US 20110212541A1

(19) **United States**

(12) **Patent Application Publication**

Tyler et al.

(10) **Pub. No.: US 2011/0212541 A1**

(43) **Pub. Date: Sep. 1, 2011**

(54) **COMPOSITIONS AND METHODS TO PROTECT CELLS BY BLOCKING ENTRY OF PATHOGEN PROTEINS**

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(21) Appl. No.: **12/944,345**

(22) Filed: **Nov. 11, 2010**

Related U.S. Application Data

(63) Continuation-in-part of application No. 12/468,470, filed on May 19, 2009, Continuation-in-part of application No. PCT/US2009/044489, filed on May 19, 2009.

(60) Provisional application No. 61/260,227, filed on Nov. 11, 2009, provisional application No. 61/128,080, filed on May 19, 2008, provisional application No. 61/160,059, filed on Mar. 13, 2009.

Publication Classification

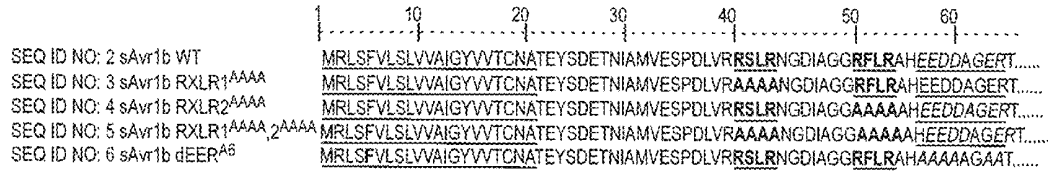
(51) **Int. Cl.**

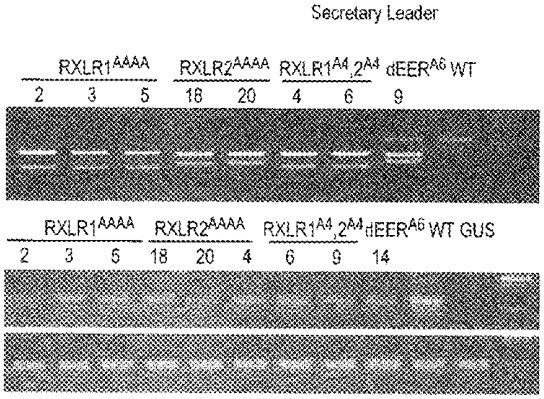
G01N 33/53	(2006.01)
C12N 5/04	(2006.01)
C12N 5/07	(2010.01)
C12N 5/071	(2010.01)
C12N 5/077	(2010.01)
C12N 5/078	(2010.01)
C12N 5/079	(2010.01)

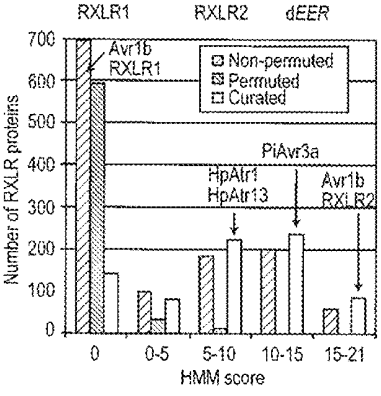
(52) **U.S. Cl.** **436/501**; 435/410; 435/412; 435/414; 435/415; 435/417; 435/416; 435/325; 435/350; 435/351; 435/366; 435/368; 435/369; 435/370; 435/371; 435/372

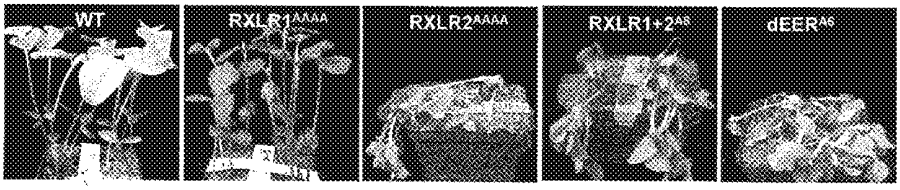
(57) **ABSTRACT**

Pathogenic effector proteins include one or more virulence motifs of amino acid consensus sequence BXZ, where B=RK or H; X=any amino acid or is absent; Z=L, M, I, W, Y or F) which bind to target polar lipids on a host (plant or animal) cell as a prerequisite for translocation of the pathogenic effector proteins into the cell. Translocation is prevented by binding blocking compounds to one or more motifs of the effector protein or to the lipid ligands of the host cell. The blocking compounds include synthetic or naturally occurring polypeptides which bind the polar lipids or the motifs, various polar lipids, the hydrophilic head-groups of polar lipids, etc. Suitable blocking compounds can be identified by assays demonstrating binding to the motifs or to the target polar lipids.









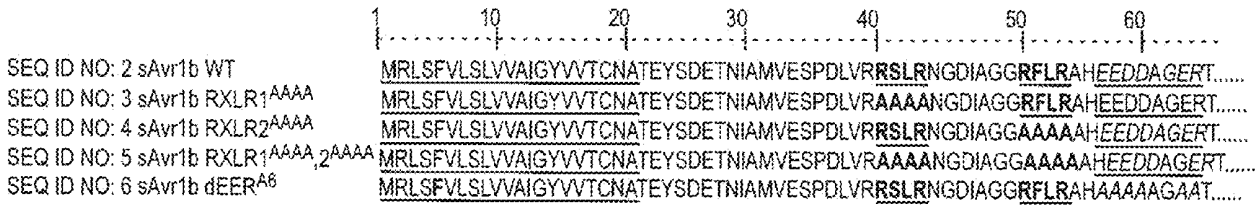


Figure 1A

Figure 1B

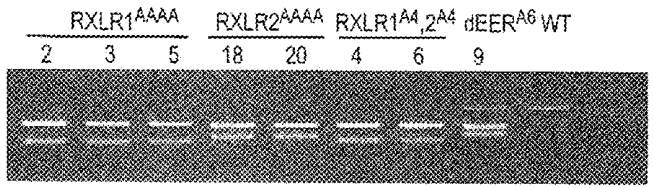
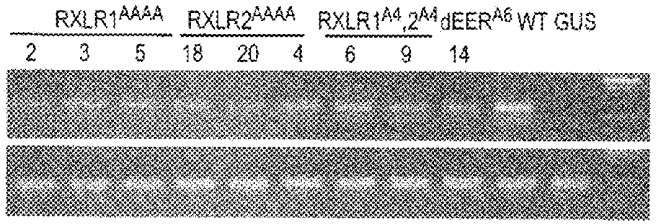


Figure 1C



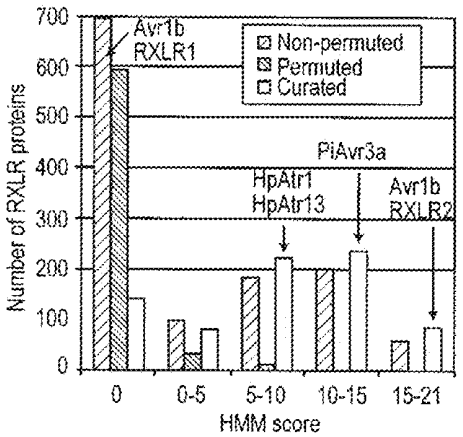
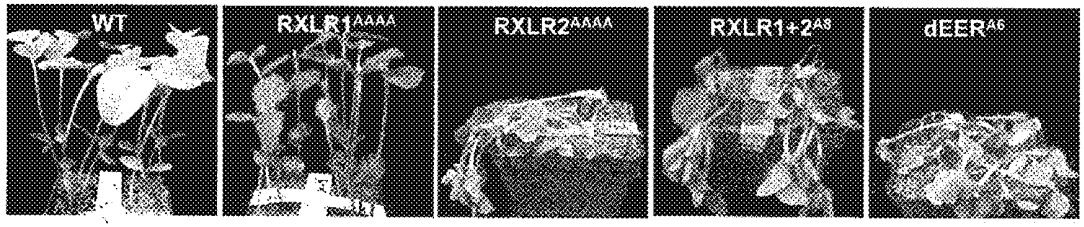


Figure 1D

Figure 1E



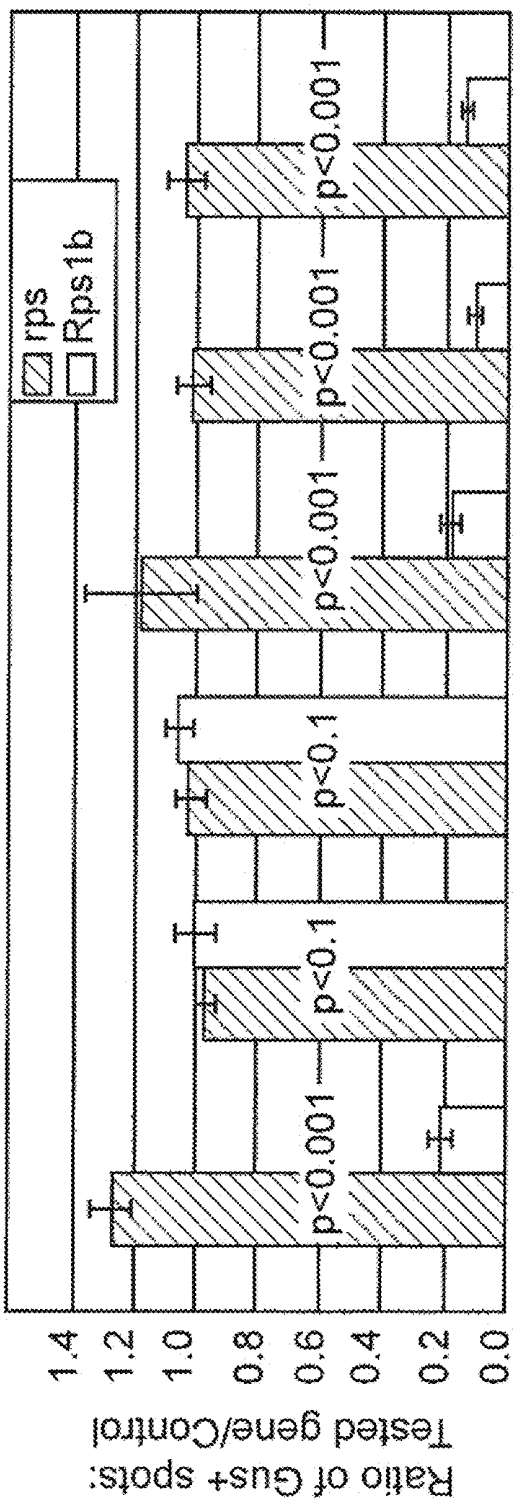

Ratio of Gus+ spots:
Tested gene/Control
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
rps
Rps1b
p<0.001
p<0.1
p<0.001
p<0.1
p<0.001
p<0.001
p<0.001
sAvr1b WT SEQ ID NO: 22
sAvr1b RXLR2AAAA SEQ ID NO: 28
sAvr1b dEERA6 SEQ ID NO: 29
mAvr1b WT SEQ ID NO: 19
mAvr1b RXLR2AAAA SEQ ID NO: 20
mAvr1b dEERA6 SEQ ID NO: 23

Figure 2

SEQ ID NO: 2 sAvr1b WT MRLSFVLSLVVAIGYVVTCNATEYSDETNIAMVESPDLVRRSLRNGDIAGGRFLRAHEEDDAGERtfsvt.....

SEQ ID NO: 4 sAvr1bRXLR2^{AAAA} MRLSFVLSLVVAIGYVVTCNATEYSDETNIAMVESPDLVRRSLRNGDIAGGAAAAAHEEDDAGERtfsvt.....

SEQ ID NO: 8 PsAvh4/6::Avr1bCt MGLHKGFFVAVALLALLIVAAPADAITDESQPRDATIVDAPLTGRGANARYLRTSTSIIKAPDAQLP-STKAAIASSVTKEEEERKISTGLSKLRQKLSKRFHDIPDWLLQLQAFLSVGLHHLtfsvt.....

SEQ ID NO: 7 HpAvh341::Avr1bCt MRLHYVGPVVAAALAASAHGLQVVSDSASDLQRTDEARQQPYINDKTKRFLTSEDKDLPLLVTS-DGYASLLPQGGDNDRVLRSADIGDGDYEEERSKIKKRHKRKSHGHGVLDtfsvt.....

SEQ ID NO: 9 mAvr1bCt M( )tfsvt.....

Figure 3A

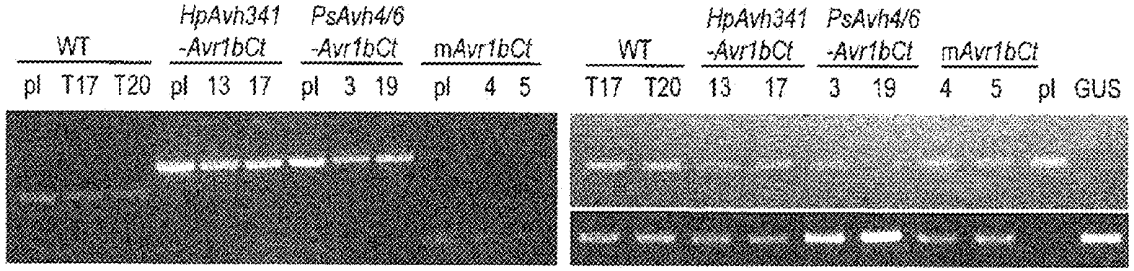


Figure 3B

Figure 3C

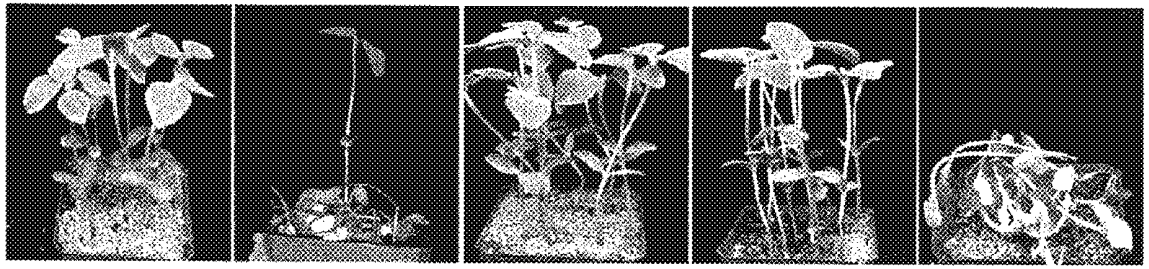


Figure 3D

SEQ ID NO: 2 2 sAvr1b MRLSFVLSLVVAIGYVVTCNATEYSDETNIAMVESPDLVRRSLRNGDIAGG-**RFLR**----------AH*EEDDAGERTFSV*....

SEQ ID NO: 41 sAvr1b RXLR2^{Arg9} MRLSFVLSLVVAIGYVVTCNATEYSDETNIAMVESPDLVRRSLRNGDIAGG-**RRRRRRRRR**---AH*EEDDAGERTFSV*....

SEQ ID NO: 42 sAvr1b RXLR2^{TAT} MRLSFVLSLVVAIGYVVTCNATEYSDETNIAMVESPDLVRRSLRNGDIAGGYGRKKRRQRRRAH*EEDDAGERTFSV*....

SEQ ID NO: 43 sAvr1b^{PfGBP} MRLSFVLSLVVAIGYVVTCNA----------DKYEKAVDYGFRES**RILAE**G*EDTCARKEKTTLRKSKQKTFSV*....

SEQ ID NO: 44 sAvr1b^{PfHRP} MRLSFVLSLVVAIGYVVTCNA----------FNNNLCSKNAKGLNLNK**RLLHE**TQAH*VDDAAHHAHHVADTFSV*....

SEQ ID NO: 45 sAvr1b^{Pf1615c} MRLSFVLSLVVAIGYVVTCNA----------SYNKINSSSTYTHS**RILKQ**LEFITL*EEKTVNALQEMLDDSVTFSV*....

Figure 4A

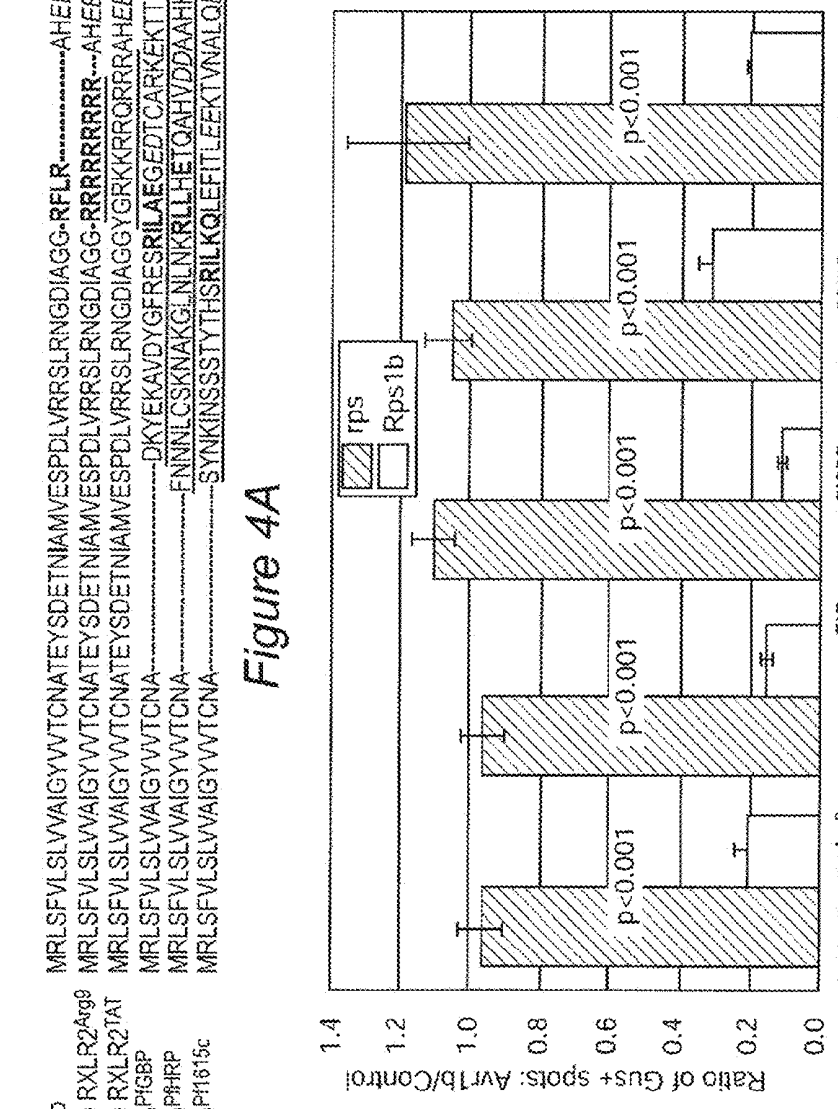


Figure 4B

		Phenotype of *P. sojae* Transformants Rps1b	rps	Cell Death in Bombardment Assay Rps1b	rps
SEQ ID NO: 22	sAvr1b WT	A	V	Y	N
SEQ ID NO: 28	sAvr1b RXLR2^{AAAA}	V	V	N	N
SEQ ID NO: 29	sAvr1b dEER^{A6}	V	V	N	N
SEQ ID NO: 19	mAvr1b WT	NT		Y	N
SEQ ID NO: 20	mAvr1b RXLR2^{AAAA}	NT		Y	N
SEQ ID NO: 21	mAvr1b dEER^{A6}	NT		Y	N
SEQ ID NO: 10	sAvr1b RXLR1^{AAAA}	A	V	NT	
SEQ ID NO: 5	sAvr1b RXLR1^{AAAA},2^{AAAA}	V	V	NT	
SEQ ID NO: 7 SEQ ID NO: 8	- PsAvh171::Avr1bCt - HpAvh341::Avr1bCt	A	V	NT	
SEQ ID NO: 33-37, 40	sAvr1b RXLR2	NT		N	N
SEQ ID NO: 38, 39	sAvr1b RXLR2	NT		P	N
SEQ ID NO: 41, 42	sAvr1b RXLR2$^{Arg9/TAT}$	NT		Y	N
SEQ ID NO: 43-45	sAvr1b$^{PfGBP/PfHRP/Pf1615c}$	NT		Y	N

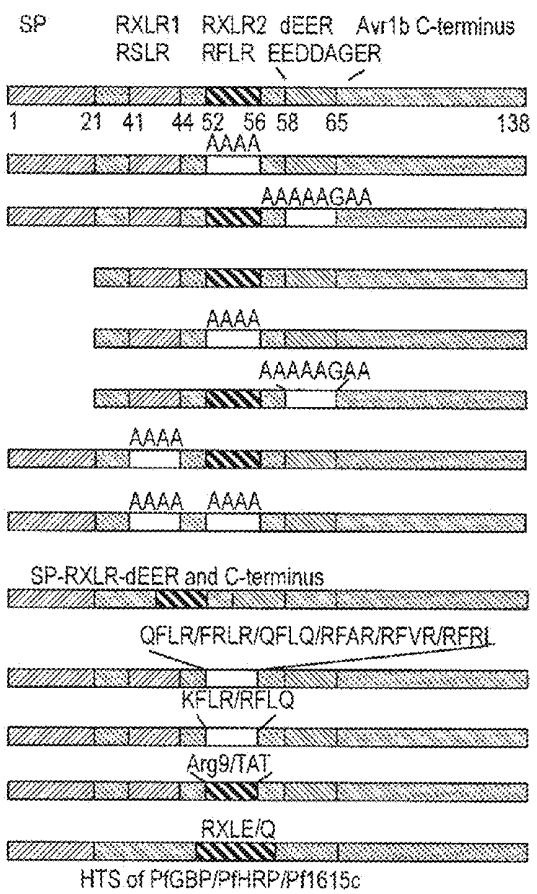


Figure 5

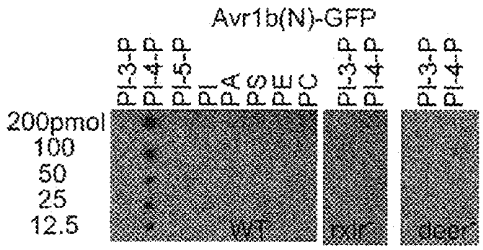


Figure 6A

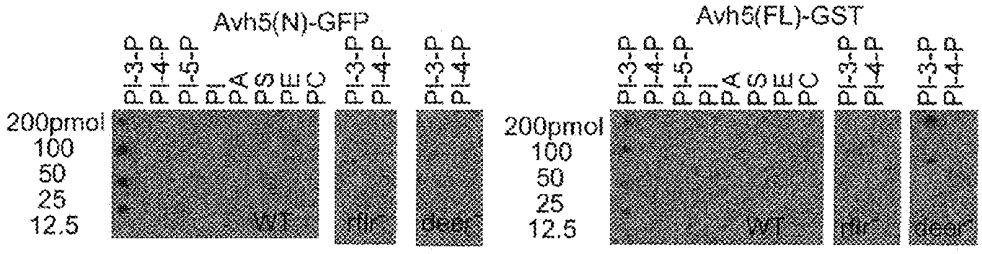


Figure 6B

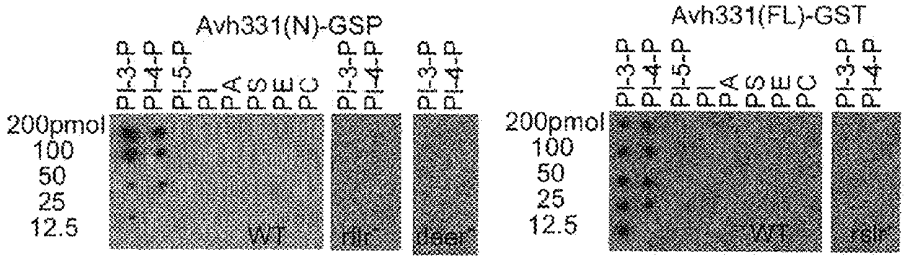


Figure 6C

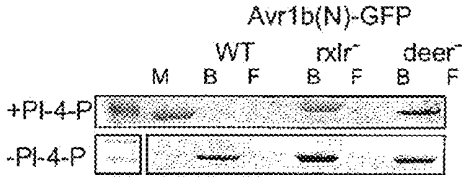
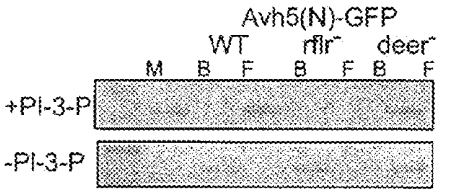


Figure 6D



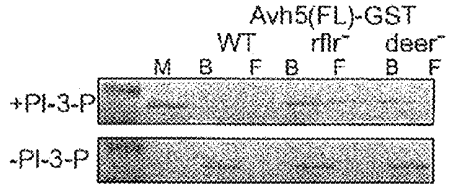


Figure 6E

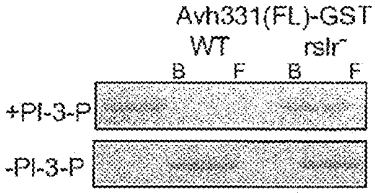


Figure 6F

	Protein	Sequence	Binding PI-3-P	Binding PI-4-P	Relative Ablation	Root Cell Entry	Human Cell Entry	Inhibition by IP2
SEQ ID NO: 46	Avr1b	TEYSDETNIAMVESPDLVRRSLRNGDIAGGRFLRAHEEDDAGERTFSVTD	-	+	1.00	Y	Y	Y
SEQ ID NO: 47	Avr1b rxlr⁻	TEYSDETNIAMVESPDLVRAAAANGDIAGGAAAAAHEEDDAGERTFSVTD	-	-	0.00	N	N	nt
SEQ ID NO: 48	Avr1b deer⁻	TEYSDETNIAMVESPDLVRRSLRNGDIAGGRFLRAHAAAAAGERTFSVTD	-	-	0.00	N	N	nt
SEQ ID NO: 116	Avh331	LTCATSEQQTRPELCFFFSVRSSWPSTISDGACLALVSAEQGATAGRNT LSLRSMMATEDMATSTRSLRSQATNVDDDANVSIENRGM	+	+	1.07	Y	Y	Y
SEQ ID NO: 117	Avh331 rslr⁻	LTCATSEQQTRPELCFFFSVRSSWPSTISDGACLALVSAEQGATAGRNT LSLRSMMATEDMATSTAAAASQATNVDDDANVSIENRGM	-	-	0.00	N	N	nt
SEQ ID NO: 118	Avh331 deer⁻	LTCATSEQQTRPELCFFFSVRSSWPSTISDGACLALVSAEQGATAGRNT LSLRSMMATEDMATSTRSLRSQATNVAAAANVSIANAGM	-	-	0.00	N	N	N
SEQ ID NO: 113	Avh5	TRVPDDANLQSVNAPVQTVTRSRRFLRTADTDIVYEPKVHNPGK	+	-	nt	Y	Y	Y
SEQ ID NO: 114	Avh5 rslr⁻rslr⁻	TRVPDDANLQSVNAPVQTVTRSRAAAATADTDIVYEPKVHNPGK	-	-	nt	N	N	nt
SEQ ID NO: 115	Avh5 deer⁻	TRVPDDANLQSVNAPVQTVTRSRRFLRTAATAIVYAPAVHNPGK	-	-	nt	N	N	nt
SEQ ID NO: 119	AvrL567	MEHVPAELTRVSEGYTRFYRSPTASVILSGLVKVKWDNEQMTMP	+	+	0.70	Y	Y	Y
SEQ ID NO: 120	AvrL567rfyr⁻de⁻	MEHVPAELTRVSEGYTAAAASPTASVILSGLVKVKWANAQMTMP	-	-	0.00	N	N	nt
SEQ ID NO: 123	PfHRPII	FNNNLCSKNAKGLNLNKRLLHETQAHVDDAHHAHHVAD	+	±	1.15	Y	Y	Y
SEQ ID NO: 124	PfHRPII pexel⁻	FNNNLCSKNAKGLNLNKAAAAATQAHVDDAHHAHHVAD	-	-	nt	N	N	nt
SEQ ID NO: 121	PfGBP	DKYEKAVDYGFRESRILAEGEDTCARKEKTTLRKSKQK	±	±	0.97	Y	nt	nt
SEQ ID NO: 122	PfGBP pexel⁻	DKYEKAVDYGFRESAAAAAGEDTCARKEKTTLRKSKQK	-	-	nt	N	nt	nt
SEQ ID NO: 125	Pf1615c	SYNKINSSSTYTHSRILKQLEFITLEEKTVNALQEMLDDSV	+	-	1.11	Y	nt	nt
SEQ ID NO: 126	Pf1615c pexel⁻	SYNKINSSSTYTHSAAAAALEFITLEEKTVNALQEMLDDSV	-	-	nt	N	nt	nt
SEQ ID NO: 112	Arg9	RRRRRRRRR	±	±	1.13	Y	Y	N

Figure 6G

secretion signal peptide

Avr1b- MRLSFVLSLVVAIGYVVTCNA|*TEYSDETNIAMVESPDLVRRSLRNGDIAGGRFLRAHEEDDAGER*|TFSVTDLWNKVAAKKLAKA

6xHis-tag EK Site HA-tag

Arg_9-GFP- MRGSHHHHHHGMASMTGGQQMGRNLYDDDDKDRWGSRS|*RRRRRRRRR*|EFRSTMSGYPYDVPDYAGSMGSGIQRPTST SSLVAAAAT*MSKEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTL*

Figure 6H

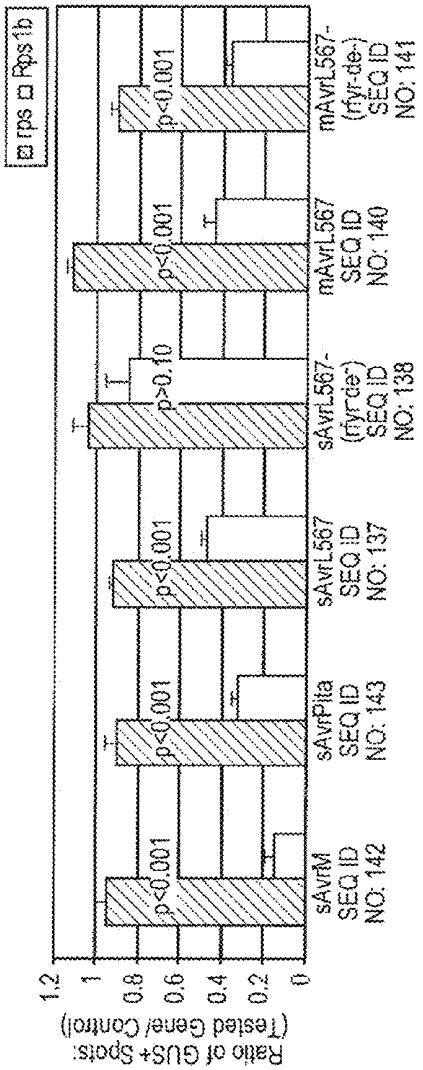


Figure 7A

Figure 7B

			Relative Ablation
SEQ ID NO: 1	Avr1b	TEYSDETNIAMVESPDLVRRSLRNDIAGGRFLRAHEEDDAGERTFSV····	1.00
SEQ ID NO: 3	Avr1b(AAAA)	----------AAAA----------	0.00
SEQ ID NO: 38	Avr1b(1K)	----------K----------	0.42
SEQ ID NO: 147	Avr1b(1H)	----------H----------	0.89
SEQ ID NO: 37	Avr1b(1Q)	----------Q----------	0.00
SEQ ID NO: 148	Avr1b(3F)	----------F----------	1.01
SEQ ID NO: 149	Avr1b(3Y)	----------Y----------	0.84
SEQ ID NO: 150	Avr1b(3I)	----------I----------	0.52
SEQ ID NO: 151	Avr1b(3M)	----------M----------	0.89
SEQ ID NO: 40	Avr1b(3V)	----------V----------	0.00
SEQ ID NO: 35	Avr1b(3A)	----------A----------	0.00
SEQ ID NO: 39	Avr1b(4Q)	----------Q----------	0.74
SEQ ID NO: 152	Avr1b(4G)	----------G----------	0.88
SEQ ID NO: 153	Avr1b(2M3V)	----------MV----------	0.71
SEQ ID NO: 154	Avr1b(2L3T4G)	----------LTG----------	0.56

Figure 7C

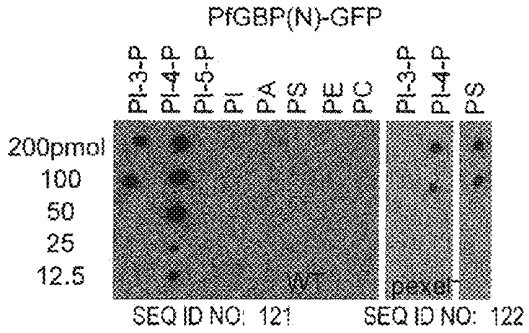


Figure 8A

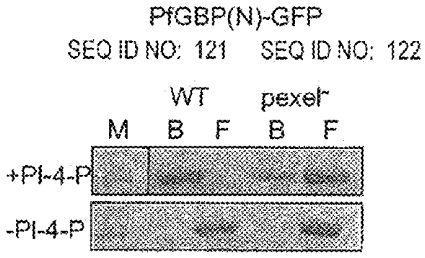


Figure 8D

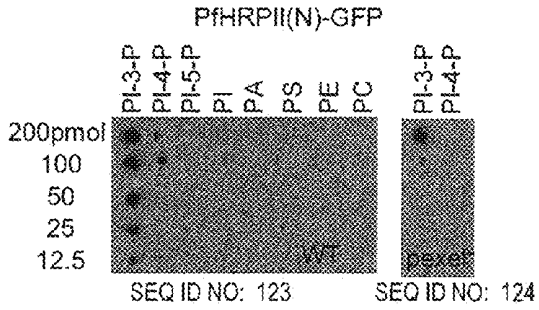


Figure 8B

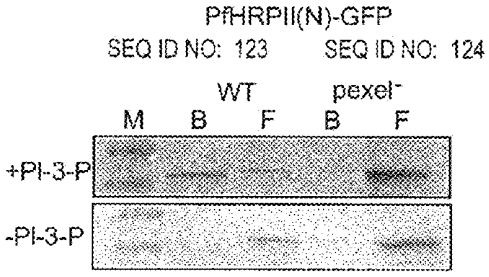


Figure 8E

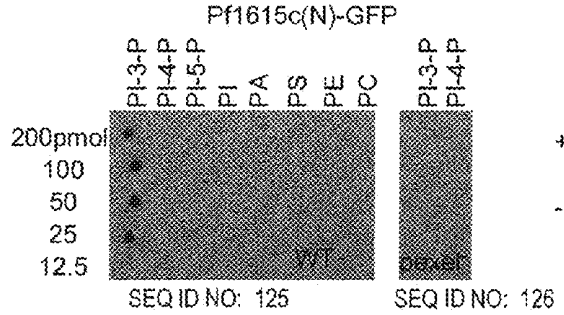


Figure 8C

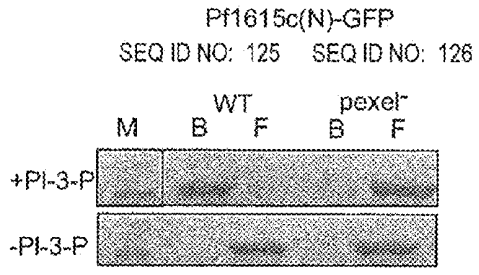


Figure 8F

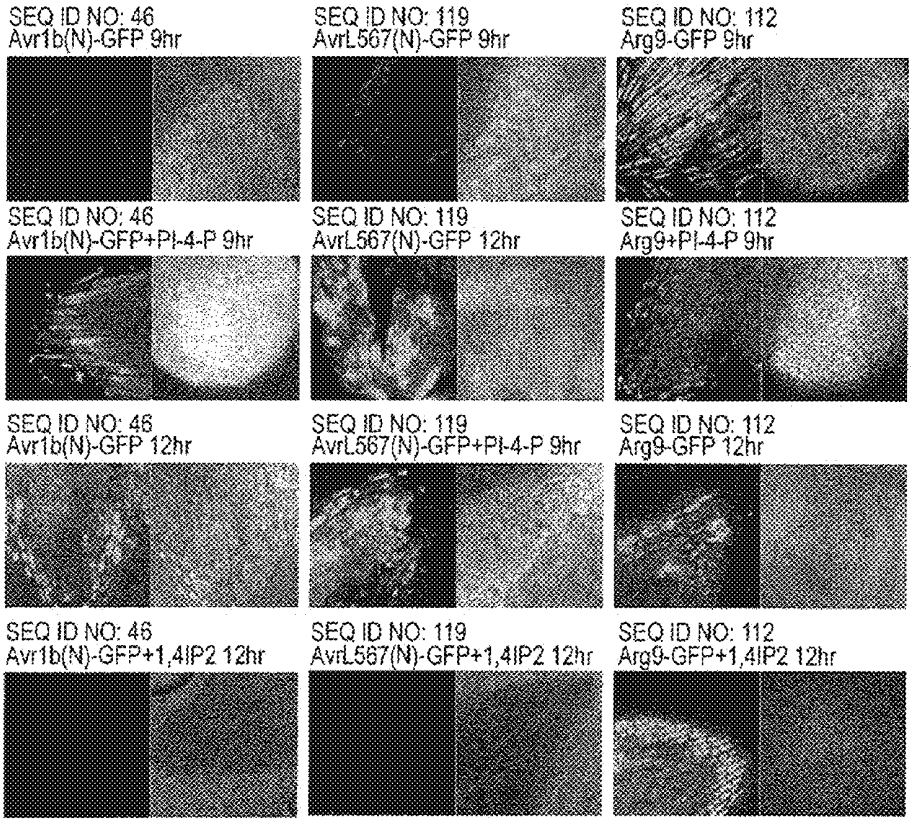


Figure 9A Figure 9B Figure 9C

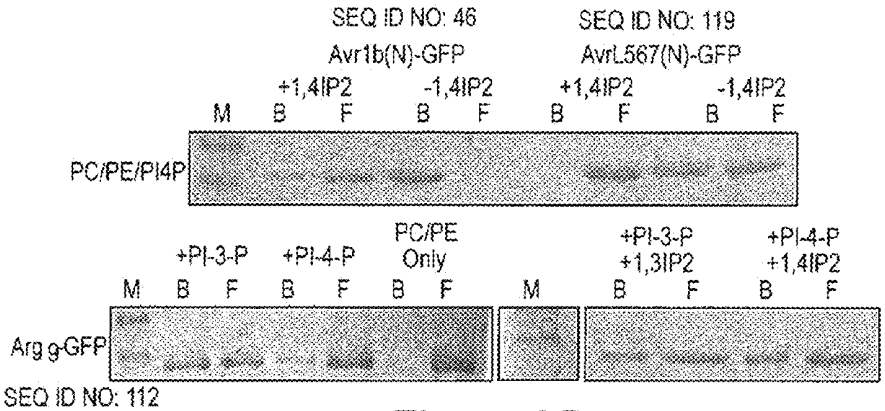
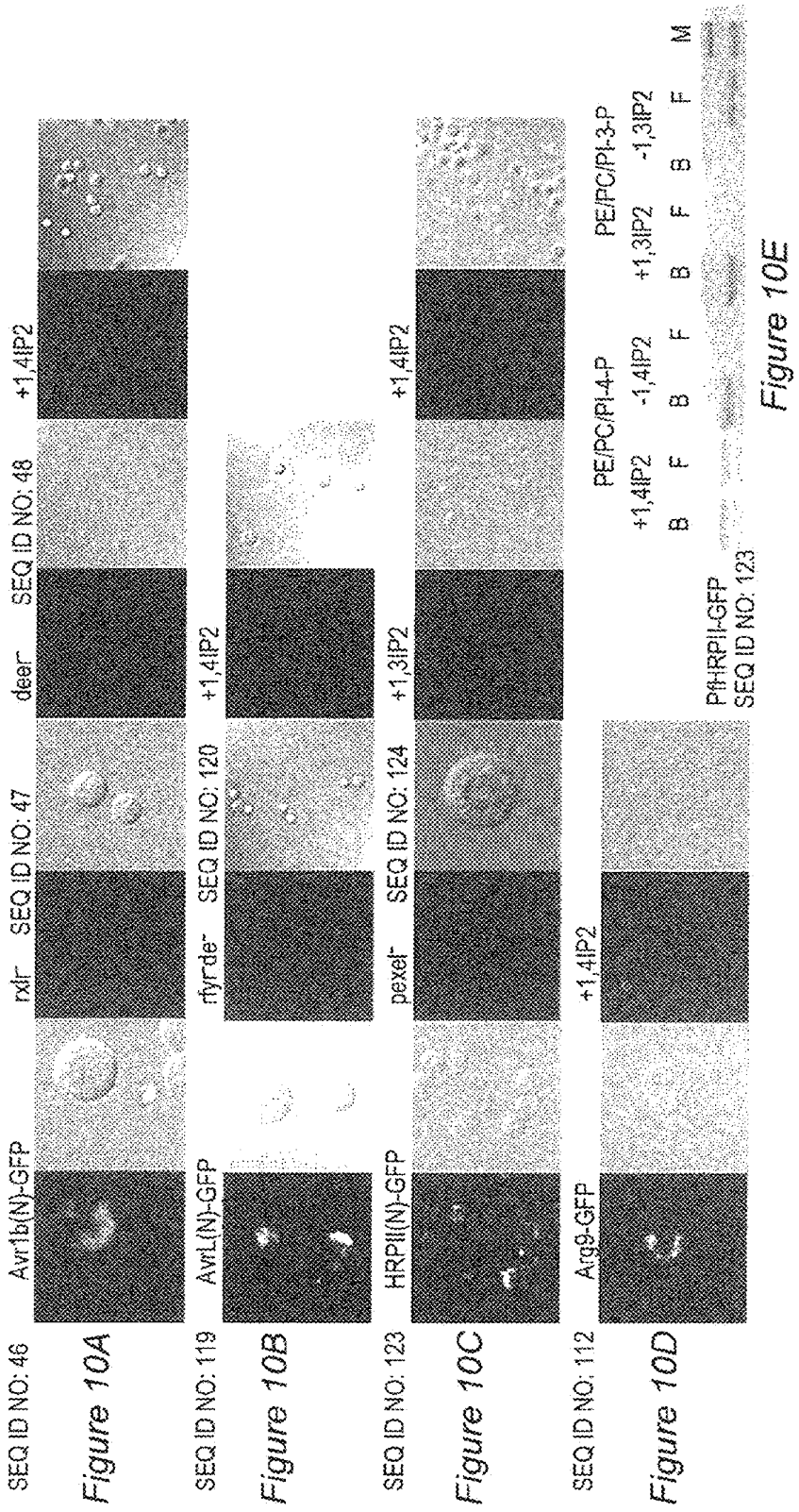


Figure 9D


SEQ ID NO: 46
Avr1b(N)-GFP
rxlr
SEQ ID NO: 47
deer
SEQ ID NO: 48
+1,4IP2
Figure 10A
SEQ ID NO: 119
AvrL(N)-GFP
rfyrde-
SEQ ID NO: 120
+1,4IP2
Figure 10B
SEQ ID NO: 123
HRPII(N)-GFP
pexel-
SEQ ID NO: 124
+1,3IP2
+1,4IP2
Figure 10C
SEQ ID NO: 112
Arg9-GFP
+1,4IP2
PE/PC/PI-4-P
+1,4IP2
-1,4IP2
PE/PC/PI-3-P
+1,3IP2
-1,3IP2
B F B F B F M
PfHRPII-GFP
SEQ ID NO: 123
Figure 10D
Figure 10E

SEQ ID NO:	Plasmid Name	Sources	Construct	Construction strategy
1	pUN	pHAMT35N (5)	*Npt* II gene for G418 resistance fused to *P. sojae* rpL41 promoter in pUC19	Ham34 promoter of pHAMT35N replaced by *P. sojae* rpL41 promoter using primers UF and UR
2	pHamAvr1b	pHAMT35N	*Avr1b*-1 gene fused to Ham34 promoter and terminator for *P. sojae* transformation in pUC19	NptII gene of pHAMT35N replaced with *P. sojae Avr1b*-1 using PrimerC and PrimerD
3	M1	pHAMT35N	*Avr1b*-1(RXLR1^{AAAA}) mutant fused to Ham34 promoter and terminator	Same as pHamAvr1b with mutation introduced by primers motif1Fand motif1R
4	M2	pHAMT35N	*Avr1b*-1(RXLR2^{AAAA}) mutant fused to Ham34 promoter and terminator	Same as pHamAvr1b with mutation introduced by primers motif2F and motif2R
5	M1+2	pHAMT35N	*Avr1b*-1(RXLR1^{AAAA},2^{AAAA}) mutant fused to Ham34 promoter and terminator	Same as pHamAvr1b with mutation introduced by primers motif1+2F and motif1+2R
6	M3	pHAMT35N	*Avr1b*-1(dEER^{AA}) mutant fused to Ham34 promoter and terminator	Same as pHamAvr1b with mutation introduced by primers motif3F and motif3R
7	pHamAvh341	pHAMT35N	*HpAvh341* fused with C-terminal domain of *Avr1b*-1, driven by Ham34 promoter and terminator	NptII gene replaced with HpAvh341-Avr1b fusion using primers HpAvh341F, HpAvh341R and PrimerD
8	pHamAvh171	pHAMT35N	Ps *Avh171* (=*Avr*4/6) fused with C-terminal of *Avr1b*-1 driven by Ham34 promoter and terminator	NptII gene replaced with Ps Avh171-Avr1b fusion using primers PsAvh171F, PsAvh171R and PrimerD
9	pHamAvr1bCt	pHAMT35N	C-terminus of *Avr1b*-1 gene fused to Ham34 promoter and terminator for *P. sojae* transformation in pUC19	NptII gene of pHAMT35N replaced with *P. sojae Avr1b*-1 C terminus using primers 1bRXLR(-)F and PrimerD
10	UNM1	pUN and M1	Ham34::Avr1b (RXLR1^{AAAA}) inserted together with rpL41::NptII for *P. sojae* transformation	Selection and Gus expression cassettes in pCambia1305.2 replaced by inserts from pUN and M1, respectively
11	UNM2	pUN and M2	Ham34::Avr1b (RXLR2^{AAAA}) inserted together with rpL41::NptII for *P. sojae* transformation	Selection and Gus expression cassettes in pCambia1305.2 replaced by inserts from pUN and M2, respectively
12	UNM1+2	pUN and M1+2	Ham34::Avr1b (RXLR1^{AAAA},2^{AAAA}) inserted together with rpL41::NptII for *P. sojae* transformation	Selection and Gus expression cassettes in pCambia1305.2 replaced by inserts from pUN and M1+2, respectively

Figure 11A

SEQ ID NO:	Plasmid Name	Sources	Construct	Construction strategy
13	UNM3	pUN and M3	Ham34::Avr1b(dEER^{AB}) inserted together with rpL41::NptII for *P. sojae* transformation	Selection and Gus expression cassettes in pCambia1305.2 replaced by inserts from pUN and M3, respectively
14	pCambiaAvr1b	pCambia1305.2	CaMV 35S promoter fused to full length *Avr1b*-1 in GUS-containing vector	HMT gene in pCambia1305.2 replaced by *Avr1b*-1 using primers Avr1bfull_F and Avr1bR
15	pCambiaM2	pCambia1305.2	CaMV 35S promoter fused to *Avr1b*-1 (RXLR2^{AAAA}) in GUS-containing vector	HMT gene in pCambia1305.2 replaced by Avr1b(RXLR2) using primers Avr1bfull_F and Avr1bR
14	pCambia-mAvr1b	pCambia1305.2	CaMV 35S promoter fused to leaderless *Avr1b*-1 in GUS-containing vector	HMT gene in pCambia1305.2 replaced by mature *Avr1b*-1 using primers Avr1bF and Avr1bR
15	pCambia-mM2	pCambia1305.2	CaMV 35S promoter fused to leaderless *Avr1b*-1(RXLR2^{AAAA}) in GUS-containing vector	HMT gene in pCambia1305.2 replaced by mAvr1b(RXLR2) using primers Avr1bF and Avr1bR
16	pCa-GUS(-)	pCambia1305.2	Empty vector as the control	GUS expression cassette was removed by *Sph* I restriction and re-ligation for co-transformation experiments
17	pCaAvr1b	pCambiaAvr1b	CaMV 35S promoter fused to *Avr1b*-1 in GUS-free vector	
18	pCaM2	pCambiaM2	CaMV 35S promoter fused to *Avr1b*-1 (RXLR2^{AAAA}) in GUS-free vector	
19	pCa-mAvr1b	pCambia-mAvr1b	CaMV 35S promoter fused to leaderless *Avr1b*-1 in GUS-free vector	
20	pCa-mM2	pCambia-mM2	CaMV 35S promoter fused to leaderless *Avr1b*-1(RXLR2^{AAAA}) in GUS-free vector	
21	pUCAvr1b	pCambiaAvr1b	CaMV 35S promoter fused to *Avr1b*-1 with *Xma* I site	Avr1b expression cassette was inserted into pUC19 by PCR with primers Avr1b_EcoRI and Avr1b_HindIII
22	pUCAvr1bXK	pUCAvr1b	*Kpn* I site added to 3' end pUCAvr1b to facilitate later constructions	Amplification with primers Avr1b_EcoRI, Avr1b_HindIII and Avr1b_genegun_KpnI
23	pUCmAvr1b(dEER)	pUCAvr1bXK and M3	CaMV 35S promoter fused to mature *Avr1b*-1(dEER^{AB}) using *Xma* I and *Kpn* I sites	Ligation of *Xma* I-*Kpn* I fragment from M3 into pUCAvr1bXK

Figure 11B

SEQ ID NO:	Plasmid Name	Sources	Construct	Construction strategy
24	pUCmAvr1bGFP	pAcGFP1-N	Fusion of leaderless *Avr1b*-1 with *AcGFP* from pAcGFP1-N (Clontech, # 632485) placed under control of CaMV 35S promoter	AcGFP fused to relevant Avr1b sequence by PCR with primers Avr1bF or Avr1bfull_F plus GFPF and GFPR. PCR product inserted into pUCAvr1bXK using *Xma* I and *Kpn* I
25	pUCsAvr1bGFP	pUCAvr1bXK	Fusion of normal *Avr1b*-1 with *AcGFP* placed under control of CaMV 35S promoter	
26	pUCGFP	pUCsAvr1bGFP	CaMV 35S promoter fused to *AcGFP*	Deletion of Avr1b sequences by self-ligation of *Xma* I/*Age* I restricted pUCsAvr1bGFP
27	pUCsGFP		CaMV 35S promoter fusion of Avr1b secretory leader to *AcGFP* placed under control of CaMV 35S promoter	Deletion of Avr1b sequences encoding mature protein by self-ligation of *Nco* I restricted pUCsAvr1bGFP
28	pUCM2GFP	pUCAvr1bXK	*Avr1b*-1(RXLR2^{AAAA})-*AcGFP* fusion placed under control of CaMV 35S promoter	AcGFP fused to relevant Avr1b sequence by PCR with primers Avr1bfull_F, GFPF and GFPR. PCR product inserted into pUCAvr1bXK using *Xma* I and *Kpn* I
29	pUCM3GFP		*Avr1b*-1(dEER^{A6})::*AcGFP* fusion placed under control of CaMV 35S promoter	
30	pUCAvr1b(R9)GFP		*Avr1b*-1(RXLR2^{Arg9})::*AcGFP* fusion placed under control of CaMV 35S promoter	
31	pUCAvr1b(TAT)GFP		*Avr1b*-1(RXLR2^{TAT})::*AcGFP* fusion placed under control of CaMV 35S promoter	
32	pUCNgo	pUCAvr1bXK	Addition of NgoMIV site upstream of RFLR in N-terminus of Avr1b (T150C) in pUCAvr1bXK to facilitate later manipulations	GCCGGT in was mutated to GCCGGc using primer Avr1bSac
33	pUCRFRL	pUCAvr1bXK	CaMV 35S promoter fused to *Avr1b*-1 genes carrying indicated mutations	Wild type Avr1b in pUCAv1bXK was replaced with the corresponding mutants using *Xma* I and *Kpn* I
34	pUCFRLR			
35	pUCRFAR			
36	pUCQFLQ			
37	pUCQFLR	pUCNgo		Avr1b in pUCNgo was replaced with the corresponding mutants by *NgoMIV*I and *Kpn* I
38	pUCKFLR			
39	pUCRFLQ			

Figure 11C

SEQ ID NO:	Plasmid Name	Sources	Construct	Construction strategy
40	pUCRFVR			
41	pUCAvr9R			
42	pUCAvrTAT			
43	pUCAvrPfGBP	pUCAvr1bXK		Wild type Avr1b in pUCAvr1bXK was replaced with the corresponding mutants using *Xma* I and *Kpn* I
44	pUCAvrPfHRP			
45	pUCAvrPf1615			
46	pAvr1bGFP	pR9GFP	Replacement of codons encoding nine arginine motif in pR9GFP with Avr1b residues 33 to 71 from wild type Avr1b or from Avr1b RXLR or dEER mutants	Amplification with primers AvrGFPF, AvrGFPR1 and AvrGFPR2
47	pAvr1b(M1+2)GFP			
48	pAvr1b(M3)GFP			

Figure 11D

SEQ ID NO:	Name	Applications	Sequence (from 5' to 3')*
49	UF	*Hind* III and *Xma* I sites added to rpL41 promoter to drive G418 resistance gene	ataagcttgaatTCTGGCGTTCATCTCCGACG
50	UR		ttcccgggTGGATGCTCAGATGctagcGTC
51	HamF	*Bremia* Ham34 promoter internal primer	TTCTCCTTTTCACTCTCACG
52	HamR	*Bremia* Ham34 Terminator internal primer	AGACACAAAATCTGCAACTTC
53	Avr1bReF	*Avr1b*-1 internal primers for PCR	ACCTTCAGCGTGACTGACCT
54	Avr1bReR		GCGATTGCCAACCAGTTCT
55	ActinF	*P. sojae Actin* gene internal primers for the reference in RT-PCR	CGACATCCGTAAGGACCTGT
56	ActinR		TTCGAGATCCACATCTGCTG
57	PrimerC	*Kpn* I sites added flanking *Avr1b*-1 for insertion downstream of HAM34 promoter	ggggtaccgacaacaATGCGTCTATCTTTTGTGCT
58	PrimerD		ggggtaccTCAGCTCTGATACCGGTGAA
59	Avr1bF	*Xho* I site and initiation codon added to 5' end of mature *Avr1b*-1 for insertion downstream of CaMV 35S promoter	atcgcactcgagctttcgcagatcccgggggcaatgagatatgACTGAGTACTCCGACGAA
60	Avr1bR	*Xho* I site to 3' end of *Avr1b*-1 for insertion downstream of CaMV 35S promoter	atcgcactcgagcttgtcgatcgacagatccggtcggcatctactTCAGCTCTGATACCGGTG
61	Avr1bfull_F	Same as Avr1bF but for secretory *Avr1b*-1	atcgcactcgagctttcgcagatcccgggggcaatgagatATGCGTCTATCTTTTGTG
62	Motif1F	Introduction of RXLR1^{AAAA} mutation, creating a *Pst* I site	TCGTCCGTgctgcagctgctAACGGCGACATTGCCGGTGG
63	Motif1R		TCGCCGTTagcagctgcagcACGGACGAGATCTGGAGATT
64	Motif2F	Introduction of RXLR2^{AAAA} mutation, creating a *Pst* I site	CCGGTGGAgctgcagctgctGCTCATGAAGAGGACGATGC
65	Motif2R		TCATGAGCagcagctgcagcTCCACCGGCAATGTCGCCGT
66	Motif1+2F	Introduction of RXLR1^{AAAA} & RXLR2^{AAAA} mutations, creating 2 *Pst* I sites	gctgcagctgctAACGGCGACATTGCCGGTGGAgctgcacctgctGCTCATGAAGAGGACGATGC
67	Motif1+2R		agcagctgcagcTCCACCGGCAATGTCGCCGTTagcagctgcagcACGGACGAGATCTGGAGATT
68	Motif3F	Introduction of dEER^{AA} mutation, creating a *Pst* I site	gctgcagcagctGCGGGGgctgctACCTTCAGCGTGACTGACCT
69	Motif3R		agcagcCCCCGCagctgctgcagcATGAGCTCGAAGAAATCTTC
70	HpAvh341F	5' flanking *Xma* I site added to Hp Avh341 for insertion downstream of HAM34 promoter	attcccgggacaacaATGCGACTCCACTACGTG
71	HpAvh341R	For fusion with *Avr1b*-1	GTCAGTCACGCTGAAGGTATCGAGAACGCCATGCCCAT

Figure 12A

SEQ ID NO:	Name	Applications	Sequence (from 5' to 3')*
72	PsAvh171F	5' flanking *Xma* I site added to PsAvh171 for insertion downstream of HAM34 promoter	attcccgggacaacaATGGGCCTCCACAAGGGCT
73	PsAvh171R	For fusion with *Avr1b*-1	GTCAGTCACGCTGAAGGT|TAGGTGGTGTAGTCCGAC
74	1bRXLR(-)F	For deletion of N-terminus of *Avr1b*-1	aacccgggacaacaatgACCTTCAGCGTGACTGAC
75	Avr1b_EcoRI	Primers for making moving Avr1b expression cassette into pUC19 vector with *Xma* I and *Kpn* I sites flanking *Avr1b*-1 gene	GGAGgaaTTcGCTGGCTGGTGGCAGGAT
76	Avr1b_HindIII		GTATTGGCTAGAGaAGCTTGCCA
77	Avr1b_gene gun_KpnI		AGAAACTCGAGCTTGTCGATCGACAGATCCGGTCGGCAggTACcTCAGCTCTGATAC
78	M2_F1	Replacement of RFLR with mutation encoding RFRL	GAAGATTTCgaCttGCTCATGAAG
79	M2_R1		CTTCATGAGCaaGtcGAAATCTTC
80	M2_F2	Replacement of RFLR with the mutation encoding FRLR	TGCCGGTGGAtttagaCTTCGAGCTC
81	M2_R2		GAGCTCGAAGtctaaaTCCACCGGCA
82	M2_F3	Replacement of RFLR with the mutation encoding RFAR	GAAGATTTgcaCGAGCTCAT
83	M2_R3		ATGAGCTCGtgcAAATCTTC
84	M2_F4	Replacement of RFLR with the mutation encoding QFLQ	GGTGGAcagTTTCTTCaaGCTCATGAAG
85	M2_R4		AGCttGAAGAAActgTCCACCGGCAATG
86	GFPF	For fusion with *Avr1b*-1 to make *Avr1b*-1-*AcGFP*	CTTTCACCGGTATCAGAGC|ggtaccgccacc|atgGTGAGCAAGGGCGCCGAG
87	GFPR	Addition of *Kpn* I after stop codon of GFP	AAGgtaCCtcaCTTGTACAGCTCATCCAT
88	Avr1bSac	Addition of NgoMIV site upstream of RFLR	TCATGAGCTCGAAGAAATCTTCCgCCGGCAATG
89	AvrRFLQ	Replacement of RFLR with the mutation encoding RFLQ	CATTGCCGGcGGAAGATTTCTTCaAGC
90	AvrQFLR	Replacement of RFLR with the mutation encoding QFLR	CATTGCCGGcGGAcaATTTC
91	AvrRFVR	Replacement of RFLR with the mutation encoding RFVR	CATTGCCGGcGGAAGATTTgTTC
92	AvrKFLR	Replacement of RFLR with the mutation encoding KFLR	CATTGCCGGcGGAAagTTTCTTC
93	Avr9R1	Replacement of RFLR with the seq-uence encoding the 9 arginine motif	cgtcgacgtcggcgacgcGCTCATGAAGAGGACGATG
94	Avr9R2		CATTGCCGGcGGAcgacggcgacgtcgacgtcggcgacg
95	AvrTAT1	Replacement of RFLR with the sequence encoding the TAT motif	taagaaacgccgtcagcgacgtcgaGCTCATGAAGAGGACGATG
96	AvirTAT2		CATTGCCGGcGGAtatggacgtaagaaacgccgtcagc
97	GBPF1	Replacement of RFLR-dEER with the sequence from Pf	gaaggagaagactacactccggaaaagcaagcaaaag|ACCTTCAGCGTGACTGACC

Figure 12B

SEQ ID NO:	Name	Applications	Sequence (from 5' to 3')*
98	GBPF2	GBP130	ctcgtatactggcagagggcgaagatacctgcgcaaggaaggagaagactacact
99	GBPF3		gtatgagaaagcggtagattacggctttcgagagtctcgtatactggcagag
100	GBPR		ctaccgctttctcatacttatc|TGCGTTGCAGGTCACGAC
101	HRPF1	Replacement of RFLR-dEER with the sequence from Pf HRPII	tgtcgacgatgcgcaccatgcacaccatgttgcagat|ACCTTCAGCGTGACTGACC
102	HRPF2		aacctcaacaagagactgttgcacgagacacaagcacatgtcgacgatgcgcacc
103	HRPF3		acaataacctgtgtagtaagaatgctaaaggcttgaacctcaacaagagactg
104	HRPR1		actacacaggttattgttaaa|TGCGTTGCAGGTCACGAC
105	1615F1	Replacement of RFLR-dEER with the sequence from Pf 1615c	cagtcaatgcattacaagaaatgttagatgatagtgtc|ACCTTCAGCGTGACTGACC
106	1615F2		ctcaagcagttggagttcatcacattggaagagaagacagtcaatgcattacaag
107	1615F3		aagatcaactcgtcatctacttatacacacagtagaatactcaagcagttggagttc
108	1615R1		agatgacgagttgatcttgttgtaact|TGCGTTGCAGGTCACGAC
109	AvrGFPF	Replacement of codons encoding nine arginine motif in pR9GFP with Avr1b residues 33 to 71 from wild type Avr1b or from Avr1b RXLR or dEER mutants	gatctagatctGTGGAATCTCCAGATCTC
110	AvrGFPR1		GTCATATGGATAGCCGGACAT|GTCAGTCACGCTGAAGGT
111	AvrGFPR2		GATCCCATGGAGCCAGCATAGTCTGGGACGTCATATGGATAGCCGGA

Figure 12C

SEQ ID NO:	Plasmid	Recipient	Expression	*Description**	Cloning Strategy†
112	Arg9-GFP		*E. coli*	*9Arg fused to the N-terminus of GFP.*	Received from H.J.Lee (Chang, M., Chou, J. C. & Lee, H. J. Cellular internalization of fluorescent proteins via arginine-rich intracellular delivery peptide in plant cells. Plant Cell Physiol 46, 482-8 (2005)
46	Avr1b(N)-GFP	Arg9-GFP	*E. coli*	*Amino acids 33-71 of Avr1b fused to the N-terminus of GFP.*	Described in Figure 11
47	Avr1b(N)(rxlr)-GFP	Arg9-GFP	*E. coli*	*Amino acids 33-71 of Avr1b fused to the N-terminus of GFP. RSLR and RFLR both mutated to AAAA.*	Described in Figure 11
48	Avr1b(N)(deer)-GFP	Arg9-GFP	*E. coli*	*Amino acids 33-71 of Avr1b fused to the N-terminus of GFP. EEDDAGER mutated to AAAAAGAA.*	Described in Figure 11
113	Avh5(N)-GFP	Arg9-GFP	*E. coli*	*Amino acids 19-63 of Avh5 fused to the N-terminus of GFP.*	2-Step PCR of Avh5 using Avh5-ExpGFP-BglII and Avh5R2 then Avh5-ExpGFP-BglII and LinkerR2. BglII and NcoI cloning.
114	Avh5(N)(rflr)-GFP	Arg9-GFP	*E. coli*	*Amino acids 19-63 of Avh5 fused to the N-terminus of GFP. RFLR mutated to AAAA.*	2-Step PCR of Avh5RXLR mutant from pGEX4T1 using Avh5-ExpGFP-BGIII and Avh5R2 then Avh5-ExpGFP-BglII and LinkerR2. BglII and NcoI cloning.
115	Avh5(N)(deer)-GFP	Arg9-GFP	*E. coli*	*Amino acids 19-63 of Avh5 fused to the N-terminus of GFP. DTDIVYEPK mutated to ATAIVYAPA*	2-Step PCR of Avh5dEER mutant from pGEX4T1 using Avh5-ExpGFP-BGIII and Avh5R2 then Avh5-ExpGFP-BglII and LinkerR2. BglII and NcoI cloning.
116	Avr1k(N)-GFP	Arg9-GFP	*E. coli*	*Amino acids 21-108 of Avr1k fused to the N-terminus of GFP.*	2-Step PCR of Avr1k using Avr1k-ExpGFP-BglII and Avr1kR2 then Avr1k-ExpGFP-BglII and LinkerR2. BglII and NcoI cloning.

Figure 13A

SEQ ID NO:	Plasmid	Recipient	Expression	*Description**	Cloning Strategy†
117	Avr1k(N)(rslr⁻)-GFP	Arg9-GFP	*E. coli*	*Amino acids 21-108 of Avr1k fused to the N-terminus of GFP. RSLR mutated to AAAA*	2-Step PCR of Avr1kRXLR mutant from pGEX4T1 using Avr1k-ExpGFP-BglII and Avr1kR2 then Avr1k-ExpGFP-BglII and LinkerR2. BglII and NcoI cloning.
118	Avr1k(N)(deer⁻)-GFP	Arg9-GFP	*E. coli*	*Amino acids 21-108 of Avr1k fused to the N-terminus of GFP. DDDANVSIENR mutated to AAAANVSIANA*	2-Step PCR of Avr1kdEER mutant from pGEX4T1 using Avr1k-ExpGFP-BglII and Avr1kR2 then Avr1k-ExpGFP-BglII and LinkerR2. BglII and NcoI cloning.
119	AvrL567(N)-GFP	Arg9-GFP	*E. coli*	*Amino acids 24-67 of AvrL fused to the N-terminus of GFP*	2-Step PCR of AvrL567 from pUCmAvrL567 using AvrL-ExpGFP-BglII and AvrL5R2 then AvrL-ExpGFP-BglII and LinkerR2. BglII and NcoI cloning.
120	AvrL567(N)(rfyr⁻de⁻)-GFP	Arg9-GFP	*E. coli*	*Amino acids 24-67 of AvrL fused to the N-terminus of GFP. RFYRSPTASVILSGLVKVKWDNE mutated to AAAASPTASVILSGLVKVKWANA*	2-Step PCR of AvrL567m from pUCmAvrL567(rfyr⁻de⁻) using AvrL-ExpGFP-BglII and AvrL5R2 then AvrL-ExpGFP-BglII and LinkerR2. BglII and NcoI cloning.
121	PfGBP(N)-GFP	Arg9-GFP	*E. coli*	*Amino acids 70-107 of PfGBP fused to the N-terminus of GFP*	2-Step PCR of PfGBP using PfGBP-ExpGFP-BglII and PfGBPR2 then PfGBP-ExpGFP-BglII and LinkerR2. BglII and NcoI cloning.
122	PfGBP(N)(pexel⁻)-GFP	Arg9-GFP	*E. coli*	*Amino acids 70-107 of PfGBP fused to the N-terminus of GFP. RILAE mutated to AAAAA*	3-Step PCR of PFGBP mutating RILAE to AAAAA using PfGBPF1 & PfGBPR2, then PfGBPF2 and PfGBPR2, then PfGBPExp-BglII and Linker2. BglII and NcoI cloning.

Figure 13B

SEQ ID NO:	Plasmid	Recipient	Expression	*Description**	Cloning Strategy†
123	PfHRPII(N)-GFP	Arg9-GFP	*E. coli*	*Amino acids 27-63 of PfHRPII fused to the N-terminus of GFP*	2-Step PCR of PfHRPII using PfHRPII-ExpGFP-BglII and PfHRPIIR2 then PfHRPII-ExpGFP-BglII and LinkerR2. BglII and NcoI cloning.
124	PfHRPII(N)(pexel-)-GFP	Arg9-GFP	*E. coli*	*Amino acids 27-63 of PfHRPII fused to the N-terminus of GFP. RLLHE mutated to AAAAA*	4-Step PCR of PfHRPII mutating RLLHE to AAAAA using PfHRPIIF1 and PfHRPIIR2, then PfHRPIIF2 and PfHRPIIR2, then PfHRPIIF3 and PfHRPIIR2, then PfHRPII-ExpGFP-BglII and LinkerR2. BglII and NcoI cloning.
125	Pf1615c(N)-GFP	Arg9-GFP	*E. coli*	*Amino acids 25-65 Pf1615c fused to the N-terminus of GFP*	2-Step PCR of Pf1615c using Pf1615c-ExpGFP-BglII and Pf1615cR2 then Pf1615c-ExpGFP-BglII and LinkerR2. BglII and NcoI cloning.
126	Pf1615c(N)(pexel-)-GFP	Arg9-GFP	*E. coli*	*Amino acids 25-65 Pf1615c fused to the N-terminus of GFP. RILKQ mutated to AAAAA*	3-Step PCR of Pf1615c mutating RILKQ to AAAAA using Pf1615cF1 and Pf1615cR2, then Pf1615cF2 and Pf1615cR2, then Pf1615c-ExpGFP and LinkerR2. BglII and NcoI cloning.
127	GST-Avr1k	pGEX4T1	*E. coli*	*mature Avr1k fused to the C-terminus of GST*	PCR of Avr1k using Avr1kF-GST-BamHI and Avr1kR-GST-SalI. BamHI and SalI.
128	GST-Avr1k(rslr-)	pGEX4T1	*E. coli*	*mature Avr1k fused to the C-terminus of GST. RSLR mutated to AAAA*	2-Step PCR of Avr1kRXLR using Avr1kF-GST-BamHI and Avr1kR2-RXLR, and Avr1kF2-RXLR and Avr1kR-GST-SalI. Products were fused using Avr1kF-GST-BamHI and Avr1kR-GST-SalI.

Figure 13C

SEQ ID NO:	Plasmid	Recipient	Expression	*Description**	Cloning Strategy†
129	GST-Avh5	pGEX4T1	*E. coli*	*mature Avh5 fused to the C-terminus of GST*	PCR of Avh5 using Avh5F-GST-BamHI and Avh5R-GST-SalI. BamHI and SalI
130	GST-Avh5(rflr-)	pGEX4T1	*E. coli*	*mature Avh5 fused to the C-terminus of GST.RFLR mutated to AAAA*	2-Step PCR of Avh5 using Avh5F-GST-BamHI and Avh5-RXLRF, and Avh5-RXLRR and Avh5R-GST-SalI. Products were fused using Avh5F-GST-BamHI and Avrh5R-GST-SalI.
131	GST-Avh5(deer-)	pGEX4T1	*E. coli*	*mature Avh5 fused to the C-terminus of GST. DTDiVYEPK mutated to ATAIVYAPA*	2-Step PCR of Avh5 using Avh5F-GST-BamHI and Avh5-dEERF, and Avh5-dEER and Avh5R-GST-SalI. Products were fused using Avh5F-GST-BamHI and Avrh5R-GST-SalI.
132	pUCsAvr1k	pUCAvr1bXK	Transient soybean expression	*mature Avr1k fused to the secreted leader of Avr1b in the transient assay vector*	PCR of Avr1k using Avr1kF-NcoI and Avr1kR-KpnI. NcoI and KpnI.
133	pUCsAvr1k(rslr-)	pUCAvr1bXK	Transient soybean expression	*mature Avr1k fused to the secreted leader of Avr1b in the transient assay vector. RSLR mutated to AAAA*	PCR of Avr1k(rflr-) using Avr1kF-NcoI and Avr1kR-KpnI. NcoI and KpnI.
134	pUCsAvr1k(deer-)	pUCAvr1bXK	Transient soybean expression	*mature Avr1k fused to the secreted leader of Avr1b in the transient assay vector. AAAANVSIANA*	PCR of Avr1k(deer-) using Avr1kF-NcoI and Avr1kR-KpnI. NcoI and KpnI.
135	pUCmAvr1k	pUCAvr1bXK	Transient soybean expression	*mature Avr1k cloned into transient bombardment vector with Avr1b signal peptide*	PCR of Avr1k using Avr1kF-XmaI and Avr1kR-Kpn.I XmaI and KpnI.

Figure 13D

SEQ ID NO:	Plasmid	Recipient	Expression	*Description**	Cloning Strategy†
136	pUCmAvr1k(rslr)	pUCAvr1bXK	Transient soybean expression	*mature Avr1k cloned transient bombardment vector with Avr1b signal peptide. RSLR mutated to AAAA*	PCR of Avr1k(rflr) using Avr1kF-XmaI and Avr1kR-KpnI. XmaI and KpnI.
137	pUCmAvr1k(deer)	pUCAvr1bXK	Transient soybean expression	*mature Avr1k cloned into transient bombardment vector with Avr1b signal peptide.*	PCR of Avr1k(deer) using Avr1kF-XmaI and Avr1kR-KpnI. XmaI and KpnI.
138	pUCsAvrL567-Avr1b	pUCNgo	Transient soybean expression	*Amino acids 24-67 of AvrL replaced the RXLR region of sAvr1b in the transient assay vector*	4-Step PCR Avr1b. AvrLF1 and Avr1b-KpnI, then AvrLF2 Avr1b-KpnI, then AvrLF3 and Avr1b-KpnI, then AvrLF4 and Avr1b-KpnI.
139	pUCsAvrL567(rfyr-de-)-Avr1b	pUCNgo	Transient soybean expression	*Amino acids 24-67 of AvrL replaced the RXLR region of sAvr1b in the transient assay vector. RFYR-DE of AvrL muated to AAAA-AA*	2-Step PCR AvrL567-Avr1b. AvrLF and AvrLmR. AvrLmF and Avr1b-KpnI. Fuse the two pieces using AvrLF and Avr1b-KpnI.
140	pUCmAvrL567-Avr1b	pUCAvr1bXK	Transient soybean expression	*Amino acids 24-67 of AvrL replaced the RXLR region of mAvr1b in the transient assay vector*	PCR pUCsAvrL567, mAvrLF and Avr1b-KpnI of. XmaI and KpnI.
141	pUCmAvrL567(rfyr-de-)-Avr1b	pUCAvr1bXK	Transient soybean expression	*Amino acids 24-67 of AvrL replaced the RXLR region of mAvr1b in the transient assay vector. RFYR-DE of AvrL muated to AAAA-AA*	PCR pUCsAvrL567(rfyr-de-). mAvrLF and Avr1b-KpnI. XmaI and KpnI.
142	pUCsAvrM-Avr1b	pUCAvr1bXK	Transient soybean expression	*N-terminus of AvrM replaced the RXLR region of sAvr1b in the transient assay vector.*	3-Step PCR.AvrMF1 and AvrMR, AvrMF2 and AvrMR, AvrMF3 and Avr1b-KpnI. NcoI and KpnI.

Figure 13E

SEQ ID NO:	Plasmid	Recipient	Expression	*Description**	Cloning Strategy†
143	pUCsAvrPita-Avr1b	pUCAvr1bXK	Transient soybean expression	*N-terminus AvrPita replaced the RXLR region of sAvr1b in the transient assay vector.*	4-Step PCR. AvrPita. AvrPitaF and AvrPitaR1, AvrPitaF and AvrPitaR2. Avr1b. AvrPitaF1mid and Avr1b-KpnI of Avr1b. AvrPitaF2mid and Avr1b-KpnI. Fusion using both products. AvrPitaF and Avr1b-KpnI. NcoI and KpnI.
144	pUCsAvr1b(KRRAYIER)	pUCAvr1bXK	Transient soybean expression	*RFLR motif of Avr1b was replaced with KRRAYIER by PCR and fused to pUCAvr1bXK. XmaI/KpnI*	PCR of Avr1b using Avr1b(KRRAYIER)F and Avr1b-KpnI. NgoMIV and KpnI.
145	pUCsAvr1b(RAALK)	pUCAvr1bXK	Transient soybean expression	*RFLR motif of Avr1b was replaced with by RAALK PCR and fused to pUCAvr1bXK. XmaI/KpnI*	PCR of Avr1b using Avr1b(RAALK)F and Avr1b-KpnI. NgoMIV and KpnI.
146	pUCsAvr1b (RLFKLIFKTDSTDIQ)	pUCAvr1bXK	Transient soybean expression	*RFLR motif of Avr1b was replaced with RLFKLIFKTDSTDIQ by PCR and fused to pUCAvr1bXK. XmaI/KpnI*	3-Step PCR. PCR of Avr1b Avr1bFull-F and Avr1b(RLFKLIFKTDSTDIQ)R. PCR of Avr1b Avr1b(RLFKLIFKTDSTDIQ)F and Avr1b-KpnI. PCR fusion of products. Avr1bFull-F and Avr1b-KpnI. XmaI & KpnI.
38	pUCsAvr1b(KFLR)	pUCAvr1bNgo	Transient soybean expression	*RFLR motif of Avr1b was replaced with KFLR by PCR and fused to pUCAvr1bXK. NgoMIV/KpnI*	Described in Figure 11
147	pUCsAvr1b(HFLR)	pUCAvr1bNgo	Transient soybean expression	*RFLR motif of Avr1b was replaced with HFLR by PCR and fused to pUCAvr1bXK. NgoMIV/KpnI*	PCR of Avr1b using Avr1b(HFLR)F and Avr1b-KpnI. NgoMIV and KpnI.
37	pUCsAvr1b(QFLR)	pUCAvr1bNgo	Transient soybean expression	*RFLR motif of Avr1b was replaced with QFLR by PCR and fused to pUCAvr1bXK. NgoMIV/KpnI*	Described in Figure 11

Figure 13F

SEQ ID NO:	Plasmid	Recipient	Expression	*Description**	Cloning Strategy†
148	pUCsAvr1b(RFFR)	pUCAvr1bNgo	Transient soybean expression	*RFLR motif of Avr1b was replaced with RFFR by PCR and fused to pUCAvr1bXK. NgoMIV/KpnI*	PCR of Avr1b using Avr1b(RFFR)F and Avr1b-KpnI. NgoMIV and KpnI.
149	pUCsAvr1b(RFYR)	pUCAvr1bNgo	Transient soybean expression	*RFLR motif of Avr1b was replaced with RFYR by PCR and fused to pUCAvr1bXK. NgoMIV/KpnI*	PCR of Avr1b using Avr1b(RFYR)F and Avr1b-KpnI. NgoMIV and KpnI.
150	pUCsAvr1b(RFIR)	pUCAvr1bNgo	Transient soybean expression	*RFLR motif of Avr1b was replaced with RFIR by PCR and fused to pUCAvr1bXK. NgoMIV/KpnI*	PCR of Avr1b using Avr1b(RFIR)F and Avr1b-KpnI. NgoMIV and KpnI.
151	pUCsAvr1b(RFMR)	pUCAvr1bNgo	Transient soybean expression	*RFLR motif of Avr1b was replaced with RFMR by PCR and fused to pUCAvr1bXK. NgoMIV/KpnI*	PCR of Avr1b using Avr1b(RFMR)F and Avr1b-KpnI. NgoMIV and KpnI.
40	pUCsAvr1b(RFVR)	pUCAvr1bNgo	Transient soybean expression	*RFLR motif of Avr1b was replaced with RFVR by PCR and fused to pUCAvr1bXK. NgoMIV/KpnI*	Described in Figure 11
35	pUCsAvr1b(RFAR)	pUCAvr1bNgo	Transient soybean expression	*RFLR motif of Avr1b was replaced with RFAR by PCR and fused to pUCAvr1bXK. NgoMIV/KpnI*	Described in Figure 11
39	pUCsAvr1b(RFLQ)	pUCAvr1bNgo	Transient soybean expression	*RFLR motif of Avr1b was replaced with RFLQ by PCR and fused to pUCAvr1bXK. NgoMIV/KpnI*	Described in Figure 11
152	pUCsAvr1b(RFLG)	pUCAvr1bNgo	Transient soybean expression	*RFLR motif of Avr1b was replaced with RFLG by PCR and fused to pUCAvr1bXK. NgoMIV/KpnI*	PCR of Avr1b using Avr1b(RFLG)F and Avr1b-KpnI. NgoMIV and KpnI.
153	pUCsAvr1b(RMVR)	pUCAvr1bNgo	Transient soybean expression	*RFLR motif of Avr1b was replaced with RMVR by PCR and fused to pUCAvr1bXK NgoMIV/KpnI*	PCR of Avr1b using Avr1b(RMVR)F and Avr1b-KpnI. NgoMIV and KpnI

Figure 13G

SEQ ID NO:	Plasmid	Recipient	Expression	*Description**	Cloning Strategy†
154	pUCsAvr1b(RLGT)	pUCAvr1bNgo	Transient soybean expression	*RFLR motif of Avr1b was replaced with RLGT by PCR and fused to pUCAvr1bXK NgoMIV/KpnI*	PCR of Avr1b using Avr1b(RLGT)F and Avr1b-KpnI. NgoMIV and KpnI
155	pUCsAvr1b(RLTQ)	pUCAvr1bNgo	Transient soybean expression	*RFLR motif of Avr1b was replaced with RLTQ by PCR and fused to pUCAvr1bXK NgoMIV/KpnI*	PCR of Avr1b using Avr1b(RLTQ)F and Avr1b-KpnI. NgoMIV and KpnI
41	pUCAvr1b(Arg9)	pUCAvr1bNgo	Transient soybean expression	*RFLR motif of Avr1b was replaced with 9 Arg residues by PCR and fused to pUCAvr1bXK NgoMIV/KpnI*	Described in Figure 11
224	Pita(N)-GFP	Arg9-GFP	*E. coli*	*Amino acids 26-100 of Avr Pita fused to the N-terminus of GFP*	2-Step PCR using PitaF and PitaR and LinkerR2. BglII and NcoI.
225	Pitam(N)-GFP	Arg9-GFP	*E. coli*	*Amino acids 26-100 of Avr Pita fused to the N-terminus of GFP. Mutation of putative RXLR motifs* KRRAY, RYSQ, RAALK, HAVK, RLFR to SASAS, AASA, ASSAA, ASAA, AASA.	2-Step PCR using PitaF and PitaR and LinkerR2. BglII and NcoI.
226	Ps87(N)-GFP	Arg9-GFP	*E. coli*	*Amino acids 23-69 of Ps87 fused to the N-terminus of GFP.*	2 Step PCR using 87F and 87R and LinkerR2. BglII and NcoI
227	Ps87m(N)-GFP	Arg9-GFP	*E. coli*	*Amino acids 23-69 of Ps87 fused to the N-terminus of GFP. KRLTG mutated to AAAAA*	2 Step PCR using 87F and 87R and LinkerR2. BglII and NcoI
228	AvrM(N)-GFP	Arg9-GFP	*E. coli*	*Amino acids 54-151 of AvrM fused to the N-terminus of GFP.*	2 Step PCR using AvrMF and AvrMR and LinkerR2. BglII and NcoI

Figure 13H

SEQ ID NO:	Plasmid	Recipient	Expression	*Description**	Cloning Strategy†
229	AvrMm(N)-GFP	Arg9-GFP	*E. coli*	*Amino acids 54-151 of AvrM fused to the N-terminus of GFP.* HPIQ, KSGT, KDMK, KALK, KLGT, RGFLR, KFLK, KLST, KNVR mutated to AAAA,AAAA,AAAA,AAAA,AAAA,AAAA,AAAA,AAAA	2 Step PCR using AvrMF and AvrMR and LinkerR2. BglII and NcoI
230	P123(N)-GFP	Arg9-GFP	*E. coli*	*Amino acids 23- 59 of AvrP123 were fused to the N-terminus of GFP.*	2 Step PCR using P123F and P123R and LinkerR2. BglII and NcoI.
231	P123m(N)-GFP	Arg9-GFP	*E. coli*	*Amino acids 23- 59 of AvrP123 were fused to the N-terminus of GFP. RLTQ was mutated to AAAA*	2 Step PCR using P123F and P123R and LinkerR2. BglII and NcoI.
232	P4(N)-GFP	Arg9-GFP	*E. coli*	*Amino acids 29-61 of AvrP4 were fused to the N-terminus of GFP.*	2 Step PCR using P4F and P4R and LinkerR2. BglII and NcoI.
233	P4m(N)-GFP	Arg9-GFP	*E. coli*	*Amino acids 29-61 of AvrP4 were fused to the N-terminus of GFP.RDIQ was mutated to AAAA.*	2 Step PCR using P4F and P4R and LinkerR2. BglII and NcoI.

Figure 13I

SEQ ID NO:	Primer Name	Function	Sequence (5' to 3')*
156	LinkerR2	Recreates the linker region between GFP and Arg9 for RXLR regions for all GFP expression constructs. NcoI	GCATC**CCATGG**AGCCAGCATAGTCTGGGACGT CATATGGATAGCCGGACATGG
157	Avr1k-GFPExp-BglII	Forward primer for Avr1k RXLR Region. BglII site for cloning into GFP expression vector	ATGC**AGATCT**CTCACTTGCGCCACCTCCGAGC
158	Avr1kR2	Reverse primer for Avr1k RXLR region. Adds nucleotides to facilitate space between GFP and RXLR	CATATGGATAGCCGGACATGGTGGATCTGTC GACTCTGTTTTCAATCG
159	Avr1kdEERR2	Reverse primer for Avr1k RXLR region dEER mutant. Adds nucleotides to facilitate space between GFP and RXLR	CATATGGATAGCCGGACATGGTGGATCTGTCG ACTGCGTTTGCAAT
160	Avh5-GFPExp-BglII	Forward primer for Avh5 RXLR Region. BglII site for cloning into GFP expression vector	AGTC**AGATCT**ACAAGAGTCCCCGACGA
161	Avh5R2	Reverse primer for Avh5 RXLR region. Adds nucleotides to facilitate space between GFP and RXLR	CATATGGATAGCCGGACATGGTGGATCTG TCGACTTGCCAGGATTATG
162	AvrL-GFPExp-BglII	Forward primer for AvrL567 RXLR Region. BglII site for cloning into GFP expression vector	ATCG**AGATCT**ATGGGAATGGAACATG
163	AvrLRevMod1	Reverse primer for AvrL567 RXLR region. Adds nucleotides to facilitate space between GFP and RXLR	GATAGCCGGACATGGTGGATCTGTCGACCCACA GGTCAGTCACGC
164	AvrLRevMod2	Adds remaining nucelotides for linker sequence between GFP Expression vector and RXLR region	TCCCATGGAGCCAGCATAGTCTGGGACGTCATA TGGATAGCCGGACATGGTGGATCT
165	PfGBP-GFPExp-BglII	Forward primer for PfGBP RXLR Region. BglII site for cloning into GFP expression vector	ATCG**AGATCT**GATAAGTATGAGAAAGCG
166	PfGBPR2	Reverse primer for PfGBP7 RXLR region. Adds nucleotides to facilitate space between GFP and RXLR	CATATGGATAGCCGGACATGGTGGATCTGTCGAC CGTTTGCTTGCTTTTCCGG
167	PfGFPm-GFPExp-F1	Forward primer 1 for PfGBP RXLR Region. RILAE to AAAAA	GATTACGGCTTTCGAGAGTCTgcagcagcagcagca GGCGAAGATACCTGCG
168	PfGFPm-GFPExp-F2	Forward primer 2 for PfGBP RXLR Region. RILAE to AAAAA	ATGCAGATCTGATAAGTATGAGAAAGCGGTAGATT ACGGCTTTCGAGAGTCT
169	PfHRPII-GFPExp-BglII	Forward primer for PfHRPII RXLR Region. BglII site for cloning into GFP expression vector	ATGCAGATCTTTTAACAATAACC
170	PfHRPIIR2	Reverse primer for PfHRPII RXLR region. Adds nucleotides to facilitate space between GFP and RXLR	CATATGGATAGCCGGACATGGTGGATCTGTCGAC ATCTGCAACATGG

Figure 14A

SEQ ID NO:	Primer Name	Function	Sequence (5' to 3')*
171	PfHRPIIm-GFPExp-F1	Forward primer 1 for PfGBP RXLR Region. RLLHE to AAAAA	GGCTTGAACCTCAACAAGgcagcagcagcagca ACACAAGCACATG
172	PfHRPIIm-GFPExp-F2	Forward primer 2 for PfGBP RXLR Region. RLLHE to AAAAA	GTAGTAAGAATGCTAAAGGCTTGAACCTCAACAAG
173	PfHRPIIm-GFPExp-F3	Forward primer 3 for PfGBP RXLR Region. RLLHE to AAAAA	ATGC**AGATC**TTTTAACAATAACCTGTGTAGTAAGA ATGCTAAAGGC
174	Pf1615cGFPExp-BglII	Forward primer for Pf1615c RXLR Region. BglII site for cloning into GFP expression vector	ATGC**AGATC**TAGTTACAACAAGATCAAC
175	Pf1615cR2	Reverse primer for Pf1615c RXLR region. Adds nucleotides to facilitate space between GFP and RXLR	CATATGGATAGCCGGACATGGTGGATCTGTCGAC ACTATCATCTAAC
176	Pf1615cm-GFPExp-F1	Forward primer 1 for Pf1615c RXLR Region. RILKQ to AAAAA	CATCTACTTATACACACAGTgcagcagcagcagca TTGGAGTTCATCACATTGG
177	Pf1615cm-GFPExp-F2	Forward primer 2 for Pf1615c RXLR Region. RILKQ to AAAAA	ATGCAGATCTAGTTACAACAAGATCAACTCGTCATC TACTTATACACACAGTgcagca
178	Avr1kF-GST-BamHI	Forward primer for mature Avr1k. BamHI site for cloning into PGEX4T1 vector	GCGT**GGATCC**CTCACTTGCGCCACCTCCG
179	Avr1kR-GST-SalI	Reverse primer for mature Avr1k. SalI site for cloning into PGEX4T1 vector	TCGA**GTCGAC**TCAGATAATCATGATGCTGT
180	Avh5F-GST-BamHI	Forward primer for mature Avh5. BamHI site for cloning into PGEX4T1 vector	GCGT**GGA**T**CC**ACAAGAGTCCCCGACGA
181	Avh5R-GST-SalI	Reverse primer for mature Avh5. SalI site for cloning into PGEX4T1 vector	TCGA**GTCGAC**TCACTTGGCCTCTTGCGAT
182	Avr1kF2-RXLR	Forward primer for producing RXLR mutation in Avr1k. RSLR to AAAA	CAgcggcggcggcgTCTCAAGCTACGAACG
183	Avr1kR2-RXLR	Reverse primer for producing RXLR mutation in Avr1k. RSLR to AAAA	GTTCGTAGCTTGAGAcgccgccgccgcTGTCGAG GTTGCCATGTC
184	Avr1kF2-dEER	Forward primer for producing dEER mutation in Avr1k. DDDANVSIENR to AAAANVSIANA	GGCTAACGTTTCGATTgcgAACgcgGGATGAACCCTTCA G
185	Avr1kR2-dEER	Reverse primer for producing dEER mutation in Avr1k. DDDANVSIENR to AAAANVSIANA	CGCAATCGAAACGTTAGCcgccgccgcCACG TTCGTAG

Figure 14B

SEQ ID NO:	Primer Name	Function	Sequence (5' to 3')'
186	Avr1kF-NcoI	Forward primer for mature Avr1k. NcoI site for cloning into transient assay vector with Avr1b signal peptide	GCGT**CCATGG**GAGCTCACTTGCGCCACCTCCG
187	Avr1kR-KpnI	Reverse primer for mature Avr1k. KpnI site for cloning into transient assay vector	TCGA**GGTACC**TCAGATAATCATGATGCTGT
188	Avr1kF-XmaI	Forward primer for mature Avr1k. XmaI site for cloning into transient assay vector	AGAT**CCCGGG**GGGCAGTGAGATATGCTCACTTGCGC CACCTCCGAGCAACAG
189	AvrL567-F4	Forward primer for AvrL567 RXLR region NcoI site for cloning into transient assay vector with Avr1b signal peptide	ATCG**CCATGG**AATGGAACATGTACCAGCAGAGTT GACCAGAGTCAGCGAAGGG
190	AvrL567-F3	Forward primer for AvrL567 RXLR region	ACCAGAGTCAGCGAAGGGTATACACGATTTTA CCGGTCCCCAACGGCTAGTGTAATAC
191	AvrL567-F2	Forward primer for AvrL567 RXLR region	CAACGGCTAGTGTAATACTGTCAGGATTGGTA AAGGTTAAATGGGATAATGAACAAATG
192	AvrL567-F1	Forward primer for AvrL567 RXLR region	TGGGATAATGAACAAATGACGATGCCGACCTT CAGCGTGACTGACCTGTGG
193	AvrL567-F	Forward primer for AvrL567 RXLR region XmaI site for cloning into transient assay vector	AGAT**CCCGGG**GGGCAATGAGATATGATGGAACATGTA CCAGCAG
194	AvrL567MR	Reverse primer for AvrL567 mutation. RFYR-DxE to AAAA-AxA	TCCTGACAGTATTACACTAGCCGTTGG GGAcgcagcggctgcTGTATACCCTTCGCTG
195	AvrL567MF	Forward primer for AvrL567 mutation. RFYR-DxE to AAAA-AxA	GTGTAATACTGTCAGGATTGGTAAAGGTT AAATGGgctAATgcaCAAATGACGATGCCG
77	Avr1b-KpnI Dou et al[8]	Reverse Primer for Avr1b in the transient assay vector	AGAAACTCGAGCTTGTCGATCGACAGATCCGGTCGGC A**gg**T**AC**cTCAGCTCTGATAC
196	Avr1bFull-F Dou et al[8]	Forward primer for Avr1b with signal peptide. XmaI site	atcgcactcgagctttcgcagat**cccgggg**ggcaatgagatATGCGTCT ATCTTTTGTG
197	AvrPitaF	Forward primer for fusing N-terminus of AvrPita wild type into Avr1b	ATCG**CCATGG**GACACCCAGTTTACGATTACAATC
198	AvrPitaF2mid	Forward primer for fusing N-terminus of AvrPita wild type into Avr1b	CACGCCGTTAAAAATGACAATCGGTTATTTAGAT TAATCTTTAAAACTGACAGCACAG

Figure 14C

SEQ ID NO:	Primer Name	Function	Sequence (5' to 3')*
199	AvrPitaF1mid	Forward primer for fusing N-terminus of AvrPita wild type into Avr1b	CTTTAAAACTGACAGCACAGATATTCAAAACACC
200	AvrPitaR1	Reverse primer for fusing N-terminus of AvrPita wild type into Avr1b	TTCAGCGTGACTGACCTG
201	AvrPitaR2	Reverse primer for fusing N-terminus of AvrPita wild type into Avr1b	CCACGAGGCGAGCTCGGCACAACTTTTTAGCGC
202	AvrM-F3	Forward primer for fusing N-terminus of AvrM wild type into Avr1b	GGCACGAATTTC
203	AvrM-F2	Forward primer for fusing N-terminus of AvrM wild type into Avr1b	CCGATTGTCATTTTTAACGGCGTGATAGCCCCAC
204	AvrM-F1	Forward primer for fusing N-terminus of AvrM wild type into Avr1b	GAGGCGAGCTCGGCAC
205	AvrM-R	Reverse Primer for fusing N-terminus of AvrM wild type into Avr1b	ATCG**GCCATGG**GAAACAACCTTGGAACAGTACCGGA
206	Avr1b(KRRAYIER)F	Forward primer for replacing RFLR motif of Avr1b with KRRAYIER	TGTGCCACATC
207	Avr1b(RAALK)F	Forward primer for replacing RFLR motif of Avr1b with RAALK	CAGTACCGGATGTGCCACATCAAATTCCAAATGA
208	Avr1b (RLFKLIFKTDSTDiQ)F	Forward primer for replacing RFLR motif of Avr1b with RFLKLIFKTDSTDiQ	CAAAAGTGGTACTCCTGCCATTG
209	Avr1b (RLFKLIFKTDSTDiQ)R	Reverse primer for replacing RFLR motif of Avr1b with RFLKLIFKTDSTDiQ	CAAAAGTGGTACTCCTGCCATTGAAGACCCAAAA
210	Avr1b(KFLR)F Dou et al[8]	Forward primer for replacing RFLR motif of Avr1b with KFLR	GATATGAAAGGATTCAATAAGGCTC
211	Avr1b(HFLR)F	Forward primer for replacing RFLR motif of Avr1b with HFLR	CCACAGGTCAGTCACGCTGAAGGTTCGTACATTT
212	Avr1b(QFLR)F Dou et al [8]	Forward primer for replacing RFLR motif of Avr1b with QFLR	TTATCTTTTTCTGCCATGTATG
			GACATT**GCCGGC**GGAaaaaggcgggcttatatt
			gaacgcGCTCATGAAGAGGACGATGC
			GACATT**GCCGGC**GGAcgtgccgcgctaaaaAG
			TGCTCATGAAGAGGACGATGC
			ctttaaaactgacagcacagatattcaaGCTCATGA
			AGAGGACGATGCG
			ctgtgctgtcagtttaaagatttaatttaaataaccgTCC
			GCCGGCAATGTCGCCGTTC
			CATT**GCCGGc**GGAAAagTTTCTTC
			CGACATT**GCCGGC**GGAcacTTTCTTCGAGCTCATGAAG
			AGGACGATG
			CATT**GCCGGc**GGAcaATTTC

Figure 14D

SEQ ID NO:	Primer Name	Function	Sequence (5' to 3')*
213	Avr1b(RFFR)F	Forward primer for replacing RFLR motif of Avr1b with RFFR	CGACATT**GCCGGC**GGAAGATTTtTTCGAGCTCATGAAG AGGACGATG
214	Avr1b(RFYR)F	Forward primer for replacing RFLR motif of Avr1b with RFYR	CGACATT**GCCGGC**GGAAGATTTtaTCGAGCTCATGA AGAGGACGATG
215	Avr1b(RFIR)F	Forward primer for replacing RFLR motif of Avr1b with RFIR	CGACATT**GCCGGC**GGAAGATTTaTTCGAGCTCATG AAGAGGACGATG
216	Avr1b(RFMR)F	Forward primer for replacing RFLR motif of Avr1b with RFMR	CGACATT**GCCGGC**GGAAGATTTaTgCGAGCTCATG AAGAGGACGATG
217	Avr1b(RFVR)F Dou et al [8]	Forward primer for replacing RFLR motif of Avr1b with RFVR	CATT**GCCGG**cGGAAGATTTgTTC
218	Avr1b(RFAR)F Dou et al [8]	Forward primer for replacing RFLR motif of Avr1b with RFAR	CATT**GCCGG**cGGAAGATTTgcTCG
219	Avr1b(RFLQ)F Dou et al [8]	Forward primer for replacing RFLR motif of Avr1b with RFLQ	CATT**GCCGG**cGGAAGATTTCTTCaAGC
220	Avr1b(RFLG)F	Forward primer for replacing RFLR motif of Avr1b with RFLG	CGACATT**GCCGGC**GGAAGATTTCTTgGAGCTCAT GAAGAGGACGATG
221	Avr1b(RMVR)F	Forward primer for replacing RFLR motif of Avr1b with RMVR	CGACATT**GCCGGC**GGAAGAaTggTTCGAGCTCA TGAAGAGGACGATG
222	Avr1b(RLGT)F	Forward primer for replacing RFLR motif of Avr1b with RLGT	CGACATT**GCCGGC**GGAAGAcTTggaacAGCTCA TGAAGAGGACGATG
223	Avr1b(RLTQ)F	Forward primer for replacing RFLR motif of Avr1b with RLTQ	CGACATT**GCCGGC**GGAAGAcTTacTCaAGCTCA TGAAGAGGACGATG
234	P4ForGFPExp-BglII	Forward primer to PCR AvrP4 or AvrP4 mutant	atgcagatctGAATTCTTAGAGGATGCACGAGATATCC
235	P4RevGFPR2	Reverse primer to PCR AvrP4 or AvrP4 mutant	CTGACAGCTCGCGCGATAGGCAAGAAAAAGTCGACAG ATCCACCATGTCCGGCTATCCATATG
236	P123ForGFPExp-BglII	Forward primer to PCR AvrP123 or AvrP123 mutant	atgcagatctCAGTATGTTGTTGATCCAGG
237	P123RevGFPR2	Reverse primer to PCR AvrP123 or AvrP123 mutant	CATATGGATAGCCGGACATGGTGGATCTGTCGACACA ACTTGGGGTGGCTTCACATTCCAC
238	Ps87ForGFP-BglII	Forward primer to PCR Ps87 or Ps87 mutant	ATGCAGATCTACTCTGTTGAACGTGACT

Figure 14E

SEQ ID NO:	Primer Name	Function	Sequence (5' to 3')*
239	Ps87RevGFP2	Reverse primer to PCR Ps87 or Ps87 mutant	CATATGGATAGCCGGACATGGTGGATCTGTCGACGTT TTGAATATCTGTGC
240	AvrMForGFP-BglII	Forward primer to PCR AvrM or AvrM mutant	atgcagatctATGGGAAACAACCTTGGAACAGTACCG
241	AvrMRevGFPR2	Reverse primer to PCR AvrM or AvrM mutant	CATATGGATAGCCGGACATGGTGGATCTGTCGACTCG TACATTTTTATCTTTTTCTGCCATG
242	AvrPitaForGFP-BglII	Forward primer to PCR AvrPita or AvrPita mutant	AGTCAGATCTCACCCAGTTTACGATTACAATCC
243	AvrPitaRevGFPR2	Forward primer to PCR AvrPita or AvrPita mutant	CATATGGATAGCCGGACATGGTGGATCTGTCGACGTT TTGAATATCTGTGC
244	Ps87m8R	For replacing KRLTG with AAAAA	GAAACgcagcagctgcggcaAAACCTCGAGGGCAATGTGTC
245	Ps87m8F	For replacing KRLTG with AAAAA	GTTTtgcagccgctgctgcGTTTCTCTCTTTCATCATTTC
246	AvrMmR1	Reverse Primers for replacing HPIQ, KDMK, KALK, KLGT, RGFLR, KFLK, KLST motifs in AvrM with ASSA, SASA, SAAA, AAAA, SAASA, SAAS, ASSA	CATTtgcagatgaagcTGGCACATCCGGTACTGTTC
247	AvrMmR2		cagcgctATTGAATCCtgctgaggcactTGGGTCTTCAATGGC AGGAG
248	AvrMmR3		GACGAagccgcagcggcTTCGGATTCTGGAGTAGAtg
249	AvrMmR4		CAAAAGGcgcagaggctgcactGTCAAATTCTGGTTGAGGG ATC
250	AvrMmR5		gatgcCTGAACTTGGTCCGGactagcggctgaCATTTTTGCT CCAAAAGGcgcag
251	AvrMmF1	Reverse Primers for replacing HPIQ, KDMK, KALK, KLGT, RGFLR, KFLK, KLST motifs in AvrM with ASSA, SASA, SAAA, AAAA, SAASA, SAAS, ASSA	GTGCCAgcttcatctgcaATGACAAAAGTGGTACTCCTG
252	AvrMmF2		cagcaGGATTCAATagcgctgccgcaTCTACTCCAGAATCCG AAAAAC

Figure 14F

SEQ ID NO:	Primer Name	Function	Sequence (5' to 3')*
253	AvrMmF3		GAAgccgctgcggctTCGTCAGTTGAAGGGATCCCTC
254	AvrMmF4		CagtgcagcctctgcgCCTTTTGGAGCAAAAATG
255	AvrMmF5		gtCCGGACCAAGTTCAGgcatcttcagccGATGATCTCATCA CATACATG
256	AvrP4mR	Reverse primer used to replace RDIQ in AvrP4 with AAAA	
257	AvrP4mF	Forward primer used to replace RDIQ in AvrP4 with AAAA	
258	AvrP123mF	Forward primer used to replace RLTQ in AvrP123 with AAAA	
259	AvrP123mR	Reverse primer used to replace RLTQ in AvrP123 with AAAA	

Figure 14G

SEQ ID NO:	Protein		RXLR Motifs of each fungal or mutations therein	PA Binding	Root Cell Entry
224	AvrPita-GFP	wild-type	KRRAY, RYSQ, RAALK, HAVK, RLFR	Y	Y
225	AvrPitam-GFP	mutant	SASAS, AASA, ASSAA, ASAA, AASA	N	N
226	Ps87-GFP	wild-type	KRLTG	Y	NT
227	Ps87m-GFP	mutant	AAAAA	N	NT
228	AvrM-GFP	wild-type	HPIQ, KSGT, KDMK, KALK, KLGT, RGFLR, KFLK, KLST, KNVR	Y	NT
229	AvrMm-GFP	mutant	AAAA,AAAA,AAAA,AAAA,AAAA,AAAA,AAAA,AAAA	N	NT
230	AvrP123-GFP	wild-type	RLTQ	Y	NT
231	AvrP123m-GFP	mutant	AAAA	N	NT
232	AvrP4-GFP	wild-type	RDIQ	Y	NT
233	AvrP4m-GFP	mutant	AAAA	N	NT

Figure 15

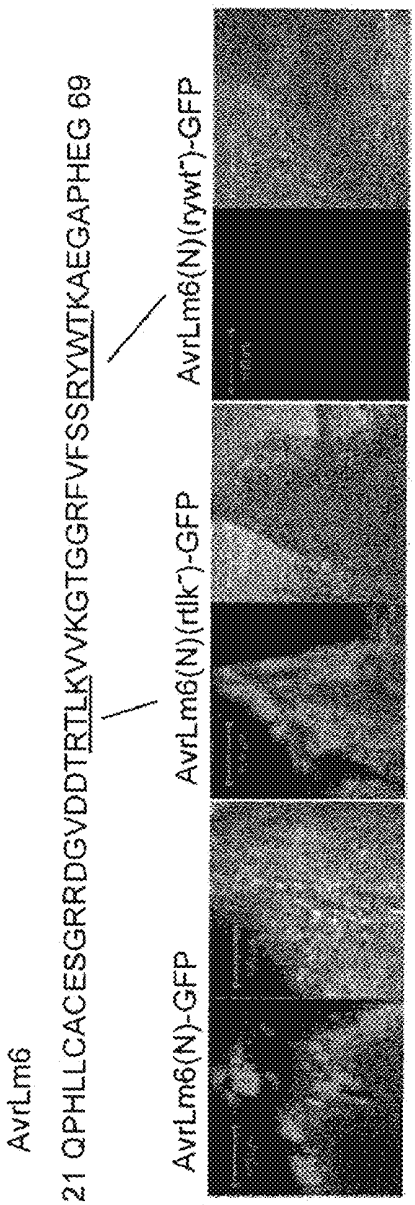


Figure 16A

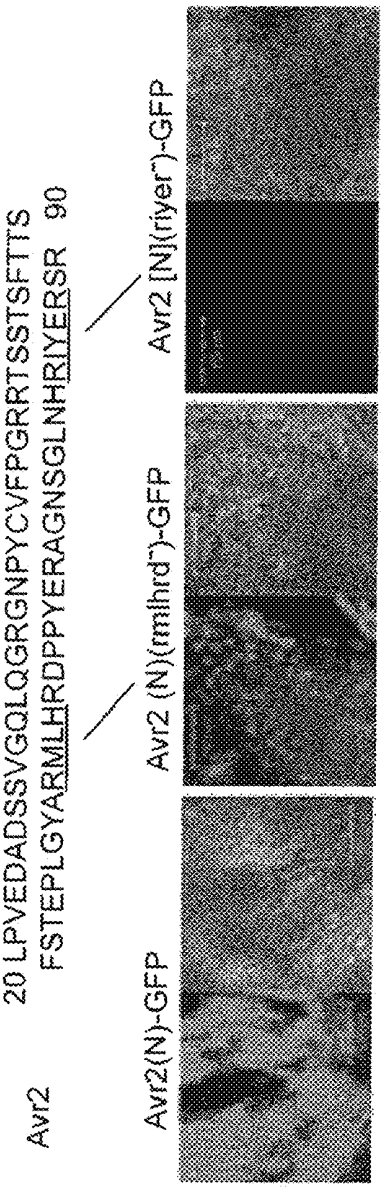


Figure 16B

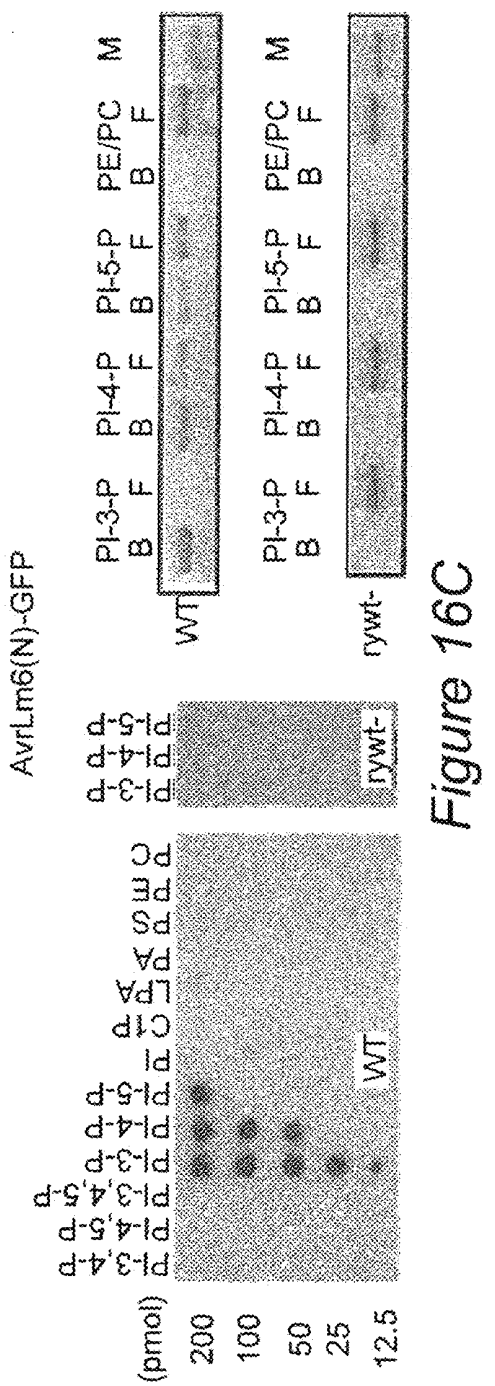


Figure 16C

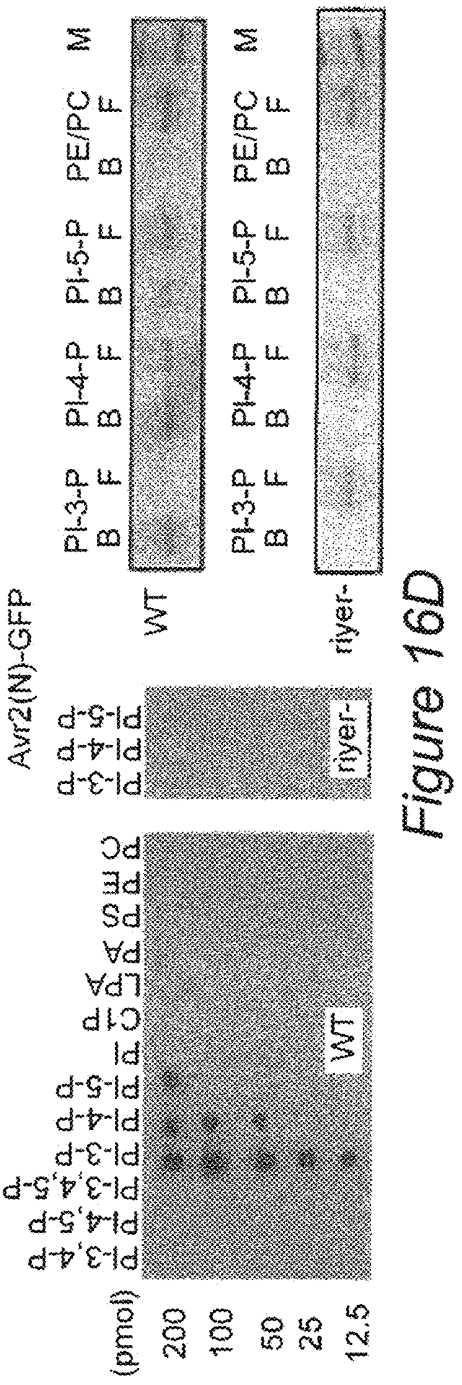


Figure 16D

Af2 VAMGVSEQRKANERKMDARRMARFNIDIETSGETQEEDEIRGKRIVLRDNKVYLDDPLPANRKHPSHTAESFYIDYP

Cng2 QQGQKANAREQHRGRKTNLTIKLPGAHSYKAKFEGCMVVLQDKKLYVEHAGCESLAYAHP

AvrLm4/7 CREASISGEIRYPQGTCPTKTEALNDCNKVTKGLIDFSQSHQRAWGIDMTAKVQ

Figure 17A

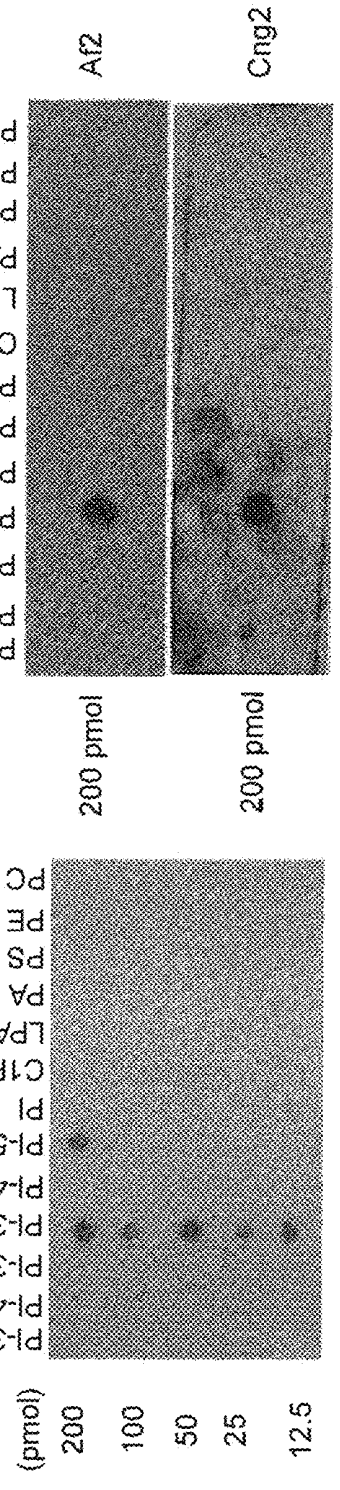


Figure 17B

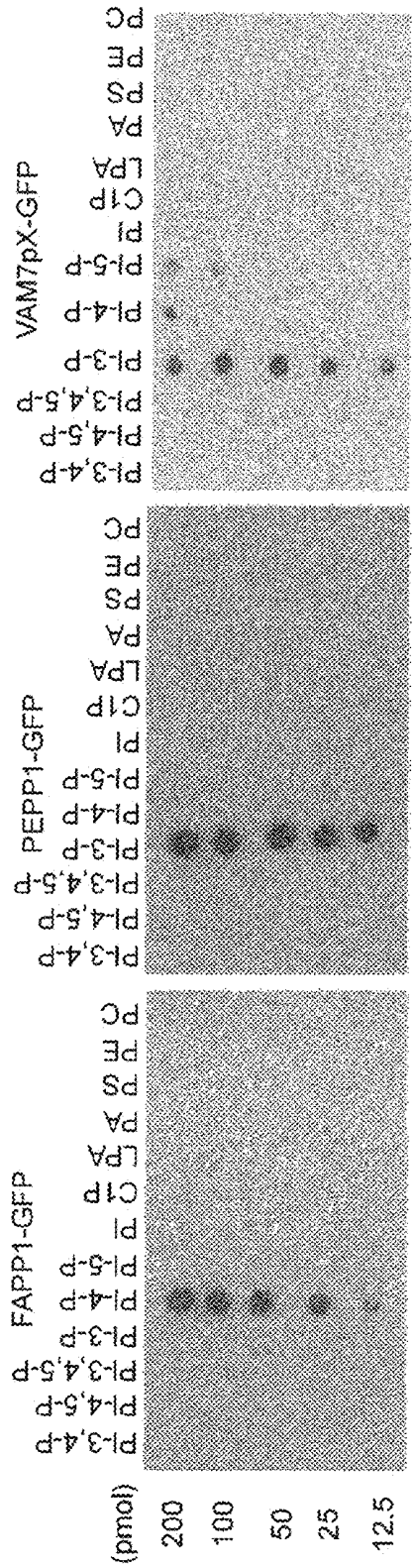


Figure 18A

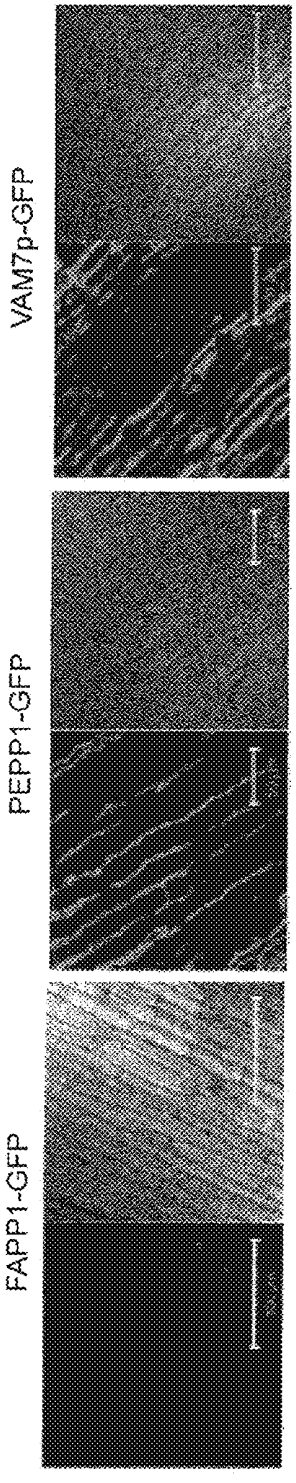


Figure 18B

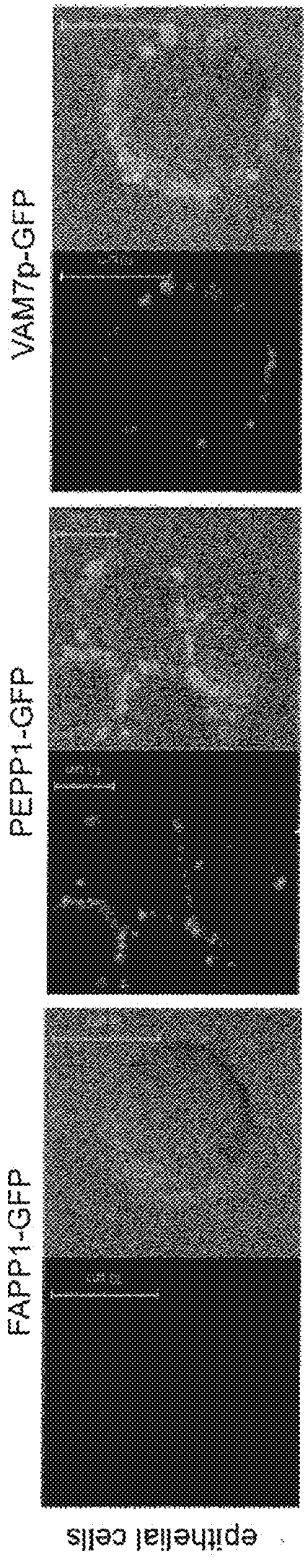


Figure 18C

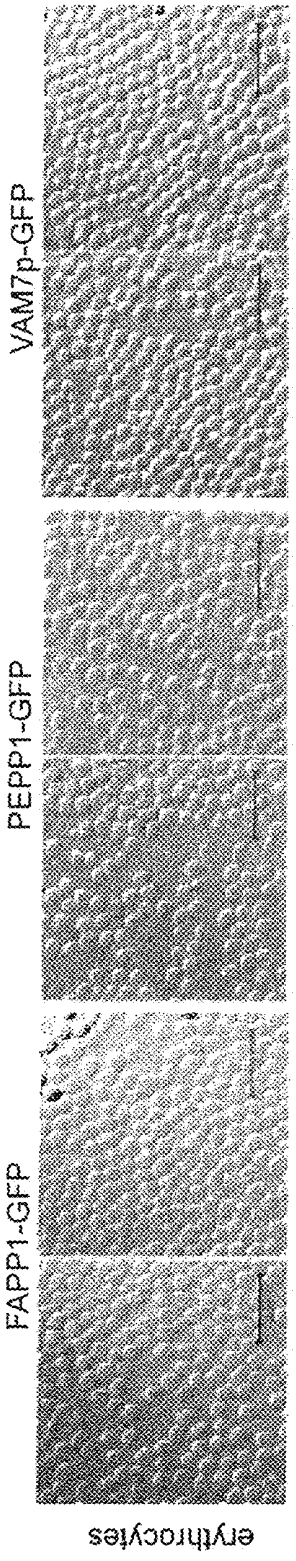


Figure 18D

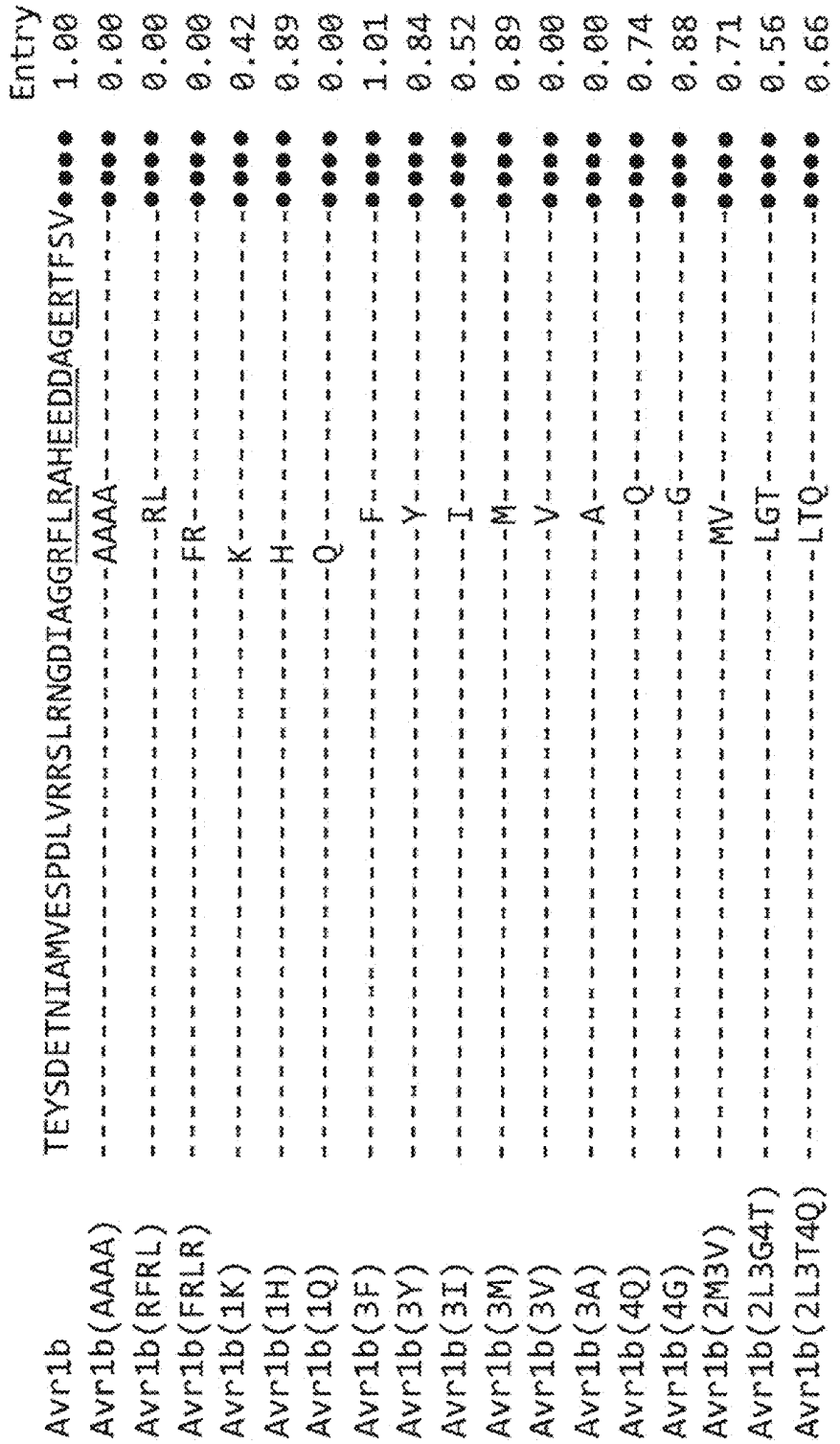

Entry
Avr1b TEYSDETNIAMVESPDLVRRSLRNGDIAGGRFLRAHEEDDAGERTFSV
Avr1b(AAAA) 1.00
Avr1b(RFRL) 0.00
Avr1b(FRLR) 0.00
Avr1b(1K) 0.00
Avr1b(1H) 0.42
Avr1b(1Q) 0.89
Avr1b(3F) 0.00
Avr1b(3Y) 1.01
Avr1b(3I) 0.84
Avr1b(3M) 0.52
Avr1b(3V) 0.89
Avr1b(3A) 0.00
Avr1b(4Q) 0.00
Avr1b(4G) 0.74
Avr1b(2M3V) 0.88
Avr1b(2L3G4T) 0.71
Avr1b(2L3T4Q) 0.56
0.66

Figure 19

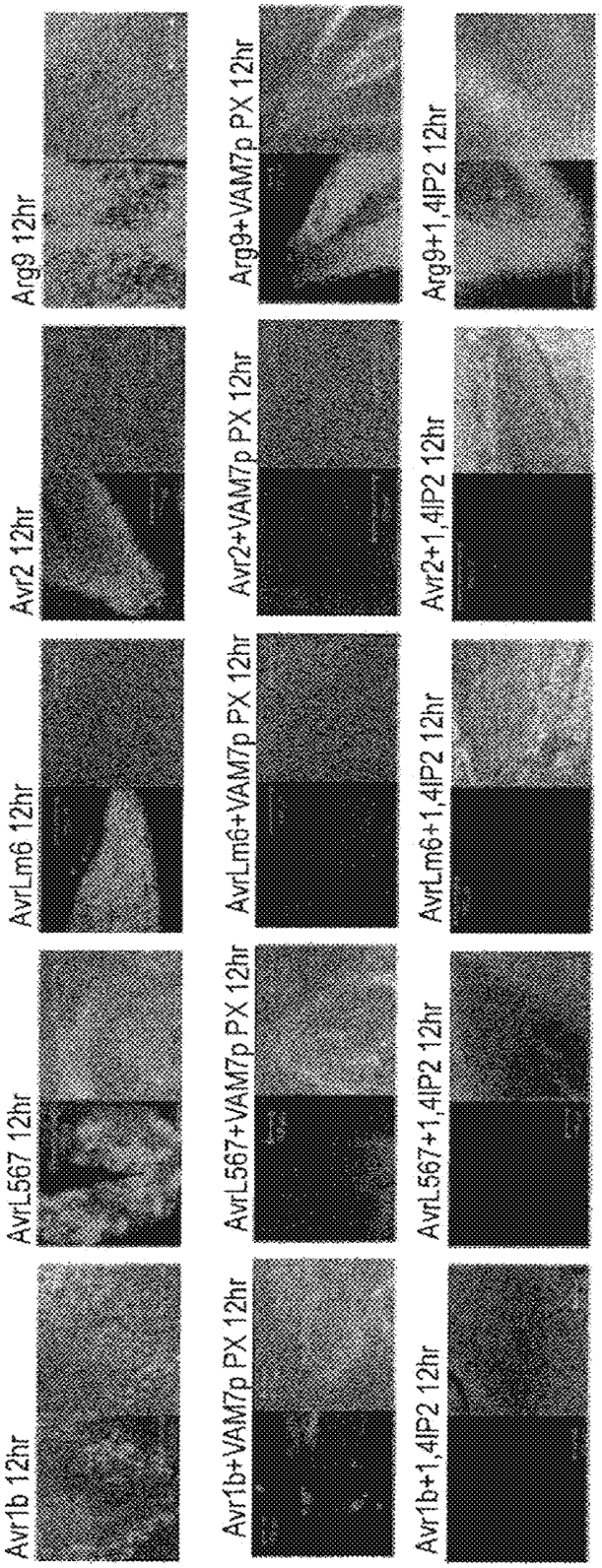

Avr1b 12hr
AvrL567 12hr
AvrLm6 12hr
Avr2 12hr
Arg9 12hr
Avr1b+VAM7p PX 12hr
AvrL567+VAM7p PX 12hr
AvrLm6+VAM7p PX 12hr
Avr2+VAM7p PX 12hr
Arg9+VAM7p PX 12hr
Avr1b+1,4IP2 12hr
AvrL567+1,4IP2 12hr
AvrLm6+1,4IP2 12hr
Avr2+1,4IP2 12hr
Arg9+1,4IP2 12hr

Figure 20A

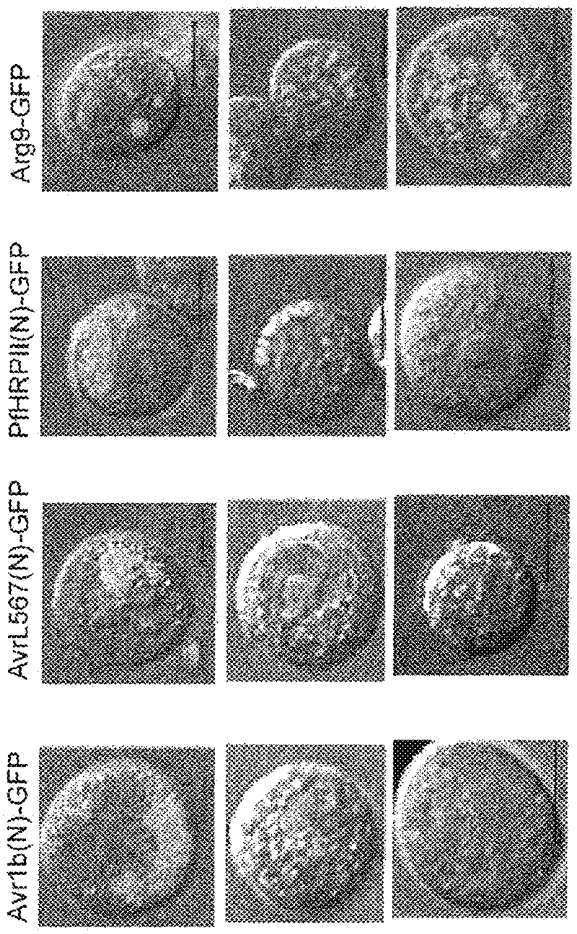


Figure 20B

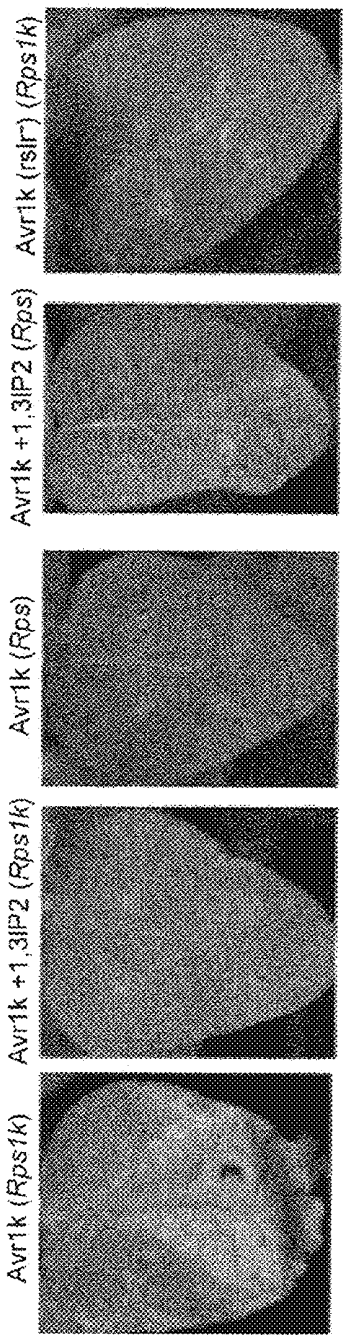


Figure 20C

COMPOSITIONS AND METHODS TO PROTECT CELLS BY BLOCKING ENTRY OF PATHOGEN PROTEINS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Patent Application Ser. No. 61/128,080, filed May 19, 2008; Ser. No. 61/160,059, filed Mar. 13, 2009; and Ser. No. 61/260,227, filed Nov. 11, 2009. This application is a continuation-in-part of U.S. patent application Ser. No. 12/468,470 filed May 19, 2009; and of International patent application PCT/US09/044,489, filed May 19, 2009. The complete contents of each of these applications are herein incorporated by reference.

STATEMENT OF GOVERNMENT INTEREST

[0002] This invention was made with funding under USDA/CSREES/NRICGP Grant No. 2007-35319-18100, and the United States government has certain rights in the invention.

SEQUENCE LISTING

[0003] This application includes as the Sequence Listing the complete contents of the accompanying text file "Sequence.txt", created Nov. 10, 2010, containing 307,236 bytes, hereby incorporated by reference.

BACKGROUND OF THE INVENTION

[0004] 1. Field of the Invention

[0005] The present invention generally relates to prevention of microbial, especially oomycete or fungal, disease and, more particularly, to cellular targets for blocking entry of pathogen effector proteins into plant or animal cells. The invention also provides compositions and methods for identifying compounds that block entry of pathogen effector proteins into cells, and treatments using such compounds.

[0006] 2. Background Description

[0007] Fungi and parasites such as *Plasmodium* are eukaryotes, which are organisms that have complex internal cell structures (bacteria and viruses have simpler structures and are excluded). Infections by parasites and fungi are especially difficult to develop drugs for because humans are also eukaryotes, so many drugs toxic to these organisms are also toxic to humans. In addition to the malaria parasite, *Plasmodium*, other eukaryotic pathogens of humans include the parasites *Schistosoma, Onchocerca, Trypanosoma*, and *Leishmania*, fungi that afflict AIDS patients such as *Candida, Histoplasma, Cryptococcus* and *Aspergillus*, and the Valley Fever fungus, *Coccidioides*, that affects healthy people in the Southwest. Fungal spores are also responsible for allergies, asthma and mold-related illnesses.

[0008] Eukaryotic pathogens of plants are also a major problem in agriculture, horticulture and forestry, and include fungi and fungal-like organisms related to marine algae called oomycetes. These diseases cause billions of dollars in losses each year. Some fungal plant pathogens include rust fungi, such as the new virulent wheat rust fungus, Ug99, that is sweeping through Africa and the middle east, and the rice blast fungus which causes major losses to the US and Asian rice crop each year. Oomycete pathogens include the late blight pathogen of potato (*Phytophthora infestans*) that causes the Irish potato famine and still causes $5 billion in losses worldwide annually, *Phytophthora ramorum* that causes Sudden Oak Death in California, and *Phytophthora sojae* that caused $1-2b damage to the US soybean crop. Worldwide transport of plants and plant products across diverse ecosystems has hastened the spread of many plant pathogens. With the increased pressure on agricultural production systems due to competing needs for food and biofuels, there is an urgent need to explore new highly efficacious strategies for biotechnology-based approaches to disease control.

[0009] Eukaryotic pathogens of both humans and plants release protein toxins called effectors that have the ability to infiltrate inside host cells, across the membrane barrier that normally surrounds the host cells. Once the effectors enter the host cell, they reprogram the cells to suppress or block the immune responses of the host and to make the host tissue more congenial for reproduction and spread of the pathogen. Therefore, drugs that could block the entry of effector proteins into host cells would potentially suppress infection by a broad range of eukaryotic pathogens important to medicine and agriculture.

[0010] Like animals, plants have evolved defense mechanisms that afford some protection from pathogens. Constitutive defenses include structures such as the cuticle and preformed anti-microbial chemicals. Plants have also evolved an active defense response that is induced by detection of an attacking pathogen. The response includes rapid synthesis of anti-microbial chemicals and proteins, and a programmed cell death (PCD) response, called the hypersensitive response (HR). The ability of plants to detect and respond to pathogens is mediated by various receptors and signal transduction pathways that have close similarities to the innate immunity mechanisms of animals. Unfortunately, however, pathogens of both plants and animals have evolved mechanisms to avoid or suppress host defenses, thereby retaining the ability to cause many destructive diseases affecting crops and forests.

[0011] Oomycetes are fungus-like organisms many of which are pathogens. For example, most of the more than 80 species of the oomycete genus *Phytophthora* are destructive pathogens, including the potato late blight pathogen, *Phytophthora infestans*, which caused the Irish potato famine in the 18th century, the soybean root and stem rot pathogen *P. sojae*, and *Phytophthora ramorum*, the causative agent of Sudden Oak Death that is currently ravishing oak forests in California. The closely related oomycete genus *Pythium* contains more than 100 species, most of which are also pathogens. The oomycetes also include a number of commercially important and diverse downy mildew pathogens that are obligate parasites, often with narrow host ranges.

[0012] The sequencing of Expressed Sequence Tags (ESTs) and genomes from several oomycete pathogens has been completed or is under way. Draft genome sequences for the soybean pathogen *Phytophthora sojae* and for *P. ramorum* have been completed; those of *P. infestans* and the *Arabidopsis* downy mildew pathogen *Hyaloperonospora arabidopsidis* are nearing completion; and genome sequencing of the broad host range plant pathogens *Phytophthora capsici* and *Pythium ultimum* and the fish pathogen *Saprolegnia parasitica* is also underway. In addition, substantial libraries of EST sequences are available for most of these species, as well as for *Phytophthora parasitica* and the Saprolegniomycete plant pathogens *Aphanomyces euteiches* and *Aphanomyces cochlioides*. The mining of these pathogen sequences by comparative genomics and the prediction of which proteins

are secreted by the pathogens has resulted in identification of large numbers of candidate genes that potentially encode proteins involved in plant infection.

[0013] Among these are the so-called "effector proteins" or "effectors". Effectors, which are secreted by plant pathogens and have the ability to enter plant cells, have been documented for many classes of plant pathogens, including bacteria, fungi, oomycetes and nematodes. Once inside a host cell, the major function of an effector protein is to suppress the signal transduction pathways that mediate plants defense responses, and many effector proteins also suppress host programmed cell death. The activities of fungal effector proteins are known to include chitin-binding, cytotoxicity, metalloprotease activity, and protease inhibition. Pathogen effectors may also reprogram the plant cell to promote nutrition of the pathogen.

[0014] In response to pathogen attacks mediated by effectors, plants have evolved certain resistance ("R") genes that encode receptor proteins having the ability to bind and sequester, and thereby inactivate, the pathogen effector proteins. (In fact, effectors were initially discovered based on their ability to trigger responses mediated by R gene-encoded host receptors). Pathogen genes encoding effectors are referred to as avirulence (Avr) genes, because, in practice, they actually prevent infection of host plants which contain cognate receptor proteins by binding to the receptor, thereby alerting the plant to their presence, and initiating an anti-pathogen response. In contrast, genes encoding plant effectors for which cognate plant receptors do not exist are referred to as virulence genes.

[0015] Genetic mapping of oomycete Avr genes led to the cloning of the first four effector genes: Avr1b-1 from *P. sojae* (Shan, W., Cao, M., Leung, D. & Tyler, B. M. The Avr1b locus of *Phytophthora sojae* encodes an elicitor and a regulator required for avirulence on soybean plants carrying resistance gene Rps1b. Mol. Plant. Microbe Interact 17, 394-403 (2004); Avr3a from *P. infestans* (Armstrong, M. R. et al. An ancestral oomycete locus contains late blight avirulence gene Avr3a, encoding a protein that is recognized in the host cytoplasm. Proc Natl Acad Sci USA 102, 7766-71 (2005); and ATR1 (Rehmany, A. P., Gordon, A., Rose, L. E., Allen, R. L., Armstrong, M. R., Whisson, S. C., Kamoun, S., Tyler, B. M., Birch, P. R., and Beynon, J. L. (2005). Differential recognition of highly divergent downy mildew avirulence gene alleles by RPP1 resistance genes from two *Arabidopsis* lines. Plant Cell 17, 1839-1850), and ATR13 (Allen, R. L., Bittner-Eddy, P. D., Grenville-Briggs, L. J., Meitz, J. C., Rehmany, A. P., Rose, L. E., and Beynon, J. L. (2004). Host-parasite coevolutionary conflict between *Arabidopsis* and downy mildew. Science 306, 1957-1960), both from *H. arabidopsidis*. Many other effector genes have subsequently been identified and analyses have shown that all effector genes encode small secreted hydrophilic proteins that lack disulfide bonds. Significantly, effector proteins have the ability to enter plant cells unaided by any other pathogen encoded molecules. Thus, the mechanism of entry must lie in the effector proteins themselves. Sequence comparisons have led to the identification of two common motifs in the N-terminus region of effector proteins: 1) RxLR or RXLR (which stands for "arginine, any amino acid, leucine, arginine"); and 2) dEER (which stands for "aspartate which is not highly conserved, glutamate, glutamate, arginine") (Birch, P. R., Rehmany, A. P., Pritchard, L., Kamoun, S., and Beynon, J. L. 2006. Trends Microbiol 14, 8-11; Tyler, 2006. Science 313, 1261-1266; Rehmany, et al. 2005. Plant Cell 17, 1839-1850). These motifs have been suspected of being responsible for the ability of effector proteins to enter plant cells. This speculation has been encouraged by the observation that a similar N-terminal "Pexel" motif (RxLxE/Q, i.e. "arginine, any amino acid, leucine, any amino acid, then aspartate or glutamate or glutamine") is required for effectors of the malaria parasite, *Plasmodium*, to cross the host parasitiphorous vacuolar membrane into the cytoplasm of red blood cells. In addition, experimental evidence has shown that mutations in either the RxLR or dEER motifs can alter an effector's ability to translocate into host cells.

[0016] Effectors of fungal plant pathogens have also been predicted to translocate into host cells because many plants (e.g. flax and rice) possess intracellular receptors, encoded by major resistance (R) genes, which mediate a rapid defense response when fungal effectors are present. However, prior to the present invention, fungal effectors had not been well characterized and the presence of amino acid sequence motifs that mediated entry into host cells had not been demonstrated.

[0017] In spite of previous suspicions concerning putative involvement of the RxLR and dEER motifs in effector translocation, the precise mode of and requirements for translocation of effector proteins were not known. And, in fact, it was previously not known whether fungal pathogens even possessed these or analogous motifs. This lack of knowledge had hindered the development of effective methods to combat the infection of both plant and animal host cells by oornycete, fungal and *Plasmodium* pathogens. Further, the lack of detailed characterization of the RxLR and dEER motifs and their flanking sequences has prevented the selection, from an enormous pool of genomic sequence data, of genes that likely encode additional effector proteins, the identification of which could lead to strategies for inhibiting their pathogenic action in cells.

SUMMARY OF THE INVENTION

[0018] The present invention provides methods to block the entry of pathogen effector proteins into host cells (e.g., "translocation"), thereby preventing host cell infection. The methods are based on the discovery that binding of polar lipids such as phosphatidyl-inositol-3-phosphate (PI-3-P) and/or phosphatidyl-inositol-4-phosphate (PI-4-P) and/or phosphatidic acid to effector molecules via a virulence motif is a prerequisite to translocation of the effector into a host cell, and that when binding is blocked, translocation, and hence infection of the cell, does not occur. The motifs have the sequence "BXZ" where B=arginine, lysine or histidine; X=any amino acid or no amino acid (i.e. X may be absent); and Z=leucine, methionine, isoleucine, tryptophan, tyrosine or phenylalanine. The BXZ motif encompasses a family of motifs, which frequently occur at or near the N-terminus of an effector protein, examples of which include but are not limited to RxLR (which may function in concert with a dEER motif), Pexel, RYWT, RIYER, RSLR, RRLLR, RRFLR, and RFYR, and others, all of which may collectively be referred to herein as "virulence motifs.

[0019] Binding may be prevented by any of several strategies including but not limited to i) blocking the effector motif itself, and ii) blocking the lipids of the cell to which the motif binds. The motif itself may be blocked by e.g. inositol 1,4-diphosphate, or by other inositol containing phosphatidic acids, phospholipids and sphingolipids, or any other compound which binds to one or the virulence motif. Blocking of

the lipid (generally at or on the cell surface) can be accomplished using, for example, proteins or peptides or other molecules that bind the lipids (e.g. mimetics of the motifs, or proteins or other compounds that destroy, remove or block access to phosphatidyl-inositol-3-phosphate (PI-3-P) and/or phosphatidyl-inositol-4-phosphate (PI-4-P) and/or phosphatidic acid and/or any other polar lipid that is bound by an effector) thereby preventing effector binding to a motif. According to the invention, the entry of effector proteins from oomycetes, fungi, and other types of pathogens, including human pathogens (e.g. *Plasmodium*) may be blocked. For example, *Plasmodium* effector proteins include a Pexel motif which is selectively bound as a prerequisite for translocation. Blocking of effector entry prevents the pathogen from inhibiting host cell defense mechanisms and allows the host to mount an effective response to the pathogen.

[0020] The invention also provides elucidation of the structural requirements of the virulence motifs in oomycetes and fungi, and of the sequences which flank the motifs, leading to the ability to predict which genes in the genome of a pathogen are likely to encode effector molecules.

[0021] According to an embodiment the invention, translocation of an effector protein from a pathogen, such as a bacteria, fungus, oomycete, protozoa or nematode, into a host including animals (including humans) and plants is prevented by selectively binding a blocking compound to one or more BXZ virulence motifs of the effector protein. According to another embodiment, translocation of an effector protein from a pathogen is prevented by selectively binding a blocking compound to one or more polar lipids which would otherwise bind an effector motif. By preventing entry of the effector protein into the cell, the host cell defense mechanisms are permitted to mount an effective defense against the pathogen (it being recognized that after entry, the effector protein would compromise the host cell defense mechanisms). Thus, the invention provides a mechanism to avoid the adverse outcomes attributed to pathogenic effector proteins, and it is applicable in promoting the health and viability of both plants and animals.

[0022] Another embodiment of the invention pertains to identifying compounds which are suitable for use in protecting cells (animal and plant) from pathogenic effector proteins. In operation, an assay is used to determine whether or not a compound binds to one or more motifs of an effector protein which are bound by phosphoinositides or another polar lipid as a prerequisite for translocation. The assay may include pathogenic effector proteins which include a BXZ motif (e.g. RxLRPexel, RYWT, RIYER, RSLR, RRLLR, RRFLR, and RFYR or similar motifs), and/or may include protein substrates which present one or more BXZ motifs in a manner which can be bound by a candidate compound. Alternatively, an assay may include one or more polar lipids which bind to the motifs, in order to identify compounds which bind and thus would block motif binding. Such assays may include competition assays between candidate compounds and compounds (e.g. peptides or proteins) which contain the motif(s). The assay may be in the solid or liquid phase and may employ fluorescent, phosphorescent, chemiluminescent, colorimetric, or other suitable labels to indicate binding of a candidate compound to one or more motifs which are required to be bound by phosphoinositides or another polar lipid as a prerequisite for translocation.

[0023] Yet another embodiment of the invention pertains to a methodology of identifying whether an amino acid sequence of a protein in a pathogen is part of an effector protein. In this embodiment, hidden Markov modeling (HMM) is used to compare flanking sequences of a BXZ sequence (e.g. of an RxLR sequence) to determine whether the structural features for the motif are present. Through identification of effector proteins, effective strategies for preventing entry of the effector proteins into a cell (animal or plant) can be pursued.

BRIEF DESCRIPTION OF THE DRAWINGS

[0024] FIG. **1**A-E. RxLR and dEER motifs are required for Avr1b function in *P. sojae* transformants. (A) Sequences of mutations in the RxLR1, RxLR2 and dEER motifs. Bold indicates amino acids of the RxLR motifs and the alanines used to replace them in the mutations. Italics indicate the dEER motif and the alanines used to replace it in the mutant. (B) Pst I restriction analysis of PCR products amplified from Avr1b-1 transformants using primers specific for the HAM34 promoter and terminator regions. Pst I restriction profiles of Avr1b(RxLR1^{AAAA}), Avr1b(RxLR2^{AAAA}), Avr1b (RxLR1^{AAAA}, 2^{AAAA}), Avr1b(dEER^{A6}) and wild type (WT) Avr1b are distinguished from each other because the mutations introduce a Pst I site. Avr1b(dEER^{A6})-9 was confirmed by sequencing the PCR product. C, Detection of Avr1b mRNA in *P. sojae* stable transformants by RT-PCR. Upper panel shows amplification with primers internal to the Avr1b C-terminus. Lower panel shows amplification with *P. sojae* actin primers. *P. sojae* stable transformants were the same as for (B) except that an amplification reaction is also shown from RNA from a *P. sojae* transformant containing a β-glucuronidase gene (GUS). No amplification was observed when reverse transcriptase was omitted from the reactions. (D) Distributions of HMM scores of RxLR flanking regions for all RxLR-containing secreted proteins from *P. sojae* and *P. ramorum* (non-permuted), for all secreted proteins retaining an RxLR string after sequence permutation (permuted), and for all high quality RxLR-effector candidates identified by Jiang et al (2008) (curated). The locations on the distribution of the HMM scores of the RxLR strings of known avirulence proteins and HpAvh341 are shown by the arrows. (E) Phenotype of L77-1863 (Rps1b) seedlings inoculated on the hypocotyls with transformants carrying the indicated wild type or mutant Avr1b-1 genes and photographed 4 days later.

[0025] FIG. **2**. RxLR and dEER functions confirmed by particle bombardment assay. Soybean leaves were bombarded using a double-barreled device that delivered Avr1b-1 DNA-bearing particles to one side of the leaf and control (empty vector) DNA to the other; both sides received GUS DNA. Ratio of blue spots in the presence of Avr1b-1 compared to the control. sAvr1b indicates a gene encoding secretory Avr1b and mAvr1b indicates one encoding mature Avr1b (lacking the secretory leader). WT indicates wild-type RxLR motif, RxLR2^{AAAA} indicates the four alanine replacement of the RxLR2 motif, dEERA6 indicates the six alanine replacement of the dEER motif. Averages and standard errors are from 16 pairs of shots. p values comparing results from cultivars with Rps1b (L77-1863) or without (rps; Williams) were calculated using the Wilcoxon rank sum test.

[0026] FIG. **3**A-D. *P. sojae* stable transformants show that two other Avh proteins can replace the RxLR and dEER region of Avr1b. (A) Sequences of the N-termini of wild type and mutant Avr1b proteins, and of fusions with two other Avh proteins. Underlined, secretory leader; bold, RxLR motifs; italics, dEER motifs. The C-terminal sequence of Avr1b is

shown in lowercase. (B) PCR analysis of DNA from *P. sojae* stable transformants. WT: p1=pHamAvr1b plasmid DNA, T17 and T20=two transformants with wild type Avr1b-1 transgenes. HpAvh341-Avr1bCt: p1=pHamAvh341 plasmid DNA (encoding Hp Avh341-Avr1bCt), 13 and 17=two transformants containing pHamAvh341. PsAvr4/6-Avr1bCt: pHamAvh171 plasmid DNA (encoding Ps Avr4/6-Avr1bCt), 3 and 19=two transformants containing pHamAvh171. mAvr1bCt: p1=pHamAvr1bCt plasmid DNA (encoding mAvr1bCt protein), 4 and 5=two transformants containing pHamAvr1bCt. The sizes of the PCR products for Avr1b-1, pHamAvh341, pHamAvh171 and pHamAvr1bCt are 577 bp, 721 bp, 748 bp and 385 bp respectively C, Detection of Avr1b mRNA in *P. sojae* stable transformants by RT-PCR. Upper panel shows amplification with primers internal to the Avr1b C-terminus. Lower panel shows amplification with *P. sojae* actin primers. *P. sojae* stable transformants were the same as for (B) except that an amplification reaction is also shown from RNA from a *P. sojae* transformant containing a β-glucuronidase gene (GUS). p1=pHamAvr1b plasmid DNA as template. No amplification was observed when reverse transcriptase was omitted from the reactions (D) Phenotype of L77-1863 (Rps1b) seedlings inoculated on the hypocotyls with the indicated transformants carrying wild type or mutant Avr1b-1 genes and photographed 4 days later. HpAvh341-Avr1b-17, PsAvr4/6-Avr1b-3 and mAvr1bCt-5 gave similar results to HpAvh341-Avr1b-13, PsAvr4/6-Avr1b-19 and mAvr1bCt-4 (Table 1).

[0027] FIGS. **4**A and B. Functional replacement of Avr1b host targeting signal with protein transduction motifs and *Plasmodium* host targeting signals. (A) Sequences of modified Avr1b proteins. PfGBP, PfHRP and Pf1615c refer to the *Plasmodium* Pf GBP-130, Pf HRPII and Pf PFE1615c proteins. All non-native Avr1b sequences are underlined, Avr1b RxLR2 and *Plasmodium* RxLXE/Q motifs are in bold, and acidic residues in the dEER region are in italics. The Avr1b secretory leader was used in all constructs. (B) Ratio of blue spots in the presence of Avr1b-1 compared to the control, assayed as described in FIG. **2**. Constructs are as in (A). Averages and standard errors are from 8 pairs of shots.

[0028] FIG. **5**. Summary of Avr1b-1 mutations and their phenotypes in *P. sojae* stable transformants and soybean transient expression assays. A, Avirulent; V, Virulent; NT, Not Tested; Y, significantly fewer blue (GUS-positive) tissue patches from GUS expression resulting from Avr1b-induced cell death; N, not significantly fewer blue tissue patches; P, partial reduction in blue tissue patches; SP, signal peptide.

[0029] FIGS. **6**A-H. Binding of oomycete effector proteins to phosphoinositides. a-c, Filter-binding assays. d-f, Liposome binding assays. RxLR and dEER mutations are described in FIGS. **6**G and H. (N)-GFP indicates a fusion of the N-terminal domain to GFP. (FL)-GST indicates a fusion of the full length effector proteins (without signal peptide) to GST. In d-f, B and F indicate liposome-bound and -free proteins respectively; M=size markers. PI-3-P=phosphatidylinositol-3-phosphate; PI-4-P=phosphatidyl inositol-4-phosphate; PI-5-P=phosphatidyl inositol-5-phosphate; PI=phosphatidyl inositol; PA=phosphatidic acid; PS=phosphatidyl serine; PE=phosphatidyl ethanolamine; PC=phosphatidyl choline. No mutant proteins bound to PI-5-P, PT, PA, PS, PE or PC (not shown).

[0030] FIGS. **7**A-C. Identification of host-targeting signals in fungal effectors a, Particle bombardment cell re-entry assays of fungal effectors fused to Avr1b. N-terminal sequences of AvrL567, AvrM and AvrPi-ta (shown in b) were fused to the secretory leader (s) and C-terminal domain of Avr1b. AvrL567-Avr1b fusions lacking the secretory leader (m) or with mutations in the putative RxLR and dEER motif (rfyr-de-) were also assayed. Effector re-entry resulting in cell killing was measured by double-barreled particle bombardment in which parallel bombardments with a beta-glucuronidase (GUS) reporter gene, with and without the Avr1b fusion, were compared in the presence of resistance gene Rps1b (cultivar L77-1863) or in its absence (rps; cultivar Williams). Averages and standard errors shown are from 14-16 pairs of bombardments. P values were calculated using the Wilcoxon rank sum test. b, N-terminal sequences of effectors tested in a, with RXLR-like motifs shaded and dEER-like motifs underlined. The start of the Avr1b C-terminal domain used for all fusions is boxed. Three sequences containing potential motifs from AvrPi-ta and one from AvrL567 were inserted into Avr1b in place of the RFLR motif. Cell entry activity of each sequence is given as relative ablation. Ablation=[1−(GUS+spots on Rps1b)/(GUS+spots on rps)]. Relative ablation=ablation of construct/ablation of wild-type Avr1b. In the sequence alignment, dashes indicate identical residues, periods indicate gaps in the alignment and * * * * indicates Avr1b sequences.

[0031] FIGS. **8**A-F. Binding of *P. falciparum* effector fusion proteins to phosphoinositides a-c, Filter binding assays Mutant proteins did not bind to PI-5-P, PI, PA, PS, PE or PC (not shown) except PfGBP(N)-GFP(pexel-) which bound weakly to PS. d-f, Binding of wild-type and mutant fusion proteins to PT-3-P or PI-4-P in liposomes; B and F indicate liposome-bound and -free proteins respectively; M=size markers.

[0032] FIGS. **9**A-D. Modulation of effector entry into root cells by phosphoinositides a, Stimulation of Avr1b(N)-GFP entry by PI-4-P and inhibition by IP2. b, Stimulation of AvrL567(N)-GFP entry by PI-4-P and inhibition by IP2. c, Entry of Arg9-GFP is not stimulated by PI-4-P nor inhibited by IP2. In each case, 1 mg/ml protein was incubated with soybean root tips for 9 hr or 12 hr then washed and photographed. Either 250 μM di-octanoyl-PI-4-P or 500 μM IP2 was preincubated with the proteins for 30 min prior to exposure to the roots. Paired light micrographs and fluorescence optical sections are from the same root tips in each case. Lighting and photographic exposure were identical for all photographs. d, Inhibition of effector-binding to liposomes by IP2. Binding of Avr1b(N)-GFP, AvrL567(N)-GFP and Arg9-GFP to liposomes containing PI-4-P was measured in the presence or absence of 300 μM inositol 1,4 diphosphate (1,4IP2). Also, binding of Arg9-GFP to liposomes containing PI-3-P was measured in the presence or absence of 300 μM inositol 1,3 diphosphate (1,3IP2).

[0033] FIGS. **10**A-E. Effector entry into human cells and inhibition by inositol diphosphates a-d, Cells of the human lung epithelial cell line A549 were incubated with the indicated fusion proteins (1 mg/ml) for 15 hr, in the presence or absence of 430 μM inositol 1,3 diphosphate (1,3IP2), 440 μM inositol 1,4 diphosphate (1,4IP2) or 240 μM dioctanoyl-PI-4-P, then washed and photographed. Paired light micrographs and fluorescence optical sections are from the same cells in each case. Lighting and photographic exposure were identical for all photographs.

[0034] FIGS. **11**A-B. Description of plasmids used in Example 1.

[0035] FIGS. **12**A-B. Oligonucleotides used for plasmid construction. Uppercase letters indicate bases that match the initial template. Lower case letters indicate mutations or 5' extensions that do not match the initial template. Restriction sites introduced into the amplicon are underlined. A pipe (|) indicates the boundary between Avr1b-1 sequences and fused sequences (Avh, GFP or *Plasmodium* RXLX motif) in the fusion oligonucleotides.

[0036] FIGS. **13** A-F. Description of plasmids used in Example 2.

[0037] FIG. **14**A-F. Oligonucleotides used. Restriction sites are in bold. Mutations created by the primers are in lower case.

[0038] FIG. **15**. Binding of fungal effector proteins to phosphatidic acid shown in tabular form. Filter-binding assay were used to test which polar lipids were bound bind by the indicated fungal effector proteins. The N-terminus of each fungal effector (documented in the sequence list) was fused to GFP, the fusion proteins were purified from *E. coli*, and then tested for binding to the same polar lipids as documented in FIG. **6**. Mutant proteins contained amino acid substitutions in the motifs listed in the row above (A=alanine; S=serine). All the wild-type proteins listed bound phosphatidic acid, but none of the mutants did.

[0039] FIG. **16**A-D. Effectors from non-haustorial fungal pathogens enter via RXLR-mediated PI-3-P binding. A. N-terminus of AvrLm6 (SEQ ID NO: 319) showing functional and non-functional RXLR motifs. 1 mg/mL GFP fusion proteins were incubated with soybean root cells for 12 hr then washed for 2 hr. B. N-terminus of Avr2 (SEQ ID NO: 326) showing functional and non-functional RXLR motifs. 1 mg/mL GFP fusion proteins were incubated with soybean root cells for 12 hr then washed for 2 hr. C. Binding of AvrLm6-GFP to lipids in filter-(left) and liposome-(right) binding assays. D. Binding of Avr2-GFP to lipids in filter-(left) and liposome-(right) binding assays. In both C and D lipids are: PI phosphatidyl (ptd)-inositol; C1P=ceramide-1 phosphate; LPA=lysophosphatidic acid; PA=phosphatidic acid; PS=ptd-serine; PE=ptd-ethanolamine; PC=ptd-choline. In the liposome assays (right panels), B=bound; F=free; M=markers.

[0040] FIGS. **17**A and B. Binding of three fungal effectors to phosphoinositides. A. N-terminal sequences of effector-like proteins Af2 from *Aspergillus fumigatus* (Af2; XP 752996.1), CNg2 from *Cryptococcus neoformans* (Cng2; AAW43853.1) and AvrLm4/7 from *Leptosphaeria macularis*. Candidate RXLR-like motifs are boxed. B. Sequences shown in A were fused to GFP and the expressed proteins tested for lipid binding using filter-binding assays as described in FIG. **16**D.

[0041] FIG. **18**A-D. PI-3-P is located on the surface of root cells and epithelial cells, but not erythrocytes A. Binding of biosensors to phosphoinositides in filter assays, as described for FIG. **16**. B. Binding of biosensors to root cells. Fusion proteins were incubated with soybean root cells for 12 hr then washed for 2 hr. Pairs of fluorescence and light micrographs are shown. Bars=50 μM or 100 μM. C. Binding of biosensors to epithelial cells. Fusion proteins were incubated with cells for 2 hr then washed for 30 min. Pairs of fluorescence micrographs and fluorescence/light overlays are shown. Bars=10 μM. D. Binding of biosensors to human erythrocytes. Fusion proteins were incubated with cells for 2 hr then washed for 30 min. Two independent fluorescence/light overlays are shown. Bars=20 μM.

[0042] FIG. **19**. Mutations of the Avr1b peptide (SEQ ID NO: 305) containing the RXLR motif assayed using the double barrel particle bombardment assay. Cell entry activity measured as cell death in the presence of Rps1b relative to wild-type Avr1b. Dashes indicate identical residues; ● ● ● ● indicates Avr1b sequences.

[0043] FIG. **20**A-C. PI-3-P binding proteins and inositol diphosphate block effector entry A. Blocking binding of effector-GFP fusions into root cells. Fusion proteins were incubated with soybean root cells for 12 hr then washed for 2 hr. Inositol 1,4 diphosphate (500 μM) was preincubated with the fusion proteins for 30 min. 5 mg/ml VAMp7 PX proteins was preincubated with the roots for 2 hr. Pairs of fluorescence and light micrographs are shown. Bars=100 μM. B. Binding of biosensors to epithelial cells. Fusion proteins were incubated with cells for 2 hr then washed for 30 min. Inositol 1,4 diphosphate (500 μM) was preincubated with the fusion proteins for 30 min. 5 mg/ml VAMp7 PX proteins was preincubated with the cells for 2 hr. Overlays of fluorescence and light micrographs are shown. Bars=10 μM. C. Full-length Avr1k protein, with or without the RXLR mutation, was produced in *E. coli*. 0.25 mg/mL protein was infiltrated into the primary unifoliate leaves of 13 day old seedlings of cultivars Williams (no rps gene) or Williams 82 (Rps1k). Where indicated, the protein was co-infiltrated with 500 χM 1,3IP2. The plants leaves were photographed 5 days after infiltration.

DETAILED DESCRIPTION

[0044] Since many resistance genes against oomycetes encode intracellular proteins, and since several cognate oomycete avirulence genes encode secreted proteins, it has been inferred that there must be a mechanism for translocating the avirulence proteins into the plant cells. Since the RxLR and dEER motifs were first identified during the *Phytophthora* genome sequence annotation, there has been extensive speculation that these motifs are involved in transporting avirulence proteins into host cells. Importantly, proteins in this family use the N-terminal motifs RxLR and dEER to cross the host plasma cell membrane autonomously, i.e. no other proteins are necessary to effect this translocation. Once inside the host cell, the proteins suppress host defense signaling. The importance of this effector family is underlined by the fact that plants have evolved intracellular defense receptors to detect the effectors and trigger a rapid counter-attack.

[0045] The present invention establishes that effectors of fungal plant pathogens contain virulence motifs with consensus sequence BXZ, where B is R, K or H; X is any amino acid and may be absent; and Z is a hydrophobic amino acid, generally L, M, I, W, Y or F. The sequence BXZ represents three contiguous amino acids, or two contiguous amino acids is X is absent. The BXZ family of motifs includes exemplary motifs such as RxLR (which may function with a dEER motif, an exemplary RxLR motif being RSLR) and related functional variants thereof (e.g. RRFLR, RRFLR), as well as exemplary motifs RFYR, RYWT, RIYER, etc). The virulence motifs are responsible for binding of the pathogen effector proteins to polar lipids (e.g. phosphatidyl-inositol-3-phosphate (PI-3-P) and/or phosphatidyl-inositol-4-phosphate (PI-4-P) and/or phosphatidic acid) at or near the surface of a host cell. Stimulation of host cell entry by, for example, PI-4-P, and inhibition by inositol 1, 4 diphosphate suggests that the binding of effectors to polar lipids (such as phosphoinositides, phospholipids and sphingolipids) mediates cell entry of the effectors. All effectors that were tested could also enter

human cells, suggesting that this mode of effector entry may be very widespread in plant and animal (including human) pathogenesis, including that which utilizes the *Plasmodium* Pexel ("P") motif. Identification of this broad spectrum of effectors containing virulence motifs thereof constitutes a novel target class, and raises the possibility of targeted blockade of pathogen effector proteins. This knowledge can be exploited to develop new classes of antibiotic treatments to prevent a wide variety of pathogenic fungal, Plasmodial and oomycete infections in plants and animals.

[0046] The invention also identifies the sequence requirements for the function of the virulence motifs and/or domains. With respect to the BXZ motif, it has been determined that generally only the presence of arginine, lysine or histidine at the first position and the presence of leucine, isoleucine, methionine, tyrosine, phenylalanine or tryptophan at the third position are required to enable function. However, in some embodiments, methionine or leucine at the second position may allow function if none of leucine, isoleucine, methionine, tyrosine, phenylalanine or tryptophan are present at the third position. In some embodiments, the sequences flanking the motifs are required for function. As used herein the term "domain", in some embodiments, refers to a region or regions of the primary sequence of an effector protein containing more than one virulence motif, e.g. both the RxLR and dEER motifs, or one or more analogous virulence motifs as described herein. The sequence requirements can be defined by a hidden markov model. For example, mutational analysis of the RxLR motif shows that, in some embodiments, the requirement for the first and third positions are quite strict. Furthermore, reversing the order of residues 1 and 2 or of 3 and 4 also abolishes activity, indicating that the mere presence of positive charge and hydrophobicity within the motif are insufficient. The arginine at position 4 is more flexible and can be replaced by lysine or glutamine. Naturally occurring functional variants of RxLR include lysine, histidine, threonine, glycine and alanine at the fourth position.

[0047] As a result of these findings, the invention provides methods to inhibit the entry, into a host cell, of effector proteins expressed by pathogens and containing the virulence motifs. The method is carried out by blocking the interaction, for example, by the binding of the motifs to a natural ligand such as a polar lipid, exemplified by phospholipids (e.g. phosphoinositides) and/or sphigolipids. Blocking may be accomplished by any of several means, for example, by exposing one or more virulence motifs to one or more molecules or molecular species which are capable of binding to or otherwise interacting with the virulence motifs, thus preventing the polar lipid (e.g. phosphoinositide, phospholipid or sphingolipid) from binding to the virulence motif. Herein, molecular species such as phosphoinositides, phospholipids and/or sphigolipids which, in nature, bind to one or more motifs of an effector molecule as described herein, causing the effector protein to translocate into the targeted host cell, may be referred to as "natural molecules" or "natural ligands" of the motif. Conversely, the motifs disclosed herein may be considered "natural ligands" of the polar lipids to which they bind. These designations distinguish them from the blocking molecules of the invention, which are added exogenously to cells and used to prevent binding of the natural ligands to the motifs, thereby preventing translocation of the effector protein into the cell. The blocking molecules may or may not be molecules that occur in nature, but if they are, then when used in the present invention, they are isolated or substantially purified, or chemically synthesized.

[0048] Blocking molecules of choice include but are not limited to lipid-derived molecules which bind to the motif but not in a manner that results in entry of the effector protein into the cell, e.g. molecules that are sterically related to natural ligands but which do not comprise all requisite properties for enabling translocation of the effector. In other embodiments, the blocking molecules are inositol or inositol derivatives (e.g. various phosphorylated inositols such as inositol monophosphate, various inositol diphosphates such as inositol 1, 4 diphosphate, and other similar molecules); or peptides that bind to the motif and block access to the motif by natural ligands; or peptides that bind to the motif and target the effector for protease degradation; or peptides that bind to the motif and anchor the effector to an external structure such as a cell wall or cell matrix such that the effector cannot enter the cell; or molecules that bind to the motif and cause chemical modification of the effector so that it can no longer enter cells; or other "small molecule" compounds that possess the geometric and charge requisites for binding to one or more of the motifs, thereby blocking the binding of the natural ligand that is responsible for effector translocation.

[0049] In one embodiment of the invention, the blocking molecule is a peptide, in particular a peptide with an amino acid primary sequence that is designed to include amino acid residues with charges suitable for interacting with and/or binding to the charged residues of the motif. In such a peptide, the amino acid sequence is designed so that charged atoms or groups (especially of the side chains) are spatially arranged in a manner that allows, for example, negatively charged side chains to be within bonding distance of positively charged side chains of e.g. R residues of the motif, or for aliphatic side chains of the peptide to interact with aliphatic side chains of the motif, etc. Approaches to synthetic peptide design are described, for example, by Devlin et al. (Devlin, H., Panganiban, L. C. and Devlin, P. E. (1990) Random peptide libraries: a source of specific protein binding molecules. Science, 249, 404-406) and Scott and Smith (Scott, J. K. and Smith, G. P. (1990) Searching for peptide ligands with an epitope library. Science, 249, 386-390). Such peptides may be designed to be stable by e.g. by avoiding the use of known protease cleavage sites in the sequence; by introducing various non-natural amino acids; or by various modifications to amino acids (e.g. amidation, sulfonation, etc.) that increase the stability of the molecule, so long a such modifications do not interfere with binding to the effector motif.

[0050] The binding or interaction of the blocking molecule (s) may be of any suitable type, and will depend on the nature of the blocking molecule. For example, the binding may be covalent and hence essentially irreversible. Thus, in some embodiments of the invention, the blocking molecule is one that, upon contact with one or more chemically reactive functional groups of the motif or polar lipid, forms a covalent bond with the one or more functional groups that participate in binding, or with functional groups of adjacent portions of the molecule (e.g. adjacent residues of and effector protein) in a manner that blocks access to the motif (e.g. by phospholipids and/or sphingolipids that are natural ligands of the motif) and/or to the polar lipid, which would otherwise permit translocation of the effector into the host cell that the pathogen is trying to infect. Usually, however, the binding is non-covalent and comprises, for example, electrostatic and/or charge interactions, hydrophobic interactions, van der Waals interactions,

etc. For a blocking molecule to be effective, a Kd better than ten-fold less than the concentration of the competing natural ligand (polar lipid or motif) in the region of the host membrane is preferred (a lower Kd indicates tighter binding). In this manner, binding of the natural ligand is prevented or at least attenuated or slowed so as to render the natural ligands ineffective in enabling the effector molecule to enter the targeted host cell, and infection of the host by the pathogen which manufactured the effector molecule is prevented, or attenuated or slowed. Those of skill in the art will recognize that much benefit can accrue from a treatment that inhibits a pathogen, even if inhibition is not absolute, but merely attenuates or slows the symptoms of infection. "Inhibition" or "prevention of infection" as used herein is intended to encompass all such degrees of inhibition, blocking, etc. In addition, in the case of plants, the overall biomass of harvested plants or plant products, and therefore the usefulness of the crop, may be advantageously increased even if some plants remain affected by the pathogen after treatment as described herein.

[0051] "Motifs" to which natural ligand binding is blocked include BXZ motifs as described herein, as well as RxLR motifs, dEER motifs, the Pexel motif, and the RYWT, RIYER, RSLR, RRLLR, RRFLR, and RFYR motifs. Those of skill in the art will recognize that many effector proteins contain both an RxLR motif and a dEER motif, or one or more virulence motifs as described herein. According to the invention, in one embodiment, the binding of a blocking molecule (which in some embodiments may be a natural ligand such as a phospholipid or sphingolipid) to one or more (e.g. either one or the other, or both, of the RxLR and dEER motifs) is blocked, and blocking occurs in a manner that prevents the effector protein that bears the motif(s) from entering the host cell. In another embodiment, the binding of a natural ligand to a Pexel motif is blocked, and blocking occurs in a manner that prevents the effector protein that bears the motif from entering a host cell. In another embodiment, the binding of a natural ligand to a RYWT, RIYER, RSLR, RRLLR, RRFLR, and/or RFYR motif is blocked, and blocking occurs in a manner that prevents the effector protein that bears the motif from entering a host cell. In some embodiments, the blocking molecule binds to or interacts directly with residues of one or more of the virulence motifs, if two or more virulence motifs are present in an effector. However, this need not always be the case, as binding to a single motif may be sufficient. In other embodiments, the blocking molecule (or molecules) binds to or interacts with adjacent residues. "Adjacent residues" may, but need not necessarily be, adjacent in primary sequence to the motif. They may also be in proximity due to the secondary or tertiary structure of the effector molecule. For example, in one embodiment, the effector protein comprises an RXLR motif followed by at least one aspartate or one glutamate residue within a 60 amino acid carboxy terminal flanking sequence. In other words, within the effector protein, the sequence which is attached directly to the carboxy terminus of the RxLR motif (which, in primary sequence, follows immediately after the carboxyl terminal R of the motif) contains at least one aspartate residue and/or at least one glutamate residue within the first 60 amino acids of the sequence.

[0052] In addition, the RxLR motifs that are targeted for blocking by the methods of the invention include but are not limited to those which comprise at least one of a two or three amino acid sequence selected from the group consisting of: arginine, any amino acid, leucine; histidine, any amino acid, leucine; lysine, any amino acid, leucine; arginine, any amino acid, isoleucine; histidine, any amino acid, isoleucine; lysine, any amino acid, isoleucine; arginine, any amino acid, methionine; histidine, any amino acid, methionine; lysine, any amino acid, methionine; arginine, any amino acid, tyrosine; histidine, any amino acid, tyrosine; lysine, any amino acid, tyrosine; arginine, any amino acid, phenylalanine; histidine, any amino acid, phenylalanine; lysine, any amino acid, phenylalanine; arginine, any amino acid, tryptophan; histidine, any amino acid, tryptophan; lysine, any amino acid, tryptophan; arginine, any amino acid, valine; histidine, any amino acid, valine; lysine, any amino acid, valine; arginine, leucine; histidine, leucine; lysine, leucine; arginine, isoleucine; histidine, isoleucine; lysine, isoleucine; arginine, methionine; histidine, methionine; lysine, methionine; arginine, tyrosine; histidine, tyrosine; lysine, tyrosine; arginine, phenylalanine; histidine, phenylalanine; lysine, phenylalanine; arginine, tryptophan; histidine, tryptophan; lysine, tryptophan; arginine, valine; histidine, valine; and lysine, valine. In some embodiments, the R of the RxLR motif is preceded by R, i.e. the motif is RRxLR, with "x" being any amino acid, or in particular L or F. These particular sequence may be represented by standard conventions using the single letter abbreviation for the amino acid and an "x" for the variable residue, e.g. as RXL for "arginine, any amino acid, leucine".

[0053] In addition, blocking may be accomplished by exposing one or more of the polar lipids to which the motifs bind (i.e. "target lipids") to one or more molecules or molecular species which are capable of binding to or otherwise interacting with the targeted polar lipid, thus preventing the motif (and hence the effector molecule) from binding to the polar lipid. In this embodiment, blocking molecules include but are not limited to: peptides, proteins, and other molecules which bind the polar lipid(s), for example, peptide mimetics of one or more effector motifs, small molecules or drugs which bind the polar lipids, various charged species which bind to the polar lipids, etc. The blocking molecule may bind to the natural target lipid (e.g. phosphoinositide, phospholipid, sphingolipid or other polar lipid) in order to block the binding of the effector to its target. In one embodiment the blocking molecule may be a naturally occurring protein that binds to the target lipid, such as a protein containing, for example, a C1, C2, PH, FYVE, PX, ENTH, ANTH, BAR, FERM, PDZ, and tubby domains (Stahelin, R. V. (2009). Lipid binding domains: more than simple lipid effectors. Lipid Res 50 Suppl, S299-304). In another embodiment, the blocking molecule may be a peptide with an amino acid primary sequence that is designed to include amino acid residues with charges suitable for interacting with and/or binding to the target phosphoinositide, phospholipid or sphingolipid. In yet another embodiment, the blocking molecule may be a polypeptide (e.g. a peptide, polypeptide, etc.) which includes one or more motif sequences and/or is a mimetic of one or more motif sequences. Blocking molecules that target the polar lipid ligands of the motif may bind to any portion of the lipid that prevents effector binding, or even to adjacent molecules or cellular components that sterically interfere with motif-lipid binding.

[0054] The host cells that are protected from effector protein invasion include many species of plant and animal cells, including human cells. Examples of plant cells that can benefit from the practice of the invention include but are not limited to: wheat, maize, rice, sorghum, barley, oats, millet,

soybean, common bean (e.g. *Phaseolus* species), green pea (*Pisum* species), cowpea, chickpea, alfalfa, clover, tomato, potato, tobacco, pepper, egg plant, grape, strawberry, raspberry, cranberry, blueberry, blackberry, hops, walnut, apple, peach, plum, pistachio, apricot, almond, pear, avocado, cacao, coffee, tea, pineapple, passionfruit, coconut, date and oil palm, citrus, safflower, carrot, sesame, common bean, banana, citrus (e.g. orange, lemon, grapefruit), papaya, macadamia, guava, pomegranate, pecan, *Brassica* species (canola, cabbage, cauliflower, mustard etc), cucurbits (pumpkin, cantaloupe, squash, zucchini, melons etc), cotton, sugar cane, sugar beets, sunflower, lettuce, onion, garlic, ornamental cut flowers, grasses used in lawns, athletic fields, golf courses and pastures (e.g. *Festuca, Lolium, Zoysia, Agrostis, Cynodon, Dactylis, Phleum, Phalaris, Poa, Bromua* and *Agropyron* species), etc.

[0055] Examples of animal cells that may benefit from the practice of the invention include but are not limited to: humans, cattle, sheep, pigs, goats, horses, cats, dogs, chickens, turkeys, bees, salmon, trout, bass, catfish, shellfish, crayfish, lobsters, shrimp, crabs, etc.

[0056] Many types of invasive pathogens may be targeted and their effector proteins prevented from entering host cells by the methods of the invention. Examples of such pathogens include but are not limited to: any *Phytophthora* species, e.g. *Phytophthora infestans, Phytophthora sojae, Phytophthora ramorum, Phytophthora parasitica, Phytophthora capsici, Phytophthora nicotianae, Phytophthora cinnamomi, Phytophthora cryptogea, Phytophthora drechsleri, Phytophthora cactorum, Phytophthora cambivora, Phytophthora citrophthera, Phytophthora citricola, Phytophthora megasperma, Phytophthora palmivora, Phytophthora Megakarya, Phytophthora boehmeriae, Phytophthora kernoviae, Phytophthora erythroseptica, Phytophthora fragariae, Phytophthora heveae, Phytophthora lateralis, Phytophthora syringae; any Pythium* species, e.g. *Pythium ultimum, Pythium aphanidermatum, Pythium irregulare, Pythium graminicola, Pythium arrhenomanes, Pythium insidiosum*; any downy mildew species; any *Peronospora* species, e.g. *Peronospora tabacina, Peronospora destructor, Peronospora sparsa, Peronospora vicaie*; any *Bremia* species, e.g. *Bremia lactucae*; any *Plasmopora* species, e.g. *Plasmopora viticola, Plasmopara halstedii*; any *Pseudoperonospora* species, e.g. *Pseudoperonospora cuhensis, Pseudoperonospora humuli*; any *Sclerospora* species e.g. *Sclerospora graminicola*; any *Peronosclerospora* species, e.g. *Peronosclerospora philippinesis, Peronosclerospora sorghi, Peronosclerospora sacchari*; any *Sclerophthora* species, e.g. *Sclerophthora rayssiae, Sclerophthora macrospora*; any *Albugo* species, e.g. *Albugo candida*; any *Aphanomyces* species, e.g. *Aphanomyces cochlioides, Aphanomyces euteiches, Aphanomyces invadans*; any *Saprolegnia* species, e.g. *Saprolegnia parasitica*; any *Achlya* species; any rust fungi; any smut fungi; any bunt fungi; any powdery mildew fungi; any *Puccinia* species, *Puccinia striiformis, Puccinia graminis, Puccinia triticina* (syn. *Puccinia recondita*), *Puccinia sorghi, Puccinia schedonnardii, Puccinia cacabata*; any *Phakopsora* species, e.g. *Phakopsora pachyrhizi, Phakopsora gossypii*; any *Phoma* species, e.g. *Phoma glycinicola*; any *Ascochyta* species, e.g. *Ascochyta gossypii*; any *Cryphonectria* species, e.g. *Cryphonectria parasitica*; any *Magnaporthe* species, e.g. *Magnaporthe oryzae*; any *Gaeumannomyces* species, e.g. *Gaeumannomyces graminis*; any *Synchytrium* species, e.g. *Synchytrium endobioticum*; any *Ustilago* species, e.g. *Ustilago maydis, Ustilago tritici, Ustilaginoidea virens*; any *Tilletia* species, e.g. *Tilletia indica, Tilletia caries, Tilletia foetida, Tilletia barclayana*; any *Erysiphe* species, e.g. *Erysiphe necator* (formerly *Uncinula necator*); any *Blumeria* species, e.g. *Blumeria graminis; Podosphaera oxyacanthae*; any *Alternaria* species, e.g. *Alternaria alternata*; any *Botrytis* species, e.g. *Botrytis cinerea*; any *Diaporthe* species, e.g. *Diaporthe phaseolorum*; any *Fusarium* species, e.g. *Fusarium graminearum, Fusarium oxysporum* (e.g. f.sp. *lycopersici*), *Fusarium moniliforme, Fusarium solani*; any *Leptosphaeria* species, e.g. *Leptosphaeria maculans, Leptosphaeria maydis*; any *Macrophomina* species, e.g. *Macrophomina phaseolina*; any *Monilinia* species, e.g. *Monilinia fructicola*; any *Mycosphaerella* species, e.g. *Mycosphaerella graminicola, Mycosphaerella fijiensis, Mycosphaerella tassiana, Mycosphaerella zeae-maydis*; any *Phialophora* species, e.g. *Phialophora gregata*; any *Phymatotrichopsis* species, e.g. *Phymatotrichopsis omnivora*; any *Taphrina* species, e.g. *Taphrina deformans*; any *Aspergillus* species, e.g. *Aspergillus flavus, Aspergillus parasiticus, Aspergillus famigatus*; any *Verticillium* species, e.g. *Verticillium dahliae, Verticillium albo-atrum, Rhizoctonia solani, Ophiostoma ulmi* (syn. *Ceratocystis ulmi*), *Ophiostoma novo-ulmi*; any *Septoria* species, e.g. *Septoria avenae*; any *Pyrenophora* species, e.g. *Pyrenophora tritici-repentis*; any *Colletotrichum* species, e.g. *Colletotrichum graminicola*; any *Sclerotinia* species, e.g. *Sclerotinia sclerotiorum*; any *Sclerotium* species, e.g *Sclerotium rolfsii*; any *Thielaviopsis* species, e.g *Thielaviopsis basicola*; any *Coccidioides* species, e.g. *Coccidioides immitus*; any *Paracoccidioides* species, e.g. *Paracoccidioides braziliensis*; any *Pneumocystis* species, e.g. *Pneumocystis carinii*; any *Histoplasma* species, e.g. *Histoplasma capsulatum*; any *Cryptococcus* species, e.g. *Cryptococcus neoformans*; any *Candida* species, e.g. *Candida albicans*; any apicomplexan parasite species such as: any *Plasmodium* species, e.g. *Plasmodium falciparum, Plasmodium vivax, Plasmodium ovale, Plasmodium malariae*; any *Babesia* species, e.g. *Babesia bovis, Babesia bigemina*; any *Cryptosporidium* species, e.g. *Cryptosporidium parvum*; any *Toxoplasma* species, e.g. *Toxoplasma gondii*; any *Trypanosomatid* species such as: any *Trypanosoma* species, e.g. *Trypanosoma brucei, Trypanosoma cruzi, Trypanosoma congolense, Trypanosoma vivax*; any *Leishmania* species, e.g. *Leismania donovani*. Any amebozoan parasites; any *Entamoeba* species, e.g. *Entamoeba histolytica*; any *Mastigamoeba* species; any *Schistosoma* species; any *Onchocerca* species; any *Giardia* species; any microsporidial species; any *Enterocytozoon* species; any *Encephalitozoon* species, e.g. *Encephalitozoon cuniculi*, etc.

[0057] As a result of the practice of the methods of the invention, entry of a pathogen effector protein into the host cell is prevented, inhibited, slowed, or otherwise decreased or lessened. As a result, the host cell can mount a robust or normal immune response to the pathogen, and infection of the host organism is averted (prevented), or the degree of infection (i.e. the deleterious symptoms that typically accompany the presence of an infection by the pathogen) are eliminated or decreased. Thus, some aspects of the invention also include methods of preventing or attenuating the symptoms of infection usually caused in a host organism by a pathogen which employs effector proteins comprising one or more virulence motifs as described herein to enter host cells. In some embodiments, the methods are used to prevent infection and/or symptoms of infection. In other embodiments, infection may have already started but the methods of the invention can

be used to curtail the spread of the infection to other organisms, or to lessen the symptoms in an organism that is already afflicted. This is the case, in particular, with *Plasmodium* infections, where the methods of the invention are especially useful in preventing the subsequent rounds of parasite multiplication after initial infection, or with other pathogens that multiply logarithmically. In addition, the invention provides methods of maintaining a host cell's ability to mount an immune response to a pathogen, the pathogen being one that produces effector proteins that comprise one or more of the motifs described herein, and the method involving blocking the effector protein from entering the host cell by preventing the binding of its natural ligand.

[0058] The mode of administration of the blocking molecules of the invention will depend on several factors, including the nature of the molecule and the host. Generally, the blocking molecule will be in a composition or formulation suitable for administration. If the host organism is a plant, application is generally in the form of a foliar spray or watering solution of e.g. an aqueous or oil solution that includes the blocking molecule in a concentration sufficient to block effector molecules of pathogens which are likely to attack the plant. For administration to an animal, which may be a human, any suitable composition, many of which are known in the art, may be employed, e.g. various pills, powders, liquids, injectable formulations, etc. Likewise, any suitable means may be used, including but not limited to by injection (e.g. subcutaneous or intramuscular), inhalation, orally, intranasally, by ingestion of a food product containing the protein, etc. In addition, the compositions may include one or more than one blocking molecule. For example, a preparation for application to plants may include molecules that block the effector proteins of one or of several different types of pathogen. In addition, the blocking molecules may be administered to plants in conjunction with other beneficial substances, such as fertilizers, various pesticides, growth factors, etc. The same is true for administration to animals, where on or more than one type of blocking molecule may be administered, and may be administered in conjunction with other beneficial substances such as chemotherapeutic agents that also have activity against the pathogen.

[0059] In some embodiments, a combination of blocking agents is utilized, e.g. two or more agents that act on or effect the effector protein, or two or more agents that acts on or effect the lipid, or a mixture of blocking agents, one or more of which acts on the effector protein, and one or more of which acts on the lipid.

[0060] In another aspect, the invention provides elucidation of the structural requirements of the virulence motifs (e.g. BXZ motifs, such as RXLR, RYWT, RIYER and related or similarly functioning motifs) in oomycetes, fungi, and other pathogens, and of the sequences which flank the motifs, thereby allowing, for example, the design of molecules to bind the motif. As a result, the invention also provides methods to predict which genes in the genome of a pathogen are likely to encode effector molecules. This is significant because, as demonstrated herein, the mere presence of a sequence conforming to the RXLR and dEER motif in a protein may not be sufficient to insure that the protein is an effector, i.e. that the protein is able to traverse the cell wall and enter the cell upon binding to phospholipids or sphingolipids. Functional virulence motifs (or functional virulence domains) may have additional requirements, particularly in the flanking sequences, as described herein. In one embodiment, the invention describes a non-random distribution of amino acid residues in the regions flanking the RXLR motif, represented by a position-weight matrix. One method of predicting whether or not a gene encodes a true effector protein involves the use of a hidden markov model (HMM) based on the position-weight matrix. This method may also be applied to the analysis of other BXZ motifs.

[0061] The development of this aspect of the invention was based in the observation of differences in activity between two putative RXLR motifs, RXLR1 and RXLR2, as described in detail in Example 1 below. The differences suggested that surrounding sequences are also important to the activity of an RXLR motif. To define the differences in the surrounding sequences a hidden markov model (HMM) was created using the 10 amino acid residues to the left and right of the RXLR motifs of all of known *P. sojae* and *P. ramorum* Avh genes. Using this HMM, the sequences surrounding RXLR2 (which was an authentic, functional motif) had a high score of 18.5, representing an excellent match to the consensus flanking sequence, and very unlikely to have been found in a random sequence. In contrast, sequences surrounding RXLR1 (a non-functional motif) had a low, non-significant score of 0.0. Using the same HMM, the sequences surrounding the RXLR motif of *P. infestans* Avr3a scored 10.9. Using a similar HMM derived from *Hyaloperonospora parasitica* Avh genes, the sequences surrounding the RXLR motifs of the *H. parasitica* Atr1 and Atr13 proteins had scores of 9.8 and 6.3 respectively. These and other comparisons described in Example 1, showed that HMM scores of zero, such as that of Avr1b RXLR1, are characteristic of RXLR strings found at random, i.e. such sequences are not likely to represent true RXLR motifs. On the other hand, HMM scores over 5.0 are characteristic of non-random occurrences of RXLR strings, and the proteins in which such non-random strings occur are likely to be authentic functional RXLR sequences. In other words, such sequences are likely, upon binding a phospholipid or sphingolipid, to promote or allow the translocation, into a host cell, of effector (avirulence) proteins in which they are located or of which they form a part. HMM scores between 0 and 5 are equivocal and cannot be assigned to either category of protein (random RXLR strings vs authentic RXLR motifs). This methodology may also be applied to other virulence motifs, e.g. RYWT, RIYER, etc.

[0062] For further discussions of the use of a hidden markov model, see U.S. Pat. No. 6,128,587 to Sjolander (Oct. 3, 2000), the complete contents of which are hereby incorporated by reference.

[0063] The invention also provides a method for screening compounds to identify those that inhibit binding of phosphoinositides, phospholipids or sphingolipids (or other natural lipid ligands) to a BXZ motif (e.g. to an RXLR motif, and optionally also to a dEER motif) in an effector protein, and which thus can inhibit translocation of effector proteins that have these motifs into cells. The method involves exposing a candidate or putative blocking compound to one or more BXZ virulence motifs (e.g. one or both of the RXLR and dEER motifs, and/or one or both of RYWT and RIYER) under conditions suitable for binding of either the natural phospholipid/sphingolipid ligands or phosphoinositides to the motifs (phosphoinositides are known to be capable of such binding). The screening is evaluated in that if the candidate compound is able to bind to one or more of the virulence motifs, and especially to two motifs when they are found to be present in a single effector (e.g. RXLR and dEER)

then the compound is selected as a compound that will inhibit binding of the natural ligands to the motifs in an effector protein, and prevent entry of the effector protein into a cell. This is especially the case if the blocking compound is able to competitively bind to the motif in the presence of a natural ligand.

[0064] Alternatively, such screening methods may be adapted and used to identify blocking compounds which bind to or otherwise interfere with the polar lipid to which the motif binds.

[0065] Blocking of effector-lipid binding may also be prevented or attenuated using genetic engineering/molecular biology techniques. Such techniques may target one or both of the effector (e.g. the motif sequence) and the lipid to which a motif binds. For example, host cells (e.g. in plants) may be genetically engineered to express inhibitory RNA (e.g. siRNA) that inhibits one or more enzymes involved in synthesis of a target lipid, or in transport of the lipid to the cell surface where it is accessible to the motif. Alternatively, host cells may be genetically engineered to produce peptides or proteins which contain one or more motifs, in a manner that promotes expression of the peptides/proteins and their binding to at least one target lipid. Other strategies will occur to those of skill in the art, and all such methods are encompassed by the invention.

[0066] The invention also provides methods for preventing pathogens from invading or infecting cells, by prophylactic ally applying one or more of the blocking compounds described herein to a substrate with which a pathogen and a cell the pathogen might infect may come in contact. The method inhibits entry, into the cell, of a pathogenic effector protein (entry of the pathogenic effector protein requiring binding of at least one motif of the effector protein as described herein to at least one polar lipid of the cell) and comprises the step of contacting a substrate which contains or is likely to contain a pathogen comprising the pathogenic effector protein with a blocking compound as described herein. By "contacting" is meant applying, permeating, coating or otherwise placing the blocking compound on the substrate. The blocking compound is capable of i) binding to at least one motif of the pathogenic effector protein; or ii) binding to at least one polar lipid of said cell (the polar lipid being the cellular ligand of the effector protein motif). Binding of the blocking compound prevents entry of the pathogenic effector protein into said cell (and hence prevents infection of the cell by the pathogen), if the pathogen comes into contact with the substrate. The blocking agent may be applied to the substrate by any suitable means, e.g. by spraying, painting, coating, etc., or even by manufacturing the substrate to contain the blocking agent (e.g. fabric), or by permeating or soaking the substrate with the blocking agent, etc. The substrate may be any suitable substrate that may be contacted by the pathogen, and which usually will be or may also come into contact with a cell which might be infected by the pathogen, or in some cases may be the cell or a collection of cells which may encounter or be exposed to the pathogen. Exemplary substrates include but are not limited to: plants (e.g. to leaves, fruit, roots, etc.) for example, by spraying or otherwise placing the blocking agent, sometimes, though not always, on an exterior surface of the plant (e.g. mature plants, plants "in the field", plants in green houses, seedlings, seeds, sprouts, etc.); fabrics (e.g. fabrics used for tents, mosquito netting, clothing, etc.), water (e.g. bodies of water, swamps, pools of standing water, wells, drinking water, etc.); skin, hair and/or fur, eyes, ear and nasal passages, the mouth, etc., e.g. of an animal (e.g. mammals such as humans, or other mammals, and also reptiles, fish, birds, etc. i.e. veterinary applications are also contemplated). For animals, application may be external by the application of e.g. lotions, sprays, rinses, mists, drops, washes, (e.g. mouthwash), etc; (internal administration is also contemplated, as described above). The substrate may also be an insect, e.g. an insect that is known or suspected of carrying the pathogen which comprises the effector protein, or is capable of synthesizing the effector protein.

[0067] The invention is further illustrated by the following Examples, which should not be interpreted as limiting the invention in any way.

EXAMPLES

Example 1

RXLR-mediated entry of *Phytophthora sojae* effector Avr1b (SEQ ID NO: 2) into soybean cells does not require pathogen encoded machinery

[0068] Effector proteins secreted by oomycete and fungal pathogens have been inferred to enter host cells, where they interact with host resistance gene products. Using the effector protein Avr1b of *Phytophthora sojae*, an oomycete pathogen of soybean, we show that a pair of sequence motifs, RXLR and dEER, plus surrounding sequences, (SEQ ID NO: 46) are both necessary and sufficient to deliver the protein into plant cells. Particle bombardment experiments demonstrate that these motifs function in the absence of the pathogen, indicating that no additional pathogen encoded machinery is required for effector protein entry into host cells. Furthermore, fusion of the Avr1b RXLR and dEER domain to green fluorescent protein (GFP) allows OFF to enter soybean root cells autonomously. The conclusion that RXLR and dEER serve to transduce oomycete effectors into host cells indicates that the more than 370 RXLR and dEER containing proteins encoded in the genome sequence of *P. sojae* are candidate effectors. We further show that the RXLR and dEER motifs can be replaced by the closely related erythrocyte targeting signals found in effector proteins of *Plasmodium*, the protozoan that causes malaria in humans. Mutational analysis of the RXLR motif shows that the required residues are very similar in the motifs of *Plasmodium* and *Phytophthora*. Thus the machinery of the hosts (soybean and human) targeted by the effectors may be very ancient.

RXLR2 and dEER Motifs of Avr1b are Required for its Avirulence Function in Transgenic *P. sojae* Lines

[0069] To test the function of the RXLR and dEER motifs of Avr1b, transgenic *P. sojae* strains that expressed either wild-type or mutant Avr1b-1 genes were created. Wild-type Avr1b contains two RXLR motifs, RXLR1 and RXLR2 (FIG. **1**A). Mutations in either or both of the RXLR motifs (SEQ ID NO: 3,4,5), in addition to a mutation in the BEER motif (FIG. **1**A) (SEQ ID NO: 6), were created. The Avr1b-1 gene constructs were fused to a strong constitutive promoter, HAM34 (Judelson, H., Tyler, B. M., and Michelmore, R. W. 1991. Mol. Plant-Microbe Interact. 4, 602-607.), and introduced into a strain, P7076, that expresses a variant Avr1b protein that does not confer avirulence against Rps1b-containing soybeans (Shan, W., Cao, M., Leung, D., and Tyler, B. M. 2004. Mol. Plant-Microbe Interact. 17, 394-403). Two independent transformants (T17 and T20) expressing wild type Avr1b-I (FIG. **1**B, C) lost the ability to infect soybean plants carrying Rps1b, but were unaffected in their ability to infect

plants lacking Rps1b (FIG. **1**E, Table 1). This demonstrated that they had acquired avirulence against Rps1b as a result of a functional Avr1b gene product. This result was confirmed using two different pairs of isolines of soybean that differed only in the presence of Rps1b, namely Williams (no Rps gene) with L77-1863 (Rps1b; Williams background) and HARO(1-7)1 (No Rps; Harosoy background) with HARO13 (Rps1b; Harosoy background) (FIG. **1**E; Table 1).

[0070] In contrast, in five independent transformants expressing the RXLR2^{AAAA} (SEQ ID NO 4) mutant, there was no gain of avirulence against Rps1b cultivars, despite the presence of abundant mRNA from the transgene (FIG. **1**E, Table 1). Thus, the RXLR^{2} motif is necessary for Avr1b activity when the protein is delivered by the pathogen. Since the RXLR^{1} motif was intact in the RXLR2^{AAAA} mutant, the motif appeared to be non-functional. Consistent with this inference, the RXLR1^{AAAA} mutation (SEQ ID NO 3) did not abolish avirulence in three independent transformants (FIG. **1**E, Table 1). As expected, avirulence was lost in the RXLR1^{AAAA}, RXLR2^{AAAA} double mutants (FIG. **1**E, Table 1) (SEQ ID NO: 5). A mutation in the dEER motif (SEQ ID NO: 6) also abolished avirulence (in two independent transformants) indicating that this motif is also required for the function of the protein (FIG. **1**E, Table 1).

TABLE 1

Molecular characterization and avirulence testing of *P. sojae* stable transformants

Strains	Transgene (PCR)[a]	Expression (RT-PCR)[b]	Transformant Validation[c]	Avirulence (Surviving seedlings)[d] Rps1[b]	rps	p[e]
P7076 (Gus)						
GUS	no	no		1/23	1/22	0.77
P7076 (sAvr1b WT)						
T17	yes	yes	Pst I	20/30	0/21	3.9E−07
T20	yes	yes	Sequence	25/44	2/28	1.2E−05
P7076 (sAvr1b RXLR1^{AAAA})						
RXLR1−2	yes	yes	Pst I	32/36	3/20	5.0E−08
RXLR1−3	yes	yes	Pst I	31/54	3/21	6.4E−04
RXLR1−5	yes	yes	Pst I	37/57	7/23	5.1E−03
P7076 (sAvr1b RXLR2^{AAAA})						
RXLR2−18	yes	yes	Pst I	6/44	3/17	0.48
RXLR2−20	yes	yes	Pst I	4/46	3/19	0.33
P7076 (sAvr1b RXLR1^{AAAA}; RXLR2^{AAAA})						
RXLR1+2−4	yes	yes	Pst	5/31	2/16	0.55
RXLR1+2−6	yes	yes	Pst I	4/43	1/21	0.47
P7076 (sAvr1b dEER^{A6})						
dEER−9	yes	yes	Sequence	4/59	2/23	0.79
dEER−14	yes	yes	Pst I	4/40	3/15	0.28
Ps Avr4/6−Avr1bCt						
4/6−1b−3	yes	yes	size	15/24	3/11	0.057
4/6−1b−19	yes	yes	size	14/26	3/16	0.025
Hp 341−Avr1bCt						
341−1b−13	yes	yes	size	16/19	0/11	6.6E−06
341−1b−17	yes	yes	size	23/24	0/7	3.0E−06
mAvr1bCt						
mAvr1bCt−4	yes	yes	size	3/20	3/16	0.77
mAvr1bCt−5	yes	yes	size	2/21	1/15	0.63

[a]The presence of transgenes was verifiedby PCR as described in the Materials and Methods. + = transgene present; − = transgene not detected.
[b]Transgene expression was determined by qualitative RT-PCR (RT-PCR) and by quantitative RT-PCR (q-PCR) as described in the Materials and Methods. Yes = transgene transcripts present; no = transgene transcripts not detected; ND = not determined.
[c]The presence of the relevant mutation in the transforming plasmid was verified by sequencing in every case. The presence of the correct mutation within the transgenes of each transformed strain was verified after PCR amplification of the Avr1b−1 transgene by Pst I digestion or by sequencing in the case of the mutants (e.g. FIG. 1) or by size in the case of the Avh gene fusions and N-terminal deletion (e.g. FIG. 4).
[d]The avirulence of each transgenic strain was tested by inoculation of seedlings containing Rps1b (L77-1863) or no rps gene (Williams), as described in the Materials and Methods. The number of surviving seedlings/total inoculated seedlings is shown, summed from all replicates
[e]Fisher's exact test (one tailed) was used to compare the frequency of seedling survival between rps and Rps1b plants. A significant p value (0.05) indicates that the transformant's phenotype is avirulent.

[0071] The difference in activity between RXLR1 (SEQ ID NO: 3) and RXLR2 (SEQ ID NO: 4) suggests that surrounding sequences are important to the activity of an RXLR motif.

To define the differences in the surrounding sequences a hidden markov model (HMM) was created using the 10 amino acid residues to the left and right of the RXLR motifs of all of the *P. sojae* and *P. ramorum* Avh genes (Tyler et al., 2006; Jiang et al., 2008). Using this HMM, the sequences surrounding RXLR2 (SEQ ID NO: 5) had a high score of 18.5, representing an excellent match to the consensus flanking sequence, very unlikely to have been found in a random sequence. In contrast, sequences surrounding RXLR1 (SEQ ID NO: 3) had a low, non-significant score of 0.0. Using the same HMM, the sequences surrounding the RXLR motif of *P. infestans* Avr3a scored 10.9. Using a similar HMM derived from *Hyaloperonospora parasitica* Avh genes, the sequences surrounding the RXLR motifs of the *H. parasitica* Atr1 and Atr13 proteins had scores of 9.8 and 6.3 respectively.

[0072] To establish the significance of these HMM scores, the *Phytophthora* HMM was used to score the RXLR motifs of 1240 RXLR-containing sequences identified from a pool of all putative secreted *P. sojae* and *P. ramorum* proteins by Jiang et al. (2008). As a control, 639 RXLR-containing sequences were scored found after permuting the sequences of all the putative secreted *P. sojae* and *P. ramorum* proteins (Jiang et al., 2008). As shown in FIG. **1**D, the RXLR strings of 698 (56%) of the 1240 real proteins had an HMM score of zero, while the RXLR strings of 595 (93%) of the permuted proteins had a zero score, and only 13 (1.8%) scored above 5.0. In contrast, of 765 proteins that Jiang et al. (2008) identified as high quality candidate effectors, only 18% had an HMM score of zero, and 543 (72%) had a score over 5.0. From this comparison we conclude that HMM scores of zero, such as that of Avr1b RXLR1 (SEQ ID NO: 3), are characteristic of RXLR strings found at random, while scores over 5.0 are characteristic of non-random occurrences of RXLR strings and of the RXLR strings of functional avirulence proteins. HMM scores between 0 and 5 are equivocal. The curated Avh genes with a score of zero may represent pseudogenes as many of them were identified principally by C-terminal sequence similarity.

The Interaction Between Avr1b and the Rps1b Gene Product Occurs Within Host Cells and Does Not Require the RXLR and dEER Motifs

[0073] To confirm that the site of interaction of Avr1b with the Rps1b gene product is within the plant cell, particle bombardment was used to introduce DNA encoding Avr1b proteins lacking a secretory leader into soybean cells together with DNA encoding β-glucuronidase (GUS). This assay measures the functional interaction of the Avr1b protein with the intracellular product of the soybean Rps1b gene; when the two proteins interact, programmed cell death is triggered in the transformed cells ablating the development of tissue patches expressing GUS. Since the Avr1b protein lacks its normal secretory leader, the protein should be synthesized in the plant cytoplasm. To facilitate the comparison of test and control bombardments, a novel double-barreled attachment for the Bio-Rad Gene Gun was utilized (Dou et al., 2008). The gun shooting two different DNA samples side-by-side into a leaf in the same shot, which greatly improves the reproducibility of the results (Dou et al., 2008). FIG. **2** shows that delivery of DNA encoding leader-less Avr1b protein (SEQ ID NO: 19) into soybean cells significantly reduced the number of blue GUS-positive patches when the Rps1b gene was present, but not when Rps1b was absent (FIG. **2**A). This is consistent with a cytoplasmic location for the Avr1b-Rps1b interaction. When RXLR2 or dEER motifs were replaced by four or six alanine residues, respectively [FIG. **2**A, mAvr1b (RXLR2^{AAAA})(SEQ ID NO: 20) and mAvr1b(dEER^{A6}) (SEQ ID NO: 23)], the interaction of the cytoplasmic, leader-less Avr1b with Rps1b was unaffected (FIG. **2**A), indicating that the RXLR2 and dEER motifs were not required for the interaction.

RXLR-Mediated Transit into Soybean Cells Does Not Require the Pathogen

[0074] To test whether RXLR function requires the presence of the pathogen, the bombardment assay was used to determine the effect of the RXLR2^{AAAA} mutation on secreted Avr1b protein (SEQ ID NO: 18). When soybean cells were bombarded with DNA encoding wild type Avr1b (SEQ ID NO: 22), including its normal secretory leader, a reduction in GUS-positive blue spots was observed comparable to that observed for the non-secreted protein [FIG. **2**, sAvr1b(WT)]. However when the RXLR2^{AAAA} (SEQ ID NO: 28) or dEERA6 (SEQ ID NO: 29) mutations were present in the bombarded DNA, there was no reduction in the number of blue spots [FIG. **2**, sAvr1b(RXLR2^{AAAA}) (SEQ ID NO: 11) and sAvr1b(dEER^{A6}) (SEQ ID NO: 13)]. From these results it may be inferred first that the secretory leader is functional in soybean and targets Avr1b protein to the outside of the cell; second, that the RXLR2 (but not RXLR1) and dEER motifs are required for Avr1b protein to re-enter the cell, which confirms the conclusion from the *P. sojae* transformation experiments. Importantly, the results also show that RXLR-dEER-mediated entry does not require the presence of the pathogen.

[0075] To support the inference that the secretory leader of Avr1b was correctly exporting the protein from the plant cells in the bombardment assay, a gene encoding *Aequorea coerulescens* green fluorescent protein (acGFP; "GFP" herein) fused either to the Avr1b leader (SEQ ID NO: 27) or to full-length Avr1b (SEQ ID NO: 25) was constructed. These fusions enabled tracking of the proteins and checking their stability. To aid in visualization onion bulb epidermal cells were used rather than soybean cells. GFP was exported from the cells and accumulated in the apoplast when the secretory leader was attached to GFP but accumulated in the cytoplasm and nucleus when the leader was not attached (not shown). When full length Avr1b was fused to GFP (SEQ ID NO: 25), the proteins also accumulated in the apoplast if a mutation was present in either the RXLR2 motif (SEQ ID No: 28) or in the dEER motif (SEQ ID No: 29). This observation confirmed that the protein encoded by these mutants was stable and correctly targeted outside of the cells. When cells expressing Avr1b-GFP fusion proteins with RXLR mutations were plasmolyzed by treatment with 0.8M mannitol for 15 min, the GFP was associated with the cell wall and not with the plasma cell membrane (not shown). Furthermore, GFP protein could be seen diffusing into the apoplast between pairs of neighboring cells not shown). Similar observations were made when cells expressing secreted GFP or Avr1b-GFP fusion proteins with a dEER mutation were plasmolyzed (not shown). If the RXLR2 and dEER motifs were intact however, the sAvr1b-GFP protein fusion accumulated in the cytoplasm and nucleus of the cells, similar to the mAvr1b-GFP (SEQ ID NO: 24) fusion lacking the leader. When cells expressing sAvr1b-GFP fusion proteins were plasmolyzed by treatment with 0.8M mannitol for 15 min, the GFP could be observed to have either fully or partially returned to the inside of the cells.

These results supported our conclusion that the RXLR2 and dEER motifs act together to enable Avr1b protein to re-enter the plant cells.

The Avr1b RXLR and dEER Motifs are Sufficient to Target GFP to Soybean Cells

[0076] The RXLR and dEER region of Avr1b was fused to GFP (SEQ ID NO: 46), and the fusion protein was synthesized in *E. coli* and partially purified. Root tips of soybean seedlings were incubated with the isolated fusion protein for 12 hours, washed for four hours in water, then observed under light and UV microscopy to localize the OFF. GFP accumulated inside many of the root cells, whereas buffer alone did not produce any fluorescence. The optical sections produced by the confocal microscope revealed that the protein penetrated approximately 10 cell layers deep during the 12 hour incubation. The characteristic accumulation of GFP in the nuclei of the treated cells is comparable to the pattern observed when GFP is expressed in planta, and verifies that the GFP is located inside the cells. The nuclear localization of the protein also indicates that the cells are alive. If mutations were present in the RXLR or dEER motifs of the fusion protein, GFP did not accumulate inside the soybean root cells. When the RXLR and dEER region was replaced by the artificial protein transduction motif Arg9 (SEQ ID NO: 112), GFP once again entered the soybean root cells and accumulated in the nuclei.

Avr1b RXLR and dEER Motifs can be Replaced by RXLR and dEER-Containing Protein Sequences Encoded by Bioinformatically Identified Avh Genes

[0077] To determine if the RXLR and dEER motifs of bioinformatically identified Avh genes could functionally replace the RXLR2 and dEER motifs of Avr1b-1, full length Avh genes from *P. sojae* and *H. parasitica* were fused to an Avr1b-1 N-terminal deletion mutant lacking the RXLR and dEER motifs. The fusion genes were then introduced into *P. sojae* and the transformants were tested for avirulence on Rps1b-containing soybean cultivars. Both Avh genes, *P. sojae* Avh171 (since identified as Avr4/6; Dau et al., 2008) (SEQ ID NO: 8) and *H. parasitica* Avh341 (SEQ ID NO: 7), could replace the requirement for the RXLR2 and dEER motifs as judged by the avirulence of the transformants on Rps1b-containing cultivars, whereas transformants containing only the C-terminus of Avr1b fused to an initiator methionine remained virulent (FIG. **3** and Table 1). This result indicates that the RXLR and dEER motifs form a distinct transferable functional domain of Avr1b and other Avh proteins. The HMM scores of the RXLR-dEER motifs of Ps Avr4/6 and Hp Avh341 are both well within the functional range (6.9 and 14.2, respectively).

The Avr1b Host Targeting Signal can be Functionally Replaced by Autonomous Protein Transduction Motifs

[0078] Protein transduction domains (PTDs) capable of autonomously carrying proteins across plasma cell membranes have been described and characterized in the HIV-1 Tat protein. Arginine-rich peptides such as Arg9 can also carry out this function. To compare RXLR and dEER mediated effector delivery with the function of PTDs, the RXLR2 motif of Avr1b was replaced with the TAT PTD (SEQ ID NO: 42) or with Arg9 (FIG. **4**A) (SEQ ID NO: 41). The resultant proteins were treated using the particle bombardment assay, and both PTDs could functionally replace the RXLR2 motif of Avr1b, restoring the avirulence reaction of Avr1b with Rps1b (FIG. **4**B). Furthermore, when the version of secreted Avr1b that contained the Arg9 sequence in place of the RXLR2 motif was fused to GFP (SEQ ID NO: 30), the fusion protein accumulated in the cytoplasm and the nucleus of bombarded onion bulb cells rather than the apoplast, confirming that Arg9 could functionally replace RXLR2 (not shown). Similar results were obtained when the version of secreted Avr1b that contained the TAT PTD was fused in place of the RXLR2 motif to GFP (SEQ ID NO: 31). Finally, when Arg9 was fused to GFP (SEQ ID NO: 112), the isolated proteins could enter soybean root cells directly (not shown).

The Avr1b Host Targeting Signal is Interchangeable with Host Targeting Signals from *Plasmodium* Effectors

[0079] To test if the erythrocyte targeting signals of *Plasmodium* effector proteins could functionally replace the RXLR and dEER region of Avr1b, the residues of Avr1b from the end of the secretory leader to the end of the dEER motif were replaced with the mature N-termini of three different *Plasmodium* effector proteins that are targeted to the erythrocyte cytoplasm, namely PfGBP-130 (SEQ ID NO: 121), PfHRPII (SEQ ID NO: 123) and PfPFE1615c (SEQ ID NO: 125) (Bhattacharjee, S., Hiller, N. L., Liolios, K., Win, J., Kanneganti, T. D., Young, C., Kamoun, S., and Haldar, K. 2006. PLoS Pathog 2, e50.). The entire 37-41 amino acid region of each *Plasmodium* effector required for transduction was used (FIG. **4**A). As shown in FIG. **4**B, all three *Plasmodium* host targeting domains could functionally replace the Avr1b N-terminus in targeting Avr1b to the soybean cytoplasm, assuming that they do not simply interfere with secretion.

Functional Characterization of the RXLR Motif

[0080] To experimentally characterize the sequence requirements of the RXLR motif, a series of mutations were introduced into the motif in a version of the Avr1b-1 gene that retained the secretory leader, and assayed the mutants using the bombardment assay (Table 2). Mutations which targeted the arginine at position 1 or the leucine at position 3 has the strongest effect on the ability of Avr1b to ablate GUS-positive tissue patches. Replacement of R1 with lysine reduced function significantly (33% ablation compared to 78%; $p<0.001$) while glutamine replacement completely abolished it. Replacement of L3 with alanine or even the relatively conservative valine also completely abolished function. Replacement of the arginine at position 4 with a glutamine slightly but significantly reduced function (58% ablation compared to 72%; $p<0.001$). Reversing the order within the first and second two pairs of positively-charged and hydrophobic residues (RFLR->FRLR; RFLR->RFRL) completely abolished avirulence activity, indicating that positions of R1 and L3 were critical, not just their presence.

TABLE 2

Function of RXLR2 mutants of Avr1b assayed by particle bombardment

SEQ ID NO	RXLR2 sequence[a]	Ratio of GUS-positive spots[b] rps	Rps1b	abla-tion[c]	p value[d]	Activity
22	RFLR	1.26 ± 0.07	0.28 ± 0.03	0.78	<0.001	Yes
20	AAAA	0.93 ± 0.04	0.96 ± 0.05	0	>0.1	No
38	KFLR	1.04 ± 0.04	0.70 ± 0.04	0.33[e]	<0.001	Partial
37	QFLR	0.95 ± 0.03	0.99 ± 0.03	0	>0.1	No

TABLE 2-continued

Function of RXLR2 mutants of Avr1b assayed by particle bombardment

SEQ ID NO	RXLR2 sequence[a]	Ratio of GUS-positive spots[b] rps	Rps1b	abla-tion[c]	p value[d]	Activ-ity
31	FRLR	1.00 ± 0.04	0.98 ± 0.05	0	>0.1	No
34	RFLQ	0.98 ± 0.07	0.41 ± 0.08	0.58[e]	<0.001	Partial
36	QFLQ	1.03 ± 0.05	1.05 ± 0.05	0	>0.1	No
35	RFAR	0.94 ± 0.03	0.91 ± 0.05	0	>0.1	No
40	RFVR	0.95 ± 0.05	1.03 ± 0.07	0	>0.1	No
33	RFRL	1.02 ± 0.04	0.96 ± 0.04	0	>0.1	No

[a]Amino acid sequence of RXLR2 in wild-type and mutants. RFLR is the wild-type. Altered residues are underlined.
[b]Ratio of blue spots in the presence of various RXLR2 mutants of Avr1b-1, compared to the control empty vector when bombarded onto leaves from rps plants (Williams) or Rps1b plants (L77-1863). Averages and standard errors are from 16 pairs of shots.
[c]Ablation calculated as 1 − (Rps1b ratio)/(rps ratio) for ratios significantly different between rps and Rps1b.
[d]p values comparing results from rps and Rps1b cultivars were calculated using the Wilcoxon rank sum test.
[e]Ablations for KFLR and RFLQ were significantly different than wildtype (RFLR) with $p < 0.001$.

[0081] This example demonstrates that

1) both the RXLR2 and dEER motifs of Avr1b are required for this protein to confer avirulence on *P. sojae* transformants (summarized in FIG. **5**);

2) the RXLR2 and dEER motifs are not required to trigger an interaction with the Rps1b gene product when the Avr1b protein is synthesized in the soybean cytoplasm;

3) when Avr1b protein is directed to be secreted out of the soybean cell, the RXLR2 and dEER motifs are once more required for the protein to trigger an interaction with Rps1b, which is consistent with the motifs being required for the Avr1b protein to re-enter the soybean cell across the plasma cell membrane; 4) fusion of the RXLR and dEER region to GFP (SEQ ID NO: 46) enabled the isolated fusion protein to enter soybean root cells in the absence of the pathogen, but only if the RXLR and dEER motifs were both intact; and 5) RXLR-dependent entry of Avr1b does not require the presence of the pathogen. These observations lead to the conclusion that the RXLR and dEER motifs do indeed have the function of transporting avirulence proteins into host cells.

[0082] In addition, the data presented in this Example characterizes the RXLR2 and dEER motifs as follows: 1) arginine at position 1 and leucine at position 3 are essential for function of the RXLR motif. However, there is not a strong requirement for the arginine at position 4. Therefore by functional assays, the oomycete RXLR motif resembles the *Plasmodium* motif (RxL×D/E/Q) even more closely than previously noted; and 2) the amino acid sequences flanking the RXLR2 and dEER motifs are required in addition to the motifs themselves for the transit of Avr1b into soybean. Further, the region from residues 33 to 71 (19aa to the left of RXLR2 and baa to the right of dEER) were sufficient for protein translocation.

[0083] The Avr1b protein requires not only the RXLR motif itself, but also non-random surrounding sequences including the dEER motif. These surrounding sequences are not enriched in positive and hydrophobic residues, but instead are enriched in acidic and hydrophilic residues. Furthermore, our RXLR mutagenesis results show that the presence of basic and hydrophobic residues is not sufficient for RXLR function; instead the order of the amino acid residues is very important, and very subtle mutations such as RFLR→RFVR or QFLR abolish function. Therefore, oomycete effectors may utilize a novel mechanism for translocation across the membrane, possibly involving host cell surface machinery (such as a receptor) that is more complex than just the phospholipid bilayer. The *Plasmodium* Pexel/VTF motif also requires surrounding sequences that are enriched in acidic and hydrophilic residues and is functionally interchangeable with the oomycete RXLR domain in both erythrocytes and in soybean tissue (this study). Thus oomycetes and *Plasmodium* both may target host cell surface machinery that is common to plants and vertebrate animals but different than that targeted by animal PTDs. The targeted machinery, if common, must not only be very ancient, but also must serve an irreplaceable function in the host organisms since it must have been preserved against strong negative selection pressure resulting from exploitation by the pathogens.

[0084] These results do not indicate which specific flanking sequences are required. However, HMMs constructed from the 10 amino acid residues flanking the upstream and downstream sides of all *P. sojae* and *P. ramorum* Avh RXLR motifs, clearly separated the RXLR motifs of functional avirulence proteins from RXLR motifs obtained by chance from real or permuted proteins sequences. These findings indicate that reliable bioinformatic searches for RXLR effector candidates should include the use of HMMs to evaluate the sequences flanking putative RXLR and dEER motifs. METHODS: Plasmids and oligonucleotides used in the study are depicted in tabular form as FIGS. **11**A and B and FIGS. **12**A and B, respectively.

P. sojae isolates and transformation: *P. sojae* isolate P7076 (Race 19) was routinely grown and maintained on V8 agar). The *P. sojae* transformation procedure was described by Dou et al (Dou, D., Kale, S. D., Wang, X., Chen, Y., Wang, Q., Wang, X., Jiang, R. H. Y., Arredondo, F. D., Anderson, R., Thakur, P., McDowell, J., Wang, Y., and Tyler, B. M. (2008) Plant Cell 20(4), 1118-1133).

Characterization, of *P. sojae* transformants: *P. sojae* transformants were selected that grew well on V8 medium with 50 μg/ml G418, and were cultured in V8 liquid medium for 3 days. The mycelia were harvested, frozen in liquid nitrogen and ground to a powder for DNA or RNA extraction. Genomic DNA was isolated from mycelium using known techniques. DNA samples were quantified using a Nanodrop ND-1000 spectrophotometer (Thermo Scientific). The presence of Avr1b-1 transgenes was verified by PCR amplification from 100 ng genomic DNA using a program of 94° C. for 2 min, 30 cycles of 94° C. for 30 s, 56° C. for 30 s, 72° C. for 30 s, and 72° C. for 5 min with primers of HamF and HamR (TS1). All the transformed *P. sojae* were double-checked by Pst I restriction and/or sequence. RNA was extracted from each sample using RNeasy Plant Mini Kit (QIAGEN, cat #74904) with β-mercaptoethanol added buffer RLT and genomic DNA was removed using RNase-Free DNase (QIAGEN, cat #79254) according to the manufacturer's recommendations. RNA was quantified using a Nanodrop ND-1000 spectrophotometer. Avr1b-1 transgene transcription was verified by RT-PCR using the internal primers, Avr1bReF and Avr1bReR (TS1) and *P. sojae* actin was used as the reference.

Phenotypic assays for avirulence: Avr1b phenotypic expression was assayed using soybean cultivars HARO(1-7) (rps), Haro13 (Harosoy background, Rps1b), Williams (rps) and L77-1863 (Williams background, Rps1b). Seedlings were

grown in the greenhouse or in a growth chamber (Percival AR-36L) with a program of 24° C. at daytime and 22° C. at night with a 14 hr day length under fluorescent light (250 μmol photons s-1m-2). The virulence of each transformant was evaluated using hypocotyl inoculation. 1-2 days after the first primary leaf appeared, the hypocotyl of the soybean was wounded with a short incision and the incision was inoculated with a small piece of V8 agar cut from the edge of a 3 day old colony. Thereafter, the plants were incubated in a growth chamber under the conditions described above. The numbers of dead and surviving plants were counted 4 days after inoculation, and summed over 2-5 replicates. The differences between the numbers of surviving plants from rps and Rps1b cultivars were compared using Fisher's exact test. Only the transformants producing a significant difference between rps and Rps1b cultivars were judged as avirulent.

Particle bombardment assays: Particle bombardment assays were carried out using a double-barreled extension of the Bio-Rad He/1000 Particle Delivery System ((Dou, D., Kale, S. D., Wang, X., Chen, Y., Wang, Q., Wang, X., Jiang, R. H. Y., Arredondo, F. D., Anderson, R., Thakur, P., McDowell, J., Wang, Y., and Tyler, B. M. (2008) Plant Cell 20(4), 1118-1133). Analyzing the bombardment data as a ratio between the test and control shots improves the reproducibility of the measurements greatly. The avirulence activity of the Avr1b-1 constructs was measured as the reduction in the number of blue spots comparing the Avr1b-1+GUS bombardment with the GUS+control bombardment. For each paired shot the logarithm of the ratio of the spot numbers of Avr1b-1 to that of the control was calculated, then the log-ratios obtained from the Rps1b and non-Rps1b leaves were compared using the Wilcoxon rank sum test.

Bombardment assays of onion bulb cells with GFP constructs: Preparation of DNA-particle mixtures was as described above. 5 mm hemispherical layers of yellow and white onion bulbs were bombarded without the double barrel attachment under a 26 psi vacuum, using a rupture pressure of 1100 psi. The onion layers were incubated between 24-48 hr at 25° C., then viewed with a Zeiss Axioskop2 Plus microscope using a 480 nm filter for GFP fluorescence. Images were captured using a Qimaging Retiga 1300 Camera. To further confirm the GFP had been secreted out of the onion cells, plasmolysis was performed for 15 min in 0.8 M mannitol and cells were observed in a Zeiss LSM510 laser scanning confocal microscope (Jena, Germany) with an argon laser excitation wavelength of 488 nm.

RXLR-GFP Fusion Protein Expression and Purification: Residues 33 to 71 of Avr1b (VESPDLVRRSLRNGDIAGGRFLRAHEEDDAGERTFSVTD (SEQ ID NO: 46) including the RXLR1, RXLR2 and dEER motifs were fused to GFP, replacing the Arg9 encoding sequences in vector pR9GFP (SEQ ID NO: 112), called pR9 by Chang et al., (Chang, M., Chou, J. C. and Lee, H. J. (2005) Plant and Cell Physiology 46, 482-488). pR9GFP, which also adds an N-terminal His6 tag, was derived by Chang et al (2005) from Ptat-HA. C43 (DE3) *E. coli* cells containing RXLR-GFP fusion constructs or pR9 were grown in 200 mL of LB containing ampicillin 100 μg/mL in a 1 L baffled flask shaken at 240 rpm at 37° C. until reaching an OD of 0.4, at which point the cells were induced by addition of 1 mL of 1M IPTG (final [5 mM]). After 4 hours further growth at the same conditions, the cells were harvested by centrifugation at 4° C. and then stored at −20° C. Visual confirmation of GFP expression was noted by the green color of the bacterial cell pellet. To extract the GFP fusion proteins, cells were thawed on ice for 20 min then 4 mL of lysis buffer (50 mM NaH_2PO_4, 300 mM NaCl, 10 mM imidazole, pH 8.0) were added per 1 g of wet cell weight. Lysozyme (Sigma-Aldrich, cat# L6876) was added to a final concentration of 1 mg/mL then the suspension was incubated for 20 min on ice. Sonication (Branson sonifier 150D, with Double stepped micro tip, 3 mm) was done at 300 W at 15 sec bursts four times with 15 sec cooling periods between each burst. The lysate was centrifuged at 10,000×g for 30 minutes at 4° C., then the supernatant was transferred to a fresh tube and kept on ice until use. 5 μL of each sample was stored for SDS-PAGE analysis. Protein purification using Ni-NTA affinity chromatography was performed using the QiaExpressionist protocol. 2 mL of 50% Ni-NTA super flow slurry (Qiagen) was loaded on a column. The column was washed twice with 5 mL of wash buffer (50 mM NaH_2PO_4, 300 mM NaCl, 20 mM imidazole, pH 8.0). The protein sample was loaded onto the column and then the column was washed twice with 10 vol (10 mL) of wash buffer. The protein was eluted with 4 mL of elution buffer (50 mM NaH_2PO_4, 300 mM NaCl, 200 mM imidazole, pH 8.0) into 1 mL fractions. These fractions were pooled and concentrated to 3001 using a centrifugal protein concentrator (Amicon Centriplus Centrifugal Filter Device MWCO-3 kDa) at 13,500×g. The sample was then mixed with an equal volume of 50 mM MES buffer pH 5.8. The protein concentration was measured at 280 nm using a nanodrop spectrophotometer (ND-1000) and adjusted to 8 mg/mL. All purified GFP preparations fluoresced normally under UV illumination.

RXLR-GFP Fusion Protein Root Cell Transduction Assay: Root tips were cut into lengths of between 0.5 cm and 1 cm, and then were washed with water. Each root tip was completely submerged in 20 μL of the protein solution (8 mg/ml in 25 mM MES pH 5.8) in a eppendorf tube. The samples were incubated overnight at 28° C. (~12 hours). The roots were then washed in 200 mL of water for 4 hours while shaken at 100 rpm on a rotary shaker. The roots were then viewed using a Zeiss LSM510 laser scanning confocal microscope with an argon laser excitation wavelength of 488 nm. For nuclear staining, the roots were stained with DAPI (4',6-diamidino-2-phenylindole) (Sigma-Aldrich cat# D8417) and viewed with a 405 nm filter.

Hidden Markof Model Analysis: By using the program HMMER 2.3.2 (Eddy, S. R. (1998). Profile hidden Markov models. Bioinformatics 14, 755-763; and website located at hmmer.janelia.org), an HMM was built from the full set of 765 high quality candidate effectors identified from the *P. sojae* and *P. ramorum* genomes by Jiang et al (Jiang, R. H. Y., Tripathy, S., Govers, F. & Tyler, B. M. Proc. Natl. Acad. Sci. USA 105, 4874-4879 (2008), using the 10 amino acids on the left side of each RXLR motif together with the 10 amino acids on the right side each RXLR motif. The same procedure was used to build an HMM from a curated list of 191 high quality candidate effectors from *Hyaloperonospora parasitica* developed at the *H. parasitica* genome annotation jamboree in August 2007 and available at pmgn.vbi.vt.edu. To estimate the significance of HMM scores, all proteins (1240) with a predicted N-terminal signal peptide (SP) and the string RXLR located between 30 and 60 amino acids after the SP cleavage site were obtained by translating the genome sequences of *P. sojae* and *P. ramorum* in all reading frames. The sequences of all the putative secreted proteins were permuted (other than the signal peptide) and RXLR-containing sequences were again identified; 639 of the permuted proteins

had RXLR strings, indicating that about 639 of the 1240 detected RXLR motifs could be expected by chance. The distributions of HMM scores the set of 1240 real proteins, the 639 permuted proteins and the 765 curated proteins were then calculated. The frequency that a permuted protein received a score between 0 and 5.0 was 0.044. The frequency that a permuted protein received a score better than 5.0 was 0.018. Accession Numbers The sequences reported herein have been deposited in the GenBank database, namely Hp Avh341 (EF681127). Accession numbers for sequences already in GenBank are Ps Avr1b-1 (AAM20936), Ps Avr4/6 (ABS50087), Pi Avr3a (CA172345); Hp Atr1 (AY842877), Hp Atr13 (AY785301).

Example 2

Effector Host-Targeting Signals of Eukaryotic Pathogens Bind Phosphoinositides or Phosphatidic Acid

[0085] Pathogens of both plants and animals produce effectors and/or toxins that act within the cytoplasm of host cells to suppress host defenses and cause disease. Effector proteins of oomycete plant pathogens utilize N-terminal motifs, RXLR and dEER, to enter host cells, and a similar motif, Pexel (RxLxE/D/Q), is used by *Plasmodium* effectors to enter erythrocytes. This Example shows that effectors of fungal plant pathogens contain functional variants of the RXLR and dEER motifs, and that the oomycete and fungal RXLR and dEER motifs, as well as the *Plasmodium* Pexel motifs, are responsible for binding of the effectors to phosphatidyl-inositol-3-phosphate (PI-3-P) and/or phosphatidyl-inositol-4-phosphate (PI-4-P). Stimulation of host cell entry by PI-4-P, and inhibition by inositol 1,4 diphosphate suggest that phosphoinositide binding mediates cell entry. All the effectors could also enter human cells, suggesting that phosphoinositide-mediated effector entry may be very widespread in plant, animal and human pathogenesis.

Oomycete RXLR and dEER Domain Binds Phosphoinositides

[0086] The RXLR and dEER domain of *P. sojae* Avr1b enables translocation of green fluorescent protein (GFP) into plant cells without any pathogen-encoded machinery (see Example 1), and the same is true for two additional bioinformatically predicted effectors, Avh5 (SEQ ID NO: 129) and Avh331 (SEQ ID NO: 127). In these experiments, accumulation of the GFP fusion proteins inside the cells was confirmed by the accumulation of GFP within the nuclei of the cells (a natural property of GFP), and by plasmolysis experiments. In principle, a cell entry domain could bind either a (glyco)protein or (glyco)lipid receptor. After noting that beta-type phosphatidylinositol-4-phosphate kinases from rice and *Arabidopsis* contained a PI-4-P binding domain consisting of 14 and 11 tandem RXLR and dEER motifs respectively, experiments were conducted to test whether oomycete the RXLR and dEER domain could bind phosphoinositides. An array of 8 different lipids found in plant cell membranes were spotted in decreasing amounts onto a Hybond-C extra membrane. Then the membrane was probed with GFP fused to the N-terminal RXLR and dEER domains of Avr1b (SEQ ID NO: 46), Avh331 (SEQ ID NO: 116) or Avh5 (SEQ ID NO: 113). FIG. **6** shows that the Avr1b- and Avh331-GFP fusions bound to PI-4-P while Avh331- and Avh5-GFP fusions bound to PI-3-P. Alanine substitutions mutations in either the RXLR or the dEER motif of any of the three fusions abolished binding, just as they abolished entry into soybean root cells. Fusions of full-length Avh5 (SEQ ID NO: 129) or Avh331 (SEQ ID NO: 127) proteins at their N-termini to glutathione-S-transferase (GST) could also bind the same phosphoinositides as just their N-terminal domains fused at their C-termini to GFP and binding by the full length proteins also required intact RXLR and dEER motifs (FIG. **6**) (full-length Avr1b could not be produced in *E. coli*).

[0087] To independently confirm binding of the effector RXLR and dEER domains to the phosphoinositides, the binding of the fusion proteins to liposomes composed of phosphatidyl-choline (PC) and phosphatidyl-ethanolamine (PE) was tested. In the absence of phosphoinositides, neither the effector N terminus-GFP fusion proteins nor the full length GST-effector fusion proteins bound the liposomes (FIG. **6**). However, when either PI-3-P or PI-4-P were included, all the fusion proteins bound to the liposomes. In every case, when any of the RXLR or the dEER motifs were mutated by alanine substitutions, the mutant fusion proteins lost their ability to bind the liposomes (FIG. **6**).

Identification of Fungal Effector Translocation Domains

[0088] To test whether fungal effectors contain N-terminal cell entry domains, N-terminal segments from the fungal effectors AvrL567 (SEQ ID NO: 138) and AvrM (SEQ ID NO: 142) of *M. lini* and from AvrPi-ta (SEQ ID NO: 143) of *M. oryzae* were fused to the C-terminus of Avr1b, in the presence of the Avr1b secretory leader, then tested the fusions in a particle bombardment cell re-entry assay that measures the ability of a motif to carry an Avr1b reporter protein back into soybean leaf cells after secretion. FIG. **7**A shows that all three fungal N-terminal segments had significant ability to deliver Avr1b back into soybean leaf cells.

[0089] Since the fungal effectors contained no obvious RXLR or dEER motifs, we decided to define experimentally the range of residues within the RXLR motif of Avr1b that could permit cell entry, using the particle bombardment cell re-entry assay. The results revealed that lysine (K) or histidine (H) but not glutamine (Q) could replace the arginine at position 1 in the motif, that any large hydrophobic residue (isoleucine, I; methionine, M; phenylalanine, F; tyrosine, Y) could replace the leucine at position 3, albeit with varying efficiencies, but valine (V) and alanine (A) could not. At position 4, all residues tested (lysine, K; glutamine, Q; glycine, G) allowed function. Furthermore, the presence of either an L or M residue at position 2 could substitute for a large hydrophobic residue at position 3.

[0090] Using this information, one, seven and four potential cell entry motifs were identified in N-terminal regions of AvrL567 (SEQ ID NO: 138), AvrM (SEQ ID NO: 142) and AvrPi-ta (SEQ ID NO: 143), respectively (FIG. **7**B). The single motif in AvrL567, RFYR, had a particularly good match to the oomycete RXLR motif, and RFYR had already been shown to be functional (FIGS. **7**B and **7**C). Four of the candidate motifs in the AvrPi-ta N-terminus, including two that overlapped at one residue (RFLK and KLIFK (SEQ ID NO: 146)), were tested for cell entry activity by substituting them for the RXLR motif of Avr1b. The two single motifs and the overlapping pair were all active in the cell re-entry assay (FIG. **7**B).

[0091] The N-terminus of AvrL567 was subjected to further analysis by mutagenesis and root cell entry assays. Alanine substitutions in the RFYR motif and in two downstream acidic residues that might act as a dEER motif (FIG. **7**B) (SEQ ID NO: 139), abolished the activity of the AvrL567

N-terminal domain in the particle bombardment cell re-entry assay (FIGS. **7**A and B). To confirm the cell entry activity of the AvrL567 N-terminal domain, it was fused to GFP (creating AvrL567(N)-GFP (SEQ ID NO: 119)), with and without (SEQ ID NO: 120) the alanine substitutions, and then the fusion proteins were tested for cell entry in the soybean root uptake assay. The GFP-fusion with the intact AvrL567 N-terminus (SEQ ID NO: 119) efficiently accumulated in the root cells, including the nuclei, whereas the fusion with the mutated RFYR and acidic residues (rfyr-de-) (SEQ ID NO: 120) did not (not shown). Thus the RFYR motif and the two downstream acidic residues appear to act as a RXLR and dEER motif in *M. lini* AvrL567.

Fungal and Apicomplexan Effectors Bind Phosphoinositides

[0092] Both filter binding and liposome binding were used to test whether the N-terminal domain of AvrL567 bound phosphoinositides. AvrL567(N)-GFP (SEQ ID NO: 119) bound PI-3-P in both assays. Binding of AvrL567(N)-GFP to PI-4-P was also be detected in the liposome assay though it is not as strong as to PI-3-P. Mutation of the RXLR and dEER-like motif to alanines (rfyr-de-mutant) (SEQ ID NO: 120) resulted in a loss of binding to the phosphoinositides in both assays.

[0093] Filter binding assays were used to determine if five additional fungal effectors could bind phospholipids. The N-terminal sequences of the following effectors were fused to GFP: *Magnaporthe grisea* AvrPita (SEQ ID NO: 224), *Puccinia graminis* Ps87 (SEQ ID NO: 226); *Melampsora lini* AvrM (SEQ ID NO: 228); *Melampsora lini* AvrP123 (SEQ ID NO: 230); *Melampsora lini* AvrP4 (SEQ ID NO: 232). The results, summarized in tabular form in FIG. **15**, showed that all five effectors bound phosphatidic acid. Mutations in RXLR-like motifs found in AvrPtia (SEQ ID NO: 225), Ps87 (SEQ ID NO: 227), AvrM (SEQ ID NO: 228), AvrP123 (SEQ ID NO: 230) and AvrP4 (SEQ ID NO: 232) all abolished binding to phosphatidic acid. In the case of AvrPita, the mutant protein (SEQ ID NO: 225) was unable to enter soybean root cells, whereas the wildtype protein (SEQ ID NO: 224) could enter root cells, suggesting that binding of AvrPita to phosphatidic acid was required to enter plant cells.

[0094] The host targeting signals (HTS) of three *Plasmodium falciparum* effectors, PfGBP (SEQ ID NO: 121), PfHRPII (SEQ ID NO: 123), and Pf1615c (SEQ ID NO: 125) can carry Avr1b into soybean leaf cells and onion bulb epidermal cells8. The three signals can also carry purified GFP into soybean root cells and this activity requires intact Pexel motifs. To test whether the three signals also could bind phosphoinositides, the HTS-GFP fusion proteins were tested using filter binding and liposome binding assays. The PfGBP HTS fusion (SEQ ID NO: 121) could bind PI-4-P and also, more weakly, PI-3-P (FIG. **8**A). The PfHRPII HTS fusion (SEQ ID NO: 123) could bind PI-3-P, and also rather weakly, PI-4-P (FIG. **8**B) The Pf1615c HTS fusion (SEQ ID NO: 125) could bind specifically to PI-3-P (FIG. **8**C). Liposome binding assays confirmed binding of all the fusion proteins to PI-3-P or PI-4-P (FIGS. **8**D-F). In both assays, alanine substitutions in the Pexel motifs of each effector abolished phosphoinositide binding (FIG. **8**A-F) (SEQ ID NO: 122, 124, 126).

Modulation of Effector Entry by Exogenous Phosphoinositides

[0095] The binding of phosphoinositides to the effector cell entry domains suggested that these phospholipids might serve as a cell entry receptor in each case. Tomato cells secreted PI-4-P when stimulated by fungal xylanase, suggesting that free PI-4-P might exist in the plant apoplast24. Therefore, increasing the concentration of free phosphoinositide by exogenous addition might stimulate RXLR and dEER-mediated uptake. To test this hypothesis, a soluble form of PI-4-P, di-octanoyl-PI-4-P (250 μM), was mixed with the Avr1b GFP fusion, Avr1b(N)-GFP, for 30 min prior to exposure to soybean roots. After 9 hr, strong stimulation of Avr1b(N)-GFP uptake by PI-4-P was evident (FIG. **9**A). The phospholipids, PI, PC and PE all did not stimulate uptake. Uptake of the fungal AvrL567(N)-GFP fusion (SEQ ID NO: 119) was also strongly stimulated by PI-4-P (FIG. **9**B), even though it binds most strongly to PI-3-P.

[0096] A synthetic cell entry motif composed of nine-arginine residues (Arg9) (SEQ ID NO: 112) was previously shown to deliver Avr1b into soybean leaf cells and into onion epidermal leaf cells in particle bombardment cell re-entry assays. The motif could also enable uptake of purified GFP into soybean root cells8 and into maize and onion cells. The mechanism of uptake has been proposed to be a plant form of macropinocytosis. The Arg9-GFP fusion protein binds PI-3-P, PI-4-P and phosphatidyl serine, albeit weakly (FIG. **9**D). FIG. **9**C shows that di-octanoyl-PI-4-P does not stimulate uptake of the Arg9-GFP fusion protein in soybean root cells, suggesting that the stimulation by PI-4-P is specific to RXLR and dEER-mediated uptake. This conclusion is supported by the observation that exogenous PI-4-P did not promote the uptake of Avr1b(N)-GFP (SEQ ID NO: 46) and AvrL567(N)-GFP (SEQ ID NO: 119) proteins containing alanine substitutions in the RXLR and dEER motifs.

[0097] Inositol-1,4-diphosphate (IP2) represents the hydrophilic head-group of PI-4-P. Preincubation with 100 μM IP2 inhibited binding of Avr1b(N)-GFP (SEQ ID NO: 46) to PI-4-P-containing liposomes and could completely block binding of AvrL567(N)-GFP (SEQ ID NO: 119) to PI-4-P-containing liposomes, presumably via competitive inhibition. To test whether IP2 could block effector uptake in planta, which would imply that a PI-4-P-like molecule mediated uptake in planta, Avr1b(N)-GFP (SEQ ID NO: 46) or AvrL567(N)-GFP (SEQ ID NO: 119) was preincubated with 500 μM IP2 for 30 min prior to exposure to soybean roots. IP2 almost completely blocked uptake of both Avr1b(N)-GFP (FIG. **9**A) (SEQ ID NO: 46) or AvrL567(N)-GFP (FIG. **9**B) (SEQ ID NO: 119) into soybean cells. IP2 could not inhibit the binding of Arg9-GFP to liposomes (FIG. **9**D) and uptake of Arg9-GFP (SEQ ID NO: 112) was completely unaffected by preincubation with IP2 (FIG. **9**C), supporting the conclusion that IP2 specifically blocks RXLR and dEER motif-mediated protein uptake.

Effector Entry into Human Cells

[0098] Phosphatidyl-inositol-phosphates are universally found in eukaryotic cells. Since a number of human and animal diseases are caused by fungi and oomycetes, as well as by apicomplexan parasites, we tested the possibility that RXLR and dEER motifs might mediate protein entry into human cells, using the human lung epithelial cell line A549 as a model. Avr1b(N)-GFP (FIG. **10**A) (SEQ ID NO: 46), AvrL567(N)-GFP (FIG. **10**B) (SEQ ID NO: 119) and PfHRPII(N)-GFP (FIG. **10**C) (SEQ ID NO: 123) (SEQ ID NO: 60) could all enter the A549 cells, but entry did not occur if alanine substitutions were present in the RXLR or Pexel motifs of the proteins (SEQ ID NO: 47,48,120,124). In these experiments, accumulation of the GFP fusion proteins inside

the cells was confirmed by the accumulation of GFP within vesicle-like structures within the cells, and by the fact that the cells were treated with protease (trypsin) prior to photographing. Protein accumulation was strongly inhibited in each case by 1,4-IP2, supporting the hypothesis that entry was mediated by phosphoinositide binding. Exogenous di-octanoyl-PI-4-P did not stimulate accumulation, suggesting that the availability of PI-4-P or other phosphatidylinositides in the growth medium was not limiting. Inositol 1,3 diphosphate (1, 3-1P2), the headgroup of PI-3-P, could also inhibit entry of PfHRPII (N)-GFP (FIG. **10**C) (SEQ ID NO: 123), consistent with the observation that the protein bound PI-3-P more strongly than PI-4-P in the filter-binding assay.

Discussion: Two independent assays, namely filter-binding and liposome-binding, demonstrated that the N-terminus of all seven effectors tested could bind to either PI-3-P or PI-4-P, but not to PI-5-P nor to any other phospholipids tested. The primary structures of the RXLR and dEER effector domains do not resemble any known phosphoinositide binding domains. However, the binding of the pathogen RXLR and dEER domains to phosphoinositides is concordant with the binding of the RXLR and dEER domains of rice and *Arabidopsis* (3-type PI-4-kinases. In the oomycete effector proteins, the dEER motif is variably spaced from the RXLR motif, so if residues from both motifs contact the phosphoinositide head group, the protein must fold so as to bring the two motifs into proximity. The three dimensional structure of the RXLR and dEER or Pexel domain is not yet available for any oomycete or apicomplexan effector proteins, respectively. However, the crystal structure of AvrL567 has been determined. In this structure, the RFYR motif adopts a beta-stranded conformation on the surface of the protein. It will be interesting to determine if the structure of AvrL567 changes in solution in the presence of a phosphoinositide.

[0099] The stimulation of protein entry into soybean root cells by PI-4-P and the inhibition of entry by IP2 together support the hypothesis that binding to phosphoinositides mediates entry of these pathogen effectors into plant cells. Similar findings with a human lung epithelial cell line suggest the possibility that effectors of oomycetes and fungi that infect humans and other animals might enter host cells via a similar mechanism. This mechanism appears to be different than reported for other peptides with cell entry activity because entry of those other peptides is not dependent on phosphoinositides.

[0100] These data demonstrate that several fungal effectors contain N-terminal domains that are capable of carrying Avr1b into soybean leaf cells. Within these domains are RXLR-like motifs that can replace the Avr1b RXLR motif in carrying reporter proteins into host cells. In the one case tested in detail so far, AvrL567, the motif RFYR was identified as necessary for the activity of the N-terminal cell entry domain, and for the binding of the domain to PI-3-P. The mutagenesis survey of the Avr1b RXLR motif and the diverse functional motifs found in the fungal effectors together suggest that a wide diversity of RXLR-like sequences support binding of phosphoinositides. Bioinformatic screens with the highly redundant motif suggested by the data identifies huge numbers of matches, most of which are likely spurious as judged by searches of permuted protein sequences. Thus, it is very likely that there are additional requirements for phosphoinositide binding. Both the RXLR and dEER motifs of Avr1b and the Pexel motifs of *Plasmodium* effectors are insufficient by themselves to facilitate cell entry; in both cases flanking sequences are required.

[0101] Other than in apicomplexan parasites, eukaryotic pathogens of humans and other animals have not been reported to produce effector proteins that can cross host membranes into the cytoplasm of host cells. The finding that phosphoinositide-binding effectors from oomycete and fungal plant pathogens can cross the membranes of human cells predicts that oomycete and fungal pathogens of humans and other animals may also utilize this mechanism to debilitate their hosts. Possible examples include oomycete pathogens of marine animals from the genera *Saprolegnia* and *Aphanomyces*, extracellular fungal pathogens such as *Pneumocystis carinii, Coccidioides iinnzitus* and *Aspergillus fumigatus*, and intra-phagosomal fungal pathogens of humans such as *Cryptococcus neoformans* and *Histoplasma capsulatum.*

[0102] The binding of phosphoinositides or other polar lipids to effector cell entry domains from diverse kingdoms will provide a powerful biochemical tool for screening or directly isolating new candidate effector proteins from all classes of microbes. It may also enable detection of phosphoinositide-binding plant proteins (or other polar-lipid-binding proteins) that can traffic through the apoplast and enter into target cells to transduce signals. Some precedents for such proteins already exist, such as the *Drosophila* antennapedia transcription factor that can move from cell to cell via an arginine-rich cell entry motif.

[0103] Understanding the role of phosphoinositides and other polar lipids in pathogen effector entry also opens the possibility of targeting cell entry domains for preventative or therapeutic intervention in both agriculture and medicine. The finding that 1P2 can block effector entry into both plant and human cells provides a proof-of-concept for this approach.

Methods Summary

[0104] Cloning was performed according to known molecular biology techniques. Proteins were expressed in *E. coli* BL21DE3 and purified using affinity chromatography. Plasmids and oligonucleotides used in the study are depicted in tabular form as FIGS. **13**A-F and FIGS. **14**A-D, respectively.

[0105] Soybean seeds were germinated in vermiculite for 3-5 days. Roots were washed with water thoroughly to remove any debris. Approximately 1.5 cm root tips were cut and placed into the protein solution (50 μl-25 mM MES pH 5.8, 50 μg protein) and incubated for 12-15 hr at 28° C. Then the root tips were rinsed with water and washed in 75 mL of water for 2 hr on an orbital shaker at 90 rpm. Roots were examined using a Zeiss LSM510 laser scanning confocal microscope with an argon laser excitation wavelength of 488 nm.

[0106] Lipid filter arrays were prepared by pipetting 1 μL PI-3-P, PI-5-P (Cayman Chemical), PS, PC, PE, PA, or PI-4-P (Avanti Polar Lipids, Cayman Chemical) at various concentrations on Hybond-C extra membranes.

[0107] Liposomes were prepared from a suspension of 0.71 μg/ml phosphatidyl-choline, 0.29 μg/ml phosphatidyl-ethanolamine (PC/PE) or 0.64 μg/ml phosphatidyl-choline, 0.26 μg/ml phosphatidyl-ethanolamine, 0.1 μg/ml phosphatidyl-inositol-phosphate (PC/PE/PI-x-P). The lipid mixtures were dried under vacuum overnight, then the resultant lipid films were rehydrated at 1 mg/mL (total lipid) in 20 mM Tris-HCl (pH 6.8) 100 mM NaCl, 2 mM dithiothreitol by three cycles

of freeze-thawing. Large unilamellar vesicles were formed by extruding the lipid suspension through a 0.1-μM filter (nucleopore track-etch membrane, Whatman) 20 times and were used immediately. Effector fusion proteins were centrifuged at 100,000 g for 20 min at 25° C. prior to assay to remove protein aggregates. 10 μg of protein was added to 50 μg of liposomes and incubated for 1 hr at room temperature. Protein-liposome mixtures were centrifuged at 100,000 g for 15 min at 25° C. Pellets containing liposome-bound proteins and supernatants containing free proteins, were then analyzed by SDS-PAGE.

Example 3

Assay for Screening Compound Libraries to Identify Novel Compounds that Interfere with the RXLR and dEER-Mediated Uptake of Effector Proteins into Plant or Human Cells

[0108] The binding of phosphoinositides (PI-3-P or PI-4-P) and phosphatidic acid to effector cell entry domains indicates that these phospholipids may serve as a cell entry receptors. Increasing the concentration of free phosphoinositide such as di-octanoyl-PI-4-P by exogenous addition stimulated RXLR and dEER-mediated uptake of the Avr1b GFP fusion, Avr1b (N)-GFP, into soybean roots and human cells. Furthermore, preincubation with inositol 1,4 diphosphate (IP2) inhibited binding of Avr1b(N)-GFP to PI-4-P-containing liposomes presumably via competitive inhibition. In addition, 1P2 almost completely blocked uptake of both Avr1b(N)-GFP into soybean root cells and human cells in cell culture. Therefore, an assay is devised for screening compound libraries to identify novel compounds that interfere with the RXLR and dEER-mediated uptake of effector proteins into plant or human cells, through inhibition of the binding of, or interaction between phospholipids PI-3-P or PI-4-P and RXLR and dEER motif containing proteins. Plasmids encoding the Avr1b sequence are expressed in BL21 *E. coli* cells and the protein are purified and diluted into appropriate binding buffer at an appropriate concentration, and thirty microliters are dispensed into each well coated 96 or 384 well plates using an automated dispenser. Through a robotized transfer mechanism involving steel pins, each of the Avr1b protein-containing wells (in a 96 or 384 well plate) receive 300 nanoliter of a compound from the compound libraries, followed by incubating the plate at room temperature for 60 minutes. An equal volume of 2× stock solution of fluorescently labeled soluble PI-4-P (Echelon Inc. BODIPY FL Phosphatidylinositol(4) Phosphate catalog #C-04F6a; BF-PI-4-P) is prepared in suitable buffer and 30 microliter of this solution is dispensed into each well of Avr1b coated preincubated 384 well plates using an automated dispenser. After BF-PI-4-P addition, the plate is incubated in dark for 60 minutes, followed by the measurement of fluorescence, utilizing a Synergy plate reader integrated with a biostack. The reactions are performed in duplicates and with negative controls, where the interactions are measured in the absence of the protein or fluorescently labeled BF-PI-4-P, and positive controls where the interaction is measured in the presence of a range of concentrations of inositol 1,4 diphosphate (IP2). The readouts are stored and analyzed for the identification of potential inhibitors of the reaction. Statistical analysis are performed utilizing a combination of parameters and compounds that showed statistically significant inhibition are selected. Briefly, the background absorbance is subtracted from the test reads. Subsequently, the net absorbance is compared to controls wells, that did not receive the test compounds and the percent decrease in absorbance is measured by the following formula: Percent inhibition=[(Fluorescence in test well/Fluorescence in control wells)×100]. In excess of one hundred thousand drug-like, diverse heterocyclic chemical compounds are screened during this process for their potential to inhibit the interactions between BF-PI-4-P and Avr1b. These compounds are obtained from several sources including established chemical vendors like Asinex, Analyticon, Biomol, Bionet, ChemDiv, Enamine, Maybridge, Spectrum, TimTec as well as a range of diversity oriented synthesis compounds that have been generated by academic research laboratories from around the world. Typical screening identifies several hundred compounds that inhibit the reaction at a statistically significant >40% levels. Successful events in this initial screen lead to the consolidation of select wells from the original library stock to generate a new second generation of plate for screening the activity of these compounds at three compound concentrations to allow the calculation of a preliminary 1050 value. A select group of compounds is then selected that showed >50% inhibition. Larger quantities of select compounds are ordered from the specific vendors (above) for rescreening in the soybean root or human cell uptake assays for their potential to inhibit the uptake of Avr1b (N)-GFP into soybean roots cells or human cells in culture.

Example 4

Screening Assays for Novel Compounds that Inhibit Plant Oomycete or Fungal Infection Through Blocking of RXLR and dEER Containing Effector Protein Action

[0109] To further characterize candidate protective compounds obtained from the RXLR and dEER protein screen, the ability of the compounds to protect against oomycete or fungal pathogen infection are tested in detached leaf assays. The following detached leaf assays are used for soybean, potato, tomato, tobacco, grape, rice, and wheat. The assays are used to test for infection by *Phytophthora* oomycete pathogens (soybean, potato, tomato, tobacco), downy mildew oomycete pathogens (tobacco and grape), rust fungi (soybean and wheat), *Magnaporthe* blast fungi (rice and wheat), and powdery mildew fungi (soybean, potato, tomato, tobacco, grape, wheat).

[0110] Expanded leaves are removed from young growth chamber-grown plants with the petioles intact (soybean, potato, tomato, tobacco, grape), or are clipped from the mother plant with sterile scissors (wheat and rice). The petioles or cut ends of the leaves are placed into plastic test tubes containing an aqueous solution of a suitable range of concentrations of each compound (determined from the biochemical IC_{50}). The leaves are then fastened into a horizontal position, but with the petioles or cut ends bent down into the tubes. The plants are then placed in a lighted growth chamber at 30% humidity for 6 hr to enable the compounds to be drawn into the leaves by transpiration.

[0111] The plants are then inoculated with pathogen spores. *Phytophthora* infections (*P. sojae* on soybean; *P. infestans* on tomato and potato; *P. parasitica* on tobacco) are initiated by spraying the leaves with an aqueous suspension of zoospores at a suitable concentration. Infections with rust fungi (*Phakopsora pachyrizi* for soybean; *Puccinia striiformis* f. sp. *tritici* (stripe rust) *Puccinia triticina* (leaf rust),

Puccinia graminis f. sp. *tritici* (stem rust) for wheat) are initiated by spraying the leaves with an aqueous suspension of urediniospores at a suitable concentration. Infections with downy mildew oomycetes (*Peronsopora tabacina* on tobacco; *Plasmopora viticola* on grape) and infections of *Magnaporthe* blast fungi (*Magnaporthe oryzae* for rice; *Magnaporthe grisea* on wheat) are initiated by spraying the leaves with an aqueous suspension of conidia at a suitable concentration. In each case, after spraying with the pathogen spore suspension, the plants are replaced into the growth chamber at high (90%) humidity at a suitable temperature (15° C. for *Phytophthora infestans* and downy mildew oomycetes; 25° C. for *P. sojae*; 20° C. for all others) until symptoms develop (3-7 days). Infections with powdery mildew (*Microsphaera diffusa* on soybean; *Erysiphe cichoracearum* on potato and tobacco; *Leveillula taurica* on tomato or potato; *Erysiphe necator* on grape; *Blumeria graminis* f. sp. *tritici* on wheat) are done dry. The arrays of plant leaves are placed into a dusting tower and heavily infected leaves are introduced into the top of the tower and shaken vigorously for one minute, then the spores are allowed to settle for 20 min. The plants are replaced into growth chambers maintained at 70% humidity (except *Microsphaera diffusa* which is favored by low humidity of 30%) and 25° C.

[0112] To assay disease development in each case, the leaves are photographed, and from the photographs the numbers of lesions on each leaf are counted (total lesions and sporulating lesion) and the areas of the lesions are determined digitally. The results are assessed statistically by reference to negative controls (water), positive controls (benomyl for the fungi and metalaxyl for the oomycetes).

Example 5

Protecting Plants Against Oomycete Infection by Blocking Effector Entry Using Peptide Receptor Mimics

[0113] Eukaryotic pathogens such as oomycetes, fungi and apicomplexan parasites deliver hundreds of effector proteins into the cytoplasm of their host cells. Delivery of these proteins is key to the pathogenic success of these organisms. The similarity between oomycete and apicomplexan effector delivery systems has been noted for some time. The discovery that inositol 1,4 diphosphate can inhibit oomycete and fungal effector uptake (Example 2) shows that effector entry can be blocked by externally applied small molecular weight compounds. This Example describes experiments that test whether infection by oomycetes, and possibly by fungi, can be mitigated by inhibiting effector entry using host-synthesized peptides that mimic inositol 1,4 diphosphate. Biotrophic and hemi-biotrophic oomycete pathogens that are likely to use RXLR and dEER effectors include more than 80 species of *Phytophthora* and more than 500 species of downy mildews that together attack almost every crop species and horticultural species of economic importance. Peptides that could inhibit RXLR and dEER effector entry could thus provide broad-spectrum protection against many of these pathogens. Even if protection is narrow, and multiple peptides must be selected for each species of pathogen, this approach offers an important new weapon against these highly adaptable pathogens. The fact that one fungal effector from a rust pathogen also may use phosphoinositides to enter host cells suggests that the protection provided by anti-RXLR and dEER peptides may extend to many biotrophic and hemi-biotrophic fungal pathogens such as rusts, smuts, powdery mildews and the rice blast fungus.

[0114] At least three commercially available phage display libraries are screened against a panel of effectors that have been well-characterized and/or are strongly expressed at the outset of *P. sojae* or *P. infestans* infection. The phage are eluted from the effectors using a rising concentration gradient of IP2 or soluble PI-P in order to identify those phage that have the greatest affinity for the PI-P binding sites of the effectors. The candidates obtained are evaluated for their binding to all panel members, and to RXLR and dEER mutants of the panel members. In addition, their affinity for both soluble and liposome-bound PI-4-P and PI-3-P is measured. Synthetic peptides corresponding to candidates with the highest affinities are prepared commercially and tested for their ability to inhibit uptake into plant and human cells. The most promising peptides at this point (broadest specificity, highest affinity and/or strongest inhibition of effector entry) are targeted for optimization of their breadth and affinity of binding. Two optimization strategies are used. Firstly, PCR-directed random mutagenesis of selected peptides is carried out and high affinity, broad-spectrum mutants are selected by phage display. Loss-of-activity mutants are also characterized to help identify important residues. As a parallel alternative approach, targeted mutagenesis of selected peptides is carried out based on bioinformatic analysis of all the phage peptide sequences obtained (both high quality and low quality peptides). Surface Plasmon resonance and NMR characterization of the binding of the most promising peptides to their target effector(s) also yields important information. The cycle of selecting promising peptides and optimizing them is repeated as needed, or until little further improvement is obtained. At this point the most promising peptides are fused to selected secreted plant proteins, and the chimeric proteins are expressed in plant tissues by transient expression. The expression levels and stabilities of the chimeric proteins are assessed, as well as the ability of the expressed proteins to reduce entry of effector proteins and reduce infection by *P. sojae* or *P. infestans*. The resistance of the plant tissue to additional pathogens is also evaluated. Stable transgenic plants expressing the chimeric proteins are produced, and are evaluated systematically for disease resistance against diverse pathogens.

[0115] Initially the Ph.D.-C7C random peptide phage display library available from New England Biolabs, Inc. is screened. In this library, a loop of 7 random amino acid residues is constrained by a disulfide bond at the base of the loop where it is fused to the N-terminus of the pill coat protein. This configuration was chosen because the loop will eventually be transferred to a secreted plant protein, and the disulfide bond will ensure that the loop has a similar structure in that context as on the phage. The library contains 1.2×10^9 independent phage, providing about 60% statistical coverage of the total theoretical complexity of a heptapeptide library ($207=1.3\times10^9$). Other possible libraries for screening include Ph.D.-7 and the Ph.D.-12 libraries that contain 7 or 12 random residues respectively, but without a disulfide bond; both have a complexity of around 2.8×10^9.

[0116] Two approaches are used to select RXLR and dEER-specific phage. In the first, individual effectors are screened. Since this allows interactions with residues outside the immediate RXLR and dEER region, inhibitory peptides with a narrow specificity are likely to be obtained. In a

complementary approach, the phage are selected on several different effectors successively, in order to only obtain peptides with broad specificity. Both strategies are adjusted as needed.

[0117] The one-effector-at-a-time strategy targets Avr1b, Avh331 (Avr1k), Avh5, Avh6 and Avh172. Because the first two effectors are avirulence gene products that trigger plant defense responses mediated by resistance (R) genes, the efficacy of candidate inhibitory peptides is also tested in planta by their ability to inhibit the R gene mediated response to the effectors. Avh6 and Avh172 are major early-expressed effectors, so targeting them singly also has a measurable effect on pathogen virulence. Avh5 is included because its NMR characterization is well advanced. In each case, two different fusions are produced: GFP and GST (glutathione-S-transferase) to reduce the chance of selecting phage that bind to an irrelevant part of the protein.

[0118] In the second strategy, three pools of effectors are created, and the phage are successively selected on the different pools. One example of such a set of pools is: pool 1=Avr1b+Avh331+Avh6; pool 2=Avh5+Avh172+Avh152; pool 3=Avh38+Avh260+AvrL567. Each effector listed is either an avirulence protein or a strongly-early-expressed *P. sojae* effector, or is otherwise well-characterized. By using pools, the risk that a single chosen effector may be problematic is reduced, and by using three different pools for the successive selection steps, the likelihood of finding broad specificity peptides is increased. The order of the pools used for selection is varied. The composition of the pools may be varied once data on the specificity of each effector for PI-3-P or PI-4-P is available, and/or if production of some chosen effector proteins in *E. coli* proves problematic.

[0119] Panning is carried out in microtiter tray wells; if sufficient enrichment of peptides is not seen in the wells, then the proteins are bound onto beads and the beads are used for panning. The phage are step eluted with different concentrations of inositol diphosphates (1P2) or soluble (e.g. di-hexanoyl) phosphatidyl phosphates. The choice of 1,3 IP2, 1,4 IP2, PI-3-P or PI-4-P, and the choice of concentrations is finalized once more precise data on the binding constant of the effectors for the phosphoinositides is available.

Characterization of Discovered Peptides for Binding to Multiple Effectors, and for Ability to Block Entry of Key Oomycete and Fungal Effectors into Plant Cells.

[0120] Each selected peptide is screened against a panel of all the effectors mentioned listed above, plus a selection of 10 *P. infestans* infection-induced effectors and several fungal effectors. RXLR and dEER region mutants are included to identify peptides that interact with those motifs. Phage with the broad specificity and a set of peptides with complementary sets of targets are identified. Screening is done in a western dot blot format in which effectors bound to a filter are probed with the phage and then with an anti-M13 antibody. Alternatively, the phage are panned against effectors arrayed in microtiter wells, and then detected by spotting onto an *E. coli* lawn with a replicator. The affinity of the phage for the effector is initially estimated by doing binding experiments in the presence of different concentrations of PI-Ps or IP2s. An oomycete effector protein microarray containing all 1440 effectors from *P. sofae, P. infestans, P. ramorum* and *H. arabidopsidis* is ideal for comprehensive screening of the most promising phage. The most promising peptides are tested for the ability to block effector-GFP entry into root cells. To obtain sufficient peptides for these experiments, synthetic peptides are ordered from a commercial supplier. A quantitative cell entry assay using luciferase and suspension culture cells may also be employed. Binding of the most promising peptides to key effectors is further characterized by NMR and surface plasmon resonance (SPR).

Concatenation and Mutagenesis of the Most Promising Peptides to Further Optimize Broad-Spectrum Binding and Ability to Block Effector Entry into Plant Cells.

[0121] Bioinformatic comparisons of peptide sequences having different affinities and ranges of specificity provide important starting clues about the potential for using targeted mutations to improve affinity and specificity of the identified peptides. Alternatively, phage display technology is a proven platform for improving binding via random mutagenesis. A single randomized oligonucleotide is used to mutagenize the 21 nucleotides encoding each peptide loop. Selection of phage on a range of different effectors is used to improve the breadth of specificity. Selection of phage in the presence of free peptide having the original sequence is used to select for improved affinity. An alternative approach to improving the breadth of specificity is to concatenate several peptides, with a spacer or linker sequence in between. This is an acceptable construction for in planta expression. The concatenated peptides are tested to ensure that they retain their original affinities and breadth of specificity.

Fuse Peptides to Small Secreted Plant Proteins, and Test the Effects of their Expression in Planta on Effector Entry and on Disease Resistance.

[0122] For evaluation in planta, the peptide mimics are fused to larger proteins normally produced during infection to promote the peptides' stability and reduce their potential susceptibility to endogenous plant proteases. The fusions are evaluated in three steps: (i) exogenous application of purified proteins to plant tissues; (ii) transient expression in plants; and (iii) expression in stable transgenic plants. A variety of candidate proteins are evaluated for fusions with the peptide mimics, including highly stable plant proteins such as PR1a, lipid transfer proteins, protease inhibitors and proteases. Fusion to a protease inhibitor promotes stability, while conversely, fusion to a protease more effectively targets pathogen effectors for proteolysis. Generally, the mimic is attached to the C-terminus of the "carrier" protein via a suitable spacer so that the native N-terminal secretory leader can be used. Initially a single peptide mimic is attached to each carrier. Once attachment of single peptides has been validated, multiple peptides are attached in tandem to improve the breadth of binding and/or for better efficacy against effectors with multiple phophoinositide binding sites. C-terminal green fluorescent protein (GFP) fusions are used to evaluate the stability and localization of the proteins in planta.

Expression in *E. coli* or *Pichia pastoris* and Evaluation of Purified Proteins.

[0123] Fusion proteins are expressed in *E. coli* or, due to the necessity to correctly form disulfide bonds, in eukaryotic expression system based on *Pichia pastoris*. The purified peptide-fusion proteins are tested for effector binding in vitro to ensure they retain binding activity as fusions. They are then introduced into leaf and root tissues (by infiltration and direct uptake, respectively) from soybean and *N. benthamiana* to test their stability in planta (via western blots) and to test their ability to inhibit the uptake of exogenously applied effector-reporter fusions into the plant cells. Uptake assays based on

suspension cultures cells and on protoplasts may also be used to distinguish between stability and effectiveness in effector uptake inhibition.

Transient Expression in Planta.

[0124] Excellent virus-based transient expression systems now exist for soybean and *Arabidopsis*. Infiltration of *Agrobacterium tumefaciens* strains harboring vectors designed to deliver gene expression constructs into plant cells locally (Agroinfiltration) and particle bombardment have also been used extensively. Initially a quantitative "double-barrel" particle bombardment assay is used to measure the ability of plant-expressed peptide fusion proteins to interfere with effector entry into soybean cells, using either the native effectors, Avr1b or Avh331 (i.e. Avr1k), or fusions of other effectors to an Avr1b reporter. By using GFP-fusions in conjunction with onion epidermal cell bombardment direct visualization of the localization of the peptide fusions or the targeted effector (or both together if one carries a red fluorescent protein, e.g mCherry) is possible. Bi-molecular fluorescence complementation (BiFC; "split-YFP") is used to verify effector-peptide interaction in planta in the onion system.

[0125] In order to evaluate the potential effect of peptide-fusion expression in planta on pathogen infection, the BPMV system is used to transiently express the peptide fusion proteins in soybean and Agroinfiltration to transiently express the proteins in *N. benthamiana*. Versions that include GFP to facilitate evaluation of stability and localization are used. Transcription of the constructs is confirmed using RT-PCR or northern analysis. Protein levels are evaluated by western blots, and confocal microscopy is used to verify that the proteins are being delivered to the apoplast.

[0126] Areas of plant tissue transiently expressing the peptide fusions are inoculated with *P. sojae* (soybean) or *P. infestans* (*N. benthamiana*) and disease development is evaluated. Empty vectors and vectors with the entire construct minus the peptide mimic are used as negative controls in these experiments. *N. benthamiana* tissue is tested for its response to the blue mold downy mildew pathogen *Peronospora tabacina*. Soybean leaf tissue is tested for resistance to the soybean rust fungus, *Phakopsora pachyrhizi*.

[0127] Hairy root cultures of soybean expressing the peptides are created, and assayed them for *P. sojae* resistance, to show that expression of Avr1b and Avh331 confers increased susceptibility to *P. sojae*. Stably transformed soybean, *N. benthamiana* and *Arabidopsis* plants expressing the fusion proteins are tested and display resistance to a variety of oomycete and fungal pathogens.

Example 6

Identification of Additional Virulence Motifs

[0128] The previous Examples present results showing that a fungal effector protein, AvrL567, from a rust fungus that forms haustoria (specialized feeding structures) enters plant cells via RXLR sequence motif-mediated binding to a phosphatidylinositide within the plant cell wall. In this Example, results are presented which show that effector protein Avr2 from the tomato pathogen *Fusarium oxysporum* Esp. *lycopersici* and effector protein AvrLm6 from the *Brassica* pathogen *Leptosphaeria maculans* also enter plants via the same mechanism. *Fusarium oxysporum* f.sp. *lycopersici* is a xylem dwelling pathogen and *Leptosphaeria maculans* is an apoplastic pathogen.

[0129] AvrLm6 contains two RXLR-like sequences, RYWT and RTLK. Mutations in the second motif (RYWT) but not the first (RTLK) abolish entry of AvrLm6-GFP fusions into root cells (FIG. **16**A). Avr2 also contains two RXLR-like sequences, RMLH and RIYER. Mutations in the second motif (RIYER) but not the first (RMLH) abolish entry of Avr2-green fluorescent protein (GFP) fusion proteins into root cells (FIG. **16**B). Both effector-GFP fusions bind PI-3-P strongly, PI-4-P moderately and PI-5-P weakly, but there was no binding to any other lipids (FIGS. **16**C and D). In each case, the PI-P binding is dependent on the functional RXLR-like sequences, RYWT (in AvrLm6) and RIYER (in Avr2). Entry of AvrLm6 (FIG. **16**E) and Avr2 (FIG. **16**F) is inhibited in both cases by inositol 1,4 diphosphate (FIG. **16**E), inositol 1,3 diphosphate (not shown) and by the PI-3-P binding proteins VAMp7 PX, indicating that entry into the soybean root cells is dependent on the presence of PI-3-P.

[0130] It has been found that GFP fusions to the N-termini of three more fungal effectors or effector-like proteins bind PI-3-P. The proteins are *Leptosphaeria maculans* effector AvrLm4/7 and two bioinformatically-predicted effector-like proteins from the human pathogens *Cryptococcus neoformans* (Cng2; AAW43853.1) and *Aspergillus fumigatus* (Af2; XP_752996.1). Each N-terminal domain contains potential RXLR-like motifs (FIG. **17**A).

[0131] These findings extend previously findings that several effectors from oomycete plant pathogens and apicomplexan pathogens of vertebrates (e.g. *Plasmodium falciparum*) bind phosphoinositides, particularly PI-3-P, which enables them to enter plant and animal cells.

Example 7

Occurrence of RXLR-Like Motifs in Effector Like Proteins from a Wide Diversity of Oomycetes, Fungi and Insects

[0132] Using a bioinformatic approach informed by detailed mutagenesis of the Avr1b RXLR motif, we have identified candidate RXLR-like motifs in 20 experimentally validated fungal effectors, as well as in 13 experimentally validated oomycete effectors (Table 1). The fungal effectors include an effector (MiSSP7) from a mutualistic ectomycorrhizal fungus, *Laccaria bicolor* (Martin et al., 2008).

[0133] Some sucking and chewing insects produce effector-like proteins, including hessian flies (*Mayetiola destructor*) (Behura et al., 2004) and pea aphids (*Acyrthosiphon pisum*) (Mutti et al., 2008). We have identified candidate RXLR-like motifs in the N-terminus of effectors vH9 and vH13 from *Mayetiola destructor*, and in the effector C002 from *Acyrthosiphon pisum* (Table 3).

[0134] Among oomycetes, RXLR-containing effectors have so far been documented in pathogens from the order Peronosporales. We have identified RXLR-like motifs in bioinformatically predicted effectors from *Pythium ultimum* (Pythiales) and *Albugo candida* (Albuginales), suggesting that RXLR-like effectors may be common to the entire oomycete Phylum (Table 4).

[0135] We have also identified RXLR-like motifs in bioinformatically predicted effectors from the necrotrophic plant pathogens *Pyrenophora tritici-repentis* and *Alternaria brassicicola*, and from the human pathogens *Cryptococcus neoformans, Aspergillus fumigatus* and *Coccidioides immitus* (Table 4).

[0136] Thus, phosphoinositide binding, particularly to PI-3-P, is a common property of most if not all eukaryotic effectors that can autonomously enter host plant or animal cells across their plasma membranes, including effectors produced by host-associated oomycetes, fungi and animals (e.g. insects and nematodes), and including pathogens, mutualists, commensals, ectosymbionts and endosymbionts. A further corollary is that chemical or transgenic control measures that target the interaction of RXLR-like sequences with phosphoinositides will potentially be effective against a wide range of oomycete, fungal and animal pathogens.

TABLE 3

RXLR-like sequences in experimentally verified effectors.

Effector	Species	King-dom	N-terminal Amino Acid Sequence
Avr1a	*Phytophthora sojae*	O	SENAFSAATDADQATVSKLAAAEFDTLVDV LTTESKRSLRATVDDGEER (SEQ ID NO: 304)
Avr1b	*Phytophthora sojae*	O	TEYSDETNIAMVESPDLVR*RSLR*NGDIAGGR FLRAHEEDDAGERTFSV (SEQ ID NO: 305)
Avr1k	*Phytophthora sojae*	O	LTCATSEQQTRPELCFFFSVRSSWPSTISDGA CLALVSAEQGATAGRNTL*SLRSMM*ATEDM ATST**RSLR**SQATNVDDDANVSIENR (SEQ ID NO: 306)
Avr3a	*Phytophthora sojae*	O	LSTTNANQAKIIKGTSPGGHSPRLLRAYQPD DEGDSPEDR (SEQ ID NO: 307)
Avr3c	*Phytophthora sojae*	O	VEPSATSTVEVAEVQARGADKRFLRSLQTE EE QGDSDVNEAEDGSEER (SEQ ID NO: 308)
Avr46	*Phytophthora sojae*	O	ITDESQPRDATIVDAPLTGRGANARYLRTST SIIKAPDAQLPSTKAAIAS (SEQ ID NO: 309)
Avh172	*Phytophthora sojae*	O	TAEVDSKTALAAEVPAAIRSLESDTPASRLL RTGTVTSADNEDR (SEQ ID NO: 310)
Avr3a	*Phytophthora infestans*	O	IDQTKVLVYGTPA*HYIH*DSAG**RRLLR**KNEE NEETSEER (SEQ ID NO: 311)
Avr4	*Phytophthora infestans*	O	KADSLARTVSVVDNVKVKSRFLRAQTDEK NEER (SEQ ID NO: 312)
AvrBlb1	*Phytophthora infestans*	O	AVSSNLNTAVNYASTSKIRFLSTEYNADEKR SLRGDYNNEVTKEPNTSDE (SEQ ID NO: 313)
AvrB1b2	*Phytophthora infestans*	O	VAAFPIPDESRPLSKTSPDTVAPRSLRIEAQE VIQSGR (SEQ ID NO: 314)
Atr1	*Hyaloperonospora arabidopsidis*	O	TESSETSGTIVHVFPLRDVADHRNDA LINRALRAQTALDDDEER (SEQ ID NO: 315)
Atr13	*Hyaloperonospora arabidopsidis*	O	LLHAHALHEDETGVTAGRQLRAAASEVFGL SRASFGLGKAQDPLDKFF (SEQ ID NO: 316)
AvrLm1	*Leptosphaeria maculans*	F	SPATKNNVNQPLDNISRRSEWKSVQIS PVKEHSAKTADNTENNHNLEKRVFTSP HMKRTFTLALENTFYAMAWLIDFSFS EEGEPHFSYKLQ (SEQ ID NO: 317)
AvrLm4/7	*Leptosphaeria maculans*	F	CREASISGEIRYPQGTCPTKTEALNDC NKVTKGLIDFSQSHQRAWGIDMT (SEQ ID NO: 318)
AvrLm6	*Leptosphaeria maculans*	F	QPHLLCACESGRRDGVDDT*RTLK*VVKGTGG RFVFSS**RYWT**KAEGAPHE (SEQ ID NO: 319)
Avr-Pita	*Magnaporthe oryzae*	F	HPVYDYNPIPNHIHGDLKRRAYIERYSQCS DSQASEIRAALKSCAELASWGYHAVKSD NRLFKLIFKTDSTDIQN (SEQ ID NO: 320)
Avr-Pii	*Magnaporthe oryzae*	F	LPTPASLNGNTEVATISDVKLEARSDTTYHK CSKCGYGSDDSDAYFNHKC (SEQ ID NO: 321)

TABLE 3 -continued

RXLR-like sequences in experimentally verified effectors.

Effector	Species	King-dom	N-terminal Amino Acid Sequence
Avr-Pia	*Magnaporthe oryzae*	F	RFCVYYDGHLPATRVLLMYVRIGTTATITA RGHEFEVEAKDQNCKVILTNG (SEQ ID NO: 322)
Avr-Pizt	*Magnaporthe oryzae*	F	SFVQCNHHLLYNGRHWGTIRKKAGWAV RFYEEKPGQPKRLVAICKNA (SEQ ID NO: 323)
Avr-PikD	*Magnaporthe oryzae*	F	ETGNKYIEKRAIDLSRERDPNFFDHPGIPVPE CFWFMFKNNVRQ (SEQ ID NO: 324)
Avr1 (Six4)	*Fusarium oxysporum f. sp. lycopersici*	F	LPKGEEGDIIGTFNFSSSDSQPLKIHWVDTPD SSGSNLVKRSA (SEQ ID NO: 325)
Avr2 (Six3)	*Fusarium oxysporum f. sp. lycopersici*	F	LPVEDADSSVGQLQGRGNPYCVFPGRRTSS TSFTTSFSTEPLGYA*RMLHR*DPPYERAGNSG LNH**RIYER**SRVGGLRTVIDV (SEQ ID NO: 326)
Avr3 (Six1)	*Fusariuin oxysporum f. sp. lycopersici*	F	QEAAVREPQIFFNLTYTEYLDKVAASHGSPP DKSDLPWNDTMGSFPGNETDDGVQTETGSS LSRRGHIVNLRKREPFGEESRNDRVTQD (SEQ ID NO: 327)
Six2	*Fusarium oxysporum f. sp. lycopersici*	F	NPAGDSLPDDAHLPDRRLSPSEVQALKKAQ IYPPGYIHKRVTFGEGKDAV (SEQ ID NO: 328)
Six5	*Fusarium oxysporum f. sp. lycopersici*	F	RDHQYCACQSGSGDSIDIDATTQLQNDNS KSYLWAQTSPAYWFADRHK (SEQ ID NO: 329)
Six6	*Fusarium oxysporum f. sp. lycopersici*	F	GPLAQTESESADVAEHTINYIDIAPEEFEPPK ANLSSLVSRDTLPVST (SEQ ID NO: 330)
AvrL567	*Melampsora lini*	F	MEHVPAELTRVSEGYT**RFYR**SPTASVILSG LVKVKWDNEQMTMPLFKWIG (SEQ ID NO: 331)
AvrM	*Melampsora lini*	F	SLSNNLGTVPDVPHQIPNDKSGTPAIEDPKA AIEDPKDMKGFNKALKSTPESEKLGTSSVE GIPQPEFDRGFLRPFGAKMKFLKPDQVQ KLSTDDLITYM (SEQ ID NO: 332)
AvrP123	*Melampsora lini*	F	QYVVDPGFGEIECMCGQIARLTQRPFDVE CEAT (SEQ ID NO: 333)
AvrP4	*Melampsora lini*	F	EFLEDARDIQGFSRKSGSKLEEESDSSRDRQ (SEQ ID NO: 334)
STP1	*Ustilago maydis*	F	NGSISNASHHHQRRMVRQRHIEARSAMSWL TKISSKASDWMFGSVHAPNLDKKDLPKPLV GGVAVMPKMPY (SEQ ID NO: 335)
MiSSP7	*Laccaria bicolor*	F	SPVPGEVGLVERGPIPNAVFRRVPEPNFFKD LLRALGQASQGGDLHR (SEQ ID NO: 336)
C007	*Acyrthosiphon pisum*	I	SAAEPYDEQEEASVELPMEHRQCDEYKSKI WDKAFSNQEAMQLMELTFNTGKELGSHEV (SEQ ID NO: 337)
vH13	*Mayetiola destructor*	I	SPLPLAYTDQVYDACDRQFDETVRNSQPL (SEQ ID NO: 338)

TABLE 3 -continued

RXLR-like sequences in experimentally verified effectors.

Effector	Species	King-dom	N-terminal Amino Acid Sequence
v19	*Mayetiola destructor*	I	LVLDTRAMPETDFEKALKEWNRVQTLVLIA PEQRRTMVLIAEHLTNLKKMNVDSPGGSFL YLKDGDPVIKLPSVEHFEITFRGPYGVDKNF SFYMPKLKKLIVRDADANDKKIIKFVSQHS RTLKTLDLVAANYRTLRTLGAMKHIEEFVT SPP (SEQ ID NO: 339)

Effectors named AvrXXX are avirulence gene products.
Motifs experimentally verified as functional are in bold and underlined.
Motifs experimentally determined to be non-functional are marked in italics.
Putative motifs are underlined.
Sequences shown are from the N-terminus of the respective proteins.
Note that *Laccaria bicolor* is a mutulasitic fungus.
Kingdoms:
O = oomycetes;
F = fungi;
I = insects

TABLE 4

RXLR-like sequences in bioinformatically predicted effectors.

Predicted Effector	Species	King-dom	N-terminal Amino Acid Sequence
Avh5	*Phytophthora sojae*	O	TRVPDDANLQSVNAPVQTVTRS**RRLLR**TADT DIVYEPKVHNPGKKQVFIE (SEQ ID NO: 340)
PYU1_T005878	*Pythium ultimum*	O	MMPSTDAHGYIAFPPAQYKDPATATNYNAIIT ASINTAFACKKWDDNPTANTKTF TAAFKKSG YTSLKQMLDKKVPGCQNSRTDFTPIKTKTYK TMEWQND (SEQ ID NO: 341)
PYU1_T001475	*Pythiun ultimum*	O	HSQMTVPNPKFSDVSKANSPLGTIDGPTVMPP PAGQSYAMGTDTNIKAYVEAFAKQTKWKTL KDLIMDKYVEDGNIPDRACGLTDKTYMQPLP DKYVVW (SEQ ID NO: 342)
AcEff1	*Albugo candida*	O	STMGLSNSRHLEDAVERVLGDLKLNQKDEKQ NENEVDKNNSKGKDRESS (SEQ ID NO: 343)
Af13	*Aspergillus flavus*	F	AGLPVFPNQAVLRPSLALPGDNSHRYSLPMFD LQPWERVDEIRLARKGYLYGSP (SEQ ID NO: 344)
PTRG_02320	*Pyrenophora triticirepentis*	F	QVKGNAIRCGQDDKSDQDTRNFCRFMFTSD RTLKINGEFRGNA (SEQ ID NO: 345)
AB09791.1	*Alternaria brassicicola*	F	APASYPASALGKRWVDTTGGQKMPAHFVST VRKLSTEKLKTKRQLDQLL (SEQ ID NO: 346)
Cng1	*Cryptococcus neoformans*	F	LTVPQAHRETLEEAGKLTTIAAINTKKLIKDV TVGTMSSVFPDGTDNGGRP (SEQ ID NO: 347)
Cng2	*Cryptococcus neoformans*	F	IQQGQKANAREQHRGRKTNLTIKLPGAHSYK AKFEGCMVVLQDKKLYVEHAGCESLAYAHP (SEQ ID NO: 348)
Af1	*Aspergillus fumigatus*	F	IPSAFPQDNAVNQVLLSDSYQDQSVSSISAED DAQNSAVIHIGESETMRAPSWFTSTLMARRLL ALSTTGTVSTIFPDPLPGNSHAPPSVAGLP (SEQ ID NO: 349)
Af2	*Aspergillus fumigatus*	F	VAMGVSEQRKANERKMDARRMARFNIDIETS GETQEEDEIRGKRIVLRDNKVYLDDPLPANRK HPSHTAESFYIDYP (SEQ ID NO: 350)

TABLE 4 -continued

RXLR-like sequences in bioinformatically predicted effectors.

Predicted Effector	Species	King-dom	N-terminal Amino Acid Sequence
Af3	*Aspergillus fumigatus*	F	PVVPGQTVMEPSAALPDDGDHLYTLPMFDIR PWERVSEVRLAREGYLYG (SEQ ID NO: 351)
Ci1	*Coccidioides immitus*	F	SPVFPGGDKRDALYQKPIAPAGEFPFDSSPPEA RMTIPYADNEPDSSLSIPSWPTTHLLARRLLGL STTGVLSTVFPRTNRDPALVGVP (SEQ ID NO: 352)
Ci2	*Coccidioides immitus*	F	IRSSQRSQRRQEHRSRKMNLIVSCSDPSRKSK DVDGCFVVLRNHKLWIASRPSDGEANEPSDD ATRFKASLHQCHH (SEQ ID NO: 353)

Motifs experimentally verified as functional are in bold and underlined.
Putative motifs are underlined.
Sequences shown are from the N-terminus of the respective proteins.
Note that *Cryptococcus neoformans*, *Aspergillus fumigatus* and *Coccidioides immitus* are human pathogens. *Pyrenophora tritici-repentis* and *Alternaria brassicicola* are necrotrophic plant pathogens.
Kingdoms:
O = oomycetes;
F = fungi.

Example 8

Phosphatidylinositol-3-phosphate is the Natural Target of RXLR(-Like) Effectors

[0137] Of the eight oomycete and fungal effectors tested to date, seven have a preference for binding to PI-3-P, and one (Avr1b) has a preference for PI-4-P. Neither of PI-3-P nor PI-4-P has been reported to occur in the outer leaflet of the plasma membrane of plant or animal cells (Boon et al., 2002). Two papers have reported secretion of PI-4-P by plant cells (Regente et al., 2008; Gonorazsky et al., 2008).

[0138] In order to test directly for the presence of PI-3-P and PI-4-P, we fused the PX domain of VAM7p and the PH domains of the human proteins FAPP1 and PEPP1 to green fluorescent protein (GFP). PEPP1 and FAPP1 bind very specifically to PI-3-P and PI-4-P, respectively (FIG. **18**A) (Dowler et al., 2000). VAM7p has a preference for PI-3-P but can bind weakly to PI-4-P and PI-5-P (FIG. **18**A) (Lee et al., 2006). The GFP fusion proteins were used to stain the surface of cells of human lung epithelial cell line A549 and soybean root cells. The results reveal very clearly that PI-3-P is present uniformly on the outer surface of roots cells (FIG. **18**B), and at specific sites on the surface of the epithelial cells (FIG. **18**C).

[0139] As can be seen, PI-4-P could not be detected in either case. Neither PI-3-P nor PI-4-P could be detected on the surface of erythrocytes. The lack of PI-3-P or PI-4-P on the surface of erythrocytes is significant because nearly all published studies documenting the absence of PI-3-P or PI-4-P from the outside of eukaryotic cells utilized erythrocytes. Our results suggest that erythrocytes may be an exception in this regard.

[0140] The finding of PI-3-P on the outside of plant and animal cells, combined with the preference for most effectors for PI-3-P is consistent with PI-3-P being the principal receptor mediating entry of the effectors into plant and animals cells. The absence of PI-4-P from the membranes suggests PI-4-P is unlikely to be the principal route of cell entry. However, PI-4-P has been reported to be secreted from plant cells under certain conditions (Regente et al., 2008; Gonorazky et al., 2008), and it is possible that some effectors such as Avr1b have evolved to respond to PI-4-P.

Example 9

[0141] Since several of the fungal effectors that were tested contained no obvious RXLR or dEER motifs, we used the leaf bombardment assay to define the range of residues within the RXLR motif of Avr1b that could permit cell entry. The results (FIG. **19**) revealed that lysine or histidine but not glutamine could replace the arginine at position 1 in the motif, that any large hydrophobic residue (isoleucine, methionine, phenylalanine, or tyrosine) could replace the leucine at position 3, but valine and alanine could not. At position 4, all residues tested allowed function. Furthermore, the presence of either a leucine or methionine residue at position 2 could substitute for leucine at position 3. The effector binding motif was thus refined to BXZ, where B=R, K or H; X is any amino acid and may be absent; and z=L, M, I, W, Y, or F.

Example 10

A PI-3-P-Binding Protein Blocks Entry of Effectors into Plant and Human Cells

[0142] To determine more directly if PI-3-P mediates host cell entry, we pre-incubated soybean roots and epithelial cells with unlabeled VAM7p PX protein, which binds PI-3-P, prior to exposing the cells to effector-GFP fusions. Pre-incubation with VAM7p PX protein strongly inhibited entry by GFP fusions of the oomycete effector Avr1b, and the fungal effectors AvrL567, Avr2 and AvrLm6 into soybean root cells (FIG. **20**A) but did not inhibit entry of a synthetic cell permeable protein Arg9-GFP that does not bind phosphoinositides. Similarly, VAM7p PX protein strongly inhibited the entry by GFP fusions of Avr1b, AvrL567 and the *Plasmodium* effector PfHRPII into human epithelial cells, but did not inhibit entry of Arg9-GFP.

[0143] These results strongly support the hypothesis that PI-3-P binding is necessary for the effector GFP fusions to enter plant and animal cells.

[0144] The previous examples showed that the head group mimic 1,4 inositol diphosphate (1,4IP2) could inhibit entry of effector-GFP fusions into soybean root cells and human epithelial cells (FIGS. **20**A and B). Presumably the binding of 1,4IP2 to the effectors is strong enough to compete with binding for cellular PI-3-P.

[0145] To test the ability of inositol diphosphate to inhibit entry of a native effector (not a GFP fusion) into plant cells, we produced full length protein of the oomycete effector Avr1k (from *Phytophthora sojae*) in *E. coli*. We then infiltrated the purified protein into soybean leaves which did or did not carry the resistance gene Rps1k. In the presence of Rps1k, Avr1k triggers a programmed cell death response called the hypersensitive response (HR) (FIG. **20**C, panel 1). In the presence of 1,3IP2, however, no HR was observed, consistent with 1,3IP2 blocking the entry of the effector into the leaf cells. When the RXLR motif of Avr1k (RSLR) was mutated, no HR was observed, even in the absence of 1,3IP2, confirming the RXLR motif was essential for cell entry. When the Rps1k gene was absent, no HR was observed, as expected. These results show that entry of RXLR effectors into plant cells requires binding to PI-3-P.

Example 11

Methods to Block Effector Entry Using Small-Molecule Drugs

[0146] The ability to block effector entry using 1,3IP2 or 1,4IP2 provides a proof-of-concept for treating oomycete or fungal infections of plants or animals, including humans, with drugs that block the PI-3-P-binding sites of the effectors. Such drugs may not need to fully block all effectors in order to be effective. Since a principal function of effectors is to suppress the host defense responses, even partial inhibition of effector entry may be sufficient to obtain protein. This point may be important because some forms of genetic resistance in plants (major gene resistance) rely upon entry of effectors into the plant cells (the resistance gene product encodes a receptor that detects the presence of an intracellular effector).

[0147] Drugs are also used to interfere with biosynthesis or export of PI-3-P to the outer leaflet. Inside the cell, PI-3-P can be formed by the action of phosphatidylinositol-3-kinases on phosphatidylinositol, and by the action of phosphatidylinositol 4,5 phosphatases on phosphatidylinositol 3,4 diphosphate, phosphatidylinositol 3,5 diphosphate and phosphatidylinositol 3,4,5 diphosphate. Any drug which inhibited these enzymes could lower the levels of external PI-3-P. Currently it is not known how PI-3-P reaches the outer leaflet. All known PI-3-P forming enzymes are located on the cytoplasmic face of membranes. PI-3-P could reach the external leaflet of the plasma membrane or the luminal face of secretory vesicles by the action of floppases or a scramblases. Alternatively PI-3-P might be transported to the outer leaflet by an ABC transporter or by a secreted lipid transfer protein. Any of the proteins involved in this process could be targeted with drugs, provided that they did not disrupt normal cell physiology. In addition to drugs that directly target the proteins described above, and drug that targets biosynthesis of the proteins, for example siRNAs, are also effective.

[0148] Some specific examples of drugs that may be used in the practice of the invention include but are not limited to membrane-permeant derivatives of inositol diphosphates (Li et al., 1992) and bis(hydroxymethyl)-inositol (Flu et al., 2000).

[0149] Alternatively, drugs that bind directly to PI-3-P making it unavailable to effectors are effective. For example, neomycin binds PI-4,5-P2 very effectively; thus neomycin, neomycin derivatives or other aminoglycosides that bind PI-3-P may be used.

[0150] If effective drugs cause toxicity, forms of the drugs which are activated only when in close proximity to the pathogen are used. For example, infection in both plant and animal cell systems results in local high concentrations of hydrogen peroxide. A pro-drug that is activated by oxidation or peroxidation mitigates toxicity.

Example 12

Methods to Block Effector Entry Using Polypeptides

[0151] Polypeptides with the properties described in Example 10 may also be utilized. Polypeptides may have some advantage over chemicals, in plant and animal systems, in that the host organism can be genetically engineered to produce the polypeptide, simplifying delivery and reducing cost. The ability to produce and select large numbers of variant polypeptides via phage display technologies provides additional power to improve specificity, if needed. Random peptides or single chain antibodies selected by phage display are used to block the PI-3-P binding sites of effectors. Additionally such effector-binding proteins could be fused to proteases to facilitate degradation of the effectors.

[0152] The ability to block effector entry by pre-incubation with PI-3-P-binding proteins provides a strong indication that secretion of PI-3-P-binding proteins could provide protection against infection, especially if the secreted protein could be targeted to the infection site. Additionally, secretion of enzymes which can hydrolyze PI-3-P or modify it in other ways may be effective in reducing the level of PI-3-P available to transport effectors into cells. Examples of such enzymes include but are not limited to PI-3-P 4,5 kinases, PI-3-phosphatases, or phospholipases, etc. Examples of these enzymes have been described in the literature (Falasca et al., 2006).

[0153] Additionally, enzymes (e.g. from microbes) that cause novel modifications of PI-3-P such as methylases, acetylases or glycosylases may be used. A particularly useful enzyme is a phospholipase C that can cleave PI-3-P into diacylglycerol and 1,3-inositol diphosphate; not only is the level of PI-3-P reduced but the inhibitor 1,3-inositol diphosphate would be produced as a result. Currently known phosphatidylinositol-specific phospholipase C's are specific for phosphatidylinositol, glycosyl phosphatidylinositol-protein anchors, or for phosphatidylinositol-4-phosphate and phosphatidylinositol-4,5-diphosphate. In some embodiments, systematic mutagenesis is used to modify the specificity of a phosphatidylinositol specific phospholipase C so that it could cleave PI-3-P.

[0154] Further, in cases where polypeptides that manipulate PI-3-P levels cause deleterious physiological effects on the host, transgenic hosts are produced in which the polypeptide gene is transcribed only during infection. Alternatively, or jointly with this strategy, the polypeptide is targeted to the site of infection. For example, the *Arabidopsis* protein. RPW8 is specifically targeted to haustoria of certain

oomycetes and fungi (Wang et al., 2009). RPW8 is used to target anti-effector polypeptides to the haustorial space.

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Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
20 25 30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
35 40 45

Ala Gly Gly Ala Ala Ala Ala Ala His Glu Glu Asp Asp Ala Gly Glu
50 55 60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65 70 75 80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
85 90 95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
100 105 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
115 120 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
130 135

<210> SEQ ID NO 12
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 12

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1 5 10 15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
20 25 30

Val Glu Ser Pro Asp Leu Val Arg Ala Ala Ala Ala Asn Gly Asp Ile
35 40 45

Ala Gly Gly Ala Ala Ala Ala Ala His Glu Glu Asp Asp Ala Gly Glu
50 55 60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65 70 75 80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
85 90 95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
100 105 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
115 120 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
130 135

<210> SEQ ID NO 13
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

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<400> SEQUENCE: 13

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1 5 10 15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
20 25 30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
35 40 45

Ala Gly Gly Arg Phe Leu Arg Ala His Ala Ala Ala Ala Ala Gly Ala
50 55 60

Ala Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65 70 75 80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
85 90 95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
100 105 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
115 120 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
130 135

<210> SEQ ID NO 14
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 14

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1 5 10 15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
20 25 30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
35 40 45

Ala Gly Gly Arg Phe Leu Arg Ala His Glu Glu Asp Asp Ala Gly Glu
50 55 60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65 70 75 80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
85 90 95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
100 105 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
115 120 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
130 135

<210> SEQ ID NO 15
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 15

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1 5 10 15

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Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Ala Ala Ala Ala Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 16
<211> LENGTH: 645
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 16

Met Ala Thr Thr Lys His Leu Ala Leu Ala Ile Leu Val Leu Leu Ser
1               5                   10                  15

Ile Gly Met Thr Thr Ser Ala Arg Thr Leu Leu Asp Leu Arg Asn Arg
            20                  25                  30

Arg Thr Ser Leu Tyr Pro Ile Asn Thr Glu Thr Arg Gly Val Phe Asp
        35                  40                  45

Leu Asn Gly Val Trp Asn Phe Lys Leu Asp Tyr Gly Lys Gly Leu Glu
    50                  55                  60

Glu Lys Trp Tyr Glu Ser Lys Leu Thr Asp Thr Ile Ser Met Ala Val
65                  70                  75                  80

Pro Ser Ser Tyr Asn Asp Ile Gly Val Thr Lys Glu Ile Arg Asn His
                85                  90                  95

Ile Gly Tyr Val Trp Tyr Glu Arg Glu Phe Thr Val Pro Ala Tyr Leu
            100                 105                 110

Lys Asp Gln Arg Ile Val Leu Arg Phe Gly Ser Ala Thr His Lys Ala
        115                 120                 125

Ile Val Tyr Val Asn Gly Glu Leu Val Val Glu His Lys Gly Gly Phe
    130                 135                 140

Leu Pro Phe Glu Ala Glu Ile Asn Asn Ser Leu Arg Asp Gly Met Asn
145                 150                 155                 160

Arg Val Thr Val Ala Val Asp Asn Ile Leu Asp Asp Ser Thr Leu Pro
                165                 170                 175

Val Gly Leu Tyr Ser Glu Arg His Glu Glu Gly Leu Gly Lys Val Ile
            180                 185                 190

Arg Asn Lys Pro Asn Phe Asp Phe Phe Asn Tyr Ala Gly Leu His Arg
        195                 200                 205

Pro Val Lys Ile Tyr Thr Thr Pro Phe Thr Tyr Val Glu Asp Ile Ser
    210                 215                 220

Val Val Thr Asp Phe Asn Gly Pro Thr Gly Thr Val Thr Tyr Thr Val
225                 230                 235                 240
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Asp Phe Gln Gly Lys Ala Glu Thr Val Lys Val Ser Val Val Asp Glu
                245                 250                 255

Glu Gly Lys Val Val Ala Ser Thr Glu Gly Leu Ser Gly Asn Val Glu
            260                 265                 270

Ile Pro Asn Val Ile Leu Trp Glu Pro Leu Asn Thr Tyr Leu Tyr Gln
        275                 280                 285

Ile Lys Val Glu Leu Val Asn Asp Gly Leu Thr Ile Asp Val Tyr Glu
    290                 295                 300

Glu Pro Phe Gly Val Arg Thr Val Glu Val Asn Asp Gly Lys Phe Leu
305                 310                 315                 320

Ile Asn Asn Lys Pro Phe Tyr Phe Lys Gly Phe Gly Lys His Glu Asp
                325                 330                 335

Thr Pro Ile Asn Gly Arg Gly Phe Asn Glu Ala Ser Asn Val Met Asp
            340                 345                 350

Phe Asn Ile Leu Lys Trp Ile Gly Ala Asn Ser Phe Arg Thr Ala His
        355                 360                 365

Tyr Pro Tyr Ser Glu Glu Leu Met Arg Leu Ala Asp Arg Glu Gly Leu
    370                 375                 380

Val Val Ile Asp Glu Thr Pro Ala Val Gly Val His Leu Asn Phe Met
385                 390                 395                 400

Ala Thr Thr Gly Leu Gly Glu Gly Ser Glu Arg Val Ser Thr Trp Glu
                405                 410                 415

Lys Ile Arg Thr Phe Glu His His Gln Asp Val Leu Arg Glu Leu Val
            420                 425                 430

Ser Arg Asp Lys Asn His Pro Ser Val Val Met Trp Ser Ile Ala Asn
        435                 440                 445

Glu Ala Ala Thr Glu Glu Glu Gly Ala Tyr Glu Tyr Phe Lys Pro Leu
    450                 455                 460

Val Glu Leu Thr Lys Glu Leu Asp Pro Gln Lys Arg Pro Val Thr Ile
465                 470                 475                 480

Val Leu Phe Val Met Ala Thr Pro Glu Thr Asp Lys Val Ala Glu Leu
                485                 490                 495

Ile Asp Val Ile Ala Leu Asn Arg Tyr Asn Gly Trp Tyr Phe Asp Gly
            500                 505                 510

Gly Asp Leu Glu Ala Ala Lys Val His Leu Arg Gln Glu Phe His Ala
        515                 520                 525

Trp Asn Lys Arg Cys Pro Gly Lys Pro Ile Met Ile Thr Glu Tyr Gly
    530                 535                 540

Ala Asp Thr Val Ala Gly Phe His Asp Ile Asp Pro Val Met Phe Thr
545                 550                 555                 560

Glu Glu Tyr Gln Val Glu Tyr Tyr Gln Ala Asn His Val Val Phe Asp
                565                 570                 575

Glu Phe Glu Asn Phe Val Gly Glu Gln Ala Trp Asn Phe Ala Asp Phe
            580                 585                 590

Ala Thr Ser Gln Gly Val Met Arg Val Gln Gly Asn Lys Lys Gly Val
        595                 600                 605

Phe Thr Arg Asp Arg Lys Pro Lys Leu Ala Ala His Val Phe Arg Glu
    610                 615                 620

Arg Trp Thr Asn Ile Pro Asp Phe Gly Tyr Lys Asn Ala Ser His His
625                 630                 635                 640
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His His His His Val
645

<210> SEQ ID NO 17
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 17

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1 5 10 15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
20 25 30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
35 40 45

Ala Gly Gly Arg Phe Leu Arg Ala His Glu Glu Asp Asp Ala Gly Glu
50 55 60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65 70 75 80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
85 90 95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
100 105 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
115 120 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
130 135

<210> SEQ ID NO 18
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 18

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1 5 10 15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
20 25 30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
35 40 45

Ala Gly Gly Ala Ala Ala Ala Ala His Glu Glu Asp Asp Ala Gly Glu
50 55 60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65 70 75 80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
85 90 95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
100 105 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
115 120 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
130 135

<210> SEQ ID NO 19
<211> LENGTH: 117

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<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 19

Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met Val Glu Ser Pro Asp
1 5 10 15

Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile Ala Gly Gly Arg Phe
20 25 30

Leu Arg Ala His Glu Glu Asp Asp Ala Gly Glu Arg Thr Phe Ser Val
35 40 45

Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys Leu Ala Lys Ala Met
50 55 60

Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr Glu Lys Trp Ala Lys
65 70 75 80

Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp Leu Ala Ile Ala Asp
85 90 95

Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr Asn Gly Tyr Thr Phe
100 105 110

His Arg Tyr Gln Ser
115

<210> SEQ ID NO 20
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 20

Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met Val Glu Ser Pro Asp
1 5 10 15

Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile Ala Gly Gly Ala Ala
20 25 30

Ala Ala Ala His Glu Glu Asp Asp Ala Gly Glu Arg Thr Phe Ser Val
35 40 45

Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys Leu Ala Lys Ala Met
50 55 60

Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr Glu Lys Trp Ala Lys
65 70 75 80

Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp Leu Ala Ile Ala Asp
85 90 95

Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr Asn Gly Tyr Thr Phe
100 105 110

His Arg Tyr Gln Ser
115

<210> SEQ ID NO 21
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 21

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1 5 10 15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
20 25 30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile

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        35                  40                  45

Ala Gly Gly Arg Phe Leu Arg Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 22
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 22

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Arg Phe Leu Arg Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 23
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 23

Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met Val Glu Ser Pro Asp
1               5                   10                  15

Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile Ala Gly Gly Arg Phe
            20                  25                  30

Leu Arg Ala His Ala Ala Ala Ala Ala Gly Ala Ala Thr Phe Ser Val
        35                  40                  45

Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys Leu Ala Lys Ala Met
    50                  55                  60

Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr Glu Lys Trp Ala Lys
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65 70 75 80

Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp Leu Ala Ile Ala Asp
85 90 95

Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr Asn Gly Tyr Thr Phe
100 105 110

His Arg Tyr Gln Ser
115

<210> SEQ ID NO 24
<211> LENGTH: 360
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 24

Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met Val Glu Ser Pro Asp
1 5 10 15

Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile Ala Gly Gly Arg Phe
20 25 30

Leu Arg Ala His Glu Glu Asp Asp Ala Gly Glu Arg Thr Phe Ser Val
35 40 45

Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys Leu Ala Lys Ala Met
50 55 60

Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr Glu Lys Trp Ala Lys
65 70 75 80

Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp Leu Ala Ile Ala Asp
85 90 95

Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr Asn Gly Tyr Thr Phe
100 105 110

His Arg Tyr Gln Ser Gly Thr Ala Thr Met Val Ser Lys Gly Ala Glu
115 120 125

Leu Phe Thr Gly Ile Val Pro Ile Leu Ile Glu Leu Asn Gly Asp Val
130 135 140

Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr
145 150 155 160

Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
165 170 175

Val Pro Trp Pro Thr Leu Val Thr Thr Leu Ser Tyr Gly Val Gln Cys
180 185 190

Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser
195 200 205

Ala Met Pro Glu Gly Tyr Ile Gln Glu Arg Thr Ile Phe Phe Glu Asp
210 215 220

Asp Gly Asn Tyr Lys Ser Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
225 230 235 240

Leu Val Asn Arg Ile Glu Leu Thr Gly Thr Asp Phe Lys Glu Asp Gly
245 250 255

Asn Ile Leu Gly Asn Lys Met Glu Tyr Asn Tyr Asn Ala His Asn Val
260 265 270

Tyr Ile Met Thr Asp Lys Ala Lys Asn Gly Ile Lys Val Asn Phe Lys
275 280 285

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
290 295 300

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Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
305                 310                 315                 320

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                325                 330                 335

Arg Asp His Met Ile Tyr Phe Gly Phe Val Thr Ala Ala Ala Ile Thr
            340                 345                 350

His Gly Met Asp Glu Leu Tyr Lys
        355                 360


<210> SEQ ID NO 25
<211> LENGTH: 381
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 25

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Arg Phe Leu Arg Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser Gly Thr Ala Thr Met Val
    130                 135                 140

Ser Lys Gly Ala Glu Leu Phe Thr Gly Ile Val Pro Ile Leu Ile Glu
145                 150                 155                 160

Leu Asn Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
                165                 170                 175

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
            180                 185                 190

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Ser
        195                 200                 205

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His
    210                 215                 220

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Ile Gln Glu Arg Thr
225                 230                 235                 240

Ile Phe Phe Glu Asp Asp Gly Asn Tyr Lys Ser Arg Ala Glu Val Lys
                245                 250                 255

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Thr Gly Thr Asp
            260                 265                 270

Phe Lys Glu Asp Gly Asn Ile Leu Gly Asn Lys Met Glu Tyr Asn Tyr
        275                 280                 285

Asn Ala His Asn Val Tyr Ile Met Thr Asp Lys Ala Lys Asn Gly Ile
    290                 295                 300
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Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
305                 310                 315                 320

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
                325                 330                 335

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
            340                 345                 350

Asp Pro Asn Glu Lys Arg Asp His Met Ile Tyr Phe Gly Phe Val Thr
        355                 360                 365

Ala Ala Ala Ile Thr His Gly Met Asp Glu Leu Tyr Lys
    370                 375                 380


<210> SEQ ID NO 26
<211> LENGTH: 239
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 26

Met Val Ser Lys Gly Ala Glu Leu Phe Thr Gly Ile Val Pro Ile Leu
1               5                   10                  15

Ile Glu Leu Asn Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

Leu Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Ile Gln Glu
                85                  90                  95

Arg Thr Ile Phe Phe Glu Asp Asp Gly Asn Tyr Lys Ser Arg Ala Glu
            100                 105                 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Thr Gly
        115                 120                 125

Thr Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly Asn Lys Met Glu Tyr
    130                 135                 140

Asn Tyr Asn Ala His Asn Val Tyr Ile Met Thr Asp Lys Ala Lys Asn
145                 150                 155                 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
            180                 185                 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
        195                 200                 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Tyr Phe Gly Phe
    210                 215                 220

Val Thr Ala Ala Ala Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225                 230                 235


<210> SEQ ID NO 27
<211> LENGTH: 270
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 27
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Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Ser Lys Gly Ala Glu Leu Phe Thr Gly Ile Val Pro Ile Leu Ile
        35                  40                  45

Glu Leu Asn Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
    50                  55                  60

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
65                  70                  75                  80

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
                85                  90                  95

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
            100                 105                 110

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Ile Gln Glu Arg
        115                 120                 125

Thr Ile Phe Phe Glu Asp Asp Gly Asn Tyr Lys Ser Arg Ala Glu Val
    130                 135                 140

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Thr Gly Thr
145                 150                 155                 160

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly Asn Lys Met Glu Tyr Asn
                165                 170                 175

Tyr Asn Ala His Asn Val Tyr Ile Met Thr Asp Lys Ala Lys Asn Gly
            180                 185                 190

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
        195                 200                 205

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
    210                 215                 220

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
225                 230                 235                 240

Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Tyr Phe Gly Phe Val
                245                 250                 255

Thr Ala Ala Ala Ile Thr His Gly Met Asp Glu Leu Tyr Lys
            260                 265                 270


<210> SEQ ID NO 28
<211> LENGTH: 381
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 28

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Ala Ala Ala Ala Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
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                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser Gly Thr Ala Thr Met Val
    130                 135                 140

Ser Lys Gly Ala Glu Leu Phe Thr Gly Ile Val Pro Ile Leu Ile Glu
145                 150                 155                 160

Leu Asn Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
                165                 170                 175

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
            180                 185                 190

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Ser
        195                 200                 205

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His
    210                 215                 220

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Ile Gln Glu Arg Thr
225                 230                 235                 240

Ile Phe Phe Glu Asp Asp Gly Asn Tyr Lys Ser Arg Ala Glu Val Lys
                245                 250                 255

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Thr Gly Thr Asp
            260                 265                 270

Phe Lys Glu Asp Gly Asn Ile Leu Gly Asn Lys Met Glu Tyr Asn Tyr
        275                 280                 285

Asn Ala His Asn Val Tyr Ile Met Thr Asp Lys Ala Lys Asn Gly Ile
    290                 295                 300

Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
305                 310                 315                 320

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
                325                 330                 335

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
            340                 345                 350

Asp Pro Asn Glu Lys Arg Asp His Met Ile Tyr Phe Gly Phe Val Thr
        355                 360                 365

Ala Ala Ala Ile Thr His Gly Met Asp Glu Leu Tyr Lys
    370                 375                 380


<210> SEQ ID NO 29
<211> LENGTH: 381
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 29

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Arg Phe Leu Arg Ala His Ala Ala Ala Ala Ala Gly Ala
    50                  55                  60
```

-continued

```
Ala Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser Gly Thr Ala Thr Met Val
    130                 135                 140

Ser Lys Gly Ala Glu Leu Phe Thr Gly Ile Val Pro Ile Leu Ile Glu
145                 150                 155                 160

Leu Asn Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
                165                 170                 175

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
            180                 185                 190

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Ser
        195                 200                 205

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His
    210                 215                 220

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Ile Gln Glu Arg Thr
225                 230                 235                 240

Ile Phe Phe Glu Asp Asp Gly Asn Tyr Lys Ser Arg Ala Glu Val Lys
                245                 250                 255

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Thr Gly Thr Asp
            260                 265                 270

Phe Lys Glu Asp Gly Asn Ile Leu Gly Asn Lys Met Glu Tyr Asn Tyr
        275                 280                 285

Asn Ala His Asn Val Tyr Ile Met Thr Asp Lys Ala Lys Asn Gly Ile
    290                 295                 300

Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
305                 310                 315                 320

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
                325                 330                 335

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
            340                 345                 350

Asp Pro Asn Glu Lys Arg Asp His Met Ile Tyr Phe Gly Phe Val Thr
        355                 360                 365

Ala Ala Ala Ile Thr His Gly Met Asp Glu Leu Tyr Lys
    370                 375                 380


<210> SEQ ID NO 30
<211> LENGTH: 386
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Sequence of 9 arginines  replacing
      the RXLR region of secreted Avr1b fused to GFP

<400> SEQUENCE: 30

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30
```

-continued

```
Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Arg Arg Arg Arg Arg Arg Arg Arg Arg Ala His Glu Glu
    50                  55                  60

Asp Asp Ala Gly Glu Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys
65                  70                  75                  80

Val Ala Ala Lys Lys Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys
                85                  90                  95

Glu Gln Lys Ala Tyr Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp
            100                 105                 110

Lys Ile Lys Asn Trp Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys
        115                 120                 125

Tyr Asp Arg Ile Tyr Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser Gly
    130                 135                 140

Thr Ala Thr Met Val Ser Lys Gly Ala Glu Leu Phe Thr Gly Ile Val
145                 150                 155                 160

Pro Ile Leu Ile Glu Leu Asn Gly Asp Val Asn Gly His Lys Phe Ser
                165                 170                 175

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
            180                 185                 190

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
        195                 200                 205

Val Thr Thr Leu Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
    210                 215                 220

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
225                 230                 235                 240

Ile Gln Glu Arg Thr Ile Phe Phe Glu Asp Asp Gly Asn Tyr Lys Ser
                245                 250                 255

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
            260                 265                 270

Leu Thr Gly Thr Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly Asn Lys
        275                 280                 285

Met Glu Tyr Asn Tyr Asn Ala His Asn Val Tyr Ile Met Thr Asp Lys
    290                 295                 300

Ala Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
305                 310                 315                 320

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
                325                 330                 335

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
            340                 345                 350

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Tyr
        355                 360                 365

Phe Gly Phe Val Thr Ala Ala Ala Ile Thr His Gly Met Asp Glu Leu
    370                 375                 380

Tyr Lys
385


<210> SEQ ID NO 31
<211> LENGTH: 388
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
```

-continued

<223> OTHER INFORMATION: Synthetic sequence consisting of P. sojae Avr1b with a known TAT motif from Lentivirus HIV inserted in the position of the second RXLR sequence fused to GFP

<400> SEQUENCE: 31

```
Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                  10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala His
    50                  55                  60

Glu Glu Asp Asp Ala Gly Glu Arg Thr Phe Ser Val Thr Asp Leu Trp
65                  70                  75                  80

Asn Lys Val Ala Ala Lys Lys Leu Ala Lys Ala Met Leu Ala Asp Pro
                85                  90                  95

Ser Lys Glu Gln Lys Ala Tyr Glu Lys Trp Ala Lys Lys Gly Tyr Ser
            100                 105                 110

Leu Asp Lys Ile Lys Asn Trp Leu Ala Ile Ala Asp Pro Lys Gln Lys
        115                 120                 125

Gly Lys Tyr Asp Arg Ile Tyr Asn Gly Tyr Thr Phe His Arg Tyr Gln
    130                 135                 140

Ser Gly Thr Ala Thr Met Val Ser Lys Gly Ala Glu Leu Phe Thr Gly
145                 150                 155                 160

Ile Val Pro Ile Leu Ile Glu Leu Asn Gly Asp Val Asn Gly His Lys
                165                 170                 175

Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu
            180                 185                 190

Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro
        195                 200                 205

Thr Leu Val Thr Thr Leu Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr
    210                 215                 220

Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu
225                 230                 235                 240

Gly Tyr Ile Gln Glu Arg Thr Ile Phe Phe Glu Asp Asp Gly Asn Tyr
                245                 250                 255

Lys Ser Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg
            260                 265                 270

Ile Glu Leu Thr Gly Thr Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly
        275                 280                 285

Asn Lys Met Glu Tyr Asn Tyr Asn Ala His Asn Val Tyr Ile Met Thr
    290                 295                 300

Asp Lys Ala Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn
305                 310                 315                 320

Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
                325                 330                 335

Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
            340                 345                 350

Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
        355                 360                 365

Ile Tyr Phe Gly Phe Val Thr Ala Ala Ala Ile Thr His Gly Met Asp
```

-continued

370 375 380

Glu Leu Tyr Lys
385

<210> SEQ ID NO 32
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 32

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1 5 10 15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
20 25 30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
35 40 45

Ala Gly Gly Arg Phe Leu Arg Ala His Glu Glu Asp Asp Ala Gly Glu
50 55 60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65 70 75 80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
85 90 95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
100 105 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
115 120 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
130 135

<210> SEQ ID NO 33
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 33

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1 5 10 15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
20 25 30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
35 40 45

Ala Gly Gly Arg Phe Arg Leu Ala His Glu Glu Asp Asp Ala Gly Glu
50 55 60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65 70 75 80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
85 90 95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
100 105 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
115 120 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
130 135

-continued

<210> SEQ ID NO 34
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 34

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1 5 10 15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
20 25 30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
35 40 45

Ala Gly Gly Phe Arg Leu Arg Ala His Glu Glu Asp Asp Ala Gly Glu
50 55 60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65 70 75 80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
85 90 95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
100 105 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
115 120 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
130 135

<210> SEQ ID NO 35
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 35

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1 5 10 15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
20 25 30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
35 40 45

Ala Gly Gly Arg Phe Ala Arg Ala His Glu Glu Asp Asp Ala Gly Glu
50 55 60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65 70 75 80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
85 90 95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
100 105 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
115 120 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
130 135

<210> SEQ ID NO 36
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 36

-continued

```
Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Gln Phe Leu Gln Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 37
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 37

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Gln Phe Leu Arg Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 38
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 38

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30
```

-continued

```
Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Lys Phe Leu Arg Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 39
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 39

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Arg Phe Leu Gln Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 40
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 40

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Arg Phe Val Arg Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60
```

-continued

```
Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 41
<211> LENGTH: 143
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence consisting of P. sojae
      Avr1b with 9 arginines inserted where the second RXLR sequence
      is found.

<400> SEQUENCE: 41

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Arg Arg Arg Arg Arg Arg Arg Arg Arg Ala His Glu Glu
    50                  55                  60

Asp Asp Ala Gly Glu Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys
65                  70                  75                  80

Val Ala Ala Lys Lys Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys
                85                  90                  95

Glu Gln Lys Ala Tyr Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp
            100                 105                 110

Lys Ile Lys Asn Trp Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys
        115                 120                 125

Tyr Asp Arg Ile Tyr Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135                 140


<210> SEQ ID NO 42
<211> LENGTH: 146
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence consisting of P. sojae
      Avr1b with a known TAT motif from Lentivirus HIV inserted in the
      position of the second RXLR sequence.

<400> SEQUENCE: 42

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45
```

-continued

```
Ala Gly Gly Tyr Gly Arg Lys Lys Lys Arg Arg Gln Arg Arg Arg Ala
    50                  55                  60

His Glu Glu Asp Asp Ala Gly Glu Arg Thr Phe Ser Val Thr Asp Leu
65                  70                  75                  80

Trp Asn Lys Val Ala Ala Lys Lys Leu Ala Lys Ala Met Leu Ala Asp
                85                  90                  95

Pro Ser Lys Glu Gln Lys Ala Tyr Glu Lys Trp Ala Lys Lys Gly Tyr
            100                 105                 110

Ser Leu Asp Lys Ile Lys Asn Trp Leu Ala Ile Ala Asp Pro Lys Gln
        115                 120                 125

Lys Gly Lys Tyr Asp Arg Ile Tyr Asn Gly Tyr Thr Phe His Arg Tyr
    130                 135                 140

Gln Ser
145
```

<210> SEQ ID NO 43
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence consisting of P. sojae Avr1b with a RXLR motif from Plasmodium falciparum GBP protein inserted where the second RXLR sequence is found.

<400> SEQUENCE: 43

```
Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Arg Phe Leu Arg Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135
```

<210> SEQ ID NO 44
<211> LENGTH: 132
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence consisting of P. sojae Avr1b with a RXLRsequence of Plasmodium falciparum HRPII protein inserted where the second RXLR sequence is found.

<400> SEQUENCE: 44

```
Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Phe Asn Asn Asn Leu Cys Ser Lys Asn Ala Lys
```

-continued

```
            20                  25                  30

Gly Leu Asn Leu Asn Lys Arg Leu Leu His Glu Thr Gln Ala His Val
        35                  40                  45

Asp Asp Ala His His Ala His His Val Ala Asp Thr Phe Ser Val Thr
    50                  55                  60

Asp Leu Trp Asn Lys Val Ala Ala Lys Lys Leu Ala Lys Ala Met Leu
65                  70                  75                  80

Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr Glu Lys Trp Ala Lys Lys
                85                  90                  95

Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp Leu Ala Ile Ala Asp Pro
            100                 105                 110

Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr Asn Gly Tyr Thr Phe His
        115                 120                 125

Arg Tyr Gln Ser
    130
```

<210> SEQ ID NO 45
<211> LENGTH: 135
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence consisting of P. sojae Avr1b with a RXLRsequence from Plasmodium falciparum 1615c protein inserted where the second RXLR sequence is found.

<400> SEQUENCE: 45

```
Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Ser Tyr Asn Lys Ile Asn Ser Ser Ser Thr Tyr
            20                  25                  30

Thr His Ser Arg Ile Leu Lys Gln Leu Glu Phe Ile Thr Leu Glu Glu
        35                  40                  45

Lys Thr Val Asn Ala Leu Gln Glu Met Leu Asp Asp Ser Val Thr Phe
    50                  55                  60

Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys Leu Ala Lys
65                  70                  75                  80

Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr Glu Lys Trp
                85                  90                  95

Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp Leu Ala Ile
            100                 105                 110

Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr Asn Gly Tyr
        115                 120                 125

Thr Phe His Arg Tyr Gln Ser
    130                 135
```

<210> SEQ ID NO 46
<211> LENGTH: 365
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 46

```
Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30
```

-continued

```
Arg Trp Gly Ser Arg Ser Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala
        35                  40                  45

Met Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp
    50                  55                  60

Ile Ala Gly Gly Arg Phe Leu Arg Ala His Glu Glu Asp Asp Ala Gly
65                  70                  75                  80

Glu Arg Thr Phe Ser Val Thr Asp Glu Phe Arg Ser Thr Met Ser Gly
                85                  90                  95

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ser Met Gly Ser Gly Ile
            100                 105                 110

Gln Arg Pro Thr Ser Thr Ser Ser Leu Val Ala Ala Ala Ala Thr Met
        115                 120                 125

Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
    130                 135                 140

Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
145                 150                 155                 160

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
                165                 170                 175

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser
            180                 185                 190

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His
        195                 200                 205

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
    210                 215                 220

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
225                 230                 235                 240

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
                245                 250                 255

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
            260                 265                 270

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
        275                 280                 285

Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
    290                 295                 300

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
305                 310                 315                 320

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
                325                 330                 335

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
            340                 345                 350

Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
        355                 360                 365


<210> SEQ ID NO 47
<211> LENGTH: 365
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 47

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30
```

-continued

```
Arg Trp Gly Ser Arg Ser Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala
        35                  40                  45

Met Val Glu Ser Pro Asp Leu Val Arg Ala Ala Ala Ala Asn Gly Asp
    50                  55                  60

Ile Ala Gly Gly Ala Ala Ala Ala Ala His Glu Glu Asp Asp Ala Gly
65                  70                  75                  80

Glu Arg Thr Phe Ser Val Thr Asp Glu Phe Arg Ser Thr Met Ser Gly
                85                  90                  95

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ser Met Gly Ser Gly Ile
            100                 105                 110

Gln Arg Pro Thr Ser Thr Ser Ser Leu Val Ala Ala Ala Ala Thr Met
        115                 120                 125

Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
    130                 135                 140

Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
145                 150                 155                 160

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
                165                 170                 175

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser
            180                 185                 190

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His
        195                 200                 205

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
    210                 215                 220

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
225                 230                 235                 240

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
                245                 250                 255

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
            260                 265                 270

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
        275                 280                 285

Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
    290                 295                 300

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
305                 310                 315                 320

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
                325                 330                 335

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
            340                 345                 350

Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
        355                 360                 365


<210> SEQ ID NO 48
<211> LENGTH: 365
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 48

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
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            20                  25                  30

Arg Trp Gly Ser Arg Ser Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala
        35                  40                  45

Met Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp
    50                  55                  60

Ile Ala Gly Gly Arg Phe Leu Arg Ala His Ala Ala Ala Ala Ala Gly
65                  70                  75                  80

Ala Ala Thr Phe Ser Val Thr Asp Glu Phe Arg Ser Thr Met Ser Gly
                85                  90                  95

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ser Met Gly Ser Gly Ile
            100                 105                 110

Gln Arg Pro Thr Ser Thr Ser Ser Leu Val Ala Ala Ala Ala Thr Met
        115                 120                 125

Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
    130                 135                 140

Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
145                 150                 155                 160

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
                165                 170                 175

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser
            180                 185                 190

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His
        195                 200                 205

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
    210                 215                 220

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
225                 230                 235                 240

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
                245                 250                 255

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
            260                 265                 270

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
        275                 280                 285

Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
    290                 295                 300

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
305                 310                 315                 320

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
                325                 330                 335

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
            340                 345                 350

Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
        355                 360                 365


<210> SEQ ID NO 49
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to
      amplify genes from genomes or plasmids with various restriction
      sites to faciliate cloning

<400> SEQUENCE: 49
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ataagcttga atctggcgtt catctccgac g 31

<210> SEQ ID NO 50
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 50

ttcccgggtg gatgctcaga tgctagcgtc 30

<210> SEQ ID NO 51
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 51

ttctcctttt cactctcacg 20

<210> SEQ ID NO 52
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 52

agacacaaaa tctgcaactt c 21

<210> SEQ ID NO 53
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 53

accttcagcg tgactgacct 20

<210> SEQ ID NO 54
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 54

gcgattgcca accagttct 19

<210> SEQ ID NO 55
<211> LENGTH: 20

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 55

cgacatccgt aaggacctgt 20

<210> SEQ ID NO 56
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 56

ttcgagatcc acatctgctg 20

<210> SEQ ID NO 57
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 57

ggggtaccga caacaatgcg tctatctttt gtgct 35

<210> SEQ ID NO 58
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 58

ggggtacctc agctctgata ccggtgaa 28

<210> SEQ ID NO 59
<211> LENGTH: 62
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 59

atcgcactcg agctttcgca gatcccgggg ggcaatgaga tatgactgag tactccgacg 60

aa 62

<210> SEQ ID NO 60
<211> LENGTH: 63
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to

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amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 60

atcgcactcg agcttgtcga tcgacagatc cggtcggcat ctacttcagc tctgataccg 60

gtg 63

<210> SEQ ID NO 61
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 61

atcgcactcg agctttcgca gatcccgggg ggcaatgaga tatgcgtcta tcttttgtg 59

<210> SEQ ID NO 62
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 62

tcgtccgtgc tgcagctgct aacggcgaca ttgccggtgg 40

<210> SEQ ID NO 63
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 63

tcgccgttag cagctgcagc acggacgaga tctggagatt 40

<210> SEQ ID NO 64
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 64

ccggtggagc tgcagctgct gctcatgaag aggacgatgc 40

<210> SEQ ID NO 65
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 65

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tcatgagcag cagctgcagc tccaccggca atgtcgccgt 40

<210> SEQ ID NO 66
<211> LENGTH: 65
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 66

gctgcagctg ctaacggcga cattgccggt ggagctgcag ctgctgctca tgaagaggac 60

gatgc 65

<210> SEQ ID NO 67
<211> LENGTH: 65
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 67

agcagctgca gctccaccgg caatgtcgcc gttagcagct gcagcacgga cgagatctgg 60

agatt 65

<210> SEQ ID NO 68
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 68

gctgcagcag ctgcgggggc tgctaccttc agcgtgactg acct 44

<210> SEQ ID NO 69
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 69

agcagccccc gcagctgctg cagcatgagc tcgaagaaat cttc 44

<210> SEQ ID NO 70
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 70

attcccgggg acaacaatgc gactccacta cgtg 34

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<210> SEQ ID NO 71
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 71

gtcagtcacg ctgaaggtat cgagaacgcc atgcccat 38

<210> SEQ ID NO 72
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 72

attcccgggg acaacaatgg gcctccacaa gggct 35

<210> SEQ ID NO 73
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 73

gtcagtcacg ctgaaggtta ggtggtgtag tccgac 36

<210> SEQ ID NO 74
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 74

aacccgggac aacaatgacc ttcagcgtga ctgac 35

<210> SEQ ID NO 75
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 75

ggaggaattc gctggctggt ggcaggat 28

<210> SEQ ID NO 76
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 76

gtattggcta gagaagcttg cca 23

<210> SEQ ID NO 77
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 77

agaaactcga gcttgtcgat cgacagatcc ggtcggcagg tacctcagct ctgatac 57

<210> SEQ ID NO 78
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 78

gaagatttcg acttgctcat gaag 24

<210> SEQ ID NO 79
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 79

cttcatgagc aagtcgaaat cttc 24

<210> SEQ ID NO 80
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 80

tgccggtgga tttagacttc gagctc 26

<210> SEQ ID NO 81
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 81

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gagctcgaag tctaaatcca ccggca 26

<210> SEQ ID NO 82
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 82

gaagatttgc acgagctcat 20

<210> SEQ ID NO 83
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 83

atgagctcgt gcaaatcttc 20

<210> SEQ ID NO 84
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 84

ggtggacagt ttcttcaagc tcatgaag 28

<210> SEQ ID NO 85
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 85

agcttgaaga aactgtccac cggcaatg 28

<210> SEQ ID NO 86
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 86

ctttcaccgg tatcagagcg gtaccgccac catggtgagc aagggcgccg ag 52

<210> SEQ ID NO 87
<211> LENGTH: 29

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 87

aaggtacctc acttgtacag ctcatccat 29

<210> SEQ ID NO 88
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 88

tcatgagctc gaagaaatct tccgccggca atg 33

<210> SEQ ID NO 89
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 89

cattgccggc ggaagatttc ttcaagc 27

<210> SEQ ID NO 90
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 90

cattgccggc ggacaatttc 20

<210> SEQ ID NO 91
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 91

cattgccggc ggaagatttg ttc 23

<210> SEQ ID NO 92
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

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<400> SEQUENCE: 92

cattgccggc ggaaagtttc ttc 23

<210> SEQ ID NO 93
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 93

cgtcgacgtc ggcgacgcgc tcatgaagag gacgatg 37

<210> SEQ ID NO 94
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 94

cattgccggc ggacgacggc gacgtcgacg tcggcgacg 39

<210> SEQ ID NO 95
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 95

taagaaacgc cgtcagcgac gtcgagctca tgaagaggac gatg 44

<210> SEQ ID NO 96
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 96

cattgccggc ggatatggac gtaagaaacg ccgtcagc 38

<210> SEQ ID NO 97
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 97

gaaggagaag actacactcc ggaaaagcaa gcaaaagacc ttcagcgtga ctgacc 56

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<210> SEQ ID NO 98
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 98

ctcgtatact ggcagagggc gaagatacct gcgcaaggaa ggagaagact acact 55

<210> SEQ ID NO 99
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 99

gtatgagaaa gcggtagatt acggctttcg agagtctcgt atactggcag ag 52

<210> SEQ ID NO 100
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 100

ctaccgcttt ctcatactta tctgcgttgc aggtcacgac 40

<210> SEQ ID NO 101
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 101

tgtcgacgat gcgcaccatg cacaccatgt tgcagatacc ttcagcgtga ctgacc 56

<210> SEQ ID NO 102
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 102

aacctcaaca agagactgtt gcacgagaca caagcacatg tcgacgatgc gcacc 55

<210> SEQ ID NO 103
<211> LENGTH: 53
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to

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amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 103

acaataacct gtgtagtaag aatgctaaag gcttgaacct caacaagaga ctg 53

<210> SEQ ID NO 104
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 104

actacacagg ttattgttaa atgcgttgca ggtcacgac 39

<210> SEQ ID NO 105
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 105

cagtcaatgc attacaagaa atgttagatg atagtgtcac cttcagcgtg actgacc 57

<210> SEQ ID NO 106
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 106

ctcaagcagt tggagttcat cacattggaa gagaagacag tcaatgcatt acaag 55

<210> SEQ ID NO 107
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 107

aagatcaact cgtcatctac ttatacacac agtagaatac tcaagcagtt ggagttc 57

<210> SEQ ID NO 108
<211> LENGTH: 45
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 108

agatgacgag ttgatcttgt tgtaacttgc gttgcaggtc acgac 45

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<210> SEQ ID NO 109
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 109

gatctagatc tgtggaatct ccagatctc 29

<210> SEQ ID NO 110
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 110

gtcatatgga tagccggaca tgtcagtcac gctgaaggt 39

<210> SEQ ID NO 111
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 111

gatcccatgg agccagcata gtctgggacg tcatatggat agccgga 47

<210> SEQ ID NO 112
<211> LENGTH: 324
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct fusing 9 arginine residues to a linker sequence to humanized GFP

<400> SEQUENCE: 112

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
20 25 30

Arg Trp Gly Ser Arg Ser Arg Arg Arg Arg Arg Arg Arg Arg Arg Glu
35 40 45

Phe Arg Ser Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
50 55 60

Gly Ser Met Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr Ser Ser Leu
65 70 75 80

Val Ala Ala Ala Ala Thr Met Ser Lys Gly Glu Glu Leu Phe Thr Gly
85 90 95

Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys
100 105 110

Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu

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        115                 120                 125

Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro
    130                 135                 140

Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr
145                 150                 155                 160

Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu
                165                 170                 175

Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr
            180                 185                 190

Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg
        195                 200                 205

Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly
    210                 215                 220

His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala
225                 230                 235                 240

Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn
                245                 250                 255

Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
            260                 265                 270

Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
        275                 280                 285

Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
    290                 295                 300

Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp
305                 310                 315                 320

Glu Leu Tyr Lys


<210> SEQ ID NO 113
<211> LENGTH: 359
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 113

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Arg Trp Gly Ser Arg Ser Thr Arg Val Pro Asp Asp Ala Asn Leu Gln
        35                  40                  45

Ser Val Asn Ala Pro Val Gln Thr Val Thr Arg Ser Arg Arg Phe Leu
    50                  55                  60

Arg Thr Ala Asp Thr Asp Ile Val Tyr Glu Pro Lys Val His Asn Pro
65                  70                  75                  80

Gly Lys Glu Phe Arg Ser Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro
                85                  90                  95

Asp Tyr Ala Gly Ser Met Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr
            100                 105                 110

Ser Ser Leu Val Ala Ala Ala Ala Thr Met Ser Lys Gly Glu Glu Leu
        115                 120                 125

Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn
    130                 135                 140

Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr
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145                 150                 155                 160

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
                165                 170                 175

Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe
            180                 185                 190

Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala
        195                 200                 205

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    210                 215                 220

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
225                 230                 235                 240

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                245                 250                 255

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            260                 265                 270

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        275                 280                 285

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    290                 295                 300

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
305                 310                 315                 320

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                325                 330                 335

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His
            340                 345                 350

Gly Met Asp Glu Leu Tyr Lys
        355


<210> SEQ ID NO 114
<211> LENGTH: 359
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 114

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Arg Trp Gly Ser Arg Ser Thr Arg Val Pro Asp Asp Ala Asn Leu Gln
        35                  40                  45

Ser Val Asn Ala Pro Val Gln Thr Val Thr Arg Ser Arg Ala Ala Ala
    50                  55                  60

Ala Thr Ala Asp Thr Asp Ile Val Tyr Glu Pro Lys Val His Asn Pro
65                  70                  75                  80

Gly Lys Glu Phe Arg Ser Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro
                85                  90                  95

Asp Tyr Ala Gly Ser Met Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr
            100                 105                 110

Ser Ser Leu Val Ala Ala Ala Ala Thr Met Ser Lys Gly Glu Glu Leu
        115                 120                 125

Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn
    130                 135                 140
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Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr
145                 150                 155                 160

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
                165                 170                 175

Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe
            180                 185                 190

Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala
        195                 200                 205

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    210                 215                 220

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
225                 230                 235                 240

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                245                 250                 255

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            260                 265                 270

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        275                 280                 285

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    290                 295                 300

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
305                 310                 315                 320

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                325                 330                 335

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His
            340                 345                 350

Gly Met Asp Glu Leu Tyr Lys
        355


<210> SEQ ID NO 115
<211> LENGTH: 359
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 115

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Arg Trp Gly Ser Arg Ser Thr Arg Val Pro Asp Asp Ala Asn Leu Gln
        35                  40                  45

Ser Val Asn Ala Pro Val Gln Thr Val Thr Arg Ser Arg Arg Phe Leu
    50                  55                  60

Arg Thr Ala Ala Thr Ala Ile Val Tyr Ala Pro Ala Val His Asn Pro
65                  70                  75                  80

Gly Lys Glu Phe Arg Ser Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro
                85                  90                  95

Asp Tyr Ala Gly Ser Met Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr
            100                 105                 110

Ser Ser Leu Val Ala Ala Ala Ala Thr Met Ser Lys Gly Glu Glu Leu
        115                 120                 125

Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn
    130                 135                 140
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Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr
145                 150                 155                 160

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
                165                 170                 175

Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe
            180                 185                 190

Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala
        195                 200                 205

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    210                 215                 220

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
225                 230                 235                 240

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                245                 250                 255

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            260                 265                 270

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        275                 280                 285

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    290                 295                 300

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
305                 310                 315                 320

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                325                 330                 335

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His
            340                 345                 350

Gly Met Asp Glu Leu Tyr Lys
        355


<210> SEQ ID NO 116
<211> LENGTH: 403
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 116

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Arg Trp Gly Ser Arg Ser Leu Thr Cys Ala Thr Ser Glu Gln Gln Thr
        35                  40                  45

Arg Pro Glu Leu Cys Phe Phe Phe Ser Val Arg Ser Ser Trp Pro Ser
    50                  55                  60

Thr Ile Ser Asp Gly Ala Cys Leu Ala Leu Val Ser Ala Glu Gln Gly
65                  70                  75                  80

Ala Thr Ala Gly Arg Asn Thr Leu Ser Leu Arg Ser Met Met Ala Thr
                85                  90                  95

Glu Asp Met Ala Thr Ser Thr Arg Ser Leu Arg Ser Gln Ala Thr Asn
            100                 105                 110

Val Asp Asp Asp Ala Asn Val Ser Ile Glu Asn Arg Gly Met Glu Phe
        115                 120                 125

Arg Ser Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly
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    130                 135                 140

Ser Met Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr Ser Ser Leu Val
145                 150                 155                 160

Ala Ala Ala Ala Thr Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
                165                 170                 175

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            180                 185                 190

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        195                 200                 205

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    210                 215                 220

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
225                 230                 235                 240

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                245                 250                 255

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            260                 265                 270

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        275                 280                 285

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    290                 295                 300

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
305                 310                 315                 320

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                325                 330                 335

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            340                 345                 350

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        355                 360                 365

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    370                 375                 380

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
385                 390                 395                 400

Leu Tyr Lys


<210> SEQ ID NO 117
<211> LENGTH: 403
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 117

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Arg Trp Gly Ser Arg Ser Leu Thr Cys Ala Thr Ser Glu Gln Gln Thr
        35                  40                  45

Arg Pro Glu Leu Cys Phe Phe Phe Ser Val Arg Ser Ser Trp Pro Ser
    50                  55                  60

Thr Ile Ser Asp Gly Ala Cys Leu Ala Leu Val Ser Ala Glu Gln Gly
65                  70                  75                  80

Ala Thr Ala Gly Arg Asn Thr Leu Ser Leu Arg Ser Met Met Ala Thr
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                85                  90                  95

Glu Asp Met Ala Thr Ser Thr Ala Ala Ala Ala Ser Gln Ala Thr Asn
            100                 105                 110

Val Asp Asp Asp Ala Asn Val Ser Ile Glu Asn Arg Gly Met Glu Phe
        115                 120                 125

Arg Ser Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly
    130                 135                 140

Ser Met Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr Ser Ser Leu Val
145                 150                 155                 160

Ala Ala Ala Ala Thr Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
                165                 170                 175

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            180                 185                 190

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        195                 200                 205

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    210                 215                 220

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
225                 230                 235                 240

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                245                 250                 255

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            260                 265                 270

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        275                 280                 285

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    290                 295                 300

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
305                 310                 315                 320

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                325                 330                 335

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            340                 345                 350

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        355                 360                 365

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    370                 375                 380

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
385                 390                 395                 400

Leu Tyr Lys


<210> SEQ ID NO 118
<211> LENGTH: 403
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 118

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Arg Trp Gly Ser Arg Ser Leu Thr Cys Ala Thr Ser Glu Gln Gln Thr
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        35                  40                  45

Arg Pro Glu Leu Cys Phe Phe Phe Ser Val Arg Ser Ser Trp Pro Ser
    50                  55                  60

Thr Ile Ser Asp Gly Ala Cys Leu Ala Leu Val Ser Ala Glu Gln Gly
65                  70                  75                  80

Ala Thr Ala Gly Arg Asn Thr Leu Ser Leu Arg Ser Met Met Ala Thr
                85                  90                  95

Glu Asp Met Ala Thr Ser Thr Arg Ser Leu Arg Ser Gln Ala Thr Asn
            100                 105                 110

Val Ala Ala Ala Ala Asn Val Ser Ile Ala Asn Ala Gly Met Glu Phe
        115                 120                 125

Arg Ser Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly
    130                 135                 140

Ser Met Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr Ser Ser Leu Val
145                 150                 155                 160

Ala Ala Ala Ala Thr Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
                165                 170                 175

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            180                 185                 190

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        195                 200                 205

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    210                 215                 220

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
225                 230                 235                 240

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                245                 250                 255

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            260                 265                 270

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        275                 280                 285

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    290                 295                 300

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
305                 310                 315                 320

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                325                 330                 335

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            340                 345                 350

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        355                 360                 365

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    370                 375                 380

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
385                 390                 395                 400

Leu Tyr Lys
```

<210> SEQ ID NO 119
<211> LENGTH: 359
<212> TYPE: PRT
<213> ORGANISM: Melampsora lini

-continued

<400> SEQUENCE: 119

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
20 25 30

Arg Trp Gly Ser Arg Ser Met Glu His Val Pro Ala Glu Leu Thr Arg
35 40 45

Val Ser Glu Gly Tyr Thr Arg Phe Tyr Arg Ser Pro Thr Ala Ser Val
50 55 60

Ile Leu Ser Gly Leu Val Lys Val Lys Trp Asp Asn Glu Gln Met Thr
65 70 75 80

Met Pro Glu Phe Arg Ser Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro
85 90 95

Asp Tyr Ala Gly Ser Met Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr
100 105 110

Ser Ser Leu Val Ala Ala Ala Ala Thr Met Ser Lys Gly Glu Glu Leu
115 120 125

Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn
130 135 140

Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr
145 150 155 160

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
165 170 175

Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe
180 185 190

Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala
195 200 205

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
210 215 220

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
225 230 235 240

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
245 250 255

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
260 265 270

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
275 280 285

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
290 295 300

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
305 310 315 320

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
325 330 335

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His
340 345 350

Gly Met Asp Glu Leu Tyr Lys
355

<210> SEQ ID NO 120
<211> LENGTH: 359
<212> TYPE: PRT
<213> ORGANISM: Melampsora lini

-continued

<400> SEQUENCE: 120

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
20 25 30

Arg Trp Gly Ser Arg Ser Met Glu His Val Pro Ala Glu Leu Thr Arg
35 40 45

Val Ser Glu Gly Tyr Thr Ala Ala Ala Ala Ser Pro Thr Ala Ser Val
50 55 60

Ile Leu Ser Gly Leu Val Lys Val Lys Trp Ala Asn Ala Gln Met Thr
65 70 75 80

Met Pro Glu Phe Arg Ser Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro
85 90 95

Asp Tyr Ala Gly Ser Met Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr
100 105 110

Ser Ser Leu Val Ala Ala Ala Ala Thr Met Ser Lys Gly Glu Glu Leu
115 120 125

Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn
130 135 140

Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr
145 150 155 160

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
165 170 175

Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe
180 185 190

Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala
195 200 205

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
210 215 220

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
225 230 235 240

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
245 250 255

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
260 265 270

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
275 280 285

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
290 295 300

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
305 310 315 320

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
325 330 335

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His
340 345 350

Gly Met Asp Glu Leu Tyr Lys
355

<210> SEQ ID NO 121
<211> LENGTH: 353
<212> TYPE: PRT

-continued

<213> ORGANISM: Plasmodium falciparum

<400> SEQUENCE: 121

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
20 25 30

Arg Trp Gly Ser Arg Ser Asp Lys Tyr Glu Lys Ala Val Asp Tyr Gly
35 40 45

Phe Arg Glu Ser Arg Ile Leu Ala Glu Gly Glu Asp Thr Cys Ala Arg
50 55 60

Lys Glu Lys Thr Thr Leu Arg Lys Ser Lys Gln Lys Glu Phe Arg Ser
65 70 75 80

Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ser Met
85 90 95

Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr Ser Ser Leu Val Ala Ala
100 105 110

Ala Ala Thr Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
115 120 125

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
130 135 140

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
145 150 155 160

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
165 170 175

Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
180 185 190

Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
195 200 205

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
210 215 220

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
225 230 235 240

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
245 250 255

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
260 265 270

Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
275 280 285

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
290 295 300

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
305 310 315 320

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
325 330 335

Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr
340 345 350

Lys

<210> SEQ ID NO 122
<211> LENGTH: 353
<212> TYPE: PRT

-continued

<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 122

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
20 25 30

Arg Trp Gly Ser Arg Ser Asp Lys Tyr Glu Lys Ala Val Asp Tyr Gly
35 40 45

Phe Arg Glu Ser Ala Ala Ala Ala Ala Gly Glu Asp Thr Cys Ala Arg
50 55 60

Lys Glu Lys Thr Thr Leu Arg Lys Ser Lys Gln Lys Glu Phe Arg Ser
65 70 75 80

Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ser Met
85 90 95

Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr Ser Ser Leu Val Ala Ala
100 105 110

Ala Ala Thr Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
115 120 125

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
130 135 140

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
145 150 155 160

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
165 170 175

Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
180 185 190

Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
195 200 205

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
210 215 220

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
225 230 235 240

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
245 250 255

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
260 265 270

Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
275 280 285

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
290 295 300

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
305 310 315 320

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
325 330 335

Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr
340 345 350

Lys

<210> SEQ ID NO 123
<211> LENGTH: 353
<212> TYPE: PRT

-continued

<213> ORGANISM: Plasmodium falciparum

<400> SEQUENCE: 123

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
20 25 30

Arg Trp Gly Ser Arg Ser Phe Asn Asn Asn Leu Cys Ser Lys Asn Ala
35 40 45

Lys Gly Leu Asn Leu Asn Lys Arg Leu Leu His Glu Thr Gln Ala His
50 55 60

Val Asp Asp Ala His His Ala His His Val Ala Asp Glu Phe Arg Ser
65 70 75 80

Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ser Met
85 90 95

Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr Ser Ser Leu Val Ala Ala
100 105 110

Ala Ala Thr Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
115 120 125

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
130 135 140

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
145 150 155 160

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
165 170 175

Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
180 185 190

Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
195 200 205

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
210 215 220

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
225 230 235 240

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
245 250 255

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
260 265 270

Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
275 280 285

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
290 295 300

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
305 310 315 320

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
325 330 335

Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr
340 345 350

Lys

<210> SEQ ID NO 124
<211> LENGTH: 353
<212> TYPE: PRT

-continued

<213> ORGANISM: Plasmodium falciparum

<400> SEQUENCE: 124

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
20 25 30

Arg Trp Gly Ser Arg Ser Phe Asn Asn Asn Leu Cys Ser Lys Asn Ala
35 40 45

Lys Gly Leu Asn Leu Asn Lys Ala Ala Ala Ala Ala Thr Gln Ala His
50 55 60

Val Asp Asp Ala His His Ala His His Val Ala Asp Glu Phe Arg Ser
65 70 75 80

Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ser Met
85 90 95

Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr Ser Ser Leu Val Ala Ala
100 105 110

Ala Ala Thr Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
115 120 125

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
130 135 140

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
145 150 155 160

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
165 170 175

Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
180 185 190

Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
195 200 205

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
210 215 220

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
225 230 235 240

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
245 250 255

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
260 265 270

Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
275 280 285

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
290 295 300

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
305 310 315 320

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
325 330 335

Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr
340 345 350

Lys

<210> SEQ ID NO 125
<211> LENGTH: 356
<212> TYPE: PRT

-continued

<213> ORGANISM: Plasmodium falciparum

<400> SEQUENCE: 125

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
20 25 30

Arg Trp Gly Ser Arg Ser Ser Tyr Asn Lys Ile Asn Ser Ser Ser Thr
35 40 45

Tyr Thr His Ser Arg Ile Leu Lys Gln Leu Glu Phe Ile Thr Leu Glu
50 55 60

Glu Lys Thr Val Asn Ala Leu Gln Glu Met Leu Asp Asp Ser Val Glu
65 70 75 80

Phe Arg Ser Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
85 90 95

Gly Ser Met Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr Ser Ser Leu
100 105 110

Val Ala Ala Ala Ala Thr Met Ser Lys Gly Glu Glu Leu Phe Thr Gly
115 120 125

Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys
130 135 140

Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu
145 150 155 160

Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro
165 170 175

Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr
180 185 190

Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu
195 200 205

Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr
210 215 220

Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg
225 230 235 240

Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly
245 250 255

His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala
260 265 270

Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn
275 280 285

Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
290 295 300

Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
305 310 315 320

Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
325 330 335

Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp
340 345 350

Glu Leu Tyr Lys
355

<210> SEQ ID NO 126
<211> LENGTH: 356

-continued

<212> TYPE: PRT
<213> ORGANISM: Plasmodium falciparum

<400> SEQUENCE: 126

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
20 25 30

Arg Trp Gly Ser Arg Ser Ser Tyr Asn Lys Ile Asn Ser Ser Ser Thr
35 40 45

Tyr Thr His Ser Ala Ala Ala Ala Ala Leu Glu Phe Ile Thr Leu Glu
50 55 60

Glu Lys Thr Val Asn Ala Leu Gln Glu Met Leu Asp Asp Ser Val Glu
65 70 75 80

Phe Arg Ser Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
85 90 95

Gly Ser Met Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr Ser Ser Leu
100 105 110

Val Ala Ala Ala Ala Thr Met Ser Lys Gly Glu Glu Leu Phe Thr Gly
115 120 125

Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys
130 135 140

Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu
145 150 155 160

Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro
165 170 175

Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr
180 185 190

Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu
195 200 205

Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr
210 215 220

Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg
225 230 235 240

Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly
245 250 255

His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala
260 265 270

Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn
275 280 285

Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
290 295 300

Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
305 310 315 320

Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
325 330 335

Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp
340 345 350

Glu Leu Tyr Lys
355

<210> SEQ ID NO 127

-continued

<211> LENGTH: 485
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 127

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220

Gly Ser Leu Thr Cys Ala Thr Ser Glu Gln Gln Thr Arg Pro Glu Leu
225 230 235 240

Cys Phe Phe Phe Ser Val Arg Ser Ser Trp Pro Ser Thr Ile Ser Asp
245 250 255

Gly Ala Cys Leu Ala Leu Val Ser Ala Glu Gln Gly Ala Thr Ala Gly
260 265 270

Arg Asn Thr Leu Ser Leu Arg Ser Met Met Ala Thr Glu Asp Met Ala
275 280 285

Thr Ser Thr Arg Ser Leu Arg Ser Gln Ala Thr Asn Val Asp Asp Asp
290 295 300

Ala Asn Val Ser Ile Glu Asn Arg Gly Met Asn Pro Ser Val Leu Thr
305 310 315 320

Lys Leu Gly Glu Phe Ala Ser Thr Leu Thr Ala Gly Asn Thr Ala Asn
325 330 335

Lys Leu Trp Leu Met Ala Asp Val Asp Pro Lys Ser Ala Phe Lys Leu
340 345 350

Leu Gly Leu Asp Met Pro Gly Val Arg Phe Ile Asp Asn Pro Lys Met
355 360 365

Leu Gln Trp Leu Lys Phe Thr Lys Ala Tyr Leu Asp Met Lys Lys Ser

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    370                 375                 380

Gly Phe Gly Glu Thr Ser Ala His Ala Leu Leu Tyr Glu Lys Ile Gly
385                 390                 395                 400

Gly Pro Asp Leu Ser Leu Leu Leu Leu Ser Leu Lys Asp Ala Pro Asp
                405                 410                 415

Ala Asn Ser Leu Val Gln Lys Leu Thr Asn Ser Gln Phe Gly Met Trp
            420                 425                 430

His Asp Ala Arg Ile Glu Pro Glu Gln Leu Ala Gln Thr Val Phe Lys
        435                 440                 445

Ile Gln Asp Val Arg Lys Leu Pro Lys Asn Asp Pro Lys Leu Gln Val
    450                 455                 460

Ile Asp Asp Tyr Ala Lys Tyr His Arg Lys His Arg Lys Phe Leu Asn
465                 470                 475                 480

Ser Ile Met Ile Ile
                485


<210> SEQ ID NO 128
<211> LENGTH: 485
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 128

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1               5                   10                  15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
            20                  25                  30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35                  40                  45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
    50                  55                  60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65                  70                  75                  80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                85                  90                  95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
            100                 105                 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
        115                 120                 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
    130                 135                 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145                 150                 155                 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
                165                 170                 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
            180                 185                 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
        195                 200                 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
    210                 215                 220

Gly Ser Leu Thr Cys Ala Thr Ser Glu Gln Gln Thr Arg Pro Glu Leu
225                 230                 235                 240
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Cys Phe Phe Phe Ser Val Arg Ser Ser Trp Pro Ser Thr Ile Ser Asp
                245                 250                 255

Gly Ala Cys Leu Ala Leu Val Ser Ala Glu Gln Gly Ala Thr Ala Gly
            260                 265                 270

Arg Asn Thr Leu Ser Leu Arg Ser Met Met Ala Thr Glu Asp Met Ala
        275                 280                 285

Thr Ser Thr Ala Ala Ala Ala Ser Gln Ala Thr Asn Val Asp Asp Asp
    290                 295                 300

Ala Asn Val Ser Ile Glu Asn Arg Gly Met Asn Pro Ser Val Leu Thr
305                 310                 315                 320

Lys Leu Gly Glu Phe Ala Ser Thr Leu Thr Ala Gly Asn Thr Ala Asn
                325                 330                 335

Lys Leu Trp Leu Met Ala Asp Val Asp Pro Lys Ser Ala Phe Lys Leu
            340                 345                 350

Leu Gly Leu Asp Met Pro Gly Val Arg Phe Ile Asp Asn Pro Lys Met
        355                 360                 365

Leu Gln Trp Leu Lys Phe Thr Lys Ala Tyr Leu Asp Met Lys Lys Ser
    370                 375                 380

Gly Phe Gly Glu Thr Ser Ala His Ala Leu Leu Tyr Glu Lys Ile Gly
385                 390                 395                 400

Gly Pro Asp Leu Ser Leu Leu Leu Leu Ser Leu Lys Asp Ala Pro Asp
                405                 410                 415

Ala Asn Ser Leu Val Gln Lys Leu Thr Asn Ser Gln Phe Gly Met Trp
            420                 425                 430

His Asp Ala Arg Ile Glu Pro Glu Gln Leu Ala Gln Thr Val Phe Lys
        435                 440                 445

Ile Gln Asp Val Arg Lys Leu Pro Lys Asn Asp Pro Lys Leu Gln Val
    450                 455                 460

Ile Asp Asp Tyr Ala Lys Tyr His Arg Lys His Arg Lys Phe Leu Asn
465                 470                 475                 480

Ser Ile Met Ile Ile
                485


<210> SEQ ID NO 129
<211> LENGTH: 342
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 129

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1               5                   10                  15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
            20                  25                  30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35                  40                  45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
    50                  55                  60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65                  70                  75                  80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                85                  90                  95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
            100                 105                 110
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Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
        115                 120                 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
    130                 135                 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145                 150                 155                 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
                165                 170                 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
            180                 185                 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
        195                 200                 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
    210                 215                 220

Gly Ser Thr Arg Val Pro Asp Asp Ala Asn Leu Gln Ser Val Asn Ala
225                 230                 235                 240

Pro Val Gln Thr Val Thr Arg Ser Arg Arg Phe Leu Arg Thr Ala Asp
                245                 250                 255

Thr Asp Ile Val Tyr Glu Pro Lys Val His Asn Pro Gly Lys Lys Gln
            260                 265                 270

Val Phe Ile Glu Asp Lys Leu Gln Lys Ala Leu Thr Asp Pro Lys Lys
        275                 280                 285

Asn Lys Lys Leu Tyr Ala Arg Trp Tyr Asn Ser Gly Phe Thr Val Lys
    290                 295                 300

Gln Val Glu Gly Gly Leu Asp Gln Asn Glu Asn Arg Glu Leu Glu Leu
305                 310                 315                 320

Thr Tyr Lys Asn Leu Ala Leu Gly Tyr Ala Lys Tyr Tyr Gln Ala Arg
                325                 330                 335

Arg Ser Gln Glu Ala Lys
            340


<210> SEQ ID NO 130
<211> LENGTH: 342
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 130

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1               5                   10                  15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
            20                  25                  30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35                  40                  45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
    50                  55                  60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65                  70                  75                  80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                85                  90                  95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
            100                 105                 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
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        115                 120                 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
    130                 135                 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145                 150                 155                 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
                165                 170                 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
            180                 185                 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
        195                 200                 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
    210                 215                 220

Gly Ser Thr Arg Val Pro Asp Asp Ala Asn Leu Gln Ser Val Asn Ala
225                 230                 235                 240

Pro Val Gln Thr Val Thr Arg Ser Arg Ala Ala Ala Ala Thr Ala Asp
                245                 250                 255

Thr Asp Ile Val Tyr Glu Pro Lys Val His Asn Pro Gly Lys Lys Gln
            260                 265                 270

Val Phe Ile Glu Asp Lys Leu Gln Lys Ala Leu Thr Asp Pro Lys Lys
        275                 280                 285

Asn Lys Lys Leu Tyr Ala Arg Trp Tyr Asn Ser Gly Phe Thr Val Lys
    290                 295                 300

Gln Val Glu Gly Gly Leu Asp Gln Asn Glu Asn Arg Glu Leu Glu Leu
305                 310                 315                 320

Thr Tyr Lys Asn Leu Ala Leu Gly Tyr Ala Lys Tyr Tyr Gln Ala Arg
                325                 330                 335

Arg Ser Gln Glu Ala Lys
            340


<210> SEQ ID NO 131
<211> LENGTH: 342
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 131

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1               5                   10                  15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
            20                  25                  30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35                  40                  45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
    50                  55                  60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65                  70                  75                  80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                85                  90                  95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
            100                 105                 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
        115                 120                 125
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Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
    130                 135                 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145                 150                 155                 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
                165                 170                 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
            180                 185                 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
        195                 200                 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
    210                 215                 220

Gly Ser Thr Arg Val Pro Asp Asp Ala Asn Leu Gln Ser Val Asn Ala
225                 230                 235                 240

Pro Val Gln Thr Val Thr Arg Ser Arg Arg Phe Leu Arg Thr Ala Ala
                245                 250                 255

Thr Ala Ile Val Tyr Ala Pro Ala Val His Asn Pro Gly Lys Lys Gln
            260                 265                 270

Val Phe Ile Glu Asp Lys Leu Gln Lys Ala Leu Thr Asp Pro Lys Lys
        275                 280                 285

Asn Lys Lys Leu Tyr Ala Arg Trp Tyr Asn Ser Gly Phe Thr Val Lys
    290                 295                 300

Gln Val Glu Gly Gly Leu Asp Gln Asn Glu Asn Arg Glu Leu Glu Leu
305                 310                 315                 320

Thr Tyr Lys Asn Leu Ala Leu Gly Tyr Ala Lys Tyr Tyr Gln Ala Arg
                325                 330                 335

Arg Ser Gln Glu Ala Lys
            340


<210> SEQ ID NO 132
<211> LENGTH: 279
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 132

Met Met Gln Trp Ser Ala Ile Leu Ile Arg Thr Cys Phe Ser Gly Ser
1               5                   10                  15

Gly Gly Glu Ala Leu Thr Cys Ala Thr Ser Glu Gln Gln Thr Arg Pro
            20                  25                  30

Glu Leu Cys Phe Phe Phe Ser Val Arg Ser Ser Trp Pro Ser Thr Ile
        35                  40                  45

Ser Asp Gly Ala Cys Leu Ala Leu Val Ser Ala Glu Gln Gly Ala Thr
    50                  55                  60

Ala Gly Arg Asn Thr Leu Ser Leu Arg Ser Met Met Ala Thr Glu Asp
65                  70                  75                  80

Met Ala Thr Ser Thr Arg Ser Leu Arg Ser Gln Ala Thr Asn Val Asp
                85                  90                  95

Asp Asp Ala Asn Val Ser Ile Glu Asn Arg Gly Met Asn Pro Ser Val
            100                 105                 110

Leu Thr Lys Leu Gly Glu Phe Ala Ser Thr Leu Thr Ala Gly Asn Thr
        115                 120                 125

Ala Asn Lys Leu Trp Leu Met Ala Asp Val Asp Pro Lys Ser Ala Phe
    130                 135                 140
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Lys Leu Leu Gly Leu Asp Met Pro Gly Val Arg Phe Ile Asp Asn Pro
145                 150                 155                 160

Lys Met Leu Gln Trp Leu Lys Phe Thr Lys Ala Tyr Leu Asp Met Lys
                165                 170                 175

Lys Ser Gly Phe Gly Glu Thr Ser Ala His Ala Leu Leu Tyr Glu Lys
            180                 185                 190

Ile Gly Gly Pro Asp Leu Ser Leu Leu Leu Leu Ser Leu Lys Asp Ala
        195                 200                 205

Pro Asp Ala Asn Ser Leu Val Gln Lys Leu Thr Asn Ser Gln Phe Gly
    210                 215                 220

Met Trp His Asp Ala Arg Ile Glu Pro Glu Gln Leu Ala Gln Thr Val
225                 230                 235                 240

Phe Lys Ile Gln Asp Val Arg Lys Leu Pro Lys Asn Asp Pro Lys Leu
                245                 250                 255

Gln Val Ile Asp Asp Tyr Ala Lys Tyr His Arg Lys His Arg Lys Phe
            260                 265                 270

Leu Asn Ser Ile Met Ile Ile
        275


<210> SEQ ID NO 133
<211> LENGTH: 279
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 133

Met Met Gln Trp Ser Ala Ile Leu Ile Arg Thr Cys Phe Ser Gly Ser
1               5                   10                  15

Gly Gly Glu Ala Leu Thr Cys Ala Thr Ser Glu Gln Gln Thr Arg Pro
            20                  25                  30

Glu Leu Cys Phe Phe Phe Ser Val Arg Ser Ser Trp Pro Ser Thr Ile
        35                  40                  45

Ser Asp Gly Ala Cys Leu Ala Leu Val Ser Ala Glu Gln Gly Ala Thr
    50                  55                  60

Ala Gly Arg Asn Thr Leu Ser Leu Arg Ser Met Met Ala Thr Glu Asp
65                  70                  75                  80

Met Ala Thr Ser Thr Ala Ala Ala Ala Ser Gln Ala Thr Asn Val Asp
                85                  90                  95

Asp Asp Ala Asn Val Ser Ile Glu Asn Arg Gly Met Asn Pro Ser Val
            100                 105                 110

Leu Thr Lys Leu Gly Glu Phe Ala Ser Thr Leu Thr Ala Gly Asn Thr
        115                 120                 125

Ala Asn Lys Leu Trp Leu Met Ala Asp Val Asp Pro Lys Ser Ala Phe
    130                 135                 140

Lys Leu Leu Gly Leu Asp Met Pro Gly Val Arg Phe Ile Asp Asn Pro
145                 150                 155                 160

Lys Met Leu Gln Trp Leu Lys Phe Thr Lys Ala Tyr Leu Asp Met Lys
                165                 170                 175

Lys Ser Gly Phe Gly Glu Thr Ser Ala His Ala Leu Leu Tyr Glu Lys
            180                 185                 190

Ile Gly Gly Pro Asp Leu Ser Leu Leu Leu Leu Ser Leu Lys Asp Ala
        195                 200                 205

Pro Asp Ala Asn Ser Leu Val Gln Lys Leu Thr Asn Ser Gln Phe Gly
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    210                 215                 220

Met Trp His Asp Ala Arg Ile Glu Pro Glu Gln Leu Ala Gln Thr Val
225                 230                 235                 240

Phe Lys Ile Gln Asp Val Arg Lys Leu Pro Lys Asn Asp Pro Lys Leu
                245                 250                 255

Gln Val Ile Asp Asp Tyr Ala Lys Tyr His Arg Lys His Arg Lys Phe
            260                 265                 270

Leu Asn Ser Ile Met Ile Ile
        275


<210> SEQ ID NO 134
<211> LENGTH: 279
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 134

Met Met Gln Trp Ser Ala Ile Leu Ile Arg Thr Cys Phe Ser Gly Ser
1               5                   10                  15

Gly Gly Glu Ala Leu Thr Cys Ala Thr Ser Glu Gln Gln Thr Arg Pro
            20                  25                  30

Glu Leu Cys Phe Phe Phe Ser Val Arg Ser Ser Trp Pro Ser Thr Ile
        35                  40                  45

Ser Asp Gly Ala Cys Leu Ala Leu Val Ser Ala Glu Gln Gly Ala Thr
    50                  55                  60

Ala Gly Arg Asn Thr Leu Ser Leu Arg Ser Met Met Ala Thr Glu Asp
65                  70                  75                  80

Met Ala Thr Ser Thr Arg Ser Leu Arg Ser Gln Ala Thr Asn Val Ala
                85                  90                  95

Ala Ala Ala Asn Val Ser Ile Ala Asn Ala Gly Met Asn Pro Ser Val
            100                 105                 110

Leu Thr Lys Leu Gly Glu Phe Ala Ser Thr Leu Thr Ala Gly Asn Thr
        115                 120                 125

Ala Asn Lys Leu Trp Leu Met Ala Asp Val Asp Pro Lys Ser Ala Phe
    130                 135                 140

Lys Leu Leu Gly Leu Asp Met Pro Gly Val Arg Phe Ile Asp Asn Pro
145                 150                 155                 160

Lys Met Leu Gln Trp Leu Lys Phe Thr Lys Ala Tyr Leu Asp Met Lys
                165                 170                 175

Lys Ser Gly Phe Gly Glu Thr Ser Ala His Ala Leu Leu Tyr Glu Lys
            180                 185                 190

Ile Gly Gly Pro Asp Leu Ser Leu Leu Leu Leu Ser Leu Lys Asp Ala
        195                 200                 205

Pro Asp Ala Asn Ser Leu Val Gln Lys Leu Thr Asn Ser Gln Phe Gly
    210                 215                 220

Met Trp His Asp Ala Arg Ile Glu Pro Glu Gln Leu Ala Gln Thr Val
225                 230                 235                 240

Phe Lys Ile Gln Asp Val Arg Lys Leu Pro Lys Asn Asp Pro Lys Leu
                245                 250                 255

Gln Val Ile Asp Asp Tyr Ala Lys Tyr His Arg Lys His Arg Lys Phe
            260                 265                 270

Leu Asn Ser Ile Met Ile Ile
        275
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<210> SEQ ID NO 135
<211> LENGTH: 259
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 135

Leu Thr Cys Ala Thr Ser Glu Gln Gln Thr Arg Pro Glu Leu Cys Phe
1 5 10 15

Phe Phe Ser Val Arg Ser Ser Trp Pro Ser Thr Ile Ser Asp Gly Ala
20 25 30

Cys Leu Ala Leu Val Ser Ala Glu Gln Gly Ala Thr Ala Gly Arg Asn
35 40 45

Thr Leu Ser Leu Arg Ser Met Met Ala Thr Glu Asp Met Ala Thr Ser
50 55 60

Thr Arg Ser Leu Arg Ser Gln Ala Thr Asn Val Asp Asp Asp Ala Asn
65 70 75 80

Val Ser Ile Glu Asn Arg Gly Met Asn Pro Ser Val Leu Thr Lys Leu
85 90 95

Gly Glu Phe Ala Ser Thr Leu Thr Ala Gly Asn Thr Ala Asn Lys Leu
100 105 110

Trp Leu Met Ala Asp Val Asp Pro Lys Ser Ala Phe Lys Leu Leu Gly
115 120 125

Leu Asp Met Pro Gly Val Arg Phe Ile Asp Asn Pro Lys Met Leu Gln
130 135 140

Trp Leu Lys Phe Thr Lys Ala Tyr Leu Asp Met Lys Lys Ser Gly Phe
145 150 155 160

Gly Glu Thr Ser Ala His Ala Leu Leu Tyr Glu Lys Ile Gly Gly Pro
165 170 175

Asp Leu Ser Leu Leu Leu Leu Ser Leu Lys Asp Ala Pro Asp Ala Asn
180 185 190

Ser Leu Val Gln Lys Leu Thr Asn Ser Gln Phe Gly Met Trp His Asp
195 200 205

Ala Arg Ile Glu Pro Glu Gln Leu Ala Gln Thr Val Phe Lys Ile Gln
210 215 220

Asp Val Arg Lys Leu Pro Lys Asn Asp Pro Lys Leu Gln Val Ile Asp
225 230 235 240

Asp Tyr Ala Lys Tyr His Arg Lys His Arg Lys Phe Leu Asn Ser Ile
245 250 255

Met Ile Ile

<210> SEQ ID NO 136
<211> LENGTH: 259
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 136

Leu Thr Cys Ala Thr Ser Glu Gln Gln Thr Arg Pro Glu Leu Cys Phe
1 5 10 15

Phe Phe Ser Val Arg Ser Ser Trp Pro Ser Thr Ile Ser Asp Gly Ala
20 25 30

Cys Leu Ala Leu Val Ser Ala Glu Gln Gly Ala Thr Ala Gly Arg Asn
35 40 45

Thr Leu Ser Leu Arg Ser Met Met Ala Thr Glu Asp Met Ala Thr Ser

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    50                  55                  60

Thr Ala Ala Ala Ala Ser Gln Ala Thr Asn Val Asp Asp Asp Ala Asn
65                  70                  75                  80

Val Ser Ile Glu Asn Arg Gly Met Asn Pro Ser Val Leu Thr Lys Leu
                85                  90                  95

Gly Glu Phe Ala Ser Thr Leu Thr Ala Gly Asn Thr Ala Asn Lys Leu
            100                 105                 110

Trp Leu Met Ala Asp Val Asp Pro Lys Ser Ala Phe Lys Leu Leu Gly
        115                 120                 125

Leu Asp Met Pro Gly Val Arg Phe Ile Asp Asn Pro Lys Met Leu Gln
    130                 135                 140

Trp Leu Lys Phe Thr Lys Ala Tyr Leu Asp Met Lys Lys Ser Gly Phe
145                 150                 155                 160

Gly Glu Thr Ser Ala His Ala Leu Leu Tyr Glu Lys Ile Gly Gly Pro
                165                 170                 175

Asp Leu Ser Leu Leu Leu Leu Ser Leu Lys Asp Ala Pro Asp Ala Asn
            180                 185                 190

Ser Leu Val Gln Lys Leu Thr Asn Ser Gln Phe Gly Met Trp His Asp
        195                 200                 205

Ala Arg Ile Glu Pro Glu Gln Leu Ala Gln Thr Val Phe Lys Ile Gln
    210                 215                 220

Asp Val Arg Lys Leu Pro Lys Asn Asp Pro Lys Leu Gln Val Ile Asp
225                 230                 235                 240

Asp Tyr Ala Lys Tyr His Arg Lys His Arg Lys Phe Leu Asn Ser Ile
                245                 250                 255

Met Ile Ile


<210> SEQ ID NO 137
<211> LENGTH: 259
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 137

Leu Thr Cys Ala Thr Ser Glu Gln Gln Thr Arg Pro Glu Leu Cys Phe
1               5                   10                  15

Phe Phe Ser Val Arg Ser Ser Trp Pro Ser Thr Ile Ser Asp Gly Ala
            20                  25                  30

Cys Leu Ala Leu Val Ser Ala Glu Gln Gly Ala Thr Ala Gly Arg Asn
        35                  40                  45

Thr Leu Ser Leu Arg Ser Met Met Ala Thr Glu Asp Met Ala Thr Ser
    50                  55                  60

Thr Arg Ser Leu Arg Ser Gln Ala Thr Asn Val Ala Ala Ala Ala Asn
65                  70                  75                  80

Val Ser Ile Ala Asn Ala Gly Met Asn Pro Ser Val Leu Thr Lys Leu
                85                  90                  95

Gly Glu Phe Ala Ser Thr Leu Thr Ala Gly Asn Thr Ala Asn Lys Leu
            100                 105                 110

Trp Leu Met Ala Asp Val Asp Pro Lys Ser Ala Phe Lys Leu Leu Gly
        115                 120                 125

Leu Asp Met Pro Gly Val Arg Phe Ile Asp Asn Pro Lys Met Leu Gln
    130                 135                 140

Trp Leu Lys Phe Thr Lys Ala Tyr Leu Asp Met Lys Lys Ser Gly Phe
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145                 150                 155                 160

Gly Glu Thr Ser Ala His Ala Leu Leu Tyr Glu Lys Ile Gly Gly Pro
                165                 170                 175

Asp Leu Ser Leu Leu Leu Leu Ser Leu Lys Asp Ala Pro Asp Ala Asn
            180                 185                 190

Ser Leu Val Gln Lys Leu Thr Asn Ser Gln Phe Gly Met Trp His Asp
        195                 200                 205

Ala Arg Ile Glu Pro Glu Gln Leu Ala Gln Thr Val Phe Lys Ile Gln
    210                 215                 220

Asp Val Arg Lys Leu Pro Lys Asn Asp Pro Lys Leu Gln Val Ile Asp
225                 230                 235                 240

Asp Tyr Ala Lys Tyr His Arg Lys His Arg Lys Phe Leu Asn Ser Ile
                245                 250                 255

Met Ile Ile


<210> SEQ ID NO 138
<211> LENGTH: 137
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Sequence of amino acids 24-67 of
      avrL567 replacing theRXLR region of seceted Avr1b

<400> SEQUENCE: 138

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Met Glu His Val Pro Ala Glu Leu Thr Arg Val
            20                  25                  30

Ser Glu Gly Tyr Thr Arg Phe Tyr Arg Ser Pro Thr Ala Ser Val Ile
        35                  40                  45

Leu Ser Gly Leu Val Lys Val Lys Trp Asp Asn Glu Gln Met Thr Met
    50                  55                  60

Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys Leu
65                  70                  75                  80

Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr Glu
                85                  90                  95

Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp Leu
            100                 105                 110

Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr Asn
        115                 120                 125

Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 139
<211> LENGTH: 137
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Sequence of amino acids 24-67 of
      avrL567 replacing theRXLR region of secreted Avr1b. RFYR-DE
      mutated to AAAA-AA

<400> SEQUENCE: 139

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Met Glu His Val Pro Ala Glu Leu Thr Arg Val
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            20                  25                  30

Ser Glu Gly Tyr Thr Ala Ala Ala Ala Ser Pro Thr Ala Ser Val Ile
        35                  40                  45

Leu Ser Gly Leu Val Lys Val Lys Trp Ala Asn Ala Gln Met Thr Met
    50                  55                  60

Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys Leu
65                  70                  75                  80

Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr Glu
                85                  90                  95

Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp Leu
            100                 105                 110

Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr Asn
        115                 120                 125

Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 140
<211> LENGTH: 116
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Sequence of amino acids 24-67 of
      avrL567 replacing theRXLR regio
      n of mature Avr1b.

<400> SEQUENCE: 140

Met Glu His Val Pro Ala Glu Leu Thr Arg Val Ser Glu Gly Tyr Thr
1               5                   10                  15

Arg Phe Tyr Arg Ser Pro Thr Ala Ser Val Ile Leu Ser Gly Leu Val
            20                  25                  30

Lys Val Lys Trp Asp Asn Glu Gln Met Thr Met Thr Phe Ser Val Thr
        35                  40                  45

Asp Leu Trp Asn Lys Val Ala Ala Lys Lys Leu Ala Lys Ala Met Leu
    50                  55                  60

Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr Glu Lys Trp Ala Lys Lys
65                  70                  75                  80

Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp Leu Ala Ile Ala Asp Pro
                85                  90                  95

Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr Asn Gly Tyr Thr Phe His
            100                 105                 110

Arg Tyr Gln Ser
        115


<210> SEQ ID NO 141
<211> LENGTH: 116
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Sequence of amino acids 24-67 of
      avrL567 replacing theRXLR region of mature Avr1b. RFYR-DE
      mutated to AAAA-AA

<400> SEQUENCE: 141

Met Glu His Val Pro Ala Glu Leu Thr Arg Val Ser Glu Gly Tyr Thr
1               5                   10                  15

Ala Ala Ala Ala Ser Pro Thr Ala Ser Val Ile Leu Ser Gly Leu Val
            20                  25                  30
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```
Lys Val Lys Trp Ala Asn Ala Gln Met Thr Met Thr Phe Ser Val Thr
        35                  40                  45

Asp Leu Trp Asn Lys Val Ala Ala Lys Lys Leu Ala Lys Ala Met Leu
    50                  55                  60

Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr Glu Lys Trp Ala Lys Lys
65                  70                  75                  80

Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp Leu Ala Ile Ala Asp Pro
                85                  90                  95

Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr Asn Gly Tyr Thr Phe His
            100                 105                 110

Arg Tyr Gln Ser
        115


    <210> SEQ ID NO 142
<211> LENGTH: 169
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Sequence of the N-terminus of AvrM
      replacing the RXLR region of secreted Avr1b.

<400> SEQUENCE: 142

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala His Pro Val Tyr Asp Tyr Asn Pro Ile Pro Asn
            20                  25                  30

His Ile His Gly Asp Leu Lys Arg Arg Ala Tyr Ile Glu Arg Tyr Ser
        35                  40                  45

Gln Cys Ser Asp Ser Gln Ala Ser Glu Ile Arg Ala Ala Leu Lys Ser
    50                  55                  60

Cys Ala Glu Leu Ala Ser Trp Gly Tyr His Ala Val Lys Asn Asp Asn
65                  70                  75                  80

Arg Leu Phe Lys Leu Ile Phe Lys Thr Asp Ser Thr Asp Ile Gln Asn
                85                  90                  95

Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys Leu
            100                 105                 110

Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr Glu
        115                 120                 125

Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp Leu
    130                 135                 140

Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr Asn
145                 150                 155                 160

Gly Tyr Thr Phe His Arg Tyr Gln Ser
                165


<210> SEQ ID NO 143
<211> LENGTH: 192
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Sequence of the N-terminus of
      AvrPita replacing theRXLR region of secreted Avr1b.

<400> SEQUENCE: 143

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15
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```
Val Thr Cys Asn Ala Asn Asn Leu Gly Thr Val Pro Asp Val Pro His
            20                  25                  30

Gln Ile Pro Asn Asp Lys Ser Gly Thr Pro Ala Ile Glu Asp Pro Lys
        35                  40                  45

Asp Met Lys Gly Phe Asn Lys Ala Leu Lys Ser Thr Pro Glu Ser Glu
    50                  55                  60

Lys Leu Gly Thr Ser Ser Val Glu Gly Ile Pro Gln Pro Glu Phe Asp
65                  70                  75                  80

Arg Gly Phe Leu Arg Pro Phe Gly Ala Lys Met Lys Phe Leu Lys Pro
                85                  90                  95

Asp Gln Val Gln Lys Leu Ser Thr Asp Asp Leu Ile Thr Tyr Met Ala
            100                 105                 110

Glu Lys Asp Lys Asn Val Arg Thr Phe Ser Val Thr Asp Leu Trp Asn
        115                 120                 125

Lys Val Ala Ala Lys Lys Leu Ala Lys Ala Met Leu Ala Asp Pro Ser
    130                 135                 140

Lys Glu Gln Lys Ala Tyr Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu
145                 150                 155                 160

Asp Lys Ile Lys Asn Trp Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly
                165                 170                 175

Lys Tyr Asp Arg Ile Tyr Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
            180                 185                 190


<210> SEQ ID NO 144
<211> LENGTH: 142
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 144

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Lys Arg Arg Ala Tyr Ile Glu Arg Ala His Glu Glu Asp
    50                  55                  60

Asp Ala Gly Glu Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val
65                  70                  75                  80

Ala Ala Lys Lys Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu
                85                  90                  95

Gln Lys Ala Tyr Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys
            100                 105                 110

Ile Lys Asn Trp Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr
        115                 120                 125

Asp Arg Ile Tyr Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135                 140


<210> SEQ ID NO 145
<211> LENGTH: 139
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 145
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```
Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Arg Ala Ala Leu Lys Ala His Glu Glu Asp Asp Ala Gly
    50                  55                  60

Glu Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys
65                  70                  75                  80

Lys Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala
                85                  90                  95

Tyr Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn
            100                 105                 110

Trp Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile
        115                 120                 125

Tyr Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 146
<211> LENGTH: 149
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 146

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Arg Leu Phe Lys Leu Ile Phe Lys Thr Asp Ser Thr Asp
    50                  55                  60

Ile Gln Ala His Glu Glu Asp Asp Ala Gly Glu Arg Thr Phe Ser Val
65                  70                  75                  80

Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys Leu Ala Lys Ala Met
                85                  90                  95

Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr Glu Lys Trp Ala Lys
            100                 105                 110

Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp Leu Ala Ile Ala Asp
        115                 120                 125

Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr Asn Gly Tyr Thr Phe
    130                 135                 140

His Arg Tyr Gln Ser
145


<210> SEQ ID NO 147
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 147

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15
```

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```
Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly His Phe Leu Arg Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 148
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 148

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Arg Phe Phe Arg Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 149
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 149

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45
```

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```
Ala Gly Gly Arg Phe Tyr Arg Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 150
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 150

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Arg Phe Ile Arg Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 151
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 151

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Arg Phe Met Arg Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80
```

-continued

```
Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 152
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 152

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Arg Phe Leu Gly Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 153
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 153

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Arg Met Val Arg Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110
```

-continued

```
Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 154
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 154

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Arg Leu Gly Thr Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135


<210> SEQ ID NO 155
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 155

Met Arg Leu Ser Phe Val Leu Ser Leu Val Val Ala Ile Gly Tyr Val
1               5                   10                  15

Val Thr Cys Asn Ala Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met
            20                  25                  30

Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile
        35                  40                  45

Ala Gly Gly Arg Leu Thr Gln Ala His Glu Glu Asp Asp Ala Gly Glu
    50                  55                  60

Arg Thr Phe Ser Val Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys
65                  70                  75                  80

Leu Ala Lys Ala Met Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr
                85                  90                  95

Glu Lys Trp Ala Lys Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp
            100                 105                 110

Leu Ala Ile Ala Asp Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr
        115                 120                 125

Asn Gly Tyr Thr Phe His Arg Tyr Gln Ser
    130                 135
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<210> SEQ ID NO 156
<211> LENGTH: 53
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 156

gcatcccatg gagccagcat agtctgggac gtcatatgga tagccggaca tgg 53

<210> SEQ ID NO 157
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 157

atgcagatct ctcacttgcg ccacctccga gc 32

<210> SEQ ID NO 158
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 158

catatggata gccggacatg gtggatctgt cgactctgtt ttcaatcg 48

<210> SEQ ID NO 159
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 159

catatggata gccggacatg gtggatctgt cgactgcgtt tgcaat 46

<210> SEQ ID NO 160
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 160

agtcagatct acaagagtcc ccgacga 27

<210> SEQ ID NO 161
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 161

catatggata gccggacatg gtggatctgt cgacttgcca ggattatg 48

<210> SEQ ID NO 162
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 162

atcgagatct atgggaatgg aacatg 26

<210> SEQ ID NO 163
<211> LENGTH: 45
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 163

gatagccgga catggtggat ctgtcgaccc acaggtcagt cacgc 45

<210> SEQ ID NO 164
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 164

tcccatggag ccagcatagt ctgggacgtc atatggatag ccggacatgg tggatct 57

<210> SEQ ID NO 165
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 165

atcgagatct gataagtatg agaaagcg 28

<210> SEQ ID NO 166
<211> LENGTH: 53
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 166

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catatggata gccggacatg gtggatctgt cgaccgtttg cttgcttttc cgg 53

<210> SEQ ID NO 167
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 167

gattacggct ttcgagagtc tgcagcagca gcagcaggcg aagatacctg cg 52

<210> SEQ ID NO 168
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 168

atgcagatct gataagtatg agaaagcggt agattacggc tttcgagagt ct 52

<210> SEQ ID NO 169
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 169

atgcagatct tttaacaata acc 23

<210> SEQ ID NO 170
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 170

catatggata gccggacatg gtggatctgt cgacatctgc aacatgg 47

<210> SEQ ID NO 171
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 171

ggcttgaacc tcaacaaggc agcagcagca gcaacacaag cacatg 46

<210> SEQ ID NO 172
<211> LENGTH: 35

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 172

gtagtaagaa tgctaaaggc ttgaacctca acaag 35

<210> SEQ ID NO 173
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 173

atgcagatct tttaacaata acctgtgtag taagaatgct aaaggc 46

<210> SEQ ID NO 174
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 174

atgcagatct agttacaaca agatcaac 28

<210> SEQ ID NO 175
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 175

catatggata gccggacatg gtggatctgt cgacactatc atctaac 47

<210> SEQ ID NO 176
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 176

catctactta tacacacagt gcagcagcag cagcattgga gttcatcaca ttgg 54

<210> SEQ ID NO 177
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

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<400> SEQUENCE: 177

atgcagatct agttacaaca agatcaactc gtcatctact tatacacaca gtgcagca 58

<210> SEQ ID NO 178
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 178

gcgtggatcc ctcacttgcg ccacctccg 29

<210> SEQ ID NO 179
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 179

tcgagtcgac tcagataatc atgatgctgt 30

<210> SEQ ID NO 180
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 180

gcgtggatcc acaagagtcc ccgacga 27

<210> SEQ ID NO 181
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 181

tcgagtcgac tcacttggcc tcttgcgat 29

<210> SEQ ID NO 182
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 182

cagcggcggc ggcgtctcaa gctacgaacg 30

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<210> SEQ ID NO 183
<211> LENGTH: 45
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 183

gttcgtagct tgagacgccg ccgccgctgt cgaggttgcc atgtc 45

<210> SEQ ID NO 184
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 184

ggctaacgtt tcgattgcga acgcgggatg aacccttcag 40

<210> SEQ ID NO 185
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 185

cgcaatcgaa acgttagccg ccgccgccac gttcgtag 38

<210> SEQ ID NO 186
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 186

gcgtccatgg gagctcactt gcgccacctc cg 32

<210> SEQ ID NO 187
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 187

tcgaggtacc tcagataatc atgatgctgt 30

<210> SEQ ID NO 188
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to

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amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 188

agatcccggg gggcagtgag atatgctcac ttgcgccacc tccgagcaac ag 52

<210> SEQ ID NO 189
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 189

atcgccatgg gaatggaaca tgtaccagca gagttgacca gagtcagcga aggg 54

<210> SEQ ID NO 190
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 190

accagagtca gcgaagggta tacacgattt taccggtccc caacggctag tgtaatac 58

<210> SEQ ID NO 191
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 191

caacggctag tgtaatactg tcaggattgg taaaggttaa atgggataat gaacaaatg 59

<210> SEQ ID NO 192
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 192

tgggataatg aacaaatgac gatgccgacc ttcagcgtga ctgacctgtg g 51

<210> SEQ ID NO 193
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 193

agatcccggg gggcaatgag atatgatgga acatgtacca gcag 44

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<210> SEQ ID NO 194
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 194

tcctgacagt attacactag ccgttgggga cgcagcggct gctgtatacc cttcgctg 58

<210> SEQ ID NO 195
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 195

gtgtaatact gtcaggattg gtaaaggtta aatgggctaa tgcacaaatg acgatgccg 59

<210> SEQ ID NO 196
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 196

atcgcactcg agctttcgca gatcccgggg ggcaatgaga tatgcgtcta tcttttgtg 59

<210> SEQ ID NO 197
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 197

atcgccatgg gacacccagt ttacgattac aatc 34

<210> SEQ ID NO 198
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 198

cacgccgtta aaaatgacaa tcggttattt agattaatct ttaaaactga cagcacag 58

<210> SEQ ID NO 199
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 199

ctttaaaact gacagcacag atattcaaaa caccttcagc gtgactgacc tg 52

<210> SEQ ID NO 200
<211> LENGTH: 45
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 200

ccacgaggcg agctcggcac aacttttag cgcggcacga atttc 45

<210> SEQ ID NO 201
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 201

ccgattgtca tttttaacgg cgtgatagcc ccacgaggcg agctcggcac 50

<210> SEQ ID NO 202
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 202

atcgccatgg gaaacaacct tggaacagta ccggatgtgc cacatc 46

<210> SEQ ID NO 203
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 203

cagtaccgga tgtgccacat caaattccaa atgacaaaag tggtactcct gccattg 57

<210> SEQ ID NO 204
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 204

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caaaagtggt actcctgcca ttgaagaccc aaaagatatg aaaggattca ataaggctc 59

<210> SEQ ID NO 205
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 205

ccacaggtca gtcacgctga aggttcgtac atttttatct ttttctgcca tgtatg 56

<210> SEQ ID NO 206
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 206

gacattgccg gcggaaaaag gcgggcttat attgaacgcg ctcatgaaga ggacgatgc 59

<210> SEQ ID NO 207
<211> LENGTH: 53
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 207

gacattgccg gcggacgtgc cgcgctaaaa agtgctcatg aagaggacga tgc 53

<210> SEQ ID NO 208
<211> LENGTH: 49
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 208

ctttaaaact gacagcacag atattcaagc tcatgaagag gacgatgcg 49

<210> SEQ ID NO 209
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 209

ctgtgctgtc agttttaaag attaatttaa ataaccgtcc gccggcaatg tcgccgttc 59

<210> SEQ ID NO 210
<211> LENGTH: 23

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 210

cattgccggc ggaaagtttc ttc 23

<210> SEQ ID NO 211
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 211

cgacattgcc ggcggacact ttcttcgagc tcatgaagag gacgatg 47

<210> SEQ ID NO 212
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 212

cattgccggc ggacaatttc 20

<210> SEQ ID NO 213
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 213

cgacattgcc ggcggaagat tttttcgagc tcatgaagag gacgatg 47

<210> SEQ ID NO 214
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 214

cgacattgcc ggcggaagat tttatcgagc tcatgaagag gacgatg 47

<210> SEQ ID NO 215
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

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<400> SEQUENCE: 215

cgacattgcc ggcggaagat ttattcgagc tcatgaagag gacgatg 47

<210> SEQ ID NO 216
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 216

cgacattgcc ggcggaagat ttatgcgagc tcatgaagag gacgatg 47

<210> SEQ ID NO 217
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 217

cattgccggc ggaagatttg ttc 23

<210> SEQ ID NO 218
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 218

cattgccggc ggaagatttg ctcg 24

<210> SEQ ID NO 219
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 219

cattgccggc ggaagatttc ttcaagc 27

<210> SEQ ID NO 220
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 220

cgacattgcc ggcggaagat ttcttggagc tcatgaagag gacgatg 47

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<210> SEQ ID NO 221
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 221

cgacattgcc ggcggaagaa tggttcgagc tcatgaagag gacgatg 47

<210> SEQ ID NO 222
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 222

cgacattgcc ggcggaagac ttggaacagc tcatgaagag gacgatg 47

<210> SEQ ID NO 223
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 223

cgacattgcc ggcggaagac ttactcaagc tcatgaagag gacgatg 47

<210> SEQ ID NO 224
<211> LENGTH: 390
<212> TYPE: PRT
<213> ORGANISM: Magnaporthe grisea

<400> SEQUENCE: 224

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
20 25 30

Arg Trp Gly Ser Arg Ser His Pro Val Tyr Asp Tyr Asn Pro Ile Pro
35 40 45

Asn His Ile His Gly Asp Leu Lys Arg Arg Ala Tyr Ile Glu Arg Tyr
50 55 60

Ser Gln Cys Ser Asp Ser Gln Ala Ser Glu Ile Arg Ala Ala Leu Lys
65 70 75 80

Ser Cys Ala Glu Leu Ala Ser Trp Gly Tyr His Ala Val Lys Asn Asp
85 90 95

Asn Arg Leu Phe Lys Leu Ile Phe Lys Thr Asp Ser Thr Asp Ile Gln
100 105 110

Asn Glu Phe Arg Ser Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro Asp
115 120 125

Tyr Ala Gly Ser Met Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr Ser
130 135 140

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Ser Leu Val Ala Ala Ala Ala Thr Met Ser Lys Gly Glu Glu Leu Phe
145                 150                 155                 160

Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly
                165                 170                 175

His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly
            180                 185                 190

Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
        195                 200                 205

Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser
    210                 215                 220

Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met
225                 230                 235                 240

Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly
                245                 250                 255

Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val
            260                 265                 270

Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile
        275                 280                 285

Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile
    290                 295                 300

Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg
305                 310                 315                 320

His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln
                325                 330                 335

Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr
            340                 345                 350

Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp
        355                 360                 365

His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly
    370                 375                 380

Met Asp Glu Leu Tyr Lys
385                 390


<210> SEQ ID NO 225
<211> LENGTH: 390
<212> TYPE: PRT
<213> ORGANISM: Magnaporthe grisea

<400> SEQUENCE: 225

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Arg Trp Gly Ser Arg Ser His Pro Val Tyr Asp Tyr Asn Pro Ile Pro
        35                  40                  45

Asn His Ile His Gly Asp Leu Ser Ala Ser Ala Ser Ile Glu Ala Ala
    50                  55                  60

Ser Ala Cys Ser Asp Ser Gln Ala Ser Glu Ile Ala Ser Ser Ala Ala
65                  70                  75                  80

Ser Cys Ala Glu Leu Ala Ser Trp Gly Tyr Ala Ser Ala Ala Asn Asp
                85                  90                  95

Asn Ala Ala Ser Ala Leu Ile Phe Lys Thr Asp Ser Thr Asp Ile Gln
            100                 105                 110
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Asn Glu Phe Arg Ser Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro Asp
        115                 120                 125

Tyr Ala Gly Ser Met Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr Ser
    130                 135                 140

Ser Leu Val Ala Ala Ala Ala Thr Met Ser Lys Gly Glu Glu Leu Phe
145                 150                 155                 160

Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly
                165                 170                 175

His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly
            180                 185                 190

Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
        195                 200                 205

Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser
    210                 215                 220

Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met
225                 230                 235                 240

Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly
                245                 250                 255

Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val
            260                 265                 270

Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile
        275                 280                 285

Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile
    290                 295                 300

Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg
305                 310                 315                 320

His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln
                325                 330                 335

Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr
            340                 345                 350

Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp
        355                 360                 365

His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly
    370                 375                 380

Met Asp Glu Leu Tyr Lys
385                 390


<210> SEQ ID NO 226
<211> LENGTH: 363
<212> TYPE: PRT
<213> ORGANISM: Puccinia striiformis

<400> SEQUENCE: 226

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Arg Trp Gly Ser Arg Ser Met Gly Thr Leu Leu Asn Val Thr Arg Arg
        35                  40                  45

Leu Gln Asn Asp Gly Lys Pro Pro Asp Tyr Cys Val Asp Lys Trp Asp
    50                  55                  60

Glu Met Met Lys Glu Arg Asn Lys Arg Leu Thr Gly Lys Pro Arg Gly
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65 70 75 80

Gln Cys Val Asp Glu Ile Glu Phe Arg Ser Thr Met Ser Gly Tyr Pro
85 90 95

Tyr Asp Val Pro Asp Tyr Ala Gly Ser Met Gly Ser Gly Ile Gln Arg
100 105 110

Pro Thr Ser Thr Ser Ser Leu Val Ala Ala Ala Ala Thr Met Ser Lys
115 120 125

Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
130 135 140

Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
145 150 155 160

Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
165 170 175

Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly
180 185 190

Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe
195 200 205

Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
210 215 220

Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
225 230 235 240

Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
245 250 255

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
260 265 270

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
275 280 285

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
290 295 300

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
305 310 315 320

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
325 330 335

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
340 345 350

Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
355 360

<210> SEQ ID NO 227
<211> LENGTH: 363
<212> TYPE: PRT
<213> ORGANISM: Puccinia striiformis

<400> SEQUENCE: 227

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
20 25 30

Arg Trp Gly Ser Arg Ser Met Gly Thr Leu Leu Asn Val Thr Arg Arg
35 40 45

Leu Gln Asn Asp Gly Lys Pro Pro Asp Tyr Cys Val Asp Lys Trp Asp
50 55 60

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Glu Met Met Lys Glu Arg Asn Ala Ala Ala Ala Ala Lys Pro Arg Gly
65                  70                  75                  80

Gln Cys Val Asp Glu Ile Glu Phe Arg Ser Thr Met Ser Gly Tyr Pro
                85                  90                  95

Tyr Asp Val Pro Asp Tyr Ala Gly Ser Met Gly Ser Gly Ile Gln Arg
            100                 105                 110

Pro Thr Ser Thr Ser Ser Leu Val Ala Ala Ala Ala Thr Met Ser Lys
        115                 120                 125

Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
    130                 135                 140

Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
145                 150                 155                 160

Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
                165                 170                 175

Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly
            180                 185                 190

Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe
        195                 200                 205

Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
    210                 215                 220

Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
225                 230                 235                 240

Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
                245                 250                 255

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
            260                 265                 270

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
        275                 280                 285

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    290                 295                 300

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
305                 310                 315                 320

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
                325                 330                 335

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            340                 345                 350

Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
        355                 360


<210> SEQ ID NO 228
<211> LENGTH: 413
<212> TYPE: PRT
<213> ORGANISM: Melampsora lini

<400> SEQUENCE: 228

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Arg Trp Gly Ser Arg Ser Asn Asn Leu Gly Thr Val Pro Asp Val Pro
        35                  40                  45

His Gln Ile Pro Asn Asp Lys Ser Gly Thr Pro Ala Ile Glu Asp Pro
    50                  55                  60
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Lys Asp Met Lys Gly Phe Asn Lys Ala Leu Lys Ser Thr Pro Glu Ser
65                  70                  75                  80

Glu Lys Leu Gly Thr Ser Ser Val Glu Gly Ile Pro Gln Pro Glu Phe
                85                  90                  95

Asp Arg Gly Phe Leu Arg Pro Phe Gly Ala Lys Met Lys Phe Leu Lys
            100                 105                 110

Pro Asp Gln Val Gln Lys Leu Ser Thr Asp Asp Leu Ile Thr Tyr Met
        115                 120                 125

Ala Glu Lys Asp Lys Asn Val Arg Glu Phe Arg Ser Thr Met Ser Gly
    130                 135                 140

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ser Met Gly Ser Gly Ile
145                 150                 155                 160

Gln Arg Pro Thr Ser Thr Ser Ser Leu Val Ala Ala Ala Ala Thr Met
                165                 170                 175

Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
            180                 185                 190

Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
        195                 200                 205

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
    210                 215                 220

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser
225                 230                 235                 240

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His
                245                 250                 255

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
            260                 265                 270

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
        275                 280                 285

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
    290                 295                 300

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
305                 310                 315                 320

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
                325                 330                 335

Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
            340                 345                 350

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
        355                 360                 365

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
    370                 375                 380

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
385                 390                 395                 400

Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
                405                 410


<210> SEQ ID NO 229
<211> LENGTH: 413
<212> TYPE: PRT
<213> ORGANISM: Melampsora lini

<400> SEQUENCE: 229

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
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1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Arg Trp Gly Ser Arg Ser Asn Asn Leu Gly Thr Val Pro Asp Val Pro
        35                  40                  45

Ala Ala Ala Ala Asn Asp Ala Ala Ala Ala Pro Ala Ile Glu Asp Pro
    50                  55                  60

Ala Ala Ala Ala Gly Phe Asn Ala Ala Ala Ala Ser Thr Pro Glu Ser
65                  70                  75                  80

Glu Ala Ala Ala Ala Ser Ser Val Glu Gly Ile Pro Gln Pro Glu Phe
                85                  90                  95

Asp Ala Ala Ala Ala Ala Pro Phe Gly Ala Lys Met Ala Ala Ala Ala
            100                 105                 110

Pro Asp Gln Val Gln Ala Ala Ala Ala Asp Asp Leu Ile Thr Tyr Met
        115                 120                 125

Ala Glu Lys Asp Ala Ala Ala Ala Glu Phe Arg Ser Thr Met Ser Gly
    130                 135                 140

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ser Met Gly Ser Gly Ile
145                 150                 155                 160

Gln Arg Pro Thr Ser Thr Ser Ser Leu Val Ala Ala Ala Ala Thr Met
                165                 170                 175

Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
            180                 185                 190

Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
        195                 200                 205

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
    210                 215                 220

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser
225                 230                 235                 240

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His
                245                 250                 255

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
            260                 265                 270

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
        275                 280                 285

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
    290                 295                 300

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
305                 310                 315                 320

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
                325                 330                 335

Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
            340                 345                 350

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
        355                 360                 365

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
    370                 375                 380

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
385                 390                 395                 400

Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
                405                 410
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<210> SEQ ID NO 230
<211> LENGTH: 369
<212> TYPE: PRT
<213> ORGANISM: Melampsora lini

<400> SEQUENCE: 230

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
20 25 30

Arg Trp Gly Ser Arg Ser Gln Tyr Val Val Asp Pro Gly Phe Gly Glu
35 40 45

Ile Glu Cys Met Cys Gly Gln Ile Ala Arg Leu Thr Gln Arg Pro Phe
50 55 60

Asp Val Glu Cys Glu Ala Thr Pro Ser Cys Glu Phe Arg Ser Thr Met
65 70 75 80

Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Glu Phe Arg Ser
85 90 95

Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ser Met
100 105 110

Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr Ser Ser Leu Val Ala Ala
115 120 125

Ala Ala Thr Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
130 135 140

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
145 150 155 160

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
165 170 175

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
180 185 190

Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
195 200 205

Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
210 215 220

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
225 230 235 240

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
245 250 255

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
260 265 270

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
275 280 285

Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
290 295 300

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
305 310 315 320

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
325 330 335

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
340 345 350

Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr

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        355                 360                 365

Lys


<210> SEQ ID NO 231
<211> LENGTH: 369
<212> TYPE: PRT
<213> ORGANISM: Melampsora lini

<400> SEQUENCE: 231

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                  10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Arg Trp Gly Ser Arg Ser Gln Tyr Val Val Asp Pro Gly Phe Gly Glu
        35                  40                  45

Ile Glu Cys Met Cys Gly Gln Ile Ala Ala Ala Ala Ala Arg Pro Phe
    50                  55                  60

Asp Val Glu Cys Glu Ala Thr Pro Ser Cys Glu Phe Arg Ser Thr Met
65                  70                  75                  80

Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Glu Phe Arg Ser
                85                  90                  95

Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ser Met
            100                 105                 110

Gly Ser Gly Ile Gln Arg Pro Thr Ser Thr Ser Ser Leu Val Ala Ala
        115                 120                 125

Ala Ala Thr Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
    130                 135                 140

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
145                 150                 155                 160

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
                165                 170                 175

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
            180                 185                 190

Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
        195                 200                 205

Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
    210                 215                 220

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
225                 230                 235                 240

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
                245                 250                 255

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
            260                 265                 270

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
        275                 280                 285

Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
    290                 295                 300

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
305                 310                 315                 320

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
                325                 330                 335

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
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            340                 345                 350

Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr
        355                 360                 365

Lys


<210> SEQ ID NO 232
<211> LENGTH: 350
<212> TYPE: PRT
<213> ORGANISM: Melampsora lini

<400> SEQUENCE: 232

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Arg Trp Gly Ser Arg Ser Met Gly Glu Phe Leu Glu Asp Ala Arg Asp
        35                  40                  45

Ile Gln Gly Phe Ser Arg Lys Ser Gly Ser Lys Leu Glu Glu Glu Ser
    50                  55                  60

Asp Ser Ser Arg Asp Arg Gln Glu Lys Glu Phe Arg Ser Thr Met Ser
65                  70                  75                  80

Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ser Met Gly Ser Gly
                85                  90                  95

Ile Gln Arg Pro Thr Ser Thr Ser Ser Leu Val Ala Ala Ala Ala Thr
            100                 105                 110

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
        115                 120                 125

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
    130                 135                 140

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
145                 150                 155                 160

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
                165                 170                 175

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
            180                 185                 190

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
        195                 200                 205

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
    210                 215                 220

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
225                 230                 235                 240

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
                245                 250                 255

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
            260                 265                 270

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
        275                 280                 285

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
    290                 295                 300

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
305                 310                 315                 320

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
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```
                325                 330                 335

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
            340                 345                 350


<210> SEQ ID NO 233
<211> LENGTH: 350
<212> TYPE: PRT
<213> ORGANISM: Melampsora lini

<400> SEQUENCE: 233

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Arg Trp Gly Ser Arg Ser Met Gly Glu Phe Leu Glu Asp Ala Ala Ser
        35                  40                  45

Ser Ala Gly Phe Ser Arg Lys Ser Gly Ser Lys Leu Glu Glu Glu Ser
    50                  55                  60

Asp Ser Ser Arg Asp Arg Gln Glu Lys Glu Phe Arg Ser Thr Met Ser
65                  70                  75                  80

Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ser Met Gly Ser Gly
                85                  90                  95

Ile Gln Arg Pro Thr Ser Thr Ser Ser Leu Val Ala Ala Ala Ala Thr
            100                 105                 110

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
        115                 120                 125

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
    130                 135                 140

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
145                 150                 155                 160

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
                165                 170                 175

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
            180                 185                 190

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
        195                 200                 205

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
    210                 215                 220

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
225                 230                 235                 240

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
                245                 250                 255

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
            260                 265                 270

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
        275                 280                 285

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
    290                 295                 300

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
305                 310                 315                 320

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
                325                 330                 335
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Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
340 345 350

<210> SEQ ID NO 234
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 234

atgcagatct gaattcttag aggatgcacg agatatcc 38

<210> SEQ ID NO 235
<211> LENGTH: 63
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 235

ctgacagctc gcgcgatagg caagaaaaag tcgacagatc caccatgtcc ggctatccat 60

atg 63

<210> SEQ ID NO 236
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 236

atgcagatct cagtatgttg ttgatccagg 30

<210> SEQ ID NO 237
<211> LENGTH: 61
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 237

catatggata gccggacatg gtggatctgt cgacacaact tggggtggct tcacattcca 60

c 61

<210> SEQ ID NO 238
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 238

atgcagatct actctgttga acgtgact 28

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<210> SEQ ID NO 239
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 239

catatggata gccggacatg gtggatctgt cgacgttttg aatatctgtg c 51

<210> SEQ ID NO 240
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 240

atgcagatct atgggaaaca accttggaac agtaccg 37

<210> SEQ ID NO 241
<211> LENGTH: 62
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 241

catatggata gccggacatg gtggatctgt cgactcgtac atttttatct ttttctgcca 60

tg 62

<210> SEQ ID NO 242
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 242

agtcagatct cacccagttt acgattacaa tcc 33

<210> SEQ ID NO 243
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 243

catatggata gccggacatg gtggatctgt cgacgttttg aatatctgtg c 51

<210> SEQ ID NO 244
<211> LENGTH: 41

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 244

gaaacgcagc agctgcggca aaacctcgag ggcaatgtgt c 41

<210> SEQ ID NO 245
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 245

gttttgcagc cgctgctgcg tttctctctt tcatcatttc 40

<210> SEQ ID NO 246
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 246

catttgcaga tgaagctggc acatccggta ctgttc 36

<210> SEQ ID NO 247
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 247

cagcgctatt gaatcctgct gaggcacttg ggtcttcaat ggcaggag 48

<210> SEQ ID NO 248
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 248

gacgaagccg cagcggcttc ggattctgga gtagatg 37

<210> SEQ ID NO 249
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

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<400> SEQUENCE: 249

caaaaggcgc agaggctgca ctgtcaaatt ctggttgagg gatc 44

<210> SEQ ID NO 250
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 250

gatgcctgaa cttggtccgg actagcggct gacatttttg ctccaaaagg cgcag 55

<210> SEQ ID NO 251
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 251

gtgccagctt catctgcaaa tgacaaaagt ggtactcctg 40

<210> SEQ ID NO 252
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 252

cagcaggatt caatagcgct gccgcatcta ctccagaatc cgaaaaac 48

<210> SEQ ID NO 253
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 253

gaagccgctg cggcttcgtc agttgaaggg atccctc 37

<210> SEQ ID NO 254
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 254

cagtgcagcc tctgcgcctt ttggagcaaa aatg 34

-continued

<210> SEQ ID NO 255
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 255

gtccggacca agttcaggca tcttcagccg atgatctcat cacatacatg 50

<210> SEQ ID NO 256
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 256

atcgccatgg gagaattctt agaggatgca gcgagcagcg cggggttctc c 51

<210> SEQ ID NO 257
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 257

caaatcgctg ctgcggcagc acgaccattt gatgtggaat gt 42

<210> SEQ ID NO 258
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed DNA sequence to amplify genes from genomes or plasmids with various restriction sites to faciliate cloning

<400> SEQUENCE: 258

tgctgccgca gcagcgattt gtccgcacat acattc 36

<210> SEQ ID NO 259
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 259

Ala Met Val Glu Ser Pro Asp Leu Val Arg Arg Ser Leu Arg Asn Gly
1 5 10 15

Asp Ile Ala Gly Gly Arg Phe Leu
20

<210> SEQ ID NO 260
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 260

-continued

```
Ser Leu Arg Asn Gly Asp Ile Ala Gly Gly Arg Phe Leu Arg Ala His
1               5                   10                  15

Glu Glu Asp Asp Ala Gly Glu Arg
            20
```

<210> SEQ ID NO 261
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 261

```
Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met Val Glu Ser Pro Asp
1               5                   10                  15

Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile Ala Gly Gly Arg Phe
            20                  25                  30

Leu Arg Ala His Glu Glu Asp Asp Ala Gly Glu Arg Thr Phe Ser Val
        35                  40                  45

Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys Leu Ala Lys Ala Met
    50                  55                  60

Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr Glu Lys Trp Ala Lys
65                  70                  75                  80

Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp Leu Ala Ile Ala Asp
                85                  90                  95

Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr Asn Gly Tyr Thr Phe
            100                 105                 110

His Arg Tyr Gln Ser
        115
```

<210> SEQ ID NO 262
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 262

```
Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met Val Glu Ser Pro Asp
1               5                   10                  15

Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile Ala Gly Gly Ala Ala
            20                  25                  30

Ala Ala Ala His Glu Glu Asp Asp Ala Gly Glu Arg Thr Phe Ser Val
        35                  40                  45

Thr Asp Leu Trp Asn Lys Val Ala Ala Lys Lys Leu Ala Lys Ala Met
    50                  55                  60

Leu Ala Asp Pro Ser Lys Glu Gln Lys Ala Tyr Glu Lys Trp Ala Lys
65                  70                  75                  80

Lys Gly Tyr Ser Leu Asp Lys Ile Lys Asn Trp Leu Ala Ile Ala Asp
                85                  90                  95

Pro Lys Gln Lys Gly Lys Tyr Asp Arg Ile Tyr Asn Gly Tyr Thr Phe
            100                 105                 110

His Arg Tyr Gln Ser
        115
```

<210> SEQ ID NO 263
<211> LENGTH: 49
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

-continued

<400> SEQUENCE: 263

Ser Glu Asn Ala Phe Ser Ala Ala Thr Asp Ala Asp Gln Ala Thr Val
1 5 10 15

Ser Lys Leu Ala Ala Ala Glu Phe Asp Thr Leu Val Asp Val Leu Thr
20 25 30

Thr Glu Ser Lys Arg Ser Leu Arg Ala Thr Val Asp Asp Gly Glu Glu
35 40 45

Arg

<210> SEQ ID NO 264
<211> LENGTH: 44
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 264

Thr Glu Tyr Ser Asp Glu Thr Asn Ile Ala Met Val Glu Ser Pro Asp
1 5 10 15

Leu Val Arg Arg Ser Leu Arg Asn Gly Asp Ile Ala Gly Gly Arg Phe
20 25 30

Leu Arg Ala His Glu Glu Asp Asp Ala Gly Glu Arg
35 40

<210> SEQ ID NO 265
<211> LENGTH: 86
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 265

Leu Thr Cys Ala Thr Ser Glu Gln Gln Thr Arg Pro Glu Leu Cys Phe
1 5 10 15

Phe Phe Ser Val Arg Ser Ser Trp Pro Ser Thr Ile Ser Asp Gly Ala
20 25 30

Cys Leu Ala Leu Val Ser Ala Glu Gln Gly Ala Thr Ala Gly Arg Asn
35 40 45

Thr Leu Ser Leu Arg Ser Met Met Ala Thr Glu Asp Met Ala Thr Ser
50 55 60

Thr Arg Ser Leu Arg Ser Gln Ala Thr Asn Val Asp Asp Asp Ala Asn
65 70 75 80

Val Ser Ile Glu Asn Arg
85

<210> SEQ ID NO 266
<211> LENGTH: 40
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 266

Leu Ser Thr Thr Asn Ala Asn Gln Ala Lys Ile Ile Lys Gly Thr Ser
1 5 10 15

Pro Gly Gly His Ser Pro Arg Leu Leu Arg Ala Tyr Gln Pro Asp Asp
20 25 30

Glu Gly Asp Ser Pro Glu Asp Arg
35 40

<210> SEQ ID NO 267

-continued

<211> LENGTH: 48
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 267

Val Glu Pro Ser Ala Thr Ser Thr Val Glu Val Ala Glu Val Gln Ala
1 5 10 15

Arg Gly Ala Asp Lys Arg Phe Leu Arg Ser Leu Gln Thr Glu Glu Glu
20 25 30

Gln Gly Asp Ser Asp Val Asn Glu Ala Glu Asp Gly Ser Glu Glu Arg
35 40 45

<210> SEQ ID NO 268
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 268

Ile Thr Asp Glu Ser Gln Pro Arg Asp Ala Thr Ile Val Asp Ala Pro
1 5 10 15

Leu Thr Gly Arg Gly Ala Asn Ala Arg Tyr Leu Arg Thr Ser Thr Ser
20 25 30

Ile Ile Lys Ala Pro Asp Ala Gln Leu Pro Ser Thr Lys Ala Ala Ile
35 40 45

Ala Ser
50

<210> SEQ ID NO 269
<211> LENGTH: 44
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 269

Thr Ala Glu Val Asp Ser Lys Thr Ala Leu Ala Ala Glu Val Pro Ala
1 5 10 15

Ala Ile Arg Ser Leu Glu Ser Asp Thr Pro Ala Ser Arg Leu Leu Arg
20 25 30

Thr Gly Thr Val Thr Ser Ala Asp Asn Glu Asp Arg
35 40

<210> SEQ ID NO 270
<211> LENGTH: 38
<212> TYPE: PRT
<213> ORGANISM: Phytophthora infestans

<400> SEQUENCE: 270

Ile Asp Gln Thr Lys Val Leu Val Tyr Gly Thr Pro Ala His Tyr Ile
1 5 10 15

His Asp Ser Ala Gly Arg Arg Leu Leu Arg Lys Asn Glu Glu Asn Glu
20 25 30

Glu Thr Ser Glu Glu Arg
35

<210> SEQ ID NO 271
<211> LENGTH: 33
<212> TYPE: PRT
<213> ORGANISM: Phytophthora infestans

<400> SEQUENCE: 271

-continued

Lys Ala Asp Ser Leu Ala Arg Thr Val Ser Val Val Asp Asn Val Lys
1 5 10 15

Val Lys Ser Arg Phe Leu Arg Ala Gln Thr Asp Glu Lys Asn Glu Glu
20 25 30

Arg

<210> SEQ ID NO 272
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Phytophthora infestans

<400> SEQUENCE: 272

Ala Val Ser Ser Asn Leu Asn Thr Ala Val Asn Tyr Ala Ser Thr Ser
1 5 10 15

Lys Ile Arg Phe Leu Ser Thr Glu Tyr Asn Ala Asp Glu Lys Arg Ser
20 25 30

Leu Arg Gly Asp Tyr Asn Asn Glu Val Thr Lys Glu Pro Asn Thr Ser
35 40 45

Asp Glu
50

<210> SEQ ID NO 273
<211> LENGTH: 38
<212> TYPE: PRT
<213> ORGANISM: Phytophthora infestans

<400> SEQUENCE: 273

Val Ala Ala Phe Pro Ile Pro Asp Glu Ser Arg Pro Leu Ser Lys Thr
1 5 10 15

Ser Pro Asp Thr Val Ala Pro Arg Ser Leu Arg Ile Glu Ala Gln Glu
20 25 30

Val Ile Gln Ser Gly Arg
35

<210> SEQ ID NO 274
<211> LENGTH: 44
<212> TYPE: PRT
<213> ORGANISM: Hyaloperonospora arabidopsidis

<400> SEQUENCE: 274

Thr Glu Ser Ser Glu Thr Ser Gly Thr Ile Val His Val Phe Pro Leu
1 5 10 15

Arg Asp Val Ala Asp His Arg Asn Asp Ala Leu Ile Asn Arg Ala Leu
20 25 30

Arg Ala Gln Thr Ala Leu Asp Asp Asp Glu Glu Arg
35 40

<210> SEQ ID NO 275
<211> LENGTH: 48
<212> TYPE: PRT
<213> ORGANISM: Hyaloperonospora arabidopsidis

<400> SEQUENCE: 275

Leu Leu His Ala His Ala Leu His Glu Asp Glu Thr Gly Val Thr Ala
1 5 10 15

Gly Arg Gln Leu Arg Ala Ala Ala Ser Glu Val Phe Gly Leu Ser Arg
20 25 30

-continued

Ala Ser Phe Gly Leu Gly Lys Ala Gln Asp Pro Leu Asp Lys Phe Phe
35 40 45

<210> SEQ ID NO 276
<211> LENGTH: 92
<212> TYPE: PRT
<213> ORGANISM: Leptosphaeria maculans

<400> SEQUENCE: 276

Ser Pro Ala Thr Lys Asn Asn Val Asn Gln Pro Leu Asp Asn Ile Ser
1 5 10 15

Arg Arg Ser Glu Trp Lys Ser Val Gln Ile Ser Pro Val Lys Glu His
20 25 30

Ser Ala Lys Thr Ala Asp Asn Thr Glu Asn Asn His Asn Leu Glu Lys
35 40 45

Arg Val Phe Thr Ser Pro His Met Lys Arg Thr Phe Thr Leu Ala Leu
50 55 60

Glu Asn Thr Phe Tyr Ala Met Ala Trp Leu Ile Asp Phe Ser Phe Ser
65 70 75 80

Glu Glu Gly Glu Pro His Phe Ser Tyr Lys Leu Gln
85 90

<210> SEQ ID NO 277
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Leptosphaeria maculans

<400> SEQUENCE: 277

Cys Arg Glu Ala Ser Ile Ser Gly Glu Ile Arg Tyr Pro Gln Gly Thr
1 5 10 15

Cys Pro Thr Lys Thr Glu Ala Leu Asn Asp Cys Asn Lys Val Thr Lys
20 25 30

Gly Leu Ile Asp Phe Ser Gln Ser His Gln Arg Ala Trp Gly Ile Asp
35 40 45

Met Thr
50

<210> SEQ ID NO 278
<211> LENGTH: 48
<212> TYPE: PRT
<213> ORGANISM: Leptosphaeria maculans

<400> SEQUENCE: 278

Gln Pro His Leu Leu Cys Ala Cys Glu Ser Gly Arg Arg Asp Gly Val
1 5 10 15

Asp Asp Thr Arg Thr Leu Lys Val Val Lys Gly Thr Gly Gly Arg Phe
20 25 30

Val Phe Ser Ser Arg Tyr Trp Thr Lys Ala Glu Gly Ala Pro His Glu
35 40 45

<210> SEQ ID NO 279
<211> LENGTH: 75
<212> TYPE: PRT
<213> ORGANISM: Magnaporthe oryzae

<400> SEQUENCE: 279

His Pro Val Tyr Asp Tyr Asn Pro Ile Pro Asn His Ile His Gly Asp

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1               5                   10                  15

Leu Lys Arg Arg Ala Tyr Ile Glu Arg Tyr Ser Gln Cys Ser Asp Ser
            20                  25                  30

Gln Ala Ser Glu Ile Arg Ala Ala Leu Lys Ser Cys Ala Glu Leu Ala
        35                  40                  45

Ser Trp Gly Tyr His Ala Val Lys Ser Asp Asn Arg Leu Phe Lys Leu
    50                  55                  60

Ile Phe Lys Thr Asp Ser Thr Asp Ile Gln Asn
65                  70                  75


<210> SEQ ID NO 280
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Magnaporthe oryzae

<400> SEQUENCE: 280

Leu Pro Thr Pro Ala Ser Leu Asn Gly Asn Thr Glu Val Ala Thr Ile
1               5                   10                  15

Ser Asp Val Lys Leu Glu Ala Arg Ser Asp Thr Thr Tyr His Lys Cys
            20                  25                  30

Ser Lys Cys Gly Tyr Gly Ser Asp Asp Ser Asp Ala Tyr Phe Asn His
        35                  40                  45

Lys Cys
    50


<210> SEQ ID NO 281
<211> LENGTH: 51
<212> TYPE: PRT
<213> ORGANISM: Magnaporthe oryzae

<400> SEQUENCE: 281

Arg Phe Cys Val Tyr Tyr Asp Gly His Leu Pro Ala Thr Arg Val Leu
1               5                   10                  15

Leu Met Tyr Val Arg Ile Gly Thr Thr Ala Thr Ile Thr Ala Arg Gly
            20                  25                  30

His Glu Phe Glu Val Glu Ala Lys Asp Gln Asn Cys Lys Val Ile Leu
        35                  40                  45

Thr Asn Gly
    50


<210> SEQ ID NO 282
<211> LENGTH: 47
<212> TYPE: PRT
<213> ORGANISM: Magnaporthe oryzae

<400> SEQUENCE: 282

Ser Phe Val Gln Cys Asn His His Leu Leu Tyr Asn Gly Arg His Trp
1               5                   10                  15

Gly Thr Ile Arg Lys Lys Ala Gly Trp Ala Val Arg Phe Tyr Glu Glu
            20                  25                  30

Lys Pro Gly Gln Pro Lys Arg Leu Val Ala Ile Cys Lys Asn Ala
        35                  40                  45


<210> SEQ ID NO 283
<211> LENGTH: 44
<212> TYPE: PRT
<213> ORGANISM: Magnaporthe oryzae
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-continued

<400> SEQUENCE: 283

Glu Thr Gly Asn Lys Tyr Ile Glu Lys Arg Ala Ile Asp Leu Ser Arg
1 5 10 15

Glu Arg Asp Pro Asn Phe Phe Asp His Pro Gly Ile Pro Val Pro Glu
20 25 30

Cys Phe Trp Phe Met Phe Lys Asn Asn Val Arg Gln
35 40

<210> SEQ ID NO 284
<211> LENGTH: 43
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum

<400> SEQUENCE: 284

Leu Pro Lys Gly Glu Glu Gly Asp Ile Ile Gly Thr Phe Asn Phe Ser
1 5 10 15

Ser Ser Asp Ser Gln Pro Leu Lys Ile His Trp Val Asp Thr Pro Asp
20 25 30

Ser Ser Gly Ser Asn Leu Val Lys Arg Ser Ala
35 40

<210> SEQ ID NO 285
<211> LENGTH: 81
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum

<400> SEQUENCE: 285

Leu Pro Val Glu Asp Ala Asp Ser Ser Val Gly Gln Leu Gln Gly Arg
1 5 10 15

Gly Asn Pro Tyr Cys Val Phe Pro Gly Arg Arg Thr Ser Ser Thr Ser
20 25 30

Phe Thr Thr Ser Phe Ser Thr Glu Pro Leu Gly Tyr Ala Arg Met Leu
35 40 45

His Arg Asp Pro Pro Tyr Glu Arg Ala Gly Asn Ser Gly Leu Asn His
50 55 60

Arg Ile Tyr Glu Arg Ser Arg Val Gly Gly Leu Arg Thr Val Ile Asp
65 70 75 80

Val

<210> SEQ ID NO 286
<211> LENGTH: 89
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum

<400> SEQUENCE: 286

Gln Glu Ala Ala Val Arg Glu Pro Gln Ile Phe Phe Asn Leu Thr Tyr
1 5 10 15

Thr Glu Tyr Leu Asp Lys Val Ala Ala Ser His Gly Ser Pro Pro Asp
20 25 30

Lys Ser Asp Leu Pro Trp Asn Asp Thr Met Gly Ser Phe Pro Gly Asn
35 40 45

Glu Thr Asp Asp Gly Val Gln Thr Glu Thr Gly Ser Ser Leu Ser Arg
50 55 60

Arg Gly His Ile Val Asn Leu Arg Lys Arg Glu Pro Phe Gly Glu Glu
65 70 75 80

-continued

Ser Arg Asn Asp Arg Val Thr Gln Asp
85

<210> SEQ ID NO 287
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum

<400> SEQUENCE: 287

Asn Pro Ala Gly Asp Ser Leu Pro Asp Asp Ala His Leu Pro Asp Arg
1 5 10 15

Arg Leu Ser Pro Ser Glu Val Gln Ala Leu Lys Lys Ala Gln Ile Tyr
20 25 30

Pro Pro Gly Tyr Ile His Lys Arg Val Thr Phe Gly Glu Gly Lys Asp
35 40 45

Ala Val
50

<210> SEQ ID NO 288
<211> LENGTH: 48
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum

<400> SEQUENCE: 288

Arg Asp His Gln Tyr Cys Ala Cys Gln Ser Gly Ser Gly Asp Ser Ile
1 5 10 15

Asp Ile Asp Ala Thr Thr Gln Leu Gln Asn Asp Asn Ser Lys Ser Tyr
20 25 30

Leu Trp Ala Gln Thr Ser Pro Ala Tyr Trp Phe Ala Asp Arg His Lys
35 40 45

<210> SEQ ID NO 289
<211> LENGTH: 48
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum

<400> SEQUENCE: 289

Gly Pro Leu Ala Gln Thr Glu Ser Glu Ser Ala Asp Val Ala Glu His
1 5 10 15

Thr Ile Asn Tyr Ile Asp Ile Ala Pro Glu Glu Phe Glu Pro Pro Lys
20 25 30

Ala Asn Leu Ser Ser Leu Val Ser Arg Asp Thr Leu Pro Val Ser Thr
35 40 45

<210> SEQ ID NO 290
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Melampsora lini

<400> SEQUENCE: 290

Met Glu His Val Pro Ala Glu Leu Thr Arg Val Ser Glu Gly Tyr Thr
1 5 10 15

Arg Phe Tyr Arg Ser Pro Thr Ala Ser Val Ile Leu Ser Gly Leu Val
20 25 30

Lys Val Lys Trp Asp Asn Glu Gln Met Thr Met Pro Leu Phe Lys Trp
35 40 45

Ile Gly

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50

<210> SEQ ID NO 291
<211> LENGTH: 100
<212> TYPE: PRT
<213> ORGANISM: Melampsora lini

<400> SEQUENCE: 291

Ser Leu Ser Asn Asn Leu Gly Thr Val Pro Asp Val Pro His Gln Ile
1 5 10 15

Pro Asn Asp Lys Ser Gly Thr Pro Ala Ile Glu Asp Pro Lys Ala Ala
20 25 30

Ile Glu Asp Pro Lys Asp Met Lys Gly Phe Asn Lys Ala Leu Lys Ser
35 40 45

Thr Pro Glu Ser Glu Lys Leu Gly Thr Ser Ser Val Glu Gly Ile Pro
50 55 60

Gln Pro Glu Phe Asp Arg Gly Phe Leu Arg Pro Phe Gly Ala Lys Met
65 70 75 80

Lys Phe Leu Lys Pro Asp Gln Val Gln Lys Leu Ser Thr Asp Asp Leu
85 90 95

Ile Thr Tyr Met
100

<210> SEQ ID NO 292
<211> LENGTH: 33
<212> TYPE: PRT
<213> ORGANISM: Melampsora lini

<400> SEQUENCE: 292

Gln Tyr Val Val Asp Pro Gly Phe Gly Glu Ile Glu Cys Met Cys Gly
1 5 10 15

Gln Ile Ala Arg Leu Thr Gln Arg Pro Phe Asp Val Glu Cys Glu Ala
20 25 30

Thr

<210> SEQ ID NO 293
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Melampsora lini

<400> SEQUENCE: 293

Glu Phe Leu Glu Asp Ala Arg Asp Ile Gln Gly Phe Ser Arg Lys Ser
1 5 10 15

Gly Ser Lys Leu Glu Glu Glu Ser Asp Ser Ser Arg Asp Arg Gln
20 25 30

<210> SEQ ID NO 294
<211> LENGTH: 71
<212> TYPE: PRT
<213> ORGANISM: Ustilago maydis

<400> SEQUENCE: 294

Asn Gly Ser Ile Ser Asn Ala Ser His His His Gln Arg Arg Met Val
1 5 10 15

Arg Gln Arg His Ile Glu Ala Arg Ser Ala Met Ser Trp Leu Thr Lys
20 25 30

Ile Ser Ser Lys Ala Ser Asp Trp Met Phe Gly Ser Val His Ala Pro

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        35                  40                  45

Asn Leu Asp Lys Lys Asp Leu Pro Lys Pro Leu Val Gly Gly Val Ala
    50                  55                  60

Val Met Pro Lys Met Pro Tyr
65                  70


<210> SEQ ID NO 295
<211> LENGTH: 47
<212> TYPE: PRT
<213> ORGANISM: Laccaria bicolor

<400> SEQUENCE: 295

Ser Pro Val Pro Gly Glu Val Gly Leu Val Glu Arg Gly Pro Ile Pro
1               5                   10                  15

Asn Ala Val Phe Arg Arg Val Pro Glu Pro Asn Phe Phe Lys Asp Leu
            20                  25                  30

Leu Arg Ala Leu Gly Gln Ala Ser Gln Gly Gly Asp Leu His Arg
        35                  40                  45


<210> SEQ ID NO 296
<211> LENGTH: 59
<212> TYPE: PRT
<213> ORGANISM: Acyrthosiphon pisum

<400> SEQUENCE: 296

Ser Ala Ala Glu Pro Tyr Asp Glu Gln Glu Glu Ala Ser Val Glu Leu
1               5                   10                  15

Pro Met Glu His Arg Gln Cys Asp Glu Tyr Lys Ser Lys Ile Trp Asp
            20                  25                  30

Lys Ala Phe Ser Asn Gln Glu Ala Met Gln Leu Met Glu Leu Thr Phe
        35                  40                  45

Asn Thr Gly Lys Glu Leu Gly Ser His Glu Val
    50                  55


<210> SEQ ID NO 297
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Mayetiola destructor

<400> SEQUENCE: 297

Ser Pro Leu Pro Leu Ala Tyr Thr Asp Gln Val Tyr Asp Ala Cys Asp
1               5                   10                  15

Arg Gln Phe Asp Glu Thr Val Arg Asn Ser Gln Pro Leu
            20                  25


<210> SEQ ID NO 298
<211> LENGTH: 154
<212> TYPE: PRT
<213> ORGANISM: Mayetiola destructor

<400> SEQUENCE: 298

Leu Val Leu Asp Thr Arg Ala Met Pro Glu Thr Asp Phe Glu Lys Ala
1               5                   10                  15

Leu Lys Glu Trp Asn Arg Val Gln Thr Leu Val Leu Ile Ala Pro Glu
            20                  25                  30

Gln Arg Arg Thr Met Val Leu Ile Ala Glu His Leu Thr Asn Leu Lys
        35                  40                  45
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Lys Met Asn Val Asp Ser Pro Gly Gly Ser Phe Leu Tyr Leu Lys Asp
    50                  55                  60

Gly Asp Pro Val Ile Lys Leu Pro Ser Val Glu His Phe Glu Ile Thr
65                  70                  75                  80

Phe Arg Gly Pro Tyr Gly Val Asp Lys Asn Phe Ser Phe Tyr Met Pro
                85                  90                  95

Lys Leu Lys Lys Leu Ile Val Arg Asp Ala Asp Ala Asn Asp Lys Lys
            100                 105                 110

Ile Ile Lys Phe Val Ser Gln His Ser Arg Thr Leu Lys Thr Leu Asp
        115                 120                 125

Leu Val Ala Ala Asn Tyr Arg Thr Leu Arg Thr Leu Gly Ala Met Lys
    130                 135                 140

His Ile Glu Glu Phe Val Thr Ser Pro Pro
145                 150


<210> SEQ ID NO 299
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Phytophthora sojae

<400> SEQUENCE: 299

Thr Arg Val Pro Asp Asp Ala Asn Leu Gln Ser Val Asn Ala Pro Val
1               5                   10                  15

Gln Thr Val Thr Arg Ser Arg Arg Phe Leu Arg Thr Ala Asp Thr Asp
            20                  25                  30

Ile Val Tyr Glu Pro Lys Val His Asn Pro Gly Lys Lys Gln Val Phe
        35                  40                  45

Ile Glu
    50


<210> SEQ ID NO 300
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Pythium ultimum

<400> SEQUENCE: 300

Met Met Pro Ser Thr Asp Ala His Gly Tyr Ile Ala Phe Pro Pro Ala
1               5                   10                  15

Gln Tyr Lys Asp Pro Ala Thr Ala Thr Asn Tyr Asn Ala Ile Ile Thr
            20                  25                  30

Ala Ser Ile Asn Thr Ala Phe Ala Gly Lys Lys Trp Asp Asp Asn Pro
        35                  40                  45

Thr Ala Asn Thr Lys Thr Phe Thr Ala Ala Phe Lys Lys Ser Gly Tyr
    50                  55                  60

Thr Ser Leu Lys Gln Met Leu Asp Lys Lys Val Pro Gly Cys Gln Asn
65                  70                  75                  80

Ser Arg Thr Asp Phe Thr Pro Ile Lys Thr Lys Thr Tyr Lys Thr Met
                85                  90                  95

Glu Trp Gln Asn Asp
            100


<210> SEQ ID NO 301
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Pythium ultimum
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-continued

<400> SEQUENCE: 301

His Ser Gln Met Thr Val Pro Asn Pro Lys Phe Ser Asp Val Ser Lys
1 5 10 15

Ala Asn Ser Pro Leu Gly Thr Ile Asp Gly Pro Thr Val Met Pro Pro
20 25 30

Pro Ala Gly Gln Ser Tyr Ala Met Gly Thr Asp Thr Asn Ile Lys Ala
35 40 45

Tyr Val Glu Ala Phe Ala Lys Gln Thr Lys Trp Lys Thr Leu Lys Asp
50 55 60

Leu Ile Met Asp Lys Tyr Val Glu Asp Gly Asn Ile Pro Asp Arg Ala
65 70 75 80

Cys Gly Leu Thr Asp Lys Thr Tyr Met Gln Pro Leu Pro Asp Lys Tyr
85 90 95

Val Val Trp

<210> SEQ ID NO 302
<211> LENGTH: 49
<212> TYPE: PRT
<213> ORGANISM: Albugo candida

<400> SEQUENCE: 302

Ser Thr Met Gly Leu Ser Asn Ser Arg His Leu Glu Asp Ala Val Glu
1 5 10 15

Arg Val Leu Gly Asp Leu Lys Leu Asn Gln Lys Asp Glu Lys Gln Asn
20 25 30

Glu Asn Glu Val Asp Lys Asn Asn Ser Lys Gly Lys Asp Arg Glu Ser
35 40 45

Ser

<210> SEQ ID NO 303
<211> LENGTH: 54
<212> TYPE: PRT
<213> ORGANISM: Aspergillus flavus

<400> SEQUENCE: 303

Ala Gly Leu Pro Val Phe Pro Asn Gln Ala Val Leu Arg Pro Ser Leu
1 5 10 15

Ala Leu Pro Gly Asp Asn Ser His Arg Tyr Ser Leu Pro Met Phe Asp
20 25 30

Leu Gln Pro Trp Glu Arg Val Asp Glu Ile Arg Leu Ala Arg Lys Gly
35 40 45

Tyr Leu Tyr Gly Ser Pro
50

<210> SEQ ID NO 304
<211> LENGTH: 43
<212> TYPE: PRT
<213> ORGANISM: Pyrenophora triticirepentis

<400> SEQUENCE: 304

Gln Val Lys Gly Asn Ala Ile Arg Cys Gly Gln Asp Asp Lys Ser Asp
1 5 10 15

Gln Asp Thr Arg Asn Phe Cys Arg Phe Met Phe Thr Ser Asp Arg Thr
20 25 30

Leu Lys Ile Asn Gly Glu Phe Arg Gly Asn Ala

-continued

35 40

<210> SEQ ID NO 305
<211> LENGTH: 49
<212> TYPE: PRT
<213> ORGANISM: Alternaria brassicicola

<400> SEQUENCE: 305

Ala Pro Ala Ser Tyr Pro Ala Ser Ala Leu Gly Lys Arg Trp Val Asp
1 5 10 15

Thr Thr Gly Gly Gln Lys Met Pro Ala His Phe Val Ser Thr Val Arg
20 25 30

Lys Leu Ser Thr Glu Lys Leu Lys Thr Lys Arg Gln Leu Asp Gln Leu
35 40 45

Leu

<210> SEQ ID NO 306
<211> LENGTH: 51
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 306

Leu Thr Val Pro Gln Ala His Arg Glu Thr Leu Glu Glu Ala Gly Lys
1 5 10 15

Leu Thr Thr Ile Ala Ala Ile Asn Thr Lys Lys Leu Ile Lys Asp Val
20 25 30

Thr Val Gly Thr Met Ser Ser Val Phe Pro Asp Gly Thr Asp Asn Gly
35 40 45

Gly Arg Pro
50

<210> SEQ ID NO 307
<211> LENGTH: 61
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 307

Ile Gln Gln Gly Gln Lys Ala Asn Ala Arg Glu Gln His Arg Gly Arg
1 5 10 15

Lys Thr Asn Leu Thr Ile Lys Leu Pro Gly Ala His Ser Tyr Lys Ala
20 25 30

Lys Phe Glu Gly Cys Met Val Val Leu Gln Asp Lys Lys Leu Tyr Val
35 40 45

Glu His Ala Gly Cys Glu Ser Leu Ala Tyr Ala His Pro
50 55 60

<210> SEQ ID NO 308
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Aspergillus fumigatus

<400> SEQUENCE: 308

Ile Pro Ser Ala Phe Pro Gln Asp Asn Ala Val Asn Gln Val Leu Leu
1 5 10 15

Ser Asp Ser Tyr Gln Asp Gln Ser Val Ser Ser Ile Ser Ala Glu Asp
20 25 30

Asp Ala Gln Asn Ser Ala Val Ile His Ile Gly Glu Ser Glu Thr Met

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        35                  40                  45

Arg Ala Pro Ser Trp Phe Thr Ser Thr Leu Met Ala Arg Arg Leu Leu
    50                  55                  60

Ala Leu Ser Thr Thr Gly Thr Val Ser Thr Ile Phe Pro Asp Pro Leu
65                  70                  75                  80

Pro Gly Asn Ser His Ala Pro Pro Ser Val Ala Gly Leu Pro
                85                  90


<210> SEQ ID NO 309
<211> LENGTH: 77
<212> TYPE: PRT
<213> ORGANISM: Aspergillus fumigatus

<400> SEQUENCE: 309

Val Ala Met Gly Val Ser Glu Gln Arg Lys Ala Asn Glu Arg Lys Met
1               5                   10                  15

Asp Ala Arg Arg Met Ala Arg Phe Asn Ile Asp Ile Glu Thr Ser Gly
            20                  25                  30

Glu Thr Gln Glu Glu Asp Glu Ile Arg Gly Lys Arg Ile Val Leu Arg
        35                  40                  45

Asp Asn Lys Val Tyr Leu Asp Asp Pro Leu Pro Ala Asn Arg Lys His
    50                  55                  60

Pro Ser His Thr Ala Glu Ser Phe Tyr Ile Asp Tyr Pro
65                  70                  75


<210> SEQ ID NO 310
<211> LENGTH: 49
<212> TYPE: PRT
<213> ORGANISM: Aspergillus fumigatus

<400> SEQUENCE: 310

Pro Val Val Pro Gly Gln Thr Val Met Glu Pro Ser Ala Ala Leu Pro
1               5                   10                  15

Asp Asp Gly Asp His Leu Tyr Thr Leu Pro Met Phe Asp Ile Arg Pro
            20                  25                  30

Trp Glu Arg Val Ser Glu Val Arg Leu Ala Arg Glu Gly Tyr Leu Tyr
        35                  40                  45

Gly


<210> SEQ ID NO 311
<211> LENGTH: 89
<212> TYPE: PRT
<213> ORGANISM: Coccidioides immitus

<400> SEQUENCE: 311

Ser Pro Val Phe Pro Gly Gly Asp Lys Arg Asp Ala Leu Tyr Gln Lys
1               5                   10                  15

Pro Ile Ala Pro Ala Gly Glu Phe Pro Phe Asp Ser Ser Pro Pro Glu
            20                  25                  30

Ala Arg Met Thr Ile Pro Tyr Ala Asp Asn Glu Pro Asp Ser Ser Leu
        35                  40                  45

Ser Ile Pro Ser Trp Pro Thr Thr His Leu Leu Ala Arg Arg Leu Leu
    50                  55                  60

Gly Leu Ser Thr Thr Gly Val Leu Ser Thr Val Phe Pro Arg Thr Asn
65                  70                  75                  80
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-continued

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Arg Asp Pro Ala Leu Val Gly Val Pro
                85

<210> SEQ ID NO 312
<211> LENGTH: 76
<212> TYPE: PRT
<213> ORGANISM: Coccidioides immitus

<400> SEQUENCE: 312

Ile Arg Ser Ser Gln Arg Ser Gln Arg Arg Gln Glu His Arg Ser Arg
1               5                   10                  15

Lys Met Asn Leu Ile Val Ser Cys Ser Asp Pro Ser Arg Lys Ser Lys
            20                  25                  30

Asp Val Asp Gly Cys Phe Val Val Leu Arg Asn His Lys Leu Trp Ile
        35                  40                  45

Ala Ser Arg Pro Ser Asp Gly Glu Ala Asn Glu Pro Ser Asp Asp Ala
    50                  55                  60

Thr Arg Phe Lys Ala Ser Leu His Gln Cys His His
65                  70                  75
```

1. A method of inhibiting entry, into a cell, of a pathogenic effector protein, said entry of said pathogenic effector protein into said cell requiring binding of at least one motif of said effector protein to at least one polar lipid of said cell, comprising the step of

i) binding a blocking compound to said at least one motif of said pathogenic effector protein; or

ii) binding a blocking compound to said at least one polar lipid of said cell,

wherein said step of binding prevents entry of said pathogenic effector protein into said cell.

2. The method of claim **1**, wherein said at least one motif comprises an amino acid sequence BXZ, where

B is an amino acid selected from arginine, lysine and histidine;

X is any amino acid and may be present or absent; and

Z is an amino acid selected from leucine, methionine, isoleucine, tryptophan, tyrosine and phenylalanine.

3. The method of claim **2**, and wherein said at least one motif is selected from the group consisting of RxLR, RSLR, Pexel, RYWT, RIYER, RRLLR, RRFLR, and RFYR.

4. The method of claim **3**, wherein said at least one motif is RIYER or RYWT.

5. The method of claim **1**, wherein said blocking compound is a polypeptide that binds to said at least one motif.

6. The method of claim **5**, wherein said polypeptide is a synthetic peptide.

7. The method of claim **1**, wherein said blocking compound is a polar lipid.

8. The method of claim **7** wherein said polar lipid is selected from phosphoinositides, phospholipids, and sphingolipids.

9. The method of claim **8** wherein said phosphoinositide is selected from the group consisting of phosphatidyl-inositol-3-phosphate (PI-3-P), phosphatidyl-inositol-4-phosphate (PI-4-P), phosphatidyl-inositol-5-phosphate (PI-5-P), phosphatidyl-inositol-3,4-diphosphate (PI-3,4-P2), phosphatidyl-inositol-3,5-diphosphate (PI-3,5-P2), phosphatidyl-inositol-4,5-diphosphate (PI-4,5-P2), phosphatidyl-inositol-3,4,5-triphosphate (PI-3,4,5-P3), lysophosphatidyl-inositol-3-phosphate (LPI-3-P), lysophosphatidyl-inositol-4-phosphate (LPI-4-P), lysophosphatidyl-inositol-5-phosphate (LPI-5-P), lysophosphatidyl-inositol-3,4-diphosphate (LPI-3,4-P2), lysophosphatidyl-inositol-3,5-diphosphate (LPI-3,5-P2), lysophosphatidyl-inositol-4,5-diphosphate (LPI-4,5-P2), and lysophosphatidyl-inositol-3,4,5-triphosphate (LPI-3,4,5-P3), and phosphatidyl-inositol (PI), and lysophosphatidyl-inositol (LPI).

10. The method of claim **7** wherein said polar lipid is selected from the group consisting of phosphatidyl-serine (PS), phosphatidyl-glycerol (PG), phosphatidyl-ethanolamine (PE), phosphatidyl-choline (PC), lysophosphatidyl-serine (LPS), lysophosphatidyl-glycerol (LPG), lysophosphatidyl-ethanolamine (LPE), lysophosphatidyl-choline (LPC), phosphatidic acid (PA), lysophosphatidic acid (LPA), sphingosine-1-phosphate (S-1-P), ceramide-1-phosphate (C-1-P), a glycosylphosphatidylinositol (GPI)-protein anchor, a glycosylsphingosylinositol (GSI)-protein anchor, a glycosyl phosphoryl inositol ceramide (GPIC) and sphingomyelin (SM).

11. The method of claim **1**, wherein said blocking compound is selected from the group consisting of: an inositol phosphate, an inositol sulfate, an inositol carboxylate, an inositol arsenate, an inositol phosphorothioate, a hexose phosphate, a hexose sulfate, a hexose carboxylate, a hexose arsenate, a hexose phosphorothioate, a hexitol phosphate, a hexitol sulfate, a hexitol carboxylate, a hexitol arsenate, a hexitol phosphorothioate, a polyol phosphate, a polyol sulfate, a polyol carboxylate, a polyol arsenate, a polyol phosphorothioate, a phosphorylated glycan, a sulfated glycan, a carboxylated glycan, a glycan arsenate, or a glycan phosphorothioate.

12. The method of claim **11**, wherein said blocking compound is a polypeptide that binds to said at least one polar lipid.

13. The method of claim **12**, wherein said polypeptide is or comprises a portion of a lipid-binding protein.

14. The method of claim **13**, wherein said polypeptide comprises a domain selected from the group consisting of C1, C2, PH, FYVE, PX, ENTH, ANTH, BAR, FERM, PDZ, and tubby domains.

15. The method of claim **12**, wherein said polypeptide is a synthetic peptide.

16. The method of claim **1**, wherein said host cell is a plant cell.

17. The method of claim **16**, wherein said plant cell is of a type selected from the group consisting of wheat, maize, rice, sorghum, barley, oats, millet, soybean, common bean (*Phaseolus* species), green pea (*Pisum* species), cowpea, chickpea, alfalfa, clover, tomato, potato, tobacco, pepper, egg plant, grape, strawberry, raspberry, cranberry, blueberry, blackberry, hops, walnut, apple, peach, plum, pistachio, apricot, almond, pear, avocado, cacao, coffee, tea, pineapple, passionfruit, coconut, date and oil palm, citrus, orange, lemon, grapefruit, safflower, carrot, sesame, common bean, banana, citrus, papaya, macadamia, guava, pomegranate, pecan, *Brassica* species, canola, cabbage, cauliflower, mustard, cucurbits, pumpkin, cantalope, squash, zucchini, melon, cotton, sugar cane, sugar beets, sunflower, lettuce, onion, garlic, ornamental cut flowers; and grass.

18. The method of claim **1** wherein said host cell is an animal cell.

19. The method of claim **18**, wherein said animal cell is from or in an animal selected from the group consisting of cattle, sheep, pigs, goats, horses, cats, dogs, chickens, turkeys, bees, salmon, trout, bass, catfish, shellfish, crayfish, lobsters, shrimp, and crabs.

20. The method of claim **19** wherein said animal cell is a human cell.

21. The method of claim **19** wherein said animal cell is a red blood cell, a lymphocyte, a macrophage, a neutrophil, a dendritic cell, a spleen cell, a thymus cell, a liver cell, a nerve cell, a brain cell, a lung cell, a muscle cell, or an epithelial cell.

22. The method of claim **1** wherein said pathogenic effector protein is from an oomycete.

23. The method of claim **22** wherein said oomycete is selected from the group consisting of: a *Phytophthora* species, *Phytophthora infestans, Phytophthora sojae, Phytophthora ramorum, Phytophthora parasitica, Phytophthora capsici, Phytophthora nicotianae, Phytophthora cinnamomi, Phytophthora cryptogea, Phytophthora drechsleri, Phytophthora cactorum, Phytophthora cambivora, Phytophthora citrophthora, Phytophthora citricola, Phytophthora megasperma, Phytophthora palmivora, Phytophthora megakarya, Phytophthora boehmeriae, Phytophthora kernoviae, Phytophthora erythroseptica, Phytophthora fragariae, Phytophthora heveae, Phytophthora lateralis, Phytophthora syringae*, a *Pythium* species, *Pythium ultimum, Pythium aphanidermatum, Pythium irregulare, Pythium graminicola, Pythium arrhenomanes, Pythium insidiosum*, a downy mildew species, a *Peronospora* species, *Peronospora tabacina, Peronospora destructor, Peronospora sparsa, Peronospora viciae*, a *Bremia* species, *Bremia lactucae*, a *Plasmopora* species, *Plasmopora viticola, Plasmopara halstedii*, a *Pseudoperonospora* species, *Pseudoperonospora cubensis, Pseudoperonospora humuli*, a *Sclerospora* species, *Sclerospora graminicola*, a *Peronosclerospora* species, *Peronosclerospora philippinesis, Peronosclerospora sorghi, Peronosclerospora sacchari*, a *Sclerophthora* species, *Sclerophthora rayssiae, Sclerophthora macrospora*, a *Albugo* species, *Albugo candida*, a *Aphanomyces* species, *Aphanomyces cochlioides, Aphanomyces euteiches, Aphanomyces invadans*, a *Saprolegnia* species, *Saprolegnia parasitica*, and a *Achlya* species.

24. The method of claim **1** wherein said pathogenic effector protein is from a fungus.

25. The method of claim **24** wherein said fungus is selected from the group consisting of: a rust fungus, a smut fungus, a bunt fungus, a powdery mildew fungus, a *Puccinia* species, *Puccinia striiformis, Puccinia graminis, Puccinia triticina* (syn. *Puccinia recondita*), *Puccinia sorghi, Puccinia schedonnardii, Puccinia cacabata*, a *Phakopsora* species, *Phakopsora pachyrhizi, Phakopsora gossypii*, a *Phoma* species, *Phoma glycinicola*, a *Ascochyta* species, *Ascochyta gossypii*, a *Cryphonectria* species, *Cryphonectria parasitica*, a *Magnaporthe* species, *Magnaporthe oryzae*, a *Gaeumannomyces* species, *Gaeumannomyces graminis*, a *Synchytrium* species, *Synchytrium endobioticum*, a *Ustilago* species, *Ustilago maydis, Ustilago tritici, Ustilaginoidea vixens*, a *Tilletia* species, *Tilletia indica, Tilletia caries, Tilletia foetida, Tilletia barclayana*, a *Erysiphe* species, *Erysiphe necator*, a *Blumeria* species, *Blumeria graminis, Podosphaera oxyacanthae*, a *Alternaria* species, *Alternaria alternata*, a *Botrytis* species, *Botrytis cinerea*, a *Diaporthe* species, *Diaporthe phaseolorum*, a *Fusarium* species, *Fusarium graminearum, Fusarium oxysporum, Fusarium moniliforme, Fusarium solani*, a *Leptosphaeria* species, *Leptosphaeria maculans, Leptosphaeria maydis*, a *Macrophomina* species, *Macrophomina phaseolina*, a *Monilinia* species, *Monilinia fructicola*, a *Mycosphaerella* species, *Mycosphaerella graminicola, Mycosphaerella fijiensis, Mycosphaerella tassiana, Mycosphaerella zeae-maydis*, a *Phialophora* species, *Phialophora gregata*, a *Phymatotrichopsis* species, *Phymatotrichopsis omnivora*, a *Taphrina* species, *Taphrina deformans*, a *Aspergillus* species, *Aspergillus flavus, Aspergillus parasiticus, Aspergillus fumigatus*, a *Verticillium* species, *Verticillium dahliae, Verticillium albo-atrum, Rhizoctonia solani, Ophiostoma ulmi, Ophiostoma novo-ulmi*, a *Septoria* species, *Septoria avenae*, a *Pyrenophora* species, *Pyrenophora triticirepentis*, a *Colletotrichum* species, *Colletotrichum graminicola*, a *Sclerotinia* species, *Sclerotinia sclerotiorum*, a *Sclerotium* species, *Sclerotium rolfsii*, a *Thielaviopsis* species, *Thielaviopsis basicola*, a *Coccidioides* species, *Coccidioides immitus*, a *Paracoccidioides* species, *Paracoccidioides braziliensis*, a *Pneumocystis* species, *Pneumocystis carinii*, a *Histoplasma* species, *Histoplasma capsulatum*, a *Cryptococcus* species, *Cryptococcus neoformans*, a *Candida* species, *Candida albicans*, a microsporidial species, a *Enterocytozoon* species, a *Encephalitozoon species* and *Encephalitozoon cuniculi*.

26. The method of claim **1**, wherein said pathogen effector protein is from a protozoon.

27. The method of claim **26** wherein said protozoon is selected from the group consisting of: an apicomplexan parasite, a *Plasmodium* species, *Plasmodium falciparum, Plasmodium vivax, Plasmodium ovale, Plasmodium malariae*, a *Babesia* species, *Babesia bovis, Babesia bigemina*, a *Cryptosporidium* species, *Cryptosporidium parvum*, a *Toxoplasma* species, *Toxoplasma gondii*, a *Trypanosomatid* species, a *Trypanosoma* species, *Trypanosoma brucei, Trypanosoma cruzi, Trypanosoma congolense, Trypanosoma vivax*, a *Leishmania* species, *Leismania donovani*, an amebozoan parasite, an *Entamoeba* species, *Entamoeba histolytica*, a *Mastigamoeba* species, a *Schistosoma* species, a *Onchocerca* species, and a *Giardia* species.

28. The method of claim **1** wherein said step of binding includes the step of providing to a plant or animal a sufficient quantity of said blocking compound so that it is present to bind to said target molecule prior to entry of said pathogenic effector protein into cells of said plan or animal.

29. A method for screening compounds to identify whether they are potential blocking compounds for inhibiting entry of pathogenic effector proteins into a cell, comprising the steps of:

providing one or more proteins each of which has one or more motifs which are bound by polar lipids as a prerequisite to translocation;

exposing a candidate compound to said one or more proteins; and

determining whether said candidate compound binds to said one or more motifs of said one or more proteins, and, if binding occurs, determining that said compound is a potential blocking compound for inhibiting entry of pathogenic effector proteins into a cell,

wherein said one or more motifs comprises an amino acid sequence BXZ, where

B is an amino acid selected from arginine, lysine and histidine;

X is any amino acid and may be present or absent; and

Z is an amino acid selected from leucine, methionine, isoleucine, tryptophan, tyrosine and phenylalanine.

30. The method of claim **29** wherein said one or more proteins provided in said providing step are pathogenic effector proteins derived from a bacterial, protozoal, fungal, oomycete or nematode source.

31. A method for screening compounds to identify whether they are potential blocking compounds for inhibiting entry of pathogenic effector proteins into a cell, comprising the steps of:

providing one or more polar lipids, each of which binds to one or more motifs of an effector protein as a prerequisite to translocation of said effector protein into said cell;

exposing a candidate compound to said one or more polar lipids; and

determining whether said candidate compound binds to said one or morepolar lipids, and, if binding occurs, determining that said compound is a potential blocking compound for inhibiting entry of pathogenic effector proteins into said cell,

wherein said one or more motifs comprises an amino acid sequence BXZ, where

B is an amino acid selected from arginine, lysine and histidine;

X is any amino acid and may be present or absent; and

Z is an amino acid selected from leucine, methionine, isoleucine, tryptophan, tyrosine and phenylalanine.

32. The method of claim **31**, wherein said effector proteins are pathogenic effector proteins derived from a bacterial, protozoal, fungal, oomycete or nematode source.

33. A method of inhibiting entry, into a cell, of a pathogenic effector protein, said entry of said pathogenic effector protein into said cell requiring binding of at least one motif of said effector protein to at least one polar lipid of said cell, comprising the step of

contacting a substrate which contains or is likely to contain a pathogen comprising said pathogenic effector protein with a blocking compound, said blocking compound being capable of

i) binding to said at least one motif of said pathogenic effector protein; or

ii) binding to said at least one polar lipid of said cell,

wherein binding of said blocking compound prevents entry of said pathogenic effector protein into said cell if said pathogen comes into contact with said substrate.

34. The method of claim **33**, wherein said substrate is selected from the group consisting of plants, fabric, water, skin and fur.

* * * * *

专利名称(译)	通过阻断病原体蛋白质的进入来保护细胞的组合物和方法		
公开(公告)号	US20110212541A1	公开(公告)日	2011-09-01
申请号	US12/944345	申请日	2010-11-11
[标]申请(专利权)人(译)	弗吉尼亚科技知识产权公司		
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发明人	TYLER, BRETT KALE, SHIV ANTIGNANI, VINCENZO		
IPC分类号	G01N33/53 C12N5/04 C12N5/07 C12N5/071 C12N5/077 C12N5/078 C12N5/079		
CPC分类号	A01N37/46 A01N57/12 A01N57/24 A01N61/00 C12N15/8282 A61K31/683 A61K31/685 G01N33/502 A61K38/00 A61K31/6615		
优先权	61/260227 2009-11-11 US 61/128080 2008-05-19 US 61/160059 2009-03-13 US		
外部链接	Espacenet USPTO		

摘要(译)

致病性效应蛋白包括氨基酸共有序列BXZ的一个或多个毒力基序，其中B = RK或H; X =任何氨基酸或不存在; Z = L，M，I，W，Y或F）与宿主（植物或动物）细胞上的目标极性脂质结合，作为致病效应蛋白易位到细胞中的先决条件。通过将阻断化合物与效应蛋白的一个或多个基序或宿主细胞的脂质配体结合来防止易位。阻断化合物包括结合极性脂质或基序的合成或天然存在的多肽，各种极性脂质，极性脂质的亲水性头部基团等。合适的阻断化合物可通过证明与基序或靶标结合的测定来鉴定。极性脂质。