD tripeptide cell-adhesion motif (Senchou et al., 2004). The RXLR motif is conserved in diverse oomycete genera among dissimilar oomycete proteins, some of which have been characterized as candidate pathogenicity factors (Senchou et al., 2004) or avirulence genes (*ATR1^{NdWsB}*) (Shan et al., 2004; Armstrong et al., 2005). Conservation of the RXLR motif in such an impressive array of proteins implies a functional significance in oomycetes.

No Cys-rich proteins from oomycetes were found that carry the RXLR motif. Therefore, proteins carrying the RXLR motif differ from the Cys-rich class of pathogen proteins that have been implicated in fungus-plant and oomycete-plant interactions (Templeton et al., 1994).

The RXLR motif shares some notable similarities with the recently described host-targeting signal, which is conserved in numerous, dissimilar proteins from malaria parasites (*Plasmodium* species) and demonstrated to be required for the translocation of these *Plasmodium* proteins into the host cell (Hiller et al., 2004; Marti et al., 2004). In particular, the *Plasmodium* signal is positioned within 60 amino acids of a secretory signal sequence, and the most highly conserved residues of the motif are Arg and Leu residues spaced, as within the RXLR motif, as RXL (Hiller et al., 2004; Marti et al., 2004). *ATR1^{NdWsB}* and *AVR3a* (Armstrong et al., 2005) are detected within the cytoplasm of host plant cells; it is tempting to speculate that, like the *Plasmodium* host-targeting signal (Hiller et al., 2004; Marti et al., 2004), the RXLR motif may play a role in translocating secreted oomycete proteins into the host plant cell. Such a hypothesis is currently untested experimentally.

Relating *ATR1^{NdWsB}* Sequences to *RPP1* Recognition Specificities

The sequences of *ATR1^{NdWsB}* from eight pathogen isolates can be related to the different recognition specificities of *RPP1*-Nd and *RPP1*-WsB. Isolates recognized by *RPP1*-Nd (Emoy2, Hiks1, and Waco5) share the same allele, but *RPP1*-WsB-recognized alleles (from Emoy2, Maks9, Noks1, and Emco5) encode four protein sequences with extensive sequence variation. *ATR1^{NdWsB}*-Maks9, which is not recognized by *RPP1*-Nd, differs by only five amino acids from *ATR1^{NdWsB}*-Emoy2, which is recognized by *RPP1*-Nd. This suggests that the specificity of *RPP1*-Nd recognition resides within the region spanning these five amino acids (amino acids 92 to 192).

Comparison of the Noks1 and Cala2 alleles revealed that these two sequences are identical for the first 107 codons. Although the *RPP1*-WsB protein can recognize *ATR1^{NdWsB}*-Noks1, it cannot recognize the *ATR1^{NdWsB}*-Cala2 allele. This restricts the region of *RPP1*-WsB recognition specificity of *ATR1^{NdWsB}* to the C-terminal portion of the protein, which differentiates the Noks1 and Cala2 alleles from each other. Further comparison of the four proteins encoded by the alleles that are recognized by *RPP1*-WsB (from isolates Emoy2, Maks9, Noks1, and Emco5) reveals a small region of identical amino acid residues shared by these

four proteins and differentiated from the proteins that are not recognized by RPP1-WsB (Cala2 and Emwa1). If recognition of these four sequences by RPP1-WsB is mechanistically the same (i.e., because of the recognition of a single region within the ATR1^{NdWsb} protein), then the most parsimonious hypothesis is that the region lies between residues 108 and 242. Coincidentally, this region overlaps the region implicated in recognition specificity of ATR1^{NdWsb} by RPP1-Nd. Extremely high levels of nonsynonymous polymorphism relative to synonymous polymorphism were seen at the C terminus of ATR1^{NdWsb}, consistent with this region experiencing diversifying selection. If this region is not involved in RPP1-specific recognition, then forces other than RPP1-WsB recognition must be postulated that have resulted in the selective maintenance of such high levels of amino acid diversity. However, it is theoretically possible that RPP1-WsB recognition of the four different ATR1^{NdWsb} proteins is not limited to a single region shared by these four sequences but extends into the highly variable C terminus. Other R-genes with multiple recognition specificities have been described, and in many cases the detected proteins do not show sequence homology (Grant et al., 1995; Rossi et al., 1998; Pedley and Martin, 2003), indicating that the multiple specificity of an R-gene is not necessarily limited to the recognition of a single sequence motif. Additional tests can now be performed, using a range of RPP1 and ATR1^{NdWsb} molecules, to determine which regions of ATR1^{NdWsb} are detected by RPP1 genes.

Dissecting the earliest molecular events that enable a plant to resist infection by downy mildew, or that enable the pathogen to evade detection and establish an infection, requires the study of both plant and downy mildew components involved in the perception of infection. We have cloned a pathogen component, ATR1^{NdWsb}, that is under immense diversifying selection pressure but retains a motif, presumably of functional significance, that should assist in identifying new candidate avirulence genes and pathogenicity factors by screening databases of oomycete proteins for its presence. Cloning of ATR1^{NdWsb} has revealed that plant RPP proteins encoded by the same genetic locus in different accessions can recognize either single or multiple forms of the same avirulence gene, yet RPP proteins encoded within a single locus of the same accession can recognize different avirulence gene products. Furthermore, virulent isolates can express avirulence alleles of ATR1^{NdWsb}. We are now in a position to test the function of the RXLR motif, elucidate the molecular basis of differential RPP recognition capabilities, and investigate what function ATR1^{NdWsb} fulfills during infection.

METHODS

Hyaloperonospora parasitica Isolates

H. parasitica isolates used in this study were gathered from naturally infected *Arabidopsis thaliana* populations; the locations of these populations and cultivation of the isolates were described previously (Holub et al., 1994; Rehmany et al., 2000).

Identification and Subcloning of ATR1Nd

H. parasitica BAC clones 9B13, 1G5, and 12113 (Rehmany et al., 2003) were sequenced by shotgun cloning of sheared BAC fragments, se-

quencing the subclones, and assembling the sequences (9B13 and 12113 were sequenced at Lark Technologies, Essex, UK; 1G5 was sequenced at Warwick HRI, Warwick, UK). The sequence prediction software MacMolly Tetra (Softgene, Berlin, Germany) was used to predict protein-coding sequences. Primers 12113-17029U (5'-CCATTCCATCAAA-CAACGGCTCTA-3') and 12113-18760L (5'-TCTGCGCATAACATTGAAACATCC-3') were used to amplify PCR products from Emoy2 and Moks9 genomic DNA, extracted as described previously (Rehmany et al., 2000, 2003). SNPs were identified after cycle sequencing (Applied Biosystems, Foster City, CA) using 12113-18760L. PCR and sequencing were repeated using template DNA from F2 individuals that were previously shown to be recombinant in this region (Rehmany et al., 2003). Primers 12113-17736U (5'-CCTGACGAGTGCATGGTAG-3') and 12113-19108L (5'-AAGCTC-GTTTGAAGACTGA-3') were used to amplify the corresponding region from isolates HiKs1, Waco5, Noks1, Cala2, Emco5, and Emwa1. The PCR products were sequenced using primers 12113-18281U (5'-TCGAACGG-GATGATTTGATTGGCG-3'), 12113-18384L (5'-TGTTACTAGCCTAGTG-GCGAGAGC-3'), 12113-18607U (5'-TCTGAGGACGACGCGAACAC-GCC-3'), and 12113-18760L.

ATR1Nd alleles and the *uidA* gene were cloned into the plant expression vector pK2GW7 (Plant Systems Biology, University of Ghent, Ghent, Belgium) using Gateway recombination (Invitrogen, Carlsbad, CA). Entry clones containing the full-length ORF from Emoy2 and Moks9 were created in pDONR207 (Invitrogen) using primer pairs 12113-17977UB1 (5'-AAAGCAGGCTTCATGCGCTGCTACTTCTC-3') and 12113-18912LB2 (5'-GAAAGCTGGGTGTTAAACAGAATATATTCTGAATA-CTC-3') and full-length attB1 and attB2 primers (Invitrogen). Entry clones (pDONR207 or pDONR221; Invitrogen) lacking the sequence encoding the signal peptide were similarly produced using primer pairs 12113-18031UB1 (5'-AAAGCAGGCTCGATGACCGAGTCGTCGGAACGTC-3') and 12113-18912LB2 for Emoy2 and Moks9, primer pairs 12113-18031UiB1 (5'-AAAGCAGGCTCGATGACCGAGTCGTCGGAAC-GTCCCGC-3') and 12113-18912LB2 for Noks1 and Emco5, and primer pairs 12113-18031UiB1 and 12113-18912LiB2 (5'-GAAAGCTGGGTGC-TACTCGCTCGCGCCCTACGAA-3') for Cala2 and Emwa1. Each pK2GW7 expression clone was sequence-verified before use in the cobombardment experiments.

Transient Expression Assays

The *uidA* gene was cloned into pK2GW7 from the pENTR-GUS (Invitrogen) entry clone for GUS expression in the cobombardment experiments. Cobombardment experiments were performed as described previously (Allen et al., 2004). Briefly, *Arabidopsis* plants were grown in 10 h of light at 18°C until 7 weeks old. Detached leaves were placed abaxially on a Whatman 3MM paper (Whatman, Middlesex, UK) support on 1% agar plates. DNA (2.5 μg) from each pK2GW7 expression clone was mixed with pK2GW7:GUS (2.5 μg) and loaded onto M17 tungsten particles (Bio-Rad, Hercules, CA); the mixture was used to make four to six replica bombardments using the manufacturer's recommended protocol. For each replicate, a leaf from both test and control plant genotypes were cobombarded together in a single shot. Bombardments were performed using a Bio-Rad PDS-1000 (He) apparatus with 1100-p.s.i. rupture discs. After bombardment, leaves were incubated at 25°C for 20 h. Histochemical GUS staining was performed using 5-bromo-4-chloro-3-indolyl glucuronide (Duchefa Biochemie, Haarlem, The Netherlands) at 37°C for 4 h (Mindrinos et al., 1994), and the tissue was cleared with methanol before scoring the leaves for numbers of blue-stained cells using a light microscope or macroscopically. Experiments were replicated at least twice.

Expression Analysis

RNA was extracted from susceptible plants 24 h after inoculation with *H. parasitica* isolates using the RNeasy plant mini kit (Qiagen, Crawley, UK)

and including a DNase treatment. First-strand cDNA was synthesized using the oligo(dT) CDSIII primer (Invitrogen) and Superscript III reverse transcriptase (Invitrogen). PCR amplifications (37 cycles) were performed using primers 12113-17977U (5'-ATGCGCGTCTGCTACTTCGTTCTC-3') and 12113-18346L (5'-CATGGAGTGGCCCCGGCGCTTCA-3') or primers MTD5 (5'-GACCCGGCTGCGAAGAAGTATGC-3') and MTD3 (5'-CCA-GCGGCCGACCAACAATG-3'). Products amplified using 12113-17977U and 12113-18346L were sequenced using the same primers.

Database Searches for Proteins with a Conserved Motif

All oomycete sequences present in GenBank, as well as the sequences of BACs spanning the *ATR1Nd* locus, were searched for putative proteins fulfilling three criteria: (1) the presence of a signal peptide predicted using SignalP based on previously published criteria (Torto et al., 2003); (2) the occurrence of the sequence RXLR within 40 amino acids of the predicted signal peptide cleavage site; and (3) a stretch of Asp and/or Glu residues in the 30 amino acids after the RXLR motif. The total number of oomycete proteins examined was 1337 (GenBank release November 29, 2004). For genomic sequences, all potential ATG start codons were identified before assessing them for the occurrence of signal peptides or the conserved motif. All analyses were performed using an Apple Macintosh OSX workstation using text string search tools.

Sequence Analysis

The nucleotide sequences from the eight isolates were aligned using ClustalX version 1.8 (Thompson et al., 1997). Minor refinements to this alignment and protein prediction were performed in MacClade version 4.0 (Maddison and Maddison, 2000). Average pairwise differences were calculated and a sliding-window analysis was conducted using DnaSP version 3.51 (Rozas and Rozas, 1999). The numbers of segregating synonymous and nonsynonymous sites and the total numbers of synonymous and nonsynonymous sites were calculated using the SITES program developed by J. Hey (available at <http://lifesci.rutgers.edu/~hey/hey/HeylabSoftware.htm>). The χ^2 test was conducted using the online program from GraphPad (<http://www.graphpad.com/quickcalcs/chisquared1.cfm>). The minimum number of recombination events in the ancestry of these alleles was calculated using DnaSP version 3.51 according to the methods described by Hudson and Kaplan (1985). The GENECONV program (developed by S.A. Sawyer; available at www.math.wustl.edu/~sawyer) was used to determine whether some regions of a pair of sequences had more consecutive identical polymorphic sites than would be expected by chance.

Sequence data from this article have been deposited with the EMBL/GenBank data libraries under the following accession numbers: Emoy2 BAC clones 9B13 (AY973543), 1G5 (AY973540), and 12113 (AY973542 and AY973541); *ATR1^{NdWsb}* alleles from Emoy2 (AY842877), Hiks1 (AY842878), Waco5 (AY842879), Maks9 (AY842880), Emco5 (AY842881), Noks1 (AY842882), Cala2 (AY842883), and Emwa1 (AY842884); and MTD from Emoy2 (AY973539).

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Differential Recognition of Highly Divergent Downy Mildew Avirulence Gene Alleles by RPP1 Resistance Genes from Two Arabidopsis Lines

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