

# Supporting Information

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## SI Text

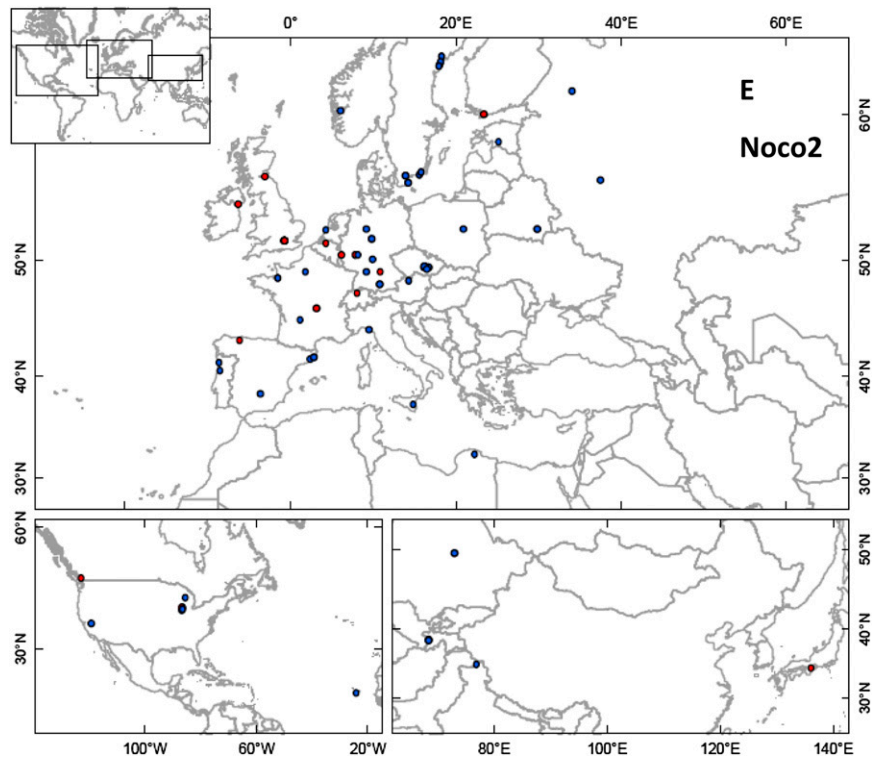
**Arabidopsis thaliana Genotypes and Growth.** The Nordborg set of 96 *A. thaliana* accessions (1) was provided by C. Dean's group (JIC, Norwich, UK). Sets of *A. thaliana* (*At*) recombinant inbred lines (RILs) were kindly provided by I. Bancroft's group (JIC, Norwich, UK) (2), with exception of the Bay-0 × Shahdara population, which was kindly provided by O. Loudet (INRA, Versailles, France) (3). *A. thaliana* plants were grown as seeds and sown on a 12:1 mixture of Scott's M2 plus Intercept to grit, and they were stratified for 2 days at 4 °C in the dark. Then, they were moved to growth chambers kept at 20–22 °C and 70% humidity under 10 h light and 14 h dark. Seeds were covered with a clear polystyrene lid for 2 days to promote germination. When necessary, accessions were vernalized in the dark for 2–3 months at 4 °C before germination.

**Hyaloperonospora arabidopsidis Materials and Infections.** The isolates Emwa1, Hiks1, Emco5, Cala2, and Emoy2 were originally collected and provided by E. Holub (HRI, Warwick, UK). Noco2 was isolated and propagated in the Sainsbury Laboratory in the United Kingdom. Propagation, inoculum preparation, infection, and incubation were conducted as described previously (4). After 7 days of incubation, the interaction was scored specifically on first true leaves as compatible, incompatible, or intermediate depending on the consistency of presence/absence of sporangiophores. Disease assessments on each genotype were done on 5–10 seedlings and repeated independently at least three times. In some accession × isolate interactions, variation in occurrence of sporulation was consistently observed within and between experiments, and this is referred to as intermediate.

1. Nordborg M, et al. (2005) The pattern of polymorphism in *Arabidopsis thaliana*. *PLoS Biol* 3:e196.
2. O'Neill CM, et al. (2008) Six new recombinant inbred populations for the study of quantitative traits in *Arabidopsis thaliana*. *Theor Appl Genet* 116:623–634.
3. Loudet O, Chaillou S, Camilleri C, Bouchez D, Daniel-Vedele F (2002) Bay-0 x Shahdara recombinant inbred line population: A powerful tool for the genetic dissection of complex traits in *Arabidopsis*. *Theor Appl Genet* 104:1173–1184.
4. Reignault P, et al. (1996) Four *Arabidopsis* RPP loci controlling resistance to the Noco2 isolate of *Peronospora parasitica* map to regions known to contain other RPP recognition specificities. *Mol Plant Microbe Interact* 9:464–473.







**Fig. S1.** Geographic distribution of resistance phenotypes in a set of 96 *A. thaliana* accessions challenged with five isolates of *H. arabidopsidis ex parasitica* (*Hpa*). Blue dots indicate resistant accessions, and red dots indicate susceptible accessions. Intermediate interactions are not reported. Accessions from the same origin may appear as a single dot but generally showed the same resistance phenotype.













**Table S1. Previously characterized resistance genes that control downy mildew resistance in *A. thaliana* with their genome location, accessions that carry them, and recognition specificities**

Chr	MRC supercluster	<i>R</i> Locus	Col-0 orthologs	Mol st	<i>H. arabidopsis</i> isolates detected					
					Cala2	Emco5	Emoy2	Emwa1	Hiks1	Noco2
I	B-2	<i>RPP7</i>	At1g58602	CNL					Col-0, Ler-0	
	B	<i>RPP27</i>							Ler-0	
		<i>RPP9</i>							Wei-0	
III	F-1	<i>RPP1<sub>W<sub>s</sub>A</sub></i>	At3g44480	TNL	Ws-0		Ws-0			Ws-0
	F-1	<i>RPP1<sub>W<sub>s</sub>B</sub></i>		TNL			Ws-0, Nd-1		Nd-1	Ws-0
	F-1	<i>RPP1<sub>W<sub>s</sub>C</sub></i>		TNL						Ws-0
	F-2	<i>RPP13</i>	At3g46530	CNL		Nd-1				
IV	H-1	<i>RPP2a</i>	At4g19510	TNL	Col-0, Oy-0					
	H-2	<i>RPP5</i>	At4g16860	TNL			Ler-0, Col-0	Ler-0, Col-0	Ler-0	Ler-0
V	J-1	<i>RPP8</i>	At5g43470	CNL		Ler-0	Ler-0			
	J	<i>RPP31</i>				Col-0				

The table represents genetic determinants of incompatible interactions identified in various host accessions against six isolates of *H. arabidopsidis*. The lines represent the loci and when known, the genes controlling resistance. Their recognition specificities are represented in columns. The intersection of line (*RPP* locus) and columns (*Ha* isolate) indicates the accession(s) in which the locus confers resistance to the isolate. Chr, chromosome; MRC, major recognition complex; Col-0 orthologs, gene references in Col-0; Mol st, molecular structure of protein encoded; TNL, Toll-like interleukin receptor-nucleotide-binding, leucine-rich repeat (NLR) encoding gene; CNL, Coiled-coil-NLR encoding gene.



Table S2. Cont.

Accession	Stock number	Host disease phenotype on challenge with <i>H. arabidopsis</i> isolate				
		<i>Emco5</i>	<i>Emwa1</i>	<i>Emoy2</i>	<i>Hiks1</i>	<i>Noco2</i>
Pna-17	CS22570	R	S	S	R	R
Pro-0	CS22649	S	S	R	S	S
Pu2-23	CS22593	I	R	R	R	R
Pu2-7	CS22592	R	—	—	—	—
Ra-0	CS22632	S	S	S	I	I
Ren-1	CS22610	R	R	R	R	R
Ren-11	CS22611	R	R	R	R	R
Rmx-A02	CS22568	—	—	—	—	—
Rmx-A180	CS22569	R	S	S	S	S
RR5-10	CS22565	R	R	S	S	S
RR5-7	CS22564	R	R	R	R	R
Se-0	CS22646	R	S	R	—	S
Shahdara	CS22652	R	R	—	S	R
Sorbo	CS22653	R	R	S	R	R
Spr1-2	CS22582	R	R	—	S	R
Spr1-6	CS22583	R	R	R	R	—
Sq-1	CS22600	I	R	R	S	R
Sq-8	CS22601	I	S	S	R	S
Tamm-2	CS22604	I	—	—	R	R
Tamm-27	CS22605	I	S	—	R	S
Ts-1	CS22647	R	S	I	R	S
Ts-5	CS22648	R	R	R	S	S
Tsu-1	CS22641	S	S	S	R	S
Ull2-3	CS22587	R	S	S	S	R
Ull2-5	CS22586	R	S	—	S	R
Uod-1	CS22612	R	R	S	S	S
Uod-7	CS22613	R	R	R	R	R
Van-0	CS22627	S	R	R	R	R
Var2-1	CS22580	I	R	—	—	S
Var2-6	CS22581	R	R	—	R	R
Wa-1	CS22644	R	R	R	R	R
Wei-0	CS22622	S	S	S	S	S
Ws-0	CS22623	S	S	R	R	R
Ws-2	CS22659	R	S	S	S	R
Wt-5	CS22637	R	R	R	R	R
Yo-0	CS22624	R	S	—	S	S
Zdr-1	CS22588	R	R	R	R	R
Zdr-6	CS22589	R	R	R	R	R

Interaction scoring: R, incompatible; S, compatible; I, intermediate; —, nonassessed. The experiment was repeated four times on five seedlings per genotype. Disease was scored specifically on first leaves.

Table S3. Summary of survey of natural variation in disease resistance interactions between 96 accessions of *A. thaliana* and five isolates of *H. arabidopsidis ex parasitica*

Phenotypes	Total	<i>Emco5</i>	<i>Emwa1</i>	<i>Emoy2</i>	<i>Hiks1</i>	<i>Noco2</i>
R	265 (60.1%)	70 (74.5%)	53 (58.9%)	41 (52.6%)	52 (59.1%)	49 (53.8%)
S	156 (35.4%)	16 (17%)	32 (35.5%)	36 (46.2%)	33 (37.5%)	39 (42.9%)
I	20 (4.6%)	8 (8.5%)	5 (5.5%)	1 (1.2%)	3 (3.4%)	3 (3.3%)
—	31	2	6	18	8	5

The summary scores of the occurrence of resistance, susceptibility, intermediate interaction, and nonassessed (n.a.) for each isolate and in total are presented with frequencies in percents between parentheses.

**Table S4. Association mapping of resistance loci against *H. arabidopsidis* in mapping intervals overlapping with MRCs using a set of 96 *A. thaliana* accessions with the 2010 genotype dataset**

Chr, MRC	Physical location	Linked marker	Associated candidate gene	Distance to candidate (kbps)	Association with <i>R</i> to <i>Hpa</i> isolate			Mapping intervals: source of resistance/recognition specificity
					<i>Emwa1</i>	<i>Emco5</i>	<i>Noco2</i>	
(A) I, MRC-B	20633251	<i>nga128</i>	?					Sorbo/E1
	21079875		At1g56540 (TNL)	0	†	‡	*	Bay-0/E1
	21187559		?					
	21657491		?		†			
	21669047		?			†		
	21908330		CW9 (RPP8-like)	0	*	‡	‡	
	22283402		At1g60320 (TNL)	10	*	*	*	
	22492711		At1g61060 (RPP8-like)	0	*	*	*	
	23270329		?					
	23704640	<i>t12p18ind8-8</i>						
(B) III, MRC-F	24379374	<i>fsi1449495</i>						
	12534916	<i>k11j14ind16-16</i>	?		—	†	—	Ga-0/E5
	14672505		?					
	15028165		?					
	15526753		?			*		
	15679305		At3g43770 (TNL)	17	‡	†	†	
	16379891		SALM	3	*	*	*	
	16977709		?		*	*	*	
	17141912		RPP13 (CNL)	0	*	*	*	Bay-0/C2
	17256068	<i>msat3.21</i>						
(C) IV, MRC-H	17277073		?			†	*	
	18180258		?			*		
	18379314		?		*	*	*	
	18470089	<i>t16k521877</i>						
	7892620	<i>ciw6</i>						
	8280764		At4g14370 (TNL)	0	*	*	*	Nok-3/E5
	8375566		At4g14610 (CNL)	5	—	—	*	
	8380918		At4g14610 (CNL)	0	*	*	*	
	8646352		?		*	—	—	
	9058122		?		*	—	—	
9277112		?		*	—	—		
9314687		?		*	—	—		
9360000	<i>msat4.15</i>							
9478782		RPP5a (TNL)	9		—	‡		
9577993		RPP5 cluster (TNL)	12	*	—	—		
9579976		RPP5 cluster (TNL)	14	†	—	—		
9680252		?		*	—	—		
9965867	<i>t6k21ind15-15</i>							
10275867		?						
10977375		?						
11951649	<i>msat4.18</i>							
12076453		?						
12603189	<i>t22a6ind10-10</i>							



**Table S5. Identification of candidate RPP loci from GWAM of resistance to five isolates of *H. arabidopsidis***

Chromosome MRC	I-B	III-F	IV-H	V-J	Total
Left border	<i>nga128</i> (20633251)	<i>k11j14ind16-16</i> (12564916)	<i>ciw6</i> (7892620)	<i>aths0191</i> (15021915)	
Right border	<i>f5i1449495</i> (24379373)	<i>t16k521877</i> (18470089)	<i>t22a6ind10-10</i> (12603189)	<i>mql58 636</i> (19218084)	
Size (Mbp)	3.72	5.97	4.7	4.78	19.17
Number of SNPs	8,734	10,783	11,280	11,054	41,851
Number of SNPs > 0.004	201 (2.3%)	207 (1.91%)	119 (1.05%)	181 (1.63%)	672 (1.6%)
>0.004 and <5 kbp apart	16	20	7	13	56
Primary candidates	4	3	2	4	13
	TNL (At1g57850) CNL (At1g58390) TNL (At1g61100) TNL (At1g63740)	RPP13 (At3g46530) EDS1 (At3g48080) CNL (At3g46710)	RPP5 (At4g16860) ACD6 (At4g14400)	TNL (At5g40920) CNL (At5g43740) TNL (At5g46270) CNL (At5g47260)	
Secondary candidates	4	2	1	1	8
	DEFL (At1g58055)  RLK (At1g26950) RbohD-interactor (At1g64060) DEFL (At1g64195)	DEFL (At3g42557)  RLK (At3g47110)	IAA1 (AXR5, At4g14560)	Avirulence-responsive (At5g39730)	
Unknown	8	15	4	8	34

The table reports loci where very strong and consistent associations were found on four genomic regions corresponding to MRC and quantitative trait loci (QTL) intervals with their corresponding left and right border markers (physical position in parentheses). The total number of tested SNPs contained in the intervals is given. Loci were first selected on the basis of strength of association (importance > 0.004) and further on the basis of consistency of association (i.e., SNPs showing association with resistance to at least two *Hpa* isolates occurred within a 5-kbp window). Primary candidates correspond to NLR encoding genes (TNL, TIR-NLR; CNL, CC-NLR). Secondary candidates include various homologs of defense-related genes or pathogen-induced genes. Loci corresponding to yet nonannotated genes or genes not clearly linked to defense were grouped as unknown.