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## Molecular mapping of the *Arabidopsis* locus *RPP11* which conditions isolate-specific hypersensitive resistance against downy mildew in ecotype RLD

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**Abstract** Isolate WELA of the plant pathogenic oomycete fungus *Peronospora parasitica* causes downy mildew in the *Arabidopsis thaliana* ecotypes Weiningen (Wei-0) and La-er, whereas ecotypes RLD and Col-0 are resistant. Genetic crosses between resistant RLD and susceptible Wei-0 showed that resistance was inherited in a simple Mendelian fashion as a monogenic dominant trait. The interactions between different isolates of *P. parasitica* and ecotypes of *A. thaliana* show race-specific variation and fit a gene-for-gene relationship. The *RPP11* resistance gene was mapped by following the co-segregation of the resistance phenotype with RFLP markers in a mapping population of 254 F<sub>3</sub> families derived from RLD × Wei-0 F<sub>2</sub> individuals. Linkage analysis using version 1.9 of the MAPMAKER program placed the *RPP11* resistance locus on chromosome III between marker m249 (two recombinants) and marker g2534 (six recombinants). Markers g2534 and g4117 are on YAC EG7H1. Marker g4117 and one end probe (N5) generated from YAC EG7H1 showed no recombinants. The YAC end probe N5, which was generated by plasmid rescue, was used to screen clones in the Eric Ward YAC library and a YAC was fished (EW19B12) which also hybridised with m249. Thus, a YAC contig has been established over the region where the resistance locus maps. Because the YACs were made with ecotype Columbia DNA it is necessary to isolate the equivalent region from RLD in order to clone the resistance locus. To this end a phage λ-DASH<sup>TM</sup> genomic library was prepared from RLD and a contig covering the relevant region of the YACs is currently under construction.

**Key words** Resistance gene · *Peronospora parasitica* · *Arabidopsis thaliana* · Molecular markers

### Introduction

Downy mildew of *Arabidopsis thaliana* was mentioned by Lindau (1901) and Gaeumann (1918), and is caused by the oomycete fungus *Peronospora parasitica*. The pathosystem was first described in detail by Koch and Slusarenko (1990) who showed that pathotypic variation occurred between host and pathogen and that resistance was associated with a hypersensitive response. Variation in the microscopic and macroscopic phenotypes of resistance in various isolate/ecotype combinations has been characterised and the inheritance of resistance studied in crosses (Holub et al. 1993; Mauch-Mani et al. 1993; Holub et al. 1994). Resistance in *Arabidopsis* to *P. parasitica* is inherited as though it were conditioned by single dominant genes in the host and this is an important pre-requisite for a map-based cloning strategy to isolate the resistance loci.

*Arabidopsis* has many advantages as a model host for investigating the molecular biology of host-pathogen interactions because of its small genome size and the availability of genetic maps, markers, and YAC-libraries (Chang et al. 1988; Guzmann and Ecker 1988; Nam et al. 1989; Ward and Jen 1990; Grill and Sommerville 1991; Hauge et al. 1993; Lister and Dean 1993; Schmidt and Dean 1993; Jarvis et al. 1994). These features all contribute to successful positional cloning strategies to isolate genes characterised only by the phenotype they confer. Model pathosystems have been developed for interactions of *Arabidopsis* with bacteria and fungi (Davis et al. 1991; Debener et al. 1991; Crute et al. 1993). For reviews see Ausubel et al. 1993; Dangl 1993; Mauch-Mani and Slusarenko 1993; Crute et al. 1994; Staskawicz et al. 1995). The *Arabidopsis* resistance gene *RPS2*, which conditions resistance against *Pseudomonas syringae* pv *tomato* isolates and other pseudomonads containing the avirulence gene *avrRpt2*, has now been

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cloned (Bent et al. 1994; Mindrinos et al. 1994) and the map positions of four genes recognizing *P. parasitica* isolates (*RPP*) have been published (Parker et al. 1993; Tör et al. 1994). In the present paper we describe the RFLP-mapping of the race-specific resistance gene *RPP11* of *A. thaliana* to the WELA isolate of *P. parasitica*.

## Materials and methods

### Plant material and crosses

Seeds of *A. thaliana* ecotypes RLD and Wei-0 were surface-sterilized with bleach (2.5%) for 15 min and washed several times with sterile tap water before sowing into growing compost mixed with perlite. The seeds were kept for 5 days at 4 °C before being transferred into a growth chamber with a photoperiod of 8 h light (approximately  $150 \mu\text{E m}^{-2} \text{s}^{-1}$ , 23 °C) and 16 h dark (18 °C). Plants for crosses were sown singly into small pots to facilitate handling whereas plants for phenotype determination were sown into flats at approximately 2 seeds  $\text{cm}^{-2}$ .

### Infection with *P. parasitica* isolate WELA

Plants were inoculated with *P. parasitica* isolate WELA 3 weeks after sowing, which corresponded to 2-weeks growth in the climate chamber. At this stage the plants had fully developed cotyledons and emerging primary leaves. Inoculum production and the inoculation of the seedlings was performed as described by Mauch-Mani and Slusarenko (1994).

### Determination of infection phenotype

Whole seedlings were stained with alcoholic trypan blue solution (Keogh et al. 1980) and cleared in chloral hydrate ( $2.5 \text{ g ml}^{-1}$ ) for about 24 h. Whole seedlings were then mounted in chloral hydrate and viewed under a microscope with bright-field optics. The resistance phenotype of  $F_1$ ,  $F_2$  and backcrosses was first determined using a dissecting microscope to score for the presence or absence of asexual sporulation of the fungus 1 week after infection. One leaf from each plant was then dissected away, cleared in chloral hydrate, and examined microscopically to confirm the macroscopically determined phenotype.

The reactions of the  $F_3$  plant families were divided into three categories. They were scored as resistant when from a subset of 40 seeds all the plants showed a hypersensitive reaction at the location of the attempted fungal penetration. A family was scored as susceptible when all the tested plants were colonized by the fungus and sexual, as well as asexual, spores could be found by 1 week after inoculation. Heterozygote families segregated for resistance and susceptibility as expected.

### Extraction and RFLP analysis of DNA from $F_3$ families

Isolation of total DNA was as described by Dolferus (1991). For RFLP analysis 1–5  $\mu\text{g}$  of DNA was digested with the appropriate restriction enzyme to reveal a polymorphism between RLD and Wei-0 for the probe in question. The digested DNA was separated on 1% agarose gels in TAE buffer (Sambrook et al. 1989) and blotted onto Hybond N membranes (Amersham; Sambrook et al. 1989). The filters were baked for 2 h at 80 °C. The RFLP markers (phage and cosmid markers) were radioactively labelled with  $^{32}\text{P}$ -dCTP using a random primed labelling kit (Boehringer). Hybridisation was carried out overnight at 60–65 °C in 10% (w/v) dextran-sulphate, 1 M NaCl and 1% SDS. Filters were washed in  $2 \times \text{SSC}$ , 1% SDS,  $2 \times 45 \text{ min}$  at 65 °C and  $0.2 \times \text{SSC}$ , 0.1% SDS,  $2 \times 45 \text{ min}$  at

65 °C. The filters were exposed to X-ray film for 1 day at –80 °C with intensifying screens.

Linkage analysis was performed with the mapmaker program (Lander and Green 1987; Lander et al. 1987) using a LOD score of 3.0.

RFLP phage, cosmid markers and the E.W. YAC library were kindly provided by the Arabidopsis Biological Resource Center at Ohio State University.

Cosmid and phage propagation and DNA extraction was done according to the methods of Sambrook et al. 1989.

The yeast DNA extraction of the clones EG7H1, EW19B12, EW12D3, the plasmid rescue, and the screening of the YAC library was done as described in Gibson and Sommerville (1992).

## Results

### Genetics of resistance

In the cross Weiningen  $\times$  RLD, 100 tested  $F_1$  plants all showed a resistant phenotype when inoculated with the WELA isolate of *P. parasitica*. Testing of an  $F_2$  population of a cross between Weiningen and RLD gave a segregation of 38 resistant to 12 susceptible plants ( $\chi^2$  3:1 = 0.014,  $P > 0.05$ ). In a representative backcross [Wei-0  $\times$  (Wei-0  $\times$  RLD)] resistance segregated eight susceptible plants to six resistant ( $\chi^2$  1:1 = 0.28,  $P > 0.05$ ). These results indicate that resistance in RLD is inherited as though it were conditioned by a single dominant gene. Since these ratios were conserved in reciprocal crosses there is no evidence for maternal effects on the inheritance of resistance in this host-isolate combination. The resistance locus in question was designated *RPP11* (Recognition of *Peronospora parasitica*) by Holub et al. (1994) in a comprehensive survey of the genetics of the interaction between *P. parasitica* isolates and *Arabidopsis* ecotypes.

### Mapping of the resistance locus

Fine mapping of the resistance locus was performed by following co-segregation of the susceptible phenotype with chromosome-3 RFLP probes in a total of 254  $F_3$  families. Phage and cosmid probes needed to be tested empirically with various restriction enzymes to determine whether they highlighted an RFLP between the RLD and Wei-0 ecotypes. This information is summarised in Table 1.

The resistance locus mapped between the phage marker m249 and the cosmid marker g2534 (Fig. 1). Two recombinants were found between *RPP11* and marker m249, and six recombinants with marker g2534. No recombinants were found with marker g4117 located between m249 and g2534. The two markers g2534 and g4117 both map to the YAC EG7H1 (Hwang et al. 1991) and the plasmid-rescued end-fragment from this YAC also showed no recombinants. A *Bam*H1/*Nde*1 digest was used to remove YAC DNA from the end-fragment of EG7H1 and this was used as a probe to isolate an overlapping YAC EW19B12, which closes the gap between the marker m249 and the YAC EG7HI. The

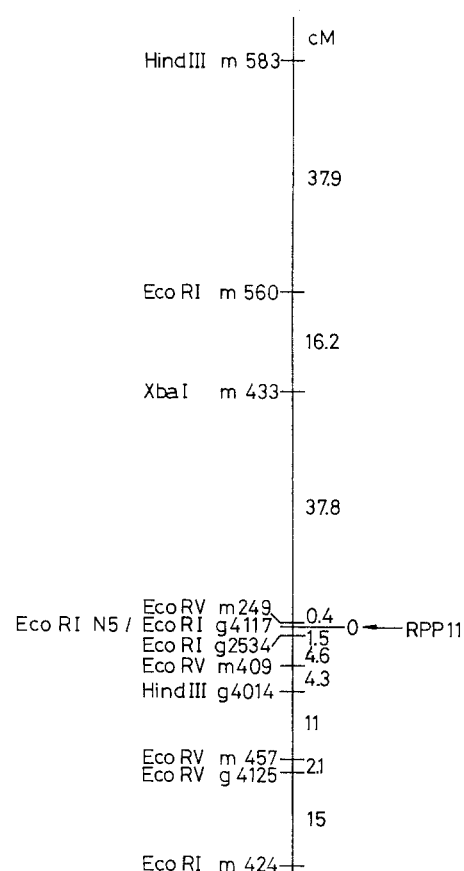
**Table 1** Probes and restriction enzymes used to highlight polymorphisms between RLD and Wei-0 ecotypes. H = *Hind*III, RI = *Eco*RI, RV = *Eco*RV, X = *Xba*I

Chromosome	Probe	Restriction enzyme	Map distance (cM)
I	m241	RI	
	m219	X	9.6
	m402	RI	30.8
	m213	RI	53.1
	m305	RI	12.3
	m421	RI	5.6
	m315	RI	6.5
	m453	RI	12.5
	m532	H	12.3
II	m605	RI	
	m283	RI	22
	m429	X	21.1
	m336	H	0
III	m583	H	
	m560	RI	37.9
	m433	X	16.2
	m249	RI	37.8
	N5	RI	0.4
	g4117	RI	0
	g2534	RI	1.5
	m409	RV	4.6
	g4014	H	4.3
	m457	RV	11
	g4125	RV	2.1
	m424	RI	15
	IV	m506	RI
m518		RI	22.5
m600		RV	36.7
V	m217	RI	
	m224	X	7
	m247	RI	31.6
	m422	RI	4.9
	m225	X	16.7

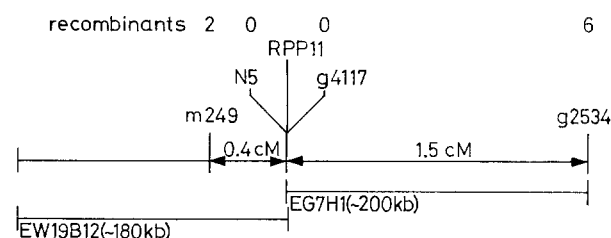
genomic organisation of the phage and cosmid markers, YACs, and the end-fragment of the YAC EG7HI is shown in Fig. 2. The YAC DNAs were isolated and used to fish cross-hybridizing phage clones from our RLD genomic library and these are currently being ordered on the physical map, and clones which potentially carry the *RPP11* gene are being subcloned into a plant transformation vector for functional testing in transgenic plants.

## Discussion

The isolation and characterization of the *RPP11* gene from *Arabidopsis* will add to the list of already cloned resistance genes and increase the composite picture of their common features. Other resistance genes effective against *Peronospora* isolates with different avirulence gene specificities (*RPP1*, *RPP2*, *RPP4* and *RPP5*) are currently being, or have been (*RPP5*, Jane Parker, personal communication), cloned from *Arabidopsis*. This series of resistance genes will be the most comprehensive so far cloned for a particular pathosystem. It will thus be



**Fig. 1** Fine mapping of *RPP11* on chromosome III in a population of 254  $F_3$  families



**Fig. 2** Physical map of the region on chromosome III around *RPP11*. The YAC, phage and cosmid clones are as described in the text

of great interest to see how these genes, which all condition resistance to different races of the same pathogen, relate to each other in structure and function. An interesting feature which has already emerged is that *RPP* genes, although dispersed throughout the genome, often seem to map in clusters. Thus, *RPP1* and *RPP11* map respectively above and below marker m249 on chromosome III and *RPP2*, *RPP4*, *RPP5* all map closely on chromosome IV (Parker et al. 1993; Tör et al. 1994; Joos et al., this work). In *Arabidopsis* only chromosome II has not yet been reported to carry a resistance locus.

Another interesting feature to emerge from studies with the *P. parasitica/Arabidopsis* pathosystem is that some resistance genes appear to be dominant, e.g. *RPP11*, whereas others show incomplete dominance, e.g., *RPP5* and *RPP6* (Mauch-Mani et al. 1993; Parker

et al. 1993). This phenomenon has been reported for the *Bremia lactucae*/lettuce pathosystem and the implications for the mechanism of resistance gene function were discussed by Crute and Norwood (1986). It will thus be particularly interesting to see how the structural features of *RPP5*, *RPP11*, and the other *RPP* genes, relate to their biochemical functions and the resistance phenotypes they confer.

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