

Supplemental Research Data – Tables S1 – S5

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**Amplification generates modular diversity at an avirulence
locus in the pathogen *Phytophthora***

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Supplemental Research Data Table S1

Table S1. BACs containing *pi3.4*. Based on the hybridization patterns with various probes, the BACs are classified in six contigs I to VI. The probes used in the hybridization and the sizes of the *Bgl*II fragments hybridizing to TDF3.4 are listed in the column headings.

contig	BAC	tdf3.4 14 kb	tdf3.4 2.3 kb	tdf3.4 9.5 kb	tdf3.4 ~15 kb	tdf3.4 ~12 kb	tdf3.4 8 kb	tdf3.4 13 kb	tdf3.1	pi3.4F- 5' end
I	BAC26D01	x								
I	BAC12I03	x								x
I	BAC37O23	x								x
I	BAC15E09	x								x
I	BAC29J11	x								x
I	BAC43G13	x								x
I	BAC22O12	x								x
I	BAC20I24		x						x	x
I	BAC34G01		x						x	
I	BAC40D03		x						x	
II	BAC09C18			x						
II	BAC27A18			x						
II	BAC45E08			x						
III	BAC03I21				x					
III	BAC18C08				x					
III	BAC13I12				x					
III	BAC22G09				x					
III	BAC27F09				x					
III	BAC40E02				x					
IV	BAC06M14					x				
IV	BAC28E04					x				
IV	BAC09H13					x				
IV	BAC28D13					x				
IV	BAC45G12					x				
IV	BAC28P02					x				
IV	BAC43M19					x				
V	BAC08E24						x			
V	BAC09F16						x			
V	BAC11F03						x			
V	BAC15O02						x			
V	BAC34B12						x			
VI	BAC05F22							x		
VI	BAC18J11							x		

Supplemental Research Data Table S2

Table S2. Composition of pools used for hybridization of the custom designed *Phytophthora* GeneChip.

	strain	<i>Avr1</i>	<i>Avr3b- Avr10- Avr11</i>	<i>Avr4</i>	<i>Avr2</i>
pool1	rE11-16	Aa	aa	Aa	Aa
	T15-1	Aa	aa	Aa	Aa
	T30-2	Aa	aa	Aa	Aa
pool2	D12-2	aa	aa	aa	Aa
	D12-23	aa	aa	aa	Aa
pool3	D12-17	Aa	Aa	aa	aa
	T15-9	Aa	Aa	aa	aa
pool4	T20-2	aa	Aa	Aa	Aa
	E12-3	aa	Aa	Aa	aa
pool 5	T35-3	aa	aa	aa	aa
pool6	T30-2	Aa	aa	Aa	Aa

Supplemental Research Data Table S3

Table S3. Eight sequences representing six genes with CNV as shown by array-CGH.

code of the array sequence	size of the sequence (bp)	intensity increase corresponds to an AVR phenotype	SwissProt hit	<i>E</i> value	copy number in <i>P. sojae</i> ^a	copy number in <i>P. ramorum</i> ^a	array-CGH intensity change (from 0 to 1) ^b
PI001829 ^c	715		Fimbrin (P54680)	1E-50	1	1	0.61
PI004035 ^c	855		Fimbrin (P54680)	1E-70	1	1	0.67
PI007379	506		-	-	0	0	0.58
PI008646	612	AVR2	-	-	0	0	0.55
PI008871	483		-	-	0	0	0.53
PI009555	413		-	-	0	0	0.84
PI003481 ^d	472	AVR3b-AVR10-AVR11	-	-	1	1	0.59
PI014715 ^d	1358	AVR3b-AVR10-AVR11	-	-	1	1	0.63

^a copy number is estimated from BLAST hit with identity percentage > 50% and *E* value < 1e-30

^b intensity change indicates copy number variation, and the calculation of intensity change is described in material and methods.

^c PI001829 and PI004035 are derived from the same gene

^d PI003481 and PI014715 are derived from *pi3.4*

Supplemental Research Data Table S4

Table S4 The presence of AFLP marker E+AA/M+CTs239 derived from *pi3.4* correlates with the AVR3b phenotype in field isolates. The phenotypes on *R1*, *R4*, *R3b*, *R10* and *R11* are indicated by avirulent (A) and virulent (V). The presence or absence of AFLP markers is indicated by + or -, respectively.

isolates	<i>R1</i>	<i>R4</i>	<i>R3b</i>	<i>R10</i>	<i>R11</i>	E+AA/ M+CTs239	E+GG/ M+CCs251	E+CA/ M+GGs826	E+AG/ M+AAs258	E+TG/ M+CTs240
80029 ^a	A	V	A	A	A	+	+	+	+	+
88133 ^a	V	A	V	V	V	-	-	-	-	-
T30-2 ^b	A	A	V	V	V	-	-	-	-	-
T15-2 ^b	V	V	A	A	A	+	+	+	+	+
85152	V	V	V	A	V	-	-	-	-	-
85192	V	V	V	V	V	-	+	+	+	+
86004	V	V	V	V	V	-	+	+	+	+
86022	V	V	V	V	A	-	+	+	+	+
87013	V	V	V	-	-	-	+	+	+	+
87194	V	V	V	V	V	-	-	-	-	-
88039	V	V	V	A	V	-	+	+	+	+
88184	V	V	V	V	V	-	-	-	-	-
88215	A	V	V	V	V	-	-	-	-	-
89005	V	V	V	V	A	-	+	+	+	+
89018	V	V	V	V	V	-	+	+	+	+
89047	V	V	A	A	A	+	+	+	+	+
89140.02	V	V	V	V	V	-	+	+	+	+
89140.10	V	V	V	V	V	-	+	+	+	+
89150.01	V	V	V	V	V	-	+	+	+	+
89153.01	V	V	V	V	V	-	-	-	-	+
89155.03	A	V	A	A	A	+	+	+	+	+
90040	V	V	V	V	V	-	-	-	-	-
90041	V	V	V	V	V	-	-	-	-	-
90101	A	A	V	V	V	-	+	+	+	+
90126	A	V	V	A	V	-	nd	-	-	-
90214.03	V	V	V	A	V	-	+	+	+	+
90222	V	V	V	V	V	-	-	-	-	-
91001	A	A	A	A	A	+	+	nd	+	+
91002	A	A	A	A	A	+	+	+	+	+
91011	A	V	V	A	V	-	+	+	+	+
91012	A	V	V	V	-	-	+	+	+	+

^a parents of the mapping population

^b F1 progeny of the mapping population

nd: not determined

Supplemental Research Data Table S5

Table S5. *P. infestans* homologues of *P. ramorum* genes located in the *pr3.4* region.

protein in <i>P. ramorum</i>	protein size (aa)	distance from <i>pr3.4</i>	<i>P. infestans</i> homologue	uni-gene code	BLAST <i>E</i> value	BLAST similarity
pro80791	1091	3 kb	PB021B03 EST	NR007K03	2E-56	81%
pro80792	223					
pro80793	129	0.5 kb	PD027G09 EST	NR011A08	7E-60	92%
pro80794-1	196					
<i>pr3.4</i>	2000		<i>pi3.4F</i>		2E-89	93%
pro71831	234	3 kb	PB014G05 EST	NR006N11	2E-66	86%
pro80796	222					
pro80796-2	593					
pro80797	1348	8,3 kb	PF034D01 EST	NR015H15	1E-121	95%