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Amplification generates modular diversity at an avirulence locus in the pathogen *Phytophthora*
 Genome Research (2006) 16: 827-840

	encoding NLS							encoding acidic domain		
	XXXXXXXXXXXXXX							XXXXXXXXXXXXXXXXXXXX		
pi3.4Fa	CTGCAGAAAGC	TGTTTAAAGCG	CAAGATCAAG	CGAGCTAAGA	AGAAACCCGC	TTCAGGTGGC	AAGGAAGAAG	GGAAAGAGCC	TGACAGTGCG	AGAGACGGCG
pi3.4T									..A..	
40D03-B7										
40D03-C6										
pi3.4Fv									..C..	
40D03-B1										
40D03-C1			T.....			G.....				
3.4-8E24	G.....			C.....	A.....	G.....				
3.4P1-2	G.....	T.....		C.....	A.....	G.T.....				T.....
3.4-6M14	G.....	T.....		C.....	A.....	G.T.....				T.....
3.4P2-2	GA.....	T.....T.....		C.....	A.....	G.T.....			..TC.....	
3.4P2-1	G.....	A.....		C.....	A.....	G.....				
3.4-27A18	G.....	A.....		C.....	A.....	G.....		A.....		
3.4-18J11	G.....	A.....		C.....	A.....	G.....				
3.4-18C08	G.....	A.....		C.....	A.....	G.....				
3.4P1-1	GG.....			C.....	A.....	G.....				A.....
pi3.4d										
	encoding acidic domain									
	XX									
pi3.4Fa	AGGAGCTAGA	AGACGACGAT	GAAGAAGAAG	AGGACGAAGA	CGAAGACTAT	GACGAAGATG	ACGACGACGA	TGACGAAGAA	GAAGAGGATT	CATGTCCGTC
pi3.4T										
40D03-B7									T.....	A.....
40D03-C6									T.....	A.....
pi3.4Fv				G.....						A.....
40D03-B1	A.....									A.....T.....
40D03-C1	A.....									A.....T.....
3.4-8E24	A.....		C.....		T.....			T.....		A.....C.....
3.4P1-2	GA.....	C.....A.....C.....	A.....		G.....					A.....
3.4-6M14	GA.....	C.....A.....C.....	A.....		G.....					A.....
3.4P2-2	A.....	C.....A.....C.....	A.....		G.....					A.....
3.4P2-1	A.....	C.....		C.....				C.....		G.....C.....
3.4-27A18	A.....	C.....		C.....				C.....		G.....C.....
3.4-18J11	A.....	C.....		C.....				C.....		G.....C.....
3.4-18C08	AG.....			AC.....	C.....			C.....		G.....C.....
3.4P1-1	A.....	C.....	C.....		C.....			C.....		G.....C.....
pi3.4d										
	encoding acidic domain									
	XX									
pi3.4Fa	GGGATGCGAC	TTGACTCTGT	ACGAGAAAGT	GCTGCGCCTG	CGTGAGAAGC	GTGCCGATGT	AGACGACGCC	ATGGGGGAGC	TGAACAAGGC	GATCGAAGAG
pi3.4T										
40D03-B7										
40D03-C6										
pi3.4Fv	T.....									
40D03-B1	T.....			T.....		T.....				
40D03-C1	T.....			T.....A.....		T.....				
3.4-8E24	T.....		A.....							
3.4P1-2	T.A.....			T.....		T.....	G.T.....	A.....		
3.4-6M14	T.A.....			T.....		T.....	G.T.....	A.....		
3.4P2-2	T.A.....						G.....	A.....		

p13.4Fa	AGTCGCGCTT	CAACCAAGCTT	GAATTCGTAG	TGCCGCTCAG	TACGCGGCAA	CTATGTTGTC	TTGAAGCTCC	GTCTCCGACT	CGGCAAAACT	GGACGCTACC
p13.4T										
40D03-B7			..CG.....							
40D03-C6			..CG.....							
p13.4Fv		G.....								
40D03-B1		G.....								
40D03-C1		G.....								
3.4-8E24		G.....	..CG..A.G.....						..A...G....	C.....
3.4P1-2	..A....A.....	T.A.....	..CG...G.....	..A.....	..AA.....	G.C.....			..A...G....	..A.....
3.4-6M14	..A....A.....	T.A.....	..CG...G.....	..A.....	..AA.....	G.C.....			..A...G....	..A.....
3.4P2-2	..A....A.....	G.A.....	..CG...G.....	..A.....	..AA...G.....	G.....			..A...G....	..A.....
3.4P2-1	..A....A.....	T.A.....	..CG...G.....	..A.....	..AA.....	CG.C.....			..A...GG....	..A.....
3.4-27A18	..T.....	-----A.....	..CG...G.....					C.....	..A...G....	..T.....
3.4-18J11	..T.....	-----A.....	..CG...G.....					C.....	..A...GT....	..T.....
3.4-18C08	..T.....	-----A.....	..CG...G.....					C.....	..A...G....	..T.....
3.4P1-1	-----	-----G.....	..CG...G.....				..C...C.....		..A...G....	
p13.4d		G.....	..CG...G.....						..A...G....	C.....

									encoding Leu Zipper	
									XX	
p13.4Fa	TGCTCAAGCT	GATGGCTGCC	TCGTGTTTAC	CACTCGCGCC	TTCTCTGCGT	TGCTCGAGCG	TATCGAGTCG	CTGCAAGCAG	AGAACAAGAA	GCTGCGTCAA
p13.4T		..C.....								
40D03-B7					..A.....					
40D03-C6										
p13.4Fv						C.....	T.....			
40D03-B1		..C.....				C.....				
40D03-C1		..C.....				C.....				
3.4-8E24		..C.....		-----A..	A-----					T..
3.4P1-2	..T.....	..C.....		-----		C.....		T..		
3.4-6M14	..T.....	..C.....		-----		C.....		T..		
3.4P2-2	..T.....	..C.....		-----		C.G....		T..		
3.4P2-1	..T.....	..C.....		-----		C.....	A.....	T..		
3.4-27A18		..C.....	T.....					T..		
3.4-18J11		..C.....					C.....		T..	
3.4-18C08		..C.....	C.....					T..		
3.4P1-1		..C.....		-----A..	A-----			C.....		
p13.4d		..C.....		-----A..	A-----		C.....			

									encoding Leu Zipper	
									XX	
p13.4Fa	CAGTTCCGAG	ACCTTCACAA	ACAGCAGAAC	GTGCTTGCTA	AGGAGAAGCG	TCAGCAGCAA	GAAGCCATTG	CAAGAGCTCA	GGATCGCAGC	GAGCAGCTCA
p13.4T										
40D03-B7										
40D03-C6										
p13.4Fv		C.....	G.....			A.....			C.....	
40D03-B1		C.....	G.....			A.....			C.....	
40D03-C1		C.....	G.....			A..A....			C.....	
3.4-8E24		C.....						A....	C.....	
3.4P1-2						A..A....	T.....		C...G....	T....
3.4-6M14						A..A....	T.....		C...G....	T....
3.4P2-2						A.TA....	T.....	G.....	C...G....	T....
3.4P2-1						A..A....	T.....		C...G....	T...G
3.4-27A18		C.....	G.....		T.....				C.....	
3.4-18J11		C.....	G.....		T.....		R.....G....		C.....	
3.4-18C08		C.....	G.....		T.....				C.....	
3.4P1-1		C.....	G.....			A..A....	T.....		C...G....	T....
p13.4d		C.....						A....	C.....	

p13.4Fa	TGCGACTGAA	ATTCGGACAG
p13.4T		
40D03-B7		
40D03-C6		
p13.4Fv		
40D03-B1		
40D03-C1		
3.4-8E24	...T.....	
3.4P1-2		
3.4-6M14		
3.4P2-2		
3.4P2-1		
3.4-27A18		
3.4-18J11	A....	
3.4-18C08		
3.4P1-1		
p13.4d	...T.....	

Figure S2. Sequence alignment of fragments derived from different *pi3.4* copies with *pi3.4F^A* (*pi3.4Fa*), *pi3.4F^V* (*pi3.4Fv*) and *pi3.4T* (*pi3.4T*). The amplified copies from BAC40D03 are 3.4-40D03-B7, 3.4-40D03-C6, 3.4-40D03-B1 and 3.4-40D03-C1. The copies derived from contig-II to contig VI are 3.4-27A18, 3.4-18C08, 3.4-6M14, 3.4-8E24 and 3.4-18J11. The copies obtained by PCR on genomic DNA are 3.4P1-1, 3.4P1-2, 3.4P2-3, 3.4P2-2 and *pi3.4d*. In the alignment nucleotides substitutions are shown, identical nucleotides are denoted with ‘.’ and deletions are marked with ‘-’.