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(54) **Title**: RNAi FOR THE CONTROL OF FUNGI AND OOMYCETES BY INHIBITING SACCHAROPINE DEHYDROGENASE GENE

(57) **Abstract**: The present invention relates to control of plant pathogens, particularly fungi or oomycetes, by inhibiting one or more biological functions, particularly by inhibiting saccharopine dehydrogenase gene(s) using RNA interference. The invention provides methods and compositions using RNA interference of plant pathogens target genes for such control. The invention is also directed to methods for making transgenic plants tolerant to said plant pathogens, and to transgenic plants and seeds generated thereof.

RNAi for the control of fungi and oomycetes by inhibiting saccharopine dehydrogenase gene

The present invention relates to control of plant pathogens and pests, particularly fungi or oomycetes, by inhibiting one or more biological functions, particularly by inhibiting fungi saccharopine dehydrogenase gene involved in the α-aminoadipate pathway for lysine biosynthesis and their oomycetes homologs using RNA interference.
The invention provides methods and compositions using RNA interference of fungi or oomycetes target genes for such control. The invention is also directed to methods for making transgenic plants tolerant to said fungi or oomycetes, and to transgenic plants and seeds generated thereof.

The technology used in the context of the present invention is RNA interference or RNAi.
The expression in an organism of a sequence homologous to a target-gene capable of inducing the formation of small double-stranded RNA (dsRNA) makes it possible, very specifically, to extinguish this gene and to observe the phenotype that results therefrom (Xiao *et al.,* 2003).

The dsRNA triggers the specific degradation of a homologous RNA only in the region of identity with the dsRNA (Zamore *et al.,* 2000; Tang *et al.,* 2003). The dsRNA is an RNA molecule which contains a double-stranded sequence, generally of at least 19 base pairs (bp) including a sense strand and an antisense strand. The dsRNA molecules are also characterized by the very large degree of complementarity between the two complementary RNA strands. The dsRNA is degraded into RNA fragments of generally 18 to 25 nucleotides (siRNA) and the cleavage sites on the target RNA are evenly spaced apart by 18 to 25 nucleotides. The small siRNAs resulting therefrom exhibit a very high degree of identity with respect to the target RNA; however, mismatches of 3 to 4 nucleotides between the siRNA and the corresponding portion of the target RNA nevertheless make it possible for the system to operate (Tang *et al.,* 2003). It has thus been suggested that these fragments of 18 to 25 nucleotides constitute RNA guides for recognition of the target (Zamore *et al.,* 2000). These small RNAs have also been detected in extracts prepared from Schneider 2 cells of *Drosophila melanogaster* which had been transfected with dsRNAs before cell lysis (Hammond *et al.,* 2000). The guiding role of the fragments of 18 to 25 nucleotides in the cleavage of the mRNAs is supported by the observation that these fragments of 19 to 25 nucleotides isolated from dsRNA are capable of being involved in the degradation of mRNA (Zamore *et al.,* 2000). Sizable homologous RNA molecules also accumulate in plant tissues which undergo the PTGS phenomenon (Post Transcriptional Gene Silencing, Hamilton and Baulcome, 1999). These small RNAs can regulate gene expression at three different levels:

- transcription (TGS for Transcriptional Gene Silencing),
- messenger RNA degradation (PTGS for Post Transcriptional Gene Silencing),
- miRNA pathway
- translation.

Regulation involving messenger RNA degradation appears to exist in all eukaryotes, whereas regulation at the transcriptional level has only been described in mammalians, plants, drosophila and *C. elegans.* As regards the regulation of translation, it has been characterized in *C. elegans* and drosophila and appears also to exist in mammals (Hannon, 2002) and plants (Ruiz Ferrer and Voinnet, 2009). In the literature, reference is made to RNAi, to PTGS, to cosuppression or to quelling (reserved for fungi) when referring to this phenomenon, depending on the organisms in which it is studied.

RNAi has in particular proved that it is effective when double-stranded RNA (dsRNA) is injected into the nematode Caenorhabditis elegans (Fire et al. 1998; Montgomery et al., 1998; WO99/32619). Inhibition of the expression of an insect target gene was also observed when this insect is fed with bacteria expressing small double-stranded RNAs corresponding to said insect target gene (WO 01/37654).

More recently, pharmaceutical compositions comprising dsRNA substantially complementary to at least part of a gene suspected to be involved in the human papilloma virus (HPV) infection together with a pharmaceutically acceptable carrier have been disclosed to treating said HPV infection (WO2009/0247607).

The introduction of dsRNA was carried out in plants in order to induce silencing of an endogenous target gene (Hamilton *et al.*, 1998, WO99/15682), to induce resistance to RNA viruses by means of the use of a transgene expressing a dsRNA having substantial identity with respect to the viral genes (Waterhouse *et al.*, 1998; Pandolfini *et al.*, 2003, WO98/36083, WO99/15682, US 5,175,102), but also to induce resistance to nematodes (Chuang and Meyerowitz, 2000, WO01/96584) or alternatively to the bacterium *Agrobacterium* (WO00/26346, Escobar *et al.*, 2001). More recently, it has been shown that plants expressing dsRNA having substantial identity against a fungal gene essential to the growth of the fungus or to its pathogenicity may also induced resistance to this fungus (WO05/071091).

Nevertheless, since that time, only few preliminary results and no commercial examples exist on RNAi-mediated resistance or tolerance to phytopathogenic fungi where the double-stranded (dsRNA) or small interfering (siRNA) molecules are expressed in the plant, or applied as part of an external composition to the seed, the plant or to the fruit of the plant or to soil or to inert substrate wherein the plant is growing or wherein it is desired to grow.

Among others, one difficulty is to find an appropriate target gene, whose inhibition by dsRNA or siRNA induces a good level of fungi tolerance, up to a level suitable for a commercial use, without deleterious effect on the plant expressing said dsRNA or siRNA or on which a composition comprising said dsRNA or siRNA is applied.

Stärkel C. attempted in her Ph. D. thesis ["Host induced gene silencing – strategies for the improvement of resistance against *Cercospora beticola* in sugar beet (B. vulgaris L.) and against *Fusarium graminearum* in wheat (T. aestivum L.) and maize (Z. mays L.)", defended in June 2011] to inhibit the growth of *Fusarium graminearum* by transforming wheat with silencing constructs targeting the homoaconitase gene, an essential gene in the lysine biosynthesis pathway. Nevertheless, no transgenic wheat plants could be generated. Moreover, the attempt to delete or silence the homoaconitase gene in *Fusarium graminearum* by transformation of the fungus with a contruct designed for the inducible silencing of the homoaconitase gene were also unsuccessful.

The present inventors have surprisingly demonstrated that inhibition of fungus or oomycetes saccharopine dehydrogenase gene, which is involved in the α-aminoadipate (AAA) pathway, via RNAi methodology causes cessation of infection, growth, development, reproduction and/or pathogenicity, and eventually results in the death of the organism.

This new target for the RNAi technology is particularly suitable, considering that AAA pathway is specifically found in some plant pathogens, including higher fungi, and not in plants, humans and animals.

Among the 20 common proteinogenic amino acids, L-lysine is the only one known to have a biosynthetic pathway which differs in plants and in higher fungi. In plants and bacteria, L-lysine is obtained through the diaminopimelate (DAP) pathway. In higher fungi and euglenoids, L-lysine is obtained through the the α-aminoadipate (AAA) pathway. Saccharopine dehydrogenase, homocitrate synthase, homoaconitase, homoisocitrate dehydrogenase, α-Aminoadipate aminotransferase, α-Aminoadipate reductase and saccharopine reductase are enzymes involved in the α-aminoadipate pathway for the biosynthesis of L-lysine.

None of the enzymes involved in these two distinct pathways (DAP and AAA pathways) are common (Xu et al., 2006, Bhattacharjee, J. K., 1985; Bhattacharjee, J. K., 1992; Vogel, H. J., 1965). As an example, fungi saccharopine dehydrogenase is involved in the Lysine biosynthesis, when the lysine-ketoglutarate from plant, sometimes also called saccharopine dehydrogenase, is responsible for lysine catabolism (Houmard et al., 2007). For humans and animals, L-lysine is an essential amino acid which can only be obtained from protein in the diet. Additionally, enzymes involved in the fungal AAA pathway are unique to lysine synthesis (Umbargar, H. E., 1978; Bhattacharjee, J. K., 1992).

The presence of a specific α-aminoadipate (AAA) pathway in higher fungi, which is not present nor in plant nor in humans or animals, leads to consider the enzymes involved in said AAA pathway as particularly attractive targets for the control of plant pathogens, particularly for fungal pathogens.

Interestingly, although lysine has been reported to be synthesized in oomycetes via the diaminopimelic pathway (Born and Blanchard, 1999), genes homologous to fungus genes of AAA pathway have been found in oomycetes, which may indicate that both pathways might be present in oomycetes. The inventors have shown that dsRNA against oomycete saccharopine dehydrogenase gene substantially reduced the growth of said oomycete, and that plants expressing dsRNA against oomycete saccharopine dehydrogenase genes could be less susceptible to said oomycete infection.

The presence of the AAA pathway for lysine biosynthesis has been demonstrated and studied for example in *Saccharomyces cerevisiae* (Broquist, H. P., 1971, Bhattacharjee, J. K., 1992), the human pathogenic fungi *Candida albicans* (Garrad, R. C. and Bhattacharjee, J. K., 1992), and the plant

pathogen *Magnaporthe grisea* (Umbargar, H. E., 1978). The saccharopine dehydrogenase enzymes involved in the AAA pathway have been intensively studied and compared in different organisms, and their technical features, including their nucleotides and aminoacids sequences, kinetics, substrate specificity, function, 3D- structure, as well as the way to purify and characterize them, are well known from the skilled man (see Xu et al., 2001, the content of which is incorporated herein by way of reference). Numerous genes from different fungi or oomycetes and their sequence data are disclosed and available in searchable public database, such as genBank.
Randall, T.A. et al. (2005) reports a list of genes of AAA pathway from the oomycete *Phytophthora infestans,* identified by their accession numbers and the sequence data thereof, incorporated herein by reference, are available in searchable public database (s) (Randall, T.A., 2005, MPMI, 18, 229-243; see in particular table 8 p 239).

In one embodiment, the present invention provides a dsRNA molecule comprising 1) a first strand comprising a sequence substantially identical to at least 18 contiguous nucleotides of a fungus or oomycete gene and ii) a second strand comprising a sequence substantially complementary to the first strand, wherein said fungus or oomycete gene is a saccharopine dehydrogenase gene.

As used herein, "RNAi" or "RNA interference" refers to the process of sequence- specific gene silencing, mediated by double-stranded RNA (dsRNA). As used herein, "dsRNA" or “dsRNA molecule” refers to RNA that is partially or completely double stranded. Double stranded RNA is also referred to small or short interfering RNA (siRNA), short interfering nucleic acid (siNA), short interfering RNA, micro-RNA (miRNA), circular interfering RNA (ciRNA), short hairpin RNA (shRNA) and the like.

As used herein, taking into consideration the substitution of uracil for thymine when comparing RNA and DNA sequences, the term "substantially identical" or “essentially homologous” as applied to dsRNA means that the nucleotide sequence of one strand of the dsRNA is at least about 80%, at least 85% identical to 18 or more contiguous nucleotides of the target gene, more preferably at least about 90 % identical to 18 or more contiguous nucleotides of the target gene, and most preferably at least about 95%, 96%, 97%, 98% or 99% identical or absolutely identical to 18 or more contiguous nucleotides of the target gene. 18 or more nucleotides means a portion, being at least about 18, 20, 21 , 22, 23, 24, 25, 50, 100, 200, 300, 400, 500, 1000, 1500, or 2000 consecutive bases or up to the full length of the target gene.

As used herein, "complementary" polynucleotides are those that are capable of base pairing according to the standard Watson-Crick complementarity rules. Specifically, purines will base pair with pyrimidines to form a combination of guanine paired with cytosine (G:C) and adenine paired with either thymine (A:T) in the case of DNA, or adenine paired with uracil (A:U) in the case of RNA. It is understood that two polynucleotides may hybridize to each other even if they are not completely complementary to each other, provided that each has at least one region that is substantially complementary to the other. As used herein, the term "substantially complementary" means that two nucleic acid sequences are complementary over at least 80% of their nucleotides. Preferably, the two nucleic acid sequences are complementary over at least 85%, 90%, 95%, 96%, 97%, 98%, 99% or more or all of their nucleotides. Alternatively, "substantially complementary" means that two nucleic acid sequences can hybridize under high stringency conditions. As used herein, the term "substantially identical" or "corresponding to" means that two nucleic acid sequences have at least 80% sequence identity. Preferably, the two nucleic acid sequences have at least 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% of sequence identity.

Also as used herein, the terms "nucleic acid" and "polynucleotide" refer to RNA or DNA that is linear or branched, single or double stranded, or a hybrid thereof. The term also encompasses RNA/DNA hybrids. When dsRNA is produced synthetically, less common bases, such as inosine, 5-methylcytosine, 6-methyladenine, hypoxanthine and others can also be used for antisense, dsRNA, and ribozyme pairing. For example, polynucleotides that contain C-5 propyne analogues of uridine and cytidine have been shown to bind RNA with high affinity and to be potent antisense inhibitors of gene expression. Other modifications, such as modification to the phosphodiester backbone, locked nucleic acid or the 2'-hydroxy in the ribose sugar group of the RNA can also be made.

Accordingly to the invention, the first strand and second strand may have identical sizes. Alternatively, the size of the first strand may be greater than that of the second strand. By way of example, the size of the first strand can be about 200 nucleotides greater than the size of the second strand. In another aspect of the invention, the size of second strand is greater than that of the first strand.

Accordingly to the invention, the dsRNA molecule comprises a first strand comprising a sequence substantially identical to at least 18 contiguous nucleotides of a fungus or oomycete saccharopine dehydrogenase gene.

In a particular embodiment, the invention provides a dsRNA molecule comprising 1) a first strand comprising a sequence substantially identical to at least 18 contiguous nucleotides of a fungus or oomycete gene and ii) a second strand comprising a sequence substantially complementary to the first strand, wherein said fungus or oomycete gene is selected from the list consisting of:

a) a polynucleotide comprising a sequence as set forth in SEQ ID N0: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43;

b) a polynucleotide encoding a polypeptide having a sequence as set forth in SEQ ID N0: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44;

c) a polynucleotide having at least 70% sequence identity, preferably at least 80%, more preferably at least 90%, even more preferably at least 95% to a polynucleotide having a sequence as set forth in SEQ ID N0: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43;

d) a polynucleotide encoding a polypeptide having at least 70% sequence identity, preferably at least 80%, more preferably at least 90%, even more preferably at least 95%, to a polypeptide having a sequence as set forth in SEQ ID N0: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44:

e) a polynucleotide hybridizing under stringent conditions to a polynucleotide having a sequence as set forth in SEQ ID N0: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43; and

f) a polynucleotide hybridizing under stringent conditions to a polynucleotide encoding a polypeptide having at least 70% sequence identity to a polypeptide having a sequence as set forth in SEQ ID N0: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44.

In accordance with the present invention, the term "identity" is to be understood to mean the number of amino acids/nucleotides corresponding with the amino acids/nucleotides of other protein/nucleic acid, expressed as a percentage. Identity is preferably determined by comparing the Seq. ID disclosed herein with other protein/nucleic acid with the help of computer programs. If sequences that are compared with one another have different lengths, the identity is to be determined in such a way that the number of amino acids, which have the shorter sequence in common with the longer sequence, determines the percentage quotient of the identity. Preferably, identity is determined by means of the computer program ClustalW, which is well known and available to the public (Thompson et al., 1994). ClustalW is made publicly available on
http://www.ebi.ac.uk/tools/clustalW2/index.html.
Preferably, Version 2.1 of the ClustalW computer program is used to determine the identity between proteins according to the invention and other proteins. In doing so, the following parameters must be set: KTUPLE=1, TOPDIAG=5, WINDOW=5, PAIRGAP=3, GAPOPEN=10, GAPEXTEND=0.05, GAPDIST=8, MAXDIV=40, MATRIX=GONNET, ENDGAPS(OFF), NOPGAP, NOHGAP.
Preferably, Version 2.1 of the ClustalW computer program is used to determine the identity between the nucleotide sequence of the nucleic acid molecules according to the invention, for example, and the nucleotide sequence of other nucleic acid molecules. In doing so, the following parameters must be set:
KTUPLE=2, TOPDIAGS=4, PAIRGAP=5, DNAMATRIX:IUB, GAPOPEN=10, GAPEXT=5, MAXDIV=40, TRANSITIONS: unweighted.

In accordance with the present invention, the term ‘hybridizing under stringent conditions” refers to polynucleotides or nucleic acid sequences which hybridize with a reference nucleic acid sequence at a level significantly greater than the background noise. The background noise may be associated with the hybridization of other DNA sequences present, in particular of other cDNAs present in a cDNA library. The level of the signal generated by the interaction between the sequence capable of selectively hybridizing and the sequences defined by the sequence IDs above according to the invention is generally 10 times, preferably 100 times, greater than that of the interaction of the other DNA sequences generating the background noise. The level of interaction can be measured, for example, by labeling the probe with radioactive elements such as ^{32}P. The selective hybridization is generally obtained by using very severe conditions for the medium (for example 0.03 M NaCl and 0.03 M sodium citrate at approximately 50℃-60℃). The hybridization can of course be carried out according to the usual methods of the state of the art (in particular Sambrook et al., 2001, Molecular Cloning: A Laboratory Manual, third edition).

In a particular embodiment of the invention, the dsRNA molecule is applied on the plant pathogen, particularly fungi or oomycete, and/or on the plant or crop to be protected. The present invention therefore also relates to a composition comprising an effective and non-phytotoxic amount of a dsRNA molecule as defined herein.

dsRNA molecules accordingly to the invention may be made by classical chemical synthesis, by means of *in vitro* transcription or produced in organisms like animals cells, bacteria, yeasts, or plants by heterologous expression (Aalto A.P. et al, 2007 RNA. 13(3):422-9.)

The present invention therefore relates to a micro-organism producing a dsRNA molecule as herein defined.

The present invention also relates to a genetic construct which comprises at least one DNA sequence as well as heterologous regulatory element(s) in the 5' and optionally in the 3' positions, characterized in that the DNA sequence is able to form a dsRNA molecule as herein defined.
The present invention also relates to a cloning and/or expression vector, characterized in that it contains at least one genetic construct as herein defined.

The expression "effective and non-phytotoxic amount" means an amount of composition according to the invention which is sufficient to control or destroy the pathogen present or liable to appear on the crops and which does not entail any appreciable symptom of phytotoxicity for the said crops. Such an amount can vary within a wide range depending on the pathogen to be controlled, the type of crop, the climatic conditions and the compounds included in the composition according to the invention. This amount can be determined by systematic field trials, which are within the capabilities of a person skilled in the art.

Thus, according to the invention, there is provided a composition comprising, as an active ingredient, an effective amount of a dsRNA molecule as herein defined and an agriculturally acceptable support, carrier, filler and/or surfactant.

According to the invention, the term "support" denotes a natural or synthetic organic or inorganic compound with which the active compound of formula (I) is combined or associated to make it easier to apply, notably to the parts of the plant. This support is thus generally inert and should be agriculturally acceptable. The support can be a solid or a liquid. Examples of suitable supports include clays, natural or synthetic silicates, silica, resins, waxes, solid fertilisers, water, alcohols, in particular butanol organic solvents, mineral and plant oils and derivatives thereof. Mixtures of such supports can also be used.

The composition according to the invention can also comprise additional components such as, but not limited to, surfactant, protective colloids, adhesives, thickeners, thixotropic agents, penetration agents, stabilisers, sequestering agents. More generally, the active compounds can be combined with any solid or liquid additive, which complies with the usual formulation techniques.

In general, the composition according to the invention can contain from 0.05 to 99% by weight of active compound, preferably 10 to 70% by weight.

Compositions according to the invention can be used in various forms such as aerosol dispenser, capsule suspension, cold fogging concentrate, dustable powder, emulsifiable concentrate, emulsion oil in water, emulsion water in oil, encapsulated granule, fine granule, flowable concentrate for seed treatment, gas (under pressure),gas generating product, granule, hot fogging concentrate, macrogranule, microgranule, oil dispersible powder, oil miscible flowable concentrate, oil miscible liquid, paste, plant rodlet, powder for dry seed treatment, seed coated with a pesticide, soluble concentrate, soluble powder, solution for seed treatment, suspension concentrate (flowable concentrate), ultra low volume (ULV) liquid, ultra low volume (ULV) suspension, water dispersible granules or tablets, water dispersible powder for slurry treatment, water soluble granules or tablets, water soluble powder for seed treatment and wettable powder. These compositions include not only compositions which are ready to be applied to the plant or seed to be treated by means of a suitable device, such as a spraying or dusting device, but also concentrated commercial compositions which must be diluted before application to the crop.

The compounds according to the invention can also be mixed with one or more phytopharmaceutical or plant growth promoting compound, such as a fungicide, herbicide, insecticide, nematicide, acaricide, molluscicide, resistance inducer, safeners, signal compounds, biologicals, pheromone active substance or other compounds with biological activity. The mixtures thus obtained have a broadened spectrum of activity. The mixtures with other fungicide compounds are particularly advantageous.

In a particular embodiment of the invention, the dsRNA is introduced or produced into the plant to be protected. After introduction or production into the plant, the dsRNA may further be processed into relatively small fragments (siRNAs) and can subsequently become distributed throughout the plant. Alternatively, the dsRNA is introduced or produced into the plant using a regulatory element or promoter that results in expression of the dsRNA in a tissue, temporal, spatial or inducible manner and may further be processed into relatively small fragments by a plant cell containing the RNAi processing machinery.

The invention therefore relates to a genetic construct or chimeric gene which is able to produce the dsRNA of the invention inside a plant cell. Said genetic construct or chimeric gene comprises at least one DNA sequence as well as well as heterologous regulatory element(s) in the 5' and optionally in the 3' positions which are able to function in a plant, characterized in that the DNA sequence(s) is (are) able to form a dsRNA molecule as herein defined once expressed in the plant.

In a particular embodiment, the genetic construct or chimeric gene comprises:
- a promoter regulatory sequence that is functional in plant cells, operably linked to
- a DNA sequence which, when it is transcribed, generates an RNA molecule comprising at least a sense sequence and an antisense sequence which are at least partially complementary, said sense sequence comprising a sequence substantially identical to at least 18 contiguous nucleotides of a target gene (i.e in the meaning of the invention a saccharopine dehydrogenase gene), and said antisense sequence comprising a sequence substantially complementary to the sense sequence, and
- optionally a terminator regulatory sequence.

In said embodiment, the DNA sequence according to the invention may have more particularly two aspects; in the first, it comprises two nucleotide sequences, which are sense and antisense, separated by a spacer nucleotide sequence or an intron that does not exhibit any homology with the target gene. The sequence cloned in the sense and antisense orientation is that whose expression in the pathogen it is intended to inhibit. The transcription of this DNA sequence thus gives a large single-stranded RNA corresponding to the sense/spacer-intron/antisense construct. This long RNA transcript can be detected by RT-PCR. Since the sense and antisense sequences are homologous, they will pair, and the spacer or intron which separates them plays the role of a loop for folding. A dsRNA is then obtained over all the homologous regions. The dsRNA is subsequently specifically degraded by an enzymatic complex called “DICER”. The degradation of the dsRNAs then forms siRNAs (“siRNA” in the figure), small double-stranded RNAs having a size of between 19 and 25 bases. These are then the siRNAs which, by pairing with the transcribed RNAs derived from the target gene will lead to their degradation via the RNA silencing machinery enzymatic machinery.
In the second aspect, the DNA sequence comprises two nucleotide sequences, which are sense and antisense, of different sizes, the loop structure corresponding to the part of the nucleotide sequence that does not exhibit any homology with the other nucleotide sequence. The nucleotide sequence cloned in the sense orientation is essentially homologous to the sequence of the target gene whose expression it is intended to inhibit. The antisense nucleotide sequence is essentially homologous to the complementary strand of the sequence of said target gene. The transcription of this DNA sequence thus gives a large single-stranded RNA corresponding to the sense/antisense construct. This long RNA transcript can be detected by RT-PCR. The homologous sense/antisense sequences are paired. A dsRNA is then obtained over all the homologous regions. The dsRNA is subsequently specifically degraded by an enzymatic complex called “DICER”. The degradation of the dsRNAs then forms siRNAs (“siRNA” in the figure), small doubled-stranded RNAs having a size of between 18 and

25 bases. These are then the siRNAs which, by pairing with the target RNAs, will lead to their degradation via the RNA silencing machinery plant's enzymatic machinery.

In another particular embodiment, the genetic construct comprises:

- two promoter regulatory sequences that are functional in plant cells, wherein the first promoter regulatory sequence is operably linked to a DNA sequence which, when it is transcribed, generates an RNA molecule comprising at least a sense sequence, and the second promoter regulatory sequence is operably linked to a DNA sequence which, when it is transcribed, generates an RNA molecule comprising at least an antisense sequence partially complementary to the sense sequence, and wherein said sense sequence comprises a sequence substantially identical to at least 18 contiguous nucleotides of the target gene, and
- optionally terminator regulatory sequence(s).

In this particular embodiment, the genetic construct may be comprised as two chimeric genes, one comprising the first promoter regulatory sequence operably linked to the first DNA sequence which, when it is transcribed, generates an RNA molecule comprising at least a sense sequence substantially identical to at least 18 contiguous nucleotides of the target gene, and optionally a terminator regulatory sequence, and the second chimeric genes comprising the second promoter regulatory sequence operably linked to the second DNA sequence which, when it is transcribed, generates an RNA molecule comprising at least an antisense sequence partially complementary to the sense sequence, and optionally a terminator regulatory sequence.

These two chimeric genes are preferably introduced into the plant cell conjointly, but not neccessary, in order to favorize the hybridization of the two RNA single strands to form the dsRNA.

Alternatively, the genetic construct may be comprised as a construct comprising:

- a first promoter, operably linked to
- a double strand DNA sequence wherein one strand when it is transcribed under the control of the first promoter, generates an RNA molecule comprising at least a sense sequence substantially identical to at least 18 contiguous nucleotides of the target gene, and optionally a terminator regulatory sequence, and wherein the second strand, when it is transcribed under the control of the second promoter, generates an RNA molecule comprising at least an antisense sequence partially complementary to the sense sequence, and optionally a terminator regulatory sequence, and
- a second promoter, in the opposite direction that the first one.

First and second promoter regulatory sequences may be different or identical, preferably different.

The invention further relates to a cloning and/or expression vector for transforming a plant, characterized in that it contains at least one chimeric gene or genetic construct as defined herein.

The present invention further relates to a transgenic plant cell containing the dsRNA molecule of the invention and as herein defined.

The present invention therefore relates to a transgenic plant cell containing the genetic construct or chimeric gene of the invention as herein defined.

In a particular embodiment of the invention, the transgenic plant cell is a soybean, oilseed, rice or potato plant cell.

The present invention further relates to a transgenic plant, seed or part thereof, comprising a transgenic plant cell according to the invention.

In a particular embodiment of the invention, the transgenic plant, seed or part thereof, is a soybean, oilseed, rice or potato plant, seed or part thereof.

According to the invention, the expression “chimeric gene” or “expression cassette” is intended to mean a nucleotide sequence comprising, functionally linked to one another in the direction of transcription, a regulatory promoter sequence that is functional in plants, a sequence encoding a protein or an RNA chain, and, optionally, a terminator that is functional in plant cells. The term “chimeric gene” or “expression cassette” is generally intended to mean a gene for which certain elements are not present in the native gene, but have been substituted for elements present in the native gene or have been added.
According to the invention, the terms “chimeric gene” or “expression cassette” may also correspond to the case where all the elements of the gene are present in the native gene, and alternatively, the term “gene” may correspond to a chimeric gene.
The expression “chimeric gene” or “expression cassette” may also correspond to the case where the sequence encoding a protein or a RNA chain is not directly linked to a promoter, but is part, for example, of a polycistronic construct comprising several coding sequences under the control of the same promoter. In that case, each coding sequences under the control of the promoter is designed as a “chimeric gene” or “expression cassette”.

According to the invention, the expression “functionally linked to one another” means that said elements of the elemental chimeric gene are linked to one another in such a way that their function is coordinated and allows the expression of the coding sequence. By way of example, a promoter is functionally linked to a coding sequence when it is capable of ensuring the expression of said coding sequence. The construction of the chimeric gene according to the invention and the assembly of its various elements can be carried out using techniques well known to those skilled in the art, in particular those described in Sambrook et al. (2001, Molecular Cloning : A Laboratory Manual (third edition), Nolan C. ed., New York: Cold Spring Harbor Laboratory Press). The choice of the regulatory elements constituting the chimeric gene depends essentially on the plant and on the type of cell in which they must function, and those skilled in the art are capable of selecting regulatory elements that are functional in a given plant.

According to the invention, the term “promoter regulatory sequence” is intended to mean any promoter regulatory sequence of a gene that is naturally expressed in plants, in particular a promoter that is expressed especially in the leaves of plants, for instance promoters referred to as constitutive of bacterial, viral or plant origin, or else promoters referred to as light-dependent, such as that of a plant ribulose-biscarboxylase/oxygenase (RuBisCO) small subunit gene, or any known suitable promoter that can be used. Among the promoters of plant origin, mention will be made of the histone promoters as described in application EP 0 507 698, or the rice actin promoter (US 5,641,876). Among the promoters of a plant virus gene, mention will be made of that of the cauliflower mosaic virus (CaMV 19S or 35S) or of the cassava vein mosaic virus (CsVMV: WO97/48819) or the circovirus promoter (AU 689 311). Use may also be made of a promoter regulatory sequence specific for particular regions or tissues of plants, and more particularly seed-specific promoters (Datla, R. *et al.*, 1997, Biotechnology Ann. Rev., 3, 269-296), especially the napin (EP 255 378), phaseolin, glutenin, helianthinin (WO 92/17580), albumin (WO 98/45460) and oleosin (WO 98/45461) promoters. An inducible promoter can also be used, it can be advantageously chosen from the promoters of phenylalanine ammonia lyase (PAL), of HMG-CoA reductase (HMG), of chitinases, of glucanases, of proteinase inhibitors (PI), of genes of the PR1 family, of nopaline synthase (nos) or of the vspB gene (US 5 670 349), the HMG2 promoter (US 5 670 349), the apple beta-galactosidase (ABG1) promoter or the apple amino cyclopropane carboxylate synthase (ACC synthase) promoter (WO 98/45445).

The term “terminator regulatory sequence” is intended to mean any sequence that is functional in plant cells or plants, also comprising polyadenylation sequences, whether they are of bacterial origin, for instance the nos or ocs terminator of *Agrobacterium tumefaciens*, of viral origin, for instance the CaMV 35S terminator, or else of plant origin, for instance a histone terminator as described in application EP 0 633 317.

The selection step for identifying the transformed cells and/or plants having integrated the construct according to the invention can be carried out by virtue of the presence of a selectable gene present in the construct according to the invention or in the plasmid used for the transformation of the cells or of the plants and comprising said construct. The selectable gene may be in the form of a chimeric gene comprising the following elements, functionally linked in the direction of transcription: a promoter regulatory sequence that is functional in plant cells, a sequence encoding a selectable marker, and a terminator regulatory sequence that is functional in plant cells.

Among the selectable markers that can be used, mention may be made of markers containing genes for resistance to antibiotics, such as, for example, that of the hygromycin phosphotransferase gene (Gritz *et al.*, 1983, Gene 25: 179-188), of the neomycin phosphotransferase II gene inducing resistance to kanamycin (Wirtz *et al.*, 1987, DNA, 6(3): 245-253), or of the aminoglycoside 3”-adenyltransferase gene, but also markers containing genes for tolerance to herbicides, such as the *bar* gene (White *et al.*, NAR 18: 1062, 1990) for tolerance to bialaphos, the EPSPS gene (US 5,188,642) for tolerance to glyphosate or else the HPPD gene (WO 96/38567) for tolerance to isoxazoles. Mention may also be made of genes encoding readily indentifiable enzymes, such as the GUS enzyme, GFP protein or genes encoding pigments or enzymes regulating pigment production in the transformed cells. Such selectable marker genes are in particular described in patent applications WO 91/02071, WO 95/06128, WO 96/38567, and WO 97/04103.

The present invention further relates to a method of making a transgenic plant cell or plant capable of expressing a dsRNA that inhibits a fungus or oomycete saccharopine dehydrogenase gene, wherein said method comprises the steps of transforming a plant cell with a chimeric gene or genetic construct according to the invention.
The method may further comprise the step of selecting the plant cell which has been transformed.

In a particular embodiment of the invention, the invention relates to a method of making a transgenic plant cell or plant capable of expressing a dsRNA that inhibits fungus or oomycete saccharopine dehydrogenase gene , wherein said method comprises the steps of transforming a plant cell with a chimeric gene or genetic construct according to the invention, and wherein said plant cell is a soybean, oilseed, rice or potato plant cell or said plant is a soybean, oilseed, rice or potato plant.

The present invention also relates to the transformed plants or part thereof, and to plants or part thereof which are derived by cultivating and/or crossing the above regenerated plants, and to the seeds of the transformed plants.
The present invention also relates to the end products such as the meal, oil, fiber which are obtained from the plants, part thereof, or seeds of the invention.

To obtain the cells or plants according to the invention, those skilled in the art can use one of the numerous known methods of transformation.
One of these methods consists in bringing the cells or tissues of the host organisms to be transformed into contact with polyethylene glycol (PEG) and the vectors of the invention (Chang and Cohen, 1979, Mol. Gen. Genet. 168(1), 111-115; Mercenier and Chassy, 1988, Biochimie 70(4), 503-517). Electroporation is another method, which consists in subjecting the cells or tissues to be transformed and the vectors of the invention to an electric field (Andreason and Evans, 1988, Biotechniques 6(7), 650-660; Shigekawa and Dower, 1989, Aust. J. Biotechnol. 3(1), 56-62). Another method consists in directly injecting the vectors into the cells or the tissues by microinjection (Gordon and Ruddle, 1985, Gene 33(2), 121-136). Advantageously, the “biolistic” method may be used. It consists in bombarding cells or tissues with particles onto which the vectors of the invention are adsorbed (Bruce *et al.*, 1989, Proc. Natl. Acad. Sci. USA 86(24), 9692-9696; Klein *et al.*, 1992, Biotechnology 10(3), 286-291; US Patent No. 4,945,050). Preferably, the transformation of plant cells or tissues can be carried out using bacteria of the *Agrobacterium* genus, preferably by infection of the cells or tissues of said plants with *A. tumefaciens* (Knopf, 1979, Subcell. Biochem. 6, 143-173; Shaw *et al.*, 1983, Gene 23(3): 315-330) or *A. rhizogenes* (Bevan and Chilton, 1982, Annu. Rev. Genet. 16: 357-384; Tepfer and Casse-Delbart, 1987, Microbiol. Sci. 4(1), 24-28). Preferably, the transformation of plant cells or tissues with

Agrobacterium tumefaciens is carried out according to the protocol described by Hiei *et al.*, (1994, Plant J. 6(2): 271-282). Those skilled in the art will choose the appropriate method according to the nature of the host organisms to be transformed.

The plants according to the invention contain transformed plant cells as defined above. In particular, the transformed plants can be obtained by regeneration of the transformed plant cells described above. The regeneration is obtained by any appropriate method, which depends on the nature of the species.

The invention also comprises parts of these plants, and the progeny of these plants. The term “part of these plants” is intended to mean any organ of these plants, whether above ground or below ground. The organs above ground are the stems, the leaves and the flowers comprising the male and female reproductive organs. The organs below ground are mainly the roots, but they may also be tubers. The term “progeny” is intended to mean mainly the seeds containing the embryos derived from the reproduction of these plants with one another. By extension, the term “progeny” applies to all the seeds formed at each new generation derived from crosses between the transformed plants according to the invention. Progeny and seeds can also be obtained by vegetative multiplication of said transformed plants. The seeds according to the invention can be coated with an agrochemical composition comprising at least one active product having an activity selected from fungicidal, herbicidal, insecticidal, nematicidal, bactericidal or virucidal activities.

The invention further relates to a method for controlling a plant pathogen, particularly a fungus or an oomycete, comprising providing to said pathogen a dsRNA molecule according to the invention and as herein defined.

In a particular embodiment of the invention, the method relates to a method for controlling a plant pathogen, particularly a fungus or an oomycete, comprising providing to said pathogen a dsRNAaccording to the invention and as herein defined , or a composition comprising said dsRNA, wherein said plant pathogen is *Magnaporthe grisea, Phytophthora infestans, Sclerotinia sclerotiorum* or *Phakopsora pachyrhizi.*

In a particular embodiment of the invention, the method relates to a method for controlling a plant pathogen, particularly a fungus or an oomycete, comprising providing to said pathogen a dsRNA molecule according to the invention and as herein defined , or a composition comprising said dsRNA, wherein said plant is a soybean, oilseed, rice or potato plant.

The invention further relates to a method for controlling a plant, crop or seed pathogen, particularly a fungus or an oomycete, characterized in that an agronomically effective and substantially non-phytotoxic quantity of dsRNA molecule according to the invention or composition according to the invention is applied as seed treatment, foliar application, stem application, drench or drip application (chemigation) to the seed, the plant or to the fruit of the plant or to soil or to inert substrate (e.g.

inorganic substrates like sand, rockwool, glasswool; expanded minerals like perlite, vermiculite, zeolite or expanded clay), Pumice, Pyroclastic materials or stuff, synthetic organic substrates (e.g. polyurethane) organic substrates (e.g. peat, composts, tree waste products like coir, wood fibre or chips, tree bark) or to a liquid substrate (e.g. floating hydroponic systems, Nutrient Film Technique, Aeroponics) wherein the plant is growing or wherein it is desired to grow.

The invention therefore relates to a method for controlling a plant pathogen, particularly a fungus or oomycete, characterized in that an effective quantity of a dsRNA molecule according to the invention or a composition according to the invention is applied to the soil where plants grow or are capable of growing, to the leaves and/or the fruit of plants or to the seeds of plants.

In a particular embodiment of the invention, the invention relates to a method for controlling a plant pathogen, particularly a fungus or oomycete, characterized in that an effective quantity of a dsRNA molecule according to the invention or a composition according to the invention is applied to the soil where plants grow or are capable of growing, to the leaves and/or the fruit of plants or to the seeds of plants, wherein said plant pathogen is Magnaporthe grisea, Phytophthora infestans, Sclerotinia sclerotinium or Phakopsora pachyrhizi.

In a particular embodiment of the invention, the invention relates to a method for controlling a plant pathogen, particularly a fungus or oomycete, characterized in that an effective quantity of a dsRNA molecule according to the invention or a composition according to the invention is applied to the soil where plants grow or are capable of growing, to the leaves and/or the fruit of plants or to the seeds of plants, wherein said plant is a soybean, oilseed, rice or potato plant.

The expression “are applied to the plants to be treated” is understood to mean, for the purposes of the present invention, that the pesticide composition which is the subject of the invention can be applied by means of various methods of treatment such as:

- spraying onto the aerial parts of the said plants a liquid comprising one of the said compositions,
- dusting, the incorporation into the soil of granules or powders, spraying, around the said plants and in the case of trees injection or daubing,
- coating or film-coating the seeds of the said plants with the aid of a plant-protection mixture comprising one of the said compositions.

The method according to the invention can either be a curing, preventing or eradicating method.

In this method, a composition used can be prepared beforehand by mixing the two or more active compounds according to the invention.

According to an alternative of such a method, it is also possible to apply simultaneously, successively or separately compounds (A) and (B) so as to have the conjugated (A)/(B) effects, of distinct compositions each containing one of the two or three active ingredients (A) or (B).

The dose of active dsRNA compound usually applied in the method of treatment according to the invention is generally and advantageously

- for foliar treatments: from 0.0001 to 10,000 g/ha, preferably from 0,0001 to 1000 g/ha, more preferably from 0.001 to 300g/ha; in case of drench or drip application, the dose can even be reduced, especially while using inert substrates like rockwool or perlite;
- for seed treatment: from 0.0001 to 200 g per 100 kilogram of seed, preferably from 0.001 to 150 g per 100 kilogram of seed;
- for soil treatment: from 0.0001 to 10,000 g/ha, preferably from 0.001 to 5,000 g/ha.

When the dsRNA of the invention is mixed with another active phytopharmaceutical or plant growth promoting compound compound, said phytopharmaceutical or plant growth promoting compound is used in the dose usually applied.

Said phytopharmaceutical or plant growth promoting compound may be a fungicide, herbicide, insecticide, nematicide, acaricide, molluscicide, resistance inducer, safeners, or signal compounds. The dose of phytopharmaceutical active compound usually applied in the method of treatment according to the invention is generally and advantageously from 10 to 800 g/ha, preferably from 50 to 300 g/ha for applications in foliar treatment. The dose of active substance applied is generally and advantageously from 2 to 200 g per 100 kg of seed, preferably from 3 to 150 g per 100 kg of seed in the case of seed treatment.

The doses herein indicated are given as illustrative Examples of method according to the invention. A person skilled in the art will know how to adapt the application doses, notably according to the nature of the plant or crop to be treated.

Under specific conditions, for example according to the nature of the pathogen, phytopathogenic fungus or oomycete to be treated or controlled, a lower dose can offer adequate protection. Certain climatic conditions, resistance or other factors like the nature of the pathogen or the degree of infestation, for example, of the plants with these pathogens, can require higher doses of combined active ingredients. The optimum dose usually depends on several factors, for example on the type of pathogen to be treated, on the type or level of development of the infested plant or plant material, on the density of vegetation or alternatively on the method of application.

Without it being limiting, the crop treated with the pesticide composition or combination according to the invention is, for example, grapevine, cereals, vegetables, lucerne, soybean, market garden crops, turf, wood, tree or horticultural plants.

The method of treatment according to the invention can also be useful to treat propagation material such as tubers or rhizomes, but also seeds, seedlings or seedlings pricking out and plants or plants pricking out. This method of treatment can also be useful to treat roots. The method of treatment according to the invention can also be useful to treat the over-ground parts of the plant such as trunks, stems or stalks, leaves, flowers and fruit of the concerned plant, and in general every material which is susceptiblel to fungal infection (e.g due to storage like hay)

The invention further relates to a method of controlling a plant pathogen, particularly a fungus or an oomycete, comprising providing in the host plant of said plant pathogen a transformed plant cell according to the invention.

The invention further relates to a method of controlling a plant pathogen, particularly a fungus or an oomycete, comprising providing in the host plant of said plant pathogen a transformed plant cell containing a dsRNA as herein defined.

The invention further relates to a method of controlling a plant pathogen, particularly a fungus or an oomycete, comprising transforming the plant with a genetic construct according to the invention.

The invention further relates to a method of controlling a plant pathogen, particularly a fungus or an oomycete, comprising the following steps:

i) transforming a plant cell with a chimeric gene according to the invention;

ii) placing the cells thus transformed under conditions that allow the transcription of said construct,

iii) having the cells into contact with the pathogen.

In a particular embodiment of the invention, methods according to the invention are controlling a plant pathogen selected from Magnaporthe grisea, Phytophthora infestans, Sclerotinia sclerotinium or Phakopsora pachyrhizi.

In a particular embodiment of the invention, methods according to the invention are controlling a plant pathogen wherein the plant is a soybean, oilseed, rice or potato plant.

The invention further relates to a method for inhibiting the expression of a plant pathogen, particularly fungus or oomycete, saccharopine dehydrogenase gene, comprising the following steps:

i) transforming a plant cell with a chimeric gene according to the invention;

ii) placing the cells thus transformed under conditions that allow the transcription of said construct,

iii) having the cells into contact with the pathogen.

In a particular embodiment of the invention, the method according to the invention is inhibiting a fungal or oomycete saccharopine dehydrogenase gene , wherein the fungus or oomycete is Magnaporthe grisea, Phytophthora infestans, Sclerotinia sclerotinium or Phakopsora pachyrhizi.

In a particular embodiment of the invention, the method according to the invention inhibites a fungal or oomycete saccharopine dehydrogenase gene , said method comprises the following steps:

i) transforming a plant cell with a chimeric gene according to the invention;

ii) placing the cells thus transformed under conditions that allow the transcription of said construct,

iii) having the cells into contact with the pathogen;
wherein the plant is a soybean, oilseed, rice or potato plant.

According to the invention all plants and plant parts can be treated. By plants is meant all plants and plant populations such as desirable and undesirable wild plants, cultivars and plant varieties (whether or not protectable by plant variety or plant breeder's rights). Cultivars and plant varieties can be plants obtained by conventional propagation and breeding methods which can be assisted or supplemented by one or more biotechnological methods such as by use of double haploids, protoplast fusion, random and directed mutagenesis, molecular or genetic markers or by bioengineering and genetic engineering methods. By plant parts is meant all above ground and below ground parts and organs of plants such as shoot, leaf, blossom and root, whereby for example leaves, needles, stems, branches, blossoms, fruiting bodies, fruits and seed as well as roots, corms and rhizomes are listed. Crops and vegetative and generative propagating material, for example cuttings, corms, rhizomes, runners and seeds also belong to plant parts.
Among the plants that can be protected by the method according to the invention, mention may be made of major field crops like corn, soybean, cotton, *Brassica* oilseeds such as *Brassica napus* (e.g. canola), *Brassica rapa*, *B. juncea* (e.g. mustard) and *Brassica carinata*, rice, wheat, sugarbeet, sugarcane, oats, rye, barley, millet, triticale, flax, vine and various fruits and vegetables of various botanical taxa such as *Rosaceae sp.* (for instance pip fruit such as apples and pears, but also stone fruit such as apricots, cherries, almonds and peaches, berry fruits such as strawberries), *Ribesioidae sp.*, *Juglandaceae sp.*, *Betulaceae sp.*, *Anacardiaceae sp.*, *Fagaceae sp.*, *Moraceae sp.*, *Oleaceae sp.*, *Actinidaceae sp.*, *Lauraceae sp.*, *Musaceae sp.* (for instance banana trees and plantings), *Rubiaceae sp.* (for instance coffee), *Theaceae sp.*, *Sterculiceae sp.*, *Rutaceae sp.* (for instance lemons, oranges and grapefruit) ; *Solanaceae sp.* (for instance tomatoes, potatoes, peppers, eggplant), *Liliaceae sp.*, Compositiae *sp.* (for instance lettuce, artichoke and chicory - including root chicory, endive or common chicory), *Umbelliferae sp.* (for instance carrot, parsley, celery and celeriac), *Cucurbitaceae sp.* (for instance cucumber – including pickling cucumber, squash, watermelon, gourds and melons), *Alliaceae* sp. (for instance onions and leek), Cruciferae *sp.* (for instance white cabbage, red cabbage, broccoli, cauliflower, brussel sprouts, pak choi, kohlrabi, radish, horseradish, cress, Chinese cabbage), Leguminosae *sp.* (for instance peanuts, peas and beans beans - such as climbing beans and broad beans), *Chenopodiaceae sp.* (for instance mangold, spinach beet, spinach, beetroots), *Malvaceae* (for instance okra), *Asparagaceae* (for instance asparagus); horticultural and forest crops; ornamental plants; as well as genetically modified homologues of these crops.

The method of treatment according to the invention can be used in the treatment of genetically modified organisms (GMOs), e.g. plants or seeds. Genetically modified plants (or transgenic plants) are plants of which a heterologous gene has been stably integrated into genome. The expression "heterologous gene" essentially means a gene which is provided or assembled outside the plant and when introduced in the nuclear, chloroplastic or mitochondrial genome gives the transformed plant new or improved agronomic or other properties by expressing a protein or polypeptide of interest or by downregulating or silencing other gene(s) which are present in the plant (using for example, antisense technology, cosuppression technology or RNA interference – RNAi - technology). A heterologous gene that is located in the genome is also called a transgene. A transgene that is defined by its particular location in the plant genome is called a transformation or transgenic event.

Depending on the plant species or plant cultivars, their location and growth conditions (soils, climate, vegetation period, diet), the treatment according to the invention may also result in superadditive (“synergistic”) effects. Thus, for example, reduced application rates and/or a widening of the activity spectrum and/or an increase in the activity of the active compounds and compositions which can be used according to the invention, better plant growth, increased tolerance to high or low temperatures, increased tolerance to drought or to water or soil salt content, increased flowering performance, easier harvesting, accelerated maturation, higher harvest yields, bigger fruits, larger plant height, greener leaf color, earlier flowering, higher quality and/or a higher nutritional value of the harvested products, higher sugar concentration within the fruits, better storage stability and/or processability of the harvested products are possible, which exceed the effects which were actually to be expected.

At certain application rates, the active compound combinations according to the invention may also have a strengthening effect in plants. Accordingly, they are also suitable for mobilizing the defense system of the plant against attack by unwanted microorganisms. This may, if appropriate, be one of the reasons of the enhanced activity of the combinations according to the invention, for example against fungi. Plant-strengthening (resistance-inducing) substances are to be understood as meaning, in the present context, those substances or combinations of substances which are capable of stimulating the defense system of plants in such a way that, when subsequently inoculated with unwanted microorganisms, the treated plants display a substantial degree of resistance to these microorganisms. In the present case, unwanted microorganisms are to be understood as meaning phytopathogenic fungi, bacteria and viruses. Thus, the substances according to the invention can be employed for protecting plants against attack by the abovementioned pathogens within a certain period of time after the treatment. The period of time within which protection is effected generally extends from 1 to 10 days, preferably 1 to 7 days, after the treatment of the plants with the active compounds.

As already mentioned above, it is possible to treat all plants and their parts in accordance with the invention. In a preferred embodiment, wild plant species and plant cultivars, or those obtained by conventional biological breeding methods, such as crossing or protoplast fusion, and also parts thereof, are treated. In a further preferred embodiment, transgenic plants and plant cultivars obtained by genetic engineering methods, if appropriate in combination with conventional methods (Genetically Modified Organisms), and parts thereof are treated. The terms “parts” or “parts of plants” or “plant parts” have been explained above. More preferably, plants of the plant cultivars which are commercially available or are in use are treated in accordance with the invention. Plant cultivars are understood to mean plants which have new properties ("traits") and have been obtained by conventional breeding, by mutagenesis or by recombinant DNA techniques. They can be cultivars, varieties, bio- or genotypes.

The method of treatment according to the invention can be used in the treatment of genetically modified organisms (GMOs), e.g. plants or seeds. Genetically modified plants (or transgenic plants) are plants of which a heterologous gene has been stably integrated into genome. The expression “heterologous gene” essentially means a gene which is provided or assembled outside the plant and when introduced in the nuclear, chloroplastic or mitochondrial genome gives the transformed plant new or improved agronomic or other properties by expressing a protein or polypeptide of interest or by downregulating or silencing other gene(s) which are present in the plant (using for example, antisense technology, cosuppression technology, RNA interference – RNAi – technology or microRNA – miRNA - technology). A heterologous gene that is located in the genome is also called a transgene. A transgene that is defined by its particular location in the plant genome is called a transformation or transgenic event.

Depending on the plant species or plant cultivars, their location and growth conditions (soils, climate, vegetation period, diet), the treatment according to the invention may also result in superadditive (“synergistic”) effects. Thus, for example, reduced application rates and/or a widening of the activity spectrum and/or an increase in the activity of the active compounds and compositions which can be used according to the invention, better plant growth, increased tolerance to high or low temperatures, increased tolerance to drought or to water or soil salt content, increased flowering performance, easier harvesting, accelerated maturation, higher harvest yields, bigger fruits, larger plant height, greener leaf color, earlier flowering, higher quality and/or a higher nutritional value of the harvested products, higher sugar concentration within the fruits, better storage stability and/or processability of the harvested products are possible, which exceed the effects which were actually to be expected.

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Plants and plant cultivars which are preferably to be treated according to the invention include all plants which have genetic material which impart particularly advantageous, useful traits to these plants (whether obtained by breeding and/or biotechnological means).

Plants and plant cultivars which are also preferably to be treated according to the invention are resistant against one or more biotic stresses, i.e. said plants show a better defense against animal and microbial pests, such as against nematodes, insects, mites, phytopathogenic fungi, bacteria, viruses and/or viroids.

Examples of nematode or insect resistant plants are described in e.g. U.S. Patent Applications 11/765,491, 11/765,494, 10/926,819, 10/782,020, 12/032,479, 10/783,417, 10/782,096, 11/657,964, 12/192,904, 11/396,808, 12/166,253, 12/166,239, 12/166,124, 12/166,209, 11/762,886, 12/364,335, 11/763,947, 12/252,453, 12/209,354, 12/491,396, 12/497,221, 12/644,632, 12/646,004, 12/701,058, 12/718,059, 12/721,595, 12/638,591.

Plants and plant cultivars which may also be treated according to the invention are those plants which are resistant to one or more abiotic stresses. Abiotic stress conditions may include, for example, drought, cold temperature exposure, heat exposure, osmotic stress, flooding, increased soil salinity, increased mineral exposure, ozone exposure, high light exposure, limited availability of nitrogen nutrients, limited availability of phosphorus nutrients, shade avoidance.

Plants and plant cultivars which may also be treated according to the invention, are those plants characterized by enhanced yield characteristics. Increased yield in said plants can be the result of, for example, improved plant physiology, growth and development, such as water use efficiency, water retention efficiency, improved nitrogen use, enhanced carbon assimilation, improved photosynthesis, increased germination efficiency and accelerated maturation. Yield can furthermore be affected by improved plant architecture (under stress and non-stress conditions), including but not limited to, early flowering, flowering control for hybrid seed production, seedling vigor, plant size, internode number and distance, root growth, seed size, fruit size, pod size, pod or ear number, seed number per pod or ear, seed mass, enhanced seed filling, reduced seed dispersal, reduced pod dehiscence and lodging resistance. Further yield traits include seed composition, such as carbohydrate content, protein content, oil content and composition, nutritional value, reduction in anti-nutritional compounds, improved processability and better storage stability.

Plants that may be treated according to the invention are hybrid plants that already express the characteristic of heterosis or hybrid vigor which results in generally higher yield, vigor, health and resistance towards biotic and abiotic stresses). Such plants are typically made by crossing an inbred male-sterile parent line (the female parent) with another inbred male-fertile parent line (the male parent). Hybrid seed is typically harvested from the male sterile plants and sold to growers. Male sterile plants can sometimes (e.g. in corn) be produced by detasseling, i.e. the mechanical removal of the male reproductive organs (or males flowers) but, more typically, male sterility is the result of genetic determinants in the plant genome. In that case, and especially when seed is the desired product to be harvested from the hybrid plants it is typically useful to ensure that male fertility in the hybrid plants is fully restored. This can be accomplished by ensuring that the male parents have appropriate fertility restorer genes which are capable of restoring the male fertility in hybrid plants that contain the genetic determinants responsible for male-sterility. Genetic determinants for male sterility may be located in the cytoplasm. Examples of cytoplasmic male sterility (CMS) were for instance described in Brassica species (WO 92/05251, WO 95/09910, WO 98/27806, WO 05/002324, WO 06/021972 and US 6,229,072). However, genetic determinants for male sterility can also be located in the nuclear genome. Male sterile plants can also be obtained by plant biotechnology methods such as genetic engineering. A particularly useful means of obtaining male-sterile plants is described in WO 89/10396 in which, for example, a ribonuclease such as barnase is selectively expressed in the tapetum cells in the stamens. Fertility can then be restored by expression in the tapetum cells of a ribonuclease inhibitor such as barstar (e.g. WO 91/02069).

Plants or plant cultivars (obtained by plant biotechnology methods such as genetic engineering) which may be treated according to the invention are herbicide-tolerant plants, i.e. plants made tolerant to one or more given herbicides. Such plants can be obtained either by genetic transformation, or by selection of plants containing a mutation imparting such herbicide tolerance.

Herbicide-resistant plants are for example glyphosate-tolerant plants, i.e. plants made tolerant to the herbicide glyphosate or salts thereof. Plants can be made tolerant to glyphosate through different means. For example, glyphosate-tolerant plants can be obtained by transforming the plant with a gene encoding the enzyme 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS). Examples of such EPSPS genes are the AroA gene (mutant CT7) of the bacterium Salmonella typhimurium (Science 1983, 221, 370-371), the CP4 gene of the bacterium Agrobacterium sp. (Curr. Topics Plant Physiol. 1992, 7, 139-145), the genes encoding a Petunia EPSPS (Science 1986, 233, 478-481), a Tomato EPSPS (J. Biol. Chem. 1988, 263, 4280-4289), or an Eleusine EPSPS (WO 01/66704). It can also be a mutated EPSPS as described in for example EP 0837944, WO 00/66746, WO 00/66747 or WO 02/26995. Glyphosate-tolerant plants can also be obtained by expressing a gene that encodes a glyphosate oxido-reductase enzyme as described in US 5,776,760 and US 5,463,175. Glyphosate-tolerant plants can also be obtained by expressing a gene that encodes a glyphosate acetyl transferase enzyme as described in for example WO 02/036782, WO 03/092360, WO 2005/012515 and WO 2007/024782. Glyphosate-tolerant plants can also be obtained by selecting plants containing naturally-occurring mutations of the above-mentioned genes, as described in for example WO 01/024615 or WO 03/013226. Plants expressing EPSPS genes that confer glyphosate tolerance are described in e.g. U.S. Patent Applications 11/517,991, 10/739,610, 12/139,408, 12/352,532, 11/312,866, 11/315,678, 12/421,292, 11/400,598, 11/651,752, 11/681,285, 11/605,824, 12/468,205, 11/760,570, 11/762,526, 11/769,327, 11/769,255, 11/943801 or 12/362,774. Plants comprising other genes that confer glyphosate tolerance, such as decarboxylase genes, are described in e.g. U.S. Patent Applications 11/588,811, 11/185,342, 12/364,724, 11/185,560 or 12/423,926.

Other herbicide resistant plants are for example plants that are made tolerant to herbicides inhibiting the enzyme glutamine synthase, such as bialaphos, phosphinothricin or glufosinate. Such plants can be obtained by expressing an enzyme detoxifying the herbicide or a mutant glutamine synthase enzyme that is resistant to inhibition, e.g. described in U.S. Patent Application 11/760,602. One such efficient detoxifying enzyme is an enzyme encoding a phosphinothricin acetyltransferase (such as the bar or pat protein from Streptomyces species). Plants expressing an exogenous phosphinothricin acetyltransferase are for example described in U.S. Patents 5,561,236; 5,648,477; 5,646,024; 5,273,894; 5,637,489; 5,276,268; 5,739,082; 5,908,810 and 7,112,665.

Further herbicide-tolerant plants are also plants that are made tolerant to the herbicides inhibiting the enzyme hydroxyphenylpyruvatedioxygenase (HPPD). HPPD is an enzyme that catalyze the reaction in which para-hydroxyphenylpyruvate (HPP) is transformed into homogentisate. Plants tolerant to HPPD-inhibitors can be transformed with a gene encoding a naturally-occurring resistant HPPD enzyme, or a gene encoding a mutated or chimeric HPPD enzyme as described in WO 96/38567, WO

99/24585, WO 99/24586, WO 09/144079, WO 02/046387, or US 6,768,044. Tolerance to HPPD-inhibitors can also be obtained by transforming plants with genes encoding certain enzymes enabling the formation of homogentisate despite the inhibition of the native HPPD enzyme by the HPPD-inhibitor. Such plants and genes are described in WO 99/34008 and WO 02/36787. Tolerance of plants to HPPD inhibitors can also be improved by transforming plants with a gene encoding an enzyme having prephenate deshydrogenase (PDH) activity in addition to a gene encoding an HPPD-tolerant enzyme, as described in WO 04/024928. Further, plants can be made more tolerant to HPPD-inhibitor herbicides by adding into their genome a gene encoding an enzyme capable of metabolizing or degrading HPPD inhibitors, such as the CYP450 enzymes shown in WO 2007/103567 and WO 2008/150473.

Still further herbicide resistant plants are plants that are made tolerant to acetolactate synthase (ALS) inhibitors. Known ALS-inhibitors include, for example, sulfonylurea, imidazolinone, triazolopyrimidines, pryimidinyoxy(thio)benzoates, and/or sulfonylaminocarbonyltriazolinone herbicides. Different mutations in the ALS enzyme (also known as acetohydroxyacid synthase, AHAS) are known to confer tolerance to different herbicides and groups of herbicides, as described for example in Tranel and Wright (Weed Science 2002, 50, 700-712), but also, in U.S. Patents 5,605,011, 5,378,824, 5,141,870, and 5,013,659. The production of sulfonylurea-tolerant plants and imidazolinone-tolerant plants is described in U.S. Patents 5,605,011; 5,013,659; 5,141,870; 5,767,361; 5,731,180; 5,304,732; 4,761,373; 5,331,107; 5,928,937; and 5,378,824; and WO 96/33270. Other imidazolinone-tolerant plants are also described in for example WO 2004/040012, WO 2004/106529, WO 2005/020673, WO 2005/093093, WO 2006/007373, WO 2006/015376, WO 2006/024351, and WO 2006/060634. Further sulfonylurea- and imidazolinone-tolerant plants are also described in for example WO 2007/024782 and U.S. Patent Application 61/288958.

Other plants tolerant to imidazolinone and/or sulfonylurea can be obtained by induced mutagenesis, selection in cell cultures in the presence of the herbicide or mutation breeding as described for example for soybeans in US 5,084,082, for rice in WO 97/41218, for sugar beet in US 5,773,702 and WO 99/057965, for lettuce in US 5,198,599, or for sunflower in WO 01/065922.

Plants or plant cultivars (obtained by plant biotechnology methods such as genetic engineering) which may also be treated according to the invention are insect-resistant transgenic plants, i.e. plants made resistant to attack by certain target insects. Such plants can be obtained by genetic transformation, or by selection of plants containing a mutation imparting such insect resistance.

An “insect-resistant transgenic plant”, as used herein, includes any plant containing at least one transgene comprising a coding sequence encoding:

1) an insecticidal crystal protein from Bacillus thuringiensis or an insecticidal portion thereof, such as the insecticidal crystal proteins listed by Crickmore et al. (1998, Microbiology and Molecular Biology Reviews, 62: 807-813), updated by Crickmore et al. (2005) at the Bacillus thuringiensis toxin nomenclature, online at: http://www.lifesci.sussex.ac.uk/Home/Neil_Crickmore/Bt/), or insecticidal portions thereof, e.g., proteins of the Cry protein classes Cry1Ab, Cry1Ac, Cry1B, Cry1C, Cry1D, Cry1F, Cry2Ab, Cry3Aa, or Cry3Bb or insecticidal portions thereof (e.g. EP-

A 1 999 141 and WO 2007/107302), or such proteins encoded by synthetic genes as e.g. described in and U.S. Patent Application 12/249,016 ; or

2) a crystal protein from Bacillus thuringiensis or a portion thereof which is insecticidal in the presence of a second other crystal protein from Bacillus thuringiensis or a portion thereof, such as the binary toxin made up of the Cry34 and Cry35 crystal proteins (Nat. Biotechnol. 2001, 19, 668-72; Applied Environm. Microbiol. 2006, 71, 1765-1774) or the binary toxin made up of the Cry1A or Cry1F proteins and the Cry2Aa or Cry2Ab or Cry2Ae proteins (U.S. Patent Application 12/214,022 and EP-A 2 300 618); or

3) a hybrid insecticidal protein comprising parts of different insecticidal crystal proteins from Bacillus thuringiensis, such as a hybrid of the proteins of 1) above or a hybrid of the proteins of 2) above, e.g., the Cry1A.105 protein produced by corn event MON89034 (WO 2007/027777); or

4) a protein of any one of 1) to 3) above wherein some, particularly 1 to 10, amino acids have been replaced by another amino acid to obtain a higher insecticidal activity to a target insect species, and/or to expand the range of target insect species affected, and/or because of changes introduced into the encoding DNA during cloning or transformation, such as the Cry3Bb1 protein in corn events MON863 or MON88017, or the Cry3A protein in corn event MIR604; or

5) an insecticidal secreted protein from Bacillus thuringiensis or Bacillus cereus, or an insecticidal portion thereof, such as the vegetative insecticidal (VIP) proteins listed at: http://www.lifesci.sussex.ac.uk/home/Neil_Crickmore/Bt/vip.html, e.g., proteins from the VIP3Aa protein class; or

6) a secreted protein from Bacillus thuringiensis or Bacillus cereus which is insecticidal in the presence of a second secreted protein from Bacillus thuringiensis or B. cereus, such as the binary toxin made up of the VIP1A and VIP2A proteins (WO 94/21795); or

7) a hybrid insecticidal protein comprising parts from different secreted proteins from Bacillus thuringiensis or Bacillus cereus, such as a hybrid of the proteins in 1) above or a hybrid of the proteins in 2) above; or

8) a protein of any one of 5) to 7) above wherein some, particularly 1 to 10, amino acids have been replaced by another amino acid to obtain a higher insecticidal activity to a target insect species, and/or to expand the range of target insect species affected, and/or because of changes introduced into the encoding DNA during cloning or transformation (while still encoding an insecticidal protein), such as the VIP3Aa protein in cotton event COT102; or

9) a secreted protein from Bacillus thuringiensis or Bacillus cereus which is insecticidal in the presence of a crystal protein from Bacillus thuringiensis, such as the binary toxin made up of VIP3 and Cry1A or Cry1F (U.S. Patent Applications 61/126083 and 61/195019), or the binary

toxin made up of the VIP3 protein and the Cry2Aa or Cry2Ab or Cry2Ae proteins (U.S. Patent Application 12/214,022 and EP-A 2 300 618).

10) a protein of 9) above wherein some, particularly 1 to 10, amino acids have been replaced by another amino acid to obtain a higher insecticidal activity to a target insect species, and/or to expand the range of target insect species affected, and/or because of changes introduced into the encoding DNA during cloning or transformation (while still encoding an insecticidal protein)

Of course, an insect-resistant transgenic plant, as used herein, also includes any plant comprising a combination of genes encoding the proteins of any one of the above classes 1 to 10. In one embodiment, an insect-resistant plant contains more than one transgene encoding a protein of any one of the above classes 1 to 10, to expand the range of target insect species affected when using different proteins directed at different target insect species, or to delay insect resistance development to the plants by using different proteins insecticidal to the same target insect species but having a different mode of action, such as binding to different receptor binding sites in the insect.

An “insect-resistant transgenic plant”, as used herein, further includes any plant containing at least one transgene comprising a sequence producing upon expression a double-stranded RNA which upon ingestion by a plant insect pest inhibits the growth of this insect pest, as described e.g. in WO 2007/080126, WO 2006/129204, WO 2007/074405, WO 2007/080127 and WO 2007/035650.

Plants or plant cultivars (obtained by plant biotechnology methods such as genetic engineering) which may also be treated according to the invention are tolerant to abiotic stresses. Such plants can be obtained by genetic transformation, or by selection of plants containing a mutation imparting such stress resistance. Particularly useful stress tolerance plants include:

1) plants which contain a transgene capable of reducing the expression and/or the activity of poly(ADP-ribose) polymerase (PARP) gene in the plant cells or plants as described in WO 00/04173, WO 2006/045633, EP-A 1 807 519, or EP-A 2 018 431.

2) plants which contain a stress tolerance enhancing transgene capable of reducing the expression and/or the activity of the PARG encoding genes of the plants or plants cells, as described e.g. in WO 2004/090140.

3) plants which contain a stress tolerance enhancing transgene coding for a plant-functional enzyme of the nicotineamide adenine dinucleotide salvage synthesis pathway including nicotinamidase, nicotinate phosphoribosyltransferase, nicotinic acid mononucleotide adenyl transferase, nicotinamide adenine dinucleotide synthetase or nicotine amide phosphorybosyltransferase as described e.g. in EP-A 1 794 306, WO 2006/133827, WO 2007/107326, EP-A 1 999 263, or WO 2007/107326.

Plants or plant cultivars (obtained by plant biotechnology methods such as genetic engineering) which may also be treated according to the invention show altered quantity, quality and/or storage-stability of the harvested product and/or altered properties of specific ingredients of the harvested product such as:

1) transgenic plants which synthesize a modified starch, which in its physical-chemical characteristics, in particular the amylose content or the amylose/amylopectin ratio, the degree of branching, the average chain length, the side chain distribution, the viscosity behaviour, the gelling strength, the starch grain size and/or the starch grain morphology, is changed in comparison with the synthesised starch in wild type plant cells or plants, so that this is better suited for special applications. Said transgenic plants synthesizing a modified starch are disclosed, for example, in EP-A 0 571 427, WO 95/04826, EP-A 0 719 338, WO 96/15248, WO 96/19581, WO 96/27674, WO 97/11188, WO 97/26362, WO 97/32985, WO 97/42328, WO 97/44472, WO 97/45545, WO 98/27212, WO 98/40503, WO 99/58688, WO 99/58690, WO 99/58654, WO 00/08184, WO 00/08185, WO 00/08175, WO 00/28052, WO 00/77229, WO 01/12782, WO 01/12826, WO 02/101059, WO 03/071860, WO 04/056999, WO 05/030942, WO 2005/030941, WO 2005/095632, WO 2005/095617, WO 2005/095619, WO 2005/095618, WO 2005/123927, WO 2006/018319, WO 2006/103107, WO 2006/108702, WO 2007/009823, WO 00/22140, WO 2006/063862, WO 2006/072603, WO 02/034923, WO 2008/017518, WO 2008/080630, WO 2008/080631, EP 07090007.1, WO 2008/090008, WO 01/14569, WO 02/79410, WO 03/33540, WO 2004/078983, WO 01/19975, WO 95/26407, WO 96/34968, WO 98/20145, WO 99/12950, WO 99/66050, WO 99/53072, US 6,734,341, WO 00/11192, WO 98/22604, WO 98/32326, WO 01/98509, WO 01/98509, WO 2005/002359, US 5,824,790, US 6,013,861, WO 94/04693, WO 94/09144, WO 94/11520, WO 95/35026, WO 97/20936, WO 2010/012796, WO 2010/003701,

2) transgenic plants which synthesize non starch carbohydrate polymers or which synthesize non starch carbohydrate polymers with altered properties in comparison to wild type plants without genetic modification. Examples are plants producing polyfructose, especially of the inulin and levan-type, as disclosed in EP-A 0 663 956, WO 96/01904, WO 96/21023, WO 98/39460, and WO 99/24593, plants producing alpha-1,4-glucans as disclosed in WO 95/31553, US 2002031826, US 6,284,479, US 5,712,107, WO 97/47806, WO 97/47807, WO 97/47808 and WO 00/14249, plants producing alpha-1,6 branched alpha-1,4-glucans, as disclosed in WO 00/73422, plants producing alternan, as disclosed in e.g. WO 00/47727, WO 00/73422, EP 06077301.7, US 5,908,975 and EP-A 0 728 213,

3) transgenic plants which produce hyaluronan, as for example disclosed in WO 2006/032538, WO 2007/039314, WO 2007/039315, WO 2007/039316, JP-A 2006-304779, and WO 2005/012529.

4) transgenic plants or hybrid plants, such as onions with characteristics such as 'high soluble solids content', 'low pungency' (LP) and/or 'long storage' (LS), as described in U.S. Patent Applications 12/020,360 and 61/054,026.

Plants or plant cultivars (that can be obtained by plant biotechnology methods such as genetic engineering) which may also be treated according to the invention are plants, such as cotton plants, with altered fiber characteristics. Such plants can be obtained by genetic transformation, or by selection of plants contain a mutation imparting such altered fiber characteristics and include:

a) Plants, such as cotton plants, containing an altered form of cellulose synthase genes as described in WO 98/00549.

b) Plants, such as cotton plants, containing an altered form of rsw2 or rsw3 homologous nucleic acids as described in WO 2004/053219.

c) Plants, such as cotton plants, with increased expression of sucrose phosphate synthase as described in WO 01/17333.

d) Plants, such as cotton plants, with increased expression of sucrose synthase as described in WO 02/45485.

e) Plants, such as cotton plants, wherein the timing of the plasmodesmatal gating at the basis of the fiber cell is altered, e.g. through downregulation of fiber-selective β-1,3-glucanase as described in WO 2005/017157, or as described in WO 2009/143995.

f) Plants, such as cotton plants, having fibers with altered reactivity, e.g. through the expression of N-acetylglucosaminetransferase gene including nodC and chitin synthase genes as described in WO 2006/136351.

Plants or plant cultivars (that can be obtained by plant biotechnology methods such as genetic engineering) which may also be treated according to the invention are plants, such as oilseed rape or related Brassica plants, with altered oil profile characteristics. Such plants can be obtained by genetic transformation, or by selection of plants contain a mutation imparting such altered oil profile characteristics and include:

a) Plants, such as oilseed rape plants, producing oil having a high oleic acid content as described e.g. in US 5,969,169, US 5,840,946 or US 6,323,392 or US 6,063,947

b) Plants such as oilseed rape plants, producing oil having a low linolenic acid content as described in US 6,270,828, US 6,169,190, or US 5,965,755

c) Plant such as oilseed rape plants, producing oil having a low level of saturated fatty acids as described e.g. in US 5,434,283 or U.S. Patent Application 12/668303

Plants or plant cultivars (that can be obtained by plant biotechnology methods such as genetic engineering) which may also be treated according to the invention are plants, such as oilseed rape or related Brassica plants, with altered seed shattering characteristics. Such plants can be obtained by genetic transformation, or by selection of plants contain a mutation imparting such altered seed shattering characteristics and include plants such as oilseed rape plants with delayed or reduced seed shattering as described in U.S. Patent Application 61/135,230, WO 2009/068313 and WO 2010/006732.

Plants or plant cultivars (that can be obtained by plant biotechnology methods such as genetic engineering) which may also be treated according to the invention are plants, such as Tobacco plants, with altered post-translational protein modification patterns, for example as described in WO 2010/121818 and WO 2010/145846.

Particularly useful transgenic plants which may be treated according to the invention are plants containing transformation events, or combination of transformation events, that are the subject of petitions for non-regulated status, in the United States of America, to the Animal and Plant Health Inspection Service (APHIS) of the United States Department of Agriculture (USDA) whether such petitions are granted or are still pending. At any time this information is readily available from APHIS (4700 River Road, Riverdale, MD 20737, USA), for instance on its internet site (URL http://www.aphis.usda.gov/brs/not_reg.html). On the filing date of this application the petitions for nonregulated status that were pending with APHIS or granted by APHIS were those which contains the following information:

- Petition: the identification number of the petition. Technical descriptions of the transformation events can be found in the individual petition documents which are obtainable from APHIS, for example on the APHIS website, by reference to this petition number. These descriptions are herein incorporated by reference.

- Extension of Petition: reference to a previous petition for which an extension is requested.

- Institution: the name of the entity submitting the petition.

- Regulated article: the plant species concerned.

- Transgenic phenotype: the trait conferred to the plants by the transformation event.

- Transformation event or line: the name of the event or events (sometimes also designated as lines or lines) for which nonregulated status is requested.

- APHIS documents: various documents published by APHIS in relation to the Petition and which can be requested with APHIS.

Additional particularly useful plants containing single transformation events or combinations of transformation events are listed for example in the databases from various national or regional regulatory agencies (see for example http://gmoinfo.jrc.it/gmp_browse.aspx and http://www.agbios.com/dbase.php).

Particularly useful transgenic plants which may be treated according to the invention are plants containing transformation events, or a combination of transformation events, and that are listed for example in the databases for various national or regional regulatory agencies including Event 1143-14A (cotton, insect control, not deposited, described in WO 2006/128569); Event 1143-51B (cotton, insect control, not deposited, described in WO 2006/128570); Event 1445 (cotton, herbicide tolerance, not deposited, described in US-A 2002-120964 or WO 02/034946); Event 17053 (rice, herbicide tolerance, deposited as PTA-9843, described in WO 2010/117737); Event 17314 (rice, herbicide tolerance, deposited as PTA-9844, described in WO 2010/117735); Event 281-24-236 (cotton, insect control - herbicide tolerance, deposited as PTA-6233, described in WO 2005/103266 or US-A 2005-216969); Event 3006-210-23 (cotton, insect control - herbicide tolerance, deposited as PTA-6233, described in US-A 2007-143876 or WO 2005/103266); Event 3272 (corn, quality trait, deposited as PTA-9972, described in WO 2006/098952 or US-A 2006-230473); Event 40416 (corn, insect control - herbicide tolerance, deposited as ATCC PTA-11508, described in WO 2011/075593); Event 43A47 (corn, insect control - herbicide tolerance, deposited as ATCC PTA-11509, described in WO 2011/075595); Event 5307 (corn, insect control, deposited as ATCC PTA-9561, described in WO 2010/077816); Event ASR-368 (bent grass, herbicide tolerance, deposited as ATCC PTA-4816, described in US-A 2006-162007 or WO 2004/053062); Event B16 (corn, herbicide tolerance, not deposited, described in US-A 2003-126634); Event BPS-CV127-9 (soybean, herbicide tolerance, deposited as NCIMB No. 41603, described in WO 2010/080829); Event CE43-67B (cotton, insect control, deposited as DSM ACC2724, described in US-A 2009-217423 or WO2006/128573); Event CE44-69D (cotton, insect control, not deposited, described in US-A 2010-0024077); Event CE44-69D (cotton, insect control, not deposited, described in WO 2006/128571); Event CE46-02A (cotton, insect control, not deposited, described in WO 2006/128572); Event COT102 (cotton, insect control, not deposited, described in US-A 2006-130175 or WO 2004/039986); Event COT202 (cotton, insect control, not deposited, described in US-A 2007-067868 or WO 2005/054479); Event COT203 (cotton, insect control, not deposited, described in WO 2005/054480); Event DAS40278 (corn, herbicide tolerance, deposited as ATCC PTA-10244, described in WO 2011/022469); Event DAS-59122-7 (corn, insect control - herbicide tolerance, deposited as ATCC PTA 11384 , described in US-A 2006-070139); Event DAS-59132 (corn, insect control - herbicide tolerance, not deposited, described in WO 2009/100188); Event DAS68416 (soybean, herbicide tolerance, deposited as ATCC PTA-10442, described in WO 2011/066384 or WO 2011/066360); Event DP-098140-6 (corn, herbicide tolerance, deposited as ATCC PTA-8296, described in US-A 2009-137395 or WO 2008/112019); Event DP-305423-1 (soybean, quality trait, not deposited, described in US-A 2008-312082 or WO 2008/054747); Event DP-32138-1 (corn, hybridization system, deposited as ATCC PTA-9158, described in US-A 2009-0210970 or WO 2009/103049); Event DP-356043-5 (soybean, herbicide tolerance, deposited as ATCC PTA-8287, described in US-A 2010-0184079 or WO 2008/002872); Event EE-1 (brinjal, insect control, not deposited, described in WO 2007/091277); Event FI117 (corn, herbicide tolerance, deposited as ATCC 209031, described in US-A 2006-059581 or WO 98/044140); Event GA21 (corn, herbicide tolerance, deposited as ATCC 209033, described in US-A 2005-086719 or WO 98/044140); Event GG25 (corn, herbicide tolerance, deposited as ATCC 209032, described in US-A 2005-188434 or WO 98/044140); Event GHB119 (cotton, insect control - herbicide tolerance, deposited as ATCC PTA-8398, described in WO 2008/151780); Event GHB614 (cotton, herbicide tolerance, deposited as ATCC PTA-6878, described in US-A 2010-050282 or WO 2007/017186); Event GJ11 (corn, herbicide tolerance, deposited as ATCC 209030, described in US-A 2005-188434 or WO 98/044140); Event GM RZ13 (sugar beet, virus resistance , deposited as NCIMB-41601, described in WO 2010/076212); Event H7-1 (sugar beet, herbicide tolerance, deposited as NCIMB 41158 or NCIMB 41159, described in US-A 2004-172669 or WO 2004/074492); Event JOPLIN1 (wheat, disease tolerance, not deposited, described in US-A 2008-064032); Event LL27 (soybean, herbicide tolerance, deposited as NCIMB41658, described in WO 2006/108674 or US-A 2008-320616); Event LL55 (soybean, herbicide tolerance, deposited as NCIMB 41660, described in WO 2006/108675 or US-A 2008-196127); Event LLcotton25 (cotton, herbicide tolerance, deposited as ATCC PTA-3343, described in WO 03/013224 or US-A 2003-097687); Event LLRICE06 (rice, herbicide tolerance, deposited as ATCC-23352, described in US 6,468,747 or WO 00/026345); Event LLRICE601 (rice, herbicide tolerance, deposited as ATCC PTA-2600, described in US-A 2008-2289060 or WO 00/026356); Event LY038 (corn, quality trait, deposited as ATCC PTA-5623, described in US-A 2007-028322 or WO 2005/061720); Event MIR162 (corn, insect control, deposited as PTA-8166, described in US-A 2009-300784 or WO 2007/142840); Event MIR604 (corn, insect control, not deposited, described in US-A 2008-167456 or WO 2005/103301); Event MON15985 (cotton, insect control, deposited as ATCC PTA-2516, described in US-A 2004-250317 or WO 02/100163); Event MON810 (corn, insect control, not deposited, described in US-A 2002-102582); Event MON863 (corn, insect control, deposited as ATCC PTA-2605, described in WO 2004/011601 or US-A 2006-095986); Event MON87427 (corn, pollination control, deposited as ATCC PTA-7899, described in WO 2011/062904); Event MON87460 (corn, stress tolerance, deposited as ATCC PTA-8910, described in WO 2009/111263 or US-A 2011-0138504); Event MON87701 (soybean, insect control, deposited as ATCC PTA-8194, described in US-A 2009-130071 or WO 2009/064652); Event MON87705 (soybean, quality trait - herbicide tolerance, deposited as ATCC PTA-9241, described in US-A 2010-0080887 or WO 2010/037016); Event MON87708 (soybean, herbicide tolerance, deposited as ATCC PTA9670, described in WO 2011/034704); Event MON87754 (soybean, quality trait, deposited as ATCC PTA-9385, described in WO 2010/024976); Event MON87769 (soybean, quality trait, deposited as ATCC PTA-8911, described in US-A 2011-0067141 or WO 2009/102873); Event MON88017 (corn, insect control - herbicide tolerance, deposited as ATCC PTA-5582, described in US-A 2008-028482 or WO 2005/059103); Event MON88913 (cotton, herbicide tolerance, deposited as ATCC PTA-4854, described in WO 2004/072235 or US-A 2006-059590); Event MON89034 (corn, insect control, deposited as ATCC PTA-7455, described in WO 2007/140256 or US-A 2008-260932); Event MON89788 (soybean, herbicide tolerance, deposited as ATCC PTA-6708, described in US-A 2006-282915 or WO 2006/130436); Event MS11 (oilseed rape, pollination control - herbicide tolerance, deposited as ATCC PTA-850 or PTA-2485, described in WO 01/031042); Event MS8 (oilseed rape, pollination control - herbicide tolerance, deposited as ATCC PTA-730, described in WO 01/041558 or US-A 2003-188347); Event NK603 (corn, herbicide tolerance, deposited as ATCC PTA-2478, described in US-A 2007-292854); Event PE-7 (rice, insect control, not deposited, described in WO 2008/114282); Event RF3 (oilseed rape, pollination control - herbicide tolerance, deposited as ATCC PTA-730, described in WO 01/041558 or US-A 2003-188347); Event RT73 (oilseed rape, herbicide tolerance, not deposited, described in WO 02/036831 or US-A 2008-070260); Event T227-1 (sugar beet, herbicide tolerance, not deposited, described in WO 02/44407 or US-A 2009-265817); Event T25 (corn, herbicide tolerance, not deposited, described in US-A 2001-029014 or WO 01/051654); Event T304-40 (cotton, insect control - herbicide tolerance, deposited as ATCC PTA-8171, described in US-A 2010-077501 or WO 2008/122406); Event T342-142 (cotton, insect control, not deposited, described in WO 2006/128568); Event TC1507 (corn, insect control - herbicide tolerance, not deposited, described in US-A 2005-039226 or WO 2004/099447); Event VIP1034 (corn, insect control - herbicide tolerance, deposited as ATCC PTA-3925., described in WO 03/052073), Event 32316 (corn,insect control-herbicide tolerance,deposited as PTA-11507, described in WO 2011/084632), Event 4114 (corn,insect control-herbicide tolerance,deposited as PTA-11506, described in WO 2011/084621).

The composition according to the invention can also be used against fungal diseases liable to grow on or inside timber. The term “timber” means all types of species of wood and all types of working of this wood intended for construction, for example solid wood, high-density wood, laminated wood and plywood. The method for treating timber according to the invention mainly consists in contacting one or more compounds according to the invention or a composition according to the invention; this includes for example direct application, spraying, dipping, injection or any other suitable means.

Among the diseases of plants or crops that can be controlled by the methods according to the invention, mention can be made of :

Powdery mildew diseases such as :

Blumeria diseases, caused for example by *Blumeria graminis* ;

Podosphaera diseases, caused for example by *Podosphaera leucotricha* ;

Sphaerotheca diseases, caused for example by *Sphaerotheca fuliginea* ;

Uncinula diseases, caused for example by *Uncinula necator* ;

Rust diseases such as :

Gymnosporangium diseases, caused for example by *Gymnosporangium sabinae* ;

Hemileia diseases, caused for example by *Hemileia vastatrix* ;

Phakopsora diseases, caused for example by *Phakopsora pachyrhizi* or *Phakopsora meibomiae* ;

Puccinia diseases, caused for example by *Puccinia recondite*, *Puccinia graminis or Puccinia striiformis*;

Uromyces diseases, caused for example by *Uromyces appendiculatus* ;

Oomycete diseases such as :

Albugo diseases caused for example by *Albugo candida*;

Bremia diseases, caused for example by *Bremia lactucae* ;

Peronospora diseases, caused for example by *Peronospora pisi* or *P. brassicae* ;

Phytophthora diseases, caused for example by *Phytophthora infestans* ;

Plasmopara diseases, caused for example by Pla*smopara viticola* ;

Pseudoperonospora diseases, caused for example by *Pseudoperonospora humuli* or *Pseudoperonospora cubensis* ;

Pythium diseases, caused for example by *Pythium ultimum* ;

Leafspot, leaf blotch and leaf blight diseases such as :

Alternaria diseases, caused for example by *Alternaria solani* ;

Cercospora diseases, caused for example by *Cercospora beticola* ;

Cladiosporum diseases, caused for example by *Cladiosporium cucumerinum* ;

Cochliobolus diseases, caused for example by *Cochliobolus sativus* (Conidiaform: Drechslera, Syn: Helminthosporium) or *Cochliobolus miyabeanus* ;

Colletotrichum diseases, caused for example by *Colletotrichum lindemuthanium* ;

Cycloconium diseases, caused for example by *Cycloconium oleaginum* ;

Diaporthe diseases, caused for example by *Diaporthe citri* ;

Elsinoe diseases, caused for example by *Elsinoe fawcettii* ;

Gloeosporium diseases, caused for example by *Gloeosporium laeticolor* ;

Glomerella diseases, caused for example by *Glomerella cingulata* ;

Guignardia diseases, caused for example by *Guignardia bidwelli* ;

Leptosphaeria diseases, caused for example by *Leptosphaeria maculans* ; *Leptosphaeria nodorum* ;

Magnaporthe diseases, caused for example by *Magnaporthe grisea* ;

Mycosphaerella diseases, caused for example by *Mycosphaerella graminicola* ; Mycosphaerella arachidicola ; *Mycosphaerella fijiensis* ;

Phaeosphaeria diseases, caused for example by *Phaeosphaeria nodorum* ;

Pyrenophora diseases, caused for example by *Pyrenophora teres*, or *Pyrenophora tritici repentis*;

Ramularia diseases, caused for example by *Ramularia collo-cygni* , or *Ramularia areola*;

Rhynchosporium diseases, caused for example by *Rhynchosporium secalis* ;

Septoria diseases, caused for example by *Septoria apii* or *Septoria lycopercisi* ;

Typhula diseases, caused for example by *Typhula incarnata* ;

Venturia diseases, caused for example by *Venturia inaequalis* ;

Root, Sheath and stem diseases such as :

Corticium diseases, caused for example by *Corticium graminearum* ;

Fusarium diseases, caused for example by *Fusarium oxysporum* ;

Gaeumannomyces diseases, caused for example by *Gaeumannomyces graminis* ;

Rhizoctonia diseases, caused for example by *Rhizoctonia solani* ;

Sarocladium diseases caused for example by *Sarocladium oryzae*;

Sclerotium diseases caused for example by *Sclerotium oryzae*;

Tapesia diseases, caused for example by *Tapesia acuformis* ;

Thielaviopsis diseases, caused for example by *Thielaviopsis basicola* ;

Ear and panicle diseases such as :

Alternaria diseases, caused for example by *Alternaria spp.* ;

Aspergillus diseases, caused for example by *Aspergillus flavus* ;

Cladosporium diseases, caused for example by *Cladosporium spp.* ;

Claviceps diseases, caused for example by *Claviceps purpurea* ;

Fusarium diseases, caused for example by *Fusarium culmorum* ;

Gibberella diseases, caused for example by *Gibberella zeae* ;

Monographella diseases, caused for example by *Monographella nivalis* ;

Smut and bunt diseases such as :

Sphacelotheca diseases, caused for example by *Sphacelotheca reiliana* ;

Tilletia diseases, caused for example by *Tilletia caries* ;

Urocystis diseases, caused for example by *Urocystis occulta* ;

Ustilago diseases, caused for example by *Ustilago nuda* ;

Fruit rot and mould diseases such as :

Aspergillus diseases, caused for example by *Aspergillus flavus* ;

Botrytis diseases, caused for example by *Botrytis cinerea* ;

Penicillium diseases, caused for example by *Penicillium expansum* ;

Rhizopus diseases caused by example by *Rhizopus stolonifer*

Sclerotinia diseases, caused for example by *Sclerotinia sclerotiorum* ;

Verticilium diseases, caused for example by *Verticilium alboatrum* ;

Seed and soilborne decay, mould, wilt, rot and damping-off diseases :

Alternaria diseases, caused for example by *Alternaria brassicicola*

Aphanomyces diseases, caused for example by *Aphanomyces euteiches*

Ascochyta diseases, caused for example by *Ascochyta lentis*

Aspergillus diseases, caused for example by *Aspergillus flavus*

Cladosporium diseases, caused for example by *Cladosporium herbarum*

Cochliobolus diseases, caused for example by *Cochliobolus sativus* (Conidiaform: *Drechslera, Bipolaris Syn: Helminthosporium*);

Colletotrichum diseases, caused for example by *Colletotrichum coccodes*;

Fusarium diseases, caused for example by *Fusarium culmorum*;

Gibberella diseases, caused for example by *Gibberella zeae*;

Macrophomina diseases, caused for example by *Macrophomina* phaseolina

Monographella diseases, caused for example by *Monographella nivalis*;

Penicillium diseases, caused for example by *Penicillium expansum*

Phoma diseases, caused for example by *Phoma lingam*

Phomopsis diseases, caused for example by *Phomopsis sojae*;

Phytophthora diseases, caused for example by Phytophthora cactorum;

Pyrenophora diseases, caused for example by *Pyrenophora graminea*

Pyricularia diseases, caused for example by *Pyricularia oryzae*;

Pythium diseases, caused for example by *Pythium ultimum*;

Rhizoctonia diseases, caused for example by *Rhizoctonia solani*;

Rhizopus diseases, caused for example by *Rhizopus oryzae*

Sclerotium diseases, caused for example by *Sclerotium rolfsii*;

Septoria diseases, caused for example by *Septoria nodorum*;

Typhula diseases, caused for example by *Typhula incarnata*;

Verticillium diseases, caused for example by *Verticillium dahliae* ;

Canker, broom and dieback diseases such as :

Nectria diseases, caused for example by *Nectria galligena* ;

Blight diseases such as :

Monilinia diseases, caused for example by *Monilinia laxa* ;

Leaf blister or leaf curl diseases such as :

Exobasidium diseases caused for example by *Exobasidium vexans*

Taphrina diseases, caused for example by *Taphrina deformans* ;

Decline diseases of wooden plants such as :

Esca diseases, caused for example by *Phaemoniella clamydospora* ;

Eutypa dyeback, caused for example by *Eutypa lata* ;

Ganoderma diseases caused for example by *Ganoderma boninense*;

Rigidoporus diseases caused for example by *Rigidoporus lignosus*

Diseases of Flowers and Seeds such as

Botrytis diseases caused for example by *Botrytis cinerea*;

Diseases of Tubers such as

Rhizoctonia diseases caused for example by *Rhizoctonia solani*;

Helminthosporium diseases caused for example by *Helminthosporium solani*;

Club root diseases such as

Plasmodiophora diseases, cause for example by *Plamodiophora brassicae*.

Diseases caused by Bacterial Organisms such as

Xanthomonas species for example *Xanthomonas campestris* pv. oryzae;

Pseudomonas species for example *Pseudomonas syringae* pv. lachrymans;

Erwinia species for example *Erwinia amylovora*.

Legend of the figures

Fig 1 : Measurement of *Phytophthora infestans* growth inhibition in the presence of dsRNA targeting the saccharopine dehydrogenase messenger RNA.

Fig 2 : Analysis of saccharopine dehydrogenase mRNA level by qRT PCR.

Sequence listing:

SEQ ID N°1: Saccharopine dehydrogenase (LYS1) from Aspergillus clavatus.

SEQ ID N°2: Protein encoded by the above nucleic acid sequence.

SEQ ID N°3: Saccharopine dehydrogenase (LYS1) from Aspergillus fumigatus.

SEQ ID N°4: Protein encoded by the above nucleic acid sequence.

SEQ ID N°5: Saccharopine dehydrogenase (LYS1) from Botrytis cinerea.

SEQ ID N°6: Protein encoded by the above nucleic acid sequence.

SEQ ID N°7: Saccharopine dehydrogenase (LYS1) from Fusarium graminearum.

SEQ ID N°8: Protein encoded by the above nucleic acid sequence.

SEQ ID N°9: Saccharopine dehydrogenase (LYS1) from Fusarium oxysporum.

SEQ ID N°10: Protein encoded by the above nucleic acid sequence.

SEQ ID N°11: Saccharopine dehydrogenase (LYS1) from Fusarium verticilloides.

SEQ ID N°12: Protein encoded by the above nucleic acid sequence.

SEQ ID N°13: Saccharopine dehydrogenase (LYS1) from Fusarium verticilloides.

SEQ ID N°14: Protein encoded by the above nucleic acid sequence.

SEQ ID N°15: Saccharopine dehydrogenase (LYS1) from Mycosphaerella fijiensis.

SEQ ID N°16: Polypeptide encoded by the above nucleic acid sequence.

SEQ ID N°17: Saccharopine dehydrogenase (LYS1) from Magnaporthe grisea.

SEQ ID N°18: Protein encoded by the above nucleic acid sequence.

SEQ ID N°19: Saccharopine dehydrogenase (LYS1) from Monoliophthora perniciosa.

SEQ ID N°20: Protein encoded by the above nucleic acid sequence.

SEQ ID N°21: Saccharopine dehydrogenase (LYS1) from Puccinia graminis.

SEQ ID N°22: Protein encoded by the above nucleic acid sequence.

SEQ ID N°23: Saccharopine dehydrogenase (LYS1) from Phytophthora infestans.

SEQ ID N°24: Protein encoded by the above nucleic acid sequence.

SEQ ID N°25: Saccharopine dehydrogenase (LYS1) (from Phytophthora ramorum.

SEQ ID N°26: Protein encoded by the above nucleic acid sequence.

SEQ ID N°27: Saccharopine dehydrogenase (LYS1) from Phytophthora sojae.

SEQ ID N°28: Protein encoded by the above nucleic acid sequence.

SEQ ID N°29: Saccharopine dehydrogenase (LYS1) from Pyrenophora tritici-repentis.

SEQ ID N°30: Protein encoded by the above nucleic acid sequence.

SEQ ID N°31: Saccharopine dehydrogenase (LYS1) from Sclerotinia sclerotiorum.

SEQ ID N°32: Protein encoded by the above nucleic acid sequence.

SEQ ID N°33: Saccharopine dehydrogenase (LYS1) from Trichoderma reesei.

SEQ ID N°34: Protein encoded by the above nucleic acid sequence.

SEQ ID N°35: Saccharopine dehydrogenase (LYS1) from Ustilago maydis.

SEQ ID N°36: Protein encoded by the above nucleic acid sequence.

SEQ ID N°37: Saccharopine dehydrogenase (LYS1) from Verticillium albo-atrum.

SEQ ID N°38: Protein encoded by the above nucleic acid sequence.

SEQ ID N°39: Saccharopine dehydrogenase (LYS1) from Mycosphaerella graminicola.

SEQ ID N°40: Protein encoded by the above nucleic acid sequence.

SEQ ID N°41: Saccharopine dehydrogenase (LYS1) from Fusarium moniliform.
SEQ ID N°42: Protein encoded by the above nucleic acid sequence.
SEQ ID N°43: Saccharopine dehydrogenase (LYS1) from Claviceps purpurea.
SEQ ID N°44: Protein encoded by the above nucleic acid sequence.
SEQ ID N°45: Primer SACdh_Pi_T7_F
SEQ ID N°46: Primer SACdh_Pi_T7_R
SEQ ID N°47: Primer Actin forward
SEQ ID N°48: Primer Actin reverse
SEQ ID N°49: Primer β-Tub forward
SEQ ID N°50: Primer β-Tub reverse
SEQ ID N°51: Primer SACdh forward
SEQ ID N°52: Primer SACdh reverse
SEQ ID N°53: Primer pBINB33-1
SEQ ID N°54: Primer pBINB33-2
SEQ ID N°55: Primer SacdhPI R
SEQ ID N°56: Primer SacdhPI F
SEQ ID N°57: Primer LYS1 Pot 117-F
SEQ ID N°58: Primer LYS1 Pot 117-R

In the claims which follow and in the preceding description of the invention, except where the context requires otherwise due to express language or necessary implication, the word “comprise” or variations such as “comprises” or “comprising” is used in an inclusive sense, i.e. to specify the presence of the stated features but not to preclude the presence or addition of further features in various embodiments of the invention.

It is to be understood that, if any prior art publication is referred to herein, such reference does not constitute an admission that the publication forms a part of the common general knowledge in the art, in Australia or any other country.

The various aspects of the invention will be understood more fully by means of the experimental examples below.

All the methods or operations described below are given by way of example and correspond to a choice, made among the various methods available for achieving the same result. This choice has no effect on the quality of the result, and, consequently, any appropriate method can be used by those skilled in the art to achieve the same result. In particular, and unless otherwise specified in the examples, all the recombinant DNA techniques employed are carried out according to the standard protocols described in Sambrook and Russel (2001, Molecular cloning: A laboratory manual, Third edition, Cold Spring Harbor Laboratory Press, NY) in Ausubel *et al*. (1994, Current Protocols in Molecular Biology, Current protocols, USA, Volumes 1 and 2), and in Brown (1998, Molecular Biology LabFax, Second edition, Academic Press, UK). Standard materials and methods for plant molecular biology are described in Croy R.D.D. (1993, Plant Molecular Biology LabFax, BIOS Scientific Publications Ltd (UK) and Blackwell Scientific Publications (UK)). Standard materials and methods for PCR (Polymerase Chain Reaction) are also described in Dieffenbach and Dveksler (1995, PCR Primer: A laboratory manual, Cold Spring Harbor Laboratory Press, NY) and in McPherson *et al.* (2000, PCR - Basics: From background to bench, First edition, Springer Verlag, Germany).

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Examples

Example 1: *In vitro* cultivation of *Magnaporthe Grisea*

Assays were carried out using the *Magnaporthe grisea* wild-type strain P1.2 originated from the collection of the phytopathology laboratory of the CIRAD (Centre de coopération internationale en recherche agronomique pour le développement) in Montpellier. Conditions for culturing, the composition of the rice-agar medium, maintenance, and sporulation as well as protoplasts preparations are described by Silué et al. (1998).

Example 2 : *Magnaporthe grisea* transfection with dsRNA targeting saccharopine dehydrogenase and measurement of growth inhibition

The Magnaporthe grisea saccharopine dehydrogenase (SACdh) gene sequence Lys-1 (MGG_01359.6: 1426 bp) was obtained from the Broad Institute (http://www.broadinstitute.org/). A region of about 325 bp was selected for dsRNA, comprizing the nucleotides 301 through 626, was synthesized by the Geneart company and cloned into the plasmid .

For transfection, ds RNA of saccharopine dehydrogenase from *Magnaporthe grisea* was produced using the MEGAscript RNAi Kit (Ambion) according to the manufacturers' instructions. Different amounts (200µg to 2µg of ds RNA) were treated with transfection agent Lipofectamin RNAi max (Invitrogen) following manufactures' instructions. Lipofectamin-ds RNA complexes were added to 2,5 x 10^6 *Magnaporthe grisea* protoplast in a microtiterplate with TB3 media (Villalba et al., 2008), and growth was monitored for 5-7 days at a OD of 600 nm using a Infinite M1000 (Tecan) microplate reader..

Growth of *Magnaporthe grisea* protoplasts treated with ds RNA of saccharopine dehydrogenase comparing to untreated control.was monitored at several time points and showed a significant difference in growth.

Example 3 : In vitro cultivation *Phytophthora infestans* and zoospores preparation.

Phytophthora infestans strain PT78 was cultivated *in vitro* in 9cm petri dishes on pea agar medium (125g/l boiled and crushed peas, 20 g/l agar agar, carbenicillin 100mg/l) at 21℃ in the dark. Every 15 days, new medium was inoculated with four 5mm cubic plugs of mycelium.

To release the zoospores, 12 ml of ice cold water were put on a 10 days old culture and the culture was placed at 4℃ for 2 hours. The supernatant was then collected without dwasturbing the mycelium and filtered through a 100 µm sieve to remove hyphal fragments. The zoospores were placed on ice and counted with a haemocytometer.

Example 4 : *Phytophthora infestans* transfection with dsRNA targeting saccharopine dehydrogenase and measurement of growth inhibition

The *Phytophthora infestans* saccharopine dehydrogenase gene sequence Lys-1 (PITG_03530 : 3020 bp) was obtained from the *P. infestans* database of the Broad Institute. A region about 500 bp offering the best siRNA according to the BLOCKit RNAi designer software (Invitrogen) and comprizing the nucleotides 2251 through 2750, was synthesized by the Geneart company and cloned into the plasmid 0920357_SacDH_Pi_pMA..

Synthesis of dsRNA was carried out using the Megascript RNAi kit (Ambion) following the manufacturer's protocol and using as a template a PCR product amplified from the plasmid 0920357_SacDH_Pi_pMA. The forward primer used was SACdh_Pi_T7_F: 5' TAATACGACTCACTATAGGGTTGCAGGAGAGCGCAGAAAGC and the reverse primer was SACdh_Pi_T7_R : TAATACGACTCACTATAGGGTCAGTTGGAGTCCGCGTGGTGT.

dsRNA were then precipitated with 100% ethanol and sodium acetate 3M, pH5.2, washed 2 times with 70 % ethanol and the pellets were resuspended in RNase free water.

The transfection mixes were prepared in a 48 well plate by adding sequentially V8 medium (5% of V8 juice (Campbell Foods Belgium), pH5) , the appropriate amount of dsRNA and 10 µl of lipofectamine RNAi max (Invitrogen) in a final volume of 200 µl. The transfection mixture was incubated during 15 min at room temperature..

Zoospores were diluted in V8 medium to a concentration of $5x10^4$ zoospores/ml. Then, 800 µL of the zoospores solution were added in each well of the plate. The final concentration of zoospores was $4x10^5$ zoospores / ml.

Three controls were added on each plate: V8 medium, V8 medium + zoospores, V8 medium + zoospores + lipofectamine. The plates were incubated at 21℃, in the dark.

The growth of the fungus was followed by measuring the absorbance at 620 nm in a plate reader (Infinite 1000, Tecan) over 8 days The percentage of growth inhibition was calculated using the following formula: $100-(OD_{dsRNA} \times 100 / OD_{control\ lipofectamine})$. The growth of the fungi was reduced in the presence of dsRNA directed against saccharopine dehydrogenase in a concentration dependant manner (100nM and 200nM respectively) as shown in Figure 1

Example 5 : Quantitative PCR analysis of *P. infestans* saccharopine dehydrogenase messenger RNA:

To yield sufficient RNA for cDNA synthesis and real-time RT-PCR, several wells of the 48 wells plate were pooled for one concentration of dsRNA tested : 10 wells for 72h time point, 6 wells for 96h time point, 3 wells for 120h time point.

After 72h, 96h and 120h of treatment with the dsRNA, the mycelia were collected. The samples were centrifuged to remove the medium. The samples were frozen in liquid nitrogen and then lyophilized overnight.

Before RNA extraction, the mycelium was grinded. Total RNA was extracted using the RNeasy Plant mini kit (Qiagen) following the manufacturer's protocol. DNA contamination of the RNA samples was removed by DNase digestion (DNA free, Ambion). Integrity of the RNA was tested on the 2100 Bioanalyzer (RNA 6000 nano kit, Agilent) following the protocol supplied by the manufacturer. The cDNA were synthesized from 2 µg of total RNA by oligo dT priming using the kit Thermoscript RT-PCR system (Invitrogen) following the manufacturer's protocol. The cDNA were precipitated with 100 %EtOH and sodium acetate 3M, pH5.2, washed 2 times with 70 % EtOH and the pellets were resuspended in 10 µL of RNase free water. The cDNA were diluted a hundred fold for the qPCR test. Primer pairs were designed for each gene sequence by using the Primer Express 3 software (Applied Biosystems). Real time RT-PCR was performed on a 7900 Real Time PCR system (Applied Biosystems) with Power SYBR green PCR master mix (Applied Biosystems) following the manufacturer's protocol. Q-PCR was performed as follows : 95℃ for 10 min, 45 cycles at 95℃ for 15s and 60℃ 1min, followed by a dissociation stage at 95℃ for 15s, 60℃ for 1min and 95℃ for 15s.

The actin and β-tubuline genes were used as endogenous controls. The relative expression of genes was calculated with the 2ΔΔCt method. The figure 2 shows a significant reduction of the level of the saccharopine dehydrogenase messenger RNA and this reduction correlates with growth inhibition.

Table 1: Sequence of qPCR primers :

Primer name	Forward primer sequence	Reverse primer sequence
actin	CGACTCTGGTGACGGTGTGT	GCGTGAGGAAGAGCGTAACC
β-Tub	CCGCCCAGACAATTTCGT	CCTTGGCCCAGTTGTTACCA
SACdh	TGGGTGGTTTCCAAGGTCTTC	AAAGGCACCAAGCCACTGAA

Example 6 : Construction of transformation vectors containing the *Phytophthora infestans* Saccharopine Dehydrogenase gene.

a) Preparation of the plant expression vector IR 47-71

The plasmid pBinAR is a derivative of the binary vector plasmid pBin19 (Bevan, 1984) which was constructed as follows: A fragment of a length of 529 bp which comprised the nucleotides 6909-7437 of the 35S promoter of the cauliflower mosaic virus was isolated as EcoR \IKpn I fragment from the plasmid pDH51 (Pietrzak et al, 1986) and ligated between the EcoR I and Kpn I restriction sites of the polylinker of pUC18. In this manner, the plasmid pUC18-35S was formed. Using the restriction endonucleases Hind III and Pvu II, a fragment of a length of 192 bp which included the polyadenylation signal (3' terminus) of the Octopin Synthase gene (gene 3) of the T-DNA of the Ti plasmid pTiACH5 (Gielen et al, 1984) (nucleotides 11 749-11 939) was isolated from the plasmid pAGV40 (Herrera-Estrella et al, 1983). Following addition of Sph I linkers to the Pvu II restriction site, the fragment was ligated between the Sph I and Hind III restriction sites of pUC18-35S. This gave the plasmid pA7. Here, the entire polylinker comprising the 35S promoter and Ocs terminator was removed using EcoR I and Hind III and ligated into the appropriately cleaved vector pBin19. This gave the plant expression vector pBinAR (Hofgen and Willmitzer, 1990).

The promoter of the patatin gene B33 from Solanum tuberosum (Rocha-Sosa et al., 1989) was, as Dra I fragment (nucleotides -1512 - +14), ligated into the Ssf I-cleaved vector pUC19 whose ends had been blunted using T4-DNA polymerase. This gave the plasmid pUC19-B33. From this plasmid, the B33 promoter was removed using EcoR I and Sma I and ligated into the appropriately restricted vector pBinAR. This gave the plant expression vector pBinB33. To facilitate further cloning steps, the MCS

(Multiple Cloning Site) was extended. To this end, two complementary oligonucleotides were synthesized, heated at 95℃ for 5 minutes, slowly cooled to room temperature to allow good fixation (annealing) and cloned into the Sal I and Kpn I restriction sites of pBinB33. The oligonucleotides used for this purpose had the following sequence:
pBINB33-1: 5'-TCG ACA GGC CTG GAT CCT TAA TTA AAC TAG TCT CGA GGA GCT CGG TAC-3'
pBINB33-2: 5'-CGA GCT CCT CGA GAC TAG TTT AAT TAA GGA TCC AGG CCT G-3'
The plasmid obtained was named IR 47-71.

b) Preparation of the plant expression vectors pEPA248 and pEPA262 comprising a nucleic acid sequences for the *Phytophthora infestans* Saccharopine Dehydrogenase gene.
The saccharopine dehydrogenase sequence (PITG_03530: 3020 bp) was obtained from the P. infestans ORF Prot V1 database. A region about 500 bp offering the best siRNA according to the BLOCKit RNAi designer software (Invitrogen), was synthesized by the Geneart company.
A 300 bp fragment was amplified by PCR from this sequence DNA with the primers SacdhPI R (5'-agaggtaccaagcttgcgtagctgg-3') and SacdhPI F (5'-tatctcgagtctagacaacgccattggttac-3'). The amplified fragment was cloned into pCRII-Topo (Invitrogen) to obtain the plasmid pEPA250. According to Wesley *et al.* (2001), the sequence of interest was cloned in pHannibal vector to give plasmid pEPA241. Then the dsRNA expression cassette was sub-cloned into different binary (plant expression) vectors pART27 (Gleave AP, PMB 20, (1992), 1203-1207) and IR 47 to produce the plant expression vectors pEPA248 and pEPA262, respectively.
Vector pEPA248 and pEPA262 were introduced into respectively GV3101 and C58C1RIF (pGV2260) agrobacteria cells by electroporation (Rocha-Sosa et al.(1989)), in order to further transform potato plants.

Example 7: Construction of transformation vectors targeting the *Sclerotinia sclerotiorum* Saccharopine Dehydrogenase gene *lys1.*

The 351bp of a region of the *S. sclerotiorum Lys1* coding sequence (saccharopine dehydrogenase SS1G_06166.1) was synthesized by the Geneart company (pEPA293), and flanked by internal (*Xba*I, *Hind*III) and external (*Xho*I, *Kpn*I) restriction sites designed to perform a two-step cloning into the pHannibal vector (Wesley et al., 2001). The intermediate plasmid harbored two inverted copies of the *Lys1* gene fragment spaced by the pHannibal *PdK* intron and regulated by the cauliflower mosaic virus (CaMV) 35S promoter and the OCS terminator.

The entire DNA cassette was then excised with *Not*I and inserted into the pART27 binary vector (Gleave, 1992), giving the final plasmid pEPA307 with a plant selection cassette based on kanamycin resistance (nptII gene regulated by the *Nos* promoter and terminator).

The same *Not*I cassette was also inserted in a binary vector (pFCO31) with a plant selection marker based on an HPPD inhibitors resistance, to be used in Soybean transformation. The final plasmid can then transform plants with a T-DNA comprising in between the Right and Left borders, our cassette of interest and an HPPD gene regulated by a CsVMV promoter, a chloroplast transit peptide sequence and a 3'Nos terminator.

Example 8 : Construction of transformation vectors targeting the *Phakopsora pachirizi* Saccharopine Dehydrogenase gene *lys1.*

The 364bp of a region of a *Phakopsora pachirizi Lys1* E.S.T. (saccharopine dehydrogenase PHAPC_EH247326.1) was synthesized by the Geneart company (pCED42), and flanked by internal (*Xba*I, *Hind*III) and external (*Xho*I, *Kpn*I), restriction sites designed to perform a two-step cloning into the pHannibal vector (Wesley et al., 2001). The intermediate plasmid harbored two inverted copies of the *Lys1* gene fragment spaced by the pHannibal *PdK* intron and regulated by the cauliflower mosaic virus (CaMV) 35S promoter and the OCS terminator.

The entire DNA cassette was then excised with *Not*I and inserted into the pART27 binary vector (Gleave, 1992), giving the final plasmid pCED45 with a plant selection cassette based on kanamycin resistance (nptII gene regulated by by the *Nos* promoter and terminator).

The same *Not*I cassette was also inserted in a binary vector (pFCO31) with a plant selection marker based on an HPPD inhibitors resistance, to be used in Soybean transformation. The final plasmid (pCED87) can then transform plants with a T-DNA comprising inbetween the Right and Left borders, our cassette of interest and an HPPD gene regulated by a CsVMV promoter, a chloroplast transit peptide sequence and a 3'Nos terminator.

Example 9: Transformation of potato plants with plant expression vectors comprising nucleic acid molecules coding for hairpin saccharopine dehydrogenase construct pEPA262

Potato plants were transformed via Agrobacterium using the plant expression vector pEPA262, which comprises a coding nucleic acid sequence for saccharopine dehydrogenase under the control of the promoter of the patatin gene B33 from Solanum tuberosum as described by Rocha-Sosa et al. (1989). The transgenic potato plants transformed with the plasmid pEPA262, were named "537 ES ". Molecular analysis of the events of "537 ES" was performed using standart PCR methods (Sambrook et al.) to detect the presence of the nucleic acid sequence for saccharopine dehydrogenase using the following primers SacDH PI F: 5'-TATCTCGAGTCTAGACAACGCCATTGGTTAC-3' and SacDH PI R: 5'-AGAGGTACCAAGCTTGCGTAGCTGG-3'. Further selection was accomplished either by Northen blotting or by expression analysis of the the nucleic acid sequence for saccharopine dehydrogenase via RT-Q PCR leading to a selection of different events. The oligonucleotides used for this purpose had the following sequence: LYS1_Pot 117-F: 5'-TCA ATA GAA GCG AAC GCG TAA A-3' and LYS1_Pot 117-R: 5'-GTT CGG GAT CTG CTC GAT GT-3'

Example 10: Agrobacterium-mediated transformation of *Arabidopsis thaliana.*

The pART27 derived plasmids was introduced into *Agrobacterium tumefaciens* strain LBA4404 (Invitrogen Electromax) by electroporation. The obtained bacterial strains were then used for the floral dip infiltration of the *A. thaliana* Col-0 or Wassileskija plants as described by Clough & Bent (PlantJ 1998).

Example 11: Agrobacterium-mediated transformation of *Glycine max*.

The pFCO31 derived plasmids were introduced into *Agrobacterium tumefaciens* strain LBA4404 (Invitrogen Electromax) by electroporation. The obtained bacterial strains were then used for Soybean transformation as described below.

Soybean seeds are sterilized for 24h with Chlorine gas (Cl2). Seeds are then placed in Petri dishes and soaked in sterile deionized water for 20 hours prior to inoculation, in the dark, at room temperature. An overnight culture grown at 28 °C a nd 200rpm agitation of *Agrobacterium tumefaciens* in 200ml of YEP (5 g/L Yeast extract, 10 g/L Peptone, 5 g/L NaCl2. pH to 7.0) containing the appropriate antibiotic is centrifugated at 4000rpm, 4 °C, 15min. The pellet is resuspended in 40 to 50mL of infection medium to a final OD600nm between 0.6 and 1 and stored on ice. Soaked seeds are dissected, under sterile conditions, using a #15 scalpel blade to separate the cotyledons and remove the primary leaves attached to them. Each cotyledon is kept as explant for inoculation. About 100 explants are prepared and subsequently inoculated together, for 30 minutes in the *Agrobacterium* inoculum, with occasional agitation. Cocultivation is performed in classical Petri dishes containing 4 papers filter (Whatman ® grade 1) and 4 mL of Cocultivation medium (1/10X B5 major salts, 1/10X B5 minor salts, 2.8 mg/L Ferrous, 3.8 mg/L NaEDTA, 30 g/L Sucrose, 3.9 g/L MES (pH 5.4). Filter sterilized 1X B5 vitamins, GA3 (0.25 mg/L), BAP (1.67 mg/L), Cysteine (400 mg/L), Dithiothrietol (154.2 mg/L), and 200µM acetosyringone). Explants are placed on co-cultivation plates (9 per plate), adaxial (flat) side down and sealed with a single vertical string of tape (Leucopore ®) and further incubated for 5 days, at 24°C, in a 18:6 photoperio d.At the end of cocultivation, the explants are placed (6 per plate) on the Shoot Initiation Medium (1X B5 major salts, 1X B5 minor salts, 28 mg/L Ferrous, 38 mg/L NaEDTA, 30 g/L Sucrose, 0.56 g/L MES, and 8 g/L agar (pH 5.6). Filter sterilized 1X B5 vitamins, BAP (1.67 mg/L), Timentin (50 mg/L), Cefotaxime (50 mg/L), Vancomycin (50 mg/L) and Tembotrione (0.1 mg/L)), inclined at 45 °, with the cotyledonary node area imbedded in the medium and upwards. The Shoot Initiation step lasts1 month (24°C 16/8 photoperiod). After one more month, explants with green shoots are transferred on Shoot Elongation Medium (1X MS/B5 medium amended with 1 mg/l zeatin riboside (ZR), 0.1 mg/l IAA, 0.5 mg/l GA3, 3% sucrose, 100 mg/l pyroglutamic acid, 50 mg/l asparagine, 0.56 g/L MES, pH 5.6, solidified with 0.8% agar, ticarcillin (50 mg/l), cefotaxime (50 mg/l) and vancomycin (50 mg/L)), with fresh transfer every 2 weeks. Plantlets that are more than 2cm high are transferred on Rooting medium. Plantlets are cut and placed on rooting medium (1/2 MS major salts, minor salts and vitamins B5, 15 g/L Sucrose, 1mg/L IBA 8 g/L Noble agar , pH 5.7). in an 180mL vertical plastic container.

Once the roots are well formed and the apex is strong, plants are placed into soil in the greenhouse and covered with a green plastic box for acclimatization for 5 days on a 36°C heating bed. After 10 days of acclimatization, the plants are transferred into big pots, without heating bed.

Example 12: Asian Soybean Rust (*Phakopsora pachyrhizi*) assay.

Soybean plants expressing dsRNA directed against *Phakopsora pachirizi Lys1* were grown in the greenhouse in 7,5 cm pots (28,5 ℃, 50% humidity, 14h light). In an incubator, plants were sprayed with a conidia suspension (50ml at 10-15X10^4 spores/ml obtained from artificially infected soybean plants serving as a source of inoculum, for one tray of dimensions 55X34X5cm containing 15 pots). Suspension includes Tween20 at 0.033%. To ensure even inoculation multidirectional spraying is necessary. Plants are then incubated for 4 days at ca. 25 ℃ (daytime) and ca. 20 ℃ (night) with very high humidity (90% to saturation). After this period plants are transferred back to normal growing conditions. Asian soybean rust development is evaluated at regular intervals to follow kinetics of disease development and severity of symptoms. All experiments with Asian soybean rust are performed in L2 safety level culture chambers or incubators according to HCB requirements.

Example 13: Sclerotinia sclerotiorum assay

Development of the Wild-type S. sclerotiorum isolate 1980 as well as the pac 1 mutant (Rollins, 2003) fungus was studied on a whole plant assay. S. sclerotiorum was stored at 4 ℃ on potato dextrose agar (PDA, potato 200 g/l, glucose 20 g/l, agar 18 g/l). The fungus was cultured in a Petri dish containing PDA by placing a mycelial plug in the centre and was maintained under static conditions at 21℃ for 4 days. 4 weeks old Arabidopsis wild-type and transgenic plants were inoculated with 12-mm diameter agar-mycelium plugs excised from the actively growing margin of the fungal colony in the centre of the plant. Inoculated plants were kept in a growth chamber at 21℃ with 100% relative humidity under a 12-h light photoperiod with a light intensity of 34 mmol m−2 s−1 using fluorescent white lights and were monitored every 12 h to observe fungal development. Disease symptoms were monitored by number of infected leaves as well as lengths and widths of lesions.

The claims defining the invention are as follows:

1. A dsRNA molecule comprising i) a first strand comprising a sequence substantially identical to at least 18 contiguous nucleotides of a fungus or oomycete saccharopine dehydrogenase gene and ii) a second strand comprising a sequence substantially complementary to the first strand, wherein the fungus or oomycete gene is selected from the group consisting of:

a) a polynucleotide comprising a sequence as set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43;

b) a polynucleotide encoding a polypeptide having a sequence as set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44;

c) a polynucleotide having at least 70% sequence identity, preferably at least 80%, more preferably at least 90%, even more preferably at least 95% to a polynucleotide having a sequence as set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43;

d) a polynucleotide encoding a polypeptide having at least 70% sequence identity, preferably at least 80%, more preferably at least 90%, even more preferably at least 95%, to a polypeptide having a sequence as set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44;

e) a polynucleotide hybridizing under stringent conditions to a polynucleotide having a sequence as set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43; and

f) a polynucleotide hybridizing under stringent conditions to a polynucleotide encoding a polypeptide having at least 70% sequence identity to a polypeptide having a sequence as set forth in SEQ ID N0: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44.

2. A composition comprising at least a dsRNA molecule according to claim 1.

3. A composition according to claim 2, further comprising an agriculturally acceptable support, carrier, filler and/or surfactant.

4. A composition according to claim 2 or 3 further comprising a phytopharmaceutical or plant growth promoting compound.

5. A micro-organism producing a dsRNA molecule according to claim 1.

6. A genetic construct which comprises at least one DNA sequence as well as heterologous regulatory element(s) in the 5' and optionally in the 3' positions, wherein the DNA sequence(s) is able to form a dsRNA molecule according to claim 1.

7. A cloning and/or expression vector, containing at least one genetic construct according to claim 6.

8. A transgenic plant cell which comprises a dsRNA molecule according to claim 1 or a construct according to claim 6.

9. A transgenic plant, seed or part thereof, comprising a transgenic plant cell according to claim 8.

10. A transgenic plant cell according to claim 8 or transgenic plant, seed or part thereof, according to claim 9 wherein said plant is a soybean, oilseed, rice or potato plant.

11. A method of making a transgenic plant cell capable of expressing a dsRNA that inhibits a fungus or oomycete saccharopine dehydrogenase gene, said method comprising the steps of transforming a plant cell with a genetic construct according to claim 6.

12. A method of controlling a plant pathogen, particularly a fungus or oomycete, comprising providing to said pathogen a dsRNA molecule according to claim 1, or a composition according to any one of claims 2 to 4.

13. A method according to claim 12, wherein an effective quantity of a dsRNA molecule according to claim 1 or a composition according to any one of claims 2 to 4 is applied to the soil where plants grow or are capable of growing, to the leaves and/or the fruit of plants or to the seeds of plants.

14. A method according to claim 12 comprising providing in the host plant of said plant pathogen a transformed plant cell according to claim 8.

15. A method for inhibiting the expression of a plant pathogen gene, comprising the following steps:

i) transforming a plant cell with a genetic construct according to claim 6;
ii) placing the cells thus transformed under conditions that allow the transcription of said construct; and
iii) bringing the cells into contact with the plant pathogen.

16. A method according to any one of claims 11 to 15 wherein said plant pathogen is *Magnaporthe grisea, Phytophthora infestans, Sclerotinia sclerotinium* or *Phakopsora pachyrhizi.*

17. A method according to any one of claims 11 to 15 wherein said plant is soybean, oilseed, rice or potato.

Figure 1

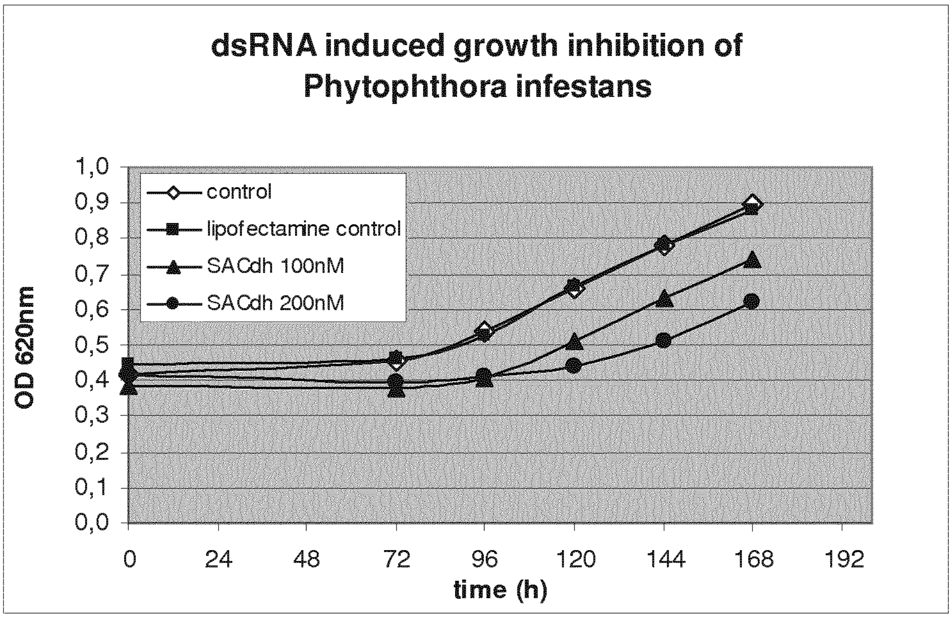
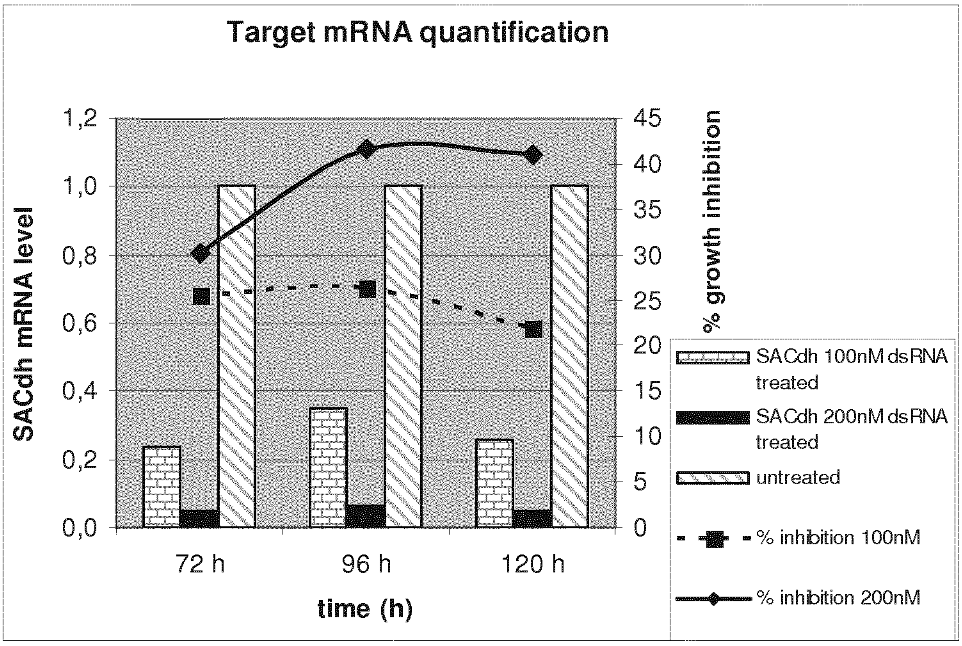


Figure 2



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1               5                   10                  15

gct cgg tct gct ttg acc ccg act acc tgc aag gcc ctt atg gat gct         96
Ala Arg Ser Ala Leu Thr Pro Thr Thr Cys Lys Ala Leu Met Asp Ala
            20                  25                  30

ggc tac gag gtg acc gtg gaa cgt tcc aga cag cgg att ttc gac gtt        144
Gly Tyr Glu Val Thr Val Glu Arg Ser Arg Gln Arg Ile Phe Asp Val
        35                  40                  45

gta cag atc ggc gcc ccc ctc gtc gag gaa ggt tca tgg gta aag gac        192
Val Gln Ile Gly Ala Pro Leu Val Glu Glu Gly Ser Trp Val Lys Asp
    50                  55                  60

gca ccc aaa gat gcc tac atc ctc ggt ctg aag gag ctt ccc gag gac        240
Ala Pro Lys Asp Ala Tyr Ile Leu Gly Leu Lys Glu Leu Pro Glu Asp
65                  70                  75                  80

gat ttt ccg ctt gag cac gta cac atc tcc ttt gcg cac tgc tac aag        288
Asp Phe Pro Leu Glu His Val His Ile Ser Phe Ala His Cys Tyr Lys
                85                  90                  95

caa cag gct ggc tgg gag aag gtg ctc agc cgg tgg ccc cgc gga ggc        336
Gln Gln Ala Gly Trp Glu Lys Val Leu Ser Arg Trp Pro Arg Gly Gly
            100                 105                 110

ggc acc ctc ttg gac ttg gag ttc ctc aca gat gag act gga cgc cga        384
Gly Thr Leu Leu Asp Leu Glu Phe Leu Thr Asp Glu Thr Gly Arg Arg
        115                 120                 125

gta gct gct ttt ggg tac tcc gcc ggt tac gca ggt tct gct ttg gcc        432
Val Ala Ala Phe Gly Tyr Ser Ala Gly Tyr Ala Gly Ser Ala Leu Ala
    130                 135                 140
```

```
att aag aac tgg gcc tgg caa ttg acg cat cct gag ggc gag ccg ctt        480
Ile Lys Asn Trp Ala Trp Gln Leu Thr His Pro Glu Gly Glu Pro Leu
145                 150                 155                 160

cct ggc gag act ccc tac gca aac cag gat ctg ttg att gag tca gtg        528
Pro Gly Glu Thr Pro Tyr Ala Asn Gln Asp Leu Leu Ile Glu Ser Val
                165                 170                 175

aag gag tcg ttg gag tct ggc aag aag ctg tcc ggc agg ccg ccc aag        576
Lys Glu Ser Leu Glu Ser Gly Lys Lys Leu Ser Gly Arg Pro Pro Lys
            180                 185                 190

gtg ctt gtc att gga gct ctt gga cgc tgt ggc aaa gga gcg gtt cag        624
Val Leu Val Ile Gly Ala Leu Gly Arg Cys Gly Lys Gly Ala Val Gln
        195                 200                 205

ctg gcc aag gat gtc ggc att cct gag tcg gat atc atc cag tgg gat        672
Leu Ala Lys Asp Val Gly Ile Pro Glu Ser Asp Ile Ile Gln Trp Asp
    210                 215                 220

ata gaa gag acc aag aag ggt ggc ccc ttc aga gag att gtc gag gat        720
Ile Glu Glu Thr Lys Lys Gly Gly Pro Phe Arg Glu Ile Val Glu Asp
225                 230                 235                 240

gca gac att ttc atc aac tgc atc tac ctc tcc gct aag atc cct cct        768
Ala Asp Ile Phe Ile Asn Cys Ile Tyr Leu Ser Ala Lys Ile Pro Pro
                245                 250                 255

ttc gtc aac acc gaa act ctg tct tct cct aac cgc cgc ttg tcc gtc        816
Phe Val Asn Thr Glu Thr Leu Ser Ser Pro Asn Arg Arg Leu Ser Val
            260                 265                 270

att tgt gac gtg agc gcc gac aca acc aat ccc aac aat cct atc cct        864
Ile Cys Asp Val Ser Ala Asp Thr Thr Asn Pro Asn Asn Pro Ile Pro
        275                 280                 285

gtc tat tcc atc aca acc act ttc gac aag ccc aca gtc act gtt cct        912
Val Tyr Ser Ile Thr Thr Thr Phe Asp Lys Pro Thr Val Thr Val Pro
    290                 295                 300

ctt ccg gaa ctg gcc cag ggc cct cca ttg agc gtg atc agc atc gac        960
Leu Pro Glu Leu Ala Gln Gly Pro Pro Leu Ser Val Ile Ser Ile Asp
305                 310                 315                 320

cac ctc ccc tcc ctc ctt cct cgt gaa agc tcc gag atg ttc agc gaa       1008
His Leu Pro Ser Leu Leu Pro Arg Glu Ser Ser Glu Met Phe Ser Glu
                325                 330                 335

gcc tta ctg ccg agc cta ctg caa ctc aag gat aga aag aac gct cgt       1056
Ala Leu Leu Pro Ser Leu Leu Gln Leu Lys Asp Arg Lys Asn Ala Arg
            340                 345                 350

gtc tgg aag caa gca gag gac ttg ttc aac gaa aag gtt gct acc ttg       1104
Val Trp Lys Gln Ala Glu Asp Leu Phe Asn Glu Lys Val Ala Thr Leu
        355                 360                 365

ccc gag tcg atg cgc gct taa                                           1125
Pro Glu Ser Met Arg Ala
    370


<210>  4
<211>  374
<212>  PRT
<213>  Aspergillus fumigatus

<400>  4
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Met Ser Ser Asn Lys Ile Trp Leu Arg Ala Glu Thr Lys Pro Ala Glu
1               5                   10                  15


Ala Arg Ser Ala Leu Thr Pro Thr Thr Cys Lys Ala Leu Met Asp Ala
            20                  25                  30


Gly Tyr Glu Val Thr Val Glu Arg Ser Arg Gln Arg Ile Phe Asp Val
        35                  40                  45


Val Gln Ile Gly Ala Pro Leu Val Glu Glu Gly Ser Trp Val Lys Asp
    50                  55                  60


Ala Pro Lys Asp Ala Tyr Ile Leu Gly Leu Lys Glu Leu Pro Glu Asp
65                  70                  75                  80


Asp Phe Pro Leu Glu His Val His Ile Ser Phe Ala His Cys Tyr Lys
                85                  90                  95


Gln Gln Ala Gly Trp Glu Lys Val Leu Ser Arg Trp Pro Arg Gly Gly
            100                 105                 110


Gly Thr Leu Leu Asp Leu Glu Phe Leu Thr Asp Glu Thr Gly Arg Arg
        115                 120                 125


Val Ala Ala Phe Gly Tyr Ser Ala Gly Tyr Ala Gly Ser Ala Leu Ala
    130                 135                 140


Ile Lys Asn Trp Ala Trp Gln Leu Thr His Pro Glu Gly Glu Pro Leu
145                 150                 155                 160


Pro Gly Glu Thr Pro Tyr Ala Asn Gln Asp Leu Leu Ile Glu Ser Val
                165                 170                 175


Lys Glu Ser Leu Glu Ser Gly Lys Lys Leu Ser Gly Arg Pro Pro Lys
            180                 185                 190


Val Leu Val Ile Gly Ala Leu Gly Arg Cys Gly Lys Gly Ala Val Gln
        195                 200                 205


Leu Ala Lys Asp Val Gly Ile Pro Glu Ser Asp Ile Ile Gln Trp Asp
    210                 215                 220


Ile Glu Glu Thr Lys Lys Gly Gly Pro Phe Arg Glu Ile Val Glu Asp
225                 230                 235                 240


Ala Asp Ile Phe Ile Asn Cys Ile Tyr Leu Ser Ala Lys Ile Pro Pro
                245                 250                 255


Phe Val Asn Thr Glu Thr Leu Ser Ser Pro Asn Arg Arg Leu Ser Val
            260                 265                 270
```

```
Ile Cys Asp Val Ser Ala Asp Thr Thr Asn Pro Asn Asn Pro Ile Pro
        275                 280                 285


Val Tyr Ser Ile Thr Thr Thr Phe Asp Lys Pro Thr Val Thr Val Pro
    290                 295                 300


Leu Pro Glu Leu Ala Gln Gly Pro Pro Leu Ser Val Ile Ser Ile Asp
305                 310                 315                 320


His Leu Pro Ser Leu Leu Pro Arg Glu Ser Ser Glu Met Phe Ser Glu
                325                 330                 335


Ala Leu Leu Pro Ser Leu Leu Gln Leu Lys Asp Arg Lys Asn Ala Arg
            340                 345                 350


Val Trp Lys Gln Ala Glu Asp Leu Phe Asn Glu Lys Val Ala Thr Leu
        355                 360                 365


Pro Glu Ser Met Arg Ala
    370


<210>  5
<211>  1119
<212>  DNA
<213>  Botrytis cinerea


<220>
<221>  CDS
<222>  (1)..(1119)
<223>  Lys1

<400>  5
atg tct gga act act ctt cac cta cgt tct gag ttg ggc aaa gct ctt           48
Met Ser Gly Thr Thr Leu His Leu Arg Ser Glu Leu Gly Lys Ala Leu
1               5                   10                  15

gag cat cga tcc gct ctt acc ccc acc acc gcc aaa gct ctc atc gat           96
Glu His Arg Ser Ala Leu Thr Pro Thr Thr Ala Lys Ala Leu Ile Asp
            20                  25                  30

gct gga tac aca atc aac gtt gag cgc agt cca gag cgt ata ttc gac          144
Ala Gly Tyr Thr Ile Asn Val Glu Arg Ser Pro Glu Arg Ile Phe Asp
        35                  40                  45

gat gaa gag ttc gag aag gtt ggt gct act ctt gtg cca gag aac aca          192
Asp Glu Glu Phe Glu Lys Val Gly Ala Thr Leu Val Pro Glu Asn Thr
    50                  55                  60

tgg aga caa gca cca aag gat cac att atc att ggg ttg aag gaa ctg          240
Trp Arg Gln Ala Pro Lys Asp His Ile Ile Ile Gly Leu Lys Glu Leu
65                  70                  75                  80

ccc gtc gaa gaa ttt cct ctc gag cat gtt cac gta caa ttc gca cat          288
Pro Val Glu Glu Phe Pro Leu Glu His Val His Val Gln Phe Ala His
                85                  90                  95

tgt tat aaa caa cag ggc ggc tgg gac act gtt cta tca cga ttc cct          336
Cys Tyr Lys Gln Gln Gly Gly Trp Asp Thr Val Leu Ser Arg Phe Pro
            100                 105                 110
```

```
cgt gga ggt gga act ctc tta gat ctt gag ttt ttg aca gac gac aga        384
Arg Gly Gly Gly Thr Leu Leu Asp Leu Glu Phe Leu Thr Asp Asp Arg
        115                 120                 125

ggc aga aga gtt gca gcc ttt gga tac cat gct gga ttt gct ggt gca        432
Gly Arg Arg Val Ala Ala Phe Gly Tyr His Ala Gly Phe Ala Gly Ala
    130                 135                 140

gca ttg gca ctc gaa aat tgg gcg tgg caa ctc acc cac cca gca tcc        480
Ala Leu Ala Leu Glu Asn Trp Ala Trp Gln Leu Thr His Pro Ala Ser
145                 150                 155                 160

gag ccc ttc cca agt gta tcg agc tac ccc aac gaa gat gaa ttg att        528
Glu Pro Phe Pro Ser Val Ser Ser Tyr Pro Asn Glu Asp Glu Leu Ile
                165                 170                 175

gtg gat gtt aag aag gca atc gca gct gga caa gag aag acc ggc aag        576
Val Asp Val Lys Lys Ala Ile Ala Ala Gly Gln Glu Lys Thr Gly Lys
            180                 185                 190

gca cca cga gtt ttg gtt att ggt gca tta ggc aga tgt gga agt gga        624
Ala Pro Arg Val Leu Val Ile Gly Ala Leu Gly Arg Cys Gly Ser Gly
        195                 200                 205

gca gtt gac ctc tgc ttg aga gct ggt gtg cca acc gaa aat gtg ttg        672
Ala Val Asp Leu Cys Leu Arg Ala Gly Val Pro Thr Glu Asn Val Leu
    210                 215                 220

aag tgg gat atg gcc gag acc gct aag gga ggg cca ttc cca gag atc        720
Lys Trp Asp Met Ala Glu Thr Ala Lys Gly Gly Pro Phe Pro Glu Ile
225                 230                 235                 240

gtt gag agt gac atc ttc atc aac tgc ata tat ctc atg tcc aag att        768
Val Glu Ser Asp Ile Phe Ile Asn Cys Ile Tyr Leu Met Ser Lys Ile
                245                 250                 255

cca aac ttt gtc gac atg caa agc ctc gat acc cca aac cgc aaa ttg        816
Pro Asn Phe Val Asp Met Gln Ser Leu Asp Thr Pro Asn Arg Lys Leu
            260                 265                 270

tca gtc gtc tgc gat gtc agt gct gat acc acc aac ccc aac aac cca        864
Ser Val Val Cys Asp Val Ser Ala Asp Thr Thr Asn Pro Asn Asn Pro
        275                 280                 285

att cca atc tat act gtt gca acc aca ttt tca gag cca act gtt cca        912
Ile Pro Ile Tyr Thr Val Ala Thr Thr Phe Ser Glu Pro Thr Val Pro
    290                 295                 300

gtt gag gtc aag gga gaa cca aga tta agt gtc atc agt att gat cac        960
Val Glu Val Lys Gly Glu Pro Arg Leu Ser Val Ile Ser Ile Asp His
305                 310                 315                 320

ttg cca agt tta ttg cca aga gag gca agt gag gca ttt agc aag gac       1008
Leu Pro Ser Leu Leu Pro Arg Glu Ala Ser Glu Ala Phe Ser Lys Asp
                325                 330                 335

tta tta cca agt ttg ttg tct ttg aag gat tgg aga aat act cca gtc       1056
Leu Leu Pro Ser Leu Leu Ser Leu Lys Asp Trp Arg Asn Thr Pro Val
            340                 345                 350

tgg gcc aag gca gag aag tta ttc cag gaa aag gtt gct act ttg ccc       1104
Trp Ala Lys Ala Glu Lys Leu Phe Gln Glu Lys Val Ala Thr Leu Pro
        355                 360                 365

aag aac gag gca tga                                                   1119
Lys Asn Glu Ala
    370
```

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<210>  6
<211>  372
<212>  PRT
<213>  Botrytis cinerea

<400>  6

Met Ser Gly Thr Thr Leu His Leu Arg Ser Glu Leu Gly Lys Ala Leu
1               5                   10                  15


Glu His Arg Ser Ala Leu Thr Pro Thr Thr Ala Lys Ala Leu Ile Asp
            20                  25                  30


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


Asp Glu Glu Phe Glu Lys Val Gly Ala Thr Leu Val Pro Glu Asn Thr
    50                  55                  60


Trp Arg Gln Ala Pro Lys Asp His Ile Ile Ile Gly Leu Lys Glu Leu
65                  70                  75                  80


Pro Val Glu Glu Phe Pro Leu Glu His Val His Val Gln Phe Ala His
                85                  90                  95


Cys Tyr Lys Gln Gln Gly Gly Trp Asp Thr Val Leu Ser Arg Phe Pro
            100                 105                 110


Arg Gly Gly Gly Thr Leu Leu Asp Leu Glu Phe Leu Thr Asp Asp Arg
        115                 120                 125


Gly Arg Arg Val Ala Ala Phe Gly Tyr His Ala Gly Phe Ala Gly Ala
    130                 135                 140


Ala Leu Ala Leu Glu Asn Trp Ala Trp Gln Leu Thr His Pro Ala Ser
145                 150                 155                 160


Glu Pro Phe Pro Ser Val Ser Ser Tyr Pro Asn Glu Asp Glu Leu Ile
                165                 170                 175


Val Asp Val Lys Lys Ala Ile Ala Ala Gly Gln Glu Lys Thr Gly Lys
            180                 185                 190


Ala Pro Arg Val Leu Val Ile Gly Ala Leu Gly Arg Cys Gly Ser Gly
        195                 200                 205


Ala Val Asp Leu Cys Leu Arg Ala Gly Val Pro Thr Glu Asn Val Leu
    210                 215                 220


Lys Trp Asp Met Ala Glu Thr Ala Lys Gly Gly Pro Phe Pro Glu Ile
225                 230                 235                 240
```

```
Val Glu Ser Asp Ile Phe Ile Asn Cys Ile Tyr Leu Met Ser Lys Ile
                245                 250                 255


Pro Asn Phe Val Asp Met Gln Ser Leu Asp Thr Pro Asn Arg Lys Leu
            260                 265                 270


Ser Val Val Cys Asp Val Ser Ala Asp Thr Thr Asn Pro Asn Asn Pro
        275                 280                 285


Ile Pro Ile Tyr Thr Val Ala Thr Thr Phe Ser Glu Pro Thr Val Pro
    290                 295                 300


Val Glu Val Lys Gly Glu Pro Arg Leu Ser Val Ile Ser Ile Asp His
305                 310                 315                 320


Leu Pro Ser Leu Leu Pro Arg Glu Ala Ser Glu Ala Phe Ser Lys Asp
                325                 330                 335


Leu Leu Pro Ser Leu Leu Ser Leu Lys Asp Trp Arg Asn Thr Pro Val
            340                 345                 350


Trp Ala Lys Ala Glu Lys Leu Phe Gln Glu Lys Val Ala Thr Leu Pro
        355                 360                 365


Lys Asn Glu Ala
    370


<210>  7
<211>  1173
<212>  DNA
<213>  Fusarium graminearum


<220>
<221>  CDS
<222>  (1)..(1173)
<223>  Lys1

<400>  7
atg tct caa tac ccc cac atc ctc ctg cgc gct gag gag aag ccc ctc         48
Met Ser Gln Tyr Pro His Ile Leu Leu Arg Ala Glu Glu Lys Pro Leu
1               5                   10                  15

gag cac cga tct ttc tct ccc tca att atc aag act ctt gtc gac gct         96
Glu His Arg Ser Phe Ser Pro Ser Ile Ile Lys Thr Leu Val Asp Ala
            20                  25                  30

gga tat ccc gtc tct gtc gag cga tca tct aca gac ccc aag ttc aag        144
Gly Tyr Pro Val Ser Val Glu Arg Ser Ser Thr Asp Pro Lys Phe Lys
        35                  40                  45

cgc atc ttt gaa gac tcc gag tat gag gct gct ggt gcg cgc ctc gtc        192
Arg Ile Phe Glu Asp Ser Glu Tyr Glu Ala Ala Gly Ala Arg Leu Val
    50                  55                  60

aac gag ggc acc tgg ccc aac gcc gaa gcc gga act ttg att ctg ggc        240
Asn Glu Gly Thr Trp Pro Asn Ala Glu Ala Gly Thr Leu Ile Leu Gly
65                  70                  75                  80
```

```
ctc aag gag att ccc gag gaa gac ttt cct ctc aag aac gac cac att        288
Leu Lys Glu Ile Pro Glu Glu Asp Phe Pro Leu Lys Asn Asp His Ile
                85                  90                  95

tca ttt gcc cat tgt tac aag aac caa ggt gga tgg gaa aag gtc ctc        336
Ser Phe Ala His Cys Tyr Lys Asn Gln Gly Gly Trp Glu Lys Val Leu
            100                 105                 110

ggc cgc ttc cct caa gga agc agc gtt cta tac gat ttg gag ttc ctt        384
Gly Arg Phe Pro Gln Gly Ser Ser Val Leu Tyr Asp Leu Glu Phe Leu
        115                 120                 125

gtc gat gag caa gga cgc cga gtt tct gct ttc ggt ttc cac gct gga        432
Val Asp Glu Gln Gly Arg Arg Val Ser Ala Phe Gly Phe His Ala Gly
    130                 135                 140

ttc gct ggc gct gcc ctc ggt atc aag act ctt gcc cac cag ctt cag        480
Phe Ala Gly Ala Ala Leu Gly Ile Lys Thr Leu Ala His Gln Leu Gln
145                 150                 155                 160

gac ccc tcc tcc aag ctc ccc tca gtg gag aca ttc acc gat ggt cgt        528
Asp Pro Ser Ser Lys Leu Pro Ser Val Glu Thr Phe Thr Asp Gly Arg
                165                 170                 175

gga tac tac cta aac gag gag gag ctc gtt aac cag atc cga gaa gac        576
Gly Tyr Tyr Leu Asn Glu Glu Glu Leu Val Asn Gln Ile Arg Glu Asp
            180                 185                 190

ctt gcc aag gcc gag aag tct ctt gga cgc aag ccc act gct ctc gtc        624
Leu Ala Lys Ala Glu Lys Ser Leu Gly Arg Lys Pro Thr Ala Leu Val
        195                 200                 205

ctc ggt gct ctt gga cga tgt ggt aag ggt gcc gtt gac ctg ttc ctc        672
Leu Gly Ala Leu Gly Arg Cys Gly Lys Gly Ala Val Asp Leu Phe Leu
    210                 215                 220

aag gct ggc atg ccc gac gag aac atc acc cgc tgg gac ttg aac gag        720
Lys Ala Gly Met Pro Asp Glu Asn Ile Thr Arg Trp Asp Leu Asn Glu
225                 230                 235                 240

acc aag gac cga gat ggt cct tat gag gag att gcc cag gcc gat gtc        768
Thr Lys Asp Arg Asp Gly Pro Tyr Glu Glu Ile Ala Gln Ala Asp Val
                245                 250                 255

ttc ctt aac gcc atc tac ctt tcc aag ccc atc cct cct ttc atc aac        816
Phe Leu Asn Ala Ile Tyr Leu Ser Lys Pro Ile Pro Pro Phe Ile Asn
            260                 265                 270

gag gag ctt ctc gcc aag tct ggc cgc aac ttg gct gtt gtt atc gat        864
Glu Glu Leu Leu Ala Lys Ser Gly Arg Asn Leu Ala Val Val Ile Asp
        275                 280                 285

gtc tcc tgc gac acc acc aac cct cac aac ccc atc ccc atc tac tct        912
Val Ser Cys Asp Thr Thr Asn Pro His Asn Pro Ile Pro Ile Tyr Ser
    290                 295                 300

atc aac acc aca ttc gag gag ccc acc gtc ccc gtc gag atc aag aac        960
Ile Asn Thr Thr Phe Glu Glu Pro Thr Val Pro Val Glu Ile Lys Asn
305                 310                 315                 320

gac cag aac tct ctc cct cta tca gtt att agc atc gac cat ctc ccc       1008
Asp Gln Asn Ser Leu Pro Leu Ser Val Ile Ser Ile Asp His Leu Pro
                325                 330                 335

tca atg ctg ccc cgt gag gct agt gag gcc ttt agc gag ggc ctc aag       1056
Ser Met Leu Pro Arg Glu Ala Ser Glu Ala Phe Ser Glu Gly Leu Lys
            340                 345                 350
```

```
gag tct ctc ctt aca ctc aag gac cgc aag act tcg cga gtg tgg gcc       1104
Glu Ser Leu Leu Thr Leu Lys Asp Arg Lys Thr Ser Arg Val Trp Ala
        355                 360                 365

gac gcc gag aag ctc ttc aac gag aag gtt gct ctg ctt ccc gag tcc       1152
Asp Ala Glu Lys Leu Phe Asn Glu Lys Val Ala Leu Leu Pro Glu Ser
    370                 375                 380

ctg cga acc aag aga gtt taa                                           1173
Leu Arg Thr Lys Arg Val
385                 390


<210>  8
<211>  390
<212>  PRT
<213>  Fusarium graminearum

<400>  8

Met Ser Gln Tyr Pro His Ile Leu Leu Arg Ala Glu Glu Lys Pro Leu
1               5                   10                  15


Glu His Arg Ser Phe Ser Pro Ser Ile Ile Lys Thr Leu Val Asp Ala
            20                  25                  30


Gly Tyr Pro Val Ser Val Glu Arg Ser Ser Thr Asp Pro Lys Phe Lys
        35                  40                  45


Arg Ile Phe Glu Asp Ser Glu Tyr Glu Ala Ala Gly Ala Arg Leu Val
    50                  55                  60


Asn Glu Gly Thr Trp Pro Asn Ala Glu Ala Gly Thr Leu Ile Leu Gly
65                  70                  75                  80


Leu Lys Glu Ile Pro Glu Glu Asp Phe Pro Leu Lys Asn Asp His Ile
                85                  90                  95


Ser Phe Ala His Cys Tyr Lys Asn Gln Gly Gly Trp Glu Lys Val Leu
            100                 105                 110


Gly Arg Phe Pro Gln Gly Ser Ser Val Leu Tyr Asp Leu Glu Phe Leu
        115                 120                 125


Val Asp Glu Gln Gly Arg Arg Val Ser Ala Phe Gly Phe His Ala Gly
    130                 135                 140


Phe Ala Gly Ala Ala Leu Gly Ile Lys Thr Leu Ala His Gln Leu Gln
145                 150                 155                 160


Asp Pro Ser Ser Lys Leu Pro Ser Val Glu Thr Phe Thr Asp Gly Arg
                165                 170                 175


Gly Tyr Tyr Leu Asn Glu Glu Glu Leu Val Asn Gln Ile Arg Glu Asp
            180                 185                 190
```

```
Leu Ala Lys Ala Glu Lys Ser Leu Gly Arg Lys Pro Thr Ala Leu Val
        195                 200                 205


Leu Gly Ala Leu Gly Arg Cys Gly Lys Gly Ala Val Asp Leu Phe Leu
    210                 215                 220


Lys Ala Gly Met Pro Asp Glu Asn Ile Thr Arg Trp Asp Leu Asn Glu
225                 230                 235                 240


Thr Lys Asp Arg Asp Gly Pro Tyr Glu Glu Ile Ala Gln Ala Asp Val
                245                 250                 255


Phe Leu Asn Ala Ile Tyr Leu Ser Lys Pro Ile Pro Pro Phe Ile Asn
            260                 265                 270


Glu Glu Leu Leu Ala Lys Ser Gly Arg Asn Leu Ala Val Val Ile Asp
        275                 280                 285


Val Ser Cys Asp Thr Thr Asn Pro His Asn Pro Ile Pro Ile Tyr Ser
    290                 295                 300


Ile Asn Thr Thr Phe Glu Glu Pro Thr Val Pro Val Glu Ile Lys Asn
305                 310                 315                 320


Asp Gln Asn Ser Leu Pro Leu Ser Val Ile Ser Ile Asp His Leu Pro
                325                 330                 335


Ser Met Leu Pro Arg Glu Ala Ser Glu Ala Phe Ser Glu Gly Leu Lys
            340                 345                 350


Glu Ser Leu Leu Thr Leu Lys Asp Arg Lys Thr Ser Arg Val Trp Ala
        355                 360                 365


Asp Ala Glu Lys Leu Phe Asn Glu Lys Val Ala Leu Leu Pro Glu Ser
    370                 375                 380


Leu Arg Thr Lys Arg Val
385                 390


<210>  9
<211>  591
<212>  DNA
<213>  Fusarium oxysporum


<220>
<221>  CDS
<222>  (1)..(591)
<223>  Lys1

<400>  9
atg tct gaa tat ccc cac atc cta ctt cgc gct gag gag aag cct ctc         48
Met Ser Glu Tyr Pro His Ile Leu Leu Arg Ala Glu Glu Lys Pro Leu
1               5                   10                  15
```

```
gag cac cga tct ttc tcc ccc gcc gtt atc aag aca ctc gtc gat gct         96
Glu His Arg Ser Phe Ser Pro Ala Val Ile Lys Thr Leu Val Asp Ala
            20                  25                  30

gga tac ccc att tcc gtc gag cga tcg tcc aca gac ccc aag ttt aag        144
Gly Tyr Pro Ile Ser Val Glu Arg Ser Ser Thr Asp Pro Lys Phe Lys
        35                  40                  45

cgt atc ttt gag gac tca gag tat gag gct gct ggc gct cgt ctt gtc        192
Arg Ile Phe Glu Asp Ser Glu Tyr Glu Ala Ala Gly Ala Arg Leu Val
    50                  55                  60

gat acg ggt gtc tgg ccc aac gct gag cct ggg aca atc atc ctg ggg        240
Asp Thr Gly Val Trp Pro Asn Ala Glu Pro Gly Thr Ile Ile Leu Gly
65                  70                  75                  80

ctg aag gag ata ccc gag gag gac ttc ccc ctc aag aat gac cac atc        288
Leu Lys Glu Ile Pro Glu Glu Asp Phe Pro Leu Lys Asn Asp His Ile
                85                  90                  95

aca ttc gct cac tgc tac aag aat caa ggg ggc tgg gag aag gta ctc        336
Thr Phe Ala His Cys Tyr Lys Asn Gln Gly Gly Trp Glu Lys Val Leu
            100                 105                 110

ggt cgc tgg gca caa ggc ggc tca gtt ttg tat gac ttg gag ttc ttg        384
Gly Arg Trp Ala Gln Gly Gly Ser Val Leu Tyr Asp Leu Glu Phe Leu
        115                 120                 125

cac gat tct gaa ggt cgt cgg gtt tcg gcc ttc ggt ttc cac gct ggt        432
His Asp Ser Glu Gly Arg Arg Val Ser Ala Phe Gly Phe His Ala Gly
    130                 135                 140

ttt gca gga gct gcg ctc gga att aag acg ctt gct cac cag ctg cag        480
Phe Ala Gly Ala Ala Leu Gly Ile Lys Thr Leu Ala His Gln Leu Gln
145                 150                 155                 160

gac tcg tct tct aag ctc cct tca gtc gag aca ttc acc gat ggc cgc        528
Asp Ser Ser Ser Lys Leu Pro Ser Val Glu Thr Phe Thr Asp Gly Arg
                165                 170                 175

gga tac tac ctg aac gag gat gag ctc gtc aac cca gat tcg cga gga        576
Gly Tyr Tyr Leu Asn Glu Asp Glu Leu Val Asn Pro Asp Ser Arg Gly
            180                 185                 190

tct cac caa ggc tga                                                    591
Ser His Gln Gly
        195


<210>  10
<211>  196
<212>  PRT
<213>  Fusarium oxysporum

<400>  10

Met Ser Glu Tyr Pro His Ile Leu Leu Arg Ala Glu Glu Lys Pro Leu
1               5                   10                  15


Glu His Arg Ser Phe Ser Pro Ala Val Ile Lys Thr Leu Val Asp Ala
            20                  25                  30


Gly Tyr Pro Ile Ser Val Glu Arg Ser Ser Thr Asp Pro Lys Phe Lys
        35                  40                  45
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```
Arg Ile Phe Glu Asp Ser Glu Tyr Glu Ala Ala Gly Ala Arg Leu Val
    50                  55                  60


Asp Thr Gly Val Trp Pro Asn Ala Glu Pro Gly Thr Ile Ile Leu Gly
65                  70                  75                  80


Leu Lys Glu Ile Pro Glu Glu Asp Phe Pro Leu Lys Asn Asp His Ile
                85                  90                  95


Thr Phe Ala His Cys Tyr Lys Asn Gln Gly Gly Trp Glu Lys Val Leu
            100                 105                 110


Gly Arg Trp Ala Gln Gly Gly Ser Val Leu Tyr Asp Leu Glu Phe Leu
        115                 120                 125


His Asp Ser Glu Gly Arg Arg Val Ser Ala Phe Gly Phe His Ala Gly
    130                 135                 140


Phe Ala Gly Ala Ala Leu Gly Ile Lys Thr Leu Ala His Gln Leu Gln
145                 150                 155                 160


Asp Ser Ser Ser Lys Leu Pro Ser Val Glu Thr Phe Thr Asp Gly Arg
                165                 170                 175


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


Ser His Gln Gly
        195


<210>  11
<211>  1104
<212>  DNA
<213>  Fusarium verticillioides


<220>
<221>  CDS
<222>  (1)..(1104)
<223>  Lys1

<400>  11
atg tcg cct gtc gtc att cat ctc cgg acc gag aca aag cct cta gag         48
Met Ser Pro Val Val Ile His Leu Arg Thr Glu Thr Lys Pro Leu Glu
1               5                   10                  15

cgt cgc tct cca ttg tca cct gcg act gct aag gct ttg ctc ggc gct         96
Arg Arg Ser Pro Leu Ser Pro Ala Thr Ala Lys Ala Leu Leu Gly Ala
            20                  25                  30

ggc tac aca gtt cga gtt gag gaa tcc ccg gac cgc att tac aag att        144
Gly Tyr Thr Val Arg Val Glu Glu Ser Pro Asp Arg Ile Tyr Lys Ile
        35                  40                  45

gac gag ttc aga gat gtt ggg gct gaa atc gta ccc gct ggc tcg tgg        192
Asp Glu Phe Arg Asp Val Gly Ala Glu Ile Val Pro Ala Gly Ser Trp
    50                  55                  60
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```
gtg aat gca ccc aag gag gat att atc ctg gga ttg aag gag att gag        240
Val Asn Ala Pro Lys Glu Asp Ile Ile Leu Gly Leu Lys Glu Ile Glu
65                  70                  75                  80

gcg aat ggt aca ccg tta ctt cac acc tac att cac ttt gct cat gta        288
Ala Asn Gly Thr Pro Leu Leu His Thr Tyr Ile His Phe Ala His Val
                85                  90                  95

ttc aag aag caa agc ggc tgg gct act gag ctg tcc cgc ttc gca aac        336
Phe Lys Lys Gln Ser Gly Trp Ala Thr Glu Leu Ser Arg Phe Ala Asn
            100                 105                 110

gcg ggt ggc tta cta tat gac ttg gaa ttt ctt acg gac caa gat gga        384
Ala Gly Gly Leu Leu Tyr Asp Leu Glu Phe Leu Thr Asp Gln Asp Gly
        115                 120                 125

cgc cgg gta gct gca ttc gga tat tgg gcg gga tat gcc ggg acc gct        432
Arg Arg Val Ala Ala Phe Gly Tyr Trp Ala Gly Tyr Ala Gly Thr Ala
    130                 135                 140

ctg gca ctc ctg tct tgg gct cac cag ctg ctc aac cct ggc gta ccc        480
Leu Ala Leu Leu Ser Trp Ala His Gln Leu Leu Asn Pro Gly Val Pro
145                 150                 155                 160

caa gga ccg gtt ccc gtc ttc gac tct gcc tct gct ttg act gaa ctt        528
Gln Gly Pro Val Pro Val Phe Asp Ser Ala Ser Ala Leu Thr Glu Leu
                165                 170                 175

gtc aag ggt aaa gtc gac gct gca cgc tcc gcc aac cac ggc gcg ctc        576
Val Lys Gly Lys Val Asp Ala Ala Arg Ser Ala Asn His Gly Ala Leu
            180                 185                 190

cct cga ctg atc gta atc ggt gcc ctg ggc cgc tgc ggc aaa ggt gcc        624
Pro Arg Leu Ile Val Ile Gly Ala Leu Gly Arg Cys Gly Lys Gly Ala
        195                 200                 205

atc gca gca gct gag gcc att ggt gtt agt gac att ctg aaa tgg gac        672
Ile Ala Ala Ala Glu Ala Ile Gly Val Ser Asp Ile Leu Lys Trp Asp
    210                 215                 220

att gct gag acg agc aag ggt ggc cca ttt cct gaa gtc gcc tcg tct        720
Ile Ala Glu Thr Ser Lys Gly Gly Pro Phe Pro Glu Val Ala Ser Ser
225                 230                 235                 240

gat att ttt gtg aac tgc gtc tac cta ggt tcc aac aag att cca ccc        768
Asp Ile Phe Val Asn Cys Val Tyr Leu Gly Ser Asn Lys Ile Pro Pro
                245                 250                 255

ttc aca act ttt gaa gca ctc tca gga ccc ggc aga cga ctc cgg gtc        816
Phe Thr Thr Phe Glu Ala Leu Ser Gly Pro Gly Arg Arg Leu Arg Val
            260                 265                 270

att tgc gac gtc agt tgc gac ccc aac agc gag aat aac cct gtt ccc        864
Ile Cys Asp Val Ser Cys Asp Pro Asn Ser Glu Asn Asn Pro Val Pro
        275                 280                 285

gtc tac tcc agc tac agt tcg ttc gaa aac ccg act gtc cct gct tct        912
Val Tyr Ser Ser Tyr Ser Ser Phe Glu Asn Pro Thr Val Pro Ala Ser
    290                 295                 300

gag cat att gat ggt cct gaa ctg cgc atc att gct atc gat cat ctt        960
Glu His Ile Asp Gly Pro Glu Leu Arg Ile Ile Ala Ile Asp His Leu
305                 310                 315                 320

cct acc atg gtt gca cgc gag tcg agt gac gag tat tcc tca cta ctt       1008
Pro Thr Met Val Ala Arg Glu Ser Ser Asp Glu Tyr Ser Ser Leu Leu
                325                 330                 335
```

```
ctg cca agt ttg ttg act ctg gac cgc cgg gat act gag ggg gtt tgg       1056
Leu Pro Ser Leu Leu Thr Leu Asp Arg Arg Asp Thr Glu Gly Val Trp
            340                 345                 350

cag cga gca gaa cgg atc ttt cgc gag aag gtt gca gag ctg ccc tag       1104
Gln Arg Ala Glu Arg Ile Phe Arg Glu Lys Val Ala Glu Leu Pro
        355                 360                 365


<210>  12
<211>  367
<212>  PRT
<213>  Fusarium verticillioides

<400>  12

Met Ser Pro Val Val Ile His Leu Arg Thr Glu Thr Lys Pro Leu Glu
1               5                   10                  15


Arg Arg Ser Pro Leu Ser Pro Ala Thr Ala Lys Ala Leu Leu Gly Ala
            20                  25                  30


Gly Tyr Thr Val Arg Val Glu Glu Ser Pro Asp Arg Ile Tyr Lys Ile
        35                  40                  45


Asp Glu Phe Arg Asp Val Gly Ala Glu Ile Val Pro Ala Gly Ser Trp
    50                  55                  60


Val Asn Ala Pro Lys Glu Asp Ile Ile Leu Gly Leu Lys Glu Ile Glu
65                  70                  75                  80


Ala Asn Gly Thr Pro Leu Leu His Thr Tyr Ile His Phe Ala His Val
                85                  90                  95


Phe Lys Lys Gln Ser Gly Trp Ala Thr Glu Leu Ser Arg Phe Ala Asn
            100                 105                 110


Ala Gly Gly Leu Leu Tyr Asp Leu Glu Phe Leu Thr Asp Gln Asp Gly
        115                 120                 125


Arg Arg Val Ala Ala Phe Gly Tyr Trp Ala Gly Tyr Ala Gly Thr Ala
    130                 135                 140


Leu Ala Leu Leu Ser Trp Ala His Gln Leu Leu Asn Pro Gly Val Pro
145                 150                 155                 160


Gln Gly Pro Val Pro Val Phe Asp Ser Ala Ser Ala Leu Thr Glu Leu
                165                 170                 175


Val Lys Gly Lys Val Asp Ala Ala Arg Ser Ala Asn His Gly Ala Leu
            180                 185                 190


Pro Arg Leu Ile Val Ile Gly Ala Leu Gly Arg Cys Gly Lys Gly Ala
        195                 200                 205
```

```
Ile Ala Ala Ala Glu Ala Ile Gly Val Ser Asp Ile Leu Lys Trp Asp
    210                 215                 220


Ile Ala Glu Thr Ser Lys Gly Gly Pro Phe Pro Glu Val Ala Ser Ser
225                 230                 235                 240


Asp Ile Phe Val Asn Cys Val Tyr Leu Gly Ser Asn Lys Ile Pro Pro
                245                 250                 255


Phe Thr Thr Phe Glu Ala Leu Ser Gly Pro Gly Arg Arg Leu Arg Val
            260                 265                 270


Ile Cys Asp Val Ser Cys Asp Pro Asn Ser Glu Asn Asn Pro Val Pro
        275                 280                 285


Val Tyr Ser Ser Tyr Ser Ser Phe Glu Asn Pro Thr Val Pro Ala Ser
    290                 295                 300


Glu His Ile Asp Gly Pro Glu Leu Arg Ile Ile Ala Ile Asp His Leu
305                 310                 315                 320


Pro Thr Met Val Ala Arg Glu Ser Ser Asp Glu Tyr Ser Ser Leu Leu
                325                 330                 335


Leu Pro Ser Leu Leu Thr Leu Asp Arg Arg Asp Thr Glu Gly Val Trp
            340                 345                 350


Gln Arg Ala Glu Arg Ile Phe Arg Glu Lys Val Ala Glu Leu Pro
        355                 360                 365


<210>  13
<211>  1173
<212>  DNA
<213>  Fusarium verticillioides


<220>
<221>  CDS
<222>  (1)..(1173)
<223>  Lys1

<400>  13
atg tct gaa tat cct cac atc ctt ctt cgc gcc gag gag aag cct ctc           48
Met Ser Glu Tyr Pro His Ile Leu Leu Arg Ala Glu Glu Lys Pro Leu
1               5                   10                  15

gag cac cga tct ttc tcc ccc gcg gtt atc aag aca ctc gtc gat gct           96
Glu His Arg Ser Phe Ser Pro Ala Val Ile Lys Thr Leu Val Asp Ala
            20                  25                  30

gga tac ccc atc tcc gtc gag cgg tca tcc acc gat ccc aaa ttt agg          144
Gly Tyr Pro Ile Ser Val Glu Arg Ser Ser Thr Asp Pro Lys Phe Arg
        35                  40                  45

cgt atc ttt gag gac tct gaa tat gaa gct gct ggt gct cgt ctt gtc          192
Arg Ile Phe Glu Asp Ser Glu Tyr Glu Ala Ala Gly Ala Arg Leu Val
    50                  55                  60
```

```
gac acg ggt gtc tgg ccc aac gct gag cct ggg aca atc ata ctc gga        240
Asp Thr Gly Val Trp Pro Asn Ala Glu Pro Gly Thr Ile Ile Leu Gly
65                  70                  75                  80

ttg aag gag att ccc gag gag gat ttc cct ctg aag aat gat cac atc        288
Leu Lys Glu Ile Pro Glu Glu Asp Phe Pro Leu Lys Asn Asp His Ile
                85                  90                  95

aca ttt gca cac tgc tac aaa aac cag gga ggc tgg gag aag gtt ctc        336
Thr Phe Ala His Cys Tyr Lys Asn Gln Gly Gly Trp Glu Lys Val Leu
            100                 105                 110

ggt cgt tgg tct cgc ggc ggg tct act ctg tat gac ttg gag ttt ttg        384
Gly Arg Trp Ser Arg Gly Gly Ser Thr Leu Tyr Asp Leu Glu Phe Leu
        115                 120                 125

cat gac gct gaa ggc cga cgt gtt tct gcg ttt ggt ttc cac gca ggc        432
His Asp Ala Glu Gly Arg Arg Val Ser Ala Phe Gly Phe His Ala Gly
    130                 135                 140

ttc gcc ggg gct gcg ctt gga ata aag aca ctt tcc cac cag ctg cag        480
Phe Ala Gly Ala Ala Leu Gly Ile Lys Thr Leu Ser His Gln Leu Gln
145                 150                 155                 160

gac ccg tca tct aag ctt ccg tct gtc gag aca ttc acc gat ggc cgc        528
Asp Pro Ser Ser Lys Leu Pro Ser Val Glu Thr Phe Thr Asp Gly Arg
                165                 170                 175

gga tat tac ctg aac gaa gat gag ctc gtc aac cag att cgc gag gat        576
Gly Tyr Tyr Leu Asn Glu Asp Glu Leu Val Asn Gln Ile Arg Glu Asp
            180                 185                 190

ctc gcc aag gct gag aag gct ctc gga cgc aag ccc act gct ctc gtc        624
Leu Ala Lys Ala Glu Lys Ala Leu Gly Arg Lys Pro Thr Ala Leu Val
        195                 200                 205

ctt ggt gct ctt gga cga tgt ggc aag ggt gct gtg gac ctt ttc ctc        672
Leu Gly Ala Leu Gly Arg Cys Gly Lys Gly Ala Val Asp Leu Phe Leu
    210                 215                 220

aag gcc ggc atg cct gat gag aac atc acc cgt tgg gac ttg aac gaa        720
Lys Ala Gly Met Pro Asp Glu Asn Ile Thr Arg Trp Asp Leu Asn Glu
225                 230                 235                 240

acc aag gac cgt gat gga cct tac gag gaa att gcg aag gct gat gtc        768
Thr Lys Asp Arg Asp Gly Pro Tyr Glu Glu Ile Ala Lys Ala Asp Val
                245                 250                 255

ttc ctt aac gcc atc tac ctc tcc aag ccc atc ccc cct ttc atc aac        816
Phe Leu Asn Ala Ile Tyr Leu Ser Lys Pro Ile Pro Pro Phe Ile Asn
            260                 265                 270

caa gaa ctc ctc gcc aag aag ggt cgc aac ctc gct gta gtc atc gac        864
Gln Glu Leu Leu Ala Lys Lys Gly Arg Asn Leu Ala Val Val Ile Asp
        275                 280                 285

gtt tct tgt gat acc aca aac ccc cac aac ccc atc ccc atc tac tcc        912
Val Ser Cys Asp Thr Thr Asn Pro His Asn Pro Ile Pro Ile Tyr Ser
    290                 295                 300

atc aac acc acc ttc gag gac ccc acc gtc ccc gtc gag atc aag gac        960
Ile Asn Thr Thr Phe Glu Asp Pro Thr Val Pro Val Glu Ile Lys Asp
305                 310                 315                 320

gac cag aac aac ctc ccc ctt tcc gtc atc agc atc gac cac ctt ccc       1008
Asp Gln Asn Asn Leu Pro Leu Ser Val Ile Ser Ile Asp His Leu Pro
                325                 330                 335
```

```
tcc atg ctt ccc cgc gag gct agt gag gcc ttt agt gag ggt ctc aag       1056
Ser Met Leu Pro Arg Glu Ala Ser Glu Ala Phe Ser Glu Gly Leu Lys
            340                 345                 350

gag tct ctg ctt aca ctc aag gat cgc aaa act tcg cgg gtg tgg gct       1104
Glu Ser Leu Leu Thr Leu Lys Asp Arg Lys Thr Ser Arg Val Trp Ala
        355                 360                 365

gat gct gag aag ctc ttc cat gag aag gtt gct acg ttg ccg gag gag       1152
Asp Ala Glu Lys Leu Phe His Glu Lys Val Ala Thr Leu Pro Glu Glu
    370                 375                 380

ttg aga acc aag aac gtt taa                                           1173
Leu Arg Thr Lys Asn Val
385                 390


<210>  14
<211>  390
<212>  PRT
<213>  Fusarium verticillioides

<400>  14

Met Ser Glu Tyr Pro His Ile Leu Leu Arg Ala Glu Glu Lys Pro Leu
1               5                   10                  15


Glu His Arg Ser Phe Ser Pro Ala Val Ile Lys Thr Leu Val Asp Ala
            20                  25                  30


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


Arg Ile Phe Glu Asp Ser Glu Tyr Glu Ala Ala Gly Ala Arg Leu Val
    50                  55                  60


Asp Thr Gly Val Trp Pro Asn Ala Glu Pro Gly Thr Ile Ile Leu Gly
65                  70                  75                  80


Leu Lys Glu Ile Pro Glu Glu Asp Phe Pro Leu Lys Asn Asp His Ile
                85                  90                  95


Thr Phe Ala His Cys Tyr Lys Asn Gln Gly Gly Trp Glu Lys Val Leu
            100                 105                 110


Gly Arg Trp Ser Arg Gly Gly Ser Thr Leu Tyr Asp Leu Glu Phe Leu
        115                 120                 125


His Asp Ala Glu Gly Arg Arg Val Ser Ala Phe Gly Phe His Ala Gly
    130                 135                 140


Phe Ala Gly Ala Ala Leu Gly Ile Lys Thr Leu Ser His Gln Leu Gln
145                 150                 155                 160


Asp Pro Ser Ser Lys Leu Pro Ser Val Glu Thr Phe Thr Asp Gly Arg
                165                 170                 175
```

```
Gly Tyr Tyr Leu Asn Glu Asp Glu Leu Val Asn Gln Ile Arg Glu Asp
            180                 185                 190


Leu Ala Lys Ala Glu Lys Ala Leu Gly Arg Lys Pro Thr Ala Leu Val
        195                 200                 205


Leu Gly Ala Leu Gly Arg Cys Gly Lys Gly Ala Val Asp Leu Phe Leu
    210                 215                 220


Lys Ala Gly Met Pro Asp Glu Asn Ile Thr Arg Trp Asp Leu Asn Glu
225                 230                 235                 240


Thr Lys Asp Arg Asp Gly Pro Tyr Glu Glu Ile Ala Lys Ala Asp Val
                245                 250                 255


Phe Leu Asn Ala Ile Tyr Leu Ser Lys Pro Ile Pro Pro Phe Ile Asn
            260                 265                 270


Gln Glu Leu Leu Ala Lys Lys Gly Arg Asn Leu Ala Val Val Ile Asp
        275                 280                 285


Val Ser Cys Asp Thr Thr Asn Pro His Asn Pro Ile Pro Ile Tyr Ser
    290                 295                 300


Ile Asn Thr Thr Phe Glu Asp Pro Thr Val Pro Val Glu Ile Lys Asp
305                 310                 315                 320


Asp Gln Asn Asn Leu Pro Leu Ser Val Ile Ser Ile Asp His Leu Pro
                325                 330                 335


Ser Met Leu Pro Arg Glu Ala Ser Glu Ala Phe Ser Glu Gly Leu Lys
            340                 345                 350


Glu Ser Leu Leu Thr Leu Lys Asp Arg Lys Thr Ser Arg Val Trp Ala
        355                 360                 365


Asp Ala Glu Lys Leu Phe His Glu Lys Val Ala Thr Leu Pro Glu Glu
    370                 375                 380


Leu Arg Thr Lys Asn Val
385                 390


<210>  15
<211>  1223
<212>  DNA
<213>  Mycosphaerella fijiensis


<220>
<221>  CDS
<222>  (3)..(1223)
<223>  Lys1
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<400>  15
ga agg tca aca ctt aaa aaa gac tca tat tcc gcg tcg act ata atc          47
   Arg Ser Thr Leu Lys Lys Asp Ser Tyr Ser Ala Ser Thr Ile Ile
   1               5                   10                  15

gta caa gat cag tgt ctc aca atg tcg cct aca gtc ctt cat ttc aga         95
Val Gln Asp Gln Cys Leu Thr Met Ser Pro Thr Val Leu His Phe Arg
                20                  25                  30

gca gag acc aag cca tta gag cat cgc tcg gca gtc aca ccg aca atc        143
Ala Glu Thr Lys Pro Leu Glu His Arg Ser Ala Val Thr Pro Thr Ile
            35                  40                  45

gca aag aaa ctt gtc gaa gct ggc tat gaa gtc cac gtc gaa cga tcg        191
Ala Lys Lys Leu Val Glu Ala Gly Tyr Glu Val His Val Glu Arg Ser
        50                  55                  60

cag ctc agc ata ttc gca gac tcc gag tat gaa ggc act ggt gct aag        239
Gln Leu Ser Ile Phe Ala Asp Ser Glu Tyr Glu Gly Thr Gly Ala Lys
    65                  70                  75

cta gtg cct act gga tcg tgg aca gag gca ccg aag gag cac att gtc        287
Leu Val Pro Thr Gly Ser Trp Thr Glu Ala Pro Lys Glu His Ile Val
80                  85                  90                  95

att ggc ttg aag gaa ctc ccc gag gag gac ttt cct ttg aag cat gtt        335
Ile Gly Leu Lys Glu Leu Pro Glu Glu Asp Phe Pro Leu Lys His Val
                100                 105                 110

cat gtg caa ttt gct cac tgc tac aaa gga caa ggt ggc tgg gac aag        383
His Val Gln Phe Ala His Cys Tyr Lys Gly Gln Gly Gly Trp Asp Lys
            115                 120                 125

gtt ctc agt aga ttt cca aac ggc aga ggc aca tta ctt gac ctt gaa        431
Val Leu Ser Arg Phe Pro Asn Gly Arg Gly Thr Leu Leu Asp Leu Glu
        130                 135                 140

ttc ttg gaa gat gag caa gga cga aga gtc gct gca ttt ggc tac cat        479
Phe Leu Glu Asp Glu Gln Gly Arg Arg Val Ala Ala Phe Gly Tyr His
    145                 150                 155

gcc gga ttt gct ggt gcc gca ctt gct ctc atg gcc tgg tct cac cag        527
Ala Gly Phe Ala Gly Ala Ala Leu Ala Leu Met Ala Trp Ser His Gln
160                 165                 170                 175

ctc gtg cac ggc aag gac agc cct ctt ccg gga gtg aca cca tac gaa        575
Leu Val His Gly Lys Asp Ser Pro Leu Pro Gly Val Thr Pro Tyr Glu
                180                 185                 190

aac gaa ggt ctc ctt att tcc gat gtc aag aag gcc atc gaa gct ggc        623
Asn Glu Gly Leu Leu Ile Ser Asp Val Lys Lys Ala Ile Glu Ala Gly
            195                 200                 205

aag gcc aag ggc ggt tgc ctc cca aga gtg ctc gtt att ggc gga ctc        671
Lys Ala Lys Gly Gly Cys Leu Pro Arg Val Leu Val Ile Gly Gly Leu
        210                 215                 220

ggc aga tgc ggt cgt ggt gcc gtt gac ctc tgt gtc aag gct ggc gtg        719
Gly Arg Cys Gly Arg Gly Ala Val Asp Leu Cys Val Lys Ala Gly Val
    225                 230                 235

gaa gac att cta aag tgg gat ctt cca gaa aca agt gcc aaa cca gga        767
Glu Asp Ile Leu Lys Trp Asp Leu Pro Glu Thr Ser Ala Lys Pro Gly
240                 245                 250                 255

cca tac cag gag atc atc gag tct gac gtg ttt gtc aac tgc atc tac        815
Pro Tyr Gln Glu Ile Ile Glu Ser Asp Val Phe Val Asn Cys Ile Tyr
                260                 265                 270
```

```
ttg tcg gcc aag atc ccg ccc ttc atc gac cag gca tct ctc gca tcg        863
Leu Ser Ala Lys Ile Pro Pro Phe Ile Asp Gln Ala Ser Leu Ala Ser
            275                 280                 285

cca aac cgc aaa ctg tct gtg gtc tgt gat gta tcc tgc gat acc acg        911
Pro Asn Arg Lys Leu Ser Val Val Cys Asp Val Ser Cys Asp Thr Thr
        290                 295                 300

aac cca aac aat cct atc cca atc tac gac atc aac acg act ttc gac        959
Asn Pro Asn Asn Pro Ile Pro Ile Tyr Asp Ile Asn Thr Thr Phe Asp
    305                 310                 315

aag cca acg gtg cct gtc aag ctc tcc gct gag gcc aat gat ctt ccg       1007
Lys Pro Thr Val Pro Val Lys Leu Ser Ala Glu Ala Asn Asp Leu Pro
320                 325                 330                 335

ttg agc gta atc agt atc gac cat ctc cca tcc tta ctg ccg cga gaa       1055
Leu Ser Val Ile Ser Ile Asp His Leu Pro Ser Leu Leu Pro Arg Glu
                340                 345                 350

gct tcc gaa gct ttc agc tcc gcg ctg ctg ccc agc ttg ctt caa ttg       1103
Ala Ser Glu Ala Phe Ser Ser Ala Leu Leu Pro Ser Leu Leu Gln Leu
            355                 360                 365

aac gac tgg aag aac gca cgt gtt tgg caa caa gcc gag aag ctg ttc       1151
Asn Asp Trp Lys Asn Ala Arg Val Trp Gln Gln Ala Glu Lys Leu Phe
        370                 375                 380

aag gac aaa tgc gcc act ctc cca gaa ggc gca atc gat agc cat gcc       1199
Lys Asp Lys Cys Ala Thr Leu Pro Glu Gly Ala Ile Asp Ser His Ala
    385                 390                 395

gag ctt ctt gct tcg caa tct tga                                       1223
Glu Leu Leu Ala Ser Gln Ser
400                 405


<210>  16
<211>  406
<212>  PRT
<213>  Mycosphaerella fijiensis

<400>  16

Arg Ser Thr Leu Lys Lys Asp Ser Tyr Ser Ala Ser Thr Ile Ile Val
1               5                   10                  15


Gln Asp Gln Cys Leu Thr Met Ser Pro Thr Val Leu His Phe Arg Ala
            20                  25                  30


Glu Thr Lys Pro Leu Glu His Arg Ser Ala Val Thr Pro Thr Ile Ala
        35                  40                  45


Lys Lys Leu Val Glu Ala Gly Tyr Glu Val His Val Glu Arg Ser Gln
    50                  55                  60


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


Val Pro Thr Gly Ser Trp Thr Glu Ala Pro Lys Glu His Ile Val Ile
                85                  90                  95
```

```
Gly Leu Lys Glu Leu Pro Glu Glu Asp Phe Pro Leu Lys His Val His
            100                 105                 110


Val Gln Phe Ala His Cys Tyr Lys Gly Gln Gly Gly Trp Asp Lys Val
        115                 120                 125


Leu Ser Arg Phe Pro Asn Gly Arg Gly Thr Leu Leu Asp Leu Glu Phe
    130                 135                 140


Leu Glu Asp Glu Gln Gly Arg Arg Val Ala Ala Phe Gly Tyr His Ala
145                 150                 155                 160


Gly Phe Ala Gly Ala Ala Leu Ala Leu Met Ala Trp Ser His Gln Leu
                165                 170                 175


Val His Gly Lys Asp Ser Pro Leu Pro Gly Val Thr Pro Tyr Glu Asn
            180                 185                 190


Glu Gly Leu Leu Ile Ser Asp Val Lys Lys Ala Ile Glu Ala Gly Lys
        195                 200                 205


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


Arg Cys Gly Arg Gly Ala Val Asp Leu Cys Val Lys Ala Gly Val Glu
225                 230                 235                 240


Asp Ile Leu Lys Trp Asp Leu Pro Glu Thr Ser Ala Lys Pro Gly Pro
                245                 250                 255


Tyr Gln Glu Ile Ile Glu Ser Asp Val Phe Val Asn Cys Ile Tyr Leu
            260                 265                 270


Ser Ala Lys Ile Pro Pro Phe Ile Asp Gln Ala Ser Leu Ala Ser Pro
        275                 280                 285


Asn Arg Lys Leu Ser Val Val Cys Asp Val Ser Cys Asp Thr Thr Asn
    290                 295                 300


Pro Asn Asn Pro Ile Pro Ile Tyr Asp Ile Asn Thr Thr Phe Asp Lys
305                 310                 315                 320


Pro Thr Val Pro Val Lys Leu Ser Ala Glu Ala Asn Asp Leu Pro Leu
                325                 330                 335


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


Ser Glu Ala Phe Ser Ser Ala Leu Leu Pro Ser Leu Leu Gln Leu Asn
        355                 360                 365
```

```
Asp Trp Lys Asn Ala Arg Val Trp Gln Gln Ala Glu Lys Leu Phe Lys
    370                 375                 380


Asp Lys Cys Ala Thr Leu Pro Glu Gly Ala Ile Asp Ser His Ala Glu
385                 390                 395                 400


Leu Leu Ala Ser Gln Ser
                405


<210>  17
<211>  1098
<212>  DNA
<213>  Magnaporthe grisea


<220>
<221>  CDS
<222>  (1)..(1098)
<223>  Lys1

<400>  17
atg tcg tcc att ctg cac ttg cgg tca gag acc aag cca ttg gag cac         48
Met Ser Ser Ile Leu His Leu Arg Ser Glu Thr Lys Pro Leu Glu His
1               5                   10                  15

cgg tcc gcc cta act ccc act acc acc aag gcc ttg att gag gcc ggt         96
Arg Ser Ala Leu Thr Pro Thr Thr Thr Lys Ala Leu Ile Glu Ala Gly
            20                  25                  30

tac acc gtc aat gtc gag cgc agt ccc gtc cgc atc ttc gac gac gcc        144
Tyr Thr Val Asn Val Glu Arg Ser Pro Val Arg Ile Phe Asp Asp Ala
        35                  40                  45

gag ttc gag gct gtt ggc gca acc ctc gtc ccc gag ggc agc tgg gag        192
Glu Phe Glu Ala Val Gly Ala Thr Leu Val Pro Glu Gly Ser Trp Glu
    50                  55                  60

cag att ccc aag gac cac atc gtc att gga ctg aag gag ttg gag gag        240
Gln Ile Pro Lys Asp His Ile Val Ile Gly Leu Lys Glu Leu Glu Glu
65                  70                  75                  80

aag gac ttc cct ttg aag cac aca cac atc cag ttc gcc cac tgc tac        288
Lys Asp Phe Pro Leu Lys His Thr His Ile Gln Phe Ala His Cys Tyr
                85                  90                  95

aag aac caa gga ggc tgg gac aag gtc ctc cgg agg tat cac gat ggc        336
Lys Asn Gln Gly Gly Trp Asp Lys Val Leu Arg Arg Tyr His Asp Gly
            100                 105                 110

gag gga atg ctc ctc gac att gag ttc ctc gag aag gac ggc cgt cgt        384
Glu Gly Met Leu Leu Asp Ile Glu Phe Leu Glu Lys Asp Gly Arg Arg
        115                 120                 125

gtt gct gct ttc ggc tac tgg gcc ggc ttt gcc ggt gcc gcg ctg gcc        432
Val Ala Ala Phe Gly Tyr Trp Ala Gly Phe Ala Gly Ala Ala Leu Ala
    130                 135                 140

ctt cag aac tgg gcc tgg cag ctg acc aac agc ggc gag ccc ctg ccg        480
Leu Gln Asn Trp Ala Trp Gln Leu Thr Asn Ser Gly Glu Pro Leu Pro
145                 150                 155                 160

agc gtc gag agc cgc cct aac gag gct gcc ttg gtc ggc gac atc aag        528
Ser Val Glu Ser Arg Pro Asn Glu Ala Ala Leu Val Gly Asp Ile Lys
                165                 170                 175
```

```
gag gct ctt gct ggg ggc aag gaa aag gcc ggc agg ctg ccc cgc gtc       576
Glu Ala Leu Ala Gly Gly Lys Glu Lys Ala Gly Arg Leu Pro Arg Val
            180                 185                 190

atc gtc atc ggt gcc ctg ggc cgc tgc ggt cgt ggt gcc gtc gac atg       624
Ile Val Ile Gly Ala Leu Gly Arg Cys Gly Arg Gly Ala Val Asp Met
        195                 200                 205

tgc aag aag gcc ggc ata ccg gat gag aac atc ctc aag tgg gat atg       672
Cys Lys Lys Ala Gly Ile Pro Asp Glu Asn Ile Leu Lys Trp Asp Met
    210                 215                 220

gag gag acg gcc ccc ggt gga ccg ttc aag gag att gtc gag agt gac       720
Glu Glu Thr Ala Pro Gly Gly Pro Phe Lys Glu Ile Val Glu Ser Asp
225                 230                 235                 240

atc ttt gtc aac tgc atc tac ctg aac aag cag atc ccg ccg ttt gtg       768
Ile Phe Val Asn Cys Ile Tyr Leu Asn Lys Gln Ile Pro Pro Phe Val
                245                 250                 255

acc atg gag tcg ctc aac acg cca gag cgc aag ctc tcc gtc atc aac       816
Thr Met Glu Ser Leu Asn Thr Pro Glu Arg Lys Leu Ser Val Ile Asn
            260                 265                 270

gac tgc tcg gct gac acg acc aac ccc ttt aac cct gtt ccc gtg tac       864
Asp Cys Ser Ala Asp Thr Thr Asn Pro Phe Asn Pro Val Pro Val Tyr
        275                 280                 285

act gtg gcc acg act ttc gac aag ccc act gtg ccg gtc gat ggc ttg       912
Thr Val Ala Thr Thr Phe Asp Lys Pro Thr Val Pro Val Asp Gly Leu
    290                 295                 300

agc cat ggc ccg ccc ctg agc gtt atc agc atc gac cac ctg ccg agt       960
Ser His Gly Pro Pro Leu Ser Val Ile Ser Ile Asp His Leu Pro Ser
305                 310                 315                 320

ctg ctc ccg cgg gag gct tcg gag tcg ttc agc aac gac ttg ttg cca      1008
Leu Leu Pro Arg Glu Ala Ser Glu Ser Phe Ser Asn Asp Leu Leu Pro
                325                 330                 335

tat ctc ctg aag ctg aag gac tgg aag agt gac ccg gtg tgg gct ggc      1056
Tyr Leu Leu Lys Leu Lys Asp Trp Lys Ser Asp Pro Val Trp Ala Gly
            340                 345                 350

gcc gag aag ctg ttc cac gag aag gtc aag acc ctg ccg tag              1098
Ala Glu Lys Leu Phe His Glu Lys Val Lys Thr Leu Pro
        355                 360                 365


<210>  18
<211>  365
<212>  PRT
<213>  Magnaporthe grisea

<400>  18

Met Ser Ser Ile Leu His Leu Arg Ser Glu Thr Lys Pro Leu Glu His
1               5                   10                  15


Arg Ser Ala Leu Thr Pro Thr Thr Thr Lys Ala Leu Ile Glu Ala Gly
            20                  25                  30


Tyr Thr Val Asn Val Glu Arg Ser Pro Val Arg Ile Phe Asp Asp Ala
        35                  40                  45
```

```
Glu Phe Glu Ala Val Gly Ala Thr Leu Val Pro Glu Gly Ser Trp Glu
    50                  55                  60


Gln Ile Pro Lys Asp His Ile Val Ile Gly Leu Lys Glu Leu Glu Glu
65                  70                  75                  80


Lys Asp Phe Pro Leu Lys His Thr His Ile Gln Phe Ala His Cys Tyr
                85                  90                  95


Lys Asn Gln Gly Gly Trp Asp Lys Val Leu Arg Arg Tyr His Asp Gly
            100                 105                 110


Glu Gly Met Leu Leu Asp Ile Glu Phe Leu Glu Lys Asp Gly Arg Arg
        115                 120                 125


Val Ala Ala Phe Gly Tyr Trp Ala Gly Phe Ala Gly Ala Ala Leu Ala
    130                 135                 140


Leu Gln Asn Trp Ala Trp Gln Leu Thr Asn Ser Gly Glu Pro Leu Pro
145                 150                 155                 160


Ser Val Glu Ser Arg Pro Asn Glu Ala Ala Leu Val Gly Asp Ile Lys
                165                 170                 175


Glu Ala Leu Ala Gly Gly Lys Glu Lys Ala Gly Arg Leu Pro Arg Val
            180                 185                 190


Ile Val Ile Gly Ala Leu Gly Arg Cys Gly Arg Gly Ala Val Asp Met
        195                 200                 205


Cys Lys Lys Ala Gly Ile Pro Asp Glu Asn Ile Leu Lys Trp Asp Met
    210                 215                 220


Glu Glu Thr Ala Pro Gly Gly Pro Phe Lys Glu Ile Val Glu Ser Asp
225                 230                 235                 240


Ile Phe Val Asn Cys Ile Tyr Leu Asn Lys Gln Ile Pro Pro Phe Val
                245                 250                 255


Thr Met Glu Ser Leu Asn Thr Pro Glu Arg Lys Leu Ser Val Ile Asn
            260                 265                 270


Asp Cys Ser Ala Asp Thr Thr Asn Pro Phe Asn Pro Val Pro Val Tyr
        275                 280                 285


Thr Val Ala Thr Thr Phe Asp Lys Pro Thr Val Pro Val Asp Gly Leu
    290                 295                 300


Ser His Gly Pro Pro Leu Ser Val Ile Ser Ile Asp His Leu Pro Ser
305                 310                 315                 320
```

```
Leu Leu Pro Arg Glu Ala Ser Glu Ser Phe Ser Asn Asp Leu Leu Pro
                325                 330                 335


Tyr Leu Leu Lys Leu Lys Asp Trp Lys Ser Asp Pro Val Trp Ala Gly
            340                 345                 350


Ala Glu Lys Leu Phe His Glu Lys Val Lys Thr Leu Pro
        355                 360                 365


<210>  19
<211>  453
<212>  DNA
<213>  Moniliophthora perniciosa


<220>
<221>  CDS
<222>  (1)..(453)
<223>  Lys1

<400>  19
atg aaa ttc aca ctc cct cgt ctt cga cca ctc acc att gga atc cgc         48
Met Lys Phe Thr Leu Pro Arg Leu Arg Pro Leu Thr Ile Gly Ile Arg
1               5                   10                  15

cgg gaa gac cct act cga att tgg gaa cga cgg gct cct cta acc ccc         96
Arg Glu Asp Pro Thr Arg Ile Trp Glu Arg Arg Ala Pro Leu Thr Pro
            20                  25                  30

gac tcc gtt tac gag ctt gtc aag gac aag gcg gta caa gtt cat gtc        144
Asp Ser Val Tyr Glu Leu Val Lys Asp Lys Ala Val Gln Val His Val
        35                  40                  45

gaa ggc tgc gac agg agg ata ttc aag gac gag gaa tac ata aag gcc        192
Glu Gly Cys Asp Arg Arg Ile Phe Lys Asp Glu Glu Tyr Ile Lys Ala
    50                  55                  60

ggt gca aca atc cga ccc aac ctg aac gat gca cat gtt gta atg ggc        240
Gly Ala Thr Ile Arg Pro Asn Leu Asn Asp Ala His Val Val Met Gly
65                  70                  75                  80

att aaa gag ccc cca ttg gac aga tta ttg ctt gat cct ctt cct cta        288
Ile Lys Glu Pro Pro Leu Asp Arg Leu Leu Leu Asp Pro Leu Pro Leu
                85                  90                  95

tcc aac acc acg tcg aaa cat gag cga aca tac atg aag ttt tct cat        336
Ser Asn Thr Thr Ser Lys His Glu Arg Thr Tyr Met Lys Phe Ser His
            100                 105                 110

act tgg aaa ggt caa gcc tac aat atg cca tta ctt tct gca ttc tta        384
Thr Trp Lys Gly Gln Ala Tyr Asn Met Pro Leu Leu Ser Ala Phe Leu
        115                 120                 125

aac att cac cca ttc cat ggc gct tat aat gac cca ctg gcc cac act        432
Asn Ile His Pro Phe His Gly Ala Tyr Asn Asp Pro Leu Ala His Thr
    130                 135                 140

aat tgg ata atg aac tcc tga                                            453
Asn Trp Ile Met Asn Ser
145                 150


<210>  20
<211>  150
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```
<212>  PRT
<213>  Moniliophthora perniciosa

<400>  20

Met Lys Phe Thr Leu Pro Arg Leu Arg Pro Leu Thr Ile Gly Ile Arg
1               5                   10                  15


Arg Glu Asp Pro Thr Arg Ile Trp Glu Arg Arg Ala Pro Leu Thr Pro
            20                  25                  30


Asp Ser Val Tyr Glu Leu Val Lys Asp Lys Ala Val Gln Val His Val
        35                  40                  45


Glu Gly Cys Asp Arg Arg Ile Phe Lys Asp Glu Glu Tyr Ile Lys Ala
    50                  55                  60


Gly Ala Thr Ile Arg Pro Asn Leu Asn Asp Ala His Val Val Met Gly
65                  70                  75                  80


Ile Lys Glu Pro Pro Leu Asp Arg Leu Leu Leu Asp Pro Leu Pro Leu
                85                  90                  95


Ser Asn Thr Thr Ser Lys His Glu Arg Thr Tyr Met Lys Phe Ser His
            100                 105                 110


Thr Trp Lys Gly Gln Ala Tyr Asn Met Pro Leu Leu Ser Ala Phe Leu
        115                 120                 125


Asn Ile His Pro Phe His Gly Ala Tyr Asn Asp Pro Leu Ala His Thr
    130                 135                 140


Asn Trp Ile Met Asn Ser
145                 150


<210>  21
<211>  1116
<212>  DNA
<213>  Puccinia graminis


<220>
<221>  CDS
<222>  (1)..(1116)
<223>  Lys1

<400>  21
atg tca ggc gat caa cca ctc cta tgg ctg cga tgc gag acc aaa ccg         48
Met Ser Gly Asp Gln Pro Leu Leu Trp Leu Arg Cys Glu Thr Lys Pro
1               5                   10                  15

ttc gag cat cgc tca gca tta act ccc ttg acc gcc aaa aaa ctc atc         96
Phe Glu His Arg Ser Ala Leu Thr Pro Leu Thr Ala Lys Lys Leu Ile
            20                  25                  30

gat gct gga ttc aag ctg gta gta gaa cgg gat cct caa cgg ttc ttc        144
Asp Ala Gly Phe Lys Leu Val Val Glu Arg Asp Pro Gln Arg Phe Phe
        35                  40                  45
```

```
gct gat gac gaa ttt gca aaa gtc gga tgt gaa ctg gtc gaa cac aac        192
Ala Asp Asp Glu Phe Ala Lys Val Gly Cys Glu Leu Val Glu His Asn
    50                  55                  60

tcg tgg ccc aag gct ccc tcc aat gca att atc atc gga ttg aag gag        240
Ser Trp Pro Lys Ala Pro Ser Asn Ala Ile Ile Ile Gly Leu Lys Glu
65                  70                  75                  80

ttg cct ccg aat gat gat tcg ccc ctc atc cat acc cat gtc atg ttc        288
Leu Pro Pro Asn Asp Asp Ser Pro Leu Ile His Thr His Val Met Phe
                85                  90                  95

ggc cat tgt tac aag caa caa gca ggc tac cag gac atc cta agt cga        336
Gly His Cys Tyr Lys Gln Gln Ala Gly Tyr Gln Asp Ile Leu Ser Arg
            100                 105                 110

ttc aaa cga ggc ggg gga act ttg ctc gac atg gaa ttc ttg cag gac        384
Phe Lys Arg Gly Gly Gly Thr Leu Leu Asp Met Glu Phe Leu Gln Asp
        115                 120                 125

gag cac acc aaa cgc aga gtg gct gcc ttt ggc ttc cac gcc gga ttc        432
Glu His Thr Lys Arg Arg Val Ala Ala Phe Gly Phe His Ala Gly Phe
    130                 135                 140

aat ggc tct gct gtc ggt cta ctt gcg ctt ggg tcg atg tta tcc ggg        480
Asn Gly Ser Ala Val Gly Leu Leu Ala Leu Gly Ser Met Leu Ser Gly
145                 150                 155                 160

gag gga agt ttg aaa gga ttg aag cct ttc aaa gat gaa gac gaa ttg        528
Glu Gly Ser Leu Lys Gly Leu Lys Pro Phe Lys Asp Glu Asp Glu Leu
                165                 170                 175

att act cga ggg aag aaa gaa ttc gat cga gtg gtc gcc aag cta ggt        576
Ile Thr Arg Gly Lys Lys Glu Phe Asp Arg Val Val Ala Lys Leu Gly
            180                 185                 190

cga cat cct aag gcc cta gtg att ggt tca ttg gga cgc tgt ggc tcc        624
Arg His Pro Lys Ala Leu Val Ile Gly Ser Leu Gly Arg Cys Gly Ser
        195                 200                 205

gga gct gtt aca ttt ttc aag aaa att gga ttg aac aag gat gac gtc        672
Gly Ala Val Thr Phe Phe Lys Lys Ile Gly Leu Asn Lys Asp Asp Val
    210                 215                 220

gtt gaa tgg gac atg gca gag act gcc aaa ggt ggc cca ttc caa gaa        720
Val Glu Trp Asp Met Ala Glu Thr Ala Lys Gly Gly Pro Phe Gln Glu
225                 230                 235                 240

att ctt gaa gcc gat atc ttc atc aat tgc atc tac ttg agt agc aaa        768
Ile Leu Glu Ala Asp Ile Phe Ile Asn Cys Ile Tyr Leu Ser Ser Lys
                245                 250                 255

atc ccc agc ttt gtc acc cgg gag aca ata gcc gca gca gga gat tct        816
Ile Pro Ser Phe Val Thr Arg Glu Thr Ile Ala Ala Ala Gly Asp Ser
            260                 265                 270

cgc cag ctg agg gtt gta gtc gat gtg tcc tgt gat acc acc aat ccg        864
Arg Gln Leu Arg Val Val Val Asp Val Ser Cys Asp Thr Thr Asn Pro
        275                 280                 285

aac aat cct att ccg ata tat gac gtc aac act aca ttc gat tct cca        912
Asn Asn Pro Ile Pro Ile Tyr Asp Val Asn Thr Thr Phe Asp Ser Pro
    290                 295                 300

acc gtg cct gtc cag cta gat gct gga ctg cca agc tta gaa gtt tgc        960
Thr Val Pro Val Gln Leu Asp Ala Gly Leu Pro Ser Leu Glu Val Cys
305                 310                 315                 320
```

```
tcg ata gat cat ctg cca aca ctt ctg ccc aga gaa gcc tcc gaa caa       1008
Ser Ile Asp His Leu Pro Thr Leu Leu Pro Arg Glu Ala Ser Glu Gln
                325                 330                 335

ttt tcg aac gat ctc ctt cct acg ctt ttg caa tta aaa acg ttg gat       1056
Phe Ser Asn Asp Leu Leu Pro Thr Leu Leu Gln Leu Lys Thr Leu Asp
            340                 345                 350

caa tct aaa gtt tgg act gaa gca agg gat ttg ttt cac aag atg gtc       1104
Gln Ser Lys Val Trp Thr Glu Ala Arg Asp Leu Phe His Lys Met Val
        355                 360                 365

aat tcc atc tag                                                       1116
Asn Ser Ile
    370


<210>  22
<211>  371
<212>  PRT
<213>  Puccinia graminis

<400>  22

Met Ser Gly Asp Gln Pro Leu Leu Trp Leu Arg Cys Glu Thr Lys Pro
1               5                   10                  15


Phe Glu His Arg Ser Ala Leu Thr Pro Leu Thr Ala Lys Lys Leu Ile
            20                  25                  30


Asp Ala Gly Phe Lys Leu Val Val Glu Arg Asp Pro Gln Arg Phe Phe
        35                  40                  45


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


Ser Trp Pro Lys Ala Pro Ser Asn Ala Ile Ile Ile Gly Leu Lys Glu
65                  70                  75                  80


Leu Pro Pro Asn Asp Asp Ser Pro Leu Ile His Thr His Val Met Phe
                85                  90                  95


Gly His Cys Tyr Lys Gln Gln Ala Gly Tyr Gln Asp Ile Leu Ser Arg
            100                 105                 110


Phe Lys Arg Gly Gly Gly Thr Leu Leu Asp Met Glu Phe Leu Gln Asp
        115                 120                 125


Glu His Thr Lys Arg Arg Val Ala Ala Phe Gly Phe His Ala Gly Phe
    130                 135                 140


Asn Gly Ser Ala Val Gly Leu Leu Ala Leu Gly Ser Met Leu Ser Gly
145                 150                 155                 160


Glu Gly Ser Leu Lys Gly Leu Lys Pro Phe Lys Asp Glu Asp Glu Leu
                165                 170                 175
```

```
Ile Thr Arg Gly Lys Lys Glu Phe Asp Arg Val Val Ala Lys Leu Gly
            180                 185                 190


Arg His Pro Lys Ala Leu Val Ile Gly Ser Leu Gly Arg Cys Gly Ser
        195                 200                 205


Gly Ala Val Thr Phe Phe Lys Lys Ile Gly Leu Asn Lys Asp Asp Val
    210                 215                 220


Val Glu Trp Asp Met Ala Glu Thr Ala Lys Gly Gly Pro Phe Gln Glu
225                 230                 235                 240


Ile Leu Glu Ala Asp Ile Phe Ile Asn Cys Ile Tyr Leu Ser Ser Lys
                245                 250                 255


Ile Pro Ser Phe Val Thr Arg Glu Thr Ile Ala Ala Ala Gly Asp Ser
            260                 265                 270


Arg Gln Leu Arg Val Val Val Asp Val Ser Cys Asp Thr Thr Asn Pro
        275                 280                 285


Asn Asn Pro Ile Pro Ile Tyr Asp Val Asn Thr Thr Phe Asp Ser Pro
    290                 295                 300


Thr Val Pro Val Gln Leu Asp Ala Gly Leu Pro Ser Leu Glu Val Cys
305                 310                 315                 320


Ser Ile Asp His Leu Pro Thr Leu Leu Pro Arg Glu Ala Ser Glu Gln
                325                 330                 335


Phe Ser Asn Asp Leu Leu Pro Thr Leu Leu Gln Leu Lys Thr Leu Asp
            340                 345                 350


Gln Ser Lys Val Trp Thr Glu Ala Arg Asp Leu Phe His Lys Met Val
        355                 360                 365


Asn Ser Ile
    370


<210>  23
<211>  3045
<212>  DNA
<213>  Phytophthora infestans


<220>
<221>  CDS
<222>  (1)..(3045)
<223>  Lys1

<400>  23
atg tcg ggc aag tgt gta ggc atc gtc cgc gag gta tac aac aaa tgg         48
Met Ser Gly Lys Cys Val Gly Ile Val Arg Glu Val Tyr Asn Lys Trp
1               5                   10                  15
```

```
gag cgt cga gcg ccg ctc aca ccc gca cac gtt aag gag cta gtg gcg           96
Glu Arg Arg Ala Pro Leu Thr Pro Ala His Val Lys Glu Leu Val Ala
            20                  25                  30

cgt ggc gtg cag gtg ctg gtt cag ccg tcc acg gca cgc gtc ttc tca          144
Arg Gly Val Gln Val Leu Val Gln Pro Ser Thr Ala Arg Val Phe Ser
        35                  40                  45

gac gac cag tat gtt cgc gcc gga gcc aca ctg tcc gag aat ttg gcg          192
Asp Asp Gln Tyr Val Arg Ala Gly Ala Thr Leu Ser Glu Asn Leu Ala
    50                  55                  60

ccg gcg aat gtc att gtg ggg gtc aag cag gtg ccc gag ccg gca ctg          240
Pro Ala Asn Val Ile Val Gly Val Lys Gln Val Pro Glu Pro Ala Leu
65                  70                  75                  80

ctg gcg gac aag acg tac ctc ttc ttc agt cat acc atc aaa gcg cag          288
Leu Ala Asp Lys Thr Tyr Leu Phe Phe Ser His Thr Ile Lys Ala Gln
                85                  90                  95

ccc gag aac atg gcg ctg ctg gac gcc gtg cta cag cgt cgc gtc acg          336
Pro Glu Asn Met Ala Leu Leu Asp Ala Val Leu Gln Arg Arg Val Thr
            100                 105                 110

cta atc gac tac gaa tgt atc aca gag gag agt ggt aag cgt ctc att          384
Leu Ile Asp Tyr Glu Cys Ile Thr Glu Glu Ser Gly Lys Arg Leu Ile
        115                 120                 125

gcc ttc ggc gga aat gcc ggt cgt gca gga atg att gcg ggc ttc cga          432
Ala Phe Gly Gly Asn Ala Gly Arg Ala Gly Met Ile Ala Gly Phe Arg
    130                 135                 140

ggt ctc gga gaa cgt ctc atc aac atg gga atc tcc tcg ccc ttc gtc          480
Gly Leu Gly Glu Arg Leu Ile Asn Met Gly Ile Ser Ser Pro Phe Val
145                 150                 155                 160

aac atc gcg tcc tcc tac atg tac gca gac tta gag cac gct aaa gac          528
Asn Ile Ala Ser Ser Tyr Met Tyr Ala Asp Leu Glu His Ala Lys Asp
                165                 170                 175

gca gtg gaa gct gca ggt aga agg att cga aca gat ggt ctg ccg ggt          576
Ala Val Glu Ala Ala Gly Arg Arg Ile Arg Thr Asp Gly Leu Pro Gly
            180                 185                 190

gac ttg gcg cca atg aca ttc gcc ttt act ggc aat ggc aat gtg tct          624
Asp Leu Ala Pro Met Thr Phe Ala Phe Thr Gly Asn Gly Asn Val Ser
        195                 200                 205

aaa gga gct cag gag atc ttc aag ctc atg ccg cac gag atg gtg cat          672
Lys Gly Ala Gln Glu Ile Phe Lys Leu Met Pro His Glu Met Val His
    210                 215                 220

cct tcg gaa cta cca aag ctg cca aaa aac aat cgt att ctc tac ggt          720
Pro Ser Glu Leu Pro Lys Leu Pro Lys Asn Asn Arg Ile Leu Tyr Gly
225                 230                 235                 240

aca gtc atc gac gat ccg gcc tac ttt gtt aag cct cag ccg ggt ttc          768
Thr Val Ile Asp Asp Pro Ala Tyr Phe Val Lys Pro Gln Pro Gly Phe
                245                 250                 255

acg ggt gag act acg aga gct cac tac tac cag aat cca cac caa tac          816
Thr Gly Glu Thr Thr Arg Ala His Tyr Tyr Gln Asn Pro His Gln Tyr
            260                 265                 270

gaa gct gct ttc cat gaa aaa gtg ttg cca tac acc tca atg ctc gtc          864
Glu Ala Ala Phe His Glu Lys Val Leu Pro Tyr Thr Ser Met Leu Val
        275                 280                 285
```

```
aac tgt atg tac tgg gac gac cgt ttt cca aga ttg gcc acg cga gag        912
Asn Cys Met Tyr Trp Asp Asp Arg Phe Pro Arg Leu Ala Thr Arg Glu
    290                 295                 300

cag att cgt gag ctt cgc aag tct ggg aac cac aaa ttg ctc ggg atc        960
Gln Ile Arg Glu Leu Arg Lys Ser Gly Asn His Lys Leu Leu Gly Ile
305                 310                 315                 320

gct gat atc tcg tgc gat atc ggc gga agt atc gag ttt ctg gag cgt       1008
Ala Asp Ile Ser Cys Asp Ile Gly Gly Ser Ile Glu Phe Leu Glu Arg
                325                 330                 335

gct act gaa att gag cgt ccg ttc gct ctg tac gac gtt gtt gaa gat       1056
Ala Thr Glu Ile Glu Arg Pro Phe Ala Leu Tyr Asp Val Val Glu Asp
            340                 345                 350

aaa atg cgc gaa gat gga gac agc cga ggc ctc gaa gga gac gac ggc       1104
Lys Met Arg Glu Asp Gly Asp Ser Arg Gly Leu Glu Gly Asp Asp Gly
        355                 360                 365

att atg atg atg ggt gtc gat atc tta ccg agt gaa ctg gca cgc gag       1152
Ile Met Met Met Gly Val Asp Ile Leu Pro Ser Glu Leu Ala Arg Glu
    370                 375                 380

tcg agt cag cag ttc ggt gac cgc ttg gtc gga tac gtc acg gcg ctg       1200
Ser Ser Gln Gln Phe Gly Asp Arg Leu Val Gly Tyr Val Thr Ala Leu
385                 390                 395                 400

tcg agt gct tct tcg tcc aac gtt cct cta cat gaa cag aaa gag ctg       1248
Ser Ser Ala Ser Ser Ser Asn Val Pro Leu His Glu Gln Lys Glu Leu
                405                 410                 415

cct gct gag cta cgt gga gct tgt atc gcc agc aat ggt gtg ctt gca       1296
Pro Ala Glu Leu Arg Gly Ala Cys Ile Ala Ser Asn Gly Val Leu Ala
            420                 425                 430

cct aaa tac gag tat atc cac cgt atg cga gcc gag cgc gag cgc agc       1344
Pro Lys Tyr Glu Tyr Ile His Arg Met Arg Ala Glu Arg Glu Arg Ser
        435                 440                 445

aag cag tac aag ttc ttg gat gct caa caa cag gtc gct ggg agt acg       1392
Lys Gln Tyr Lys Phe Leu Asp Ala Gln Gln Gln Val Ala Gly Ser Thr
    450                 455                 460

tgc gtt cta ctg gag ggg cac ctg ttt gat acc gga ctt att aac cag       1440
Cys Val Leu Leu Glu Gly His Leu Phe Asp Thr Gly Leu Ile Asn Gln
465                 470                 475                 480

gta ctc aac ctc att gaa gac cat gat ggg ggt ttc cac ctt cta gac       1488
Val Leu Asn Leu Ile Glu Asp His Asp Gly Gly Phe His Leu Leu Asp
                485                 490                 495

tgc gaa gta cgc cca aat gtt gga gtc ggg gac agt ggt gac agc acc       1536
Cys Glu Val Arg Pro Asn Val Gly Val Gly Asp Ser Gly Asp Ser Thr
            500                 505                 510

agt tcg aac gcc atc gtg cag att agt atg agt gac cgt gaa gcg ctg       1584
Ser Ser Asn Ala Ile Val Gln Ile Ser Met Ser Asp Arg Glu Ala Leu
        515                 520                 525

gat gct atc atc acc aag atc cgc tcc tta gct gag ctt act tct ggt       1632
Asp Ala Ile Ile Thr Lys Ile Arg Ser Leu Ala Glu Leu Thr Ser Gly
    530                 535                 540

gcg aag gct acg gtc aca gaa cta ccc gat ctg tgc ggc aca gac tac       1680
Ala Lys Ala Thr Val Thr Glu Leu Pro Asp Leu Cys Gly Thr Asp Tyr
545                 550                 555                 560
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tcc aag acg cga ggt gtc gtg aga aaa gat gca gca gcc aat act atg       1728
Ser Lys Thr Arg Gly Val Val Arg Lys Asp Ala Ala Ala Asn Thr Met
                565                 570                 575

gct gaa gta tcg gtc tcc agc ccg aag aag cgg aag gtt gtg tgt ttt       1776
Ala Glu Val Ser Val Ser Ser Pro Lys Lys Arg Lys Val Val Cys Phe
            580                 585                 590

ggc gct gga ttg gtg gcg tca cca ctt gtg gag tat cta tca aga gag       1824
Gly Ala Gly Leu Val Ala Ser Pro Leu Val Glu Tyr Leu Ser Arg Glu
        595                 600                 605

caa gga aac gaa gtt cat gtg gtg tcg ggt att gag agg gaa gta aag       1872
Gln Gly Asn Glu Val His Val Val Ser Gly Ile Glu Arg Glu Val Lys
    610                 615                 620

gag atg atg cgc aaa atc tct cgt cga aac atc aag cct cac gta gtg       1920
Glu Met Met Arg Lys Ile Ser Arg Arg Asn Ile Lys Pro His Val Val
625                 630                 635                 640

aac gtc gct gaa gat gct gct gga gtc gac aaa ctt tgc gct gaa gcc       1968
Asn Val Ala Glu Asp Ala Ala Gly Val Asp Lys Leu Cys Ala Glu Ala
                645                 650                 655

gat tgc gtt gtg tcg cta ctg cca gcg acc atg cac acg aca att gct       2016
Asp Cys Val Val Ser Leu Leu Pro Ala Thr Met His Thr Thr Ile Ala
            660                 665                 670

cag cgc tgc att cag cat gcg act cct ctc gtg acg gct agc tat gtg       2064
Gln Arg Cys Ile Gln His Ala Thr Pro Leu Val Thr Ala Ser Tyr Val
        675                 680                 685

tca cca gaa atg aag gag ctg gac gct agg gca aag aag gca ggt att       2112
Ser Pro Glu Met Lys Glu Leu Asp Ala Arg Ala Lys Lys Ala Gly Ile
    690                 695                 700

ccg atc ctc tgt gag att ggt ctc gac cct ggt atg gat cac atg agt       2160
Pro Ile Leu Cys Glu Ile Gly Leu Asp Pro Gly Met Asp His Met Ser
705                 710                 715                 720

gcc atg aaa gtc att gat gaa gtg aag gcc ctc tcc ggg aag gtc atg       2208
Ala Met Lys Val Ile Asp Glu Val Lys Ala Leu Ser Gly Lys Val Met
                725                 730                 735

acc ttc tcg tct gtc tgt ggc ggc ttg cca gct cct gaa gca gcg gac       2256
Thr Phe Ser Ser Val Cys Gly Gly Leu Pro Ala Pro Glu Ala Ala Asp
            740                 745                 750

aac gcc att ggt tac aag ttc agt tgg agt ccg cgt ggt gtg ctc acg       2304
Asn Ala Ile Gly Tyr Lys Phe Ser Trp Ser Pro Arg Gly Val Leu Thr
        755                 760                 765

gcg gca ctg aat gca gcc cag tac cgc aaa gac ggc aaa gtc atc aac       2352
Ala Ala Leu Asn Ala Ala Gln Tyr Arg Lys Asp Gly Lys Val Ile Asn
    770                 775                 780

gtg gca ggt gaa gac tta ctc aat aga agc gaa cgc gta aac ttc ttg       2400
Val Ala Gly Glu Asp Leu Leu Asn Arg Ser Glu Arg Val Asn Phe Leu
785                 790                 795                 800

ccg gcg ttc aac atc gag cag atc ccg aac cgt aat tcg ctt cct tac       2448
Pro Ala Phe Asn Ile Glu Gln Ile Pro Asn Arg Asn Ser Leu Pro Tyr
                805                 810                 815

ggc gat atc tat ggc atc cca gag gca cac tcg ctg tat cgt gga act       2496
Gly Asp Ile Tyr Gly Ile Pro Glu Ala His Ser Leu Tyr Arg Gly Thr
            820                 825                 830
```

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ctg cga tac ggt gga tgc tgt caa att ctg tac cag cta cgc aag ctt       2544
Leu Arg Tyr Gly Gly Cys Cys Gln Ile Leu Tyr Gln Leu Arg Lys Leu
        835                 840                 845

ggc ctc ttt gac atg gac cca tcc aaa ccc att cca gcg act tgg ccg       2592
Gly Leu Phe Asp Met Asp Pro Ser Lys Pro Ile Pro Ala Thr Trp Pro
    850                 855                 860

gat ctt ctg acg cag ttg ggt ggt ttc caa ggt ctt cgc gaa gac gcc       2640
Asp Leu Leu Thr Gln Leu Gly Gly Phe Gln Gly Leu Arg Glu Asp Ala
865                 870                 875                 880

cat ggg ttc ctt cag tgg ctt ggt gcc ttt gat aaa tca aat cct gtg       2688
His Gly Phe Leu Gln Trp Leu Gly Ala Phe Asp Lys Ser Asn Pro Val
                885                 890                 895

gtt aaa gcc ccg tcc atc ctt gac gct ttc tgc gct ctc ctg caa gat       2736
Val Lys Ala Pro Ser Ile Leu Asp Ala Phe Cys Ala Leu Leu Gln Asp
            900                 905                 910

aag ttg tcg tac caa cca gga gaa cgc gac atg gcc atc atg cat cat       2784
Lys Leu Ser Tyr Gln Pro Gly Glu Arg Asp Met Ala Ile Met His His
        915                 920                 925

gag ttc ggc atc gag tac gag gat ggc aag aag gaa aag cgt acg tca       2832
Glu Phe Gly Ile Glu Tyr Glu Asp Gly Lys Lys Glu Lys Arg Thr Ser
    930                 935                 940

aca ttc gtg ggc tac ggg tcc gag aag ggc gac acg atc atg gct aaa       2880
Thr Phe Val Gly Tyr Gly Ser Glu Lys Gly Asp Thr Ile Met Ala Lys
945                 950                 955                 960

acg gtt gga tta agt gct gct atc ggc gtc cag ttg atc ttg cag gac       2928
Thr Val Gly Leu Ser Ala Ala Ile Gly Val Gln Leu Ile Leu Gln Asp
                965                 970                 975

gca gtt caa ggt cgt ggt gtg ctt acc ccc aca acc ccc gac atc tac       2976
Ala Val Gln Gly Arg Gly Val Leu Thr Pro Thr Thr Pro Asp Ile Tyr
            980                 985                 990

ggt cct gca ctg gcc cgt ctc gag  gtc gaa ggt gtg cgc  ttc att gaa     3024
Gly Pro Ala Leu Ala Arg Leu Glu  Val Glu Gly Val Arg  Phe Ile Glu
        995                 1000                 1005

aaa aca  ttc cca cag cat taa                                          3045
Lys Thr  Phe Pro Gln His
    1010


<210>  24
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<212>  PRT
<213>  Phytophthora infestans

<400>  24

Met Ser Gly Lys Cys Val Gly Ile Val Arg Glu Val Tyr Asn Lys Trp
1               5                   10                  15


Glu Arg Arg Ala Pro Leu Thr Pro Ala His Val Lys Glu Leu Val Ala
            20                  25                  30


Arg Gly Val Gln Val Leu Val Gln Pro Ser Thr Ala Arg Val Phe Ser
        35                  40                  45
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Asp Asp Gln Tyr Val Arg Ala Gly Ala Thr Leu Ser Glu Asn Leu Ala
    50                  55                  60


Pro Ala Asn Val Ile Val Gly Val Lys Gln Val Pro Glu Pro Ala Leu
65                  70                  75                  80


Leu Ala Asp Lys Thr Tyr Leu Phe Phe Ser His Thr Ile Lys Ala Gln
                85                  90                  95


Pro Glu Asn Met Ala Leu Leu Asp Ala Val Leu Gln Arg Arg Val Thr
            100                 105                 110


Leu Ile Asp Tyr Glu Cys Ile Thr Glu Glu Ser Gly Lys Arg Leu Ile
        115                 120                 125


Ala Phe Gly Gly Asn Ala Gly Arg Ala Gly Met Ile Ala Gly Phe Arg
    130                 135                 140


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


Asn Ile Ala Ser Ser Tyr Met Tyr Ala Asp Leu Glu His Ala Lys Asp
                165                 170                 175


Ala Val Glu Ala Ala Gly Arg Arg Ile Arg Thr Asp Gly Leu Pro Gly
            180                 185                 190


Asp Leu Ala Pro Met Thr Phe Ala Phe Thr Gly Asn Gly Asn Val Ser
        195                 200                 205


Lys Gly Ala Gln Glu Ile Phe Lys Leu Met Pro His Glu Met Val His
    210                 215                 220


Pro Ser Glu Leu Pro Lys Leu Pro Lys Asn Asn Arg Ile Leu Tyr Gly
225                 230                 235                 240


Thr Val Ile Asp Asp Pro Ala Tyr Phe Val Lys Pro Gln Pro Gly Phe
                245                 250                 255


Thr Gly Glu Thr Thr Arg Ala His Tyr Tyr Gln Asn Pro His Gln Tyr
            260                 265                 270


Glu Ala Ala Phe His Glu Lys Val Leu Pro Tyr Thr Ser Met Leu Val
        275                 280                 285


Asn Cys Met Tyr Trp Asp Asp Arg Phe Pro Arg Leu Ala Thr Arg Glu
    290                 295                 300


Gln Ile Arg Glu Leu Arg Lys Ser Gly Asn His Lys Leu Leu Gly Ile
305                 310                 315                 320
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Ala Asp Ile Ser Cys Asp Ile Gly Gly Ser Ile Glu Phe Leu Glu Arg
                325                 330                 335


Ala Thr Glu Ile Glu Arg Pro Phe Ala Leu Tyr Asp Val Val Glu Asp
            340                 345                 350


Lys Met Arg Glu Asp Gly Asp Ser Arg Gly Leu Glu Gly Asp Asp Gly
        355                 360                 365


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


Ser Ser Gln Gln Phe Gly Asp Arg Leu Val Gly Tyr Val Thr Ala Leu
385                 390                 395                 400


Ser Ser Ala Ser Ser Ser Asn Val Pro Leu His Glu Gln Lys Glu Leu
                405                 410                 415


Pro Ala Glu Leu Arg Gly Ala Cys Ile Ala Ser Asn Gly Val Leu Ala
            420                 425                 430


Pro Lys Tyr Glu Tyr Ile His Arg Met Arg Ala Glu Arg Glu Arg Ser
        435                 440                 445


Lys Gln Tyr Lys Phe Leu Asp Ala Gln Gln Gln Val Ala Gly Ser Thr
    450                 455                 460


Cys Val Leu Leu Glu Gly His Leu Phe Asp Thr Gly Leu Ile Asn Gln
465                 470                 475                 480


Val Leu Asn Leu Ile Glu Asp His Asp Gly Gly Phe His Leu Leu Asp
                485                 490                 495


Cys Glu Val Arg Pro Asn Val Gly Val Gly Asp Ser Gly Asp Ser Thr
            500                 505                 510


Ser Ser Asn Ala Ile Val Gln Ile Ser Met Ser Asp Arg Glu Ala Leu
        515                 520                 525


Asp Ala Ile Ile Thr Lys Ile Arg Ser Leu Ala Glu Leu Thr Ser Gly
    530                 535                 540


Ala Lys Ala Thr Val Thr Glu Leu Pro Asp Leu Cys Gly Thr Asp Tyr
545                 550                 555                 560


Ser Lys Thr Arg Gly Val Val Arg Lys Asp Ala Ala Ala Asn Thr Met
                565                 570                 575


Ala Glu Val Ser Val Ser Ser Pro Lys Lys Arg Lys Val Val Cys Phe
            580                 585                 590
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Gly Ala Gly Leu Val Ala Ser Pro Leu Val Glu Tyr Leu Ser Arg Glu
        595                 600                 605


Gln Gly Asn Glu Val His Val Val Ser Gly Ile Glu Arg Glu Val Lys
    610                 615                 620


Glu Met Met Arg Lys Ile Ser Arg Arg Asn Ile Lys Pro His Val Val
625                 630                 635                 640


Asn Val Ala Glu Asp Ala Ala Gly Val Asp Lys Leu Cys Ala Glu Ala
                645                 650                 655


Asp Cys Val Val Ser Leu Leu Pro Ala Thr Met His Thr Thr Ile Ala
            660                 665                 670


Gln Arg Cys Ile Gln His Ala Thr Pro Leu Val Thr Ala Ser Tyr Val
        675                 680                 685


Ser Pro Glu Met Lys Glu Leu Asp Ala Arg Ala Lys Lys Ala Gly Ile
    690                 695                 700


Pro Ile Leu Cys Glu Ile Gly Leu Asp Pro Gly Met Asp His Met Ser
705                 710                 715                 720


Ala Met Lys Val Ile Asp Glu Val Lys Ala Leu Ser Gly Lys Val Met
                725                 730                 735


Thr Phe Ser Ser Val Cys Gly Gly Leu Pro Ala Pro Glu Ala Ala Asp
            740                 745                 750


Asn Ala Ile Gly Tyr Lys Phe Ser Trp Ser Pro Arg Gly Val Leu Thr
        755                 760                 765


Ala Ala Leu Asn Ala Ala Gln Tyr Arg Lys Asp Gly Lys Val Ile Asn
    770                 775                 780


Val Ala Gly Glu Asp Leu Leu Asn Arg Ser Glu Arg Val Asn Phe Leu
785                 790                 795                 800


Pro Ala Phe Asn Ile Glu Gln Ile Pro Asn Arg Asn Ser Leu Pro Tyr
                805                 810                 815


Gly Asp Ile Tyr Gly Ile Pro Glu Ala His Ser Leu Tyr Arg Gly Thr
            820                 825                 830


Leu Arg Tyr Gly Gly Cys Cys Gln Ile Leu Tyr Gln Leu Arg Lys Leu
        835                 840                 845


Gly Leu Phe Asp Met Asp Pro Ser Lys Pro Ile Pro Ala Thr Trp Pro
    850                 855                 860
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```
Asp Leu Leu Thr Gln Leu Gly Gly Phe Gln Gly Leu Arg Glu Asp Ala
865                 870                 875                 880


His Gly Phe Leu Gln Trp Leu Gly Ala Phe Asp Lys Ser Asn Pro Val
                885                 890                 895


Val Lys Ala Pro Ser Ile Leu Asp Ala Phe Cys Ala Leu Leu Gln Asp
            900                 905                 910


Lys Leu Ser Tyr Gln Pro Gly Glu Arg Asp Met Ala Ile Met His His
        915                 920                 925


Glu Phe Gly Ile Glu Tyr Glu Asp Gly Lys Lys Glu Lys Arg Thr Ser
    930                 935                 940


Thr Phe Val Gly Tyr Gly Ser Glu Lys Gly Asp Thr Ile Met Ala Lys
945                 950                 955                 960


Thr Val Gly Leu Ser Ala Ala Ile Gly Val Gln Leu Ile Leu Gln Asp
                965                 970                 975


Ala Val Gln Gly Arg Gly Val Leu Thr Pro Thr Thr Pro Asp Ile Tyr
            980                 985                 990


Gly Pro Ala Leu Ala Arg Leu Glu  Val Glu Gly Val Arg  Phe Ile Glu
        995                 1000             1005


Lys Thr  Phe Pro Gln His
    1010


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<223>  Lys1

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gtg ggc atc gtg cgc gag gtg tac aac aag tgg gag cgc cgc gcg ccg          48
Val Gly Ile Val Arg Glu Val Tyr Asn Lys Trp Glu Arg Arg Ala Pro
1               5                   10                  15

ctc acc ccc gcg cac gtc cgc gag ctc gtg cag cgc ggc gtg cag gtg          96
Leu Thr Pro Ala His Val Arg Glu Leu Val Gln Arg Gly Val Gln Val
            20                  25                  30

ttg gtg cag ccg tct acg gcg cgc gtc ttc tca gac gag cag tac gtg         144
Leu Val Gln Pro Ser Thr Ala Arg Val Phe Ser Asp Glu Gln Tyr Val
        35                  40                  45

cga gcg ggc gcc aag ctg gcc gag gac ctg gcg ccc gcc aat atc atc         192
Arg Ala Gly Ala Lys Leu Ala Glu Asp Leu Ala Pro Ala Asn Ile Ile
    50                  55                  60
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gtg ggc gtc aag cag gta ccg gag ccg gcg ctt ctg gcg gac aag aca        240
Val Gly Val Lys Gln Val Pro Glu Pro Ala Leu Leu Ala Asp Lys Thr
65                  70                  75                  80

tac ctc ttc ttc agc cat acc atc aag gcg cag cct gag aac atg gcg        288
Tyr Leu Phe Phe Ser His Thr Ile Lys Ala Gln Pro Glu Asn Met Ala
                85                  90                  95

ctc ctg gat gcc gtg ctg cag cgc cgc gtc acg ctc atc gac tac gag        336
Leu Leu Asp Ala Val Leu Gln Arg Arg Val Thr Leu Ile Asp Tyr Glu
            100                 105                 110

tgc atc aca gag gag agc ggc aag cgc ctc atc gcc ttc gga ggc aac        384
Cys Ile Thr Glu Glu Ser Gly Lys Arg Leu Ile Ala Phe Gly Gly Asn
        115                 120                 125

gcg ggg cga gca gga atg atc gcg ggc ttc cgg ggg ctt ggg gaa cgc        432
Ala Gly Arg Ala Gly Met Ile Ala Gly Phe Arg Gly Leu Gly Glu Arg
    130                 135                 140

ctc atc aac atg ggc atc tcc tcg ccc ttt gtg aac gta gcg tcg gcc        480
Leu Ile Asn Met Gly Ile Ser Ser Pro Phe Val Asn Val Ala Ser Ala
145                 150                 155                 160

tac atg tac tcg gac ttg gag cac gca aaa gac gcc gta gaa gct gcg        528
Tyr Met Tyr Ser Asp Leu Glu His Ala Lys Asp Ala Val Glu Ala Ala
                165                 170                 175

ggc agg agg att cgg tcc gat gga ttg cca ggc gag ctg gcg ccc atg        576
Gly Arg Arg Ile Arg Ser Asp Gly Leu Pro Gly Glu Leu Ala Pro Met
            180                 185                 190

gcc ttc gcc ttc acg ggc aat ggc aac gtg tcc aaa ggg gcg cag gag        624
Ala Phe Ala Phe Thr Gly Asn Gly Asn Val Ser Lys Gly Ala Gln Glu
        195                 200                 205

atc ttc aag ctc atg cca cat gaa atg gtg cat ccg tca gag ctg cca        672
Ile Phe Lys Leu Met Pro His Glu Met Val His Pro Ser Glu Leu Pro
    210                 215                 220

aac ttg ccg aag aac aac cac atc ctg tac ggc acc gtg gtt gat gac        720
Asn Leu Pro Lys Asn Asn His Ile Leu Tyr Gly Thr Val Val Asp Asp
225                 230                 235                 240

ccg gcc ttc ttt gtg aag ccg cag gct ggc aac agc ggc acg gcc tcg        768
Pro Ala Phe Phe Val Lys Pro Gln Ala Gly Asn Ser Gly Thr Ala Ser
                245                 250                 255

cgc gca cac tac tac cag aac cca cac cag tac gac cct gcc ttc cac        816
Arg Ala His Tyr Tyr Gln Asn Pro His Gln Tyr Asp Pro Ala Phe His
            260                 265                 270

gag aag gtg ctg ccg tac acg tcc atg ttg gtg aac tgc atg tac tgg        864
Glu Lys Val Leu Pro Tyr Thr Ser Met Leu Val Asn Cys Met Tyr Trp
        275                 280                 285

gac gac cgt ttc ccg cga ttg gtt acg cgc gaa cag atc cgt gag ctt        912
Asp Asp Arg Phe Pro Arg Leu Val Thr Arg Glu Gln Ile Arg Glu Leu
    290                 295                 300

cga ggc tct gga aac caa aag ctg ctg ggc att gcc gat att tcg tgc        960
Arg Gly Ser Gly Asn Gln Lys Leu Leu Gly Ile Ala Asp Ile Ser Cys
305                 310                 315                 320

gat att ggc ggc agt gtt gaa ttt ttg gag cgc gcg acg gaa att gaa       1008
Asp Ile Gly Gly Ser Val Glu Phe Leu Glu Arg Ala Thr Glu Ile Glu
                325                 330                 335
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cgc ccg ttc gcg ctg tac gat gtc gct gaa gac aaa atg cgc gag gat       1056
Arg Pro Phe Ala Leu Tyr Asp Val Ala Glu Asp Lys Met Arg Glu Asp
            340                 345                 350

ggc gat agt cga ggg ctc gaa ggg gat aac ggc atc atg atg atg ggg       1104
Gly Asp Ser Arg Gly Leu Glu Gly Asp Asn Gly Ile Met Met Met Gly
        355                 360                 365

gtc gat ata ttg cca agc gaa ctt cca cgc gag tct agt caa cag ttc       1152
Val Asp Ile Leu Pro Ser Glu Leu Pro Arg Glu Ser Ser Gln Gln Phe
    370                 375                 380

ggc gac cgt ctg gtc gca tac gtg gcg gcg ctg tcg aat gct tcc tca       1200
Gly Asp Arg Leu Val Ala Tyr Val Ala Ala Leu Ser Asn Ala Ser Ser
385                 390                 395                 400

tcc agt gtc cca ctt cat gag caa aag gag cta cct gct gag ctc cgt       1248
Ser Ser Val Pro Leu His Glu Gln Lys Glu Leu Pro Ala Glu Leu Arg
                405                 410                 415

ggc gcc tgc atc gca agc aaa gga gta ctc gcc cca aaa tac gag tac       1296
Gly Ala Cys Ile Ala Ser Lys Gly Val Leu Ala Pro Lys Tyr Glu Tyr
            420                 425                 430

att cac cgt atg cgt gcc gaa cgt gag cgc agt aag cag tac aag ttc       1344
Ile His Arg Met Arg Ala Glu Arg Glu Arg Ser Lys Gln Tyr Lys Phe
        435                 440                 445

ctg gat gcg cag cag gaa gtt gcg ggg agc acg tgt att ctg ctt gaa       1392
Leu Asp Ala Gln Gln Glu Val Ala Gly Ser Thr Cys Ile Leu Leu Glu
    450                 455                 460

ggt cac ctc ttc gat aca gga ctt atc aac caa gtg ctc aac ctc att       1440
Gly His Leu Phe Asp Thr Gly Leu Ile Asn Gln Val Leu Asn Leu Ile
465                 470                 475                 480

gag gac cat gat ggc gga ttc cac ctt gtg gac tgt gaa gtg cgg ccg       1488
Glu Asp His Asp Gly Gly Phe His Leu Val Asp Cys Glu Val Arg Pro
                485                 490                 495

aac gtt gct gtc agc gac agt ggc gac tgt acc ata tcg aat gct atc       1536
Asn Val Ala Val Ser Asp Ser Gly Asp Cys Thr Ile Ser Asn Ala Ile
            500                 505                 510

gtc cag ata agc atg aac gat cga gct gcg ctg gat gaa att atc tca       1584
Val Gln Ile Ser Met Asn Asp Arg Ala Ala Leu Asp Glu Ile Ile Ser
        515                 520                 525

aag gtt cgc tct ctt gct gac ctt acc tcc ggt gcc aag gct act gtc       1632
Lys Val Arg Ser Leu Ala Asp Leu Thr Ser Gly Ala Lys Ala Thr Val
    530                 535                 540

act gag ctt ccc gac ttg tgc ggt aca aac tac tcg aag aca cgt ggt       1680
Thr Glu Leu Pro Asp Leu Cys Gly Thr Asn Tyr Ser Lys Thr Arg Gly
545                 550                 555                 560

gct gta gta cgg aag gac gcg gct gcc aat acg act acc gac gtg tcg       1728
Ala Val Val Arg Lys Asp Ala Ala Ala Asn Thr Thr Thr Asp Val Ser
                565                 570                 575

gtc tca agc cca aag agg cga aag att gta tgc ttt ggc gcc ggg ttg       1776
Val Ser Ser Pro Lys Arg Arg Lys Ile Val Cys Phe Gly Ala Gly Leu
            580                 585                 590

gtg gca tcg ccc ctt gtg gag tat ctg tcg cgt gaa caa gtc aac gaa       1824
Val Ala Ser Pro Leu Val Glu Tyr Leu Ser Arg Glu Gln Val Asn Glu
        595                 600                 605
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gtt cat gtg gtg tct ggc ctc gag ggt gag gta aag gga att atg cgc       1872
Val His Val Val Ser Gly Leu Glu Gly Glu Val Lys Gly Ile Met Arg
    610                 615                 620

aag atc tct cgc cga aac atc aag cct cat gtt gta aac gta gct gaa       1920
Lys Ile Ser Arg Arg Asn Ile Lys Pro His Val Val Asn Val Ala Glu
625                 630                 635                 640

gac act gcc gga gtt gac aag ctt tgt gca gaa gct gat tgt gtc gtg       1968
Asp Thr Ala Gly Val Asp Lys Leu Cys Ala Glu Ala Asp Cys Val Val
                645                 650                 655

tca ctt ttg cca gcg acc atg cac aca acg att gcc gag cgc tgt att       2016
Ser Leu Leu Pro Ala Thr Met His Thr Thr Ile Ala Glu Arg Cys Ile
            660                 665                 670

cag cac gcg aca cca ctt gtg act gca agt tat gtg tct ccg gag atg       2064
Gln His Ala Thr Pro Leu Val Thr Ala Ser Tyr Val Ser Pro Glu Met
        675                 680                 685

aaa gag ctg gac tcc aag gca aag caa gct ggc atc cct atc ctc tgt       2112
Lys Glu Leu Asp Ser Lys Ala Lys Gln Ala Gly Ile Pro Ile Leu Cys
    690                 695                 700

gaa att ggt ctt gac cct ggc atg gat cac atg agc gcg atg aaa gtt       2160
Glu Ile Gly Leu Asp Pro Gly Met Asp His Met Ser Ala Met Lys Val
705                 710                 715                 720

att gat gag gtg aag gcg cac tct ggg aag atc aag tct ttc tcg tct       2208
Ile Asp Glu Val Lys Ala His Ser Gly Lys Ile Lys Ser Phe Ser Ser
                725                 730                 735

gta tgt ggc ggg ctg ccg gcg cct gag gca gcg gac aac gct att ggt       2256
Val Cys Gly Gly Leu Pro Ala Pro Glu Ala Ala Asp Asn Ala Ile Gly
            740                 745                 750

tac aag ttc agc tgg agt ccg cgc ggt gtg cta aca gca gcg ctg aat       2304
Tyr Lys Phe Ser Trp Ser Pro Arg Gly Val Leu Thr Ala Ala Leu Asn
        755                 760                 765

gca gct caa tac cgc aaa gac gac aaa gtc att aat gtg gcc ggt gaa       2352
Ala Ala Gln Tyr Arg Lys Asp Asp Lys Val Ile Asn Val Ala Gly Glu
    770                 775                 780

gac ttg cta aac agc agt gag cgc gtg aac ttc ctg cca gcg ttc aac       2400
Asp Leu Leu Asn Ser Ser Glu Arg Val Asn Phe Leu Pro Ala Phe Asn
785                 790                 795                 800

att gag cag att cca aac cgt aat tcg ctg ccg tac ggc gat atc tac       2448
Ile Glu Gln Ile Pro Asn Arg Asn Ser Leu Pro Tyr Gly Asp Ile Tyr
                805                 810                 815

ggc att ccg gaa gca cac tca ttg tat cgc ggc act ctg cgc tat ggt       2496
Gly Ile Pro Glu Ala His Ser Leu Tyr Arg Gly Thr Leu Arg Tyr Gly
            820                 825                 830

ggc tgc tgt caa att ttg tac caa cta cgt aag ctc ggc ctc ttc gac       2544
Gly Cys Cys Gln Ile Leu Tyr Gln Leu Arg Lys Leu Gly Leu Phe Asp
        835                 840                 845

atg gac cca tcc aag ccc att cca gct act tgg cca gac ctt ctc act       2592
Met Asp Pro Ser Lys Pro Ile Pro Ala Thr Trp Pro Asp Leu Leu Thr
    850                 855                 860

caa tta ggt gga cac caa gac ctt cgt gaa gat gcc agc ggg ttc ctt       2640
Gln Leu Gly Gly His Gln Asp Leu Arg Glu Asp Ala Ser Gly Phe Leu
865                 870                 875                 880
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cag tgg ctt ggt gcc ttt gat cgc acc acg cct att gtt aag gca ccg       2688
Gln Trp Leu Gly Ala Phe Asp Arg Thr Thr Pro Ile Val Lys Ala Pro
                885                 890                 895

tcc gtt ctc gac gct ttc tgt aca ttg ctg cag gac aag tta tcg tac       2736
Ser Val Leu Asp Ala Phe Cys Thr Leu Leu Gln Asp Lys Leu Ser Tyr
            900                 905                 910

cag ccg ggt gaa cgc gac atg gcc atc atg cac cat gaa ttc ggc att       2784
Gln Pro Gly Glu Arg Asp Met Ala Ile Met His His Glu Phe Gly Ile
        915                 920                 925

gag tac gaa gat ggc aaa agg gaa aaa cgc acg tca acg ttc gtg ggc       2832
Glu Tyr Glu Asp Gly Lys Arg Glu Lys Arg Thr Ser Thr Phe Val Gly
    930                 935                 940

tat ggc tcc gag aag ggc gac aca atc atg gca aaa act gtc ggc ttg       2880
Tyr Gly Ser Glu Lys Gly Asp Thr Ile Met Ala Lys Thr Val Gly Leu
945                 950                 955                 960

agt gca gct att ggc gtg cag ctg att ttg cag gac gcc gtc cag ggc       2928
Ser Ala Ala Ile Gly Val Gln Leu Ile Leu Gln Asp Ala Val Gln Gly
                965                 970                 975

cga ggt gtg cta acc ccg aca acc cct gac atc tac ggc cca gcc ctc       2976
Arg Gly Val Leu Thr Pro Thr Thr Pro Asp Ile Tyr Gly Pro Ala Leu
            980                 985                 990

gcc cgt ctc gaa gtc gaa ggt gtg  cgc ttc atc gag aag                  3015
Ala Arg Leu Glu Val Glu Gly Val  Arg Phe Ile Glu Lys
        995                 1000                 1005


<210>  26
<211>  1005
<212>  PRT
<213>  Phytophthora ramorum

<400>  26

Val Gly Ile Val Arg Glu Val Tyr Asn Lys Trp Glu Arg Arg Ala Pro
1               5                   10                  15


Leu Thr Pro Ala His Val Arg Glu Leu Val Gln Arg Gly Val Gln Val
            20                  25                  30


Leu Val Gln Pro Ser Thr Ala Arg Val Phe Ser Asp Glu Gln Tyr Val
        35                  40                  45


Arg Ala Gly Ala Lys Leu Ala Glu Asp Leu Ala Pro Ala Asn Ile Ile
    50                  55                  60


Val Gly Val Lys Gln Val Pro Glu Pro Ala Leu Leu Ala Asp Lys Thr
65                  70                  75                  80


Tyr Leu Phe Phe Ser His Thr Ile Lys Ala Gln Pro Glu Asn Met Ala
                85                  90                  95


Leu Leu Asp Ala Val Leu Gln Arg Arg Val Thr Leu Ile Asp Tyr Glu
            100                 105                 110
```

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Cys Ile Thr Glu Glu Ser Gly Lys Arg Leu Ile Ala Phe Gly Gly Asn
        115                 120                 125


Ala Gly Arg Ala Gly Met Ile Ala Gly Phe Arg Gly Leu Gly Glu Arg
    130                 135                 140


Leu Ile Asn Met Gly Ile Ser Ser Pro Phe Val Asn Val Ala Ser Ala
145                 150                 155                 160


Tyr Met Tyr Ser Asp Leu Glu His Ala Lys Asp Ala Val Glu Ala Ala
                165                 170                 175


Gly Arg Arg Ile Arg Ser Asp Gly Leu Pro Gly Glu Leu Ala Pro Met
            180                 185                 190


Ala Phe Ala Phe Thr Gly Asn Gly Asn Val Ser Lys Gly Ala Gln Glu
        195                 200                 205


Ile Phe Lys Leu Met Pro His Glu Met Val His Pro Ser Glu Leu Pro
    210                 215                 220


Asn Leu Pro Lys Asn Asn His Ile Leu Tyr Gly Thr Val Val Asp Asp
225                 230                 235                 240


Pro Ala Phe Phe Val Lys Pro Gln Ala Gly Asn Ser Gly Thr Ala Ser
                245                 250                 255


Arg Ala His Tyr Tyr Gln Asn Pro His Gln Tyr Asp Pro Ala Phe His
            260                 265                 270


Glu Lys Val Leu Pro Tyr Thr Ser Met Leu Val Asn Cys Met Tyr Trp
        275                 280                 285


Asp Asp Arg Phe Pro Arg Leu Val Thr Arg Glu Gln Ile Arg Glu Leu
    290                 295                 300


Arg Gly Ser Gly Asn Gln Lys Leu Leu Gly Ile Ala Asp Ile Ser Cys
305                 310                 315                 320


Asp Ile Gly Gly Ser Val Glu Phe Leu Glu Arg Ala Thr Glu Ile Glu
                325                 330                 335


Arg Pro Phe Ala Leu Tyr Asp Val Ala Glu Asp Lys Met Arg Glu Asp
            340                 345                 350


Gly Asp Ser Arg Gly Leu Glu Gly Asp Asn Gly Ile Met Met Met Gly
        355                 360                 365


Val Asp Ile Leu Pro Ser Glu Leu Pro Arg Glu Ser Ser Gln Gln Phe
    370                 375                 380
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Gly Asp Arg Leu Val Ala Tyr Val Ala Ala Leu Ser Asn Ala Ser Ser
385                 390                 395                 400


Ser Ser Val Pro Leu His Glu Gln Lys Glu Leu Pro Ala Glu Leu Arg
                405                 410                 415


Gly Ala Cys Ile Ala Ser Lys Gly Val Leu Ala Pro Lys Tyr Glu Tyr
            420                 425                 430


Ile His Arg Met Arg Ala Glu Arg Glu Arg Ser Lys Gln Tyr Lys Phe
        435                 440                 445


Leu Asp Ala Gln Gln Glu Val Ala Gly Ser Thr Cys Ile Leu Leu Glu
    450                 455                 460


Gly His Leu Phe Asp Thr Gly Leu Ile Asn Gln Val Leu Asn Leu Ile
465                 470                 475                 480


Glu Asp His Asp Gly Gly Phe His Leu Val Asp Cys Glu Val Arg Pro
                485                 490                 495


Asn Val Ala Val Ser Asp Ser Gly Asp Cys Thr Ile Ser Asn Ala Ile
            500                 505                 510


Val Gln Ile Ser Met Asn Asp Arg Ala Ala Leu Asp Glu Ile Ile Ser
        515                 520                 525


Lys Val Arg Ser Leu Ala Asp Leu Thr Ser Gly Ala Lys Ala Thr Val
    530                 535                 540


Thr Glu Leu Pro Asp Leu Cys Gly Thr Asn Tyr Ser Lys Thr Arg Gly
545                 550                 555                 560


Ala Val Val Arg Lys Asp Ala Ala Ala Asn Thr Thr Thr Asp Val Ser
                565                 570                 575


Val Ser Ser Pro Lys Arg Arg Lys Ile Val Cys Phe Gly Ala Gly Leu
            580                 585                 590


Val Ala Ser Pro Leu Val Glu Tyr Leu Ser Arg Glu Gln Val Asn Glu
        595                 600                 605


Val His Val Val Ser Gly Leu Glu Gly Glu Val Lys Gly Ile Met Arg
    610                 615                 620


Lys Ile Ser Arg Arg Asn Ile Lys Pro His Val Val Asn Val Ala Glu
625                 630                 635                 640


Asp Thr Ala Gly Val Asp Lys Leu Cys Ala Glu Ala Asp Cys Val Val
                645                 650                 655
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Ser Leu Leu Pro Ala Thr Met His Thr Thr Ile Ala Glu Arg Cys Ile
            660                 665                 670


Gln His Ala Thr Pro Leu Val Thr Ala Ser Tyr Val Ser Pro Glu Met
        675                 680                 685


Lys Glu Leu Asp Ser Lys Ala Lys Gln Ala Gly Ile Pro Ile Leu Cys
    690                 695                 700


Glu Ile Gly Leu Asp Pro Gly Met Asp His Met Ser Ala Met Lys Val
705                 710                 715                 720


Ile Asp Glu Val Lys Ala His Ser Gly Lys Ile Lys Ser Phe Ser Ser
                725                 730                 735


Val Cys Gly Gly Leu Pro Ala Pro Glu Ala Ala Asp Asn Ala Ile Gly
            740                 745                 750


Tyr Lys Phe Ser Trp Ser Pro Arg Gly Val Leu Thr Ala Ala Leu Asn
        755                 760                 765


Ala Ala Gln Tyr Arg Lys Asp Asp Lys Val Ile Asn Val Ala Gly Glu
    770                 775                 780


Asp Leu Leu Asn Ser Ser Glu Arg Val Asn Phe Leu Pro Ala Phe Asn
785                 790                 795                 800


Ile Glu Gln Ile Pro Asn Arg Asn Ser Leu Pro Tyr Gly Asp Ile Tyr
                805                 810                 815


Gly Ile Pro Glu Ala His Ser Leu Tyr Arg Gly Thr Leu Arg Tyr Gly
            820                 825                 830


Gly Cys Cys Gln Ile Leu Tyr Gln Leu Arg Lys Leu Gly Leu Phe Asp
        835                 840                 845


Met Asp Pro Ser Lys Pro Ile Pro Ala Thr Trp Pro Asp Leu Leu Thr
    850                 855                 860


Gln Leu Gly Gly His Gln Asp Leu Arg Glu Asp Ala Ser Gly Phe Leu
865                 870                 875                 880


Gln Trp Leu Gly Ala Phe Asp Arg Thr Thr Pro Ile Val Lys Ala Pro
                885                 890                 895


Ser Val Leu Asp Ala Phe Cys Thr Leu Leu Gln Asp Lys Leu Ser Tyr
            900                 905                 910


Gln Pro Gly Glu Arg Asp Met Ala Ile Met His His Glu Phe Gly Ile
        915                 920                 925
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```
Glu Tyr Glu Asp Gly Lys Arg Glu Lys Arg Thr Ser Thr Phe Val Gly
    930                 935                 940


Tyr Gly Ser Glu Lys Gly Asp Thr Ile Met Ala Lys Thr Val Gly Leu
945                 950                 955                 960


Ser Ala Ala Ile Gly Val Gln Leu Ile Leu Gln Asp Ala Val Gln Gly
                965                 970                 975


Arg Gly Val Leu Thr Pro Thr Thr Pro Asp Ile Tyr Gly Pro Ala Leu
            980                 985                 990


Ala Arg Leu Glu Val Glu Gly Val  Arg Phe Ile Glu Lys
        995                 1000                 1005


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<213>  Phytophthora sojae


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<223>  Lys1

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atg acg ggc aag tgc gtg ggc atc gtc cgc gag gtg tac aac aag tgg           48
Met Thr Gly Lys Cys Val Gly Ile Val Arg Glu Val Tyr Asn Lys Trp
1               5                   10                  15

gag cgg cgc gcg ccg ctc acg ccc gcg cac gtc cgg gag ctc gtg cag           96
Glu Arg Arg Ala Pro Leu Thr Pro Ala His Val Arg Glu Leu Val Gln
            20                  25                  30

cgc ggc atc cag gtg ctg gtg cag ccg tcc acg gcg cgc gtc ttc tcg          144
Arg Gly Ile Gln Val Leu Val Gln Pro Ser Thr Ala Arg Val Phe Ser
        35                  40                  45

gac gag cag tac gtg cgc gcg ggc gcc act ttg tcc gag gac ctg gcg          192
Asp Glu Gln Tyr Val Arg Ala Gly Ala Thr Leu Ser Glu Asp Leu Ala
    50                  55                  60

ccc gcc aac gtc atc gtg ggc gtc aag cag gtg ccc gag ccg gcg ctg          240
Pro Ala Asn Val Ile Val Gly Val Lys Gln Val Pro Glu Pro Ala Leu
65                  70                  75                  80

ctg gcc gac aag acg tac ctc ttc ttc agc cac acc atc aag gcg cag          288
Leu Ala Asp Lys Thr Tyr Leu Phe Phe Ser His Thr Ile Lys Ala Gln
                85                  90                  95

ccg gag aac atg gcg ttg ctg gac gcc gtg ctg cag cgc cgc atc acg          336
Pro Glu Asn Met Ala Leu Leu Asp Ala Val Leu Gln Arg Arg Ile Thr
            100                 105                 110

ctc gtc gac tac gag tgc atc aca gag gag agc ggc aag cgc ctc atc          384
Leu Val Asp Tyr Glu Cys Ile Thr Glu Glu Ser Gly Lys Arg Leu Ile
        115                 120                 125

gcc ttc ggg ggc aac gcc ggc cgc gcc ggt atg atc gcg ggc ttc cgg          432
Ala Phe Gly Gly Asn Ala Gly Arg Ala Gly Met Ile Ala Gly Phe Arg
    130                 135                 140
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ggg ctt gga gag cgc ctc atc aac atg ggc gtc tcc tcg ccc ttc gtg        480
Gly Leu Gly Glu Arg Leu Ile Asn Met Gly Val Ser Ser Pro Phe Val
145                 150                 155                 160

aac gtc gcg tcc gcc tac atg tac tcg gac ttg gag cac gcc aag gac        528
Asn Val Ala Ser Ala Tyr Met Tyr Ser Asp Leu Glu His Ala Lys Asp
                165                 170                 175

gcg gtg gag gcc gcg ggc aag agg atc cgc tcg gac gga ctg ccg agc        576
Ala Val Glu Ala Ala Gly Lys Arg Ile Arg Ser Asp Gly Leu Pro Ser
            180                 185                 190

gag ctg gtg ccc atg acg ttc gca ttc acg ggc aac ggc aat gtg tca        624
Glu Leu Val Pro Met Thr Phe Ala Phe Thr Gly Asn Gly Asn Val Ser
        195                 200                 205

aag ggc gcg cag gag atc ttc aag ctt atg ccc cac gag atg gtg cat        672
Lys Gly Ala Gln Glu Ile Phe Lys Leu Met Pro His Glu Met Val His
    210                 215                 220

ccg tcg gag ctg ccc aag cta ccg aag aac aac cgt att ctg tac ggc        720
Pro Ser Glu Leu Pro Lys Leu Pro Lys Asn Asn Arg Ile Leu Tyr Gly
225                 230                 235                 240

aca gtg atc gac aac ccg gac tac ttc gtc aag ccc cag ccg gga ttc        768
Thr Val Ile Asp Asn Pro Asp Tyr Phe Val Lys Pro Gln Pro Gly Phe
                245                 250                 255

agc ggc aca ccc tcc cgc gcg cac tac tac cag aac cca cac cag tac        816
Ser Gly Thr Pro Ser Arg Ala His Tyr Tyr Gln Asn Pro His Gln Tyr
            260                 265                 270

gag cct gct ttc cac gag aag gtg ctg ccc tac acg tcc atg ctg gtg        864
Glu Pro Ala Phe His Glu Lys Val Leu Pro Tyr Thr Ser Met Leu Val
        275                 280                 285

aac tgc atg tac tgg gac gac cgc ttc ccg cgg cta gtc acg cga gag        912
Asn Cys Met Tyr Trp Asp Asp Arg Phe Pro Arg Leu Val Thr Arg Glu
    290                 295                 300

cag atc cga gag ctt cga ggc tct ggg aac cat aag ctg ctg ggg atc        960
Gln Ile Arg Glu Leu Arg Gly Ser Gly Asn His Lys Leu Leu Gly Ile
305                 310                 315                 320

gcg gac att tcg tgc gat att ggc ggc agc gtg gag ttc ttg gag cgc       1008
Ala Asp Ile Ser Cys Asp Ile Gly Gly Ser Val Glu Phe Leu Glu Arg
                325                 330                 335

gcc acg gag atc gaa cga cca ttc gct ctg tac gat gtc gct gaa gac       1056
Ala Thr Glu Ile Glu Arg Pro Phe Ala Leu Tyr Asp Val Ala Glu Asp
            340                 345                 350

aag atg cgt gag gac ggc gac agt cga ggc ctt gaa ggc gac gat ggc       1104
Lys Met Arg Glu Asp Gly Asp Ser Arg Gly Leu Glu Gly Asp Asp Gly
        355                 360                 365

att atg atg atg ggc gtc gat atc ctg ccg agc gag ttg gcg cgc gag       1152
Ile Met Met Met Gly Val Asp Ile Leu Pro Ser Glu Leu Ala Arg Glu
    370                 375                 380

tca agc cag cag ttt ggt gac cgc ttg gtg gga tac gtc acg gcg cta       1200
Ser Ser Gln Gln Phe Gly Asp Arg Leu Val Gly Tyr Val Thr Ala Leu
385                 390                 395                 400

tcg agt gtc act tca tcg aat gta cct ctg cac gag caa aag gag ctg       1248
Ser Ser Val Thr Ser Ser Asn Val Pro Leu His Glu Gln Lys Glu Leu
                405                 410                 415
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ccg gct gaa ctg cgt ggc gct tgt att gcc agc aaa ggt gtt ttg gcg       1296
Pro Ala Glu Leu Arg Gly Ala Cys Ile Ala Ser Lys Gly Val Leu Ala
            420                 425                 430

ccc agg tac gag tac att cat cgg atg cgt gcc gaa cgt gag cgc agc       1344
Pro Arg Tyr Glu Tyr Ile His Arg Met Arg Ala Glu Arg Glu Arg Ser
        435                 440                 445

aag cag ttc aag ttc ctg gat gct cag cag gag gtt gca ggc agc acg       1392
Lys Gln Phe Lys Phe Leu Asp Ala Gln Gln Glu Val Ala Gly Ser Thr
    450                 455                 460

tgc ctg tta ctg gaa gga cac ctc ttt gat aca ggc ctc atc aac cag       1440
Cys Leu Leu Leu Glu Gly His Leu Phe Asp Thr Gly Leu Ile Asn Gln
465                 470                 475                 480

gta ctg aat ctc atc gag gac cac gat gga ggc ttc cac ctc gtg gac       1488
Val Leu Asn Leu Ile Glu Asp His Asp Gly Gly Phe His Leu Val Asp
                485                 490                 495

tgc gag gtc cga ccg aac att gca gcc gga gac agc ggc ttc agc act       1536
Cys Glu Val Arg Pro Asn Ile Ala Ala Gly Asp Ser Gly Phe Ser Thr
            500                 505                 510

gtg tcg aat gct ata gtc cag gtt agc atg agt gac cgt gct gct ttg       1584
Val Ser Asn Ala Ile Val Gln Val Ser Met Ser Asp Arg Ala Ala Leu
        515                 520                 525

gac gac att att gcg aag atc cgc tcc ctt gcc gat ctt acg tct ggt       1632
Asp Asp Ile Ile Ala Lys Ile Arg Ser Leu Ala Asp Leu Thr Ser Gly
    530                 535                 540

gcc aag gcc atc gtc acg gag ctt ccc gac ttg tgc ggc acg aat tat       1680
Ala Lys Ala Ile Val Thr Glu Leu Pro Asp Leu Cys Gly Thr Asn Tyr
545                 550                 555                 560

tcg aag act cgt ggt gcc gtg gtg cgc aag gat gct gct gct aat acg       1728
Ser Lys Thr Arg Gly Ala Val Val Arg Lys Asp Ala Ala Ala Asn Thr
                565                 570                 575

gcg gcg gac gtg tca gtc tcg agc ccg aag aag cga cag atc gtg tgt       1776
Ala Ala Asp Val Ser Val Ser Ser Pro Lys Lys Arg Gln Ile Val Cys
            580                 585                 590

ttt ggc gct gga tta gtg gca tcc ccg ctt gtt gag tac ctg tct cgc       1824
Phe Gly Ala Gly Leu Val Ala Ser Pro Leu Val Glu Tyr Leu Ser Arg
        595                 600                 605

gag caa ggc aat gaa gtg cac gtg gtg tcc ggt atc gag ggt gaa gtg       1872
Glu Gln Gly Asn Glu Val His Val Val Ser Gly Ile Glu Gly Glu Val
    610                 615                 620

aag ggg gtg atg cgc aaa atc tct cgc cgt aac att aag cct cac gtg       1920
Lys Gly Val Met Arg Lys Ile Ser Arg Arg Asn Ile Lys Pro His Val
625                 630                 635                 640

gtg aac gta gct gag gac ggt gct ggc gtt gac aag ctc tgt gca gaa       1968
Val Asn Val Ala Glu Asp Gly Ala Gly Val Asp Lys Leu Cys Ala Glu
                645                 650                 655

gcc gat tgt gtt gtg tca cta tta cca gct aca atg cac aca acc atc       2016
Ala Asp Cys Val Val Ser Leu Leu Pro Ala Thr Met His Thr Thr Ile
            660                 665                 670

gcc cag cgt tgc atc caa cat gga acg cct ctc gtg act gca agc tac       2064
Ala Gln Arg Cys Ile Gln His Gly Thr Pro Leu Val Thr Ala Ser Tyr
        675                 680                 685
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gtg tct ccg gag atg aaa gag ttg gat gcc aaa gcc aag aaa gcc ggc       2112
Val Ser Pro Glu Met Lys Glu Leu Asp Ala Lys Ala Lys Lys Ala Gly
    690                 695                 700

att cca ata ctg tgt gaa att ggc ctt gat cct ggc atg gat cac atg       2160
Ile Pro Ile Leu Cys Glu Ile Gly Leu Asp Pro Gly Met Asp His Met
705                 710                 715                 720

agc gct atg aag gtc atc gac gaa gtg aag gct cac tcc gga aag atc       2208
Ser Ala Met Lys Val Ile Asp Glu Val Lys Ala His Ser Gly Lys Ile
                725                 730                 735

ctg tca ttt tca tcc gtg tgt ggt gga ctt cca gct cct gaa gct gct       2256
Leu Ser Phe Ser Ser Val Cys Gly Gly Leu Pro Ala Pro Glu Ala Ala
            740                 745                 750

gac aac gcc att ggt tac aag ttc agc tgg agt ccg cgc ggc gtg ctt       2304
Asp Asn Ala Ile Gly Tyr Lys Phe Ser Trp Ser Pro Arg Gly Val Leu
        755                 760                 765

act gca gca ctg aac gcg gcg caa tac cgc aaa gac ggc aag atc gtc       2352
Thr Ala Ala Leu Asn Ala Ala Gln Tyr Arg Lys Asp Gly Lys Ile Val
    770                 775                 780

aac gtc gca ggc gaa gac ttg ctt aac agc agc gaa cct gtg aac ttc       2400
Asn Val Ala Gly Glu Asp Leu Leu Asn Ser Ser Glu Pro Val Asn Phe
785                 790                 795                 800

ttg cct gcg ttt aac atc gag cag atc ccg aac cgt gac tca ctg ccg       2448
Leu Pro Ala Phe Asn Ile Glu Gln Ile Pro Asn Arg Asp Ser Leu Pro
                805                 810                 815

tac ggc gag atc tac gtc att cct gag gcg cac tcg ctg tat cgt gga       2496
Tyr Gly Glu Ile Tyr Val Ile Pro Glu Ala His Ser Leu Tyr Arg Gly
            820                 825                 830

aca ctg cgc tac gga ggt tgt tgc cga atc ctg tac cag ctg cgc aag       2544
Thr Leu Arg Tyr Gly Gly Cys Cys Arg Ile Leu Tyr Gln Leu Arg Lys
        835                 840                 845

ctt ggt ctc ttt gac atg gac ccg tcc aag ccc att cca gct acg tgg       2592
Leu Gly Leu Phe Asp Met Asp Pro Ser Lys Pro Ile Pro Ala Thr Trp
    850                 855                 860

cca gac ctt atc tcc cag ctt ggt gga cac caa ggc ctt cgc gaa gac       2640
Pro Asp Leu Ile Ser Gln Leu Gly Gly His Gln Gly Leu Arg Glu Asp
865                 870                 875                 880

gcc aat gga ttc ctt caa tgg ctc ggt gcc ttc gat cac agc act ccc       2688
Ala Asn Gly Phe Leu Gln Trp Leu Gly Ala Phe Asp His Ser Thr Pro
                885                 890                 895

gta gtg cga gcc cca tcc atc ctc gac gca ttc tgc gca ctg ttg cag       2736
Val Val Arg Ala Pro Ser Ile Leu Asp Ala Phe Cys Ala Leu Leu Gln
            900                 905                 910

gac aag tta tct tac caa cct gga gaa cgt gat atg gcc atc atg cac       2784
Asp Lys Leu Ser Tyr Gln Pro Gly Glu Arg Asp Met Ala Ile Met His
        915                 920                 925

cat gaa ttc ggc atc gag tac gaa gac ggc aag aag gaa aag cgc acg       2832
His Glu Phe Gly Ile Glu Tyr Glu Asp Gly Lys Lys Glu Lys Arg Thr
    930                 935                 940

tca acg ttc gtg ggt tac ggc tcc gat aag ggc gac acc atc atg gct       2880
Ser Thr Phe Val Gly Tyr Gly Ser Asp Lys Gly Asp Thr Ile Met Ala
945                 950                 955                 960
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```
aaa acc gtt ggg ttg agt gca gcg att ggt gtg cag ttg atc ttg cag       2928
Lys Thr Val Gly Leu Ser Ala Ala Ile Gly Val Gln Leu Ile Leu Gln
                965                 970                 975

gac gca gtc caa ggc cga ggc gtg ctt aca ccg acg acc cct gac atc       2976
Asp Ala Val Gln Gly Arg Gly Val Leu Thr Pro Thr Thr Pro Asp Ile
            980                 985                 990

tac ggg cca gcc ctc gcg cga ctt  gag gtt gaa ggt gtt  cgc ttc atc     3024
Tyr Gly Pro Ala Leu Ala Arg Leu  Glu Val Glu Gly Val  Arg Phe Ile
        995                 1000                 1005

gaa aag  acg ttc ccg cag cct  taa                                     3048
Glu Lys  Thr Phe Pro Gln Pro
    1010                 1015


<210>  28
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<212>  PRT
<213>  Phytophthora sojae

<400>  28

Met Thr Gly Lys Cys Val Gly Ile Val Arg Glu Val Tyr Asn Lys Trp
1               5                   10                  15


Glu Arg Arg Ala Pro Leu Thr Pro Ala His Val Arg Glu Leu Val Gln
            20                  25                  30


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


Asp Glu Gln Tyr Val Arg Ala Gly Ala Thr Leu Ser Glu Asp Leu Ala
    50                  55                  60


Pro Ala Asn Val Ile Val Gly Val Lys Gln Val Pro Glu Pro Ala Leu
65                  70                  75                  80


Leu Ala Asp Lys Thr Tyr Leu Phe Phe Ser His Thr Ile Lys Ala Gln
                85                  90                  95


Pro Glu Asn Met Ala Leu Leu Asp Ala Val Leu Gln Arg Arg Ile Thr
            100                 105                 110


Leu Val Asp Tyr Glu Cys Ile Thr Glu Glu Ser Gly Lys Arg Leu Ile
        115                 120                 125


Ala Phe Gly Gly Asn Ala Gly Arg Ala Gly Met Ile Ala Gly Phe Arg
    130                 135                 140


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


Asn Val Ala Ser Ala Tyr Met Tyr Ser Asp Leu Glu His Ala Lys Asp
                165                 170                 175
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Ala Val Glu Ala Ala Gly Lys Arg Ile Arg Ser Asp Gly Leu Pro Ser
            180                 185                 190

Glu Leu Val Pro Met Thr Phe Ala Phe Thr Gly Asn Gly Asn Val Ser
        195                 200                 205

Lys Gly Ala Gln Glu Ile Phe Lys Leu Met Pro His Glu Met Val His
    210                 215                 220

Pro Ser Glu Leu Pro Lys Leu Pro Lys Asn Asn Arg Ile Leu Tyr Gly
225                 230                 235                 240

Thr Val Ile Asp Asn Pro Asp Tyr Phe Val Lys Pro Gln Pro Gly Phe
                245                 250                 255

Ser Gly Thr Pro Ser Arg Ala His Tyr Tyr Gln Asn Pro His Gln Tyr
            260                 265                 270

Glu Pro Ala Phe His Glu Lys Val Leu Pro Tyr Thr Ser Met Leu Val
        275                 280                 285

Asn Cys Met Tyr Trp Asp Asp Arg Phe Pro Arg Leu Val Thr Arg Glu
    290                 295                 300

Gln Ile Arg Glu Leu Arg Gly Ser Gly Asn His Lys Leu Leu Gly Ile
305                 310                 315                 320

Ala Asp Ile Ser Cys Asp Ile Gly Gly Ser Val Glu Phe Leu Glu Arg
                325                 330                 335

Ala Thr Glu Ile Glu Arg Pro Phe Ala Leu Tyr Asp Val Ala Glu Asp
            340                 345                 350

Lys Met Arg Glu Asp Gly Asp Ser Arg Gly Leu Glu Gly Asp Asp Gly
        355                 360                 365

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

Ser Ser Gln Gln Phe Gly Asp Arg Leu Val Gly Tyr Val Thr Ala Leu
385                 390                 395                 400

Ser Ser Val Thr Ser Ser Asn Val Pro Leu His Glu Gln Lys Glu Leu
                405                 410                 415

Pro Ala Glu Leu Arg Gly Ala Cys Ile Ala Ser Lys Gly Val Leu Ala
            420                 425                 430

Pro Arg Tyr Glu Tyr Ile His Arg Met Arg Ala Glu Arg Glu Arg Ser
        435                 440                 445
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Lys Gln Phe Lys Phe Leu Asp Ala Gln Gln Glu Val Ala Gly Ser Thr
    450                 455                 460


Cys Leu Leu Leu Glu Gly His Leu Phe Asp Thr Gly Leu Ile Asn Gln
465                 470                 475                 480


Val Leu Asn Leu Ile Glu Asp His Asp Gly Gly Phe His Leu Val Asp
                485                 490                 495


Cys Glu Val Arg Pro Asn Ile Ala Ala Gly Asp Ser Gly Phe Ser Thr
            500                 505                 510


Val Ser Asn Ala Ile Val Gln Val Ser Met Ser Asp Arg Ala Ala Leu
        515                 520                 525


Asp Asp Ile Ile Ala Lys Ile Arg Ser Leu Ala Asp Leu Thr Ser Gly
    530                 535                 540


Ala Lys Ala Ile Val Thr Glu Leu Pro Asp Leu Cys Gly Thr Asn Tyr
545                 550                 555                 560


Ser Lys Thr Arg Gly Ala Val Val Arg Lys Asp Ala Ala Ala Asn Thr
                565                 570                 575


Ala Ala Asp Val Ser Val Ser Ser Pro Lys Lys Arg Gln Ile Val Cys
            580                 585                 590


Phe Gly Ala Gly Leu Val Ala Ser Pro Leu Val Glu Tyr Leu Ser Arg
        595                 600                 605


Glu Gln Gly Asn Glu Val His Val Val Ser Gly Ile Glu Gly Glu Val
    610                 615                 620


Lys Gly Val Met Arg Lys Ile Ser Arg Arg Asn Ile Lys Pro His Val
625                 630                 635                 640


Val Asn Val Ala Glu Asp Gly Ala Gly Val Asp Lys Leu Cys Ala Glu
                645                 650                 655


Ala Asp Cys Val Val Ser Leu Leu Pro Ala Thr Met His Thr Thr Ile
            660                 665                 670


Ala Gln Arg Cys Ile Gln His Gly Thr Pro Leu Val Thr Ala Ser Tyr
        675                 680                 685


Val Ser Pro Glu Met Lys Glu Leu Asp Ala Lys Ala Lys Lys Ala Gly
    690                 695                 700


Ile Pro Ile Leu Cys Glu Ile Gly Leu Asp Pro Gly Met Asp His Met
705                 710                 715                 720
```

```
Ser Ala Met Lys Val Ile Asp Glu Val Lys Ala His Ser Gly Lys Ile
                725                 730                 735


Leu Ser Phe Ser Ser Val Cys Gly Gly Leu Pro Ala Pro Glu Ala Ala
            740                 745                 750


Asp Asn Ala Ile Gly Tyr Lys Phe Ser Trp Ser Pro Arg Gly Val Leu
        755                 760                 765


Thr Ala Ala Leu Asn Ala Ala Gln Tyr Arg Lys Asp Gly Lys Ile Val
    770                 775                 780


Asn Val Ala Gly Glu Asp Leu Leu Asn Ser Ser Glu Pro Val Asn Phe
785                 790                 795                 800


Leu Pro Ala Phe Asn Ile Glu Gln Ile Pro Asn Arg Asp Ser Leu Pro
                805                 810                 815


Tyr Gly Glu Ile Tyr Val Ile Pro Glu Ala His Ser Leu Tyr Arg Gly
            820                 825                 830


Thr Leu Arg Tyr Gly Gly Cys Cys Arg Ile Leu Tyr Gln Leu Arg Lys
        835                 840                 845


Leu Gly Leu Phe Asp Met Asp Pro Ser Lys Pro Ile Pro Ala Thr Trp
    850                 855                 860


Pro Asp Leu Ile Ser Gln Leu Gly Gly His Gln Gly Leu Arg Glu Asp
865                 870                 875                 880


Ala Asn Gly Phe Leu Gln Trp Leu Gly Ala Phe Asp His Ser Thr Pro
                885                 890                 895


Val Val Arg Ala Pro Ser Ile Leu Asp Ala Phe Cys Ala Leu Leu Gln
            900                 905                 910


Asp Lys Leu Ser Tyr Gln Pro Gly Glu Arg Asp Met Ala Ile Met His
        915                 920                 925


His Glu Phe Gly Ile Glu Tyr Glu Asp Gly Lys Lys Glu Lys Arg Thr
    930                 935                 940


Ser Thr Phe Val Gly Tyr Gly Ser Asp Lys Gly Asp Thr Ile Met Ala
945                 950                 955                 960


Lys Thr Val Gly Leu Ser Ala Ala Ile Gly Val Gln Leu Ile Leu Gln
                965                 970                 975


Asp Ala Val Gln Gly Arg Gly Val Leu Thr Pro Thr Thr Pro Asp Ile
            980                 985                 990
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Tyr Gly Pro Ala Leu Ala Arg Leu  Glu Val Glu Gly Val  Arg Phe Ile
        995                 1000                1005


Glu Lys  Thr Phe Pro Gln Pro
    1010                 1015


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<212>  DNA
<213>  Pyrenophora tritici-repentis


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<222>  (1)..(1164)
<223>  Lys1

<400>  29
atg gct ttc ccc aca cta cat gcc cgc gca gag gct aaa cct ctt gaa         48
Met Ala Phe Pro Thr Leu His Ala Arg Ala Glu Ala Lys Pro Leu Glu
1               5                   10                  15

cac cgc tcg tgt ctc aca ccc aca acc gca aag aag ctg ctc gat gct         96
His Arg Ser Cys Leu Thr Pro Thr Thr Ala Lys Lys Leu Leu Asp Ala
            20                  25                  30

ggc tac cct gtc ctc gtc gag cgc tcg ccc aag gac ccc aac tac gcc        144
Gly Tyr Pro Val Leu Val Glu Arg Ser Pro Lys Asp Pro Asn Tyr Ala
        35                  40                  45

cgt atc ttc aaa gac gac gag ttc gag gag gta ggc gcg acg ctc atc        192
Arg Ile Phe Lys Asp Asp Glu Phe Glu Glu Val Gly Ala Thr Leu Ile
    50                  55                  60

gag gaa ggc gca tac aag acg gcc ccc aag gac cgc atc atc atc ggc        240
Glu Glu Gly Ala Tyr Lys Thr Ala Pro Lys Asp Arg Ile Ile Ile Gly
65                  70                  75                  80

cta aag gag ctg cca gag gac aag ttc ccg ctc gag cac aca ttc gta        288
Leu Lys Glu Leu Pro Glu Asp Lys Phe Pro Leu Glu His Thr Phe Val
                85                  90                  95

cac ttt gca cat tgc tac aag cag caa ggc gga tgg gaa aac gta ttg        336
His Phe Ala His Cys Tyr Lys Gln Gln Gly Gly Trp Glu Asn Val Leu
            100                 105                 110

gcg agg ttc ccc cgt ggc ggt ggc aca ttg tat gac ctc gag ttc ctg        384
Ala Arg Phe Pro Arg Gly Gly Gly Thr Leu Tyr Asp Leu Glu Phe Leu
        115                 120                 125

caa gat gag tca ggc agg cgc gtt gct gcc ttt ggc tac cac gcc ggt        432
Gln Asp Glu Ser Gly Arg Arg Val Ala Ala Phe Gly Tyr His Ala Gly
    130                 135                 140

ttc gtc ggc gct gct ctt gcc atc aag aca tgg gct tgg caa ctc acc        480
Phe Val Gly Ala Ala Leu Ala Ile Lys Thr Trp Ala Trp Gln Leu Thr
145                 150                 155                 160

cat ccc aac ggc gag ccc ctt cct ggt cta gag acc ttc act gag gga        528
His Pro Asn Gly Glu Pro Leu Pro Gly Leu Glu Thr Phe Thr Glu Gly
                165                 170                 175

cgc ggc tac tac aac aac gag agc gag ttg att acc caa ctc aag gaa        576
Arg Gly Tyr Tyr Asn Asn Glu Ser Glu Leu Ile Thr Gln Leu Lys Glu
            180                 185                 190
```

```
gat gtc gca gcc ggc gaa aag atc gca gga cac aag ccc agc agt ctg        624
Asp Val Ala Ala Gly Glu Lys Ile Ala Gly His Lys Pro Ser Ser Leu
        195                 200                 205

gtg cta ggt gct ctc ggc cgc tgc ggc tct ggt gcc gtc gac ctc ctt        672
Val Leu Gly Ala Leu Gly Arg Cys Gly Ser Gly Ala Val Asp Leu Leu
    210                 215                 220

gag aag att ggc tgc cct gag atc aag aag tgg gat ctt gcc gag acc        720
Glu Lys Ile Gly Cys Pro Glu Ile Lys Lys Trp Asp Leu Ala Glu Thr
225                 230                 235                 240

aag gag cgc gac ggc cca tac ccc gaa att gtc gaa tct gac atc ttc        768
Lys Glu Arg Asp Gly Pro Tyr Pro Glu Ile Val Glu Ser Asp Ile Phe
                245                 250                 255

gtc aac tgc atc tac ctt tcc aag ccc atc ccg cct ttt gtc aac aag        816
Val Asn Cys Ile Tyr Leu Ser Lys Pro Ile Pro Pro Phe Val Asn Lys
            260                 265                 270

gag agt ctc aag tcg cca aac cgc aga ctc agc gtc gtt tgc gat gtc        864
Glu Ser Leu Lys Ser Pro Asn Arg Arg Leu Ser Val Val Cys Asp Val
        275                 280                 285

agc tgt gac act act aac cct cat aac ccc att ccc atc tac gat atc        912
Ser Cys Asp Thr Thr Asn Pro His Asn Pro Ile Pro Ile Tyr Asp Ile
    290                 295                 300

aac acc acc ttt gac aag ccc aca gtt gag gtt tct gtc gag ggt gac        960
Asn Thr Thr Phe Asp Lys Pro Thr Val Glu Val Ser Val Glu Gly Asp
305                 310                 315                 320

ggt cct aga cta tct gtc atc tcc att gac cac ctt ccc tct gcg ttg       1008
Gly Pro Arg Leu Ser Val Ile Ser Ile Asp His Leu Pro Ser Ala Leu
                325                 330                 335

cct cgt gag tct tca gaa gcc ttt agc aac gct ctg ctg cct agc ttg       1056
Pro Arg Glu Ser Ser Glu Ala Phe Ser Asn Ala Leu Leu Pro Ser Leu
            340                 345                 350

atg gct ctg aag gac cgc gcg aca acg cct gtg tgg cag ggt gct gag       1104
Met Ala Leu Lys Asp Arg Ala Thr Thr Pro Val Trp Gln Gly Ala Glu
        355                 360                 365

aag ctc ttc caa gag aag gtt cag acg ctg ccg ggt ggt gtc ccc gca       1152
Lys Leu Phe Gln Glu Lys Val Gln Thr Leu Pro Gly Gly Val Pro Ala
    370                 375                 380

aag gag gta tag                                                       1164
Lys Glu Val
385


<210>  30
<211>  387
<212>  PRT
<213>  Pyrenophora tritici-repentis

<400>  30

Met Ala Phe Pro Thr Leu His Ala Arg Ala Glu Ala Lys Pro Leu Glu
1               5                   10                  15


His Arg Ser Cys Leu Thr Pro Thr Thr Ala Lys Lys Leu Leu Asp Ala
            20                  25                  30
```

```
Gly Tyr Pro Val Leu Val Glu Arg Ser Pro Lys Asp Pro Asn Tyr Ala
        35                  40                  45


Arg Ile Phe Lys Asp Asp Glu Phe Glu Glu Val Gly Ala Thr Leu Ile
    50                  55                  60


Glu Glu Gly Ala Tyr Lys Thr Ala Pro Lys Asp Arg Ile Ile Ile Gly
65                  70                  75                  80


Leu Lys Glu Leu Pro Glu Asp Lys Phe Pro Leu Glu His Thr Phe Val
                85                  90                  95


His Phe Ala His Cys Tyr Lys Gln Gln Gly Gly Trp Glu Asn Val Leu
            100                 105                 110


Ala Arg Phe Pro Arg Gly Gly Gly Thr Leu Tyr Asp Leu Glu Phe Leu
        115                 120                 125


Gln Asp Glu Ser Gly Arg Arg Val Ala Ala Phe Gly Tyr His Ala Gly
    130                 135                 140


Phe Val Gly Ala Ala Leu Ala Ile Lys Thr Trp Ala Trp Gln Leu Thr
145                 150                 155                 160


His Pro Asn Gly Glu Pro Leu Pro Gly Leu Glu Thr Phe Thr Glu Gly
                165                 170                 175


Arg Gly Tyr Tyr Asn Asn Glu Ser Glu Leu Ile Thr Gln Leu Lys Glu
            180                 185                 190


Asp Val Ala Ala Gly Glu Lys Ile Ala Gly His Lys Pro Ser Ser Leu
        195                 200                 205


Val Leu Gly Ala Leu Gly Arg Cys Gly Ser Gly Ala Val Asp Leu Leu
    210                 215                 220


Glu Lys Ile Gly Cys Pro Glu Ile Lys Lys Trp Asp Leu Ala Glu Thr
225                 230                 235                 240


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


Val Asn Cys Ile Tyr Leu Ser Lys Pro Ile Pro Pro Phe Val Asn Lys
            260                 265                 270


Glu Ser Leu Lys Ser Pro Asn Arg Arg Leu Ser Val Val Cys Asp Val
        275                 280                 285


Ser Cys Asp Thr Thr Asn Pro His Asn Pro Ile Pro Ile Tyr Asp Ile
    290                 295                 300
```

```
Asn Thr Thr Phe Asp Lys Pro Thr Val Glu Val Ser Val Glu Gly Asp
305                 310                 315                 320


Gly Pro Arg Leu Ser Val Ile Ser Ile Asp His Leu Pro Ser Ala Leu
                325                 330                 335


Pro Arg Glu Ser Ser Glu Ala Phe Ser Asn Ala Leu Leu Pro Ser Leu
            340                 345                 350


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


Lys Leu Phe Gln Glu Lys Val Gln Thr Leu Pro Gly Gly Val Pro Ala
    370                 375                 380


Lys Glu Val
385


<210>  31
<211>  1119
<212>  DNA
<213>  Sclerotinia sclerotiorum


<220>
<221>  CDS
<222>  (1)..(1119)
<223>  Lys1

<400>  31
atg tct gga act act ctt cac cta cgt tct gag ttg gga aaa gct ctt         48
Met Ser Gly Thr Thr Leu His Leu Arg Ser Glu Leu Gly Lys Ala Leu
1               5                   10                  15

gag cat aga tca gct ctt acc ccc act aca gcc aaa gct ctc atc gat         96
Glu His Arg Ser Ala Leu Thr Pro Thr Thr Ala Lys Ala Leu Ile Asp
            20                  25                  30

gct gga tac aca att aat gtc gag cgc agc cca gaa cgt ata ttc gac        144
Ala Gly Tyr Thr Ile Asn Val Glu Arg Ser Pro Glu Arg Ile Phe Asp
        35                  40                  45

gat gag gag ttc gag aag gtt gga gct act ctc gtg cca gaa gat aca        192
Asp Glu Glu Phe Glu Lys Val Gly Ala Thr Leu Val Pro Glu Asp Thr
    50                  55                  60

tgg aga caa gca cca aag gat cat att att att ggt ttg aag gaa cta        240
Trp Arg Gln Ala Pro Lys Asp His Ile Ile Ile Gly Leu Lys Glu Leu
65                  70                  75                  80

cct gtc gaa gac ttt ccc ctc gag cat gtc cac gta caa ttc gca cac        288
Pro Val Glu Asp Phe Pro Leu Glu His Val His Val Gln Phe Ala His
                85                  90                  95

tgt tac aaa caa caa ggt ggc tgg gac acc gtt cta tca cga ttt cct        336
Cys Tyr Lys Gln Gln Gly Gly Trp Asp Thr Val Leu Ser Arg Phe Pro
            100                 105                 110

cgc ggc ggc gga act ctc tta gat ctc gaa ttt ttg aca gac gat aaa        384
Arg Gly Gly Gly Thr Leu Leu Asp Leu Glu Phe Leu Thr Asp Asp Lys
        115                 120                 125
```

```
ggc aga aga gtt gca gct ttc gga tac cac gct gga ttt gct ggt gca        432
Gly Arg Arg Val Ala Ala Phe Gly Tyr His Ala Gly Phe Ala Gly Ala
    130                 135                 140

gca ttg gca ctc gaa act tgg gca tgg caa ctc act cat tca gca tca        480
Ala Leu Ala Leu Glu Thr Trp Ala Trp Gln Leu Thr His Ser Ala Ser
145                 150                 155                 160

gag cca ttc cca agc gta tca agc tat cct aac gaa gat gag ttg att        528
Glu Pro Phe Pro Ser Val Ser Ser Tyr Pro Asn Glu Asp Glu Leu Ile
                165                 170                 175

gcc gac gta aag aaa gca atc gca gct gga caa gaa aag aca ggc aag        576
Ala Asp Val Lys Lys Ala Ile Ala Ala Gly Gln Glu Lys Thr Gly Lys
            180                 185                 190

gca cca cga gtt ttg gtt atc gga gca ttg ggc aga tgt gga agt gga        624
Ala Pro Arg Val Leu Val Ile Gly Ala Leu Gly Arg Cys Gly Ser Gly
        195                 200                 205

gca gtt gat ctc tgc ttg aga gcc ggt gtg cca acc gag aat gtc ttg        672
Ala Val Asp Leu Cys Leu Arg Ala Gly Val Pro Thr Glu Asn Val Leu
    210                 215                 220

aag tgg gat atg gca gag act gcc aag gga gga cca ttt cca gag att        720
Lys Trp Asp Met Ala Glu Thr Ala Lys Gly Gly Pro Phe Pro Glu Ile
225                 230                 235                 240

gtc gag agt gac atc ttc att aac tgc ata tac ctc atg tcc aag att        768
Val Glu Ser Asp Ile Phe Ile Asn Cys Ile Tyr Leu Met Ser Lys Ile
                245                 250                 255

ccg aac ttt gtc gac atg caa agc ctc gat acc cca aac cgc aaa ttg        816
Pro Asn Phe Val Asp Met Gln Ser Leu Asp Thr Pro Asn Arg Lys Leu
            260                 265                 270

tca gtc gtc tgc gac gtc agt gct gat acc aca aat ccc aac aat cca        864
Ser Val Val Cys Asp Val Ser Ala Asp Thr Thr Asn Pro Asn Asn Pro
        275                 280                 285

att cca atc tat acc gtt gcg acc aca ttt tca gag cca act gtc cca        912
Ile Pro Ile Tyr Thr Val Ala Thr Thr Phe Ser Glu Pro Thr Val Pro
    290                 295                 300

gtc gag gtc aag gga gac ccc aga cta agc gtc atc agc att gat cac        960
Val Glu Val Lys Gly Asp Pro Arg Leu Ser Val Ile Ser Ile Asp His
305                 310                 315                 320

tta cca agt cta ttg cca aga gaa gca agc gag gca ttc agc aag gac       1008
Leu Pro Ser Leu Leu Pro Arg Glu Ala Ser Glu Ala Phe Ser Lys Asp
                325                 330                 335

ttg cta cca agt ttg ttg aca tta aag gac tgg aga agt act cca gtc       1056
Leu Leu Pro Ser Leu Leu Thr Leu Lys Asp Trp Arg Ser Thr Pro Val
            340                 345                 350

tgg gcg aag gcc gag aag ttg ttt cag gag aag gtt gcc aca ttg cct       1104
Trp Ala Lys Ala Glu Lys Leu Phe Gln Glu Lys Val Ala Thr Leu Pro
        355                 360                 365

aag aag gag gca tga                                                   1119
Lys Lys Glu Ala
    370


<210>  32
<211>  372
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```
<212>  PRT
<213>  Sclerotinia sclerotiorum

<400>  32

Met Ser Gly Thr Thr Leu His Leu Arg Ser Glu Leu Gly Lys Ala Leu
1               5                   10                  15


Glu His Arg Ser Ala Leu Thr Pro Thr Thr Ala Lys Ala Leu Ile Asp
            20                  25                  30


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


Asp Glu Glu Phe Glu Lys Val Gly Ala Thr Leu Val Pro Glu Asp Thr
    50                  55                  60


Trp Arg Gln Ala Pro Lys Asp His Ile Ile Ile Gly Leu Lys Glu Leu
65                  70                  75                  80


Pro Val Glu Asp Phe Pro Leu Glu His Val His Val Gln Phe Ala His
                85                  90                  95


Cys Tyr Lys Gln Gln Gly Gly Trp Asp Thr Val Leu Ser Arg Phe Pro
            100                 105                 110


Arg Gly Gly Gly Thr Leu Leu Asp Leu Glu Phe Leu Thr Asp Asp Lys
        115                 120                 125


Gly Arg Arg Val Ala Ala Phe Gly Tyr His Ala Gly Phe Ala Gly Ala
    130                 135                 140


Ala Leu Ala Leu Glu Thr Trp Ala Trp Gln Leu Thr His Ser Ala Ser
145                 150                 155                 160


Glu Pro Phe Pro Ser Val Ser Ser Tyr Pro Asn Glu Asp Glu Leu Ile
                165                 170                 175


Ala Asp Val Lys Lys Ala Ile Ala Ala Gly Gln Glu Lys Thr Gly Lys
            180                 185                 190


Ala Pro Arg Val Leu Val Ile Gly Ala Leu Gly Arg Cys Gly Ser Gly
        195                 200                 205


Ala Val Asp Leu Cys Leu Arg Ala Gly Val Pro Thr Glu Asn Val Leu
    210                 215                 220


Lys Trp Asp Met Ala Glu Thr Ala Lys Gly Gly Pro Phe Pro Glu Ile
225                 230                 235                 240


Val Glu Ser Asp Ile Phe Ile Asn Cys Ile Tyr Leu Met Ser Lys Ile
                245                 250                 255
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```
Pro Asn Phe Val Asp Met Gln Ser Leu Asp Thr Pro Asn Arg Lys Leu
            260                     265                 270


Ser Val Val Cys Asp Val Ser Ala Asp Thr Thr Asn Pro Asn Asn Pro
        275                 280                 285


Ile Pro Ile Tyr Thr Val Ala Thr Thr Phe Ser Glu Pro Thr Val Pro
    290                 295                 300


Val Glu Val Lys Gly Asp Pro Arg Leu Ser Val Ile Ser Ile Asp His
305                 310                 315                 320


Leu Pro Ser Leu Leu Pro Arg Glu Ala Ser Glu Ala Phe Ser Lys Asp
                325                 330                 335


Leu Leu Pro Ser Leu Leu Thr Leu Lys Asp Trp Arg Ser Thr Pro Val
            340                 345                 350


Trp Ala Lys Ala Glu Lys Leu Phe Gln Glu Lys Val Ala Thr Leu Pro
        355                 360                 365


Lys Lys Glu Ala
    370


<210>  33
<211>  1170
<212>  DNA
<213>  Trichoderma reesei


<220>
<221>  CDS
<222>  (1)..(1170)
<223>  Lys1

<400>  33
gtt caa cta ttt tcc ccc tca tta tca tac cac aaa aaa caa caa caa         48
Val Gln Leu Phe Ser Pro Ser Leu Ser Tyr His Lys Lys Gln Gln Gln
1               5                   10                  15

tca att cgt gcc aaa atg cct acc gtc atc cat ctg aga gcc gat acc         96
Ser Ile Arg Ala Lys Met Pro Thr Val Ile His Leu Arg Ala Asp Thr
            20                  25                  30

aag ccg ttt gag cgt cgc tcg ccg ctg tcc ccc cca acc gcc aag gcc        144
Lys Pro Phe Glu Arg Arg Ser Pro Leu Ser Pro Pro Thr Ala Lys Ala
        35                  40                  45

ctc ctc gac gct ggc tac gtc gtc cgc gtt gag cga tct tca gag cgc        192
Leu Leu Asp Ala Gly Tyr Val Val Arg Val Glu Arg Ser Ser Glu Arg
    50                  55                  60

atc tac aag gac gaa gag ttc gag gcc gtt ggc gcc gaa ttg gtc cct        240
Ile Tyr Lys Asp Glu Glu Phe Glu Ala Val Gly Ala Glu Leu Val Pro
65                  70                  75                  80

gcc gga tca tgg atc aag gct ccc aag gag gac atc atc ctg ggc ctc        288
Ala Gly Ser Trp Ile Lys Ala Pro Lys Glu Asp Ile Ile Leu Gly Leu
                85                  90                  95
```

```
aag gag ctg ccc gac gac gac att gac ctg cct cac aca tac atc cac        336
Lys Glu Leu Pro Asp Asp Asp Ile Asp Leu Pro His Thr Tyr Ile His
            100                 105                 110

ttc cag cac atc ttc aag aag cag ctc ggc tgg gcg ccc tcc ctg aag        384
Phe Gln His Ile Phe Lys Lys Gln Leu Gly Trp Ala Pro Ser Leu Lys
        115                 120                 125

cgc ttt gct cgc gcc ggc ggc acg ctc tac gac ctg gaa ttc ctg act        432
Arg Phe Ala Arg Ala Gly Gly Thr Leu Tyr Asp Leu Glu Phe Leu Thr
    130                 135                 140

gag gag aac ggc cgc aga atc gcg gcc ttt ggc tac ttt gct gga tat        480
Glu Glu Asn Gly Arg Arg Ile Ala Ala Phe Gly Tyr Phe Ala Gly Tyr
145                 150                 155                 160

gcc ggc gcc gcc att gcc ttc atc tcg tgg gct cac cag atc ctc aac        528
Ala Gly Ala Ala Ile Ala Phe Ile Ser Trp Ala His Gln Ile Leu Asn
                165                 170                 175

ccc ggc gtc ccc cag ccc ccg gtg cct ctg ttc gac agc gcg cct gct        576
Pro Gly Val Pro Gln Pro Pro Val Pro Leu Phe Asp Ser Ala Pro Ala
            180                 185                 190

ctg gtc gcg cat gtc aag gct gcg ctc gag ccc gcg att cgt gcc aac        624
Leu Val Ala His Val Lys Ala Ala Leu Glu Pro Ala Ile Arg Ala Asn
        195                 200                 205

aac ggc caa ctt ccc cgc gtc att gtg att ggc gct ctg gga cga tgc        672
Asn Gly Gln Leu Pro Arg Val Ile Val Ile Gly Ala Leu Gly Arg Cys
    210                 215                 220

ggc aag gga gcc gtg gac ttt tgc cgc gag gtt ggt ctt cct gag gac        720
Gly Lys Gly Ala Val Asp Phe Cys Arg Glu Val Gly Leu Pro Glu Asp
225                 230                 235                 240

tcc atc ctc aag tgg gat atg cag gag act gcc aag gga ggg cct ttc        768
Ser Ile Leu Lys Trp Asp Met Gln Glu Thr Ala Lys Gly Gly Pro Phe
                245                 250                 255

gag gaa atc acc act tcc gac atc ttc atc aac tgc gtc tac ctt ggc        816
Glu Glu Ile Thr Thr Ser Asp Ile Phe Ile Asn Cys Val Tyr Leu Gly
            260                 265                 270

cct act ccc act cct ccc ttt gtc aca ttc gaa tcg ctt gcg acc cca        864
Pro Thr Pro Thr Pro Pro Phe Val Thr Phe Glu Ser Leu Ala Thr Pro
        275                 280                 285

gag aga cga ctc cgc gtc att gcc gat atc tcg tgt gat ccc aac agc        912
Glu Arg Arg Leu Arg Val Ile Ala Asp Ile Ser Cys Asp Pro Asn Ser
    290                 295                 300

gag aac aac ccg atc ccc ttg tac tcc acc tgg tcc agc ttt gac aag        960
Glu Asn Asn Pro Ile Pro Leu Tyr Ser Thr Trp Ser Ser Phe Asp Lys
305                 310                 315                 320

ccc acg atc ccg aca tcc aag ccc gtt gac ggc cct gag ctg aga atc       1008
Pro Thr Ile Pro Thr Ser Lys Pro Val Asp Gly Pro Glu Leu Arg Ile
                325                 330                 335

att gcc atc gac cac ctc ccc acc ttg att gcc cgc gag tcc agc gat       1056
Ile Ala Ile Asp His Leu Pro Thr Leu Ile Ala Arg Glu Ser Ser Asp
            340                 345                 350

gag tac tct ggc ctg ctg ctg ccg gcc ctg ctc act ctg gac aag cgg       1104
Glu Tyr Ser Gly Leu Leu Leu Pro Ala Leu Leu Thr Leu Asp Lys Arg
        355                 360                 365
```

```
gat act gag ggt gtc tgg acg aga gcg gag aag aca tac aag gac aga       1152
Asp Thr Glu Gly Val Trp Thr Arg Ala Glu Lys Thr Tyr Lys Asp Arg
    370                 375                 380

gtg gct gag ctg cct tag                                               1170
Val Ala Glu Leu Pro
385


<210>  34
<211>  389
<212>  PRT
<213>  Trichoderma reesei

<400>  34

Val Gln Leu Phe Ser Pro Ser Leu Ser Tyr His Lys Lys Gln Gln Gln
1               5                   10                  15


Ser Ile Arg Ala Lys Met Pro Thr Val Ile His Leu Arg Ala Asp Thr
            20                  25                  30


Lys Pro Phe Glu Arg Arg Ser Pro Leu Ser Pro Pro Thr Ala Lys Ala
        35                  40                  45


Leu Leu Asp Ala Gly Tyr Val Val Arg Val Glu Arg Ser Ser Glu Arg
    50                  55                  60


Ile Tyr Lys Asp Glu Glu Phe Glu Ala Val Gly Ala Glu Leu Val Pro
65                  70                  75                  80


Ala Gly Ser Trp Ile Lys Ala Pro Lys Glu Asp Ile Ile Leu Gly Leu
                85                  90                  95


Lys Glu Leu Pro Asp Asp Asp Ile Asp Leu Pro His Thr Tyr Ile His
            100                 105                 110


Phe Gln His Ile Phe Lys Lys Gln Leu Gly Trp Ala Pro Ser Leu Lys
        115                 120                 125


Arg Phe Ala Arg Ala Gly Gly Thr Leu Tyr Asp Leu Glu Phe Leu Thr
    130                 135                 140


Glu Glu Asn Gly Arg Arg Ile Ala Ala Phe Gly Tyr Phe Ala Gly Tyr
145                 150                 155                 160


Ala Gly Ala Ala Ile Ala Phe Ile Ser Trp Ala His Gln Ile Leu Asn
                165                 170                 175


Pro Gly Val Pro Gln Pro Pro Val Pro Leu Phe Asp Ser Ala Pro Ala
            180                 185                 190


Leu Val Ala His Val Lys Ala Ala Leu Glu Pro Ala Ile Arg Ala Asn
        195                 200                 205
```

```
Asn Gly Gln Leu Pro Arg Val Ile Val Ile Gly Ala Leu Gly Arg Cys
    210                 215                 220


Gly Lys Gly Ala Val Asp Phe Cys Arg Glu Val Gly Leu Pro Glu Asp
225                 230                 235                 240


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


Glu Glu Ile Thr Thr Ser Asp Ile Phe Ile Asn Cys Val Tyr Leu Gly
            260                 265                 270


Pro Thr Pro Thr Pro Pro Phe Val Thr Phe Glu Ser Leu Ala Thr Pro
        275                 280                 285


Glu Arg Arg Leu Arg Val Ile Ala Asp Ile Ser Cys Asp Pro Asn Ser
    290                 295                 300


Glu Asn Asn Pro Ile Pro Leu Tyr Ser Thr Trp Ser Ser Phe Asp Lys
305                 310                 315                 320


Pro Thr Ile Pro Thr Ser Lys Pro Val Asp Gly Pro Glu Leu Arg Ile
                325                 330                 335


Ile Ala Ile Asp His Leu Pro Thr Leu Ile Ala Arg Glu Ser Ser Asp
            340                 345                 350


Glu Tyr Ser Gly Leu Leu Leu Pro Ala Leu Leu Thr Leu Asp Lys Arg
        355                 360                 365


Asp Thr Glu Gly Val Trp Thr Arg Ala Glu Lys Thr Tyr Lys Asp Arg
    370                 375                 380


Val Ala Glu Leu Pro
385


<210>  35
<211>  1173
<212>  DNA
<213>  Ustilago maydis


<220>
<221>  CDS
<222>  (1)..(1173)
<223>  Lys1

<400>  35
atg tct aca agc cgc caa ccc ctc tac ctc cga tgc gag atg aag ccg         48
Met Ser Thr Ser Arg Gln Pro Leu Tyr Leu Arg Cys Glu Met Lys Pro
1               5                   10                  15

gcc gag cac cgt gcc gcg ctc acc cca acc acc gcc aag gca ctc att         96
Ala Glu His Arg Ala Ala Leu Thr Pro Thr Thr Ala Lys Ala Leu Ile
            20                  25                  30
```

```
gac gct ggg ttc gac atc acg gtc gag tcc gac cct caa cgt atc ttt        144
Asp Ala Gly Phe Asp Ile Thr Val Glu Ser Asp Pro Gln Arg Ile Phe
        35                  40                  45

gac gac aaa gag tac acc gag gta ggg tgc aag ctt gcc cct cac aac        192
Asp Asp Lys Glu Tyr Thr Glu Val Gly Cys Lys Leu Ala Pro His Asn
    50                  55                  60

acg ttt cac tcc ctg ccc gcc gac atc ccc atc atc ggt ctc aag gag        240
Thr Phe His Ser Leu Pro Ala Asp Ile Pro Ile Ile Gly Leu Lys Glu
65                  70                  75                  80

ctt gag gag cct ggt ccg gat ctg cct cac acc cac att cag ttt gct        288
Leu Glu Glu Pro Gly Pro Asp Leu Pro His Thr His Ile Gln Phe Ala
                85                  90                  95

cac tgc tac aag aag cag gcc ggt tgg gcg gat gtt ctg ggt cga ttc        336
His Cys Tyr Lys Lys Gln Ala Gly Trp Ala Asp Val Leu Gly Arg Phe
            100                 105                 110

aag cgc gga ggc gga aag ctc tac gat ttg gag ttt ttg gag gac aag        384
Lys Arg Gly Gly Gly Lys Leu Tyr Asp Leu Glu Phe Leu Glu Asp Lys
        115                 120                 125

aac ggc cgt cgt gta gcc gcg ttt ggt tgg cac gcc ggc ttt gca ggc        432
Asn Gly Arg Arg Val Ala Ala Phe Gly Trp His Ala Gly Phe Ala Gly
    130                 135                 140

gct gca ctt ggt ctg ttg gct ttg gct gaa cag gtg caa ggt gaa gac        480
Ala Ala Leu Gly Leu Leu Ala Leu Ala Glu Gln Val Gln Gly Glu Asp
145                 150                 155                 160

caa agg ctg ggt gct caa aag gct tac ccc aac gag cag gcg ctc atc        528
Gln Arg Leu Gly Ala Gln Lys Ala Tyr Pro Asn Glu Gln Ala Leu Ile
                165                 170                 175

gca cac gcc aag cag cag att gag ttc atc aag aaa tcg cgc tcg gac        576
Ala His Ala Lys Gln Gln Ile Glu Phe Ile Lys Lys Ser Arg Ser Asp
            180                 185                 190

ggc aaa gtg aag gcg ctc gtc gtc gga gct ttg gga cga tgt ggt cgt        624
Gly Lys Val Lys Ala Leu Val Val Gly Ala Leu Gly Arg Cys Gly Arg
        195                 200                 205

gga gcc att gac ttt ttc gaa aag gcc ggc gtc gct tct gag gac att        672
Gly Ala Ile Asp Phe Phe Glu Lys Ala Gly Val Ala Ser Glu Asp Ile
    210                 215                 220

gtc cgc tgg gac atc cag gag acc tca gcc aag cac ggt ccc tac caa        720
Val Arg Trp Asp Ile Gln Glu Thr Ser Ala Lys His Gly Pro Tyr Gln
225                 230                 235                 240

gag ctg ctc gac gta gac atc ttt gtc aac tgc atc tac ctc acc tct        768
Glu Leu Leu Asp Val Asp Ile Phe Val Asn Cys Ile Tyr Leu Thr Ser
                245                 250                 255

aaa atc ccg cct ttc ctc gac caa cct acg atc caa gcc gct ggt ccc        816
Lys Ile Pro Pro Phe Leu Asp Gln Pro Thr Ile Gln Ala Ala Gly Pro
            260                 265                 270

tcg cgt cgt ctc ggc gtc gtc gtc gac gta tcg tgc gac act acc aac        864
Ser Arg Arg Leu Gly Val Val Val Asp Val Ser Cys Asp Thr Thr Asn
        275                 280                 285

ccc aac aac cct ctc ccc atc tac gac atc aac acc acc ttt gac aaa        912
Pro Asn Asn Pro Leu Pro Ile Tyr Asp Ile Asn Thr Thr Phe Asp Lys
    290                 295                 300
```

```
cct acc gtc gac gtc aac acg ggc aaa ggt aac ccg agc ttg acc gtc        960
Pro Thr Val Asp Val Asn Thr Gly Lys Gly Asn Pro Ser Leu Thr Val
305                 310                 315                 320

atc tcg atc gac cat ctg ccc act ctg ctg cct agg gag agc tcc gag       1008
Ile Ser Ile Asp His Leu Pro Thr Leu Leu Pro Arg Glu Ser Ser Glu
                325                 330                 335

ggt ttc agc aac gac ctg ttg ccc agt ctg ttg cag ttg ccc tac gtg       1056
Gly Phe Ser Asn Asp Leu Leu Pro Ser Leu Leu Gln Leu Pro Tyr Val
            340                 345                 350

ctc ggt aag gac acc acc aag ctc gac acg ttg gac gaa gga aag gga       1104
Leu Gly Lys Asp Thr Thr Lys Leu Asp Thr Leu Asp Glu Gly Lys Gly
        355                 360                 365

gcc gtc tgg cag aga gcc gaa aag ctc ttc cat aag cac ttg gca gag       1152
Ala Val Trp Gln Arg Ala Glu Lys Leu Phe His Lys His Leu Ala Glu
    370                 375                 380

gct gag cag cac aca gct tga                                           1173
Ala Glu Gln His Thr Ala
385                 390


<210>  36
<211>  390
<212>  PRT
<213>  Ustilago maydis

<400>  36

Met Ser Thr Ser Arg Gln Pro Leu Tyr Leu Arg Cys Glu Met Lys Pro
1               5                   10                  15


Ala Glu His Arg Ala Ala Leu Thr Pro Thr Thr Ala Lys Ala Leu Ile
            20                  25                  30


Asp Ala Gly Phe Asp Ile Thr Val Glu Ser Asp Pro Gln Arg Ile Phe
        35                  40                  45


Asp Asp Lys Glu Tyr Thr Glu Val Gly Cys Lys Leu Ala Pro His Asn
    50                  55                  60


Thr Phe His Ser Leu Pro Ala Asp Ile Pro Ile Ile Gly Leu Lys Glu
65                  70                  75                  80


Leu Glu Glu Pro Gly Pro Asp Leu Pro His Thr His Ile Gln Phe Ala
                85                  90                  95


His Cys Tyr Lys Lys Gln Ala Gly Trp Ala Asp Val Leu Gly Arg Phe
            100                 105                 110


Lys Arg Gly Gly Gly Lys Leu Tyr Asp Leu Glu Phe Leu Glu Asp Lys
        115                 120                 125


Asn Gly Arg Arg Val Ala Ala Phe Gly Trp His Ala Gly Phe Ala Gly
    130                 135                 140
```

```
Ala Ala Leu Gly Leu Leu Ala Leu Ala Glu Gln Val Gln Gly Glu Asp
145                 150                 155                 160


Gln Arg Leu Gly Ala Gln Lys Ala Tyr Pro Asn Glu Gln Ala Leu Ile
                165                 170                 175


Ala His Ala Lys Gln Gln Ile Glu Phe Ile Lys Lys Ser Arg Ser Asp
            180                 185                 190


Gly Lys Val Lys Ala Leu Val Val Gly Ala Leu Gly Arg Cys Gly Arg
        195                 200                 205


Gly Ala Ile Asp Phe Phe Glu Lys Ala Gly Val Ala Ser Glu Asp Ile
    210                 215                 220


Val Arg Trp Asp Ile Gln Glu Thr Ser Ala Lys His Gly Pro Tyr Gln
225                 230                 235                 240


Glu Leu Leu Asp Val Asp Ile Phe Val Asn Cys Ile Tyr Leu Thr Ser
                245                 250                 255


Lys Ile Pro Pro Phe Leu Asp Gln Pro Thr Ile Gln Ala Ala Gly Pro
            260                 265                 270


Ser Arg Arg Leu Gly Val Val Val Asp Val Ser Cys Asp Thr Thr Asn
        275                 280                 285


Pro Asn Asn Pro Leu Pro Ile Tyr Asp Ile Asn Thr Thr Phe Asp Lys
    290                 295                 300


Pro Thr Val Asp Val Asn Thr Gly Lys Gly Asn Pro Ser Leu Thr Val
305                 310                 315                 320


Ile Ser Ile Asp His Leu Pro Thr Leu Leu Pro Arg Glu Ser Ser Glu
                325                 330                 335


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


Leu Gly Lys Asp Thr Thr Lys Leu Asp Thr Leu Asp Glu Gly Lys Gly
        355                 360                 365


Ala Val Trp Gln Arg Ala Glu Lys Leu Phe His Lys His Leu Ala Glu
    370                 375                 380


Ala Glu Gln His Thr Ala
385                 390


<210>  37
<211>  1137
<212>  DNA
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<213>  Verticillium albo-atrum


<220>
<221>  CDS
<222>  (1)..(1137)
<223>  Lys1

<400>  37
atg tct ggc atc acc cta cac ctc cgg tcc gag acc aag ccg ctg gag         48
Met Ser Gly Ile Thr Leu His Leu Arg Ser Glu Thr Lys Pro Leu Glu
1               5                   10                  15

cac cgc agt gct ctg acc ccc ttc acg gca tcc gag ctg atc aag gct         96
His Arg Ser Ala Leu Thr Pro Phe Thr Ala Ser Glu Leu Ile Lys Ala
            20                  25                  30

ggc tac acc ctc aat gtc gag cgc agc cct gtt cgc atc ttc gac gat        144
Gly Tyr Thr Leu Asn Val Glu Arg Ser Pro Val Arg Ile Phe Asp Asp
        35                  40                  45

gcc gag ttc gag aag att ggc gcc acc ctc gtc ccc gag ggt agc tgg        192
Ala Glu Phe Glu Lys Ile Gly Ala Thr Leu Val Pro Glu Gly Ser Trp
    50                  55                  60

acc gaa gcc ccc caa gac cac atc att gtt ggc ctc aag gag ctt ctt        240
Thr Glu Ala Pro Gln Asp His Ile Ile Val Gly Leu Lys Glu Leu Leu
65                  70                  75                  80

gag gag gat ttc cct ctg aag cac gtt cac gtc cag ttt gcg cac tgc        288
Glu Glu Asp Phe Pro Leu Lys His Val His Val Gln Phe Ala His Cys
                85                  90                  95

tac aag cag cag ggc ggg tgg gag aac gtc ctg gcc cgc ttc cct cgt        336
Tyr Lys Gln Gln Gly Gly Trp Glu Asn Val Leu Ala Arg Phe Pro Arg
            100                 105                 110

ggt ggc ggc acc ctc tac gac ctc gaa ttc ctc gag aag gag gtc gcc        384
Gly Gly Gly Thr Leu Tyr Asp Leu Glu Phe Leu Glu Lys Glu Val Ala
        115                 120                 125

ccc ggc cgc ttt gcc cga gtc gcc gcc ttt ggc tgg agc gcc ggt ttc        432
Pro Gly Arg Phe Ala Arg Val Ala Ala Phe Gly Trp Ser Ala Gly Phe
    130                 135                 140

tct ggt gct gct ctg gct ctc cag aac tgg gcc tgg cag ctc aac aac        480
Ser Gly Ala Ala Leu Ala Leu Gln Asn Trp Ala Trp Gln Leu Asn Asn
145                 150                 155                 160

ccc ggc aag ccc ctg cct tcg gtc gag agc tat ccc aac gag gac gag        528
Pro Gly Lys Pro Leu Pro Ser Val Glu Ser Tyr Pro Asn Glu Asp Glu
                165                 170                 175

ctc atc act gct gtc aag aag agc att gcc gag ggc aag gag aag gcc        576
Leu Ile Thr Ala Val Lys Lys Ser Ile Ala Glu Gly Lys Glu Lys Ala
            180                 185                 190

ggc aag cta ccc cag gtc ctc gtg atc ggc gcc ctc ggc cgc tgc ggc        624
Gly Lys Leu Pro Gln Val Leu Val Ile Gly Ala Leu Gly Arg Cys Gly
        195                 200                 205

agc ggt gcc gtc gag ctg tgc cgc cgc gtc ggc ctg ccc gag gag cag        672
Ser Gly Ala Val Glu Leu Cys Arg Arg Val Gly Leu Pro Glu Glu Gln
    210                 215                 220

atc ctc aag tgg gat ctc gag gag acg aag aag ggc ggc ccc ttc acc        720
Ile Leu Lys Trp Asp Leu Glu Glu Thr Lys Lys Gly Gly Pro Phe Thr
225                 230                 235                 240
```

```
gag att gtt gag agc gac atc ttt gtc aac tgc atc tac ctc aac agc         768
Glu Ile Val Glu Ser Asp Ile Phe Val Asn Cys Ile Tyr Leu Asn Ser
                245                 250                 255

aag att ccc aac ttt gtc gac ttt gag tct ctc aag tcg ccc aag agg         816
Lys Ile Pro Asn Phe Val Asp Phe Glu Ser Leu Lys Ser Pro Lys Arg
            260                 265                 270

cag ctg tcc gtc gtc tgc gac gtc tct gct gac acc acc aac ccc aac         864
Gln Leu Ser Val Val Cys Asp Val Ser Ala Asp Thr Thr Asn Pro Asn
        275                 280                 285

aac cct gtc ccc atc tac acc gtc gcc aca acc ttc gac aag ccc aca         912
Asn Pro Val Pro Ile Tyr Thr Val Ala Thr Thr Phe Asp Lys Pro Thr
    290                 295                 300

gtg ccc gtc gag gga ctc gag aac ccg ccc ctg agc gtc atc agc att         960
Val Pro Val Glu Gly Leu Glu Asn Pro Pro Leu Ser Val Ile Ser Ile
305                 310                 315                 320

gat cac ctt ccc agc ctc ctc ccc cgt gag gcc tcc gag acg tac agc        1008
Asp His Leu Pro Ser Leu Leu Pro Arg Glu Ala Ser Glu Thr Tyr Ser
                325                 330                 335

aag gac ctg ctg ccg tac ctg ctc acg ctg aag gac cgc aag acg gac        1056
Lys Asp Leu Leu Pro Tyr Leu Leu Thr Leu Lys Asp Arg Lys Thr Asp
            340                 345                 350

ccc gtc tgg acg agg gct gag aag ctc ttc aac gac aag gtc gct acg        1104
Pro Val Trp Thr Arg Ala Glu Lys Leu Phe Asn Asp Lys Val Ala Thr
        355                 360                 365

ctg ccg gcc gac ctg cag aag cct gct cag tga                            1137
Leu Pro Ala Asp Leu Gln Lys Pro Ala Gln
    370                 375


<210>  38
<211>  378
<212>  PRT
<213>  Verticillium albo-atrum

<400>  38

Met Ser Gly Ile Thr Leu His Leu Arg Ser Glu Thr Lys Pro Leu Glu
1               5                   10                  15


His Arg Ser Ala Leu Thr Pro Phe Thr Ala Ser Glu Leu Ile Lys Ala
            20                  25                  30


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


Ala Glu Phe Glu Lys Ile Gly Ala Thr Leu Val Pro Glu Gly Ser Trp
    50                  55                  60


Thr Glu Ala Pro Gln Asp His Ile Ile Val Gly Leu Lys Glu Leu Leu
65                  70                  75                  80


Glu Glu Asp Phe Pro Leu Lys His Val His Val Gln Phe Ala His Cys
                85                  90                  95
```

```
Tyr Lys Gln Gln Gly Gly Trp Glu Asn Val Leu Ala Arg Phe Pro Arg
            100                 105                 110


Gly Gly Gly Thr Leu Tyr Asp Leu Glu Phe Leu Glu Lys Glu Val Ala
        115                 120                 125


Pro Gly Arg Phe Ala Arg Val Ala Ala Phe Gly Trp Ser Ala Gly Phe
    130                 135                 140


Ser Gly Ala Ala Leu Ala Leu Gln Asn Trp Ala Trp Gln Leu Asn Asn
145                 150                 155                 160


Pro Gly Lys Pro Leu Pro Ser Val Glu Ser Tyr Pro Asn Glu Asp Glu
                165                 170                 175


Leu Ile Thr Ala Val Lys Lys Ser Ile Ala Glu Gly Lys Glu Lys Ala
            180                 185                 190


Gly Lys Leu Pro Gln Val Leu Val Ile Gly Ala Leu Gly Arg Cys Gly
        195                 200                 205


Ser Gly Ala Val Glu Leu Cys Arg Arg Val Gly Leu Pro Glu Glu Gln
    210                 215                 220


Ile Leu Lys Trp Asp Leu Glu Glu Thr Lys Lys Gly Gly Pro Phe Thr
225                 230                 235                 240


Glu Ile Val Glu Ser Asp Ile Phe Val Asn Cys Ile Tyr Leu Asn Ser
                245                 250                 255


Lys Ile Pro Asn Phe Val Asp Phe Glu Ser Leu Lys Ser Pro Lys Arg
            260                 265                 270


Gln Leu Ser Val Val Cys Asp Val Ser Ala Asp Thr Thr Asn Pro Asn
        275                 280                 285


Asn Pro Val Pro Ile Tyr Thr Val Ala Thr Thr Phe Asp Lys Pro Thr
    290                 295                 300


Val Pro Val Glu Gly Leu Glu Asn Pro Pro Leu Ser Val Ile Ser Ile
305                 310                 315                 320


Asp His Leu Pro Ser Leu Leu Pro Arg Glu Ala Ser Glu Thr Tyr Ser
                325                 330                 335


Lys Asp Leu Leu Pro Tyr Leu Leu Thr Leu Lys Asp Arg Lys Thr Asp
            340                 345                 350


Pro Val Trp Thr Arg Ala Glu Lys Leu Phe Asn Asp Lys Val Ala Thr
        355                 360                 365
```

```
Leu Pro Ala Asp Leu Gln Lys Pro Ala Gln
    370                 375


<210>  39
<211>  1125
<212>  DNA
<213>  Mycosphaerella graminicola


<220>
<221>  CDS
<222>  (1)..(1125)
<223>  Lys1

<400>  39
atg tct tct tca cca cta act ttg cac atc cgc gcg gaa acc aag ccc         48
Met Ser Ser Ser Pro Leu Thr Leu His Ile Arg Ala Glu Thr Lys Pro
1               5                   10                  15

ctc gaa cat cgc acc gct gtt ccg ccc aag gtt gcg agg aaa ctt gtc         96
Leu Glu His Arg Thr Ala Val Pro Pro Lys Val Ala Arg Lys Leu Val
            20                  25                  30

gag gcg ggt tac gtg gtc aac gtc gag cgg agt cca ttg agc atc ttc        144
Glu Ala Gly Tyr Val Val Asn Val Glu Arg Ser Pro Leu Ser Ile Phe
        35                  40                  45

ccg gac aac gag tac gaa gga aca gga gct acg ctt gtg ccg act ggt        192
Pro Asp Asn Glu Tyr Glu Gly Thr Gly Ala Thr Leu Val Pro Thr Gly
    50                  55                  60

tct tgg acg gaa gca ccc aag gac cat atc gtt gtg gga ttg aag gag        240
Ser Trp Thr Glu Ala Pro Lys Asp His Ile Val Val Gly Leu Lys Glu
65                  70                  75                  80

ttg ccg gag gag gat ttc gcg ttg gtg cat acg cat gtt cag ttc gca        288
Leu Pro Glu Glu Asp Phe Ala Leu Val His Thr His Val Gln Phe Ala
                85                  90                  95

cat tgc tat aag aat cag ggc gga tgg gag aaa gtc ttg agt cga ttc        336
His Cys Tyr Lys Asn Gln Gly Gly Trp Glu Lys Val Leu Ser Arg Phe
            100                 105                 110

ccg aga ggt gga ggg acg ctg ctt gac ttg gag ttc ctc gaa gat gag        384
Pro Arg Gly Gly Gly Thr Leu Leu Asp Leu Glu Phe Leu Glu Asp Glu
        115                 120                 125

caa gga cga cga gtt gcg gct ttc ggc tac cac gcc gga ttc gca gga        432
Gln Gly Arg Arg Val Ala Ala Phe Gly Tyr His Ala Gly Phe Ala Gly
    130                 135                 140

gca gct ctc tcc ctc atc aca tgg gcc tgg caa ctc gag cac ggc acc        480
Ala Ala Leu Ser Leu Ile Thr Trp Ala Trp Gln Leu Glu His Gly Thr
145                 150                 155                 160

tcc aag ccc gtg cct gga gtc acc gcc tac gag aac gaa aca ctc ctc        528
Ser Lys Pro Val Pro Gly Val Thr Ala Tyr Glu Asn Glu Thr Leu Leu
                165                 170                 175

gtc aac gac gtg aag aaa gcc gtc gag aag ggc aag tcg atc gcc ggc        576
Val Asn Asp Val Lys Lys Ala Val Glu Lys Gly Lys Ser Ile Ala Gly
            180                 185                 190

cac ctt ccg cga gtt ctg gtc atc ggc gct ctc gga cgt tgt ggc cgt        624
His Leu Pro Arg Val Leu Val Ile Gly Ala Leu Gly Arg Cys Gly Arg
        195                 200                 205
```

```
gga gcc gtc gac ctc tgc gtc aaa gct ggt ctg caa gac atc ctc aaa           672
Gly Ala Val Asp Leu Cys Val Lys Ala Gly Leu Gln Asp Ile Leu Lys
    210                 215                 220

tgg gac ctg caa gag acc aaa gcc aaa cca ggc ccc tac caa gaa atc           720
Trp Asp Leu Gln Glu Thr Lys Ala Lys Pro Gly Pro Tyr Gln Glu Ile
225                 230                 235                 240

atc gag tcc gac gtc ttt gta aac tgc atc tac ctc tcc gcc aaa atc           768
Ile Glu Ser Asp Val Phe Val Asn Cys Ile Tyr Leu Ser Ala Lys Ile
                245                 250                 255

cct cca ttc atc gac gca cct tcc ctc gcc tcc ccg acc cgc aaa ctc           816
Pro Pro Phe Ile Asp Ala Pro Ser Leu Ala Ser Pro Thr Arg Lys Leu
            260                 265                 270

agc gtc gtc tgt gac gtc tcc tgc gac acc acg aat cca cac aat ccg           864
Ser Val Val Cys Asp Val Ser Cys Asp Thr Thr Asn Pro His Asn Pro
        275                 280                 285

att ccg att tac tcc atc aat acg acg ttt gac aag ccc acc gtg cct           912
Ile Pro Ile Tyr Ser Ile Asn Thr Thr Phe Asp Lys Pro Thr Val Pro
    290                 295                 300

gtg gaa ctg tcc tca gag gcg aac gat gtg ccg ttg agt gtg att agc           960
Val Glu Leu Ser Ser Glu Ala Asn Asp Val Pro Leu Ser Val Ile Ser
305                 310                 315                 320

atc gac cac ttg ccg agt ttg ttg ccg aga gag gcg agc gag gca ttc          1008
Ile Asp His Leu Pro Ser Leu Leu Pro Arg Glu Ala Ser Glu Ala Phe
                325                 330                 335

agc gag gca ttg ttg ccg agt ttg ttg gag ttg aag gag agg aag acg          1056
Ser Glu Ala Leu Leu Pro Ser Leu Leu Glu Leu Lys Glu Arg Lys Thr
            340                 345                 350

gcg cgg gtg tgg agg cag gcg gag aag ttg ttc gag gac aag gtg gct          1104
Ala Arg Val Trp Arg Gln Ala Glu Lys Leu Phe Glu Asp Lys Val Ala
        355                 360                 365

agt ctg ccg aag ggt tcg tac                                              1125
Ser Leu Pro Lys Gly Ser Tyr
    370                 375


<210>  40
<211>  375
<212>  PRT
<213>  Mycosphaerella graminicola

<400>  40

Met Ser Ser Ser Pro Leu Thr Leu His Ile Arg Ala Glu Thr Lys Pro
1               5                   10                  15


Leu Glu His Arg Thr Ala Val Pro Pro Lys Val Ala Arg Lys Leu Val
            20                  25                  30


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


Pro Asp Asn Glu Tyr Glu Gly Thr Gly Ala Thr Leu Val Pro Thr Gly
    50                  55                  60
```

```
Ser Trp Thr Glu Ala Pro Lys Asp His Ile Val Val Gly Leu Lys Glu
65                  70                  75                  80


Leu Pro Glu Glu Asp Phe Ala Leu Val His Thr His Val Gln Phe Ala
                85                  90                  95


His Cys Tyr Lys Asn Gln Gly Gly Trp Glu Lys Val Leu Ser Arg Phe
            100                 105                 110


Pro Arg Gly Gly Gly Thr Leu Leu Asp Leu Glu Phe Leu Glu Asp Glu
        115                 120                 125


Gln Gly Arg Arg Val Ala Ala Phe Gly Tyr His Ala Gly Phe Ala Gly
    130                 135                 140


Ala Ala Leu Ser Leu Ile Thr Trp Ala Trp Gln Leu Glu His Gly Thr
145                 150                 155                 160


Ser Lys Pro Val Pro Gly Val Thr Ala Tyr Glu Asn Glu Thr Leu Leu
                165                 170                 175


Val Asn Asp Val Lys Lys Ala Val Glu Lys Gly Lys Ser Ile Ala Gly
            180                 185                 190


His Leu Pro Arg Val Leu Val Ile Gly Ala Leu Gly Arg Cys Gly Arg
        195                 200                 205


Gly Ala Val Asp Leu Cys Val Lys Ala Gly Leu Gln Asp Ile Leu Lys
    210                 215                 220


Trp Asp Leu Gln Glu Thr Lys Ala Lys Pro Gly Pro Tyr Gln Glu Ile
225                 230                 235                 240


Ile Glu Ser Asp Val Phe Val Asn Cys Ile Tyr Leu Ser Ala Lys Ile
                245                 250                 255


Pro Pro Phe Ile Asp Ala Pro Ser Leu Ala Ser Pro Thr Arg Lys Leu
            260                 265                 270


Ser Val Val Cys Asp Val Ser Cys Asp Thr Thr Asn Pro His Asn Pro
        275                 280                 285


Ile Pro Ile Tyr Ser Ile Asn Thr Thr Phe Asp Lys Pro Thr Val Pro
    290                 295                 300


Val Glu Leu Ser Ser Glu Ala Asn Asp Val Pro Leu Ser Val Ile Ser
305                 310                 315                 320


Ile Asp His Leu Pro Ser Leu Leu Pro Arg Glu Ala Ser Glu Ala Phe
                325                 330                 335
```

```
Ser Glu Ala Leu Leu Pro Ser Leu Leu Glu Leu Lys Glu Arg Lys Thr
            340                 345                 350


Ala Arg Val Trp Arg Gln Ala Glu Lys Leu Phe Glu Asp Lys Val Ala
        355                 360                 365


Ser Leu Pro Lys Gly Ser Tyr
    370                 375


<210>  41
<211>  1170
<212>  DNA
<213>  Fusarium moniliforme


<220>
<221>  CDS
<222>  (1)..(1170)
<223>  Lys1

<400>  41
atg tct gac tat ccc cac att ctc ctt cgc gct gag gag aag cct ctc         48
Met Ser Asp Tyr Pro His Ile Leu Leu Arg Ala Glu Glu Lys Pro Leu
1               5                   10                  15

gag cac cga tct ttc tcc ccc gca att atc aag aca ctc gtt gat gct         96
Glu His Arg Ser Phe Ser Pro Ala Ile Ile Lys Thr Leu Val Asp Ala
            20                  25                  30

gga tac ccc att tcc gtc gag cga tcg tct acc gac ccc aag ttc aag        144
Gly Tyr Pro Ile Ser Val Glu Arg Ser Ser Thr Asp Pro Lys Phe Lys
        35                  40                  45

cgt atc ttt gag gac tca gaa tat gag gct gct ggt gct cgt ctt gtc        192
Arg Ile Phe Glu Asp Ser Glu Tyr Glu Ala Ala Gly Ala Arg Leu Val
    50                  55                  60

gat acg ggt gtc tgg ccc aac gct gag cct gga aca atc att ctc ggc        240
Asp Thr Gly Val Trp Pro Asn Ala Glu Pro Gly Thr Ile Ile Leu Gly
65                  70                  75                  80

cta aaa gag cta cct tct gag gac ttc ccg ctc aag aat gac cac att        288
Leu Lys Glu Leu Pro Ser Glu Asp Phe Pro Leu Lys Asn Asp His Ile
                85                  90                  95

aca ttt gca cat tgt tac aag aac caa ggc ggg tgg gag cag gtc ctc        336
Thr Phe Ala His Cys Tyr Lys Asn Gln Gly Gly Trp Glu Gln Val Leu
            100                 105                 110

ggt cgc tgg gca cgc ggt ggc agc cgg ctt tac gac ctc gag ttt ctt        384
Gly Arg Trp Ala Arg Gly Gly Ser Arg Leu Tyr Asp Leu Glu Phe Leu
        115                 120                 125

gtg gac gaa caa ggt cgg cgt gtt tct gca ttt ggg tac cac gcg ggc        432
Val Asp Glu Gln Gly Arg Arg Val Ser Ala Phe Gly Tyr His Ala Gly
    130                 135                 140

ttc gcc ggt gct gcg ctc gga atc aag aca ctc gct cac cag ctg cag        480
Phe Ala Gly Ala Ala Leu Gly Ile Lys Thr Leu Ala His Gln Leu Gln
145                 150                 155                 160

ggc tcg tcc tct aaa ctt cct tct gtc gag aca ttc act gat ggc cgc        528
Gly Ser Ser Ser Lys Leu Pro Ser Val Glu Thr Phe Thr Asp Gly Arg
                165                 170                 175
```

```
gga tat tac ttg aac gaa gat gag ctc gtc aac cag att cgt gag gat        576
Gly Tyr Tyr Leu Asn Glu Asp Glu Leu Val Asn Gln Ile Arg Glu Asp
            180                 185                 190

ctc gct aag gct gaa aag gct ctc gga cgt aag ccc act gct ctc gtc        624
Leu Ala Lys Ala Glu Lys Ala Leu Gly Arg Lys Pro Thr Ala Leu Val
        195                 200                 205

ctt ggt gct ctt gga cga tgt ggt aag ggt gcc gtg gac ctt ttc ctg        672
Leu Gly Ala Leu Gly Arg Cys Gly Lys Gly Ala Val Asp Leu Phe Leu
    210                 215                 220

aag gcc ggc atg cct gat gac aac att acc cgc tgg gac ttg aac gag        720
Lys Ala Gly Met Pro Asp Asp Asn Ile Thr Arg Trp Asp Leu Asn Glu
225                 230                 235                 240

act aag gac cgt gat ggc cct tac gag gag atc gcc aag gct gat gtc        768
Thr Lys Asp Arg Asp Gly Pro Tyr Glu Glu Ile Ala Lys Ala Asp Val
                245                 250                 255

ttc ctc aac gcc atc tac ctc tcc aag ccc att ccc cct ttc atc aac        816
Phe Leu Asn Ala Ile Tyr Leu Ser Lys Pro Ile Pro Pro Phe Ile Asn
            260                 265                 270

caa gaa ctc ctt gcc aag caa ggt cgc aac ctc gct gtt gtc atc gac        864
Gln Glu Leu Leu Ala Lys Gln Gly Arg Asn Leu Ala Val Val Ile Asp
        275                 280                 285

gtt tct tgt gac acc aca aac cct cac aac cct atc ccc atc tac tcc        912
Val Ser Cys Asp Thr Thr Asn Pro His Asn Pro Ile Pro Ile Tyr Ser
    290                 295                 300

atc aac acc acc ttt gag gac cca acc gtc ccc gtt gag atc aag gac        960
Ile Asn Thr Thr Phe Glu Asp Pro Thr Val Pro Val Glu Ile Lys Asp
305                 310                 315                 320

gat cag aac aac ctc ccc cta tcc gtc atc agc att gat cac ctc cct       1008
Asp Gln Asn Asn Leu Pro Leu Ser Val Ile Ser Ile Asp His Leu Pro
                325                 330                 335

tcc atg ctt ccc cgc gag gct agt gag gcc ttt agt gag ggt ctc aag       1056
Ser Met Leu Pro Arg Glu Ala Ser Glu Ala Phe Ser Glu Gly Leu Lys
            340                 345                 350

gag tct ctg ctc aca ctc aag gat cgc gag act tcg cgg gtg tgg act       1104
Glu Ser Leu Leu Thr Leu Lys Asp Arg Glu Thr Ser Arg Val Trp Thr
        355                 360                 365

gat gct gag aag ctc ttc cat gag aag gtt gcc ctg ttg ccc gag gag       1152
Asp Ala Glu Lys Leu Phe His Glu Lys Val Ala Leu Leu Pro Glu Glu
    370                 375                 380

ttg aga acc aag agt gtt                                               1170
Leu Arg Thr Lys Ser Val
385                 390


<210>  42
<211>  390
<212>  PRT
<213>  Fusarium moniliforme

<400>  42

Met Ser Asp Tyr Pro His Ile Leu Leu Arg Ala Glu Glu Lys Pro Leu
1               5                   10                  15
```

```
Glu His Arg Ser Phe Ser Pro Ala Ile Ile Lys Thr Leu Val Asp Ala
            20                  25                  30

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

Arg Ile Phe Glu Asp Ser Glu Tyr Glu Ala Ala Gly Ala Arg Leu Val
    50                  55                  60

Asp Thr Gly Val Trp Pro Asn Ala Glu Pro Gly Thr Ile Ile Leu Gly
65                  70                  75                  80

Leu Lys Glu Leu Pro Ser Glu Asp Phe Pro Leu Lys Asn Asp His Ile
                85                  90                  95

Thr Phe Ala His Cys Tyr Lys Asn Gln Gly Gly Trp Glu Gln Val Leu
            100                 105                 110

Gly Arg Trp Ala Arg Gly Gly Ser Arg Leu Tyr Asp Leu Glu Phe Leu
        115                 120                 125

Val Asp Glu Gln Gly Arg Arg Val Ser Ala Phe Gly Tyr His Ala Gly
    130                 135                 140

Phe Ala Gly Ala Ala Leu Gly Ile Lys Thr Leu Ala His Gln Leu Gln
145                 150                 155                 160

Gly Ser Ser Ser Lys Leu Pro Ser Val Glu Thr Phe Thr Asp Gly Arg
                165                 170                 175

Gly Tyr Tyr Leu Asn Glu Asp Glu Leu Val Asn Gln Ile Arg Glu Asp
            180                 185                 190

Leu Ala Lys Ala Glu Lys Ala Leu Gly Arg Lys Pro Thr Ala Leu Val
        195                 200                 205

Leu Gly Ala Leu Gly Arg Cys Gly Lys Gly Ala Val Asp Leu Phe Leu
    210                 215                 220

Lys Ala Gly Met Pro Asp Asp Asn Ile Thr Arg Trp Asp Leu Asn Glu
225                 230                 235                 240

Thr Lys Asp Arg Asp Gly Pro Tyr Glu Glu Ile Ala Lys Ala Asp Val
                245                 250                 255

Phe Leu Asn Ala Ile Tyr Leu Ser Lys Pro Ile Pro Pro Phe Ile Asn
            260                 265                 270

Gln Glu Leu Leu Ala Lys Gln Gly Arg Asn Leu Ala Val Val Ile Asp
        275                 280                 285
```

```
Val Ser Cys Asp Thr Thr Asn Pro His Asn Pro Ile Pro Ile Tyr Ser
    290                 295                 300


Ile Asn Thr Thr Phe Glu Asp Pro Thr Val Pro Val Glu Ile Lys Asp
305                 310                 315                 320


Asp Gln Asn Asn Leu Pro Leu Ser Val Ile Ser Ile Asp His Leu Pro
                325                 330                 335


Ser Met Leu Pro Arg Glu Ala Ser Glu Ala Phe Ser Glu Gly Leu Lys
            340                 345                 350


Glu Ser Leu Leu Thr Leu Lys Asp Arg Glu Thr Ser Arg Val Trp Thr
        355                 360                 365


Asp Ala Glu Lys Leu Phe His Glu Lys Val Ala Leu Leu Pro Glu Glu
    370                 375                 380


Leu Arg Thr Lys Ser Val
385                 390


<210>  43
<211>  856
<212>  DNA
<213>  Claviceps purpurea


<220>
<221>  CDS
<222>  (3)..(854)
<223>  Lys1

<400>  43
ct ggc tac aaa gtt tcc gtg gag cgc tca cca tcg gac ccc gac ttt          47
   Gly Tyr Lys Val Ser Val Glu Arg Ser Pro Ser Asp Pro Asp Phe
   1               5                   10                  15

gtc cgc atc ttc caa gac tct gaa tat gag gcg gct gga gct tct ctg          95
Val Arg Ile Phe Gln Asp Ser Glu Tyr Glu Ala Ala Gly Ala Ser Leu
                20                  25                  30

gtt ccc act ggc gtg tgg ccc aag gct gcg cca aac act ctg atc gtt         143
Val Pro Thr Gly Val Trp Pro Lys Ala Ala Pro Asn Thr Leu Ile Val
            35                  40                  45

ggt ctc aag gag atc ccc gaa gag ggc ttt tct ctc acc aat gac cac         191
Gly Leu Lys Glu Ile Pro Glu Glu Gly Phe Ser Leu Thr Asn Asp His
        50                  55                  60

ctg acc ttt gcc cat tgc tac aag aag caa gct ggc tgg aca cag gtt         239
Leu Thr Phe Ala His Cys Tyr Lys Lys Gln Ala Gly Trp Thr Gln Val
    65                  70                  75

ctc gga cgc ttt gtc gca ggc aaa tcg acc ctc tac gac ctg gag ttt         287
Leu Gly Arg Phe Val Ala Gly Lys Ser Thr Leu Tyr Asp Leu Glu Phe
80                  85                  90                  95

ctg gtc gat agc act gga aga cgc atc tct gct ttc gga ttc cac gct         335
Leu Val Asp Ser Thr Gly Arg Arg Ile Ser Ala Phe Gly Phe His Ala
                100                 105                 110
```

```
ggc ttc acg ggc gct gct ttg gga gtg aag aac tgg gct tgg caa ctg        383
Gly Phe Thr Gly Ala Ala Leu Gly Val Lys Asn Trp Ala Trp Gln Leu
            115                 120                 125

gcc aat cca gcc aag aag ctt ccc gcc gtg tcc aca ttc act gac ggc        431
Ala Asn Pro Ala Lys Lys Leu Pro Ala Val Ser Thr Phe Thr Asp Gly
        130                 135                 140

aag gga tac tat gtg aac gaa acc gag ttg gtg gag caa atc cgc aag        479
Lys Gly Tyr Tyr Val Asn Glu Thr Glu Leu Val Glu Gln Ile Arg Lys
    145                 150                 155

gat ctc gag gca gga gag aag att ctt ggc cgt aag cca aca gcc ttt        527
Asp Leu Glu Ala Gly Glu Lys Ile Leu Gly Arg Lys Pro Thr Ala Phe
160                 165                 170                 175

gtc ctg gga gct ttg ggt cgc tgc ggc agg ggt gct tgc gat ttg ttc        575
Val Leu Gly Ala Leu Gly Arg Cys Gly Arg Gly Ala Cys Asp Leu Phe
                180                 185                 190

ctc aag gca ggc ttg ccc gaa gag aac atc acc cga tgg gat ttg gcc        623
Leu Lys Ala Gly Leu Pro Glu Glu Asn Ile Thr Arg Trp Asp Leu Ala
            195                 200                 205

gaa acc cgc gac cgc caa ggc ccg tac gag gag att gct cag cac gat        671
Glu Thr Arg Asp Arg Gln Gly Pro Tyr Glu Glu Ile Ala Gln His Asp
        210                 215                 220

atc ttc ctg aac gct atc tat ctc tcc gag ccc atc cca cct ttt gtc        719
Ile Phe Leu Asn Ala Ile Tyr Leu Ser Glu Pro Ile Pro Pro Phe Val
    225                 230                 235

aac aac gag ctt ctt tct aag cct ggc cgc aaa ttg agt gtt gtc ata        767
Asn Asn Glu Leu Leu Ser Lys Pro Gly Arg Lys Leu Ser Val Val Ile
240                 245                 250                 255

gac gtc tcc tgc gac acc acc aac ccc cac aac ccc atc ccc atc tac        815
Asp Val Ser Cys Asp Thr Thr Asn Pro His Asn Pro Ile Pro Ile Tyr
                260                 265                 270

agc atc aac acc acc ttc gac agc ccc acc gtt gcc gtc aa                 856
Ser Ile Asn Thr Thr Phe Asp Ser Pro Thr Val Ala Val
            275                 280


<210>  44
<211>  284
<212>  PRT
<213>  Claviceps purpurea

<400>  44

Gly Tyr Lys Val Ser Val Glu Arg Ser Pro Ser Asp Pro Asp Phe Val
1               5                   10                  15


Arg Ile Phe Gln Asp Ser Glu Tyr Glu Ala Ala Gly Ala Ser Leu Val
            20                  25                  30


Pro Thr Gly Val Trp Pro Lys Ala Ala Pro Asn Thr Leu Ile Val Gly
        35                  40                  45


Leu Lys Glu Ile Pro Glu Glu Gly Phe Ser Leu Thr Asn Asp His Leu
    50                  55                  60
```

```
Thr Phe Ala His Cys Tyr Lys Lys Gln Ala Gly Trp Thr Gln Val Leu
65                  70                  75                  80


Gly Arg Phe Val Ala Gly Lys Ser Thr Leu Tyr Asp Leu Glu Phe Leu
                85                  90                  95


Val Asp Ser Thr Gly Arg Arg Ile Ser Ala Phe Gly Phe His Ala Gly
            100                 105                 110


Phe Thr Gly Ala Ala Leu Gly Val Lys Asn Trp Ala Trp Gln Leu Ala
        115                 120                 125


Asn Pro Ala Lys Lys Leu Pro Ala Val Ser Thr Phe Thr Asp Gly Lys
    130                 135                 140


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


Leu Glu Ala Gly Glu Lys Ile Leu Gly Arg Lys Pro Thr Ala Phe Val
                165                 170                 175


Leu Gly Ala Leu Gly Arg Cys Gly Arg Gly Ala Cys Asp Leu Phe Leu
            180                 185                 190


Lys Ala Gly Leu Pro Glu Glu Asn Ile Thr Arg Trp Asp Leu Ala Glu
        195                 200                 205


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


Phe Leu Asn Ala Ile Tyr Leu Ser Glu Pro Ile Pro Pro Phe Val Asn
225                 230                 235                 240


Asn Glu Leu Leu Ser Lys Pro Gly Arg Lys Leu Ser Val Val Ile Asp
                245                 250                 255


Val Ser Cys Asp Thr Thr Asn Pro His Asn Pro Ile Pro Ile Tyr Ser
            260                 265                 270


Ile Asn Thr Thr Phe Asp Ser Pro Thr Val Ala Val
        275                 280


<210>  45
<211>  41
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer


<220>
<221>  primer_bind
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<222>  (1)..(41)

<400>  45
taatacgact cactataggg ttgcaggaga gcgcagaaag c                           41


<210>  46
<211>  42
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer


<220>
<221>  primer_bind
<222>  (1)..(42)

<400>  46
taatacgact cactataggg tcagttggag tccgcgtggt gt                          42


<210>  47
<211>  20
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer


<220>
<221>  primer_bind
<222>  (1)..(20)

<400>  47
cgactctggt gacggtgtgt                                                   20


<210>  48
<211>  20
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer


<220>
<221>  primer_bind
<222>  (1)..(20)

<400>  48
gcgtgaggaa gagcgtaacc                                                   20


<210>  49
<211>  18
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer


<220>
<221>  primer_bind
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```
<222>  (1)..(18)

<400>  49
ccgcccagac aatttcgt                                                    18


<210>  50
<211>  20
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer


<220>
<221>  primer_bind
<222>  (1)..(20)

<400>  50
ccttggccca gttgttacca                                                  20


<210>  51
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer


<220>
<221>  primer_bind
<222>  (1)..(21)

<400>  51
tgggtggttt ccaaggtctt c                                                21


<210>  52
<211>  20
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer


<220>
<221>  primer_bind
<222>  (1)..(20)

<400>  52
aaaggcacca agccactgaa                                                  20


<210>  53
<211>  48
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer


<220>
<221>  primer_bind
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```
<222>  (1)..(48)

<400>  53
tcgacaggcc tggatcctta attaaactag tctcgaggag ctcggtac                    48


<210>  54
<211>  40
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer


<220>
<221>  primer_bind
<222>  (1)..(40)

<400>  54
cgagctcctc gagactagtt taattaagga tccaggcctg                             40


<210>  55
<211>  31
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer


<220>
<221>  primer_bind
<222>  (1)..(31)

<400>  55
tatctcgagt ctagacaacg ccattggtta c                                      31


<210>  56
<211>  25
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer


<220>
<221>  primer_bind
<222>  (1)..(25)

<400>  56
agaggtacca agcttgcgta gctgg                                             25


<210>  57
<211>  22
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer


<220>
<221>  primer_bind
```

```
<222>  (1)..(22)

<400>  57
tcaatagaag cgaacgcgta aa                                                22


<210>  58
<211>  20
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer


<220>
<221>  primer_bind
<222>  (1)..(20)

<400>  58
gttcgggatc tgctcgatgt                                                   20
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