Supplemental Research Data - Figure S1

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

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Ps3.4        1 MEGELGDGGGVPPDVAQELNEEGHEGQEVAEQEAEQEAPDYATPELVRPLANWEISRDHLVFADMCGLDTGKRHILHVLEPRLEGEHGSVLLTAAGNTVQ
Pr3.4        1 MEGEELSDGGLLSEVVQEQLEDG--------QGTQQGVPDYATSELVRPLNNWEIARDHLVFSKMNGLDTGKRRILHVVEPMHGKEHGGVLLTAAGNTVQ
Pi3.4A       1 MEYAELGEDATSATTAQEQNESA--------QEVEPEALDYVTSQLVRPLSNWEISRDHLVFADICGLDTGKRHILHLLEPAIVGVHGGVLLTAAGNTVQ
Pi3.4V       1 MEYAELGEDATSATTAQEQNESA--------QEVEPEALDYVTSQLVRPLSNWEISRDHLVFADICGLDTGKRHILHLLEPAIVGVHGGVLLTAAGNTVQ
consensus    1 **  .... ..... .**..*..        *... .. ** *. *****.****.******....*******.***..**.... **.***********

                                                   WD40 domain
Ps3.4      101 LLTMMPQVAPSGSSVQSRRYLFGFGGSGIGSLAVHPSGEFFAVGEKGVKPNISIYRYPQITVSQVLRNGTERAYASVEFSQDGETLASVGSAPDFLLTVW
Pr3.4       93 LLTMTPHVSVSGSNVKYRRYIFGFGGSGVGSLAVHPSGEFFAVGDKGVRPNISIYRYPQITVSHVLRNGTERAYASVEFSKDGETLASVGSAPDFLLTVW
Pi3.4A      93 LLTMSPQVAASSSNIQSRRYVFGFGGSGIGSLAVHPSRQFFAVGGKGVKPNISIYRYPEISVSHVLRNGTERAYASVEFSKDGDTLASVGSGPDFLLTVW
Pi3.4V      93 LLTMSPQVAASSSNIQSRRYVFGFGGSGIGSLAVHPSRQFFAVGGKGVKPNISIYRYPEISVSHVLRNGTERAYASVEFSKDGDTLASVGSGPDFLLTVW
consensus  101 ****.*.*..* *....***.*******.********  *****.***.********* *.**.****************.**.*******.********

Ps3.4      201 NWREEQTVLRCKAFGQDVFSVRFAPTDSGFLATSGVGHIRLWKMAATFTGLKLQGDIGKFGKSELSDIEAFCVLPDKKVLSGTERGVLLLWDGNFIKCEI
Pr3.4      193 NWREEQTVLRCKAFGQDVFSVRFAPTDSGFLASSGVGHIRLWKMAATFTGLKLQGDIGKFGKSELSDIEAFCVLPDKKVLSGTERGVLLLWDGNFIKCEI
Pi3.4A     193 KWREEQTVLRCKAFGQDVFSVRFAPTDSGFLATSGVGHIRLWKMAATFTGLKLQGDIGKFGKSELSDIEAFCVLPDKKVLSGTERGILLLWDGNFIKCEI
Pi3.4V     193 KWREEQTVLRCKAFGQDVFSVRFAPTDSGFLATSGVGHIRLWKMAATFTGLKLQGDIGKFGKSELSDIEAFCVLPDKKVLSGTERGILLLWDGNFIKCEI
consensus  201  ******************************.*********************************************************.**************

Ps3.4      301 LTSRRHLPHAGTINVVDFDEAEGLIVTAGKDGFVRFWSFNSIDSADVATDETVALVPMRRQIQIKPQMDIRAVVKEDSGRYLLQDGVGGVHLLVLKSNDE
Pr3.4      293 LTSRRHLPHTGTINVVDFDEEEGHIVTAGRDGYVRFWSFDSIDSADVAADETVALVPMKRQVFVKPQMDIRAVVKEDTSRYLLQDGAGGVHLLLLKSNDE
Pi3.4A     293 MTSRRHLPHAGTINVVDFDEDESHIVTAGKDGYVRFWSFDSIDSADVPVDETVALVPMKRQVLVMPQMDIRAVVKQDTGRYLLQDGAGGVHLLLLINNDE
Pi3.4V     293 MTSRRHLPHAGTINVVDFDEDESHIVTAGKDGYVRFWSFDSIDSADVPVDETVALVPMKRQVLVMPQMDIRAVVKQDTGRYLLQDGAGGVHLLLLINNDE
consensus  301 .********.**********.* .*****.**.******.******* .*********.**... ********** *..*******.******.*  ***

Ps3.4      401 HQVEFDYVANDTGRATGIACSPYEHIAATCGEDGSVRAWDYVSGACLMTVFPEQSFTDEKNNSNDRASLAPASTITWTPNSAAVINDTITQSRQVAVGFD
Pr3.4      393 HEVELDYVSNDTGRATDVACSPYEHLAATCGEDGSVRAWDYVSGSCLMTVHPEQGRMEDQDNTSDRTTLAAATTIRWVPDSAAVVTDLVPASRQVAVGFD
Pi3.4A     393 HHVEMDYVANDTGRATGIACSPYEHLAVICGEDGGVRAWDYVSGTCLLAVFPELSCLEDQDN-VDYTTLGAATTIAWVPNSAAVINDNIPSSRQVAVGFD
Pi3.4V     393 HHVEMDYVANDTGRATGIACSPYEHLAVICGEDGGVRAWDYVSGTCLLAVFPELSCLEDQDN-VDYTTLGAATTIAWVPNSAAVINDNIPSSRQVAVGFD
consensus  401 *.**.***.*******..*******.*  ***** *********.**. *.** .......*..* ..*..*.**.*.*.****..*....*********

Ps3.4      501 DGLVRVMLMDIDHRAWVRINIFKPHSKRVTCMAYSHSGSAFVTASADGTFFLFQVVPNIKSSKFSKYPCEYEPYGFQRVPAAVIAVCWRGDDEAILATLA
Pr3.4      493 DGLVRVLLMDVEHRAWVRINVFKPHTRRVTCMAYSHSGSTFVTASDDGTFFLFQVVPSIKSSKFAKYQCEYEPFGFQRVPASVIAICWREDDEAVLVTLV
Pi3.4A     492 DGLVRILLMDVDHRAWVLLNVFKPHRKRVTCVAYSHSGSAFVSASADGTFFLFHVVPNIKSSKYVKYQPEYEPYGFQHVPGSVAAICWRDDDAAVLVTLA
Pi3.4V     492 DGLVRILLMDVDHRAWVLLNVFKPHRKRVTCVAYSHSGSAFVSASADGTFFLFHVVPNIKSSKYVKYQPEYEPYGFQHVPGSVAAICWRDDDAAVLVTLA
consensus  501 *****..***..***** .*.*****..****.*******.**.**.******* ***.*****..**. ****.***.**..* *.***.** *.*.**.

Ps3.4      601 NGQVLEFFLPSGELYAKTTGDKEDADSFETAHESDEPALIAG-TKSAERESYELHLSSREWALRQRKRFMSVKELDTLEAQYPSITAPQVEDKIRNQFQV
Pr3.4      593 NGQVFEFFLPSQELHGKTEGSSEDGDGSEGIHDIDELADRTDSTNVSERESYELHLSSREWTLHQRNRFMSVKELETLEAQHPSITALQTEEKVRNQFQV
Pi3.4A     592 NGQVLEYFVS-GELDGNTGEKSDTTTTDESMFQS---------EVSAERESFELHLSTREWVLQQRNRFMTVKELEILEAQYPNVSSPETEEKIRNQFQV
Pi3.4V     592 NGQVLEYFVS-GELDGNTGEKSDTTTTDESMFQS---------EVSAERESFELHLSTREWVLQQRNRFMTVKELEILEAQYPNVSSPETEEKIRNQFQV
consensus  601 ****.*.*. ..**.. *. ... . ..*.. .... .      ...****.*****.***.*.**.***.****. ****.* .. . .*.*.******

Ps3.4      700 EIKPGNPGSKALAALYTVVPEKDKGKPLSRASKDRIYLSCQAPLDGNLFVAQHDLPTPFQELASETGGNITSLELSTSEKFLLCGMSNGKFQIRSARRPH
Pr3.4      693 EVRPANGTTKAWAALYTVVPEKDKGKPLGRTNKDRIYLSCQAPLDGNLFVVQHDQPTPQQEMASETGGHITSLELSTSERFLLCGLSNGKFQLRSARRPH
Pi3.4A     682 EVKPANGRAKALAALFTPVTEQD--------TEDRIYLSCQAPLDGTLFIVQHDRSMPLQELASESAGHITSLSLSSSERFILCGLSNGKFQLRSARRPH
Pi3.4V     682 EVKPANGRAKALAALFTPVTEQD--------TEDRIYLSCQAPLDGTLFIVQHDRSMPLQELASESAGHITSLSLSSSERFILCGLSNGKFQLRSARRPH
consensus  701 *..*.*...**.***.* * * *..... . . ************* **..***.  *.**.***..*.**** **.**.*.***.******.*******

Ps3.4      800 AFLSGEFHDYAASSADGRLHLALSFDDSYAITVGSDGNLSICRVYSEKVEEASAVLSGKFESMIAEATIARDQAFEKQEAVVTMQQKAMSDDKSDDDPSN
Pr3.4      793 AFISGEFHDYTASSSNGRLHLALSFDDSYVVAVGCDGNLSICRLHSDKVEEASKLLAGKYESLLAEAAIARDQAREKQETVITMQQKAMDD-KNEDEASN
Pi3.4A     774 AFISGEFHDYAASTSNDKLYLATSYDDSYVVAVGSDGNVSICRVHSNRVEEAAKLLTVKYKSILAEADIARDQAREKQDSVLTMQRKAMED-KGEGDPSN
Pi3.4V     774 AFISGEFHDYAASTSNDKLYLATSYDDSYVVAVGSDGNVSICRVHSNRVEEAAKLLTVKYKSILAEADIARDQAREKQDSVLTMQRKAMED-KGEGDPSN
consensus  801 **.*******.**... .* ** *.****...**.***.****..*..**** ..*. *. *..***.******.***..*.*** ***.* *.. ..**

Ps3.4      900 SGGGASNTDLSALPAFHGAKAYAAYIENKLSPSVAAAMDNEEFQGVIRFVSDARSTEGLPNVTP--RHGDSAGKT-GVPGAGLIQLGVADLANPREAYTI
Pr3.4      892 TGGGSASTDLRDLPAFHAAKAYATYIEGKLSPSVGAATDNEEFQGVIRLVGDQKSTDGLPEAAPPIRDDASSNKTNGVPAAALTQLGVADLTNPREAYTI
Pi3.4A     873 SEG-TANTDLSALPAFHGAKAYAAYIESKLSSRVAAAKDKEEYLGVTRLASDDQSIEGLPKATPPSRDDGKAQTG--VAATALLQLSVEDIADSKEAYTI
Pi3.4V     873 SEG-TANTDLSALPAFHGAKAYAAYIESKLSSRVAAAKDKEEYLGVTRLASDDQSIEGLPKATPPSRDDGKAQTG--VAATALLQLSVEDIADSKEAYTI
consensus  901 . *....***..*****.*****.***.***  *.**.* **.  ** *. .*..* .***...*..*... ..   .* . .*.** * *..  .*****

Ps3.4      997 EDAKLKSEADARARSTLSKQDSTRAVLSKMRKQLQELQAQDAALPSQSRVDPEEWEIDLDYGDLLTRQGDEACDEVRKELAFAVEKEELLLLKMRETYVG
Pr3.4      992 EDAKLKSEADARARSTLSKQDSTRAVISKMRAQLLDLQAQDAALPFQSRVDPEDWEIDLDYGELLTRQGDEACEEVRKELAFAVEKEELLLLKMRNTYVG
Pi3.4A     970 EDAKLKSEADARVRSTLRKQDSTRAVLNQMRTELQELQAQDAALPPQSRVDSEEWEIDLDYGDLLTRQGDEACDEVRKELAFAVEKEELLLLKMRETYVG
Pi3.4V     970 EDAKLKSEADARVRSTLRKQDSTRAVLNQMRTELQELQAQDAALPPQSRVDSEEWEIDLDYGDLLTRQGDEACDEVRKELAFAVEKEELLLLKMRETYVG
Pi3.4T       1 ----------------------------MRTELQELQAQDAALPPQSRVDSEEWEIDLDYGDLLTRQGDEACDEVRKELAFAVEKEELLLLKMRETYVG
consensus 1001 ************ **** ********.  **. *..*********.***** *.********.**********.********************.****
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Ps3.4     1097 PLAVELLTLRAFESGLSVQSFRTMKMPVTLQKRLAEIHIAD-AAKKQASVGLKPAGSTRRPSVLDIMEKDTPLDEAFPLKEDERRMIMSYHEPAVDGTHG
Pr3.4     1092 PLAVELMTLRAFESGLSVQSFRTMKMPPTLQKRLAEIHTAEAAAKIQLPAGGKAGGVPRRASVLDIMEKDMPLDEEFPLKEDERRMIMSHIEPAVGGS-G
Pi3.4A    1070 PLAVELLTLRAFESGLSVQSFRTMKMPATLQKRLAEIHTADAAAKKQPSTGAKTG-PRRRASVLDIMEKDTALDEDFPLKEDERRKLMSHNDPAVGGNGA
Pi3.4V    1070 PLAVELLTLRAFESGLSVQSFRTMKMPATLQKRLAEIHTADAAAKKQPSTGAKTG-PRRRASVLDIMEKDTALDEDFPLKEDERRKLMSHNDPAVGGNGA
Pi3.4T      72 PLAVKLLTLRAFESGLSVQSFRTMKMPATLQKRLAEIHTADAAAKKQPSTGAKTG-PRRRASVLDIMEKDTALDEDFPLKEDERRKLMSHNDPAVGGNCA
consensus 1101 ******.********************.**********.*..***.*...*.*.....**.*********. ***.********* .**...***.*...

Ps3.4     1196 GAGWSPAAQESGGSKSVHGFEARKRLRTERKERLARWRSNKPGEDADDPRDVVAIAFAQRNMGDYKLKTAADYVVPEHQRVNAVKKLRQMALLEESLYSA
Pr3.4     1191 AAGWTVVS-ETGSSKSVHGFEARKRLRTERKDRLTRWMNSKPGEDADDPRDVVAIAFAQRNMGDYKLKTAADYVVPEHQRVNAVKKLRQIALLEESLYAA
Pi3.4A    1169 ASSGPTAVQETSGSKSVHGFEARKQLRTERKERLARWQSNKPGEDADDPRDVVAIAFAQRNMGDYKLKTAPDYVVPEHQRVNAVKKLRQMALLEESLYAA
Pi3.4V    1169 ASSGPTAVQETSGSKSVHGFEARKQLRTERKERLARWQSNKPGEDADDPRDVVAIAFAQRNMGDYKLKTAPDYVVPEHQRVNAVKKLRQMALLEESLYAA
Pi3.4T     171 ASSGPTAVQETSGSKSVHGFEARKRLRTERKERLARWQSNKPGEDADDPRDVVAIAFAQRNMGDYKLKTAPDYVVPEHQRVNAAKKLRQMALLEESLYAA
consensus 1201 .   .....*. .*********** ******.**.**...***************************** *****************.********.*

Ps3.4     1296 RLRFNAKVLELRELKVQLINELRHDQERLVKLRATLAAGDDGSSAQPPPPPSGLSIDLREWPEQRERVSDGDIELFLKEKKVISHSQTQSADANVSMTRL
Pr3.4     1290 RLRFNAKVLELRELKVQLINELRRDQERLIELLVALAAKGSGGGSSAPPAPAGLAVDLREWPEQRERVSDADIELFLREKKVISHSQSQTAGSEISLTRT
Pi3.4A    1269 RLRFNAKVLELRELKVQLINELHRDQERLVELRAALASSG---ATPSSVPSKDLVVDLREWPEQRERVSDADIELFLREQKVISHVQTQTGEADLALTRI
Pi3.4V    1269 RLRFNAKVLELRELKVQLINELHRDQERLVELRAALASSG---ATPSSVPSKDLVVDLREWPEQRERVSDADIELFLREQKVISHVQTQTGEADLALTRI
Pi3.4T     271 RLRFNAKVLELRELKVQLINELHRDQERLVELRAALASSG---ATPSSVSSKDLVVDLREWPEQRERVSDADIELFLREQKVISHVQTQTGEAHLALTRI
consensus 1301 **********************..*****..*...** .. . ....  . . *..**************.******.* ***** *.*...... .**.

Ps3.4     1396 SGAENPHQTSDRSIAAVARALEGPNSTLTAGNEVLTGLTIGHLHLQMEDGAAVASAATVSAPATGSQALGSNGGNFDEDDVSVREYLMRQEALLLERKQR
Pr3.4     1390 GGAEKHHQSSDRSIAAVARAIEGPGSTVSTGSSASVGITIGHLHLQMDDGGAAATATAAPAASTGSSSLGLDGGNFDGDDVAVREYLMRQEALLLERKQR
Pi3.4A    1366 GGAEKRPQSADRSIAAVARALEG-----TSGKEAAKGVTIGHLHLQMDDG--TAAAATASSAHAG----ALNVENMDEDDVVVHEYLMRQEALLLERKQQ
Pi3.4V    1366 GGAEKRPQSADRSIAAVARALEG-----TSGKEAAKGVTIGHLHLQMDDS--TAAAATASSAHAG----ALNVGNMDEDDVVVHEYLMRQEALLLERKQQ
Pi3.4T     368 GGAEKRPQSADRSIAAVARALEG-----TSGKEAAKGVTIGHLHLQMDDG--TAAAATASSAHAG----ALNVENMDEDDVVVHEYLMRQEALLLERKQQ
consensus 1401 .***.. *. **********.**. .....*.....*.*********.*....*.*.... .. *.  .... .* *.***.*.**************

Ps3.4     1496 REIVAFDAAVAHLRREKLALEVGFKQAELRLFTLFSELSLLESFESKENLLSSKLEKSKSEKAQIVAELRDVQELLASKKRELDEWSRQERAVQGEFLTL
Pr3.4     1490 REVVAFDAAVAHLRRERLALGVGFKQAELRLFTLVSELSLLESFESKENLLSNKLEKSKGEKAQIMAELRDVQDLLASKKHELDEWSRQERSVQAEFLML
Pi3.4A    1455 REIASFDAAVAHLRHEKLALEVRFKQAELRLFTLLSELSLLESFESKENLLSSKLEKSKGEKAQIVADLRDVQDLLTIKKRDLDEWARQEKAVQAEFLTL
Pi3.4V    1455 REIASFDAAVAHLRHEKLALEVGFKQAELRLFTLLSELSLLESFESKENLLSSKLEKSKGEKAQIVADLRDVQDLLTIKKRDLDEWARQEKAVQAEFLTL
Pi3.4T     457 REIASFDAAVAHLRHEKLALEVGFKQAELRLFTLLSELSLLESFESKENLLSSKLEKSKGEKAQIVADLRDVQDLLTIKKRDLDEWARQEKAVQAEFLTL
consensus 1501 **.  *********.*.***.* ***********.*****************.******.*****.*.*****.**  **..**** ***..**.***.*

                                        NLS                                Acidic domain
Ps3.4     1596 VNGGTGSSTTPHPSFSALQKLFKRKIKRAKKKPTASG-KDDGKDGNGQSPESARDGEEQEEEEEEEDEDEDYDEDDDDDDEEEEDTCPPGCDLTLYEKV
Pr3.4     1590 VNGGTGSTATPHPSFAALQKLFKRKIKRAKKKPTASGGKEEGKDGNGQSPESARDGEEQEEEEEEEEDEDEDYDEDDDDDDEEEEDACPLGCDLTLYEKV
Pi3.4A    1555 VNGGTGSSATPHPSFAALQKLFKRKIKRAKKKP-ASGGKEEGKE-----PDSARDGEELEDDDEEEEDEDEDYDEDDDDDDEEEEDSCPSGCDLTLYEKV
Pi3.4V    1555 VNGGTGSSATPHPSFAALQKLFKRKIKRAKKKP-ASGGKEEGKE-----PDSARDGEELEDDDEEEEDEDEDYDEDDDDDDEEEEDTCPSGCDLTLYEKV
Pi3.4T     557 VNGGTGSSATPHPSFAALQKLFKRKIKRAKKKP-ASGGKEEGKE-----PDSARDGEELEDDDEEEEDEDEDYDEDDDDDDEEEEDSCPSGCDLTLYEKV
consensus 1601 *******..******.****************.***.*..**......*.******* *...********************** **.**********

Ps3.4     1695 LALREKRADVDDAVGELNKAIEELRKAGERQAAKQRAIDKELAATEQDTQQFQSEKQSRFNQLDVVVALSTRQLRCLESPSPNQLNWLLPAQAAGCLVFT
Pr3.4     1690 LALREKRADVDDAMGELNKAIEELRKAGDRQAAKQRAIDKELAATEQDTQQFQSEKQSRFNQLDVVVPLSTRQLRCLEPPSPNQQGWLLSAQAAGCLVFT
Pi3.4A    1649 LALREKRADVDDAMGELNKAIEELRKAGERQTAKQRAIDKELAATEQDTQHFQSEKQSRFNQLEFVVPLSTRQLCCLEAPSPTRQNWTLPAQADGCLVFT
Pi3.4V    1649 LALREKRADVDDAMGELNKAIEELRKAGERQTAKQRAIDKELAATEQDTQQFQSEKQSRFNQLDVVVPLSTRQLCCLEAPSPTRQNWTLPAQADGCLVFT
Pi3.4T     651 LALREKRADVDDAMGELNKAIEELRKAGERQTAKQRAIDKELAATEQDTQHFQSEKQSRFNQLEFVVPLSTRQLCCLEAPSPTRQNWTLPAQAAGCLVFT
consensus 1701 *************.**************.** ***************** ************  **.****** ***.***  ..* *.*** ******
                                Leu zipper
Ps3.4     1795 TQAFAALTERIESLQAENKQLRQQFRDLHKQQSVLAREKRLQQETIARSQERSEQLQRLKFGQLVDLEVLDRACDASAVDELQARVKLREVEGERTLRRV
Pr3.4     1790 TRAFSALTERIESLQAENKHLRQQFRDLHKQQSVLAREKRLQQESIARAQERSEQLQRLKFGQLVDLEVLDRACDASSMDELQTRVKLREVEGERALRRV
Pi3.4A    1749 TRAFSALSERIESLQAENKKLRQQFRDLHKQQNVLAKEKRQQQEAIARAQDRSEQLMRLKFGQLVDLEVLDRACDASSVDELQTRVKLREVEGERALRRA
Pi3.4V    1749 TRAFSALSERIESLQAENKKLRQQFRDLHKQQNVLAKEKRQQQEAIARAQDRSEQLMRLKFGQLVDLEVLDRACDASSVDELQTRVKLREVEGERALRRA
Pi3.4T     751 TRAFSALSERIESLQAENKKLRQQFRDLHKQQNVLAKEKRQQQEAIARAQDRSEQLMRLKFGQLVDLEVLDRACDASSVDELQTRVKLREVEGERALRRA
consensus 1801 *.**.**.***********.************ ***.*** ***.***.*.***** *******************..****.***********.***

Ps3.4     1895 KQMHPQLQHAILQATEQNTALLAQIAALTERQAELERELNRSQGSGSGSGG--DGSGLLSLEDDAALAEREMKERNKLVRLVKLQAREVEALKQEIGLLR
Pr3.4     1890 KQTHPQFQHAILQATEQKTALLTQIAELTERQAELERELNHNQGGGSGSSGGRDGGGLLNMEDDAALAEREMKERNKLVRLVKLQAREVEALKQEIGLLR
Pi3.4A    1849 KQTHPQLQHAILQATEQNTALLAQIAALTERQAELERELNRHQGGGS-SSG--DSGGVLSLDDDEALVEREMKERNKLVRLVKLQAREVEALKQEIGLLR
Pi3.4V    1849 KQTHPQLQHAILQATEQNTALLAQIAALTERQAILERELNRHQGGGS-SSG--DSGGVLSLDDDEVLAEREMKERNKLVRLVKLQAREVEALKQEIGLLR
Pi3.4T     851 KQTHPQLQHAILQATEQNTALLAQIAALTERQAELERELNRHQGGGS-SSG--DSGGVLSLDDDEALVEREMKERNKLVRLVKLQAREVEALKQEIGLLR
consensus 1901 **.***.**********.****.***.****** ******..**.**.*.*  * .*.*...**  * ******************************

Ps3.4     1993 GKDGKVYAPRV
Pr3.4     1990 GKDGKVYAPRG
Pi3.4A    1946 GKDGKVYAPRG
Pi3.4V    1946 GKDGKVYAPRG
Pi3.4T     948 GKDGKVYAPRG
consensus 2001 **********.
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Figure S1. Sequence alignment of Ps3.4, Pr3.4, Pi3.4F^{A}, Pi3.4F^{V} and Pi3.4T. The polymorphisms in blue are between Pi3.4T and Pi3.4F (A and V), in black between Pi3.4F^{V} and both, Pi3.4F^{A} and Pi3.4T, and in red between Pi3.4F^{A} and both, Pi3.4F^{V} and Pi3.4T. The predicted protein domains are shaded.