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(54) **NUCLEIC ACIDS ENCODING
PSEUDOMONAS HOP PROTEINS AND USE
THEREOF**

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(21) Appl. No.: **10/114,828**

(22) Filed: **Apr. 2, 2002**

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(51) **Int. Cl.**
C12N 15/82 (2006.01)
C12N 15/31 (2006.01)
C12N 15/63 (2006.01)

(52) **U.S. Cl.** **800/301**; 800/279; 536/23.7; 424/93.2; 435/320.1; 435/252.3

(58) **Field of Classification Search** 800/301; 536/23.7; 435/252.3, 418, 252.2
See application file for complete search history.

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Petnicki-Ocwieja et al., "Genomewide Identification of Proteins Secreted by the Hrp Type III Protein Secretion System of Pseudomonas syringae pv. Tomato DC3000," *PNAS* 99(11):7652-7657 (2002), with supplemental material available online at www.pnas.org.

* cited by examiner

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(57) **ABSTRACT**

The present invention relates to isolated nucleic acid molecules encoding a type III—secreted bacterial protein capable of modifying a cell death pathway in a plant cell. One aspect of the present invention involves an isolated nucleic acid molecule having a nucleotide sequence that encodes the HopPtoD2 protein of *Pseudomonas syringae* pv. *syringae* DC 3000. Expression vectors, host cells, and transgenic plants which include the DNA molecules of the present invention are also disclosed. The nucleic acid molecules of the present invention can be used to impart disease resistance to a plant and to make a plant hypersusceptible to colonization by nonpathogenic bacteria.

12 Claims, 1 Drawing Sheet

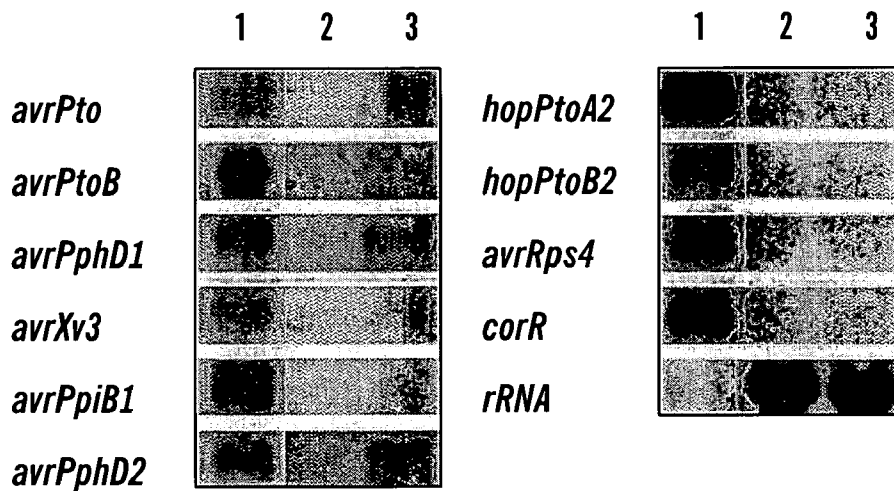


FIG. 1

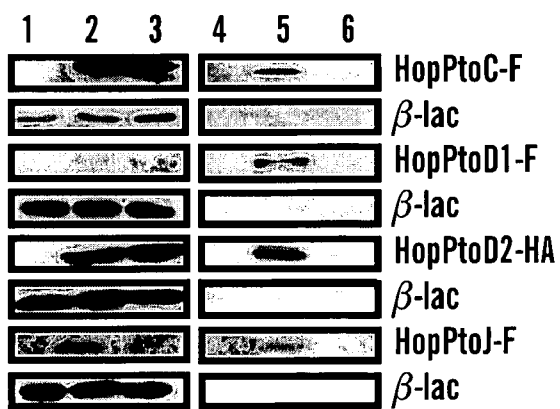


FIG. 2A

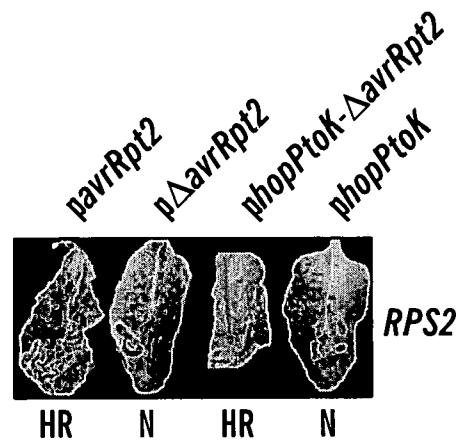


FIG. 2B

**NUCLEIC ACIDS ENCODING
PSEUDOMONAS HOP PROTEINS AND USE
THEREOF**

This application claims benefit of U.S. Provisional Patent Application Ser. Nos. 60/280,918, filed Apr. 2, 2001, and 60/356,408, filed Feb. 12, 2002, each of which is hereby incorporated by reference in its entirety.

This work was supported by National Science Foundation Grant Nos. DBI-0077622 and MCB-9982646 and National Research Initiative Competitive Grants Program, U.S. Department of Agriculture, Grant Nos. 97-35303-4488 and 01-35319-10019. The U.S. Government may have certain rights in this invention.

FIELD OF THE INVENTION

The present invention relates to isolated DNA molecules corresponding to the open reading frames of *Pseudomonas syringae* pv. tomato DC3000, the isolated avirulence effector proteins and hrp-dependent outer proteins encoded thereby, as well as their various uses.

BACKGROUND OF THE INVENTION

The plant pathogenic bacterium *Pseudomonas syringae* is noted for its diverse and host-specific interactions with plants. A specific strain may be assigned to one of at least 40 pathovars based on its host range among different plant species and then further assigned to a race based on differential interactions among cultivars of the host. In host plants the bacteria typically grow to high population levels in leaf intercellular spaces and then produce necrotic lesions. In nonhost plants or in host plants with race-specific resistance, the bacteria elicit the hypersensitive response (HR), a rapid, defense-associated programmed death of plant cells in contact with the pathogen (Alfano & Collmer, *J. Bacteriol.* 179:5655-5662 (1997)). The ability to produce either of these reactions in plants appears to be directed by hrp (HR and pathogenicity) and hrc (HR and conserved) genes that encode a type III protein secretion pathway and by avr (avirulence) and hop (Hrp-dependent outer protein) genes that encode effector proteins injected into plant cells by the pathway (Alfano & Collmer, *J. Bacteriol.* 179:5655-5662 (1997)). These effectors may also betray the parasite to the HR-triggering R-gene surveillance system of potential hosts (hence the avr designation), and plant breeding for resistance based on such gene-for-gene (avr-R) interactions may produce complex combinations of races and differential cultivars (Keen, *Annu. Rev. Genet.* 24:447-463 (1990)). hrp/hrc genes are probably universal among necrosis-causing gram-negative plant pathogens, and they have been sequenced in *P. syringae* pv. *syringae* (Psy) 61, *Erwinia amylovora* Ea321, *Xanthomonas campestris* pv. *vesicatoria* (Xcv) 85-10, and *Ralstonia solanacearum* GMI1000 (Alfano & Collmer, *J. Bacteriol.* 179:5655-5662 (1997)). Based on their distinct gene arrangements and regulatory components, the hrp/hrc gene clusters of these four bacteria can be divided into two groups: I (*Pseudomonas* and *Erwinia*) and II (*Xanthomonas* and *Ralstonia*). The discrepancy between the distribution of these groups and the phylogeny of the bacteria provides some evidence that hrp/hrc gene clusters have been horizontally acquired and, therefore, may represent pathogenicity islands (Pais) (Alfano & Collmer, *J. Bacteriol.* 179:5655-5662 (1997)).

Virulence effector proteins delivered to or into host cells by type III secretion systems are key factors in the patho-

genicity of many bacteria, including animal pathogens in the genera *Salmonella*, *Yersinia*, *Shigella*, and *Escherichia*, and plant pathogens in the genera *Pseudomonas*, *Erwinia*, *Xanthomonas*, *Ralstonia*, and *Pantoea* (Galán & Collmer, *Science* 284:1322-1328 (1999)). In plant pathogens, the type III secretion machinery is referred to as the hypersensitive response and pathogenicity (Hrp) system because secretion mutants typically lose their ability to elicit the defense-associated hypersensitive response in nonhost plants and to grow parasitically or be pathogenic in host plants (Alfano & Collmer, *J. Bacteriol.* 179:5655-5662 (1997)). These phenotypes demonstrate the importance of the Hrp system in bacterium-plant interactions, and global identification of effectors will be important for understanding the pathogenesis of bacteria that use type III secretion systems. Unfortunately, several factors have hindered searches for type III effector genes. These factors include: (i) effectors are often redundant with mutants having only subtle phenotypes; (ii) with few exceptions (see e.g., Miao & Miller, *Proc. Natl. Acad. Sci. USA* 97:7539-7544 (2000)) motifs that can identify proteins as substrates for type III secretion have not been recognized (Lloyd et al., *Mol. Microbiol.* 39:520-532 (2001)); (iii) many effectors show no similarity to known proteins; and (iv) some pathogens have multiple type III secretion systems which deliver different sets of effectors (Cornelis & Van Gijsegem, *Annu. Rev. Microbiol.* 54:735-774 (2000)). Thus, a complete inventory of type III effector genes is lacking for any pathogen, although it seems that pathogens such as *Salmonella* may have many such genes (Worley et al., *Mol. Microbiol.* 36:749-761 (2000)).

Plant pathogen type III effector proteins are mostly designated Avr or Hop, depending on whether their primary phenotype involves plant reaction or secretion behavior. Many effectors were initially discovered through their ability to betray the pathogen to the host R (resistance) gene surveillance system, thereby rendering the pathogen avirulent on a test plant (Keen, *Annu. Rev. Genet.* 24:447-463 (1990)). Over 25 effector genes have been identified by Avr or Hop phenotypes in various *P. syringae* pathovars and races (Vivian & Arnold, *J. Plant Pathol.* 82:163-178 (2000); Alfano et al., *Proc. Natl. Acad. Sci. USA* 97:4856-4861 (2000)). The encoded effectors seem to determine both basic pathogenicity and host range, but the number of such proteins produced by any single strain has not been systematically investigated. *P. s. tomato* DC3000 is known to carry at least three avr genes, avrPto (Ronald et al., *J. Bacteriol.* 174:1604-1611 (1992)), avrPtoB, and avrE (Lorang & Keen, *Mol. Plant-Microbe Interact.* 8:49-57 (1995)), with the latter being in the Hrp pathogenicity island along with five other candidate effector genes (Alfano et al., *Proc. Natl. Acad. Sci. USA* 97:4856-486 (2000); Lorang & Keen, *Mol. Plant-Microbe Interact.* 8:49-57 (1995)).

The present invention is a further advance in the effort to identify, clone, and sequence Avr and Hop proteins or polypeptides from plant pathogens.

SUMMARY OF THE INVENTION

One aspect of the present invention relates to isolated nucleic acid molecules having a nucleotide sequence which (i) encodes a protein or polypeptide including SEQ ID No: 2, SEQ ID No: 4, SEQ ID No: 6, SEQ ID No: 8, SEQ ID No: 10, SEQ ID No: 12, SEQ ID No: 14, SEQ ID No: 16, SEQ ID No: 18, SEQ ID No: 20, SEQ ID No: 22, or SEQ ID No: 24; or (ii) hybridizes, under stringency conditions including a hybridization medium which includes 0.9×SSC at a temperature of 42° C., to a DNA molecule complementary to

SEQ ID No: 1, SEQ ID No: 3, SEQ ID No: 5, SEQ ID No: 7, SEQ ID No: 9, SEQ ID No: 11, SEQ ID No: 13, SEQ ID No: 15, SEQ ID No: 17, SEQ ID No: 19, SEQ ID No: 21, or SEQ ID No: 23; or (iii) includes a nucleotide sequence which is complementary to the nucleic acid molecules of (i) and (ii). Expression vectors, host cells, and transgenic plants which include the DNA molecules of the present invention are also disclosed. Methods of making such host cells and transgenic plant are disclosed.

A further aspect of the present invention relates to isolated effector proteins or polypeptides encoded by the nucleic acid molecules of the present invention. Compositions which contain the proteins or polypeptides are also disclosed.

Yet another aspect of the present invention relates to methods of imparting disease resistance to a plant. According to one approach, this method is carried out by transforming a plant cell with a heterologous DNA molecule of the present invention and regenerating a transgenic plant from the transformed plant cell, wherein the transgenic plant expresses the heterologous DNA molecule under conditions effective to impart disease resistance. According to one approach, this method is carried out by treating a plant with a protein or polypeptide of the present invention under conditions effective to impart disease resistance to the treated plant.

A further aspect of the present invention relates to a method of causing eukaryotic cell death which includes: introducing into a eukaryotic cell a cytotoxic *Pseudomonas* protein of the present invention, said introducing being performed under conditions effective to cause cell death.

A still further aspect of the present invention relates to a method of treating a cancerous condition which includes introducing a cytotoxic *Pseudomonas* protein of the present invention into cancer cells of a patient under conditions effective to cause death of cancer cells, thereby treating the cancerous condition.

Yet another aspect of the present invention relates to a method of modifying a metabolic pathway in a cell which includes: introducing into a cell a protein or polypeptide of the present invention which interacts with a native cellular protein involved in a metabolic pathway, wherein the protein or polypeptide modifies the metabolic pathway through its interaction with the native cellular protein.

It is believed that bacteria have evolved effector proteins to make exquisite alterations in host metabolism. While plant resistance and cancer cell toxicity are important uses, as mentioned above, it is believed that these effector proteins can be used to modify or effect metabolic targets in eukaryotes, including both yeasts and higher order species, such as plants and animals. It is noteworthy that several of the effector proteins being claimed in this application have homologs in other phytopathogenic bacteria. Thus, these proteins appear to represent a set of effectors that are

conserved among *Pseudomonas*, *Erwinia*, *Xanthomonas*, and *Ralstonia* spp. By disrupting the function of these effectors through, for example, transgenic expression thereof in a host plant, it is believed that use of these effectors may lead to widely applicable means for controlling diseases of plants.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is an RNA blot analysis of HrpL-dependent expression of representative virulence-implicated genes. Each well was loaded with 25 μ g of total RNA isolated from CUCPB5114 cultures carrying either vector control pCPP5031 or P_{hrpL} -hrpL plasmid pCPP5032 (lanes 2 and 3, respectively). PCR-amplified internal fragments were used as probes; lane 1 in each case contains PCR product of the corresponding probe. AvrPpiB1_{Pto} and AvrPpiB2_{Pto} are 100% identical, therefore their signals cannot be distinguished.

FIGS. 2A–B illustrate assays for Hrp system-dependent secretion in culture or translocation in plants of various Avr and Hop proteins. In FIG. 2A, DC3000 or a DC3000 hrcC mutant (Yuan & He, *J. Bacteriol.* 178:6399–6402 (1996), which is hereby incorporated by reference in its entirety) carrying test ORFs (i.e., candidate effectors) fused to either the FLAG (F) or hemagglutinin (HA) epitopes were grown in Hrp-inducing media, and cultures were separated into cell (lanes 1–3) and supernatant (lanes 4–5) fractions and analyzed by SDS-PAGE and immunoblotting. Lanes: 1 and 4, wild type DC3000; 2 and 5, wild type DC3000(pTestORF); 3 and 6, DC3000 hrcC mutant(pTestORF). As an additional control against leakage, pCPP2318 (which encodes the mature form of β -lactamase, β -lac) was included in all strains. The presence of an epitope-tagged protein in the supernatant fraction of the wild type (lane 5), but absence in the hrcC secretion mutant (lane 6), indicated that the test ORF encoded a secreted product. In FIG. 2B, AvrRpt2 translocation assays were performed with a DC3000 AvrRps4 homolog (now designated HopPtoK). Constructs that contained ORFs fused to AvrRpt2 lacking translocation signals were electroporated into *P. s. phaseolicola* 3121. Test strains were infiltrated into *A. thaliana* Col-0 (RPS2). Plant responses were scored 18 hr after inoculation for hypersensitive collapse (HR) or no visible response (N).

DETAILED DESCRIPTION OF THE INVENTION

One aspect of the present invention relates to *Pseudomonas syringae* pv. *syringae* DC 3000 nucleic acid molecules which encode Avr or Hop effector proteins.

A first nucleic acid molecule is a homolog of avrPpHE of *Pseudomonas syringae* pv. *phaseolicola* and has a nucleotide sequence according to SEQ ID No: 1 as follows:

```

atgaaaatac ataacgctgg cctaacccca cctttgccgg gcatttcgaa tggaaacgtt 60
ggaaggcg cgcaatcatc aataactcaa ccgcagagcc agcaaggctc ttatggcttg 120
ccaccagaaa gctctgagac tcgccctgat agggcgctg cgaactatcc atattcatca 180
gtacaaacac ggttgccgcc cgttgctct gctgggaaac cgctgcctga tacaccatct 240
tctttgcccc gctacttact gttgcgaagg ctggaccatc gccctgtgga tcaggaaggt 300
accaaaagtc tgatccccgc agacaaggct gtggctgaag cgcgccgtgc attgcccttt 360
ggaagagcca atattgatgt ggatgogcaa cttccaatc tggaaagtg agccccgacc 420

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cttgagcaa ggtgcttgag aaaagatgcc gaggccgccg gtcagagacc tatgcctgcg 480
aatgagccga tgaactggca tgttcttgtt gcgatgtcag gccagggtgtt cggcgcgggc 540
aactgtggcg aacatgctcg tatagcgagc ttcgcctatg gagctttggc ccaggaaaac 600
ggacgatctg aatatgaaaa catctacttg gctgcatcga ctgaggaaga tcatgtgtgg 660
gctgaaaccg acgaatccca gtctggcacc tcaacgattg tcatggatcc gtggtcaaat 720
ggttcagcca ttttgcgga ggacagtagg tttgcgaaaa atcgaaatgc tgtagagcgt 780
acggatagct ttaatctttc aaccgcagcc gaagcgggca aaattacgcg tgagacagcc 840
gagaaggctt tgacgcaggt cacaaccgca ttgcagaaac gcctggcggga tcagcaggag 900
caagtctcgc ccatcaaaa tggtcgtat cgaccagaaa aatcggtact tgatgatgca 960
tttgtccgca gagtgcgca caagttgacc tcccctgatt tgcggcgtgc actacaggtg 1020
gatattgaag cggtcggagt cgcaatgtcg ctcggcacca agggcgctca ggacgctact 1080
cgacaagccc gaccttgggt tgagcttgca gtgaaggtcg cctctcctca aggcttggcg 1140
agacgagatg tctga 1155

```

The encoded protein, designated AvrPphE_{Pro}, has an amino²⁵ acid sequence according to SEQ ID No: 2 as follows:

```

Met Lys Ile His Asn Ala Gly Leu Thr Pro Pro Leu Pro Gly Ile Ser
 1           5           10          15
Asn Gly Asn Val Gly Lys Ala Ala Gln Ser Ser Ile Thr Gln Pro Gln
 20          25          30
Ser Gln Gln Gly Ser Tyr Gly Leu Pro Pro Glu Ser Ser Glu Thr Arg
 35          40          45
Pro Asp Arg Ala Arg Ala Asn Tyr Pro Tyr Ser Ser Val Gln Thr Arg
 50          55          60
Leu Pro Pro Val Ala Ser Ala Gly Lys Pro Leu Pro Asp Thr Pro Ser
 65          70          75          80
Ser Leu Pro Gly Tyr Leu Leu Leu Arg Arg Leu Asp His Arg Pro Val
 85          90          95
Asp Gln Glu Gly Thr Lys Ser Leu Ile Pro Ala Asp Lys Ala Val Ala
100         105         110
Glu Ala Arg Arg Ala Leu Pro Phe Gly Arg Gly Asn Ile Asp Val Asp
115         120         125
Ala Gln Leu Ser Asn Leu Glu Ser Gly Ala Arg Thr Leu Ala Ala Arg
130         135         140
Cys Leu Arg Lys Asp Ala Glu Ala Ala Gly His Glu Pro Met Pro Ala
145         150         155         160
Asn Glu Pro Met Asn Trp His Val Leu Val Ala Met Ser Gly Gln Val
165         170         175
Phe Gly Ala Gly Asn Cys Gly Glu His Ala Arg Ile Ala Ser Phe Ala
180         185         190
Tyr Gly Ala Leu Ala Gln Glu Asn Gly Arg Ser Glu Tyr Glu Asn Ile
195         200         205
Tyr Leu Ala Ala Ser Thr Glu Glu Asp His Val Trp Ala Glu Thr Asp
210         215         220
Glu Ser Gln Ser Gly Thr Ser Thr Ile Val Met Asp Pro Trp Ser Asn
225         230         235         240

```

-continued

Gly Ser Ala Ile Phe Ala Glu Asp Ser Arg Phe Ala Lys Asn Arg Asn
 245 250 255
 Ala Val Glu Arg Thr Asp Thr Phe Asn Leu Ser Thr Ala Ala Glu Ala
 260 265 270
 Gly Lys Ile Thr Arg Glu Thr Ala Glu Lys Ala Leu Thr Gln Val Thr
 275 280 285
 Thr Arg Leu Gln Lys Arg Leu Ala Asp Gln Gln Glu Gln Val Ser Pro
 290 295 300
 Ile Lys Ser Gly Arg Tyr Arg Pro Glu Lys Ser Val Leu Asp Asp Ala
 305 310 315 320
 Phe Val Arg Arg Val Ser Asp Lys Leu Thr Ser Pro Asp Leu Arg Arg
 325 330 335
 Ala Leu Gln Val Asp Ile Glu Ala Val Gly Val Ala Met Ser Leu Gly
 340 345 350
 Thr Lys Gly Val Lys Asp Ala Thr Arg Gln Ala Arg Pro Leu Val Glu
 355 360 365
 Leu Ala Val Lys Val Ala Ser Pro Gln Gly Leu Ala Arg Arg Asp Val
 370 375 380

AvrPphE_{Pro} has been shown to be expressed by DC3000. It has been demonstrated that AvrPphE of *Pseudomonas syringae* pv. *phaseolicola* is recognized within plant cells and that this protein alone is required for hypersensitive response induction (Stevens et al., "Sequence variations in alleles of the avirulence gene avrPphE: R2 from *Pseudomonas syringae* pv. *phaseolicola* lead to loss of recognition of the AvrPphE protein within bean cells and a gain in cultivar-specific virulence," *Mol. Microbiol.* 29(1):165-177 (1998); Mansfield et al., "Characterization of avrPphE, a gene for cultivar-specific avirulence from *Pseudomonas syringae* pv.

phaseolicola which is physically linked to hrpY, new hrp gene identified in the halo-blight bacterium," *Mol. Plant Microbe Interact.* 7(6):726-739 (1994), each of which is hereby incorporated by reference in its entirety). AvrPphE has been shown to be secreted by a type III secretion system and translocated into plants. AvrPphE matches the R2 resistance gene of *Phaseolus*.

A second nucleic acid molecule is a homolog of avrRps4 of *Pseudomonas syringae* pv. *pisii* and has a nucleotide sequence according to SEQ ID No: 3 as follows:

```

atgaatcgca ttcaaccag ctcagtaaat tccagcttca attacacggc ccctacggag 60
gaagcgcaaa accgcttcgc ctcagcgccc gacaattccc ctctagttgt caccacaaca 120
tctatcgccc aagcgtcggg agggctacaa agggcggggg caacgctaag catgcaggcc 180
cagcgactgc gccaatgat ggggagcccg tctgagcagt gccggaggga cacaatgtta 240
gctaaagctt ttgatgctca acgcctaac attaacactc aagcaggctc ttccaacagc 300
ccacacttga acgctctcaa cacgctccaa caacgacact tcaaacctgc ggctggtggg 360
ctagaaatcc cagttacatc caactcctta ttggcggtg gcaggcaagt ctatcaaat 420
ggctcatcgt cagcgagct aagccaccga cgggtcaatg atcaggaccg cgcgcccttc 480
agggcgcttg agcggctgca cgccgagttg tttagaggtg ggccgattga gtttgtcct 540
agaggcagca acgtgttggc ctcaaactg agggatgtcg acatggacga gttcogatgtc 600
atcaactcta aagacggctg ccaaggcatt ggcaccactg gcctgggacc ctgcattgca 660
gtgtgtgcaa gaggcattga tagagaagg cttccggtgc tgggtgtcta tcaccacagt 720
ggtatcggt caccagagga taccatggct actcttgatc aagcagtcg cgataaaggt 780
gctttgcaaa tcaaatactc cctggtagcc ggcatgatca tgcctaaaga ggaagaggct 840
ggcagctatg acgacagca aagctttttg gcattgaaag gcagttattc aatcgaaggg 900
gcgcgcttgc atgtatccga aggcgaagag gacgtgcata ccggcgagga caacagtgtc 960
aatgttctgc tgatgcctga ccgcgttctg tacggtcgcg acacgctota ctgctga 1017
    
```

The encoded protein, originally designated AvrRps_{Pto} and now renamed HopPtoK, has an amino acid sequence according to SEQ ID No: 4 as follows:

```

Met Asn Arg Ile Her Thr Ser Ser Val Asn Ser Ser Phe Asn Tyr Thr
 1           5           10           15

Ala Pro Thr Glu Glu Ala Gln Asn Arg Phe Ala Ser Ala Pro Asp Asn
 20           25           30

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

Leu Gln Arg Pro Gly Ala Thr Leu Ser Met Gln Ala Gln Arg Leu Arg
 50           55           60

Gln Leu Met Gly Ser Pro Ser Glu Gln Cys Arg Arg Asp Thr Met Leu
 65           70           75           80

Ala Lys Ala Phe Asp Ala Gln Arg Leu Asn Ile Asn Thr Gln Ala Gly
 85           90           95

Ser Ser Asn Ser Pro His Leu Asn Ala Leu Asn Thr Leu Gln Gln Arg
 100          105          110

His Phe Lys Pro Ala Ala Gly Gly Leu Glu Ile Pro Val Thr Ser Asn
 115          120          125

Ser Leu Leu Gly Gly Gly Arg Gln Val Tyr Gln Ile Gly Ser Per Ser
 130          135          140

Arg Glu Leu Ser His Arg Pro Val Asn Asp Gln Asp Arg Ala Pro Phe
 145          150          155          160

Arg Ala Leu Glu Arg Leu His Ala Glu Leu Phe Arg Gly Gly Pro Ile
 165          170          175

Glu Phe Val Pro Arg Gly Ser Asn Val Leu Ala Ser Asn Val Arg Asp
 180          185          190

Val Asp Met Asp Glu Phe Asp Val Ile Asn Ser Lys Asp Gly Cys Gln
 195          200          205

Gly Ile Gly Thr Thr Gly Leu Gly Pro Cys Ile Ala Val Cys Ala Arg
 210          215          220

Gly Met Asp Arg Glu Gly Leu Pro Val Leu Gly Val Tyr His His Ser
 225          230          235          240

Gly Ile Gly Ser Pro Glu Asp Thr Met Ala Thr Leu Asp Gln Ala Met
 245          250          255

Arg Asp Lys Gly Ala Leu Gln Ile Lys Tyr Ser Leu Val Gly Gly Met
 260          265          270

Ile Met Pro Lys Glu Glu Glu Ala Gly Per Tyr Asp Asp Glu Gln Ser
 275          280          285

Phe Leu Ala Leu Lys Gly Ser Tyr Ser Ile Glu Gly Ala Arg Leu His
 290          295          300

Val Ser Glu Gly Glu Glu Asp Val His Thr Gly Glu Asp Asn Ser Val
 305          310          315          320

Asn Val Leu Leu Met Pro Asp Arg Val Leu Tyr Gly Arp Asp Thr Leu
 325          330          335

Tyr Cys

```


11

HopPtoK has been shown to be a secreted protein that is expressed by DC3000. The *Pseudomonas syringae* pv. *pisii* AvrRps4 effector matches the disease locus RPS4. It has previously been demonstrated that *Pseudomonas syringae* strains carrying avrRps4 induces a hypersensitive response on specific accessions of both Arabidopsis and soybean (Hinsch et al., "Identification of a new Arabidopsis disease

12

resistance locus, RPs4, and cloning of the corresponding avirulence gene, avrRps4, from *Pseudomonas syringae* pv. *pisii*," *Mol. Plant Microbe Interact.* 9(1):55-61 (1996), which is hereby incorporated by reference in its entirety).
 A third nucleic acid molecule is a homolog of avrPphF orf1 of *Pseudomonas syringae* pv. *phaseolicola* and has a nucleotide sequence according to SEQ ID No: 5 as follows:

```
atgaaaaacg catttgacct gcttgtggaa gggctggcta aggactacaa catgccgccc 60
ttgcctgaca agaacatat cgatgaagtc tattgctttg agtttcaaag tggatgaac 120
gtaaaagtat accaagacga atttcgctgg gtatatttca ccgctgacgt tgggacattt 180
caagatagca gtattgacac attaaactac gcgctccagc tgaacaacct tagccttaga 240
aaccttttcc tgaccttcgg aatgacgaag gagaaaaatg gtgtattgca tacacgcacc 300
cccttgattg aggtagacaa cgtgcaaatg cgcaggatat ttgaggagct tataggcggtg 360
gcaggtgaaa tcagaaaaac actaaaactc aaatag 396
```

The encoded protein has an amino acid sequence according to SEQ ID No: 6 as follows:

```
Met Lys Asn Ala Phe Asp Leu Leu Val Glu Gly Leu Ala Lys Asp Tyr
  1           5           10          15
Asn Met Pro Pro Leu Pro Asp Lys Lys His Ile Asp Glu Val Tyr Cys
          20           25          30
Phe Glu Phe Gln Ser Gly Met Asn Val Lys Val Tyr Gln Asp Glu Phe
          35           40          45
Arp Trp Val Tyr Phe Thr Ala Asp Val Gly Thr Phe Gln Asp Ser Ser
          50           55          60
Ile Asp Thr Leu Asn Tyr Ala Leu Gln Leu Asn Asn Phe Per Leu Arg
          65           70          75          80
Lys Pro Phe Leu Thr Phe Gly Met Thr Lys Glu Lys Asn Gly Val Leu
          85           90          95
His Thr Arg Thr Pro Leu Ile Glu Val Asp Asn Val Gln Met Arg Arp
          100          105          110
Ile Phe Glu Glu Leu Ile Gly Val Ala Gly Glu Ile Arg Lys Thr Leu
          115          120          125
Lys Leu Lys
          130
```

This protein is believed to be a chaperone protein for the protein of SEQ ID NO: 8 described below.

A fourth nucleic acid molecule is also homolog of avrP-phF orf2 of *Pseudomonas syringae* pv. *phaseolicola* and has a nucleotide sequence according to SEQ ID No: 7 as follows:

```
gtgtatagcc catcccatac acaacgaata acttcagctc cctctacatc cactcatggtt 60
ggtaggagata cactgacatc cattcatcag ctttcgcata gtcagagaga gcagttttctg 120
aacatgcatg atccaatgag agtaatggga cttgaccatg ataccgagct tttcagaacg 180
acggatagtc gctatataaa aaacgataaa ctgcggggca atccacaact catggcgaggt 240
atccttatgc atgaagaact gcgcccctaat cgttttgcca gccatacagg tgcccacaacca 300
cacgaagcaa gggcgtacgt tccgaaaaga ataaaagcca ccgatctagg agttccatca 360
```

-continued

ctgaacgtaa tgactggctc gctagcgcga gacggaatta gagcttatga tcacatgagt 420
 gataatcagg tctctgtcaa aatgcgactg ggagattttc tcgaaagggg tggcaaggtc 480
 tatgccgacg ctctgtctgt agctgacgat ggggaaacat cacaagctct gattgtcaca 540
 ttgcccaaag gacagaaagt gccggtcgaa agggctctga 579

The encoded protein, designated AvrPphF_{Pto}, has an amino acid sequence according to SEQ ID No: 8 as follows:

Val Tyr Ser Pro Ser His Thr Gln Arg Ile Thr Ser Ala Pro Ser Thr
 1 5 10 15
 Ser Thr His Val Gly Gly Asp Thr Lou Thr Ser Ile His Gln Leu Ser
 20 25 30
 His Ser Gln Arg Glu Gln Phe Leu Asn Met His Asp Pro Met Arg Val
 35 40 45
 Met Gly Leu Asp His Asp Thr Glu Leu Phe Arg Thr Thr Asp Ser Arg
 50 55 60
 Tyr Ile Lys Asn Asp Lys Leu Ala Gly Asn Pro Gln Ser Met Ala Ser
 65 70 75 80
 Ile Leu Met His Glu Leu Arg Pro Asn Arg Phe Ala Ser His Thr
 85 90 95
 Gly Ala Gln Pro His Glu Ala Arg Ala Tyr Val Pro Lys Arg Ile Lys
 100 105 110
 Ala Thr Asp Leu Gly Val Pro Ser Leu Asn Val Met Thr Gly Ser Leu
 115 120 125
 Ala Arg Asp Gly Ile Arg Ala Tyr Asp His Met Ser Asp Asn Gln Val
 130 135 140
 Ser Val Lys Met Arg Leu Gly Asp Phe Leu Glu Arg Gly Gly Lys Val
 145 150 155 160
 Tyr Ala Asp Ala Ser Ser Val Ala Asp Asp Gly Glu Thr Ser Gln Ala
 165 170 175
 Leu Ile Val Thr Leu Pro Lys Gly Gln Lys Val Pro Val Glu Arg Val
 180 185 190

AvrPphF_{Pto} has been shown to be expressed by DC3000. Fusion of both the homolog of AvrPphF orf1 and AvrPphF_{Pto} with the AvrRpt2 reporter (AvrRpt2Δ40) caused a hypersensitive response in Arabidopsis Col-0, suggesting that AvrPphF_{Pto} is secreted. Neither Orf1-AvrRpt2Δ40 (AvrPphF_{Pto}) nor Orf2-AvrRpt2Δ40 alone causes the hypersensitive response in Arabidopsis Col-0, although mutants of the homolog of AvrPphF orf1 have shown reduced disease symptoms on tomato. The *Pseudomonas syringae* pv. *phaseolicola* AvrPphF effector protein has been shown to

45 play a role in both development of the hypersensitive response and virulence in several plants (Tsiamis et al., "Cultivar-specific avirulence and virulence functions assigned to avrPphF in *Pseudomonas syringae* pv. *phaseolicola*, the cause of bean halo-blight disease," *EMBO J.* 19(13):3204-3214 (2000), which is hereby incorporated by reference in its entirety).

A fifth nucleic acid molecule is a homolog of avrPphD of *Pseudomonas syringae* pv. *phaseolicola* and has a nucleotide sequence according to SEQ ID No: 9 as follows:

atgaatcctc tacgatctat tcaacacaac attgcaactc cccaatcag tggcggctcag 60
 ccattagacg cgggtgggcc tcaggccag caatcccatc ctaaaaggat ttacattct 120
 caattgagcc aaagcgtca ccaggctcta gaacgccttt cagctaattgc cgaacaccaa 180
 cgccttgcat cactggtagc caacgctctg caggatggca catttcaatt tcaatccagt 240
 aaccacacgc aagtaacctt taaagcgtca atctgtctgc cagctgacac cgataccgtg 300
 agaaccgacc acttgattaa taacgagctg acggttcagg cccgattaaa tgatcaatcg 360

-continued

```

gagtacgaca tcgtcagcgc acatttgcac ggctcttcga aagccatata cttcgacgta 420
cccagcccc cgcccgcaca tggttcagca tcttctgtct tgagtgaacg gacccatcta 480
ggatagagtc gcgttctctc acaagatgca gtagacagca gtagcctgga aactccgta 540
ctgagctcgc cagaccattc tcgtccgcca tcacagccaa agcccgtgca taccgggtcg 600
gtccgcaggg actctggtag ccttgtttcc gataaccggg tagtgacggc cctgctatcg 660
tttgcgcagg ccgaccaggc atttccacca caggccgcga gcattgccgg ggtccagctg 720
gaaatgcggc cacgtcggga tattgagaaa gcaactgagg aattcaaagg cgcttcacg 780
gtggtgaagg cgcaactgat gtccgggtgc aactcgtcgg agcgtgtaga tgaggatgtc 840
aacgcagaca tccatatccc cttattgctc aaggccatcg agcggggggc tgcggcattt 900
ggccaaaacg catcaatcgg ccagaatagc gcgaaagcgt ttctgcctc atgtgctccc 960
aagatcacgt ccaatgacga tgtctctccc gagttcatca accagaaact caagggggac 1020
gacgatcttc aggttcgcct gggcgcacag gaattgttgc atgtagccac caagaaggaa 1080
ttccagctcg gcggtctagc cggcagcatc ggggtcagca gcatactcgg ctccggcatgg 1140
gagcttgggc cttctgagct gttgaaaaat gccatcttcg gcaaaaattt ctcaccgagc 1200
caatatgccc tgcaattggc tggaatcgat tcagtgcctc ctttgattat cgagtccatg 1260
gacaccatgt gcgtacttgc catcatcaag ggcataaagg gtgaggagtg gtccatgagc 1320
gatctacttc ccaagggcgt gaaggccggt gctatttctc cgggtgtgtc attcccgaat 1380
aatgttttgc agtatgcagg tttcaaatcc agagtcggcg atcttgcggc aaactcagtg 1440
acaactgaag cgccatcctt tggcgcgcc cccgggtatt caccggagg caaggaagt 1500
gaagagctga tcggtgctgg cttattccag agcatgaagg acggcgtgat ggctcattca 1560
ggcggggggg tggacaccaa aaaaacgatt gagcggatga cgcgccatgc gctggatata 1620
gctccggggc aaagcaccgc tgtcaagtcc atggggctgg catcgattgt cgggatgatt 1680
ccactgattg ccagcaacaa ggcaaccggg ctgctgtcgg aacaggtaact gcgtattttc 1740
cggagcgcgc tcttcaatcc aatcgaagcc atcgctctga acgcggtggc gcttggcggg 1800
cgtgtcaacg ttcccgggct atttgattcc gacaatgcca agcatgcacg cgtggtacaa 1860
accatccttg cgcgggccag ccagcacatg gaagctggag accgtgacat ttcgcgagag 1920
gagctacatc aaatgctggc tccccggagc gagttcctgc gccatgtggg atctgcgatt 1980
gtcaacggca tgaatgccag ctttgaggca attcccgcgc tggttcggaa gcttgatata 2040
ggtgaggctc cattggccga acgtattccg tatcaagacc tggctgtgcc cgacacgctg 2100
cggcagcccc caccctga 2118

```

The encoded protein, originally designated AvrPphD1_{Pto} and now renamed HopPtoD1, has an amino acid sequence according to SEQ ID No: 10 as follows:

```

Met Asn Pro Leu Arg Her Ile Gln His Asn Ile Ala Thr Pro Pro Ile
 1           5           10           15

Ser Gly Gly Gln Pro Leu Asp Ala Val Gly Pro Gln Ala Gln Gln Her
 20           25           30

His Pro Lys Arg Ile Ser Pro Ser Gln Leu Ser Gln Ser Ala His Gln
 35           40           45

Ala Leu Glu Arg Leu Ser Ala Asn Ala Glu His Gln Ary Leu Ala Ser
 50           55           60

```

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Leu Val Arg Asn Ala Leu Gln Asp Gly Thr Phe Gln Phe Gln Ser Ser
 65 70 75 80
 Asn His Thr Gln Val Thr Tyr Lys Ala Ser Ile Cys Leu Pro Ala Asp
 85 90 95
 Thr Asp Thr Val Arg Thr Asp His Leu Ile Asn Asn Glu Leu Thr Val
 100 105 110
 Gln Ala Arg Leu Asn Asp Gln Ser Glu Tyr Asp Ile Val Ser Ala His
 115 120 125
 Leu His Gly Ser Ser Lys Ala Ile Ser Phe Asp Val Pro Ser Pro Pro
 130 135 140
 Pro Ala His Gly Ser Ala Ser Ser Val Leu Ser Glu Arg Thr His Leu
 145 150 155 160
 Gly Met Ser Arg Val Leu Ser Gln Asp Ala Val Asp Ser Ser Ser Leu
 165 170 175
 Glu Thr Pro Leu Leu Ser Ser Pro Asp His Ser Arg Pro Pro Ser Gln
 180 185 190
 Pro Lys Pro Val His Ile Gly Ser Val Arg Arg Asp Ser Gly Ser Leu
 195 200 205
 Val Ser Asp Asn Pro Val Val Gln Ala Leu Leu Ser Phe Ala Gln Ala
 210 215 220
 Asp Gln Ala Phe Pro Pro Gln Ala Ala Ser Ile Ala Gly Val Gln Leu
 225 230 235 240
 Glu Met Arg Pro Arg Arg Asp Ile Glu Lys Ala Leu Glu Glu Phe Lys
 245 250 255
 Gly Ala Phe Thr Val Val Lys Ala Gln Leu Met Ser Gly Ala Asn Ser
 260 265 270
 Ser Glu Arg Val Asp Glu Asp Val Asn Ala Asp Ile His Ile Pro Leu
 275 280 285
 Leu Leu Lys Ala Ile Glu Arg Gly Ala Ala Ala Phe Gly Pro Asn Ala
 290 295 300
 Ser Ile Gly Gln Asn Ser Ala Lys Ala Phe Leu Ala Ser Cys Ala Pro
 305 310 315 320
 Lys Ile Thr Ser Asn Asp Asp Val Leu Ser Glu Phe Ile Asn Gln Lys
 325 330 335
 Leu Lys Gly Asp Asp Asp Leu Gln Val Arg Leu Gly Ala Gln Glu Leu
 340 345 350
 Leu His Val Ala Thr Lys Lys Glu Phe Gln Leu Gly Gly Leu Ala Gly
 355 360 365
 Ser Ile Gly Val Ser Ser Ile Leu Gly Ser Ala Trp Glu Leu Gly Ala
 370 375 380
 Ser Glu Leu Leu Lys Asn Ala Ile Phe Gly Lys Asn Phe Ser Pro Ser
 385 390 395 400
 Gln Tyr Ala Leu Gln Leu Ala Gly Ile Asp Ser Val Pro Pro Leu Ile
 405 410 415
 Ile Glu Ser Met Asp Thr Met Cys Val Leu Ala Ile Ile Lys Gly Met
 420 425 430
 Lys Gly Glu Glu Trp Ser Met Ser Asp Leu Leu Pro Lys Ala Leu Lys
 435 440 445
 Ala Gly Ala Ile Ser Ser Val Val Ser Phe Pro Asn Asn Val Leu Gln
 450 455 460
 Tyr Ala Gly Phe Lys Ser Arg Val Gly Asp Leu Ala Ala Asn Ser Val
 465 470 475 480
 Thr Thr Glu Ala Ala Ile Phe Gly Ala Ala Ser Gly Ile Pro Pro Glu
 485 490 495

-continued

Val Lys Glu Ser Glu Glu Leu Met Arg Ala Gly Leu Phe Gln Ser Met
 500 505 510
 Lys Asp Gly Val Met Ala His Ser Gly Glu Gly Val Asp Thr Lys Lys
 515 520 525
 Thr Ile Glu Arg Met Thr Arg His Ala Leu Asp Ile Ala Pro Gly Glu
 530 535 540
 Ser Thr Ala Val Lys Ser Met Gly Leu Ala Ser Ile Val Gly Met Ile
 545 550 555 560
 Pro Leu Ile Ala Ser Asn Lys Ala Thr Gly Leu Leu Ser Glu Gln Val
 565 570 575
 Leu Arg Ile Phe Arg Ser Ala Val Phe Asn Pro Ile Glu Ala Ile Ala
 580 585 590
 Leu Asn Ala Leu Ala Leu Gly Gly Arg Val Asn Val Pro Gly Leu Phe
 595 600 605
 Asp Ser Asp Asn Ala Lys His Ala Arg Val Val Gln Thr Ile Leu Ala
 610 615 620
 Arg Ala Ser Gln His Met Glu Ala Gly Asp Arg Asp Ile Ser Ala Glu
 625 630 635 640
 Glu Leu His Gln Met Leu Ala Pro Arg Ser Glu Phe Leu Arg His Val
 645 650 655
 Gly Ser Ala Ile Val Asn Gly Met Asn Ala Ser Phe Glu Ala Ile Pro
 660 665 670
 Ala Leu Val Arg Lys Leu Gly Tyr Gly Glu Ala Pro Leu Ala Glu Arg
 675 680 685
 Ile Pro Tyr Gln Asp Leu Ala Val Pro Asp Thr Ser Arg Gln Pro Ala
 690 695 700
 Pro
 705

HopPtoD1 has been shown to be a secreted protein that is expressed by DC3000.

A sixth nucleic acid molecule is another homolog of ⁴⁰avrPphD of *Pseudomonas syringae* pv. *phaseolicola* and has a nucleotide sequence according to SEQ ID No: 11 as follows:

atgaatcccc tgcaacctat tcagcacagc attacaaatt cccaaatgag tgggtggtcag 60
 caattagagg cggagggtc tcaggccac aattcctatt cccatcctga caggatttcg 120
 ctttcccaat tgagccaaag cgctcaccta gctctagatc acctttcaac tcagcctaata 180
 accgatcacc aacgcgttgc atcactggta cgcaacgctg tgcaggacgg taagttccaa 240
 ctccaatcca gtaacgacac gcaagtaacc tataaaactt cagtctgtcc gccagctaac 300
 gccgacacca tgggggccgc cacttaatt aataacgagc tgacggttca ggcccgatta 360
 aatgatcaac ttgagtacga catcgtcagc gctcatttgt atggcccttc ggaagccata 420
 tccatcgatg catccagtcc tccctoggcc aacgatctag cgtcctctgg cttgagcgaa 480
 cgtacgcacc taggtatgaa tcgtgtcctc ttacgctacg cggtgccccc tcgggaaacc 540
 gaagaccaat gtgttatggt gatcgacaaa atgccccccc ccaaacacgg caaaatgtct 600
 ttcttcgta cactaatga cttgagcaaa ctgcctttgg gaatggagac gggcgggttg 660
 tccgacctga aattggctgg ttgtgaacgt atttcttccg tcgagcaggt gaagagtatc 720
 cgcgacgccc ttggaggcgg gccgctcacc gtactagatc tgcgcaaga atctcatgcg 780

-continued

```

attgtcaacg gtttgctat caccttacgt ggcccgatgg attgggcca cgcgcgcta 840
tcccaggttg acggagcgcg acgtgaaagt gccatgatta cagaactgaa gcgcactaag 900
tctttaacgt tggtcgatgc caattatgta aaaggtaaaa aaagtaatcc tcaaacgaca 960
gaactgaaaa atttgaatgt ccggagcgcg cgagaagtcg ttacagaggc cggcgcgacc 1020
tatcgccgcg tggccattac cgaccataac aggcctagtc cggaagcgcg cgacgagcta 1080
gtagacatca tgcgccactg cctgcaggca aatgagtcgc tagttgtgca ctgtaacggc 1140
ggtcggggcc gtactaccac ggctatgata atggtcgcga tgcttaagaa cgctcgtaac 1200
cattccgcag aaacctcat cagcgcgatg gccaaagctaa gctatgacta caacatgacg 1260
gatctaggca gcatttctgc actcaagcgg ccattcctag aggcagactt aaaatttctg 1320
caggcctttc acgactatgc ccgcaacaac ccaagcggat tatctcttaa ttggacacag 1380
tggcgcgcaa aatagcgtt agaatga 1407

```

The encoded protein, originally designated AvrPphD2_{Pto} and now renamed HopPtoD2, has an amino acid sequence according to SEQ ID No: 12 as follows:

```

Met Asn Pro Leu Gln Pro Ile Gln His Ser Ile Thr Asn Ser Gln Met
 1           5           10           15
Ser Gly Gly Gln Gln Leu Glu Ala Glu Gly Ser Gln Ala His Asn Ser
 20           25           30
Tyr Her His Pro Asp Arg Ile Ser Leu Ser Gln Leu Ser Gln Ser Ala
 35           40           45
His Leu Ala Leu Asp His Leu Her Thr Gln Pro Asn Thr Asp His Gln
 50           55           60
Arg Val Ala Ser Leu Val Arg Asn Ala Val Gln Asp Gly Lys Phe Gln
 65           70           75           80
Leu Gln Ser Ser Asn Asp Thr Gln Val Thr Tyr Lys Thr Ser Val Cys
 85           90           95
Pro Pro Ala Asn Ala Asp Thr Met Gly Ala Ala His Leu Ile Asn Asn
100           105           110
Glu Leu Thr Val Gln Ala Arg Leu Asn Asp Gln Leu Glu Tyr Asp Ile
115           120           125
Val Ser Ala His Leu Tyr Gly Pro Ser Glu Ala Ile Ser Ile Asp Ala
130           135           140
Ser Ser Pro Pro Ser Ala Asn Asp Leu Ala Ser Ser Gly Len Ser Glu
145           150           155           160
Arg Thr His Leu Gly Met Asn Arg Val Leu Leu Arg Tyr Ala Val Pro
165           170           175
Pro Arg Glu Thr Glu Asp Gln Cys Val Met Val Ile Asp Lys Met Pro
180           185           190
Pro Pro Lys His Gly Lys Met Ser Phe Phe Arg Thr Thr Asn Asp Leu
195           200           205
Ser Lys Leu Pro Leu Gly Met Glu Thr Gly Gly Leu Ser Asp Leu Lys
210           215           220
Leu Ala Gly Cys Glu Arg Ile Ser Ser Val Glu Gln Val Lys Ser Ile
225           230           235           240
Arg Ala Ala Leu Gly Gly Gly Pro Leu Thr Val Leu Asp Leu Arg Glu
245           250           255

```

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Glu Ser His Ala Ile Val Asn Gly Leu Pro Ile Thr Leu Arg Gly Pro
 260 265 270

Met Asp Trp Ala Asn Ala Gly Leu Ser Gln Val Asp Gly Ala Ala Arg
 275 280 285

Glu Ser Ala Met Ile Thr Glu Leu Lys Arg Thr Lys Ser Leu Thr Leu
 290 295 300

Val Asp Ala Asn Tyr Val Lys Gly Lys Lys Ser Asn Pro Gln Thr Thr
 305 310 315 320

Glu Leu Lys Asn Leu Asn Val Arg Ser Glu Arg Glu Val Val Thr Glu
 325 330 335

Ala Gly Ala Thr Tyr Arg Arg Val Ala Ile Thr Asp His Asn Arg Pro
 340 345 350

Ser Pro Glu Ala Thr Asp Glu Leu Val Asp Ile Met Arg His Cys Leu
 355 360 365

Gln Ala Asn Glu Ser Leu Val Val His Cys Asn Gly Gly Arg Gly Arg
 370 375 380

Thr Thr Thr Ala Met Ile Met Val Asp Met Leu Lys Asn Ala Arg Asn
 385 390 395 400

His Ser Ala Glu Thr Leu Ile Thr Arg Met Ala Lys Leu Ser Tyr Asp
 405 410 415

Tyr Asn Met Thr Asp Leu Gly Ser Ile Ser Ala Leu Lys Arg Pro Phe
 420 425 430

Leu Glu Asp Arg Leu Lys Phe Leu Gln Ala Phe His Asp Tyr Ala Arg
 435 440 445

Asn Asn Pro Ser Gly Leu Ser Leu Asn Trp Thr Gln Trp Arg Ala Lys
 450 455 460

Ile Ala Leu Glu
 465

HopPtoD2 has been shown to be a secreted protein that is expressed by DC3000.

A seventh nucleic acid molecule is a homolog of avrP-piC2 of *Pseudomonas syringae* pv. *lisi* and has a nucleotide⁴⁰ sequence according to SEQ ID No: 13 as follows:

```

atgacaatcg tgtctggaca catcggaaaa cacccaagcc taaccactgt tcaagctggg 60
tcttcggctt cggctcgagaa tcaaatgcct gatcctgcac agttcagtga tggacgggtg 120
aaaaagcttc cgaccaatg gtcgtcaatt acattggcga gattcgatca ggatatttgc 180
acqaataatc atggcatcag tcagcgtgca atgtgctttg gcctttcatt gagctggatt 240
aacatgattc atgccgggaa agatcatggt acgccctatg catcggcaga aagaatgagg 300
ttctggggtt cttttgaagg ggtggtgcat gctcgtactg ttcataactt ctatcggact 360
gagcacaat tctgatgga gcaagcttcc gcaaaccccg gagtatcaag tggcgcgatg 420
gctggcacag aaagtttatt gcaagctgct gagttgaagg ggttaaagct tcaacctggt 480
ctagaggaca agtcgaactc aggcctaccc ttcctaattg cgtgtaagca gtcagggcgg 540
caggtgagca cagatgaagc tgcgctaagc tccttatgtg atgcaattgt agaaaataag 600
agaggggtaa tgggtgatata cagccaagaa attgcccacg ctttgggctt ttctgtatca 660
tcagatggca aaagagcgac cttatttggat cccaatctcg gagagtttca tacacactcg 720
aaagcgttgg ctgatactat cgaaaacata tcatcggcag atgggctgcc tttaatcggc 780
gttcaagtat tcgcttcaaa aatacactga 810
    
```

The encoded protein, originally designated AvrPpiC_{2Pto} and now renamed HopPtoC, has an amino acid sequence according to SEQ ID No: 14 as follows:

```

Met Thr Ile Val Ser Gly His Ile Gly Lys His Pro Ser Leu Thr Thr
  1           5           10           15
Val Gln Ala Gly Ser Ser Ala Ser Val Glu Asn Gln Met Pro Asp Pro
           20           25           30
Ala Gln Phe Ser Asp Gly Arg Trp Lys Lys Leu Pro Thr Gln Leu Ser
  35           40           45
Ser Ile Thr Leu Ala Arg Phe Asp Gln Asp Ile Cys Thr Asn Asn His
  50           55           60
Gly Ile Ser Gln Arg Ala Met Cys Phe Gly Leu Ser Leu Ser Trp Ile
  65           70           75           80
Asn Met Ile His Ala Gly Lys Asp His Val Thr Pro Tyr Ala Ser Ala
           85           90           95
Glu Arg Met Arg Phe Leu Gly Ser Phe Glu Gly Val Val His Ala Arg
  100          105          110
Thr Val His Asn Phe Tyr Arg Thr Glu His Lys Phe Leu Met Glu Gln
  115          120          125
Ala Ser Ala Asn Pro Gly Val Ser Ser Gly Ala Met Ala Gly Thr Glu
  130          135          140
Ser Leu Leu Gln Ala Ala Glu Leu Lys Gly Leu Lys Leu Gln Pro Val
  145          150          155          160
Leu Glu Asp Lys Ser Asn Ser Gly Leu Pro Phe Leu Ile Ala Cys Lys
  165          170          175
Gln Ser Gly Arg Gln Val Ser Thr Asp Glu Ala Ala Leu Ser Ser Leu
  180          185          190
Cys Asp Ala Ile Val Glu Asn Lys Arg Gly Val Met Val Ile Tyr Ser
  195          200          205
Gln Glu Ile Ala His Ala Leu Gly Phe Ser Val Ser Ser Asp Gly Lys
  210          215          220
Arg Ala Thr Leu Phe Asp Pro Asn Leu Gly Glu Phe His Thr His Ser
  225          230          235          240
Lys Ala Leu Ala Asp Thr Ile Glu Asn Ile Ser Ser Ala Asp Gly Leu
  245          250          255
Pro Leu Ile Gly Val Gln Val Phe Ala Ser Lys Ile His
  260          265

```

HopPtoC has been shown to be a secreted protein that is expressed by DC3000.

An eighth nucleic acid molecule is a homolog of avrP- 50 piB1 of *Pseudomonas syringae* pv. *pisii* and has a nucleotide sequence according to SEQ ID No: 15 as follows:

```

atgcacgcaa atcctttaag ctctttcaac agagctcaac atggcaatct gactaatgta 60
gaggccagcc aagttaaatc ggcaggaacc tcttccacca ctaatataga cagtaaaaac 120
attgaagaac atggttcaga cagactcagt gatttaggca gacctgatgg tggatggttt 180
ttcgagaagt cacttggcac cttgaaaaat ttaaactctg agcagttagc cggaatccat 240
gatgtactaa aattaacaga tggcgtaaag aacattgtct cttttggagc tcgggaagga 300
ggcttcgagt tgccaatgca gtttcgtcat gatttataca gatctcaaca tccggatgaa 360
aactcgccgc acgatgccgc aactcattat cttgatgcaa tcagcctgca atcaaacaaa 420

```


-continued

```

tttcaaaaac ttgaaaaact acaacatgta gatgtattta aaatgcaaaa cccgttttgg 480
gatgtcgggt acaaaaacgg aattgcgcac gcaaaaaaaa tggcattcct cataacgcca 540
gagtggctgg gttctgattt ctgtaaacag gaattccagt ggcttagcga acaaaaaaac 600
aaagacataa aatctgcatt tgtgatcttt aaagatgtag acttaaaaag caaaaatatg 660
acaagtatct tcaattttgc agacttccat aaatcacgcy tcatgatggc aagcacacct 720
ccccgaatcg gattgaataa tgtaaaaatc gaaaatagcg ttgacctgaa tttcaagagg 780
ttattaactg accgtgagtc atgggaacta aataatttcc taggcgacta a          831

```

The encoded protein, designated AvrPpiB1_{Pto}, has an amino acid sequence according to SEQ ID No: 16 as follows:

```

Met His Ala Asn Pro Leu Ser Ser Phe Asn Arg Ala Gln His Gly Asn
  1          5          10          15
Leu Thr Asn Val Glu Ala Ser Gln Val Lys Ser Ala Gly Thr Ser Ser
          20          25          30
Thr Thr Asn Ile Asp Ser Lys Asn Ile Glu Glu His Val Ala Asp Arg
          35          40          45
Leu Ser Asp Leu Gly Arg Pro Asp Gly Gly Trp Phe Phe Glu Lys Ser
          50          55          60
Leu Gly Thr Leu Lys Asn Leu Asn Leu Glu Gln Leu Ala Gly Ile His
          65          70          75          80
Asp Val Leu Lys Leu Thr Asp Gly Val Lys Asn Ile Val Ser Phe Gly
          85          90          95
Ala Arg Glu Gly Gly Phe Glu Leu Ala Met Gln Phe Arg His Asp Leu
          100          105          110
Tyr Arg Ser Gln His Pro Asp Glu Asn Ser Pro His Asp Ala Ala Thr
          115          120          125
His Tyr Leu Asp Ala Ile Ser Leu Gln Ser Asn Lys Phe Thr Lys Leu
          130          135          140
Glu Lys Leu Gln His Val Asp Val Phe Lys Met Gln Asn Pro Phe Trp
          145          150          155          160
Asp Val Gly Tyr Lys Asn Gly Ile Ala His Ala Lys Lys Met Ala Phe
          165          170          175
Phe Ile Thr Pro Glu Trp Leu Gly Ser Asp Phe Cys Lys Gln Glu Phe
          180          185          190
Gln Trp Leu Ser Glu Thr Lys Asn Lys Asp Ile Lys Ser Ala Phe Val
          195          200          205
Ile Phe Lys Asp Val Asp Leu Lys Ser Lys Asn Met Thr Ser Ile Phe
          210          215          220
Asn Phe Ala Asp Phe His Lys Ser Arg Val Met Met Ala Ser Thr Pro
          225          230          235          240
Pro Glu Ser Gly Leu Asn Asn Val Lys Ile Glu Asn Ser Val Asp Leu
          245          250          255
Asn Phe Lys Arg Leu Leu Thr Asp Arg Glu Ser Trp Glu Leu Asn Asn
          260          265          270
Phe Leu Gly Asp
          275

```

AvrPpiB1_{Pto} has been shown to be expressed by DC3000. A second copy of AvrPpiB1_{Pto} is present in the genome of DC3000. This second copy is identical and has been designated AvrPpiB2_{Pto}. The *Pseudomonas syringae* pv. *pisii* AvrPpiB effector protein was demonstrated to effect the expression of a resistance mechanism governed by the R3 resistance locus of pea (Cournoyer et al., "Molecular characterization of the *Pseudomonas syringae* pv. *pisii* plasmid-

borne avirulence gene avrPpiB which matches the R3 resistance locus in pea," *Mol. Plant Microbe Interact.* 8(5): 700-708 (1995), which is hereby incorporated by reference in its entirety).

A ninth nucleic acid molecule is a homolog of avrXv3 of *Xanthomonas campestris* pv. *vesicatoria* and has a nucleotide sequence according to SEQ ID No: 17 as follows:

```

atggggctat gtatttcaaa acactctggt agcagttaca gctacagtga tagcgacggc 60
tggcaagtgc ctgcatgccc tccaaacgcc aggtctgtat ccagtcacaa aacagcatct 120
gcgagtgaca tcgcatcagg cgatgtggat gaacgtcctg caacgttttc tcattttcaa 180
cttgcgcggt gcggtggaga gtacacgctt agcatggttt ctgcagcggc ttatcaagca 240
gaaagacggc atcgcggtaa ttaataaaa gatcgtagt c aatccatact cccatggggtc 300
caggatatatc attctaaaaa aggtttggat tacagcttcc agatcgacag aactacgact 360
gttaaagtgg ctggattcaa ctgctctatc cccaataaca gagggactcg gcatttatac 420
agcgctggta cgagtcagac aaacatgcct gtcacgcag acaacatgag cgcatgcatt 480
gctgtcgcgt gtgcggcgga aaacgtggat gctggcacgg gtgaacgtag gccggggggcg 540
aaagttcgcg tattccatct actccctttt cgacgcgaag accttgtgcc agaagaagtt 600
ttagcttctg tgcgcgatta tctgcgaac accaaagaac aggggctaac aatgcgcgta 660
gctatgcatg gagggaatac agaggggtgat ttctcagtea gcaactgcga ggcattgaaa 720
ggcctgtttg ctaatgaagg gatcccgtt gaatttgacg agacctgtgc aaaccgaacg 780
tctgaaacac tgcttggtgc cgttatctta gatgacaact cgactcattt cataaaacat 840
ctggtcgcac aataa 855
    
```

35

The encoded protein, originally designated AvrXv3_{Pto} and now renamed HopPtoJ, has an amino acid sequence according to SEQ ID No: 18 as follows:

```

Met Gly Leu Cys Ile Ser Lys His Ser Gly Ser Ser Tyr Ser Tyr Ser
 1           5           10          15
Asp Ser Asp Arg Trp Gln Val Pro Ala Cys Pro Pro Asn Ala Arg Ser
          20          25          30
Val Ser Ser His Gln Thr Ala Ser Ala Ser Asp Ile Ala Ser Gly Asp
          35          40          45
Val Asp Glu Arg Pro Ala Thr Phe Ser His Phe Gln Leu Ala Arg Cys
          50          55          60
Gly Gly Glu Tyr Thr Leu Ser Met Val Ser Ala Ala Ala Tyr Gln Ala
          65          70          75          80
Glu Arg Arg His Arg Gly Asn Leu Ile Lys Asp Arg Ser Gln Ser Ile
          85          90          95
Leu Pro Trp Val Gln Val Tyr His Ser Lys Lys Gly Leu Asp Tyr Ser
          100         105         110
Phe Gln Ile Asp Arg Thr Thr Thr Val Lys Val Ala Gly Phe Asn Cys
          115         120         125
Ser Ile Pro Asn Asn Arg Gly Thr Arg His Leu Tyr Ser Ala Gly Thr
          130         135         140
Ser Gln Thr Asn Met Pro Val Ile Ala Asp Asn Met Ser Ala Cys Ile
          145         150         155         160
    
```

-continued

Ala Val Ala Cys Ala Ala Glu Asn Val Asp Ala Gly Thr Gly Glu Arg
 165 170 175
 Arg Pro Gly Ala Lys Val Arg Val Phe His Leu Leu Pro Phe Arg Arg
 180 185 190
 Glu Asp Leu Val Pro Glu Glu Val Leu Ala Ser Val Arg Asp Tyr Leu
 195 200 205
 Arg Thr Thr Lys Glu Gln Gly Leu Thr Met Arg Val Ala Met His Gly
 210 215 220
 Gly Asn Thr Glu Gly Asp Phe Ser Val Ser Thr Ala Gln Ala Leu Lys
 225 230 235 240
 Gly Leu Phe Ala Asn Glu Gly Ile Pro Leu Glu Phe Asp Glu Thr Cys
 245 250 255
 Ala Asn Arg Thr Ser Glu Thr Leu Leu Gly Ala Val Ile Leu Asp Asp
 260 265 270
 Asn Ser Thr His Phe Ile Lys His Leu Val Ala Gln
 275 280

HopPtoJ has been shown to be a secreted protein that is expressed by DC3000. As reported in Astua-Monge et al. ("Resistance of tomato and pepper to T3 strains of *Xanthomonas campestris* pv. *vesicatoria* is specified by a plant-inducible avirulence gene," *Mol. Plant Microbe Interact.* 13:911-921 (2000), which is hereby incorporated by reference in its entirety), it has been demonstrated that the *Xanthomonas campestris* AvrXv3 effector protein elicits a hypersensitive response in tomato NIL 216 and certain pepper genotypes, which suggests that AvrXv3 is like other

effectors in functioning inside plant cells. A uidA fusion enabled demonstration that the *avrXv3* gene is part of the Hrp regulon. A domain in the C terminus of AvrXv3 is possibly responsible for transcriptional activation activity in yeast. For these reasons, it is also believed that HopPtoJ possesses similar characteristics and properties.

A tenth nucleic acid molecule is a homolog of *hrmB* of *Pseudomonas syringae* pv. *syringae* and has a nucleotide sequence according to SEQ ID No: 19 as follows:

```
atgatcatcg acaatacgtt cgcgctgaca ctgtcatgcg attacgcgcg tgagcgcctg 60
ctgttgatcg gcttgcttga gccgcacaag gacatacctc agcagtgcct tttggctggc 120
gctctcaatc cgctcctcaa tgcaggccca ggcttggcc tggatgagaa aagcggcctg 180
tatcacgctg atcaaagcat ccctcgagaa aaactcagcg tgccgacgct caaacgcgaa 240
atggcaggtc tgctggagtg gatgaggggc tggcgcgaag caagccaata g 291
```

The encoded protein, believed to be a chaperone for the protein of SEQ ID No: 22, has an amino acid sequence according to SEQ ID No: 20 as follows:

```
Met Ile Ile Asp Asn Thr Phe Ala Leu Thr Leu Ser Cys Asp Tyr Ala
 1 5 10 15
Arg Glu Arg Leu Leu Leu Ile Gly Leu Leu Glu Pro His Lys Asp Ile
 20 25 30
Pro Gln Gln Cys Leu Leu Ala Gly Ala Leu Asn Pro Leu Leu Asn Ala
 35 40 45
Gly Pro Gly Leu Gly Leu Asp Glu Lys Her Gly Leu Tyr His Ala Tyr
 50 55 60
Gln Ser Ile Pro Arg Glu Lys Leu Ser Val Pro Thr Leu Lys Arg Glu
 65 70 75 80
Met Ala Gly Leu Leu Glu Trp Met Arg Gly Trp Arg Glu Ala Ser Gln
 85 90 95
```

An eleventh nucleic acid molecule is a homolog of hrmA (also known as hopPsyA) of *Pseudomonas syringae* pv. *syringae* and has a nucleotide sequence according to SEQ ID No: 21 as follows:

```

atgaacccca ttcagtcacg cttctccagt gtgcaagagc tcagacgatc caacgttgat 60
attccggcgc tcaaagccaa tggccaactg gaggtcgcgc gcaagaggta cgagattcgt 120
gcagccgatg acggaacaat ttcggtcctt cgaccggagc aacaatccaa agcgaaaagt 180
tttttcaagg gcgcttccca gttgataggt ggcagcagcc agcgcgcgca gattgcccag 240
gcgctcaacg agaaggtcgc atcggcacgc actgtccttc accagagcgc tatgacgggc 300
ggacgcttgg acacccttga gcgggggcga agcagctcag ccacaacagc catcaaacc 360
actgcctaac aggtcgcgca aagtactttt aacagctttc atgagtgggc caaacaggca 420
gaggcgatgc gaaaccgcgc tcgaatggat atctacaaga tctataaaca agatgcacct 480
cactcacacc ccatgagcga cgagcagcaa gaagagtcc tgacacgct aaaggcattg 540
aatggcaaaa acggcattga ggtgcgcact caggaccagc acagcgcgca aaataaaaa 600
gaccgcaacc tggacaagta catcgcagag agcccggatg caaagagggt tttctatcga 660
attatcccca aacatgagcg ccgagaagat aagaatcaag ggcgattgac cattggcgtg 720
caaccccaat atgcaacaca gttgaccgc gccatggcaa ccctgatagc gaaggaaagt 780
gcaatcacgc atggcaaaat aataggcccc gcctgccacg gccaatgac cgattcggca 840
gtttgtata tcaacggtga tgttgcaaag gcagaaaagc tgggcgagaa actgaaacag 900
atgagcggca ttcctctgga tgcgttcgtt gagcacaccc ctttgagcat gcaatccctg 960
agtaaaggtc tgcctatgc agaaagcgc ctgggcgaca ccagaggcca tgggatgtcg 1020
cgagcggaag tgatcagcga tgccttgagg atggacggga tgccatttct ggccagattg 1080
aagctatcac tgtctgcca tggctatgac ccggacaacc cggcccttcg aaacacgaaa 1140
tga 1143

```

The encoded protein, designated HopPsyA_{Flv}, has an amino⁴⁰ acid sequence according to SEQ ID No: 22 as follows:

```

Met Asn Pro Ile Gln Ser Arg Phe Ser Ser Val Gln Glu Leu Arg Arg
  1           5           10          15
Ser Asn Val Asp Ile Pro Ala Leu Lys Ala Asn Gly Gln Leu Glu Val
          20          25          30
Asp Gly Lys Arg Tyr Glu Ile Arg Ala Ala Asp Asp Gly Thr Ile Ser
          35          40          45
Val Leu Arg Pro Glu Gln Gln Ser Lys Ala Lys Ser Phe Phe Lys Gly
          50          55          60
Ala Ser Gln Leu Ile Gly Gly Ser Ser Gln Arg Ala Gln Ile Ala Gln
          65          70          75          80
Ala Leu Asn Glu Lys Val Ala Ser Ala Arg Thr Val Leu His Gln Ser
          85          90          95
Ala Met Thr Gly Gly Arg Leu Asp Thr Leu Glu Arg Gly Glu Ser Ser
          100         105         110
Ser Ala Thr Thr Ala Ile Lys Pro Thr Ala Lys Gln Ala Ala Gln Ser
          115         120         125
Thr Phe Asn Ser Phe His Glu Trp Ala Lys Gln Ala Glu Ala Met Arg
          130         135         140

```

-continued

Asn Pro Ser Arg Met Asp Ile Tyr Lys Ile Tyr Lys Gln Asp Ala Pro
 145 150 155 160
 His Ser His Pro Met Ser Asp Glu Gln Gln Glu Glu Phe Leu His Thr
 165 170 175
 Leu Lys Ala Leu Asn Gly Lys Asn Gly Ile Glu Val Arg Thr Gln Asp
 180 185 190
 His Asp Ser Val Arg Asn Lys Lys Asp Arg Asn Leu Asp Lys Tyr Ile
 195 200 205
 Ala Glu Ser Pro Asp Ala Lys Arg Phe Phe Tyr Arg Ile Ile Pro Lys
 210 215 220
 His Glu Arg Arg Glu Asp Lys Asn Gln Gly Arg Leu Thr Ile Gly Val
 225 230 235 240
 Gln Pro Gln Tyr Ala Thr Gln Leu Thr Arg Ala Met Ala Thr Leu Ile
 245 250 255
 Gly Lys Glu Ser Ala Ile Thr His Gly Lys Val Ile Gly Pro Ala Cys
 260 265 270
 His Gly Gln Met Thr Asp Ser Ala Val Leu Tyr Ile Asn Gly Asp Val
 275 280 285
 Ala Lys Ala Glu Lys Leu Gly Glu Lys Leu Lys Gln Met Ser Gly Ile
 290 295 300
 Pro Leu Asp Ala Phe Val Glu His Thr Pro Leu Ser Met Gln Ser Leu
 305 310 315 320
 Ser Lys Gly Leu Ser Tyr Ala Glu Ser Ile Leu Gly Asp Thr Arg Gly
 325 330 335
 His Gly Met Ser Arg Ala Glu Val Ile Ser Asp Ala Leu Arg Met Asp
 340 345 350
 Gly Met Pro Phe Leu Ala Arg Leu Lys Leu Ser Leu Ser Ala Asn Gly
 355 360 365
 Tyr Asp Pro Asp Asn Pro Ala Leu Arg Asn Thr Lys
 370 375 380

HopPsyA_{Pto} has been shown to be a secreted protein that is expressed by DC3000. It has been shown that HopPsyA is characterized by cytotoxicity when expressed recombinantly in eukaryotes (i.e., in plants and yeast), and further that HopPsyA is capable of altering metabolic (e.g., Mad2) pathways in targeted cells (see PCT Application Publication No. WO 01/75066 to Collmer et al., published Oct. 11, 2001, which is hereby incorporated by reference in its entirety). Moreover, it has been shown that HopPsyA (HrmA) can be used to effect enhanced resistance to bacterial, fungal, and

viral pathogens upon recombinant expression thereof in plants (U.S. Pat. No. 6,342,654 to Li et al., which is hereby incorporated by reference in its entirety). Based on its shared amino acid identity of about 52% when compared to HopPsyA, it is believed that HopPsyA_{Pto} possesses these same characteristics.

A twelfth nucleic acid molecule is hopPtoB2, a homolog of hopB of *Pseudomonas syringae* pv. *syringae* DC3000, and has a nucleotide sequence according to SEQ ID No: 23 as follows:

```

gtgccgcgta tcgtcgccgg ccatgcagaa ggcgtgtgcg tggccaacgg ccggcaactat 60
gtcgaagtgt ccggtagaac ctttcaagtc cattacgaca cacatctgcy cggtggcag 120
attgtcgatc cagaaaaccc gttcgccctt tttggccagc agccgggtgcy cctagatgaa 180
caggggcaat ggcagcttgt cgcccgtcga cgtctgcytg gcgggtggcgt aggtgactcc 240
agccatgccc acctgcccga agaaacaccg ggctccagca caggctcgat tccgagcgcac 300
tacgaaatgc cggccgcat gcaggcaggc cttgatgtcg tgttgagcaa caagccctac 360
gacccgaccg ggattggcat ggagtcttac tttgagagct atttcgtgga tctgcytcag 420
agttttgtgg cgcgcagggg aaagctttat gaggatgccc ggacattttt cgccggtttt 480
tctccgccgc caaagccgca attgcctccg ctggcgcac ctgttgccat cgacaccctg 540
    
```

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attgaacacg tcttcgcgca gggtaacggc ctggttttga gtgaagcacc gaagtcggtc 600
 gccagcaaac ggctgctggt actcaacatg cgcctgctgg ccgaacagcg tgtcaagatt 660
 ctgtatatcg agcacctgct gaccgacaag cacctgtcta aactggccag gtatcgtcaa 720
 ctgggcaaaa agagccgctc aggctcgac gaactcaagc attacctgca cgatctcaac 780
 cgcgggacgc tgaacaattc cagcaaccgac tacgactatt accacctcat caaggcagcg 840
 catcgctatg gtatcgaggt gcgacggtc agctcgtcga tcagctaccc gtttctggac 900
 catccggtat tgagcgcagc caacgacacg actgcagtac aaaaaatgag caattttttc 960
 ggccatacgc tcatcagcag cgatgtcgca tccgcgccga caaaacgctg ggttgccctg 1020
 ctcgaccaga agctggccac gaccacgac ggggtattag gcattgccga aatgcagggc 1080
 gtggtcagtg tgcattgccc cgacatcccg gcaggccggc cgacgcgcat cactaaaggc 1140
 acaggcgaac tgccacgcga gggcacgcag gcccgctgcg acttcacgat tgcgttttcc 1200
 gatccgacgc tgattgtgcc ccaggcgcct caccgcacg gtaccaaact ggacgacatg 1260
 ctgctcagag aactgagggg ccaatctgcc ggtgccgggg gcgaacgctg gcccgccag 1320
 tacgattca tccgtgacga ggacgggtgcc tggcgggtgga tcgcgctga ggaactggcc 1380
 gcagacagcc cgatgacggc aatccagcaa tccctgaccg accctgtcta tgagatgcca 1440
 ctggacactc gaacaacgct tcatacgtg gcgaacttcg aaagaagggg gctcgacatg 1500
 gagtatttct ttgaagaaaag ccagtacgaa actgttcgca acgtattcgc cctgcaccgc 1560
 aaaaagctgc aacaggatgc ggccttgatc agcgtgtac agttgccgc tcgtccgacg 1620
 atgccggccg tcaaccctcg gacgaccacg gcgcagctgt ttgaaacgct gtaccagcac 1680
 accgatggca tcgtgatcgg cgagtgcgat ttttcggtcg ccagcaagaa aatgatcatc 1740
 gacaacctgc cgttgctgtc gcagcaaac gtacgaacgc tgtacatgga gcaactgttc 1800
 accgacttgc atcaggcgga tctggatcgc tttttcgaaa cagggcaaat gagcaaaccc 1860
 ctgcttcacg acctgaaagt gctggatcgg ggccatcgca ccgaccggga caaggtttac 1920
 acctttgagc aactggtcat caaggcgcag cagcacggca tggaaagtcg cgccatcgac 1980
 tgcgcagcca gctaccacct tagtggcctt gacaacgatg gttcaatcac ccgtcagcaa 2040
 atgatgaact actttcgctc gcgcaccctg gcgaggcac aggacgcat gggctcacac 2100
 aagtggatcg cgctggctcg caacagccat tccaatgtct atcaaggcgt cgtgcctggg 2160
 atcgccgagc tggaaagcgg catcggcctg cgggttatcg acgtggcacc ggggcagtcg 2220
 aagggtgtca tgcacgacct gggggagctg gtctcggcag acatctcgag aaccaaagta 2280
 cacatcaaa gcgattatcg agtggagata gaaataccgc gtgcgaagga tgccattcgg 2340
 ccacccagc ctgttaccct cgaacagcga ctggccagac cgggattggt tctggtgga 2400
 gagagtgag gcaatctgct gaccattgct caccgcgctc gcgacacctg gattcaccgc 2460
 acgccggtgc tggatcaatc cgagggcaag ctgtacctgg agcgcgtgcg ctggcccgcg 2520
 atccacctca aaccctttga tgacatggac gcgctggtag cggcgcctgga ggagatgaac 2580
 ctgacgcggg taggctga 2598

The encoded HopPtoB2 protein has an amino acid sequence according to SEQ ID No: 24 as follows:

```

Val Pro Arg Ile Val Ala Gly His Ala Glu Gly Val Cys Val Val Asn
 1           5           10           15
Gly Arg His Tyr Val Glu Leu Ser Gly Arg Thr Phe Gln Val His Tyr
 20           25           30
Asp Thr His Leu Arg Gly Trp Gln Ile Val Asp Pro Glu Asn Pro Phe
 35           40           45
Ala Phe Phe Gly Gln Gln Pro Val Arg Leu Asp Glu Gln Gly Gln Trp
 50           55           60
Gln Leu Val Ala Arg Arg Arg Leu Arg Gly Gly Gly Val Gly Asp Ser
 65           70           75           80
Ser His Ala His Leu Pro Glu Glu Thr Pro Gly Ser Ser Thr Gly Ser
 85           90           95
Ile Pro Ser Asp Tyr Glu Met Pro Ala Ala Met Gln Ala Gly Leu Asp
 100          105          110
Val Val Leu Ser Asn Lys Pro Tyr Asp Pro Thr Gly Ile Gly Met Glu
 115          120          125
Ser Tyr Phe Glu Ser Tyr Phe Val Asp Leu Arg Gln Ser Phe Val Ala
 130          135          140
Arg Arg Glu Lys Leu Tyr Glu Asp Ala Arg Thr Phe Phe Ala Gly Phe
 145          150          155          160
Ser Pro Pro Pro Lys Pro Gln Leu Pro Pro Leu Ala Pro Pro Val Ala
 165          170          175
Ile Asp Thr Leu Ile Glu His Val Phe Ala Gln Gly Asn Gly Leu Val
 180          185          190
Leu Ser Glu Ala Pro Lys Ser Val Ala Ser Lys Arg Leu Leu Leu Leu
 195          200          205
Asn Met Pro Leu Leu Ala Glu Gln Arg Val Lys Ile Leu Tyr Ile Glu
 210          215          220
His Leu Leu Thr Asp Lys His Leu Ser Lys Leu Ala Arg Tyr Arg Gln
 225          230          235          240
Leu Gly Lys Lys Ser Arg Ser Gly Ser His Glu Leu Lys His Tyr Leu
 245          250          255
His Asp Leu Asn Arg Gly Thr Leu Asn Asn Ser Ser Thr Asp Tyr Asp
 260          265          270
Tyr Tyr His Leu Ile Lys Ala Ala His Arg Tyr Gly Ile Glu Val Arg
 275          280          285
Pro Phe Ser Ser Ser Ile Ser Tyr Pro Phe Leu Asp His Pro Val Leu
 290          295          300
Ser Ala Ala Asn Asp Thr Thr Ala Val Gln Lys Met Ser Asn Phe Phe
 305          310          315          320
Gly His Thr Leu Ile Ser Ser Asp Val Ala Ser Ala Pro Thr Lys Arg
 325          330          335
Trp Val Ala Leu Leu Asp Gln Lys Leu Ala Thr Thr His Asp Gly Val
 340          345          350
Leu Gly Ile Ala Glu Met Gln Gly Val Val Ser Val His Val Arg Asp
 355          360          365
Ile Pro Ala Gly Arg Pro Thr Arg Ile Thr Lys Gly Thr Gly Glu Leu
 370          375          380
Pro Arg Glu Gly Thr Gln Ala Arg Cys Asp Phe Thr Ile Ala Phe Ser
 385          390          395          400

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-continued

Asp Pro Thr Leu Ile Val Pro Gln Ala Pro His Pro His Gly Thr Lys
 405 410 415
 Leu Asp Asp Met Leu Leu Arg Glu Leu Arg Gly Gln Ser Ala Gly Ala
 420 425 430
 Gly Gly Glu Arg Trp Ala Gly Gln Tyr Gly Phe Ile Arg Asp Glu Asp
 435 440 445
 Gly Ala Trp Arg Trp Ile Ala Pro Glu Asp Trp Pro Ala Asp Ser Pro
 450 455 460
 Met Thr Ala Ile Gln Gln Ser Leu Thr Asp Pro Val Tyr Glu Met Pro
 465 470 475 480
 Leu Asp Thr Arg Thr Thr Leu His Thr Leu Ala Asn Phe Glu Arg Arg
 485 490 495
 Gly Leu Asp Met Glu Tyr Phe Phe Glu Glu Ser Gln Tyr Glu Thr Val
 500 505 510
 Arg Asn Val Phe Ala Leu His Arg Lys Lys Leu Gln Gln Asp Ala Ala
 515 520 525
 Leu Ile Ser Ala Val Gln Leu Pro Pro Arg Pro Thr Met Pro Ala Val
 530 535 540
 Asn Pro Arg Thr Thr Thr Ala Gln Leu Phe Glu Thr Leu Tyr Gln His
 545 550 555 560
 Thr Asp Gly Ile Val Ile Gly Glu Ser His Phe Ser Val Ala Ser Lys
 565 570 575
 Lys Met Ile Ile Asp Asn Leu Pro Leu Leu Ser Gln Gln Asn Val Arg
 580 585 590
 Thr Leu Tyr Met Glu His Leu Leu Thr Asp Leu His Gln Ala Asp Leu
 595 600 605
 Asp Arg Phe Phe Glu Thr Gly Gln Met Ser Lys Thr Leu Leu His Asp
 610 615 620
 Leu Lys Val Leu Asp Arg Gly His Arg Thr Asp Pro Asp Lys Val Tyr
 625 630 635 640
 Thr Phe Glu Gln Leu Val Ile Lys Ala Gln Gln His Gly Met Glu Val
 645 650 655
 Arg Ala Ile Asp Cys Ala Ala Ser Tyr His Leu Ser Gly Leu Asp Asn
 660 665 670
 Asp Gly Ser Ile Thr Arg Gln Gln Met Met Asn Tyr Phe Ala Ser Arg
 675 680 685
 Thr Leu Arg Arg His Gln Asp Val Met Gly Ser His Lys Trp Ile Ala
 690 695 700
 Leu Val Gly Asn Ser His Ser Asn Val Tyr Gln Gly Val Val Pro Gly
 705 710 715 720
 Ile Ala Glu Leu Glu Gly Gly Ile Gly Leu Arg Val Ile Asp Val Ala
 725 730 735
 Pro Gly Gln Ser Lys Gly Val Met His Asp Leu Gly Glu Leu Val Ser
 740 745 750
 Ala Asp Ile Ser Arg Thr Lys Val His Ile Lys Gly Asp Tyr Arg Val
 755 760 765
 Glu Ile Glu Ile Pro Arg Ala Lys Asp Ala Ile Arg Pro Pro Gln Pro
 770 775 780
 Val Thr Leu Glu Gln Arg Leu Ala Arg Pro Gly Leu Phe Leu Val Glu
 785 790 795 800
 Glu Ser Glu Gly Asn Leu Leu Thr Ile Val His Arg Ala Arg Asp Thr
 805 810 815
 Trp Ile His Arg Thr Pro Val Leu Val Asn Ala Glu Gly Lys Leu Tyr
 820 825 830

-continued

Leu Glu Arg Val Arg Trp Pro Arg Ile His Leu Lys Pro Phe Asp Asp
 835 840 845

Met Asp Ala Leu Val Ala Ala Leu Glu Glu Met Asn Leu Thr Arg Val
 850 855 860

Gly
 865

HopPtoB2 has been shown to be a secreted protein that is expressed by DC3000.

Fragments of the above-identified proteins or polypeptides as well as fragments of full length proteins can also be used according to the present invention.

Suitable fragments can be produced by several means. Subclones of the gene encoding a known protein can be produced using conventional molecular genetic manipulation for subcloning gene fragments, such as described by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Springs Laboratory, Cold Springs Harbor, N.Y. (1989), and Ausubel et al. (ed.), *Current Protocols in Molecular Biology*, John Wiley & Sons (New York, N.Y.) (1999 and preceding editions), each of which is hereby incorporated by reference in its entirety. The subclones then are expressed in vitro or in vivo in bacterial cells to yield a smaller protein or polypeptide that can be tested for activity, e.g., as a product required for pathogen virulence.

In another approach, based on knowledge of the primary structure of the protein, fragments of the protein-coding gene may be synthesized using the PCR technique together with specific sets of primers chosen to represent particular portions of the protein. Erlich, H. A., et al., "Recent Advances in the Polymerase Chain Reaction," *Science* 252: 1643-51 (1991), which is hereby incorporated by reference. These can then be cloned into an appropriate vector for expression of a truncated protein or polypeptide from bacterial cells as described above.

As an alternative, fragments of a protein can be produced by digestion of a full-length protein with proteolytic enzymes like chymotrypsin or *Staphylococcus* proteinase A, or trypsin. Different proteolytic enzymes are likely to cleave different proteins at different sites based on the amino acid sequence of the particular protein. Some of the fragments that result from proteolysis may be active virulence proteins or polypeptides.

Chemical synthesis can also be used to make suitable fragments. Such a synthesis is carried out using known amino acid sequences for the polypeptide being produced. Alternatively, subjecting a full length protein to high temperatures and pressures will produce fragments. These fragments can then be separated by conventional procedures (e.g., chromatography, SDS-PAGE).

Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the properties, secondary structure and hydrophobic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which cotranslationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification, or identification of the polypeptide.

The proteins or polypeptides used in accordance with the present invention are preferably produced in purified form (preferably at least about 80%, more preferably 90%, pure)

by conventional techniques. Typically, the protein or polypeptide of the present invention is secreted into the growth medium of recombinant host cells (discussed infra). Alternatively, the protein or polypeptide of the present invention is produced but not secreted into growth medium. In such cases, to isolate the protein, the host cell (e.g., *E. coli*) carrying a recombinant plasmid is propagated, lysed by sonication, heat, or chemical treatment, and the homogenate is centrifuged to remove bacterial debris. The supernatant is then subjected to sequential ammonium sulfate precipitation. The fraction containing the protein or polypeptide of interest is subjected to gel filtration in an appropriately sized dextran or polyacrylamide column to separate the proteins. If necessary, the protein fraction may be further purified by HPLC.

Other DNA molecules encoding other effector proteins or polypeptides can also be identified by determining whether such DNA molecules hybridize under stringent conditions to a nucleic acid molecule as identified above. An example of suitable stringency conditions is when hybridization is carried out at a temperature of about 37° C. using a hybridization medium that includes 0.9× sodium citrate ("SSC") buffer, followed by washing with 0.2×SSC buffer at 37° C. Higher stringency can readily be attained by increasing the temperature for either hybridization or washing conditions or increasing the sodium concentration of the hybridization or wash medium. Nonspecific binding may also be controlled using any one of a number of known techniques such as, for example, blocking the membrane with protein-containing solutions, addition of heterologous RNA, DNA, and SDS to the hybridization buffer, and treatment with RNase. Wash conditions are typically performed at or below stringency. Exemplary high stringency conditions include carrying out hybridization at a temperature of about 42° C. up to and including about 65° C. for up to about 20 hours in a hybridization medium containing 1M NaCl, 50 mM Tris-HCl, pH 7.4, 10 mM EDTA, 0.1% sodium dodecyl sulfate (SDS), 0.2% ficoll, 0.2% polyvinylpyrrolidone, 0.2% bovine serum albumin, and 50 µg/ml *E. coli* DNA, followed by washing carried out at between about 42° C. to about 65° C. in a 0.2×SSC buffer.

The delivery of effector proteins or polypeptides can be achieved in several ways: (1) as a stable transgene; (2) transiently expressed via *Agrobacterium* or viral vectors; (3) delivered by the type III secretion systems of disarmed pathogens or recombinant nonpathogenic bacteria which express a functional, heterologous type III secretion system; or (4) delivered via topical application followed by TAT protein transduction domain-mediated spontaneous uptake into cells. Each of these is discussed infra.

The DNA molecule encoding the protein or polypeptide can be incorporated in cells using conventional recombinant DNA technology. Generally, this involves inserting the DNA molecule into an expression system to which the DNA molecule is heterologous (i.e. not normally present). The heterologous DNA molecule is inserted into the expression

system or vector in proper sense orientation and correct reading frame. The vector contains the necessary elements for the transcription and translation of the inserted protein-coding sequences.

U.S. Pat. No. 4,237,224 to Cohen and Boyer, which is hereby incorporated by reference in its entirety, describes the production of expression systems in the form of recombinant plasmids using restriction enzyme cleavage and ligation with DNA ligase. These recombinant plasmids are then introduced by means of transformation and replicated in unicellular cultures including prokaryotic organisms and eukaryotic cells grown in tissue culture.

Recombinant genes may also be introduced into viruses, such as vaccinia virus. Recombinant viruses can be generated by transfection of plasmids into cells infected with virus.

Suitable vectors include, but are not limited to, the following viral vectors such as lambda vector system gt11, gt WES.tB, Charon 4, and plasmid vectors such as pBR322, pBR325, pACYC177, pACYC1084, pUC8, pUC9, pUC18, pUC19, pLG339, pR290, pKC37, pKC101, SV 40, pBlue-script II SK +/- or KS +/- (see "Stratagene Cloning Systems" Catalog (1993) from Stratagene, La Jolla, Calif., which is hereby incorporated by reference), pQE, pIH821, pGEX, pET series (see F. W. Studier et. al., "Use of T7 RNA Polymerase to Direct Expression of Cloned Genes," *Gene Expression Technology* vol. 185 (1990), which is hereby incorporated by reference in its entirety), and any derivatives thereof. Recombinant molecules can be introduced into cells via transformation, particularly transduction, conjugation, mobilization, or electroporation. The DNA sequences are cloned into the vector using standard cloning procedures in the art, as described by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Springs Laboratory, Cold Springs Harbor, N.Y. (1989), which is hereby incorporated by reference in its entirety.

A variety of host-vector systems may be utilized to express the protein-encoding sequence(s). Primarily, the vector system must be compatible with the host cell used. Host-vector systems include but are not limited to the following: bacteria transformed with bacteriophage DNA, plasmid DNA, or cosmid DNA; microorganisms such as yeast containing yeast vectors; mammalian cell systems infected with virus (e.g., vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (e.g., baculovirus); and plant cells infected by bacteria. The expression elements of these vectors vary in their strength and specificities. Depending upon the host-vector system utilized, any one of a number of suitable transcription and translation elements can be used.

Different genetic signals and processing events control many levels of gene expression (e.g., DNA transcription and messenger RNA (mRNA) translation).

Transcription of DNA is dependent upon the presence of a promoter which is a DNA sequence that directs the binding of RNA polymerase and thereby promotes mRNA synthesis. The DNA sequences of eukaryotic promoters differ from those of prokaryotic promoters. Furthermore, eukaryotic promoters and accompanying genetic signals may not be recognized in or may not function in a prokaryotic system, and, further, prokaryotic promoters are not recognized and do not function in eukaryotic cells.

Similarly, translation of mRNA in prokaryotes depends upon the presence of the proper prokaryotic signals which differ from those of eukaryotes. Efficient translation of mRNA in prokaryotes requires a ribosome binding site called the Shine-Dalgarno ("SD") sequence on the mRNA. This sequence is a short nucleotide sequence of mRNA that

is located before the start codon, usually AUG, which encodes the amino-terminal methionine of the protein. The SD sequences are complementary to the 3'-end of the 16S rRNA (ribosomal RNA) and probably promote binding of mRNA to ribosomes by duplexing with the rRNA to allow correct positioning of the ribosome. For a review on maximizing gene expression, see Roberts and Lauer, *Methods in Enzymology*, 68:473 (1979), which is hereby incorporated by reference in its entirety.

Promoters vary in their "strength" (i.e. their ability to promote transcription). For the purposes of expressing a cloned gene, it is desirable to use strong promoters in order to obtain a high level of transcription and, hence, expression of the gene. Depending upon the host cell system utilized, any one of a number of suitable promoters may be used. For instance, when cloning in *E. coli*, its bacteriophages, or plasmids, promoters such as the T7 phage promoter, lac promoter, trp promoter, recA promoter, ribosomal RNA promoter, the P_R and P_L promoters of coliphage lambda and others, including but not limited, to lacUV5, ompF, bla, lpp, and the like, may be used to direct high levels of transcription of adjacent DNA segments. Additionally, a hybrid trp-lacUV5 (tac) promoter or other *E. coli* promoters produced by recombinant DNA or other synthetic DNA techniques may be used to provide for transcription of the inserted gene.

Bacterial host cell strains and expression vectors may be chosen which inhibit the action of the promoter unless specifically induced. In certain operations, the addition of specific inducers is necessary for efficient transcription of the inserted DNA. For example, the lac operon is induced by the addition of lactose or IPTG (isopropylthio-beta-D-galactoside). A variety of other operons, such as trp, pro, etc., are under different controls.

Specific initiation signals are also required for efficient gene transcription and translation in prokaryotic cells. These transcription and translation initiation signals may vary in "strength" as measured by the quantity of gene specific messenger RNA and protein synthesized, respectively. The DNA expression vector, which contains a promoter, may also contain any combination of various "strong" transcription and/or translation initiation signals. For instance, efficient translation in *E. coli* requires an SD sequence about 7-9 bases 5' to the initiation codon ("ATG") to provide a ribosome binding site. Thus, any SD-ATG combination that can be utilized by host cell ribosomes may be employed. Such combinations include but are not limited to the SD-ATG combination from the cro gene or the N gene of coliphage lambda, or from the *E. coli* tryptophan E, D, C, B or A genes. Additionally, any SD-ATG combination produced by recombinant DNA or other techniques involving incorporation of synthetic nucleotides may be used.

Once the isolated DNA molecule encoding the polypeptide or protein has been cloned into an expression system, it is ready to be incorporated into a host cell. Such incorporation can be carried out by the various forms of transformation noted above, depending upon the vector/host cell system. Suitable host cells include, but are not limited to, bacteria, virus, yeast, mammalian cells, insect, plant, and the like.

Because it is desirable for recombinant host cells to secrete the encoded protein or polypeptide, it is preferable that the host cell also possess a functional type III secretion system. The type III secretion system can be heterologous to host cell (Ham et al., "A Cloned *Erwinia chrysanthemi* Hrp (Type III Protein Secretion) System Functions in *Escherichia coli* to Deliver *Pseudomonas syringae* Avr Signals to

Plant Cells and Secrete Avr Proteins in Culture," *Microbiol.* 95:10206–10211 (1998), which is hereby incorporated by reference in its entirety) or the host cell can naturally possess a type III secretion system. Host cells which naturally contain a type III secretion system include many pathogenic Gram-negative bacterium, such as numerous *Erwinia* species, *Pseudomonas* species, *Xanthomonas* species, etc. Other type III secretion systems are known and still others are continually being identified. Pathogenic bacteria that can be utilized to deliver effector proteins or polypeptides are preferably disarmed according to known techniques, i.e., as described above. Alternatively, isolation of the effector protein or polypeptide from the host cell or growth medium can be carried out as described above.

Another aspect of the present invention relates to a transgenic plant which express a protein or polypeptide of the present invention and methods of making the same.

In order to express the DNA molecule in isolated plant cells or tissue or whole plants, a plant expressible promoter is needed. Any plant-expressible promoter can be utilized regardless of its origin, i.e., viral, bacterial, plant, etc. Without limitation, two suitable promoters include the nopaline synthase promoter (Fraley et al., *Proc. Natl. Acad. Sci. USA* 80:4803–4807 (1983), which is hereby incorporated by reference in its entirety) and the cauliflower mosaic virus 35S promoter (O'Dell et al., "Identification of DNA Sequences Required for Activity of the Cauliflower Mosaic Virus 35S Promoter," *Nature*, 313(6005):810–812 (1985), which is hereby incorporated by reference in its entirety). Both of these promoters yield constitutive expression of coding sequences under their regulatory control.

While constitutive expression is generally suitable for expression of the DNA molecule, it should be apparent to those of skill in the art that temporally or tissue regulated expression may also be desirable, in which case any regulated promoter can be selected to achieve the desired expression. Typically, the temporally or tissue regulated promoters will be used in connection with the DNA molecule that are expressed at only certain stages of development or only in certain tissues.

In some plants, it may also be desirable to use promoters which are responsive to pathogen infiltration or stress. For example, it may be desirable to limit expression of the protein or polypeptide in response to infection by a particular pathogen of the plant. One example of a pathogen-inducible promoter is the *gst1* promoter from potato, which is described in U.S. Pat. Nos. 5,750,874 and 5,723,760 to Strittmayer et al., each of which is hereby incorporated by reference in its entirety.

Expression of the DNA molecule in isolated plant cells or tissue or whole plants also requires appropriate transcription termination and polyadenylation of mRNA. Any 3' regulatory region suitable for use in plant cells or tissue can be operably linked to the first and second DNA molecules. A number of 3' regulatory regions are known to be operable in plants. Exemplary 3' regulatory regions include, without limitation, the nopaline synthase 3' regulatory region (Fraley, et al., "Expression of Bacterial Genes in Plant Cells," *Proc. Nat'l. Acad. Sci. USA*, 80:4803–4807 (1983), which is hereby incorporated by reference in its entirety) and the cauliflower mosaic virus 3' regulatory region (Odell, et al., "Identification of DNA Sequences Required for Activity of the Cauliflower Mosaic Virus 35S Promoter," *Nature*, 313 (6005):810–812 (1985), which is hereby incorporated by reference in its entirety).

The promoter and a 3' regulatory region can readily be ligated to the DNA molecule using well known molecular

cloning techniques described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Press, NY (1989), which is hereby incorporated by reference in its entirety.

One approach to transforming plant cells with a DNA molecule of the present invention is particle bombardment (also known as biolistic transformation) of the host cell. This can be accomplished in one of several ways. The first involves propelling inert or biologically active particles at cells. This technique is disclosed in U.S. Pat. Nos. 4,945,050, 5,036,006, and 5,100,792, all to Sanford, et al., each of which is hereby incorporated by reference in its entirety. Generally, this procedure involves propelling inert or biologically active particles at the cells under conditions effective to penetrate the outer surface of the cell and to be incorporated within the interior thereof. When inert particles are utilized, the vector can be introduced into the cell by coating the particles with the vector containing the heterologous DNA. Alternatively, the target cell can be surrounded by the vector so that the vector is carried into the cell by the wake of the particle. Biologically active particles (e.g., dried bacterial cells containing the vector and heterologous DNA) can also be propelled into plant cells. Other variations of particle bombardment, now known or hereafter developed, can also be used.

Another method of introducing the DNA molecule into plant cells is fusion of protoplasts with other entities, either minicells, cells, lysosomes, or other fusible lipid-surfaced bodies that contain the DNA molecule. Fraley, et al., *Proc. Natl. Acad. Sci. USA*, 79:1859–63 (1982), which is hereby incorporated by reference in its entirety.

The DNA molecule may also be introduced into the plant cells by electroporation. Fromm, et al., *Proc. Natl. Acad. Sci. USA*, 82:5824 (1985), which is hereby incorporated by reference in its entirety. In this technique, plant protoplasts are electroporated in the presence of plasmids containing the DNA molecule. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and regenerate.

Another method of introducing the DNA molecule into plant cells is to infect a plant cell with *Agrobacterium tumefaciens* or *Agrobacterium rhizogenes* previously transformed with the DNA molecule. Under appropriate conditions known in the art, the transformed plant cells are grown to form shoots or roots, and develop further into plants. Generally, this procedure involves inoculating the plant tissue with a suspension of bacteria and incubating the tissue for 48 to 72 hours on regeneration medium without antibiotics at 25–28° C.

Agrobacterium is a representative genus of the Gram-negative family Rhizobiaceae. Its species are responsible for crown gall (*A. tumefaciens*) and hairy root disease (*A. rhizogenes*). The plant cells in crown gall tumors and hairy roots are induced to produce amino acid derivatives known as opines, which are catabolized only by the bacteria. The bacterial genes responsible for expression of opines are a convenient source of control elements for chimeric expression cassettes. In addition, assaying for the presence of opines can be used to identify transformed tissue.

Heterologous genetic sequences such as a DNA molecule of the present invention can be introduced into appropriate plant cells by means of the Ti plasmid of *A. tumefaciens* or the Ri plasmid of *A. rhizogenes*. The Ti or Ri plasmid is transmitted to plant cells on infection by *Agrobacterium* and

is stably integrated into the plant genome. Schell, J., *Science*, 237:1176–83 (1987), which is hereby incorporated by reference in its entirety.

Plant tissue suitable for transformation include leaf tissue, root tissue, meristems, zygotic and somatic embryos, and anthers.

After transformation, the transformed plant cells can be selected and regenerated.

Preferably, transformed cells are first identified using, e.g., a selection marker simultaneously introduced into the host cells along with the DNA molecule of the present invention. Suitable selection markers include, without limitation, markers coding for antibiotic resistance, such as kanamycin resistance (Fraley, et al., *Proc. Natl. Acad. Sci. USA*, 80:4803–4807 (1983), which is hereby incorporated by reference in its entirety). A number of antibiotic-resistance markers are known in the art and other are continually being identified. Any known antibiotic-resistance marker can be used to transform and select transformed host cells in accordance with the present invention. Cells or tissues are grown on a selection media containing an antibiotic, whereby generally only those transformants expressing the antibiotic resistance marker continue to grow.

Once a recombinant plant cell or tissue has been obtained, it is possible to regenerate a full-grown plant therefrom. Thus, another aspect of the present invention relates to a transgenic plant that includes a DNA molecule of the present invention, wherein the promoter induces transcription of the first DNA molecule in response to infection of the plant by an oomycete. Preferably, the DNA molecule is stably inserted into the genome of the transgenic plant of the present invention.

Plant regeneration from cultured protoplasts is described in Evans, et al., *Handbook of Plant Cell Cultures Vol. 1*: (MacMillan Publishing Co., New York, 1983); and Vasil I. R. (ed.), *Cell Culture and Somatic Cell Genetics of Plants*, Acad. Press, Orlando, Vol. I, 1984, and Vol. III (1986), each of which is hereby incorporated by reference in their entirety.

It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to, all major species of rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, cauliflower, broccoli, turnip, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, and sugarcane.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts or a petri plate containing transformed explants is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced in the callus tissue. These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is usually reproducible and repeatable.

After the DNA molecule is stably incorporated in transgenic plants, it can be transferred to other plants by sexual crossing or by preparing cultivars. With respect to sexual crossing, any of a number of standard breeding techniques can be used depending upon the species to be crossed.

Cultivars can be propagated in accord with common agricultural procedures known to those in the field.

Diseases caused by the vast majority of bacterial pathogens result in limited lesions. That is, even when everything is working in the pathogen's favor (e.g., no triggering of the hypersensitive response because of R-gene detection of one of the effectors), the parasitic process still triggers defenses after a couple of days, which then stops the infection from spreading. Thus, the very same effectors that enable parasitism to proceed must also eventually trigger defenses. Therefore, premature expression of these effectors is believed to "turn on" plant defenses earlier (i.e., prior to infection) and make the plant resistant to either the specific bacteria from which the effector protein was obtained or many pathogens. An advantage of this approach is that it involves natural products and plants seem highly sensitive to pathogen effector proteins.

According to one embodiment, a transgenic plant is provided that contains a heterologous DNA molecule of the present invention. When the heterologous DNA molecule is expressed in the transgenic plant, plant defenses are activated, imparting disease resistance to the transgenic plant. The transgenic plant can also contain an R-gene whose product is activated by the protein or polypeptide product of the heterologous DNA molecule. The R gene can be naturally occurring in the plant or heterologously inserted therein. By disease resistance, it is believed that the effector proteins of the present invention can impart to plants resistance against bacterial, viral, and/or fungal diseases.

In addition to imparting disease resistance, it is believed that stimulation of plant defenses in transgenic plants of the present invention will also result in a simultaneous enhancement in growth and resistance to insects.

Alternative to transgenic expression is topical application of the effector proteins to plants. The embodiments of the present invention where the effector polypeptide or protein is applied to the plant can be carried out in a number of ways, including: 1) application of an isolated protein (or composition containing the same) or 2) application of bacteria which do not cause disease and are transformed with a gene encoding the effector protein of the present invention. In the latter embodiment, the effector protein can be applied to plants by applying bacteria containing the DNA molecule encoding the effector protein. Such bacteria are preferably capable of secreting or exporting the protein so that the protein can contact plant cells. In these embodiments, the protein is produced by the bacteria in planta.

Such topical application can be carried out using an effector-TAT protein, which will afford transduction domain-mediated spontaneous uptake of the effector protein into cells. Basically, this is carried out by fusing an 11-amino acid peptide (YGRKKRRQRRR, SEQ ID No: 25) by standard rDNA techniques to the N-terminus of the effector protein, and the resulting tagged protein is taken up into animal cells by a poorly understood process. This peptide is the protein transduction domain (PTD) of the human immunodeficiency virus (HIV) TAT protein (Schwarze et al., "Protein transduction: unrestricted delivery into all cells?" *Trends Cell Biol.* 10:290–295 (2000), which is hereby incorporated by reference in its entirety). Other PTDs are known and can be used for this purpose (Prochiantz, "Messenger proteins: homeoproteins, TAT and others," *Curr. Opin. Cell Biol.* 12:400–406 (2000), which is hereby incorporated by reference in its entirety). See PCT Application Publication No. WO 01/19393 to Collmer et al., which is hereby incorporated by reference in its entirety.

51

When the effector protein is topically applied to plants, it can be applied as a composition, which includes a carrier in the form, e.g., of water, aqueous solutions, slurries, or dry powders. In this embodiment, the composition contains greater than about 5 nM of the protein of the present invention.

Although not required, this composition may contain additional additives including fertilizer, insecticide, fungicide, nematocide, and mixtures thereof. Suitable fertilizers include $(\text{NH}_4)_2\text{NO}_3$. An example of a suitable insecticide is Malathion. Useful fungicides include Captan.

Other suitable additives include buffering agents, wetting agents, coating agents, and, in some instances, abrading agents. These materials can be used to facilitate the process of the present invention.

According to one embodiment, a transgenic plant including a heterologous DNA molecule of the present invention expresses one or more effector proteins, wherein the transgenic plant is capable of supporting growth of compatible nonpathogenic bacteria. The compatible nonpathogenic bacteria can be naturally occurring or it can be recombinant. Preferably, the nonpathogenic bacteria is recombinant and expresses one or more useful products. Thus, the transgenic plant becomes a green factory for producing desirable products. Desirable products include, without limitation, products that can enhance the nutritional quality of the plant or products that are desirable in isolated form. If desired in isolated form, the product can be isolated from plant tissues. To prevent competition between the non-pathogenic bacteria which express the desired product and those that do not, it is possible to tailor the needs of recombinant, non-pathogenic bacteria so that only they are capable of living in plant tissues expressing a particular effector protein or polypeptide of the present invention.

The effector proteins or polypeptides of the present invention are believed to alter the plant physiology by shifting metabolic pathways to benefit the parasite and by activating or suppressing cell death pathways. Thus, they may also provide useful tools for efficiently altering the nutrient content of plants and delaying or triggering senescence. There are agricultural applications for all of these possible effects.

Thus, a further aspect of the present invention relates more generally to a method of modifying a metabolic pathway in a cell by introducing into the cell an effector protein or polypeptide of the present invention which interacts with a native cellular protein involved in a metabolic pathway of the cell. As a result of introducing the protein or polypeptide into the cell, the protein or polypeptide modifies the metabolic pathway through its interaction with the native cellular protein. By way of example, the HopPsyA_{Pto} protein (SEQ ID No: 22) is believed to interact with Mad2.

Yet another aspect of the present invention relates to a method of causing eukaryotic cell death which is carried out by introducing into a eukaryotic cell a *Pseudomonas* protein which is cytotoxic and causes cell death. One preferred protein of the present invention is HopPsyA_{Pto} (SEQ ID No: 22), homolog of HopPsyA. The eukaryotic cell which is treated can be either in vitro or in vivo. When treating eukaryotic cells in vivo, a number of different protein- or DNA-delivery systems can be employed to introduce the effector protein into the target eukaryotic cell.

The protein- or DNA-delivery systems can be provided in the form of pharmaceutical compositions which include the delivery system in a pharmaceutically acceptable carrier, which may include suitable excipients or stabilizers. The dosage can be in solid or liquid form, such as powders,

52

solutions, suspensions, or emulsions. Typically, the composition will contain from about 0.01 to 99 percent, preferably from about 20 to 75 percent of active compound(s), together with the carrier, excipient, stabilizer, etc.

The compositions of the present invention are preferably administered in injectable or topically-applied dosages by solution or suspension of these materials in a physiologically acceptable diluent with a pharmaceutical carrier. Such carriers include sterile liquids, such as water and oils, with or without the addition of a surfactant and other pharmaceutically and physiologically acceptable carrier, including adjuvants, excipients or stabilizers. Illustrative oils are those of petroleum, animal, vegetable, or synthetic origin, for example, peanut oil, soybean oil, or mineral oil. In general, water, saline, aqueous dextrose and related sugar solution, and glycols, such as propylene glycol or polyethylene glycol, are preferred liquid carriers, particularly for injectable solutions.

Alternatively, the effector proteins can also be delivered via solution or suspension packaged in a pressurized aerosol container together with suitable propellants, for example, hydrocarbon propellants like propane, butane, or isobutane with conventional adjuvants. The materials of the present invention also may be administered in a non-pressurized form such as in a nebulizer or atomizer.

Depending upon the treatment being effected, the compounds of the present invention can be administered orally, topically, transdermally, parenterally, subcutaneously, intravenously, intramuscularly, intraperitoneally, by intranasal instillation, by intracavitary or intravesical instillation, intraocularly, intraarterially, intralesionally, or by application to mucous membranes, such as, that of the nose, throat, and bronchial tubes.

Compositions within the scope of this invention include all compositions wherein the compound of the present invention is contained in an amount effective to achieve its intended purpose. While individual needs vary, determination of optimal ranges of effective amounts of each component is within the skill of the art.

One approach for delivering an effector protein into cells involves the use of liposomes. Basically, this involves providing a liposome which includes that effector protein to be delivered, and then contacting the target cell with the liposome under conditions effective for delivery of the effector protein into the cell.

Liposomes are vesicles comprised of one or more concentrically ordered lipid bilayers which encapsulate an aqueous phase. They are normally not leaky, but can become leaky if a hole or pore occurs in the membrane, if the membrane is dissolved or degrades, or if the membrane temperature is increased to the phase transition temperature. Current methods of drug delivery via liposomes require that the liposome carrier ultimately become permeable and release the encapsulated drug at the target site. This can be accomplished, for example, in a passive manner wherein the liposome bilayer degrades over time through the action of various agents in the body. Every liposome composition will have a characteristic half-life in the circulation or at other sites in the body and, thus, by controlling the half-life of the liposome composition, the rate at which the bilayer degrades can be somewhat regulated.

In contrast to passive drug release, active drug release involves using an agent to induce a permeability change in the liposome vesicle. Liposome membranes can be constructed so that they become destabilized when the environment becomes acidic near the liposome membrane (see, e.g., *Proc. Natl. Acad. Sci. USA* 84:7851 (1987); *Biochemistry*

28:908 (1989), each of which is hereby incorporated by reference in their entirety). When liposomes are endocytosed by a target cell, for example, they can be routed to acidic endosomes which will destabilize the liposome and result in drug release.

Alternatively, the liposome membrane can be chemically modified such that an enzyme is placed as a coating on the membrane which slowly destabilizes the liposome. Since control of drug release depends on the concentration of enzyme initially placed in the membrane, there is no real effective way to modulate or alter drug release to achieve "on demand" drug delivery. The same problem exists for pH-sensitive liposomes in that as soon as the liposome vesicle comes into contact with a target cell, it will be engulfed and a drop in pH will lead to drug release.

This liposome delivery system can also be made to accumulate at a target organ, tissue, or cell via active targeting (e.g., by incorporating an antibody or hormone on the surface of the liposomal vehicle). This can be achieved according to known methods.

Different types of liposomes can be prepared according to Bangham et al., *J. Mol. Biol.* 13:238-252 (1965); U.S. Pat. No. 5,653,996 to Hsu et al.; U.S. Pat. No. 5,643,599 to Lee et al., U.S. Pat. No. 5,885,613 to Holland et al.; U.S. Pat. No. 5,631,237 to Dzau et al.; and U.S. Pat. No. 5,059,421 to Loughrey et al., each of which is hereby incorporated by reference in their entirety.

An alternative approach for delivery of effector proteins involves the conjugation of the desired effector protein to a polymer that is stabilized to avoid enzymatic degradation of the conjugated effector protein. Conjugated proteins or polypeptides of this type are described in U.S. Pat. No. 5,681,811 to Ekwuribe, which is hereby incorporated by reference in its entirety.

Yet another approach for delivery of proteins or polypeptides involves preparation of chimeric proteins according to U.S. Pat. No. 5,817,789 to Heartlein et al., which is hereby incorporated by reference in its entirety. The chimeric protein can include a ligand domain and, e.g., an effector protein of the present invention. The ligand domain is specific for receptors located on a target cell. Thus, when the chimeric protein is delivered intravenously or otherwise introduced into blood or lymph, the chimeric protein will adsorb to the targeted cell, and the targeted cell will internalize the chimeric protein, which allows the effector protein to destabilize the cell checkpoint control mechanism, affording its cytotoxic effects.

When it is desirable to achieve heterologous expression of an effector protein of the present invention in a target cell, DNA molecules encoding the desired effector protein can be delivered into the cell. Basically, this includes providing a nucleic acid molecule encoding the effector protein and then introducing the nucleic acid molecule into the cell under conditions effective to express the effector protein in the cell. Preferably, this is achieved by inserting the nucleic acid molecule into an expression vector before it is introduced into the cell.

When transforming mammalian cells for heterologous expression of an effector protein, an adenovirus vector can be employed. Adenovirus gene delivery vehicles can be readily prepared and utilized given the disclosure provided in Berkner, *Biotechniques* 6:616-627 (1988) and Rosenfeld et al., *Science* 252:431-434 (1991), WO 93/07283, WO 93/06223, and WO 93/07282, each of which is hereby incorporated by reference in their entirety. Adeno-associated viral gene delivery vehicles can be constructed and used to deliver a gene to cells. The use of adeno-associated viral

gene delivery vehicles in vitro is described in Chatterjee et al., *Science* 258:1485-1488 (1992); Walsh et al., *Proc. Nat'l Acad. Sci.* 89:7257-7261 (1992); Walsh et al., *J. Clin. Invest.* 94:1440-1448 (1994); Flotte et al., *J. Biol. Chem.* 268: 3781-3790 (1993); Ponnazhagan et al., *J. Exp. Med.* 179: 733-738 (1994); Miller et al., *Proc. Nat'l Acad. Sci.* 91:10183-10187 (1994); Einerhand et al., *Gene Ther.* 2:336-343 (1995); Luo et al., *Exp. Hematol.* 23:1261-1267 (1995); and Zhou et al., *Gene Ther.* 3:223-229 (1996), each of which is hereby incorporated by reference in their entirety. In vivo use of these vehicles is described in Flotte et al., *Proc. Nat'l Acad. Sci.* 90:10613-10617 (1993); and Kaplitt et al., *Nature Genet.* 8:148-153 (1994), each of which is hereby incorporated by reference in their entirety. Additional types of adenovirus vectors are described in U.S. Pat. No. 6,057,155 to Wickham et al.; U.S. Pat. No. 6,033,908 to Bout et al.; U.S. Pat. No. 6,001,557 to Wilson et al.; U.S. Pat. No. 5,994,132 to Chamberlain et al.; U.S. Pat. No. 5,981,225 to Kochanek et al.; and U.S. Pat. No. 5,885,808 to Spooner et al.; and U.S. Pat. No. 5,871,727 to Curiel, each of which is hereby incorporated by reference in their entirety).

Retroviral vectors which have been modified to form infective transformation systems can also be used to deliver nucleic acid encoding a desired effector protein into a target cell. One such type of retroviral vector is disclosed in U.S. Pat. No. 5,849,586 to Kriegler et al., which is hereby incorporated by reference in its entirety.

Regardless of the type of infective transformation system employed, it should be targeted for delivery of the nucleic acid to a specific cell type. For example, for delivery of the nucleic acid into tumor cells, a high titer of the infective transformation system can be injected directly within the tumor site so as to enhance the likelihood of tumor cell infection. The infected cells will then express the desired effector protein, thereby causing cytotoxic effects.

Particularly preferred is use of the effector proteins of the present invention to treat a cancerous condition (i.e., the eukaryotic cell which is affected is a cancer cell). This can be carried out by introducing or administering to a patient, a cytotoxic *Pseudomonas* protein under conditions effective to inhibit cancer cell division, thereby treating the cancer condition.

By introducing, it is intended that the effector protein is administered to the patient, preferably in the form of a composition which will target delivery to the cancer cells. Alternatively, when using DNA-based therapies, it is intended that the introducing be carried out by administering a targeted DNA delivery system to the patient such that the cancer cells are targeted and the effector protein is expressed therein. A number of known targeted delivery systems are known in the art and can be employed herewith.

EXAMPLES

The following Examples are intended to be illustrative and in no way are intended to limit the scope of the present invention.

Example 1

Detection of Protein Expression by *Pseudomonas syringae* pv. tomato DC3000

ORF-specific DNA fragments were amplified by PCR from DC3000 genomic DNA and printed onto amine-coated slides from Cell Associates (Houston). Each DNA sample

was printed three times on each slide with a BioRobotics (Boston) Microgrid II Arrayer by using MicroSpot2500 split pins. Slides were blocked according to the recommended protocol from Cell Associates. Of total RNA, 50–100 µg was used to synthesize cDNA probes for microarray analysis. RNA was mixed with 3 µg of random hexamers (Invitrogen) in a total volume of 15 µl and incubated at 65° C. for 10 min. Reactions were then placed on ice for 2 min, to which were added 3 µl of 1 mM FluoroLink Cy3- or Cy5-dUTP (Amersham Biosciences, Piscataway, N.J.), 3 µl of 0.1 M DTT, 6 µl of 5× first-strand buffer, 0.6 µl of 50×dNTPs mix (25 mM dATP, dCTP, dGTP/10 mM dTTP), and 2 µl of Superscript II (GIBCO/BRL). Reactions were incubated at room temperature for 10 min, followed by 42° C. for 110 min. RNA was hydrolyzed by adding 1.5 µl of 1 M NaOH at 65° C. for 10 min followed by neutralizing with 1.5 µl of 1 M HCl. cDNA probes were purified by using a PCR purification kit (Qiagen, Valencia, Calif.) and were resuspended in 20 µl of hybridization buffer (5×SSC, 0.1% SDS, and 25% formamide, where 1×SSC=0.15 M sodium chloride/0.015 M sodium citrate, pH 7). Denatured probes (99° C., 2 min) were hybridized to slides at 60° C. overnight in hybridization cassettes (Coming), after which slides were washed twice with 2×SSC, 0.1% SDS (60° C., 5 min), once with 2×SSC (room temperature, 5 min), and once with 0.2×SSC (room temperature, 5 min).

Microarray images were visualized by using a ScanArray 5000 (Packard), using laser and PMT settings of 100 and 90, respectively. Images were overlaid and quantified by using IMAGENE 4.1 software (BioDiscovery; Marina Del Rey, Calif.). Ratio data were extracted by using GENESIGHT 2.1 software (BioDiscovery). For these analyses, local background for each spot was corrected, and signals lower than 50 were flagged and eliminated. After flooring low signals to the value of 100, ratios of the overlaid images were calculated for individual spots. 16S rRNA was used and, to normalize the data, the 16S rRNA was expressed to similar levels in both tested strains based on RNA blots. Finally, all of the replicated data were combined, and mean ratio data and SDs were calculated for each ORF.

To corroborate the microarray results, RNA blotting was performed on 10 ORFs from similarly grown cultures. RNA blot analyses were performed as described (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Lab. Press, Plainview, N.Y.(1989), which is hereby incorporated by reference). Of each RNA sample, 25 µg was resolved on 1.2% formaldehyde-agarose gels and transferred to Nylon membranes (Hybond-N+) by capillary blotting using 20×SSC. transferred to Nylon membranes (Hybond-N+) by capillary blotting using 20×SSC. RNA was bound to the membrane by UV cross-linking. Probes were generated by PCR amplification from genomic DNA, using ORF-specific primers, and labeled with ³²P-dATP by random priming with a DECAprime II kit (Ambion). Hybridization was performed in 5×SSC, 50% formamide, 0.1% sodium-lauroylsarcosine, 0.02% SDS, and 2% blocking reagent (Roche Molecular Biochemicals) at 42° C. overnight. Membranes were then washed twice with 2×SSC/0.1% SDS for 15 min, twice with 1×SSC/0.1% SDS for 15 min, and once with 0.1×SSC/0.1% SDS for 15 min before exposure on a phosphor screen. Signals were detected and evaluated by using a Storm system (Molecular Dynamics) (FIG. 1).

The microarray experiments were in qualitative agreement with the RNA blot. These data indicate that Hrp promoter candidates with E values smaller (more significant) than 1e-4 are expressed at levels detected by the microarray and RNA blotting. However, within this group

there was no apparent relationship between the magnitude of the E value and the level of expression. Furthermore, one of 16 examined ORFs (see Fouts et al. (*Proc. Natl. Acad. Sci USA* 99: 2275–2280 (2002)), which is hereby incorporated by reference in its entirety) with an E value substantially lower than this threshold, AvrXv3 (4e-6), was expressed at a level that was detected only by RNA blot analysis (Table 1 below), indicating that significant E values do not always predict strong expression.

TABLE 1

Results of Microarray Analysis					
Des-ignation	GenBank accession number ¹	Amino acid % identity	BLASTP p value	HMM E-value	Microarray signal ratio ²
HopPsyA _{Pto}	L14926	52	9e-93	1.0e-5	11 ± 9
AvrPphE _{Pto}	U16817	67	1e-117	2.5e-4	5 ± 2
AvrPphF _{Pto}	AF231452	51	3e-36	1.7e-6	3 ± 2
AvrPphD1 _{Pto}	AJ277494	89	0	1.9e-6	30 ± 17
AvrXv3 _{Pto}	AF190120	27	7e-12	3.4e-6	ND
AvrPpiB1 _{Pto}	X84843	100	1e-152	7.8e-6	11 ± 9
AvrPpiB2 _{Pto}	X84843	100	1e-150	7.8e-6	10 ± 6
AvrPphD2 _{Pto}	AJ277494	53	2e-44	3.0e-5	27 ± 11
HopPtoB2 ³	AF232004			2.6e-3	ND
AvrRps4 _{Pto}	L43559	72	2e-44	2.5e-2	ND
Reference genes					
16S rRNA*					1
23S rRNA**					1

¹GenBank accession number AF232004 is for DC3000 sequences, all others are for homologs originally found in other bacteria.

²Microarray signal is the mean ratio and standard deviation from 3 replicates of 2 independent experiments, calculated as described in the Materials and Methods. AvrPpiB1_{Pto} and AvrPpiB2_{Pto} are 100% identical, so their signals cannot be distinguished. AvrPphD1_{Pto} and AvrPphD2_{Pto} are 62% identical. ND = not detected.

³HopPtoB1 is secreted in a Hrp-dependent manner; HopPtoB2 has duplicated regions of homology with HopPtoB1.

By using an iterative process involving computational and gene expression data, an initial inventory of *P. s. tomato* DC3000 candidate type III secretion effector proteins was obtained. These are the presumed prime agents of host metabolic subversion. These analyses have revealed that the Hrp regulon, the primary regulon known to be expressed during infection, seems to control at least 48 genes and a subsidiary regulon directing phytotoxin production. The iterative process focused on Hrp promoters in DC3000 and featured microarray experiments that tested the activity of novel Hrp promoters and demonstrated the validity of this approach for genomewide transcriptional profiling in DC3000. These findings suggest that the *P. syringae* Hrp regulon is more complex than expected and encompasses more than type III secretion system genes and effector genes.

The global search for DC3000 ORFs that are similar to known Avr/Hop proteins yielded AvrXv3_{Pto}, AvrPtoB, and the AvrPphD families as the only candidate effectors shared with *Xanthomonas* spp. (Noel et al., *Mol. Microbiol.* 41:1271–1281 (2001), which is hereby incorporated by reference in its entirety). Notably missing were members of the AvrBs2 and AvrBs3 families, which are widespread in *Xanthomonas* spp., or any members of the AvrRxxv/YopJ family, which are found in genera as diverse as *Salmonella*, *Yersinia*, *Xanthomonas*, *Erwinia*, and *Rhizobium*, and have also been reported in another strain of *P. syringae* (i.e., *P. s. syringae* B728a) (Galán & Collmer, *Science* 284:1322–1328 (1999); Alfano et al., *Proc. Natl. Acad. Sci. USA* 97:4856–4861 (2000), each of which is hereby incorporated by reference in its entirety). However, it is important to note that further searches after closure and annotation of the

DC3000 genome may yield additional homologs of known effectors. In addition, genomic projects with other pathogens will enlarge the set of candidate effector genes available for comparison.

The majority of *P. syringae* avr genes that have been cloned on the basis of Avr phenotype have come from three pathovars that parasitize legumes *glycinea*, *phaseolicola*, and *pisi*. *P. s.* tomato has a different host range and diverges from these other pathovars in rRNA comparisons (Manceau & Horvais, *Appl. Environ. Microbiol.* 63:498–505 (1997), which is hereby incorporated by reference in its entirety). Nevertheless, of the 15 avr gene families found in these legume-attacking pathovars, 6 are also found in DC3000. This finding suggests the existence of a core set of *P. syringae* effectors in addition to those in the Hrp pathogenicity island CEL.

The analyses described above and reported in Fouts et al. (*Proc. Natl. Acad. Sci USA* 99: 2275–2280 (2002), which is hereby incorporated by reference in its entirety) revealed a striking apparent redundancy among the candidate effector protein genes hopPtoA, hopPtoB, avrPphD_{Pto}, and avrPpiB1_{Pto}, as well as in three Hrp-related factors that may play a role in type III protein translocation across bacterial and plant cell walls.

All of the analyzed candidate effector genes seem to be expressed in a HrpL-dependent manner except for avrRps4_{Pto}, hopPtoA2, and hopPtoB2 (avrXv3_{Pto} was HrpL-activated, but relatively poorly). avrRps4_{Pto} was cloned originally from *Pseudomonas syringae pisi* and renders recombinant DC3000 avirulent on most *Arabidopsis* accessions (Hinsch & Staskawicz, *Mol. Plant-Microbe Interact.* 9:55–61 (1996), which is hereby incorporated by reference in its entirety), and avrXv3 is from an *Xanthomonas campestris* pv. *vesicatoria* race that is avirulent on tomato carrying the Xv3 R gene (Astua-Monge et al., *Mol. Plant-Microbe Interact.* 13:911–921 (2000), which is hereby incorporated by reference in its entirety). There exists a possibility that poor expression of these two avr genes in DC3000 is a factor in the virulence of DC3000 on *Arabidopsis* and tomato carrying the cognate R genes.

Example 2

In vitro Secretion of Effector Proteins

Secretion assays were performed using *P. s.* tomato DC3000 strains carrying a pML123 derivative containing a PCR-cloned ORF (encoding a candidate Hrp-secreted protein) fused to nucleotide sequences that encoded either the HA or FLAG epitopes along with their native ribosome binding sites and an engineered stop codon (Labes et al., *Gene* 89:37–46 (1990), which is hereby incorporated by reference in its entirety).

Four effector proteins were tested for their secretion from the above-identified strains. Primers and the constructs used to prepare the transform the host strains are identified as follows:

For HopPtoC expression, the hopPtoC gene was cloned using forward primer (agtcggatccgaataggcgctgaaaatgacaatcgtgtc, SEQ ID No: 26) containing a BamHI site and reverse primer (agtcctcagtcactgtcatcgtcctttagtctgtgtattttgaagcgaa, SEQ ID No: 27) containing an XhoI site and FLAG epitope codons. The hopPtoC gene was cloned into plasmid vector pLN50.

For HopPtoD1 expression, the hopPtoD1 gene was cloned using forward primer (ccacattggatccgattacttcacgggacagctgatagcgc, SEQ ID No: 28) containing a BamHI

site and reverse primer (attctcagtcattatcatcatcatcttataatcgggtcgggctcccgcgac, SEQ ID No: 29) containing an XhoI site and FLAG epitope codons. The hopPtoD1 gene was cloned into plasmid vector pLN167.

For HopPtoD2 expression, the hopPtoD2 gene was cloned using forward primer (atgcaagcttccaatgcctcttgca, SEQ ID No: 30) containing a HindIII site and reverse primer (atgctcagtcgaagcgaatctggaacatcgtatgggtattctaagcctattttgc, SEQ ID No: 31) containing an XhoI site and HA epitope codons. The hopPtoD2 gene was cloned into plasmid vector pLN130.

For HopPtoJ expression, the hopPtoJ gene was cloned using forward primer (agtaaagcttgagctgcacgcatcgag, SEQ ID No: 32) containing a HindIII site and reverse primer (agtatctagatcactgtcatcgtcgtcctttagtctgtgagcaccagatggtt, SEQ ID No: 33) containing an XbaI site and FLAG epitope codons. The hopPtoJ gene was cloned into plasmid vector pLN164.

Constructs carrying different epitope-tagged ORFs were electroporated into DC3000 and a DC3000 hrcC mutant and grown in Hrp-inducing conditions (Yuan & He, *J. Bacteriol.* 178:6399–6402 (1996), which is hereby incorporated by reference in its entirety). Additionally, all of the DC3000 strains also carried pCPP2318, a construct that contains blaM lacking signal peptide sequences (Charkowski et al., *J. Bacteriol.* 179:3866–3874 (1997), which is hereby incorporated by reference in its entirety). DC3000 cultures were separated into cell-bound and supernatant fractions as described (van Dijk et al., *J. Bacteriol.* 181:4790–4797 (1999), which is hereby incorporated by reference in its entirety). Proteins were separated with SDS-PAGE by standard procedures (Sambrook et al., *Molecular Cloning Second Ed.* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.) (1989), which is hereby incorporated by reference in its entirety), transferred to polyvinylidene difluoride membranes, and immunoblotted using anti-FLAG (Sigma Chemical Co., St. Louis, Mo.), -HA (Roche Molecular Biochemicals, Indianapolis, Ind.), or -β-lactamase (5 Prime→3 Prime Inc., Boulder, Colo.) as primary antibodies. Primary antibodies were recognized by goat anti-rabbit immunoglobulin G-alkaline phosphatase conjugate (Sigma Chemical Co.), which were visualized by chemiluminescence using a Western-Light chemiluminescence detection system (Tropix, Bedford, Mass.) and X-Omat X-ray film.

Each of these DC3000 proteins were found to be secreted (FIG. 2A). Because the secretability of these proteins was demonstrated (and the avirulence activity of these DC3000 homologs is unknown), the proteins were renamed as HopPtoC (AvrPpiC2 homolog), HopPtoD1 and HopPtoD2 (AvrPphD homologs), and HopPtoJ (AvrXv3 homolog).

Example 3

In vitro Translocation of Effectors

Arabidopsis thaliana accession Columbia (Col-0) and rps2–201 mutant plants were grown in a growth chamber with 12 hr of light at 24° C. (22° C. at night) and 70% relative humidity. For HopPtoK expression, the hopPtoK gene was cloned using forward primer (gcgaattcatcggtttaacacgcaaggc, SEQ ID No: 34) containing a EcoRI site and reverse primer (ttgtactcagcagtagagcgtgt, SEQ ID No: 35) containing an KpnI site. The hopPtoK gene was cloned into plasmid vector phopPtoK. In addition, a hopPtoK-^ΔavrRpt2 fusion was prepared using SEQ ID No: 34 (above) as forward primer and reverse primer (aaggatcccagagcgtgctcgcgacc, SEQ ID No: 36) containing an BamHI site to

clone the hopPtoK gene. The partial avrRpt2 gene with the N terminal 40 codons deleted was amplified using standard PCR procedures and cloned into pMOD (Madison, Wis.). After confirmation by sequence analysis, it was cloned into the KpnI and Sall sites of the broad-host-plasmid pLK, resulting in pΔavrRpt2. DNA fragments spanning 200 bp upstream of the Hrp boxes and the complete ORFs for hopPtoK was cloned into pΔavrRpt2 to produce phopPtoK-ΔavrRpt2. Additionally, the full-length hopPtoK was cloned using PCR into pLK to generate phopPtoK. Each construct was introduced in *P. s. phaseolicola* 3121 by electroporation. Bacterial strains in 10 mM MgCl₂ at a cell density of 10⁸ cfu/ml were infiltrated into *A. thaliana* Col-0 plants with a needleless syringe. Plant responses were documented 18 hours postinoculation.

The AvrRpt2 translocation assay was used to test whether the DC3000 ORF that is similar to AvrRps4 (Hinsch & Staskawicz, *Mol. Plant-Microbe Interact.* 9:55–61 (1996), which is hereby incorporated by reference in its entirety) was translocated into *Arabidopsis* plant cells (Mudgett et al., *Proc. Natl. Acad. Sci. USA* 97:13324–13329 (2000); Guttman & Greenberg, *Mol. Plant-Microbe Interact.* 14:145–155 (2001), each of which is hereby incorporated by reference in its entirety). *P. s. phaseolicola* carrying a broad-host-range plasmid expressing the AvrRps4 homolog fused to the Avr domain of AvrRpt2 (but lacking the secretion signals of AvrRpt2) elicited an RPS2-dependent HR on *A. thaliana* Col-0 (FIG. 2B), indicating that the amino terminus of the AvrRps4 homolog supplied sufficient information to direct translocation of the fusion protein into plant cells. Consequently, the AvrRps4 homolog was renamed HopPtoK. *P. s. phaseolicola* expressing HopPtoK did not elicit an HR, indicating that although translocated into host cells, HopPtoK is probably not recognized by the RPS4 protein present in *A. thaliana* Col-0, in contrast to its *P. s. pisi* 151 homolog (Hinsch & Staskawicz, *Mol. Plant-Microbe Interact.* 9:55–61 (1996), which is hereby incorporated by reference in its entirety).

Example 4

Determining Cytotoxicity of Effector in Yeast

Effector proteins of the present invention will be cloned into pFLAG-CTC (Kodak) to generate an in-frame fusion with the FLAG epitope, which will permit monitoring of protein production with anti-FLAG monoclonal antibodies. The FLAG-tagged genes will then be cloned under the control of the GAL1 promoter in the yeast shuttle vector p415GAL1 (Mumberg et al., 1994). These regulatable promoters of *Saccharomyces cerevisiae* will allow comparison of transcriptional activity and heterologous expression. The recombinant plasmids will be transformed into uracil auxotrophic yeast strains FY833/4, then selected for growth on SC-Ura (synthetic complete medium lacking uracil) based on the presence of the URA3 gene on the plasmid. The transformants will then be streaked onto SC-Ura medium plates containing either 2% galactose (which will induce expression of the effector proteins) or 2% glucose. The presence or absence of growth on the plates supplemented with 2% galactose will be observed. If no growth is observed on 2% galactose (but growth is observed in the 2% glucose control), this result will suggest that the effector protein is having a cytotoxic effect on the transformed yeast. Empty vector controls will also be used. FLAG-tagged nontoxic Avr proteins will be used to confirm that the recombinant effector genes were differentially expressed, as expected, on

plates containing galactose. To further confirm the results, albeit at lower expression levels, the recombinant effector gene will be recloned into p416GALS, which expresses foreign genes at a substantially lower level than p415GAL1.

Example 5

Determining Cytotoxicity of Effector in Plants

To determine whether effector proteins induce cell death on tobacco leaves, a transformation system that delivers the effector gene on T-DNA of *Agrobacterium tumefaciens* will be used (Rossi et al., *Plant Mol. Biol. Reporter* 11:220–229 (1993); van den Ackerveken et al., *Cell* 87:1307–1316 (1996), each of which is hereby incorporated by reference in its entirety). This delivery system works better than biolistics for transiently transforming whole plant leaves. For these experiments, vector pTA7002, kindly provided by Nam-Hai Chua and his colleagues at Rockefeller University, will be used. The unique property of this vector is that it contains an inducible expression system that uses the regulatory mechanism of the glucocorticoid receptor (Picard et al., *Cell* 54:1073–1080 (1988); Aoyama and Chua, *Plant J.* 11(3):605–612 (1997); McNellis et al., *Plant J.* 14(2):247–257 (1998), each of which is hereby incorporated by reference in its entirety). pTA7002 encodes a chimeric transcription factor consisting of the DNA-binding domain of GAL4, the transactivating domain of the herpes viral protein VP16, and the receptor domain of the rat glucocorticoid receptor. Also contained on this vector is a promoter containing GAL4 upstream activating sequences (UAS) upstream of a multiple cloning site. Thus, any gene cloned downstream of the promoter containing the GAL4-UAS can be induced by glucocorticoids, of which a synthetic glucocorticoid, dexamethasone (DEX), is available commercially. Effector proteins of the present invention will be PCR-cloned downstream of the GAL4-UAS. Thereafter, plant leaves from several different test plants will be infiltrated with *Agrobacterium* carrying recombinant pTA7002 carrying the effector ORF and after 48 hours these plants will be sprayed with DEX to induce expression of the effectors.

Tobacco (*Nicotiana tabacum*) and tomato (*Lycopersicon esculentum*) will be grown under greenhouse conditions and then maintained at 25° C. with daylight and supplemental halide illumination for HR and virulence assays. Bacteria will be grown overnight on King's medium B agar supplemented with appropriate antibiotics, suspended in 5 mM MES pH 5.6, and then infiltrated with a needleless syringe into the leaves of test plants at 10⁸ cfu/ml for HR assays and 10⁴ cfu/ml for pathogenicity assays (Charkowski et al., *J. Bacteriol.* 180:5211–5217 (1998), which is hereby incorporated by reference in its entirety). All assays will be repeated at least four times on leaves from different plants. Bacterial growth in tomato leaves will be assayed by excising disks from infiltrated areas with a cork borer, comminuting the tissue in 0.5 ml of 5 mM MES, pH 5.6, with an appropriate pestle, and then dilution plating the homogenate on King's medium B agar with 50 μg/ml rifampicin and 2 μg/ml cycloheximide to determine bacterial populations. The mean and SD from three leaf samples will be determined for each time point.

Plant leaves will be examined to determine the response of plant tissue to the expression of the effector proteins. In particular, plant tissues will be examined for tissue necrosis indicative of a hypersensitive response.

Although the invention has been described in detail for the purposes of illustration, it is understood that such detail is solely for that purpose, and variations can be made therein

by those skilled in the art without departing from the spirit and scope of the invention which is defined by the following claims.

SEQUENCE LISTING

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Thr Lys Gly Val Lys Asp Ala Thr Arg Gln Ala Arg Pro Leu Val Glu
 355 360 365

Leu Ala Val Lys Val Ala Ser Pro Gln Gly Leu Ala Arg Arg Asp Val
 370 375 380

<210> SEQ ID NO 3
 <211> LENGTH: 1017
 <212> TYPE: DNA
 <213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 3

atgaatcgca tttaaccag ctcaagtaaat tccagcttca attacacggc ccctacggag 60

gaagcgcaaa accgcttcgc ctcaagcggc gacaattccc ctctagtgtg caccacaaca 120

tctatcgccc aagcgtcgga agggctacaa aggcggggg caacgctaag catgcaggcc 180

cagcgactgc gccaatgat ggggagccg tctgagcagt gccggaggga cacaatgtta 240

gctaaagcct ttgatgctca acgcctaaac attaacactc aagcaggctc ttccaacagc 300

ccacacttga acgctctcaa cagctccaa caacgacact tcaaacctgc ggetggtggg 360

ctagaaatcc cagttacatc caactcctta ttggcggtg gcaggcaagt ctatcaaat 420

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ggctcatcgt cacgcgagct aagccaccga ccggtcaatg atcaggaccg cgcgcccttc 480
agggcgcttg agcggctgca cgccgagttg tttagaggtg ggccgattga gtttgtgcct 540
agaggcagca acgtgttgcc ctcaaacgtg agggatgtcg acatggacga gttcgtatgc 600
atcaactcta aagacggctg ccaaggcatt ggcaccactg gcctgggacc ctgcattgca 660
gtgtgtgcaa gaggcattgga tagagaaggg cttccggtgc tgggtgtcta tcaccacagt 720
ggtatcggct caccagagga taccatggct actcttgatc aagcgtatgc cgataaaggt 780
gctttgcaaa tcaaatactc cctggtaggc ggcatgatca tgcctaaaga ggaagaggct 840
ggcagctatg acgacgagca aagctttttg gcattgaaag gcagttattc aatcgaaggg 900
gcgcgcttgc atgtatccga aggcgaagag gacgtgcata ccggcgagga caacagtgtc 960
aatgttctgc tgatgctga ccgcgttctg tacgggtcgc acacgtctta ctgctga 1017

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<210> SEQ ID NO 4

<211> LENGTH: 338

<212> TYPE: PRT

<213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 4

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Met Asn Arg Ile Ser Thr Ser Ser Val Asn Ser Ser Phe Asn Tyr Thr
  1          5          10          15
Ala Pro Thr Glu Glu Ala Gln Asn Arg Phe Ala Ser Ala Pro Asp Asn
          20          25          30
Ser Pro Leu Val Val Thr Thr Thr Ser Ile Ala Gln Ala Ser Glu Gly
          35          40          45
Leu Gln Arg Pro Gly Ala Thr Leu Ser Met Gln Ala Gln Arg Leu Arg
          50          55          60
Gln Leu Met Gly Ser Pro Ser Glu Gln Cys Arg Arg Asp Thr Met Leu
          65          70          75          80
Ala Lys Ala Phe Asp Ala Gln Arg Leu Asn Ile Asn Thr Gln Ala Gly
          85          90          95
Ser Ser Asn Ser Pro His Leu Asn Ala Leu Asn Thr Leu Gln Gln Arg
          100          105          110
His Phe Lys Pro Ala Ala Gly Gly Leu Glu Ile Pro Val Thr Ser Asn
          115          120          125
Ser Leu Leu Gly Gly Gly Arg Gln Val Tyr Gln Ile Gly Ser Ser Ser
          130          135          140
Arg Glu Leu Ser His Arg Pro Val Asn Asp Gln Asp Arg Ala Pro Phe
          145          150          155          160
Arg Ala Leu Glu Arg Leu His Ala Glu Leu Phe Arg Gly Gly Pro Ile
          165          170          175
Glu Phe Val Pro Arg Gly Ser Asn Val Leu Ala Ser Asn Val Arg Asp
          180          185          190
Val Asp Met Asp Glu Phe Asp Val Ile Asn Ser Lys Asp Gly Cys Gln
          195          200          205
Gly Ile Gly Thr Thr Gly Leu Gly Pro Cys Ile Ala Val Cys Ala Arg
          210          215          220
Gly Met Asp Arg Glu Gly Leu Pro Val Leu Gly Val Tyr His His Ser
          225          230          235          240
Gly Ile Gly Ser Pro Glu Asp Thr Met Ala Thr Leu Asp Gln Ala Met
          245          250          255
Arg Asp Lys Gly Ala Leu Gln Ile Lys Tyr Ser Leu Val Gly Gly Met
          260          265          270

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Ile Met Pro Lys Glu Glu Glu Ala Gly Ser Tyr Asp Asp Glu Gln Ser
 275 280 285
 Phe Leu Ala Leu Lys Gly Ser Tyr Ser Ile Glu Gly Ala Arg Leu His
 290 295 300
 Val Ser Glu Gly Glu Glu Asp Val His Thr Gly Glu Asp Asn Ser Val
 305 310 315 320
 Asn Val Leu Leu Met Pro Asp Arg Val Leu Tyr Gly Arg Asp Thr Leu
 325 330 335

Tyr Cys

<210> SEQ ID NO 5
 <211> LENGTH: 396
 <212> TYPE: DNA
 <213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 5

atgaaaaacg catttgacct gcttgtggaa gggctggcta aggactacaa catgccgccc 60
 ttgcctgaca agaaacatat cgatgaagtc tattgctttg agtttcaaag tggatgaac 120
 gtaaaagtat accaagacga atttcgctgg gtatatttca ccgctgacgt tgggacattt 180
 caagatagca gtattgacac attaaactac gcgctccagc tgaacaactt tagccttaga 240
 aaacctttcc tgaccttcgg aatgacgaag gagaaaaatg gtgtattgca tacacgcacc 300
 cccttgattg aggtagacaa cgtgcaaatg cgcaggatat ttgaggagct tataggcgtg 360
 gcaggtgaaa tcagaaaaac actaaaactc aaatag 396

<210> SEQ ID NO 6
 <211> LENGTH: 131
 <212> TYPE: PRT
 <213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 6

Met Lys Asn Ala Phe Asp Leu Leu Val Glu Gly Leu Ala Lys Asp Tyr
 1 5 10 15
 Asn Met Pro Pro Leu Pro Asp Lys Lys His Ile Asp Glu Val Tyr Cys
 20 25 30
 Phe Glu Phe Gln Ser Gly Met Asn Val Lys Val Tyr Gln Asp Glu Phe
 35 40 45
 Arg Trp Val Tyr Phe Thr Ala Asp Val Gly Thr Phe Gln Asp Ser Ser
 50 55 60
 Ile Asp Thr Leu Asn Tyr Ala Leu Gln Leu Asn Asn Phe Ser Leu Arg
 65 70 75 80
 Lys Pro Phe Leu Thr Phe Gly Met Thr Lys Glu Lys Asn Gly Val Leu
 85 90 95
 His Thr Arg Thr Pro Leu Ile Glu Val Asp Asn Val Gln Met Arg Arg
 100 105 110
 Ile Phe Glu Glu Leu Ile Gly Val Ala Gly Glu Ile Arg Lys Thr Leu
 115 120 125
 Lys Leu Lys
 130

<210> SEQ ID NO 7
 <211> LENGTH: 579
 <212> TYPE: DNA
 <213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 7

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gtgtatagcc catcccatc acaacgaata acttcagctc cctctacatc cactcatggt 60
gggtgagata cactgacatc cattcatcag ctttcgcata gtcagagaga gcagtttctg 120
aacatgcatg atccaatgag agtaatggga cttgaccatg ataccgagct tttcagaacg 180
acggatagtc gctatataaa aaacgataaa ctcgcgggca atccacaatc catggcgagt 240
atccttatgc atgaagaact gcgccccaat cgttttgcca gccatacagg tgcccaacca 300
cacgaagcaa gggcgtacgt tccgaaaaga ataaaagcca ccgatctagg agttccatca 360
ctgaacgtaa tgactggctc gctagcgcga gacggaatta gagcttatga tcacatgagt 420
gataatcagg tctctgtcaa aatgcgactg ggagattttc tcgaaagggg tggcaaggtc 480
tatgccgacg cttcgtctgt agctgacgat ggggaaacat cacaagctct gattgtcaca 540
ttgccaaaag gacagaaagt gccggtcgaa agggctctga 579

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<210> SEQ ID NO 8
<211> LENGTH: 192
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae

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<400> SEQUENCE: 8

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Val Tyr Ser Pro Ser His Thr Gln Arg Ile Thr Ser Ala Pro Ser Thr
  1           5           10           15
Ser Thr His Val Gly Gly Asp Thr Leu Thr Ser Ile His Gln Leu Ser
           20           25           30
His Ser Gln Arg Glu Gln Phe Leu Asn Met His Asp Pro Met Arg Val
           35           40           45
Met Gly Leu Asp His Asp Thr Glu Leu Phe Arg Thr Thr Asp Ser Arg
           50           55           60
Tyr Ile Lys Asn Asp Lys Leu Ala Gly Asn Pro Gln Ser Met Ala Ser
           65           70           75           80
Ile Leu Met His Glu Glu Leu Arg Pro Asn Arg Phe Ala Ser His Thr
           85           90           95
Gly Ala Gln Pro His Glu Ala Arg Ala Tyr Val Pro Lys Arg Ile Lys
           100          105          110
Ala Thr Asp Leu Gly Val Pro Ser Leu Asn Val Met Thr Gly Ser Leu
           115          120          125
Ala Arg Asp Gly Ile Arg Ala Tyr Asp His Met Ser Asp Asn Gln Val
           130          135          140
Ser Val Lys Met Arg Leu Gly Asp Phe Leu Glu Arg Gly Gly Lys Val
           145          150          155          160
Tyr Ala Asp Ala Ser Ser Val Ala Asp Asp Gly Glu Thr Ser Gln Ala
           165          170          175
Leu Ile Val Thr Leu Pro Lys Gly Gln Lys Val Pro Val Glu Arg Val
           180          185          190

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<210> SEQ ID NO 9
<211> LENGTH: 2118
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae

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<400> SEQUENCE: 9

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atgaatcctc tacgatctat tcaacacaac attgcaactc cccaatcag tggcggtcag 60
ccattagacg cgggtgggcc tcaggcccag caatcccac ctaaaaggat ttcaccttct 120
caattgagcc aaagcgtca ccaggctcta gaacgccttt cagctaagtc cgaacaccaa 180

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cgcccttgcat cactggtacg caacgctctg caggatggca catttcaatt tcaatccagt 240
aaccacacgc aagtaaccta taaagcgtca atctgtctgc cagctgacac cgataccgtg 300
agaaccgacc acttgattaa taacgagctg acggttcagg cccgattaaa tgatcaatcg 360
gagtacgaca tcgtcagcgc acatttgcat ggctcttcga aagccatata cttegacgta 420
cccagcccc cgcccgcaca tggttcagca tcttctgtct tgagtgaacg gacccatcta 480
ggtatgagtc gcgttctctc acaagatgca gtagacagca gtagcctgga aactccgtta 540
ctgagctcgc cagaccattc tcgtccgcca tcacagccaa agcccgtgca tategggctg 600
gtccgcaggg actctggtag ccttgtttcc gataaccgg tagtgacagg cctgctatcg 660
tttgcgcagg ccgaccaggc atttccacca caggccgca gcatcgccgg ggtccagctg 720
gaaatgcggc cacgtcggga tattgagaaa gcacttgagg aattcaaagg cgccttcacg 780
gtggtgaagg cgcaactgat gtccggtgcc aactcgtcgg agcgtgtaga tgaggatgtc 840
aacgcagaca tccatatccc cttattgctc aaggccatcg agcggggggc tgcggcattt 900
ggtccaaacg catcaatcgg ccagaatagc gcgaaagcgt ttctcgcctc atgtgctccc 960
aagatcacgt ccaatgacga tgcctctcc gagttcatca accagaaact caagggggac 1020
gacgatcttc aggttcgcct gggcgcacag gaattgttgc atgtagccac caagaaggaa 1080
ttccagctcg gcggtctagc cggcagcatc ggggtcagca gcatactcgg ctccggcatgg 1140
gagcttggcg cttctgagct gttgaaaaat gccatcttcg gcaaaaattt ctcaccgagc 1200
caatatgccc tgcaattggc tggaatcgat tcagtgctc ctttgattat cgagtccatg 1260
gacaccatgt gcgtacttgc catcatcaag ggcataaagg gtgaggagtg gtccatgagc 1320
gatctacttc ccaaggcgtt gaaggccggt gctatttctc cgggtgtgtc attcccgaat 1380
aatgttttgc agtatgcagg tttcaaatcc agagtcggcg atcttgccggc aaactcagtg 1440
acaactgaag cggccatctt tggcgccgcc tccggtattc caccggaggc caaggaaagt 1500
gaagagctga tcgctgctgg cttattccag agcatgaagg acggcgtgat ggcatttca 1560
ggcgaggggg tggacaccaa aaaaacgatt gagcggatga cgcgccatgc gctggatata 1620
gctccggggc aaagcaccgc tgtcaagtcc atggggctgg catcgattgt cgggatgatt 1680
ccactgattg ccagcaacaa ggcaaccggg ctgctgtcgg aacaggtaact gcgtattttc 1740
cggagcgccg tcttcaatcc aatcgaagcc atcgtctga acgcttggc gcttggcggg 1800
cgtgtcaacg ttcccgggct atttgattcc gacaatgcca agcatgcacg cgtggtacaa 1860
accatccttg cgcgggccag ccagcacatg gaagctggag accgtgacat ttccgcagag 1920
gagctacatc aaatgctggc tcccgggagc gagttcctgc gccatgtggg atctgcgatt 1980
gtcaacggca tgaatgccag ctttgaggca attcccggcc tggttcggaa gcttgatata 2040
ggtgaggctc cattggccga acgtattccg tatcaagacc tggctgtgcc cgacacgtcg 2100
cggcagcccc caccctga 2118

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<210> SEQ ID NO 10

<211> LENGTH: 705

<212> TYPE: PRT

<213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 10

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Met Asn Pro Leu Arg Ser Ile Gln His Asn Ile Ala Thr Pro Pro Ile
  1             5             10             15

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Ser Gly Gly Gln Pro Leu Asp Ala Val Gly Pro Gln Ala Gln Gln Ser
  20             25             30

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His Pro Lys Arg Ile Ser Pro Ser Gln Leu Ser Gln Ser Ala His Gln
 35 40 45
 Ala Leu Glu Arg Leu Ser Ala Asn Ala Glu His Gln Arg Leu Ala Ser
 50 55 60
 Leu Val Arg Asn Ala Leu Gln Asp Gly Thr Phe Gln Phe Gln Ser Ser
 65 70 75 80
 Asn His Thr Gln Val Thr Tyr Lys Ala Ser Ile Cys Leu Pro Ala Asp
 85 90 95
 Thr Asp Thr Val Arg Thr Asp His Leu Ile Asn Asn Glu Leu Thr Val
 100 105 110
 Gln Ala Arg Leu Asn Asp Gln Ser Glu Tyr Asp Ile Val Ser Ala His
 115 120 125
 Leu His Gly Ser Ser Lys Ala Ile Ser Phe Asp Val Pro Ser Pro Pro
 130 135 140
 Pro Ala His Gly Ser Ala Ser Ser Val Leu Ser Glu Arg Thr His Leu
 145 150 155 160
 Gly Met Ser Arg Val Leu Ser Gln Asp Ala Val Asp Ser Ser Ser Leu
 165 170 175
 Glu Thr Pro Leu Leu Ser Ser Pro Asp His Ser Arg Pro Pro Ser Gln
 180 185 190
 Pro Lys Pro Val His Ile Gly Ser Val Arg Arg Asp Ser Gly Ser Leu
 195 200 205
 Val Ser Asp Asn Pro Val Val Gln Ala Leu Leu Ser Phe Ala Gln Ala
 210 215 220
 Asp Gln Ala Phe Pro Pro Gln Ala Ala Ser Ile Ala Gly Val Gln Leu
 225 230 235 240
 Glu Met Arg Pro Arg Arg Asp Ile Glu Lys Ala Leu Glu Glu Phe Lys
 245 250 255
 Gly Ala Phe Thr Val Val Lys Ala Gln Leu Met Ser Gly Ala Asn Ser
 260 265 270
 Ser Glu Arg Val Asp Glu Asp Val Asn Ala Asp Ile His Ile Pro Leu
 275 280 285
 Leu Leu Lys Ala Ile Glu Arg Gly Ala Ala Ala Phe Gly Pro Asn Ala
 290 295 300
 Ser Ile Gly Gln Asn Ser Ala Lys Ala Phe Leu Ala Ser Cys Ala Pro
 305 310 315 320
 Lys Ile Thr Ser Asn Asp Asp Val Leu Ser Glu Phe Ile Asn Gln Lys
 325 330 335
 Leu Lys Gly Asp Asp Leu Gln Val Arg Leu Gly Ala Gln Glu Leu
 340 345 350
 Leu His Val Ala Thr Lys Lys Glu Phe Gln Leu Gly Gly Leu Ala Gly
 355 360 365
 Ser Ile Gly Val Ser Ser Ile Leu Gly Ser Ala Trp Glu Leu Gly Ala
 370 375 380
 Ser Glu Leu Leu Lys Asn Ala Ile Phe Gly Lys Asn Phe Ser Pro Ser
 385 390 395 400
 Gln Tyr Ala Leu Gln Leu Ala Gly Ile Asp Ser Val Pro Pro Leu Ile
 405 410 415
 Ile Glu Ser Met Asp Thr Met Cys Val Leu Ala Ile Ile Lys Gly Met
 420 425 430
 Lys Gly Glu Trp Ser Met Ser Asp Leu Leu Pro Lys Ala Leu Lys
 435 440 445

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Ala	Gly	Ala	Ile	Ser	Ser	Val	Val	Ser	Phe	Pro	Asn	Asn	Val	Leu	Gln
450						455					460				
Tyr	Ala	Gly	Phe	Lys	Ser	Arg	Val	Gly	Asp	Leu	Ala	Ala	Asn	Ser	Val
465					470					475					480
Thr	Thr	Glu	Ala	Ala	Ile	Phe	Gly	Ala	Ala	Ser	Gly	Ile	Pro	Pro	Glu
				485					490						495
Val	Lys	Glu	Ser	Glu	Glu	Leu	Met	Arg	Ala	Gly	Leu	Phe	Gln	Ser	Met
			500					505						510	
Lys	Asp	Gly	Val	Met	Ala	His	Ser	Gly	Glu	Gly	Val	Asp	Thr	Lys	Lys
		515					520						525		
Thr	Ile	Glu	Arg	Met	Thr	Arg	His	Ala	Leu	Asp	Ile	Ala	Pro	Gly	Glu
	530					535					540				
Ser	Thr	Ala	Val	Lys	Ser	Met	Gly	Leu	Ala	Ser	Ile	Val	Gly	Met	Ile
545					550					555					560
Pro	Leu	Ile	Ala	Ser	Asn	Lys	Ala	Thr	Gly	Leu	Leu	Ser	Glu	Gln	Val
				565					570						575
Leu	Arg	Ile	Phe	Arg	Ser	Ala	Val	Phe	Asn	Pro	Ile	Glu	Ala	Ile	Ala
			580					585							590
Leu	Asn	Ala	Leu	Ala	Leu	Gly	Gly	Arg	Val	Asn	Val	Pro	Gly	Leu	Phe
		595				600							605		
Asp	Ser	Asp	Asn	Ala	Lys	His	Ala	Arg	Val	Val	Gln	Thr	Ile	Leu	Ala
	610					615						620			
Arg	Ala	Ser	Gln	His	Met	Glu	Ala	Gly	Asp	Arg	Asp	Ile	Ser	Ala	Glu
625					630					635					640
Glu	Leu	His	Gln	Met	Leu	Ala	Pro	Arg	Ser	Glu	Phe	Leu	Arg	His	Val
				645					650						655
Gly	Ser	Ala	Ile	Val	Asn	Gly	Met	Asn	Ala	Ser	Phe	Glu	Ala	Ile	Pro
			660					665							670
Ala	Leu	Val	Arg	Lys	Leu	Gly	Tyr	Gly	Glu	Ala	Pro	Leu	Ala	Glu	Arg
		675					680								685
Ile	Pro	Tyr	Gln	Asp	Leu	Ala	Val	Pro	Asp	Thr	Ser	Arg	Gln	Pro	Ala
	690					695					700				
Pro															
705															

<210> SEQ ID NO 11
 <211> LENGTH: 1407
 <212> TYPE: DNA
 <213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 11

atgaatcccc tgcaacctat tcagcacagc attacaaatt cccaaatgag tggtagtcag	60
caattagagg cggagggtc tcaggccac aattcctatt cccatcctga caggatttcg	120
ctttcccaat tgagccaaag cgctcaccta gctctagatc acctttcaac tcagccta	180
accgatcacc aacgcgttgc atcaactgta cgcaacgctg tgcaggacgg taagttccaa	240
cttcaatcca gtaacgacac gcaagtaacc tataaaactt cagtctgtcc gccagctaac	300
gccgacacca tggggggcgc ccacttaatt aataacgagc tgacggttca ggcccgatta	360
aatgatcaac ttgagtacga catcgtcagc gctcatttgt atggcccttc ggaagccata	420
tccatcgatg catccagtcc tccctcggcc aacgatctag cgtcctcttg cttgagcgaa	480
cgtagcgcac taggtatgaa tcgtgtcctc ttacgctacg cggtgccccc tcgggaaacc	540
gaagaccaat gtgttatggt gatcgacaaa atgccccccc ccaaacacgg caaaatgtct	600

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ttcttccgta ccactaatga cttgagcaaa ctgcctttgg gaatggagac gggcgggttg 660
tccgacctga aattgcttgg ttgtgaacct atttcttccg tgcagcaggt gaagagtatc 720
cgcgcagcgc ttggaggcgg gccgctcacc gtactagatc tgcgcgaaga atctcatgcg 780
attgtcaacg gtttgcttat caccttacgt ggcccgatgg attgggcaaa cgcggccta 840
tcccaggttg acggagcggc acgtgaaagt gccatgatta cagaactgaa gcgcaactaag 900
tctttaacct tggctgatgc caattatgta aaaggtaaaa aaagtaatcc tcaaacgaca 960
gaactgaaaa atttgaatgt ccggagcggag cgagaagtgc ttacagaggc cggcgcgacc 1020
tatcgccgcg tggccattac cgaccataac aggcctagtc cggaagcgac cgacgagcta 1080
gtagacatca tgcgccactg cctgcaggca aatgagtcgc tagttgtgca ctgtaacggc 1140
ggtcggggcc gtactaccac ggctatgata atggtcgaca tgcttaagaa cgctcgtaac 1200
cattccgcag aaacctcat cacgcgatg gccaaagctaa gctatgacta caacatgacg 1260
gatctaggca gcattttctg actcaagcgg ccattcctag aggacagact aaaatttctg 1320
caggcctttc acgactatgc ccgcaacaac ccaagcggat tatctcttaa ttggacacag 1380
tggcgcgcaa aatagcgtt agaatga 1407

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<210> SEQ ID NO 12

<211> LENGTH: 468

<212> TYPE: PRT

<213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 12

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Met Asn Pro Leu Gln Pro Ile Gln His Ser Ile Thr Asn Ser Gln Met
  1             5             10            15
Ser Gly Gly Gln Gln Leu Glu Ala Glu Gly Ser Gln Ala His Asn Ser
                20            25            30
Tyr Ser His Pro Asp Arg Ile Ser Leu Ser Gln Leu Ser Gln Ser Ala
          35            40            45
His Leu Ala Leu Asp His Leu Ser Thr Gln Pro Asn Thr Asp His Gln
      50            55            60
Arg Val Ala Ser Leu Val Arg Asn Ala Val Gln Asp Gly Lys Phe Gln
      65            70            75            80
Leu Gln Ser Ser Asn Asp Thr Gln Val Thr Tyr Lys Thr Ser Val Cys
          85            90            95
Pro Pro Ala Asn Ala Asp Thr Met Gly Ala Ala His Leu Ile Asn Asn
          100           105           110
Glu Leu Thr Val Gln Ala Arg Leu Asn Asp Gln Leu Glu Tyr Asp Ile
      115           120           125
Val Ser Ala His Leu Tyr Gly Pro Ser Glu Ala Ile Ser Ile Asp Ala
      130           135           140
Ser Ser Pro Pro Ser Ala Asn Asp Leu Ala Ser Ser Gly Leu Ser Glu
      145           150           155           160
Arg Thr His Leu Gly Met Asn Arg Val Leu Leu Arg Tyr Ala Val Pro
          165           170           175
Pro Arg Glu Thr Glu Asp Gln Cys Val Met Val Ile Asp Lys Met Pro
          180           185           190
Pro Pro Lys His Gly Lys Met Ser Phe Phe Arg Thr Thr Asn Asp Leu
          195           200           205
Ser Lys Leu Pro Leu Gly Met Glu Thr Gly Gly Leu Ser Asp Leu Lys
      210           215           220
Leu Ala Gly Cys Glu Arg Ile Ser Ser Val Glu Gln Val Lys Ser Ile

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225	230	235	240
Arg Ala Ala Leu Gly	Gly Gly Pro Leu Thr Val Leu Asp Leu Arg Glu		
	245	250	255
Glu Ser His Ala Ile Val Asn Gly Leu Pro Ile Thr Leu Arg Gly Pro			
	260	265	270
Met Asp Trp Ala Asn Ala Gly Leu Ser Gln Val Asp Gly Ala Ala Arg			
	275	280	285
Glu Ser Ala Met Ile Thr Glu Leu Lys Arg Thr Lys Ser Leu Thr Leu			
	290	295	300
Val Asp Ala Asn Tyr Val Lys Gly Lys Lys Ser Asn Pro Gln Thr Thr			
	305	310	315
Glu Leu Lys Asn Leu Asn Val Arg Ser Glu Arg Glu Val Val Thr Glu			
	325	330	335
Ala Gly Ala Thr Tyr Arg Arg Val Ala Ile Thr Asp His Asn Arg Pro			
	340	345	350
Ser Pro Glu Ala Thr Asp Glu Leu Val Asp Ile Met Arg His Cys Leu			
	355	360	365
Gln Ala Asn Glu Ser Leu Val Val His Cys Asn Gly Gly Arg Gly Arg			
	370	375	380
Thr Thr Thr Ala Met Ile Met Val Asp Met Leu Lys Asn Ala Arg Asn			
	385	390	395
His Ser Ala Glu Thr Leu Ile Thr Arg Met Ala Lys Leu Ser Tyr Asp			
	405	410	415
Tyr Asn Met Thr Asp Leu Gly Ser Ile Ser Ala Leu Lys Arg Pro Phe			
	420	425	430
Leu Glu Asp Arg Leu Lys Phe Leu Gln Ala Phe His Asp Tyr Ala Arg			
	435	440	445
Asn Asn Pro Ser Gly Leu Ser Leu Asn Trp Thr Gln Trp Arg Ala Lys			
	450	455	460
Ile Ala Leu Glu			
	465		

<210> SEQ ID NO 13
 <211> LENGTH: 810
 <212> TYPE: DNA
 <213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 13

atgacaatcg tgtctggaca catcgaaaa caccgaagcc taaccactgt tcaagctggg	60
tcttcggcct cggtcgagaa tcaaatgcct gatcctgcac agttcagtga tggacgggtg	120
aaaaagcttc cgaccaatt gtcgtcaatt acattggcga gattcgatca ggatatttgc	180
acgaataatc atggcatcag tcagcgtgca atgtgctttg gcctttcatt gagctggatt	240
aacatgattc atgccgggaa agatcatggt acgccctatg catcggcaga aagaatgagg	300
ttctggggtt ctttgaagg ggtggtgcat gctcgtactg ttcataactt ctatcggact	360
gagcacaat tctgatgga gcaagcttcc gaaaccccg gagtatcaag tggcgcgatg	420
gctggcacag aaagtttatt gcaagctgct gagttgaagg ggttaaagct tcaacctgtt	480
ctagaggaca agtcgaactc aggcctacc ttcctaattg cgtgtaagca gtcaggggcg	540
caggtgagca cagatgaagc tgcgctaagc tccttatgtg atgcaattgt agaaaataag	600
agaggggtaa tggatgata cagccaagaa attgccacg ctttgggctt ttctgtatca	660
tcagatggca aaagagcgac cttatttgat cccaatctcg gagagtttca tacacactcg	720
aaagcgttgg ctgatactat cgaaaacata tcacggcag atgggctgccc ttaaatcggc	780

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gttcaagtat tcgcttcaaa aatacactga

810

<210> SEQ ID NO 14
 <211> LENGTH: 269
 <212> TYPE: PRT
 <213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 14

Met Thr Ile Val Ser Gly His Ile Gly Lys His Pro Ser Leu Thr Thr
 1 5 10 15
 Val Gln Ala Gly Ser Ser Ala Ser Val Glu Asn Gln Met Pro Asp Pro
 20 25 30
 Ala Gln Phe Ser Asp Gly Arg Trp Lys Lys Leu Pro Thr Gln Leu Ser
 35 40 45
 Ser Ile Thr Leu Ala Arg Phe Asp Gln Asp Ile Cys Thr Asn Asn His
 50 55 60
 Gly Ile Ser Gln Arg Ala Met Cys Phe Gly Leu Ser Leu Ser Trp Ile
 65 70 75 80
 Asn Met Ile His Ala Gly Lys Asp His Val Thr Pro Tyr Ala Ser Ala
 85 90 95
 Glu Arg Met Arg Phe Leu Gly Ser Phe Glu Gly Val Val His Ala Arg
 100 105 110
 Thr Val His Asn Phe Tyr Arg Thr Glu His Lys Phe Leu Met Glu Gln
 115 120 125
 Ala Ser Ala Asn Pro Gly Val Ser Ser Gly Ala Met Ala Gly Thr Glu
 130 135 140
 Ser Leu Leu Gln Ala Ala Glu Leu Lys Gly Leu Lys Leu Gln Pro Val
 145 150 155 160
 Leu Glu Asp Lys Ser Asn Ser Gly Leu Pro Phe Leu Ile Ala Cys Lys
 165 170 175
 Gln Ser Gly Arg Gln Val Ser Thr Asp Glu Ala Ala Leu Ser Ser Leu
 180 185 190
 Cys Asp Ala Ile Val Glu Asn Lys Arg Gly Val Met Val Ile Tyr Ser
 195 200 205
 Gln Glu Ile Ala His Ala Leu Gly Phe Ser Val Ser Ser Asp Gly Lys
 210 215 220
 Arg Ala Thr Leu Phe Asp Pro Asn Leu Gly Glu Phe His Thr His Ser
 225 230 235 240
 Lys Ala Leu Ala Asp Thr Ile Glu Asn Ile Ser Ser Ala Asp Gly Leu
 245 250 255
 Pro Leu Ile Gly Val Gln Val Phe Ala Ser Lys Ile His
 260 265

<210> SEQ ID NO 15
 <211> LENGTH: 831
 <212> TYPE: DNA
 <213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 15

atgcacgcaa atcctttaag ctctttcaac agagctcaac atggcaatct gactaatgta 60
 gaggccagcc aagttaaatc gccaggaacc tottccacca ctaatataga cagtaaaaac 120
 attgaagaac atgttgacag cagactcagt gatttaggca gacctgatgg tggatggttt 180
 ttcgagaagt cacttggcac cttgaaaaat ttaaatcttg agcagtttagc cggaatccat 240
 gatgtactaa aattaacaga tggcgtaaag aacattgtct cttttggagc tcggaagga 300

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ggcttcgagt tggcaatgca gtttcgtcat gattataca gatctcaaca tccggatgaa 360
aactcgccgc acgatgccgc aactcattat cttgatgcaa tcagcctgca atcaaacaaa 420
ttacaaaaac ttgaaaaact acaacatgta gatgtattta aaatgcaaaa cccgttttgg 480
gatgtcgggt acaaaaaacg aattgcgcac gcaaaaaaaaa tggcattctt cataaaccca 540
gagtggctgg gttctgattt ctgtaaacag gaattccagt ggcttagcga acaaaaaaac 600
aaagacataa aatctgcatt tgtgatcttt aaagatgtag acttaaaaag caaaaatatg 660
acaagtatct tcaattttgc agacttccat aaatcacgcg tcatgatggc aagcacacct 720
cccgaatcgg gattgaataa tgtaaaaatc gaaaatagcg ttgacctgaa tttcaagagg 780
ttattaactg accgtgagtc atgggaacta aataatttcc taggcgacta a 831

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<210> SEQ ID NO 16
<211> LENGTH: 276
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae

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<400> SEQUENCE: 16

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Met His Ala Asn Pro Leu Ser Ser Phe Asn Arg Ala Gln His Gly Asn
  1             5             10             15
Leu Thr Asn Val Glu Ala Ser Gln Val Lys Ser Ala Gly Thr Ser Ser
             20             25             30
Thr Thr Asn Ile Asp Ser Lys Asn Ile Glu Glu His Val Ala Asp Arg
  35             40             45
Leu Ser Asp Leu Gly Arg Pro Asp Gly Gly Trp Phe Phe Glu Lys Ser
  50             55             60
Leu Gly Thr Leu Lys Asn Leu Asn Leu Glu Gln Leu Ala Gly Ile His
  65             70             75             80
Asp Val Leu Lys Leu Thr Asp Gly Val Lys Asn Ile Val Ser Phe Gly
             85             90             95
Ala Arg Glu Gly Gly Phe Glu Leu Ala Met Gln Phe Arg His Asp Leu
  100            105            110
Tyr Arg Ser Gln His Pro Asp Glu Asn Ser Pro His Asp Ala Ala Thr
  115            120            125
His Tyr Leu Asp Ala Ile Ser Leu Gln Ser Asn Lys Phe Thr Lys Leu
  130            135            140
Glu Lys Leu Gln His Val Asp Val Phe Lys Met Gln Asn Pro Phe Trp
  145            150            155            160
Asp Val Gly Tyr Lys Asn Gly Ile Ala His Ala Lys Lys Met Ala Phe
             165            170            175
Phe Ile Thr Pro Glu Trp Leu Gly Ser Asp Phe Cys Lys Gln Glu Phe
  180            185            190
Gln Trp Leu Ser Glu Thr Lys Asn Lys Asp Ile Lys Ser Ala Phe Val
  195            200            205
Ile Phe Lys Asp Val Asp Leu Lys Ser Lys Asn Met Thr Ser Ile Phe
  210            215            220
Asn Phe Ala Asp Phe His Lys Ser Arg Val Met Met Ala Ser Thr Pro
  225            230            235            240
Pro Glu Ser Gly Leu Asn Asn Val Lys Ile Glu Asn Ser Val Asp Leu
             245            250            255
Asn Phe Lys Arg Leu Leu Thr Asp Arg Glu Ser Trp Glu Leu Asn Asn
  260            265            270
Phe Leu Gly Asp

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275

<210> SEQ ID NO 17
 <211> LENGTH: 855
 <212> TYPE: DNA
 <213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 17

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atggggctat gtatttcaaa acactctggt agcagttaca gctacagtga tagcgaccgc      60
tggcaagtgc ctgcatgccc tccaaacgcc aggtctgtat ccagtcatca aacagcatct    120
gcgagtgaca tcgcatcagg cgatgtggat gaacgtcctg caacgttttc tcattttcaa    180
cttgcgcggt gcggtggaga gtacacgctt agcatggttt ctgcagcggc ttatcaagca    240
gaaagacggc atcgcggtaa ttaataaaa gatcgtagtc aatccatact cccatgggtc    300
caggtatatac attctaaaaa aggtttggat tacagcttcc agatcgacag aactacgact    360
gttaaagtgg ctggattcaa ctgctctatc cccaataaca gagggactcg gcatttatac    420
agcgcgtgta cgagtcagac aaacatgcct gtcacgcgag acaacatgag cgcattgcatt    480
gctgtcgcgt gtgcgcgga aaacgtggat gctggcacgg gtgaacgtag gccgggggcg    540
aaagttcgcg tattccatct actccctttt cgacgcgaag accttgtgcc agaagaagtt    600
ttagcttctg tgcgcgatta tctgcgaacg accaaagaac aggggctaac aatgcgcgta    660
gctatgcatg gaggaatac agagggatgat ttctcagtca gcaactgcgc gccattgaaa    720
ggcctgtttg ctaatgaagg gatcccgctt gaatttgacg agacctgtgc aaaccgaacg    780
tctgaaacac tgcttggtgc cgttatctta gatgacaact cgactcattt cataaaacat    840
ctggtcgcac aataa                                         855
    
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<210> SEQ ID NO 18
 <211> LENGTH: 284
 <212> TYPE: PRT
 <213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 18

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Met Gly Leu Cys Ile Ser Lys His Ser Gly Ser Ser Tyr Ser Tyr Ser
  1           5           10           15
Asp Ser Asp Arg Trp Gln Val Pro Ala Cys Pro Pro Asn Ala Arg Ser
  20          25          30
Val Ser Ser His Gln Thr Ala Ser Ala Ser Asp Ile Ala Ser Gly Asp
  35          40          45
Val Asp Glu Arg Pro Ala Thr Phe Ser His Phe Gln Leu Ala Arg Cys
  50          55          60
Gly Gly Glu Tyr Thr Leu Ser Met Val Ser Ala Ala Ala Tyr Gln Ala
  65          70          75          80
Glu Arg Arg His Arg Gly Asn Leu Ile Lys Asp Arg Ser Gln Ser Ile
  85          90          95
Leu Pro Trp Val Gln Val Tyr His Ser Lys Lys Gly Leu Asp Tyr Ser
  100         105         110
Phe Gln Ile Asp Arg Thr Thr Thr Val Lys Val Ala Gly Phe Asn Cys
  115         120         125
Ser Ile Pro Asn Asn Arg Gly Thr Arg His Leu Tyr Ser Ala Gly Thr
  130         135         140
Ser Gln Thr Asn Met Pro Val Ile Ala Asp Asn Met Ser Ala Cys Ile
  145         150         155         160
Ala Val Ala Cys Ala Ala Glu Asn Val Asp Ala Gly Thr Gly Glu Arg
    
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	165					170						175		
Arg Pro Gly Ala Lys Val Arg Val Phe His Leu Leu Pro Phe Arg Arg	180					185						190		
Glu Asp Leu Val Pro Glu Glu Val Leu Ala Ser Val Arg Asp Tyr Leu	195					200						205		
Arg Thr Thr Lys Glu Gln Gly Leu Thr Met Arg Val Ala Met His Gly	210					215						220		
Gly Asn Thr Glu Gly Asp Phe Ser Val Ser Thr Ala Gln Ala Leu Lys	225					230						235		240
Gly Leu Phe Ala Asn Glu Gly Ile Pro Leu Glu Phe Asp Glu Thr Cys						245						250		255
Ala Asn Arg Thr Ser Glu Thr Leu Leu Gly Ala Val Ile Leu Asp Asp						260						265		270
Asn Ser Thr His Phe Ile Lys His Leu Val Ala Gln						275						280		

<210> SEQ ID NO 19
 <211> LENGTH: 291
 <212> TYPE: DNA
 <213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 19

atgatcatcg acaatcacgtt cgcgctgaca ctgtcatgcg attacgcgcg tgagcgcttg	60
ctgttgatcg gcttgcttga gccgcacaag gacatacctc agcagtgcct tttggctggc	120
gctctcaatc cgctcctcaa tgcaggccca ggccttgcc tggatgagaa aagcgcgctg	180
tatcacgcgt atcaaagcat cctctgagaa aaactcagcg tgccgacgct caaacgcgaa	240
atggcaggtc tgctggagtg gatgaggggc tggcgcgaag caagccaata g	291

<210> SEQ ID NO 20
 <211> LENGTH: 96
 <212> TYPE: PRT
 <213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 20

Met Ile Ile Asp Asn Thr Phe Ala Leu Thr Leu Ser Cys Asp Tyr Ala	1	5	10	15
Arg Glu Arg Leu Leu Ile Gly Leu Leu Glu Pro His Lys Asp Ile	20	25	30	
Pro Gln Gln Cys Leu Leu Ala Gly Ala Leu Asn Pro Leu Leu Asn Ala	35	40	45	
Gly Pro Gly Leu Gly Leu Asp Glu Lys Ser Gly Leu Tyr His Ala Tyr	50	55	60	
Gln Ser Ile Pro Arg Glu Lys Leu Ser Val Pro Thr Leu Lys Arg Glu	65	70	75	80
Met Ala Gly Leu Leu Glu Trp Met Arg Gly Trp Arg Glu Ala Ser Gln	85	90	95	

<210> SEQ ID NO 21
 <211> LENGTH: 1143
 <212> TYPE: DNA
 <213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 21

atgaacccca ttcagtcacg cttctccagt gtgcaagagc tcagacgatc caacgttgat	60
attccggcgc tcaaagccaa tggccaactg gaggtcgcag gcaagaggta cgagattcgt	120

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gcagccgatg acggaacaat ttcggtcctt cgaccggagc aacaatccaa agcgaaaagt 180
tttttcaagg gcgcttccca gttgataggt ggcagcagcc agcgcgcgca gattgcccag 240
gcgctcaacg agaaggtcgc atcggcacgc actgtcttgc accagagcgc tatgacgggc 300
ggagcgttgg acacccttga gcggggcgaa agcagctcag ccacaacagc catcaaacc 360
actgccaaac aggtcgcgca aagtactttt aacagctttc atgagtgggc caaacaggca 420
gaggcgatgc gaaaccctgc tcgaatggat atctacaaga tctataaaca agatgcacct 480
cactcacacc ccatgagcga cgagcagcaa gaagagttcc tgcacacgct aaaggcattg 540
aatggcaaaa acggcattga ggtgcgcact caggaccacg acagcgtcag aaataaaaa 600
gaccgcaacc tggacaagta catcgcagag agcccggatg caaagaggtt tttctatcga 660
attatcccca aacatgagcg ccgagaagat aagaatcaag ggcgattgac cattggcgtg 720
caaccccaat atgcaacaca gttgaccctg gccatggcaa ccctgatagg gaaggaaagt 780
gcaatcacgc atggcaaaat aataggcccc gcctgccacg gccaatgac cgattcggca 840
gttttgata tcaacggtga tgttgcaaag gcagaaaagc tgggcgagaa actgaaacag 900
atgagcggca ttctctgga tgcgttcgtt gagcacacc ctttgagcat gcaatccctg 960
agtaaaggtc tgtcctatgc agaaagcacc ctggcgaca ccagaggcca tgggatgtcg 1020
cgagcgggaag tgatcagcga tgccttgagg atggacggga tgccatttct gccagattg 1080
aagctatcac tgtctgcaa tggctatgac ccggacaacc cgcccttcg aaacacgaaa 1140
tga 1143

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<210> SEQ ID NO 22

<211> LENGTH: 380

<212> TYPE: PRT

<213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 22

```

Met Asn Pro Ile Gln Ser Arg Phe Ser Ser Val Gln Glu Leu Arg Arg
  1             5             10             15
Ser Asn Val Asp Ile Pro Ala Leu Lys Ala Asn Gly Gln Leu Glu Val
             20             25             30
Asp Gly Lys Arg Tyr Glu Ile Arg Ala Ala Asp Asp Gly Thr Ile Ser
             35             40             45
Val Leu Arg Pro Glu Gln Gln Ser Lys Ala Lys Ser Phe Phe Lys Gly
             50             55             60
Ala Ser Gln Leu Ile Gly Gly Ser Ser Gln Arg Ala Gln Ile Ala Gln
             65             70             75             80
Ala Leu Asn Glu Lys Val Ala Ser Ala Arg Thr Val Leu His Gln Ser
             85             90             95
Ala Met Thr Gly Gly Arg Leu Asp Thr Leu Glu Arg Gly Glu Ser Ser
             100            105            110
Ser Ala Thr Thr Ala Ile Lys Pro Thr Ala Lys Gln Ala Ala Gln Ser
             115            120            125
Thr Phe Asn Ser Phe His Glu Trp Ala Lys Gln Ala Glu Ala Met Arg
             130            135            140
Asn Pro Ser Arg Met Asp Ile Tyr Lys Ile Tyr Lys Gln Asp Ala Pro
             145            150            155            160
His Ser His Pro Met Ser Asp Glu Gln Gln Glu Glu Phe Leu His Thr
             165            170            175
Leu Lys Ala Leu Asn Gly Lys Asn Gly Ile Glu Val Arg Thr Gln Asp
             180            185            190

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His Asp Ser Val Arg Asn Lys Lys Asp Arg Asn Leu Asp Lys Tyr Ile
 195 200 205

Ala Glu Ser Pro Asp Ala Lys Arg Phe Phe Tyr Arg Ile Ile Pro Lys
 210 215 220

His Glu Arg Arg Glu Asp Lys Asn Gln Gly Arg Leu Thr Ile Gly Val
 225 230 235 240

Gln Pro Gln Tyr Ala Thr Gln Leu Thr Arg Ala Met Ala Thr Leu Ile
 245 250 255

Gly Lys Glu Ser Ala Ile Thr His Gly Lys Val Ile Gly Pro Ala Cys
 260 265 270

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

Ala Lys Ala Glu Lys Leu Gly Glu Lys Leu Lys Gln Met Ser Gly Ile
 290 295 300

Pro Leu Asp Ala Phe Val Glu His Thr Pro Leu Ser Met Gln Ser Leu
 305 310 315 320

Ser Lys Gly Leu Ser Tyr Ala Glu Ser Ile Leu Gly Asp Thr Arg Gly
 325 330 335

His Gly Met Ser Arg Ala Glu Val Ile Ser Asp Ala Leu Arg Met Asp
 340 345 350

Gly Met Pro Phe Leu Ala Arg Leu Lys Leu Ser Leu Ser Ala Asn Gly
 355 360 365

Tyr Asp Pro Asp Asn Pro Ala Leu Arg Asn Thr Lys
 370 375 380

<210> SEQ ID NO 23
 <211> LENGTH: 2598
 <212> TYPE: DNA
 <213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 23

gtgcccgcgta tcgctcgcgg ccatgcagaa ggcgtgtgcg tggcaacgg ccggcactat 60
 gtcgagctgt ccggtagaac ctttcaagtc cattacgaca cacatctgcg cggctggcag 120
 attgtcgatc cagaaaacc gttcgccttt tttggccagc agccgggtgcg cctagatgaa 180
 caggggcaat ggcagcttgt cgcccgtcga cgtctgctg cgggtggcgt aggtgactcc 240
 agccatgccc acctgcccga agaaacaccg ggctccagca caggctcgat tccgagcgac 300
 tacgaaatgc cggccgccat gcaggcagc cttgatgtcg tgttgagcaa caagccctac 360
 gaccgaccg ggattggcat ggagtcttac tttgagagct atttcgtgga tctgcgtcag 420
 agttttgtgg cgcgcaggga aaagctttat gaggatgccc ggacattttt cgccggtttt 480
 tetccgccgc caaagccgca attgcctcgg ctggcgccac ctggtgccaat cgacaccctg 540
 attgaacacg tcttcgcgca gggtaacggc ctggttttga gtgaagcacc gaagtcggtc 600
 gccagcaaac ggctgctggt actcaacatg ccgctgctgg ccgaacagcg tgtcaagatt 660
 ctgtatatcg agcacctgct gaccgacaag cacctgteta aactggccag gtatcgtcaa 720
 ctgggcaaaa agagccgctc aggctcgcac gaactcaagc attacctgca cgatctcaac 780
 cgcgggacgc tgaacaatc cagcaccgac tacgactatt accacctcat caaggcagcg 840
 catcgctatg gtatcgaggt gcgaccgttc agctcgtcga tcagctaccc gtttctggac 900
 catccggtat tgagcgcagc caacgacacg actgcagtac aaaaaatgag caattttttc 960
 ggccatagc tcatcagcag cgatgtcga tccgcgccga caaaacgctg ggttgccttg 1020

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ctcgaccaga agctggccac gaccacgac ggggtattag gcattgccga aatgcagggc 1080
gtggtcagtg tgcattgccg cgacatcccg gcaggccggc cgacgcgcac cactaaaggc 1140
acaggcgaac tgccacgcga gggcacgcag gcccgctgcg acttcacgat tgcgttttcc 1200
gatccgacgc tgattgtgcc ccagggcct caccgcgacg gtaccaaact ggacgacatg 1260
ctgctcagag aactgagggg ccaatctgcc ggtgccgggg gcgaacgctg gcccgccag 1320
tacggattca tccgtgacga ggacgggtgcc tggcggtgga tcgcgcctga ggactggccc 1380
gcagacagcc cgatgacggc aatccagcaa tccctgaccg accctgtcta tgagatgcca 1440
ctggacactc gaacaacgct tcatacgtg gcgaacttcg aaagaagggg gctcgacatg 1500
gagtatttct ttgaagaaa cagtagcga actgttcgca acgtattcgc cctgcaccgc 1560
aaaaagctgc aacaggatgc gcccttgatc agcgtgtac agttgccgcc tcgtccgacg 1620
atgccggccg tcaacctcgc gacgaccacg gcgcagctgt ttgaaacgct gtaccagcac 1680
accgatggca tcgtgatcgg cgagtcgcat ttttcggtcg ccagcaagaa aatgatcatc 1740
gacaacctgc cgttgctgtc gcagcaaac gtacgaacgc tgtacatgga gcaactgttc 1800
accgacttgc atcaggcggg tctggatcgc ttttcgaaa caggcgaat gagcaaac 1860
ctgcttcacg acctgaaagt gctggatcgg ggccatcgca ccgaccggg caaggtttac 1920
acctttgagc aactggatc caaggcgcag cagcagggca tggaaagtcg cgcacatcgc 1980
tgcgagcca gctaccacct tagtggcctt gacaacgatg gttcaatcac ccgtcagcaa 2040
atgatgaact actttgcgtc gcgcaccctg gcgagcctc aggacgcat gggctcacac 2100
aagtggatcg cgctggctcg caacagccat tccaatgtct atcaaggcgt cgtgcctggt 2160
atcgccgagc tggaaagcgg catcggcctg cgggttatcg acgtggcacc gggcagctcg 2220
aagggtgtca tgcacgacct gggggagctg gtctcggcag acatctcag aaccaaagta 2280
cacatcaaa gcgattatcg agtggagata gaaataccgc gtgcgaagga tgcattcgg 2340
ccacccagc ctgttacct cgaacagcga ctggccagac cgggattggt tctggtgaa 2400
gagagtgagg gcaatctgct gaccattgct caccgcgctc gcgacacctg gattcaccgc 2460
acgcccgtgc tggatcaatgc cgagggcaag ctgtacctgg agcgcgtgcg ctggccgcgc 2520
atccacctca aaccctttga tgacatggac gcgctggtag cggcgtgga ggagatgaac 2580
ctgacgcggg taggctga 2598

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<210> SEQ ID NO 24

<211> LENGTH: 865

<212> TYPE: PRT

<213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 24

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Val Pro Arg Ile Val Ala Gly His Ala Glu Gly Val Cys Val Val Asn
  1             5             10             15
Gly Arg His Tyr Val Glu Leu Ser Gly Arg Thr Phe Gln Val His Tyr
             20             25             30
Asp Thr His Leu Arg Gly Trp Gln Ile Val Asp Pro Glu Asn Pro Phe
             35             40             45
Ala Phe Phe Gly Gln Gln Pro Val Arg Leu Asp Glu Gln Gly Gln Trp
             50             55             60
Gln Leu Val Ala Arg Arg Arg Leu Arg Gly Gly Gly Val Gly Asp Ser
             65             70             75             80
Ser His Ala His Leu Pro Glu Glu Thr Pro Gly Ser Ser Thr Gly Ser
             85             90             95

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Ile Pro Ser Asp Tyr Glu Met Pro Ala Ala Met Gln Ala Gly Leu Asp
 100 105 110
 Val Val Leu Ser Asn Lys Pro Tyr Asp Pro Thr Gly Ile Gly Met Glu
 115 120 125
 Ser Tyr Phe Glu Ser Tyr Phe Val Asp Leu Arg Gln Ser Phe Val Ala
 130 135 140
 Arg Arg Glu Lys Leu Tyr Glu Asp Ala Arg Thr Phe Phe Ala Gly Phe
 145 150 155 160
 Ser Pro Pro Pro Lys Pro Gln Leu Pro Pro Leu Ala Pro Pro Val Ala
 165 170 175
 Ile Asp Thr Leu Ile Glu His Val Phe Ala Gln Gly Asn Gly Leu Val
 180 185 190
 Leu Ser Glu Ala Pro Lys Ser Val Ala Ser Lys Arg Leu Leu Leu Leu
 195 200 205
 Asn Met Pro Leu Leu Ala Glu Gln Arg Val Lys Ile Leu Tyr Ile Glu
 210 215 220
 His Leu Leu Thr Asp Lys His Leu Ser Lys Leu Ala Arg Tyr Arg Gln
 225 230 235 240
 Leu Gly Lys Lys Ser Arg Ser Gly Ser His Glu Leu Lys His Tyr Leu
 245 250 255
 His Asp Leu Asn Arg Gly Thr Leu Asn Asn Ser Ser Thr Asp Tyr Asp
 260 265 270
 Tyr Tyr His Leu Ile Lys Ala Ala His Arg Tyr Gly Ile Glu Val Arg
 275 280 285
 Pro Phe Ser Ser Ser Ile Ser Tyr Pro Phe Leu Asp His Pro Val Leu
 290 295 300
 Ser Ala Ala Asn Asp Thr Thr Ala Val Gln Lys Met Ser Asn Phe Phe
 305 310 315 320
 Gly His Thr Leu Ile Ser Ser Asp Val Ala Ser Ala Pro Thr Lys Arg
 325 330 335
 Trp Val Ala Leu Leu Asp Gln Lys Leu Ala Thr Thr His Asp Gly Val
 340 345 350
 Leu Gly Ile Ala Glu Met Gln Gly Val Val Ser Val His Val Arg Asp
 355 360 365
 Ile Pro Ala Gly Arg Pro Thr Arg Ile Thr Lys Gly Thr Gly Glu Leu
 370 375 380
 Pro Arg Glu Gly Thr Gln Ala Arg Cys Asp Phe Thr Ile Ala Phe Ser
 385 390 395 400
 Asp Pro Thr Leu Ile Val Pro Gln Ala Pro His Pro His Gly Thr Lys
 405 410 415
 Leu Asp Asp Met Leu Leu Arg Glu Leu Arg Gly Gln Ser Ala Gly Ala
 420 425 430
 Gly Gly Glu Arg Trp Ala Gly Gln Tyr Gly Phe Ile Arg Asp Glu Asp
 435 440 445
 Gly Ala Trp Arg Trp Ile Ala Pro Glu Asp Trp Pro Ala Asp Ser Pro
 450 455 460
 Met Thr Ala Ile Gln Gln Ser Leu Thr Asp Pro Val Tyr Glu Met Pro
 465 470 475 480
 Leu Asp Thr Arg Thr Thr Leu His Thr Leu Ala Asn Phe Glu Arg Arg
 485 490 495
 Gly Leu Asp Met Glu Tyr Phe Phe Glu Glu Ser Gln Tyr Glu Thr Val
 500 505 510

-continued

Arg Asn Val Phe Ala Leu His Arg Lys Lys Leu Gln Gln Asp Ala Ala
 515 520 525
 Leu Ile Ser Ala Val Gln Leu Pro Pro Arg Pro Thr Met Pro Ala Val
 530 535 540
 Asn Pro Arg Thr Thr Thr Ala Gln Leu Phe Glu Thr Leu Tyr Gln His
 545 550 555 560
 Thr Asp Gly Ile Val Ile Gly Glu Ser His Phe Ser Val Ala Ser Lys
 565 570 575
 Lys Met Ile Ile Asp Asn Leu Pro Leu Leu Ser Gln Gln Asn Val Arg
 580 585 590
 Thr Leu Tyr Met Glu His Leu Leu Thr Asp Leu His Gln Ala Asp Leu
 595 600 605
 Asp Arg Phe Phe Glu Thr Gly Gln Met Ser Lys Thr Leu Leu His Asp
 610 615 620
 Leu Lys Val Leu Asp Arg Gly His Arg Thr Asp Pro Asp Lys Val Tyr
 625 630 635 640
 Thr Phe Glu Gln Leu Val Ile Lys Ala Gln Gln His Gly Met Glu Val
 645 650 655
 Arg Ala Ile Asp Cys Ala Ala Ser Tyr His Leu Ser Gly Leu Asp Asn
 660 665 670
 Asp Gly Ser Ile Thr Arg Gln Gln Met Met Asn Tyr Phe Ala Ser Arg
 675 680 685
 Thr Leu Arg Arg His Gln Asp Val Met Gly Ser His Lys Trp Ile Ala
 690 695 700
 Leu Val Gly Asn Ser His Ser Asn Val Tyr Gln Gly Val Val Pro Gly
 705 710 715 720
 Ile Ala Glu Leu Glu Gly Gly Ile Gly Leu Arg Val Ile Asp Val Ala
 725 730 735
 Pro Gly Gln Ser Lys Gly Val Met His Asp Leu Gly Glu Leu Val Ser
 740 745 750
 Ala Asp Ile Ser Arg Thr Lys Val His Ile Lys Gly Asp Tyr Arg Val
 755 760 765
 Glu Ile Glu Ile Pro Arg Ala Lys Asp Ala Ile Arg Pro Pro Gln Pro
 770 775 780
 Val Thr Leu Glu Gln Arg Leu Ala Arg Pro Gly Leu Phe Leu Val Glu
 785 790 795 800
 Glu Ser Glu Gly Asn Leu Leu Thr Ile Val His Arg Ala Arg Asp Thr
 805 810 815
 Trp Ile His Arg Thr Pro Val Leu Val Asn Ala Glu Gly Lys Leu Tyr
 820 825 830
 Leu Glu Arg Val Arg Trp Pro Arg Ile His Leu Lys Pro Phe Asp Asp
 835 840 845
 Met Asp Ala Leu Val Ala Ala Leu Glu Glu Met Asn Leu Thr Arg Val
 850 855 860
 Gly
 865

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 <220> FEATURE:
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 immunodeficiency virus, TAT protein transduction
 domain

-continued

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<213> ORGANISM: Artificial Sequence

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<223> OTHER INFORMATION: Description of Artificial Sequence: hopPtoJ
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<223> OTHER INFORMATION: Description of Artificial Sequence: hopPtoJ
primer

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<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

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<223> OTHER INFORMATION: Description of Artificial Sequence: hopPtoK
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<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<213> ORGANISM: Artificial Sequence

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primer

<400> SEQUENCE: 36

aaggatccgc agagcgtgtc gcgacc 26

103

What is claimed:

- 1. An isolated nucleic acid molecule comprising a nucleotide sequence which encodes a protein or polypeptide comprising SEQ ID No: 12.
- 2. The nucleic acid molecule according to claim 1, wherein the nucleic acid molecule comprises the nucleotide sequence according to SEQ ID No: 11.
- 3. The nucleic acid molecule according to claim 1, wherein the nucleic acid molecule is DNA.
- 4. An expression system comprising a vector into which is inserted the nucleic acid molecule according to claim 3.
- 5. The expression system according to claim 4, wherein the nucleic acid molecule is inserted in sense orientation relative to a promoter.
- 6. A host cell comprising the nucleic acid molecule according to claim 3.
- 7. The host cell according to claim 6, wherein the host cell is a bacterial cell or a plant cell.
- 8. The host cell according to claim 7, wherein the bacterial cell is *Agrobacterium*.
- 9. A transgenic plant comprising the nucleic acid molecule according to claim 3.

104

- 10. A method of making a transgenic plant comprising: providing nucleic acid molecule according to claim 3, and transforming a plant cell with the nucleic acid molecule, whereby the nucleic acid molecule is expressed by the transformed plant cell.
- 11. A method of making a transgenic plant comprising: transforming a plant cell with the nucleic acid molecule according to claim 3, whereby the nucleic acid molecule is expressed by the transformed plant cell, and regenerating a transgenic plant from the transformed plant cell.
- 12. A method of making a plant hypersusceptible to colonization by nonpathogenic bacteria, said method comprising: transforming a plant cell with the nucleic acid molecule of claim 3, and regenerating a transgenic plant from the transformed plant cell, wherein a transgenic plant expresses a protein or polypeptide encoded by a nucleic acid molecule, thereby rendering the transgenic plant hypersusceptible to colonization by nonpathogenic bacteria.

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