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(54) Titre : POLYPEPTIDE PRESENTANT UNE ACTIVITE D'INDUCTION DE LA DEFENSE CONTRE LE STRESS BIOTIQUE DANS DES PLANTES, SEQUENCE DE NUCLEOTIDES CODANT CE POLYPEPTIDE, MICRO-ORGANISME, COMPOSITIONS ET METHODES
(54) Title: POLYPEPTIDE HAVING INDUCING ACTIVITY FOR THE DEFENCE AGAINST BIOTIC STRESS IN PLANTS, NUCLEOTIDE SEQUENCE ENCODING THE SAME, MICROORGANISM, COMPOSITIONS AND METHODS

(57) **Abrégé/Abstract:**

Polypeptide having activity inducing pathogen plant defence, nucleotide sequence encodes it, microorganism, compositions and methods. The polypeptide is a subtilisin derived from a strain of Acremonium strictum. The polypeptide is encoded by the nucleotide sequence SEQ ID No.: 1 or sequences at least 90% homologous to the same and has the amino acid sequence SEQ ID No: 2 or sequences at least 90% homologous to the same.

ABSTRACT

Polypeptide having activity inducing pathogen plant defence, nucleotide sequence encodes it, microorganism, compositions and methods. The polypeptide is a subtilisin derived from a strain of *Acremonium strictum*. The polypeptide is encoded by the nucleotide sequence SEQ ID No.: 1 or sequences at least 90% homologous to the same and has the amino acid sequence SEQ ID No: 2 or sequences at least 90% homologous to the same.

Polypeptide having inducing activity for the defence against biotic stress in plants, nucleotide sequence encoding the same, microorganism, compositions and methods

This invention refers to a polypeptide having inducing activity for the defence against biotic stress in plants, nucleotide sequence encoding the same, microorganism, compositions and methods. More specifically, this invention refers to a subtilisin polypeptide derived from *Acremonium strictum*, wherein such polypeptide has elicitory activity. According to a particular embodiment of the invention, the polypeptide is codified by nucleotide sequence SEQ ID No. 1 or sequences being at least 90% homologous to the same, and has the amino acid sequence SEQ ID No. 2 or sequences being at least 90% homologous to the same, wherein such polypeptide has elicitory activity.

BACKGROUND

Strawberry is a fruit with remarkable characteristics, which can be eaten fresh, dried, frozen or canned. From an economic point of view, strawberry is a very important culture because of the number of input and technology used, apart from the added value it can achieve due to the fact it can be industrialized and exported.

One of the main problems of producing strawberries is the great number of diseases and pests (biotic stress) that attack the cultivars thereof, which result in limitation to the fruit's production and quality. The main cause of biotic stress for strawberries is fungal diseases.

There are many diseases, the most frequent of which are as follows:

Root and crown rot: several diseases caused by fungi among the genus *Phytophthora*, *Rhizoctonia* and *Colletotrichum* (anthracnose).

Leaf diseases: *Xanthomonas fragariae* (angular leaf spot); *Gnomonia comari* (foliar spot); *Mycosphaerella fragariae* or *Ramularia* (leaf spot); *Diplocarpon earliana* (leaf burn or spot); *Dendrophoma/Phomopsis obscurans* (stain); *Sphaerotheca macularis* (oidium); *Colletotrichum spp.* (anthracnose).

Flower and fruit diseases: *Rhizopus stolonifer* (rot); *Botrytis cinerea* (grey mould); *Colletotrichum spp.* (anthracnose).

Strawberry anthracnose, caused by a *Colletotrichum* fungal complex, is definitely the disease that most adversely affects the culture thereof, attacking almost every organ in the plant and originating great loss both in fruit production and greenhouses (seedling production), mainly in tropical and subtropical agro-climatic regions.

As a result of the wide pathogenic diversity (at least three different species), almost all kinds of strawberries are sensitive to anthracnose. In terms of culture's genetic enhancement, it is difficult to combine in a single variety genes conferring certain characteristics regarding production, greenhouse management, and resistance to diseases, and even more difficult to a disease caused by different pathogens such as anthracnose.

Culture management together with chemical treatments help reducing anthracnose incidence. However, the excessive use of agrochemicals has a high impact on the ecosystem's degradation and on farm worker's health, as well as on water pollution and in the content of toxic residues in food, apart from favouring the origination of fungicidal-resistant fungi strains and having direct effects on the elimination of pests' natural enemies. The excess of fungicidal residues in the fruit can cause serious problems when marketing or exporting strawberries for not meeting the quality standards required by local authorities or importing markets.

There is currently a major global agreement as to promoting, in general, responsible or sustainable agriculture through the development of productive systems integrating low-environmental impact agronomic procedures (integrated production). Among the different biological approaches encompassed within the term biotechnology, the use of varieties with increased resistance (resulting from conventional or molecular biotechnology-assisted genetic enhancement) as well as Biological Control Agents (BCA) is included.

BCAs may (i) act directly on the pathogen such as in the case of "antagonist microorganisms"; (ii) exert an indirect action by interacting in the host plant, providing protection against a disease, either by: hypovirulence transmission to virulent races thereby neutralizing such disease, or (iii) by activating the plant's defense mechanisms, known as "Induced Resistance" or "preimmunization".

Plants defend themselves from potential invading pathogens either through morphological structures acting as physical barriers that inhibit the pathogen's entrance and development, or by biochemical reactions occurring in different plant tissues producing toxic substances for the pathogen, or creating conditions that inhibit the microorganism's entrance and development in the host. Such defenses may be either part of the plant being a non-specific protection against a wide range of microorganisms or induced in the presence of the attacking pathogen. In this latter case, plants as well as other living beings activate their own defense systems as they recognize a pathogenic-microorganism-derived molecule or else as they detect any molecule generated during the pathogen's invasion, any of them being referred to as defense "inducer" or "elicitor".

In plant/pathogen interactions, inducing molecules alert of the presence of the invading pathogen when the pathogen is recognized by the host plant (Nürnberger, 1999. *Cell Mol. Life Sci.* 55, 167-182). In early recognition of the elicitors of the attacking pathogen, the plant produces a rapid activation of its defence mechanisms, which block the infection, stopping the pathogen's progress. In this case, the plant/pathogen interaction is said to be incompatible because it does not result in a disease, the phytopathogen strain being defined as non-virulent (Keen, 1990. *Annu. Rev. Genet.* 24, 447-463). In contrast, the plant develops the disease when it is unable to detect the pathogen's aggression or when it detects it late (the elicitors thereof), and in spite of triggering certain defence mechanisms, they are not sufficient to timely stop the invasion, thus the plant/pathogen interaction is said to be compatible and the strain is deemed virulent.

During a fungal infection, plants can recognize the aggressor via a set of elicitors. Some of the inducing molecules are derived from the pathogen (non- self factors) and can be present at the fungal surface (e.g., chitin and glucan fragments) or secreted by the pathogen (e.g., avirulence proteins); while other molecules are generated by the plant during the fungal invasion (known as self factors), such as in the case of plant cell wall fragments (e.g., oligogalacturonates, chitin, heptaglucons, monosilated glycopeptides) released from polymeric precursors by action of the

invading pathogen's hydrolytic enzymes (Knogge, 1996. *The Plant Cell* 8, 1711-1722). Thus, elicitors can be classified as pre-formed compounds, which are present on the pathogen's surface, or as induced, as when synthesized during the interaction between the pathogen and the host plant.

In general, the pathogen recognition and the subsequent activation of resistance responses to disease in plants can occur at a species level (e.g., species or non-host resistance, or cultivar non-specific host resistance, or innate immunity) or at a genotype level (cultivar specific host resistance). A cultivar's specific resistance is expressed in a given cultivar against one or a reduced number of pathogenic races and represents what is known as "gene to gene" response, being genetically determined by the complementary pair codified by the pathogen avirulence (Avr) gene and the product from a plant resistance (R) gene.

Thus, when the AVR protein is directly or indirectly recognized by a resistant host plant, it acts as a defense "specific elicitor", and can be detected by the plant surveillance system. However, innate immunity is the prevailing resistance form in all plants species. In this response, a great variety of products associated to so-called "general elicitor" microorganisms, induce the defense response in many plant species and do not depend on a specific cultivar. The term "Pathogen-Associated Molecular Pattern" (PAMP) refers to any molecule capable of activating the plant defense system, and it can be found in a wide range of pathogens (Bent and Mackey, 2007. *Annu. Rev. Phytopathol.* 45, 399-436). Kamoun (Kamoun, 2006. *Annu. Rev. Phytopathol.* 44, 41-60) reports the elicitors produced by plant pathogenic oomycetes fungi, while Stergiopoulos *et al.* (Stergiopoulos and de Wit, 2009. *Annu. Rev. Phytopathol.* 47, 233-263) describe fungal avirulence proteins reported so far.

After the recognition of the elicitor, a series of cytological shifts and biochemical responses in plant cells have been identified. In biochemical terms, it can be said that an inducer interacts with one receptor on the cell surface which detects the extracellular signal converting it in intracellular signals, the transduction of which imply (a) ionic trans-membrane fluids (i.e. entrance of Ca^{2+} , H^+ and Cl^-); (b) production of reactive oxygen species (ROS) such as H_2O_2 , O_2^- , etc., toxic for the

cells, producing “oxidative burst”; (c) nitric oxide production (NO); c) phosphorylation/ dephosphorylation of mitogen-activated protein kinases (MAPKs) and other calcium dependant protein kinases (CDPKs).

These signals give rise to early defense responses at the infection site, and late defence responses in distant plant areas.

Local defense responses to elicitors imply regulating several genes, which contribute to generate protective physiological conditions against invading pathogens. At the infection site, such responses include generation of reactive oxygen species (ROS), rapid accumulation of several enzymes and metabolites, such as for example, proteins involved in the production of signals, such as salicylic acid (SA), jasmonates and/or ethylene, and of enzymes related to phenylpropanoid metabolism (PAL: phenyl ammonium-lyase; CHS: chalcone synthase; etc.) and phytoalexin biosynthesis, low molecular weight secondary metabolites having antimicrobial activity, and the so-called PR proteins (Pathogenesis Related Proteins). Such defense is restricted to the area surrounding the pathogen penetration site.

In some cases, cells at the infection site can undergo a process of cell death, which usually becomes visible as a hypersensitive response. Hypersensitive Response (HR) consists in the rapid and localized death of the host cells invaded by the pathogen, by a necrosis phenomenon or programmed cell death (PCD). This phenomenon is associated with reinforcement in the cell wall of affected cells by local lignifications and callose accumulation, cross-linking of hydroxyproline-rich glycoproteins (HRGP), activation of the enzymes implied in molecule cross-linking as a plant strategy to limit the colonization to infection sites.

Salicylic acid (SA), is a plant hormone which among other functions inhibits catalase aggravating oxidative stress, and also coordinates the expression of PR protein subgroup which are divided in three classes: chitinases, glucanases and chitin binding proteins. In summary, to kill or successfully stop an invading microorganism a special and accurately timely coordination of induced defense responses is required.

A local infection often leads to induction of similar defense responses in non-infected plant tissues thus resulting in resistance to subsequent infections (Kuč, 1982.

BioScience 32, 854-860). This line of defense leads to the accumulation of proteins and hydrolytic enzymes throughout the organisms, thus being referred to as “systemic” (Hunt and Ryals, 1996. Crit. Rev. Plant Sci. 15, 583-606). It usually provides resistance to the primary inducing agent (virulent pathovar) and also to a wide range of other fungal, bacterial and viral pathogens (immunization). When this defense response is mediated by action of an avirulent pathogen, it is referred to as “Systemic Acquired Resistance” (SAR). Furthermore, systemic resistance may also be triggered by a rhizosphere non-pathogenic microorganism, and in this case it is referred to as “Induced Systemic Resistance” (ISR); or it may be induced by injuries (mechanical damage).

The different systemic defense responses associated with pathogen infections include induction of several PR genes, accumulation of phytoalexins, induction of EROs and micro-HR.

The foregoing suggests that the induction of a broad-spectrum systemic defense response (either SAR or ISR) can be used as “immunization” strategy in order to prevent or reduce crop diseases (Induced Resistance or IR). For strawberries, the use of IR for controlling *Phytophthora spp.* (Eikemo *et al.*, 2003. Plant Dis. 87, 345-350) and *Botrytis* (Adikaram *et al.*, 2002. Australasian Plant Pathology 31(3), 223–229) has been suggested. This host plant protection phenomenon which was originally referred to as “Cross-protection” was used as means of management of virus-caused diseases by prior inoculation with weak strains of the same virus, thus making that the virus inoculated first prevent the development of the subsequent virus. Then, it was apparent that it was also possible to increase resistance to fungal pathogen severe races by pre-inoculation with an avirulent genotype of the same fungus species or by application of a rhizosphere non-pathogenic microorganism; as mentioned above, this last phenomenon was called ISR as opposed to SAR.

Unlike the response induced by a rhizosphere non-pathogenic microorganism, field implementation of a SAR-like system, which implies direct plant infection with a live pathogenic microorganism, is not possible, since it poses serious problems, among which it is worth mentioning that it is possible that an avirulent strain used to

protect a cultivar can produce the disease in other susceptible genotypes (Fulton, 1986. Annu. Rev. Phytopathol. 24, 67-81). A biotechnological option to solve this problem and induce resistance involves inactivating the pathogen and applying portions from different pathogenic cultures (non-pathogenic extracts) that retain inducing defense activity, which at the same time lose pathogenic potential, that is, using fractions of the inactivated pathogen containing the defense inducing agent(s). Having greater knowledge of the system will allow for the direct application of elicitor molecules derived from the plant/avirulent pathogen interaction, capable of providing resistance against diseases through the induction of a broad-spectrum systemic defense response (SAR elicitor), to the expression of such pathogen avirulent gene in transgenic plants.

Very few elicitors that can effectively induce resistance are currently known. In strawberries, registered biopesticides with elicitory action include *harpin* proteins (trade name: MESSENGER®), an alternative to the use of methyl bromide, which is effective against bacterial leaf spot, tristeza caused by bacteria, bacterial blight, certain fungal diseases; and chitosan (trade name: ELEXA-4®) which is active against woolly aphids and powdery “mildew” and grey mould. However, until now, no type of biological control method to control anthracnose (*Colletotrichum* spp.) in strawberries has been suggested.

In light of the above mentioned, having determined the lack of solutions with respect to the provision of new disease treatment and/or prevention methods, the inventors herein have identified a new protein excreted to the medium by *Acremonium strictum*, and having purified it to homogeneity. This protein acts as avirulence factor (elicitor), triggering different defense mechanisms immunizing the plant, thus making it resistant to diseases, such as anthracnose produced by *Colletotrichum* spp.

SUMMARY OF THE INVENTION

A subtilisin polypeptide having elicitory (inducing) activity of the defence against biotic stress in plants, the polypeptide being derived from *Acremonium*

strictum, for example *Acremonium strictum* SS71 deposited in the German deposit center DSMZ under access code DSM 24396, and having elicitory activity is provided. The polypeptide is codified by nucleotide sequence SEQ ID No. 1 or sequences at least 90% homologous to the same, and having the amino acid sequence SEQ ID No. 2 or sequences being at least 90% homologous to the same, wherein such polypeptide has elicitory activity.

A nucleotide sequence encoding the elicitor polypeptide shown in sequence SEQ ID No: 1 or sequences at least 90% homologous is provided.

An elicitor polypeptide producing microorganism is provided, such microorganism being the strain of *Acremonium strictum* SS71 deposited in the German deposit center DSMZ under access code DSM 24396.

A composition useful for inducing resistance to biotic factors in plants is provided, the composition comprising *Acremonium strictum* conidia and excipients, e.g. comprising between 1×10^3 and 1×10^8 conidia/ml. Prefererably, the composition comprises conidia of the strain of *Acremonium strictum* SS71 deposited in the German deposit center DSMZ under access code DSM 24396.

A composition useful for inducing resistance to biotic factors in plants is provided, the composition comprising *Acremonium strictum*. Prefererably, the composition comprises an extract of the strain of *Acremonium strictum* SS71 deposited in the German deposit center DSMZ under access code DSM 24396. The extract can be cell-free supernatant or conidial extract.

A composition comprising between 2.5 and 15 µg/ml of elicitor polypeptide is provided.

A procedure for obtaining and purifying the elicitor polypeptide is provided, comprising the following steps:

- (a) culturing *Acremonium strictum*, preferably *Acremonium strictum* SS71 under access code DSM 24396;
- (b) recovering the supernatant;
- (c) concentrating the supernatant; and
- (d) ultrafiltrating the product obtained in the previous step.

A method for inducing resistance to pathogens in plants is provided, comprising the application to such a plant of a composition derived from *Acremonium strictum*, e.g. the strain of *Acremonium strictum* SS71 under access code DSM 24396. The composition can be: a conidial suspension of the strain, a cell-free extract, a conidial extract, a culture supernatant, an elicitor polypeptide solution or a combination thereof. The conidial suspension can be applied at a concentration from between 1×10^3 and 1×10^8 conidia/ml, the cell-free extract can be at a concentration between 0.4 and 9 μg protein/ml, the conidial extract can be at a concentration between 0.12 and 1.5 μg protein/ml and the elicitor polypeptide solution can be between 2.5 and 15 μg /ml. Since the elicitor generates a non-specific systemic response, the method of the invention provides protection against a wide range of pathogens, being effective for fungal, bacterial and viral protection. The method can be applied among others to the following pathogens: *Colletotrichum spp.*, *Botrytis cinera* or *Xanthomonas fragariae*. Moreover, considering the protection mechanisms triggered by the elicitor are widely spread in the plant kingdom, the method is effective for any type of plant, in particular eudicotyledons, such as strawberry (*Fragaria x ananassa*), tomato (*Solanum lycopersicon*) or *Arabidopsis thaliana*, by aspersion in the aerial parts, infiltration or irrigation.

DESCRIPTION OF THE DRAWINGS

Figure 1: Figure 1 shows in a graphic the disease severity level (DSR) of anthracnose in strawberry plants cv. Pájaro treated with extracts containing the elicitor 48 hours prior to inoculation with virulent isolate M11 of *C. acutatum*. Plants were assessed 40 DAI (Days After Inoculation) with M11. CE: Conidial extract (10 μg protein/ml) obtained by sonication; SN: liquid culture supernatant grown in PG (potatoe-glucose) medium to stationary phase (10 μg protein/ml). Ctr-PC: M11-infected plant control, which were previously inoculated with the avirulent strain (SS71) of *A. strictum*. Ctr.-Ca: M11-infected plant control without previous treatment. DSR means Disease Severity Rating.

Figure 2: Figure 2A shows heat susceptibility of elicitory activity. Assays were carried out with concentrated and dialysed culture supernatants of isolate SS71 of *A. strictum* grown in PG medium to stationary phase. (A) SN: extract without treatment. SN1: extract heated until boiling in boiling water bath for 15 min.; SN2: extract heated to 120°C by autoclaving (overpressure 1 atm.) for 15 min. Figure 2B shows susceptibility of elicitory activity to digestion with Proteinase K. SN: extract without treatment; SNA: extract treated with Proteinase K (100 µg/ml) for 1 hour at 50°C; and SNB: extract treated for 12 hours at 50°C. Controls: Ctr.-PC: M11-infected plants which were previously inoculated with the avirulent strain (SS71) of *A. strictum*. Ctr.-Ca: M11-infected plants without previous treatment. Assays were conducted 40 DAI. DSR means Disease Severity Rating.

Figure 3: Figure 3 shows the first purification step of the fungal elicitor of the invention in a profile obtained from FPLC chromatographical separation using an anion exchange Q matrix balanced at 7.5 (Pharmacia). Elution was performed with discontinuous increasing NaCl gradient (0-100%). The activity is concentrated in peak I.

Figure 4: Figure 4 shows the second purification stage of the fungal elicitor of the invention in a profile obtained from FPLC chromatographical separation using an hydrophobic interaction matrix Phenyl Superose® HP (Pharmacia) balanced with Tris-HCl (50mM, pH 7.5), EDTA (1mM) and (NH₄)₂SO₄ (1.5 M), and eluted with discontinuous decreasing (NH₄)₂SO₄ gradient (100-0 %). The activity is concentrated in pool IV.

Figure 5: Figure 5 shows proteins present in fractions I to IV (20 µg total charge) obtained by FPLC in Phenyl Superose® HP (Figure 4) separated by SDS-PAGE at 12%. The activity is concentrated in pool IV. The arrow indicates the active elicitor protein post-purified to homogeneity (Figure 6).

Figure 6: Figure 6 shows SDS-PAGE at 10% of the active subfraction (7 µg total protein) obtained by re-chromatography of pool IV via Phenyl Superose® HP eluted under the same conditions as mentioned in Figure 4, with a gradual (NH₄)₂SO₄ inverse gradient (100-0 %). The active protein elutes from the Phenyl Superose® HP column at a concentration of (NH₄)₂SO₄ of 0.5 M.

Figure 7: Figure 7 shows a picture of plants treated and non-treated with the elicitor of the invention (2.5 µg protein/ml) and after infection with the virulent isolate (M11) of *C. acutatum* at 40 days post- inoculation. The top row depicts the plants pre-treated with the elicitor and the bottom row depicts the plants treated with water (virulence control) respectively, 48 h before inoculation with pathogen M11.

Figure 8: Figure 8 shows pictures of the accumulation of reactive oxygen species (ROS) 4 h after treatment by elicitor aspersion (10 µg protein/ml) in leaves of strawberry cv Pájaro. (A) H₂O₂ accumulation detected by DAB (diaminobenzoic acid method), (B) O₂⁻ accumulation (superoxyde anion) detected by NBT (nitroblue tetrazolium method) and (C) control of water-treated leaf. Scale bars indicate 100 µm.

Figure 9: Figure 9 shows pictures of accumulation of self-fluorescent species after treatment by elicitor infiltration (50 µl, 10 µg protein /ml) in strawberry cv. Pájaro leaves. (A) Leaf treated at time zero or treated with water, (B) fluorescence 12 hours after treatment and (C) fluorescence 72 hours after treatment. Pictures were taken in a fluorescent magnifier (320 nm, Leitz). Scale bars indicate 300 µm.

Figure 10: Figure 10 shows pictures of the accumulation of callose in strawberry cv. Pájaro leaves 7 days after treatment by aspersion with the elicitor (10 µg protein/ml; A) or water (control; B); or 2 days post-inoculation with the virulent isolate of *C. acutatum* M11 treated 7 days before with elicitor (10 µg protein /ml; C); and control of plants only infected with M11 (D). Scale bars indicate 100 µm.

Figure 11: Figure 11 show a graph depicting accumulation of salicylic acid in strawberry cv. Pájaro leaves after treatment by aspersion of water □ , BTH (*S-methyl benzo*[1,2,3]thiadiazole-7-carbothiate acid) an analogue to SA (0.5 mM) ◻ and elicitor (15 µg protein/ml) ■.

Figure 12: Figure 12 shows the experimental scheme, the aspect of strawberry cv. Pájaro plants after different treatments and the DSR values after 40 DAI. One of the plants' leaves was treated with the elicitor (arrow) 7 days before infecting the rest of the aerial part by aspersion of the virulent isolate M11 of *C. acutatum* (1.5 x10⁶ conidia/ml). (A) plants pre-treated with elicitor (5 µg protein/ml), (B) plants pre-

treated with BTH (0.5 mM), (C) plants pre-treated with SA (0.5 mM) and (D) with water. DSR means Disease Severity Rating.

Figure 13: Figure 13 shows a graph depicting the disease's symptomatology in several strawberry cultivars pre-treated with the elicitor (10 µg protein/ml) derived from *A. strictum* SS71. DSR means Disease Severity Rating.

Figure 14: Figure 14 shows a graph depicting NO (nitric oxide) and ROS (H₂O₂) production measurements in tomato (*Solanum lycopersicon*) cell culture by fluorescent probes. DAF-FMDA fluorescent probe was used for NO detection and H₂DCF-DA probe was used for ROS detection, in both cases $\lambda_{\text{exi}} = 480 \text{ nm}$; $\lambda_{\text{emi}} = 525 \text{ nm}$. Incubation time was 30 minutes at room temperature. The elicitor was used at a concentration of 10 µg/ml for NO and 5 µg/ml for ROS; xylanase (inductor control) at 100 µg/ml for NO and 10 µg/ml for ROS.

Figure 15: Figure 15 shows pictures of the maximum production of intracellular hydrogen peroxide with Dichlorofluorescein diacetate (DCFH-DA) fluorescent probe in *Arabidopsis thaliana* leaves observed by fluorescent microscopy (UV-light). Pannel (A) corresponds to foliar tissue, control of plants treated by aspersion with water 2 hpt (hours post treatment) while panel (B) corresponds to treatment with elicitor at the same time (2 hpt). Scale bars indicate 100 µm.

Figure 16: Figure 16 shows pictures depicting evolution through time of superoxide radical generation as detected by dyeing with NBT in *Arabidopsis thaliana* leaves treated with elicitor 2 hpt (A), 4 hpt (B) and 6 hpt (C), and the respective controls thereof (treated with water) at each time (D-F).

Figure 17: Figure 17 shows the amino acid sequences (Edman method) of the three analyzed fragments (triptych digestion) of the 34 kDa defense elicitor polypeptide of the present invention isolated from *A. strictum*.

Figure 18: Figure 18 shows the nucleotide sequence encoding the polypeptide with elicitory activity of the present invention, A: Full nucleotide sequence of mature transcript or complementary DNA (cDNA) (SEQ ID No. 1); B Nucleotide sequences producing the maximum similarity values and source species thereof by Blast X.

Figure 19: (A): Elicitor protein sequence derived from cDNA nucleotide sequence (SEQ ID No: 2) is shown; (B): Amino acid sequences producing maximum

similarity values and source species obtained by Blast P; (C): structure of a subtilisin obtained from *Trichoderma koningii* indicating I9 inhibitor domain and S8 catalytic domain. It is shown that the obtained sequences that are fragments of the invention (34 kDa plant defense elicitor protein) are within the protein catalytic domain (peptidase S8). Each domain amino acid length is also shown.

Figure 20: Figure 20 shows absorbance shifts at $\lambda=405$ nm over time. The curves indicate the proteolytic activity of elicitor protein at 15 $\mu\text{g/ml}$ ($\blacktriangle$) and subtilisin of *Bacillus subtilis* (0.04 $\mu\text{g/ml}$) used as positive control ($\blacksquare$). Curve ($\blacklozenge$) indicates the self-proteolysis activity of the chromogenic substrate. Absorbance increase is due to the enzymatic reaction of proteolysis of chromogenic substrate N-Suc-Ala-Ala-Pro-Phe-p-NA by releasing p-NA ($\lambda=405\text{nm}$).

DETAILED DESCRIPTION OF THE INVENTION

DEFINITIONS:

For the purposes of the present patent application, the terms “elicitor or elicitors” refers to any compound capable of inducing any type of defense response in a plant. Elicitors can be molecules of very different kind: proteins, carbohydrates, lipids; small peptides, small compounds of heterogeneous origin, such as secondary metabolites, sugar and/or amino acid derivatives, fatty acids and combinations thereof.

Elicitory Capacity has the same meaning as inducing activity of the defense against stress in plants, e.g., biotic stress.

On the other hand, as used herein “Induced Resistance” (IR), refers to the phenomenon whereby a plant subjected to the appropriate stimulation of its defense by previous exposure to an elicitor acquires an increased level of resistance against pathogens.

Anthrachnose is a fungal disease that produces holonecrosis in the vegetative part of the plant. The infective form of *Colletotrichum spp.* species causing anthrachnose is conidia which, upon germination, penetrate through stomas, tricommas, or directly through the plant leaves epidermis and attack the conducting tissue (xylem), causing petiole girdling. Symptoms start to appear in petiole’s upper portion

and proceed to attack the crown (modified stem), resulting in the death of the plant. Assessment on the severity of anthracnose symptoms is performed in the petiole according to the scale set by Delp and Milholand (Delp and Milholand, 1980. Plant Dis. 64, 1071-1073) which defines a Disease Severity Rating (DSR). This DSR scale ranges from 1 to 5 increasing in accordance with the severity of the disease symptoms as determined in the petiole. The different severity levels are classified as follows:

- Infection Degree # 1: without lesions.
- Infection Degree # 2: lesions shorter than 3 mm long and shallow, dark stains along the petiole (small black spots).
- Infection Degree # 3: lesions between 3-10 mm long, dark stain generally surrounded by red colour.
- Infection Degree # 4: severe lesions and girdling of petiole, which can affect up to 50% of its length.
- Infection Degree # 5: very severe lesion, with girdling of petiole, which can affect more than 50% of its length and/or dead plant.

The protocol used to evaluate anthracnose evolution in the present application was as follows:

- 1) Lesions are assessed in the petioles of the three fully expanded youngest leaves.
- 2) In case there are several degrees of symptoms in the same plant, the maximum degree at the time of observation is used.
- 3) Disease symptoms are assessed 9, 21, 30, 40 days after inoculation (dpi: days post-inoculation) with the virulent pathogen, in accordance with the enhanced procedure by Salazar *et al.*, 2001 (REDBIO Brasil) and 2002 (REDBIO Argentina).

For practical and simplicity purposes when presenting the results in the present application, only the degrees of the symptoms 40 days after inoculation (40 dpi) for each phytopathological assay are informed herein.

Disease evolution and full recovery of the plant lot were considered as assessment standards. Plant recovery is determined by the DSR at the end of the assessment, i.e., 40 days (DSR₄₀), wherein:

- DSR₄₀=1, full recovery or lack of disease.
- DSR₄₀=2, partial recovery.
- DSR₄₀=3 a 5, disease persistence.

Plant recovery gives a measurement of the efficiency of the inducer protection regarding the product used in the plant treatment.

This application provides an elicitor that enables the prevention and/or treatment of plant diseases, such as anthracnose. More particularly, the present invention provides a polypeptide codified by nucleotide sequence SEQ ID No: 1 or sequences at least 90% homologous to the same. In a preferred embodiment, such polypeptide comprises amino acid sequence SEQ ID No: 2 or sequences at least 90% homologous to the same, wherein such polypeptide has elicitory activity. In another more preferred embodiment, the polypeptide of the present invention is derived from a strain of *Acremonium strictum*, preferably such strain is the strain *Acremonium strictum* SS71, deposited pursuant to the Treaty of Budapest on December 14, 2010 at the German deposit centre DSMZ under access code DSM 24396.

The polypeptide of the present invention was obtained after assessing several local isolates of different fungal pathogenic strains of strawberries from the North West region of Argentina, many of which correspond to the different species of *Colletotrichum* comprising the fungal complex responsible for anthracnose in the culture of strawberries: *C. fragariae*, *C. acutatum*, *C. gloeosporioides*. As a result of this assessment, the strain SS71, identified as *Acremonium strictum* which is the object of the invention, was isolated and purified, being virulent for some strawberry cultivars (i.e. cv. Chandler), while it is completely avirulent for other strawberry cultivars such as strawberry cv. Pájaro. Strain SS71 of *Acremonium strictum* expresses a polypeptide having an amino acid sequence SEQ ID No: 2 or sequences at least 90% homologous to the same, wherein such polypeptide has elicitory activity.

From the analysis carried out in the different isolates, it can be seen that the plant/pathogen interaction is highly specific, i.e., it depends on the genotype of the plant and of the pathogen (pathovar or race). Different pathovars can affect a certain strawberry genotype in different severity degrees, and vice versa, different strawberry cultivars and varieties thereof respond in different ways when challenged with the same pathogenic isolate.

A Cross-Protection system in cv. Pájaro between avirulent isolate *A. strictum* SS71 and a virulent isolate of *C. acutatum* (M11) was established. For example, this system became apparent inoculating firstly the aerial parts of healthy plants with live conidia of isolate SS71 and after three days with live conidia of isolate M11, observing that no disease was produced. Cells in conidial state were used.

It is also shown that cv. Pájaro plants after infection with *A. strictum* SS71 acquire resistance against virulent strains of *Colletotrichum* spp., *Botrytis cinera* and *Xanthomonas fragariae*. It was also found that this protection is produced as a result of the interaction between cultivar Pájaro and the avirulent pathovar, inducing a SAR-type response.

This finding has interesting implications to generate an agronomical management of culture diseases, with minor impact on human and environmental health.

In a preferred embodiment, field implementation of an agronomical biocontrol system can be performed based on cross-protection, inoculating plants directly with the living strain or conidia of SS71 of *A. strictum*. Considering that even though the strain is avirulent against cv. Pájaro, it is capable of inducing disease in susceptible varieties, it is desirable to obtain non-pathogenic extracts containing elicitory capacity to produce formulations that trigger the defensive response, and it is better to obtain and use the compound having elicitory activity in order to prepare a composition for inducing a plant's defense system.

Another preferred embodiment is applying directly the elicitor molecule of the present invention to immunize and prevent fungal diseases of cultures, such as

strawberry. Apart from being environmentally safe, this technology can further be an agronomically applicable alternative because it is harmless.

Cross-protection was observed against *C. acutatum* M11 previously inoculating cv. Pájaro plants with a suspension of live conidia of strain SS71 of *A. strictum* at a concentration of 1.5×10^6 conidia/ml.

In addition, the conidial extract of *A. strictum* SS71 obtained by sonication (CE) was analyzed and the evolution of disease symptoms was analyzed (DSR) over time (dpi) in double-treatment assays. Disease symptom analysis was done using the extremes, 1 when there was full recovery (lack of anthracnose symptoms) and 5 when there was no recovery.

When plants were sprayed with conidial extract obtained by cellular sonication to disrupt cells (CE), disease symptoms degrees similar to those of Cross-Protection controls were achieved, showing the same full recovery (DSR=1) after 40 days, similar to such controls (Figure 1); i.e. CE shows high efficiency protection against the virulent strain causing anthracnose disease. This result indicates that: (a) the presence of live conidia of the avirulent pathogen (*A. strictum* SS71) of the invention is not required to trigger the resistance against the virulent pathogen (*C. acutatum* M11); (b) the medium containing conidia of the pathogen, inactivated by cell lysis physical treatment, is capable of retaining inducing activity present in such conidia in active state with equal protection efficiency.

The presence of the active agent in the liquid culture supernatant of the avirulent pathogen of *A. strictum* of the invention grown under optimal conditions to stationary phase was analyzed. For this purpose, a conventional potatoe-glucose (PG) medium was used and the activity present in the cell-free supernatant (SN) was measured. It was seen that the supernatant of the culture grown in the PG medium (SN) reaches DSR= 1 at 30 days, a value kept during the entire assessment period (DSR₄₀=1; Figure 1), thus, SN treatment leads to early full recovery of plants. This means that SN develops maximum protection efficiency (DSR₄₀=1) in the same way as the Cross-Protection control. This result indicates that activity with maximum

protection efficiency is obtained from the liquid culture supernatant, implying that the active ingredient would be excreted to the culture medium.

Based on the above-mentioned results, it is seen that maximum protection efficiency is obtained from all assayed fractions of *A. strictum* SS71 of the invention, (DSR=1), in the same way as Cross-Protection control with CE and SN, thus it is concluded that they both present highly effective protection activity. These experiments confirm that the “inducing power” can be recovered in CE and SN portions, with which maximum protection is attained.

The protocol and experimental design used to assess the protection activity in the different fractions obtained (CE and SN) are detailed in Table 2 (see examples).

In order to characterize the elicitor, the chemical nature of the active ingredients and technological possibilities thereof were determined. The thermal stability of the elicitory activity was analyzed. For this purpose, the supernatant SN containing the active ingredient compound with “inducing power” at a high purity degree was used. In this sense, the SN was subjected to two thermal treatments with different intensity: (A) heating to boiling (100°C) for 15 minutes (SN1), being sufficient for large proteins (in general, molecular weight greater than 10,000 Da) to be denaturalized, and insufficient to destroy other compounds of different chemical nature, such as carbohydrates, lipids, etc.; and (B) autoclaving (121°C) for 15 minutes (SN2), being a more severe treatment which destroys the majority of compounds except for low molecular weight metabolites resistant to high temperatures, thermoresistant peptides, etc.

Figure 2A shows the results indicating that the supernatant subjected to both thermal treatments generates an evolution of the disease which is very similar to the *C. acutatum* M11 positive control. Both SN1 and SN2 as well as the virulent strain control show, DSR= 5 ; in the case of the heated supernatants such rating is achieved after 30 days, while in positive control it is reached after 21 days. In all cases, plants die after treatment. From this it is concluded that the defense inducing activity is practically completely lost upon severe heat exposure.

As shown in Figure 2B, the same effect is seen when the SN is incubated with Proteinase K overnight (12 hours) under optimal conditions for such enzyme activity (50°C), which is broadly used for proteolytic digestion.

The results shown indicate that the main active compound participating in the induction of the defensive response loses its activity not only because of the less severe thermal treatment (heating at 100°C for 15 minutes), probably by cleavage of peptide bonds, but also by action of a protease (Proteinase K), thus concluding that it is a compound of protein nature.

For a better understanding of the obtention procedure of the polypeptide of the present invention, an example embodiment is described herein to attribute the protection effect against *C. acutatum* associated with the full supernatant derived from the avirulent pathovar of *Acremonium strictum* (isolate SS71) of the invention to a single purified molecule. In this case, firstly the extracellular protein/s with inducing activity was/were identified. In order to do so, a purification protocol was designed and optimized to recover the protein in large quantities and of high purity degree (single band on SDS-PAGE or single peak on FPLC), to obtain such a protocol experiments were performed in 2 steps:

(a) Optimizing the fungal culture conditions for maximum production of elicitory activity.

Plant full protection is achieved by pre-treatment of plants with the axenic culture supernatant of the isolate *Acremonium strictum* SS71 in PG medium (potatoe-glucose, non-buffered, initial pH =6.75), grown at 28°C, in static form (no stirring), with continuous white light until reaching the to stationary growth phase (21 days). Total protein content in the final supernatant was 8.43 µg proteins/ ml.

(b) Isolating the extracellular protein with inducing activity form PG medium:

As shown in the examples, the activity in each purification step was followed by two parallel methods: (a) ROS production (H_2O_2 and $O_2^{\cdot-}$) 4 h post-, and (b) protection against the virulent isolate M11 of *C. acutatum*.

The purification protocol includes the following steps:

I. Initial processing for conservation:

To remove the mycelium, cultures were centrifuged at 16,300g, for 30 minutes, at 4°C. The supernatant was recovered and filtered through diathomea earth and then through a filtering membrane with a pore-diameter of 0.22 µm. This fraction corresponds to the axenic supernatant (cell-free) 1X (undiluted) which was kept frozen at -20°C until later use.

II. Concentration of sample components: The 1X Supernatant was concentrated 10 times by lyophilisation and then an additional 4X by adding PEG to the sample and dialysing overnight at 4°C with a membrane of 12 kDa cut-off. at 4 (ON).

III. Removing majority pollutants: This part was performed in two steps.

(a) ultrafiltration by using a membrane of 10 kDa cut-off: the volume of the concentrated supernatant was reduced 10 times (in total 400X), maintaining the inducing activity retained by the membrane (molecular weight greater than 10kDa);

b) Anion exchange chromatography: the retained solution with major activity was thereafter fractioned using a FPLC system (Pharmacia), and a column packed with Q Sepharose® Fast Flow matrix (Q) (Pharmacia-FPLC) balanced in Tris-HCl buffer pH 7.5 and eluted by increasing ionic strength: discontinuous increasing NaCl gradient at concentrations of 0.24M (8 min), 0.38M (8 min) and 1M (10 min). Eluted fractions were collected together in 4 protein pools which were phytopathologically assayed (Figure 3). The defense eliciting activity was found to be concentrated in peak I.

Plant pre-treatment with the Q column flow-through at pH 7.5 produces full protection against virulent isolate M11, while high – though not total – protection is achieved with protein pool II which weakly interact with the matrix (eluted with 0.24M NaCl).

These results lead to conclude that the liquid culture supernatant of avirulent isolate *Acremonium strictum* SS71 of the invention contains two or more proteins having inducing defense activity, proteins presenting different pI. However, since the maximum induction activity of resistance to anthracnose is obtained from the portion of proteins that do not interact with the anionic exchange matrix Q at pH 7.5, this basic protein pool (pI>8) was selected to continue the purification.

IV. Removing very closely related trace pollutants (“Polishing”):

Proteins unbound to the Q matrix (pool I) were separated by chromatography through a Hydrophobic Interaction matrix. For such purpose, pool I was cultured, under high ionic strength conditions, in a Phenyl Superose® HP (PS) hydrophobic interaction column adapted to a FPLC system. The matrix was previously balanced with Tris HCl buffer 50 mM pH 7.5 adding EDTA 1mM and $(\text{NH}_4)_2\text{SO}_4$ at 1.5M concentration, and after culturing it was eluted by decreasing the ionic strength by applying a $(\text{NH}_4)_2\text{SO}_4$ decreasing concentration gradient, thereby obtaining the profile shown in Figure 4. The elicitor inducing activity was found to be concentrated in peak IV.

When proteins unbound to the Q matrix were run through a PS matrix, protection activity was found to be divided among three fractions eluted by decreasing the ionic strength: pools II, III and IV, which upon observation in a 12% polyacrylamide gel did not contain single protein bands (Figure 5). The main activity is concentrated in peak IV. A new chromatographical separation was performed using the same system (matrix and buffers), but applying a $(\text{NH}_4)_2\text{SO}_4$ discontinuous gradient having 5 intermediate steps. Using this procedure 10 chromatographical peaks were obtained, which contained single proteins as observed by single bands in SDS-PAGE (10%) dyed with Coomassie® Blue-R. Defense elicitor activity detection was carried out spraying one leaf in plants ($n=4$) with each of the obtained fractions conditioned to a concentration of 2.5 μg protein/ml. Results showed that peak 7 which is eluted with $(\text{NH}_4)_2\text{SO}_4$ at 0.5 M concentration, provides plants with full protection against anthracnose ($\text{DSR}_{40}=1$) and also induces ROS production (NBT and DAB positive dyes).

As shown in Figure 6, when peak 7 is separated by SDS-PAGE at 10% a single band is intensely coloured with Coomassie® Blue-R. The active protein elutes from the column with 0.5 M of $(\text{NH}_4)_2\text{SO}_4$.

A 34 kDa basic protein was purified to homogeneity, which is capable of inducing systemic resistance against the attack by virulent isolate M11 of *C. acutatum*.

The elicitor polypeptide is a new protein, different from other previously reported proteases. To confirm this, even though no accessions of protein sequences described in *Acremonium spp.* were registered among the top 100 hits obtained by Blast-P performed with the elicitor protein sequence, the identity degree thereof was studied with all the proteins that have been reported as proteases or protease-like in this genus.

Table 1 summarizes the characteristics of amino acid sequences of *Acremonium* genus proteins (producing organism, source, extension, Mr, number of amino acids and function) and the comparison thereof with the elicitor protein (percentages of identical amino acids and gaps obtained from alignment with each of them).

In all genomic and proteomic databases, only 6 protease-like protein sequences produced by different species of *Acremonium spp.* have been reported. Two which were determined on an experimental basis and correspond to amino terminal sequences partial sequence) with proved proteolytic function (No. Acc. P85156, Sub-E1 of 40 a.a.) (No. Acc. P85157, Sub-E2 of 18 a.a.), while the remaining four are sequences inferred by homology from genomic DNA depositions. Among these later sequences, an internal protease fragment (No. Acc. AAC09289.1, Pr.) and three full length sequences corresponding to a subtilisin-like serine protease (No. Acc. BAF62454.1; Sub-E3), an alkali proteinase precursor (No. Acc. BAA00765.1; Pr.Alc) and a cephalosporine C acetylhydrolase (No. Acc. CAB87194.1; AcH) are described.

Table 1. Description of protease-like proteins of *Acremonium spp.* recorded in protein databases (Uniprot).

<i>Acremonium spp.</i> proteins described							Comparison to elicitor	
Accession No.	Description	Organism	Protein Existence	Function	Mr, Extension	Abbrev	Ident. (%)	Gaps (%)
P85156 (ASE1_ACR SP)	Subtilisin-like serine protease AS-E1	<i>Acremonium</i> sp.	Experimental evidence	Prothrombin and fibrinogen cleavage, and plasma clotting inhibition.	Amine terminus 40 aa 4.327 kDa	Sub-E2	72.50 (29/40)	0 (0/40)
P85157 (ASE2_ACR SP)	Subtilisin-like serine protease AS-E2	<i>Acremonium</i> sp.	Experimental evidence	Prothrombin and fibrinogen cleavage, and plasma clotting inhibition.	Amine terminus 18 aa 1.914 kDa	Sub-E1	61.11 (11/18)	0 (0/18)

AAC09289.1	Protease P1	<i>Acremonium coenophialum</i>	Inferred by homology (genomic DNA)		Internal fragment 92 aa	Pr.	59.78 (55/92)	0 (0/92)
BAF62454.1	Subtilisin -like serine protease	<i>Acremonium</i> sp. (F11177)	Predicted (genomic DNA)	Prothrombin cleavage	Full 535 aa 58.371 kDa	Sub-E3	39.17 (152/388)	13.78 (62/450)
BAA00765.1	Alkali protease precursor	<i>Acremonium chrysogenum</i>	Inferred by homology (genomic DNA)		Full 402 aa 42.099 kDa	Pr.Alc	44.8 (168/375)	9.42 (39/414)
CAB87194.1	cephalosporine C acetylhydrolase	<i>Acremonium chrysogenum</i>	Inferred by homology (genomic DNA)	Non-specific esterase. Deletion of cephalosporine C acetyl group	Full 383 aa 38.223 kDa	AcH	53.68 (204/280)	2.06 (8/388)

As shown in Table 1, elicitor protein alignments with Sub-E1, Sub-E2 and Pr fragments result in high identity values ranging between around 59.8 and 72.5% without breaking gaps in the sequence alignments. However, the short amino acid sequence (40 to 92 aa) of these proteins prevent any homology inference with the elicitor protein, since more than 75% of their sequence is unknown.

On the other hand, in relation to the full length proteases reported in *Acremonium* spp., the elicitor protein shows 39.2% of identity with Sub-E3 and 44.8% of identity with the Pr.Alc alkali protease; however, in both alignments very high gap percentages are obtained (13.8% and 9.4%, respectively). Sub-E3 is the only full length sequence subtilisin-like serine protease described in *Acremonium* spp. which in addition presents experimentally proven proteolytic activity (Liu et al., 2007). Nevertheless, this protease presents a very low similarity percentage (39.2%) as compared to the defense -inducing subtilisin isolated from *A. strictum*.

Surprisingly, the highest identity value (53.7% of identity and 2.1% of gaps) of the elicitor protein corresponds to the protein AcH of *A. Chrysogenum*. It is a non-specific esterase, which acts by eliminating the antibiotic cephalosporine C acetyl group. Even though it lacks proteolytic activity, AcH was included in the analysis because of its sequence similarity to serine proteases.

The following comparison shows an alignment performed with the amino terminal sequences of all proteases reported in *Acremonium* spp., including the elicitor protein, showing the variability of the amino terminal region between these proteases.

Elicitor	106	YTASTRPGTAQ
AcH	105	IQAESQEPGTAD
Sub-E1	1	DVTTAAY
Sub-E3	146	DSELEKATLSFATFNKAAEEVDATN
Pr. Alc.	120	ALVTQATPSSYAL
Sub-E2	1	YVSG

The assays performed to determine the elicitor activity are shown in Figure 7. The plants treated with the elicitor exhibit the same general status as the Cross-Protection control plants, and are completely healthy plants ($DSR_{40}=1$) of great size. It was also verified that fractions derived from the avirulent pathogen isolate SS71 of *A. strictum* of the invention do not present any type of virulence against a *Fragaria vesca* (wild strawberry) genotype which is highly susceptible to this type of fungal pathogens. These results are consistent with the possibility of using these fractions to confer field protection against anthracnose in cultured strawberry (*F. x ananassa*) cv. Pájaro.

The protocol and experimental design used to assess the induction of resistance against anthracnose by the different purification fractions obtained are detailed in Table 2 (see examples).

The defense response induced by fractions of the avirulent pathogen and by the polypeptide having elicitory activity of the present invention in strawberries has been characterized.

The events associated with the plant defense produced by the polypeptide of the invention derived from the avirulent pathogen isolate SS71 of *A. strictum* were analyzed.

Defense reactions were assessed in strawberry plant leaves of the Pájaro cultivar treated with active pre-purified extracts derived from isolate SS71 cultures of the invention, and such results were subsequently confirmed with the pure inducing protein. In these assessments, accumulation of reactive oxygen species (H_2O_2 and O_2^-) associated with the oxidative burst; nitric oxide (NO) production; accumulation of phenolic compounds; microscopic hypersensitive response (micro-HR); reinforcement of cell wall by lignification and by callose deposition; accumulation of salicylic acid and expression of genes associated with the defense response and the systemic acquired resistance (SAR) e.g. PR-proteins, were observed. The

aforementioned indicate that general induced plant defense is obtained, found in all plant species studied as of today. Some of these responses were studied and found in other plant species after application of the subtilisin protein isolated from *A. strictum* (tomato and Arabidopsis). It can be concluded from these experiments that there is a general effect in different cultures against fungal and bacterial pathogens, which is also grounded by positive resistance results against *Colletotrichum spp.* (biotrophic fungus), *Botrytis cinerea* (necrotrophic fungus) and *Xanthomonas fragariae* (bacteria). As mentioned above, the response against the elicitor of the invention includes accumulation of salicylic acid, which induces resistance not only against fungal and bacterial pathogens but also against viruses. Consequently, the present invention is also useful to induce resistance against viruses in plants. The oxidative burst was assessed by the accumulation of ROS. It was analyzed whether the protective effect observed in plants pre-treated with the elicitor was preceded by biochemical markers usually associated to the defense, and also the accumulation of superoxide ion radical (O_2^-) and hydrogen peroxide (H_2O_2) by histochemical dyeing with NBT (nitroblue tetrazolium) and DAB (diaminobenzidine), respectively.

The production of H_2O_2 (DAB +) and O_2^- ion (NBT +) was observed in application areas 2 hours after treatment (hpt) with the elicitor. Both, proximal leaflets as well as distal leaves (non-treated) were analyzed. Maximum production was observed for both ROS species 4 hpt, as shown in Fig. 8A for H_2O_2 and Fig. 8B for O_2^- ion. However, the superoxide ion detection became almost histochemically neglectable at later time points, while hydrogen peroxide levels continued at a high detection level 12 hpt. In contrast, no production of any reactive oxygen species was observed in control plants treated with either PG medium or water (Fig. 8C).

When pure protein was infiltrated through the abaxial side of a plant leaflet, ROS production was observed (DAB + and NBT+ dyes) in discrete micro sites, uniformly distributed throughout the surface of the infiltrated leaf (proximal tissue) and unfiltered leaves (distal tissue) known as systemic micro-oxidative bursts.

The accumulation of self-fluorescent compounds was assessed. Results shown in Figure 9 demonstrate that leaves infiltrated with active extracts or the pure protein exhibit a strong self-fluorescent signal at 329 nm observed under UV light at

the infiltration point, which is accompanied by a tissue necrotic lesion, whereas leaves infiltrated with water (control) do not present detectable self-fluorescence or tissue necrosis. The self-fluorescence assessment was carried out at the infiltration point at different times after induction. At 12 hpt (hours post-treatment) under UV light the apparent presence of a yellow self-fluorescence was observed (Fig. 9B), with gradual increased intensity, reaching its maximum point 72 hpt (Fig. 9C). At the infiltration point of control plants, no self-fluorescence is observed (Figure 9A). Yellow self-fluorescence is probably due to the release of phenolic compounds derived from the phenylpropanoid route (i.e. phytoalexins), which is strongly activated during HR.

Changes in cell wall composition induced by the defense response were also analyzed, by assessing deposition of callose. For this purpose, water (control), cell extracts with defense-inducing activity and purified subtilisin protein were analyzed for capacity to induce accumulation of callose in strawberry plant cell walls. Figure 10 shows plants accumulating callose 7 days after treatment with the pure elicitor protein from strain SS71 (Fig. 10B), whereas no accumulation is detected in plants treated with water (Fig. 10A). However, figure 10 also shows that callose is deposited in even higher concentrations in plants infected with the virulent isolate M11 of *C. acutatum*, in plants which had previously been induced with the elicitor 7 days prior to infection (Fig. 10C). Deposition of callose was firstly observed to occur in isolated epidermal cells and subsequently accumulating in contiguous cell groups forming a matrix acting as a sheer physical barrier to stop pathogen invasion.

Salicylic acid (SA) was quantified in phloem of strawberry plants infiltrated with pure elicitor protein at a concentration of 2.5 µg protein/ml. SA was recovered from petioles at different time points (0, 24, 48, 72 and 96 hours) after treatment (hpt), purified by reverse-phase chromatography and quantified by fluorescence spectroscopy excitation at 296 nm.

Plants treated with BTH as well as the purified subtilisin protein showed significant increase in SA concentrations in the phloem 72 hpt, reaching a concentration of 3.72 µg/ml in the phloematic exudate, while water-treated control plants presented a 2.5 times lower value (1.45 µg/ml exudate). Figure 11 shows that

plants treated with water did not present a significant increase in SA throughout the experiment, while plants treated with elicitor showed a significant increase 72 hpt, as well as BTH-treated plants (0.5 mM), used as a SAR-responsive positive control plant.

Experiments were conducted in order to determine if extracts having defense-inducing activity and the pure protein (subtilisin) were capable of translocating the defense signal and thereby inducing a SAR-like response. For this purpose, spraying of a single plant leaf was performed with the pure protein (5 µg protein/ml), and after 7 days (7dpt), the rest of the plant was infected with a conidial suspension of virulent isolate M11. BTH and SA were used as SAR-inducing positive controls, while a negative plant control was obtained by spraying with water.

As shown in the table appended to Figure 12, plants pre-treated by spraying a single leaf with the elicitor of the present invention present a DSR lower than 1.5 as of 40 days post-inoculation, as well as plants treated with BTH and SA, while plants pre-treated with water die 10 dpi (DSR=5). This confirms that the elicitor provides plants with a systemic-like protection, since plants where only one leaf had been treated didn't exhibit disease symptoms.

In order to investigate the resistance-inducing action of the elicitor polypeptide of the present invention a defense assay was performed in other strawberry cultivars and in different plant species. The pure elicitor derived from isolate SS71 of the invention provides protection to different strawberry cultivars when challenged with virulent strains of *C. acutatum*.

Different commercial varieties of strawberry presenting either an incompatible-like interaction (e.g. cvs. Pájaro and Camarosa) or a compatible-like interaction (e.g. cvs. Milsei Tudla, and Chandler) were tested for pathogen defense-induction after treatment with the elicitor from SS71. After treatment with the inducer, all plants were challenged with a virulent strain for each cultivar, *C. acutatum* M11 (isolate of cv. Chandler in Manantial-Tucumán), MP3 (isolate of

Aroma plants in Mar del Plata) or LCF 1-05 (isolate from fruits of Camarosa Lules-Tucumán).

Figure 13 shows that after treatment with the elicitor, cvs. Pájaro and Camarosa do not present disease symptoms (DSR=1) as of 40 dpi, while cvs. M. Tudla and Chandler plants presented different degrees of disease development, depending on the isolate used for infection. These results demonstrate that in general, all varieties exhibit lower disease symptom values than control plants, and in most cases showed a remarkable recovery 30 dpi (DSR= 1-2).

The elicitor derived from SS71 develops high efficiency protection against anthracnose in SS71-resistant cvs. (wherein it behaves on an avirulent basis), while leading to partial protection in SS71-susceptible cultivars (wherein it behaves on a virulent basis).

Figure 13 also shows that the protection degree particularly depends on the isolate being used. While the elicitor can rapidly control the infection caused by M11 in all the cultivars analyzed, the disease protection differs with isolates MP3 and LCF1.

These results conclude that the elicitor of the invention has a broad-spectrum inducing activity since it is capable of inducing defense responses in other cultivars and against other pathogens, though at different protection degrees.

The induction of reactions associated to defense in other plant species was studied. For example, the effect of the elicitor on a tomato cell culture (*Lycopersicon esculentum*) was investigated, analyzing if the elicitor is capable of inducing the accumulation of ROS and NO (nitric oxide) as biochemical markers of the plant defense. Purified protein (subtilisin) was added at a final concentration of 5 µg/ml or 10 µg/ml to cell cultures to assess ROS or NO evolution, respectively, by fluorescence measurements. Figure 14 shows that while tomato cells exhibit strong and rapid ROS and NO accumulation, during the first 30 minutes after adding the elicitor. Control cells did not exhibit any ROS or NO accumulation above baseline levels.

In addition, the elicitor capacity to induce ROS production in *Arabidopsis thaliana*- plants was studied. For this purpose, hydrogen peroxide production and superoxide radical production were studied in parallel. Intracellular hydrogen peroxide was assessed with a Dichlorofluorescein diacetate (DCFH-DA) fluorescent probe, observing a peak of burst as a consequence of the treatment with the pure elicitor protein. This result confirms the capacity of the protein of the invention to induce hydrogen peroxide intracellular accumulation, despite the fact that the accumulation peak does not correspond exactly to the time point to that observed for strawberries wherein the maximum peak is produced 4 hpt (Figure 15).

The accumulation of superoxide radical in leaves of *A. thaliana* was assessed with NBT (see above), observing an accumulation peak 4 hpt, coinciding with the generation of superoxide in strawberries, while control leaves did not present any reaction (Figure 16).

In order to provide a chemical and molecular characterization of the resistance inducing activity polypeptide of the present invention, the molecular weight of this protein was determined by 10% SDS-PAGE (with β -mercaptoethanol using the PD Quest software (Bio-Rad®), giving an approximate value of 34 kDa. The polypeptide presents a pI of around 9.5 determined on an experimental basis by isoelectric focusing electrophoresis.

The NH₂-terminal sequence of the previously reduced and alkylated protein transferred to a PVDF membrane, as well as three-internal-peptide sequences obtained by *in gel* tryptic digestion of the reduced and alkylated protein, were obtained. Figure 17 shows the peptide sequences with 1095.19, 2441.2 and 1938.1 MS/MS molecular mass. Alignment analysis showed that all peptide sequences have, each individually, high similarity with fungal proteases from the subtilisin family. The highest sequence identity values correspond to a subtilisin from *Arthroderma* spp. (or *Trichophyton* spp.) for the peptide with a molecular mass of 2441.2 and a subtilisin protein from *Aspergillus* spp. for the peptide with a molecular mass of 1938.1.

Oligonucleotide primers were designed from the peptide fragment sequence shown in Figure 17, knowing that the first peptide corresponds to the protein amino-

terminal end. The corresponding cDNA sequence was obtained by an amplification protocol corresponding to the entire mature elicitor protein transcript and the deduced nucleotide sequence thereof is shown in Figure 18A. Having access to the entire cDNA sequence of the elicitor, the similarity of this sequence was compared against sequences in the protein and DNA sequence databases, in order to obtain information on protein function and belonging to protein family. From this study it was concluded that the isolated sequence is actually a serine protease of the subtilisin family.

In order to complete the study and confirm the result, this protein affiliation was also studied by Blast P. For such purpose, the amino acid sequence deduced from the nucleotide sequence shown in Figure 18 was used, thereby obtaining the sequence shown in Figure 19A. This analysis confirmed that the isolated sequence corresponds to a serine protease of the subtilisin family (Fig. 19B).

In order to gain a better overview of the relative positions of domains having higher similarity, a complete sequence comparison between the *A. strictum* subtilisin amino acid sequence with sequences belonging to the subtilisin family was performed. For such purpose, subtilisin from *Trichoderma koningii*, *Metarhizium anisopliae* var. *anisopliae*, *Ophiocordyceps sinensis*, *Paecilomyces lilacinus* were selected because of having both high nucleotide (Blast X) and amino acid (Blast P) sequence identity. The structure of the subtilisin of *Trichoderma koningii* was taken as model since it has high sequence identity with the elicitor subtilisin of *A. strictum*. Figure 19C shows the relative position of the sequenced fragments from the elicitor of *A. strictum* in relation to the characterized domains of the subtilisin of *T. koningii*. The results shown let us conclude that the amino-terminal end is located in the region located between the Inhibitor I9 domain and the Peptidase S8 domain having protease function, while the other two sequenced internal peptide sequences are located in the Peptidase S8 domain. The peptidase I9 inhibitor domain was found in the immature form of all referenced subtilisins analyzed.

These results suggest that the immature elicitor protein experiences post-translational maturation, consisting in the cleavage of the inhibitor I9 domain, which can be the signal propeptide for export to the extracellular medium. Based on the

results shown above, we know that that sequences are highly conserved in the domain having protease function, therefore we can infer that such proteins show proteolytic activity.

In order to experimental determine whether the subtilisin-like elicitor protein has a proteolytic function, the capacity thereof was studied using a specific chromogenic substrate (N-Succinyl-Ala-Ala-Pro-Phe p-Nitroanilide) releasing p-NA which absorbs at 405nm when proteolytically cleaved. Figure 20 demonstrates that the elicitor protein (15 µg/ml) acts on the chromogenic substrate producing the proteolysis thereof over time, as well as the subtilisin of *Bacillus subtilis* (0.04 µg/ml) used as positive control.

After being purified to homogeneity, the elicitor protein exhibits proteolytic activity on the subtilisin specific chromogenic substrate, i.e., it has *in vitro* subtilisin-like protease function.

This invention is better illustrated according to the following examples, which are not to be construed as a limitation on the scope thereof. In contrast, it should be clearly understood that other embodiments, modifications and equivalents thereof can be applied, which upon reading the present specification can be suggested by those skilled in the art without departing from the spirit of the present invention and/or scope of the appended claims.

Examples:

Example 1: Materials and media used

Strawberry plants

Fragaria x ananassa Duchesne cultivar Pájaro strawberry plants and wild strawberry *Fragaria vesca* specie were used; all available at Pro/ Frutilla germplasm bank.

The material was produced in three stages: (1) Meristem *in vitro* culture; (2) Rustication; and 3) Stolon plant multiplication.

(1) By meristem *in vitro* culture, plant material was cleaned and multiplied under axenic and controlled growth conditions (temperature: 25°C - photoperiod: 16 h of light). (2) Then, it was rusticated in trays using a mixture of earth and perlite as a

sterile substrate (2:1). After four weeks, plants were transplanted to plastic pots, 8 cm height x 8.5 cm diameter, thereby obtaining mother seedlings. (3) These mother seedlings were grown in growth chambers under controlled temperature (25-27°C), humidity (70%) and photoperiod (16 h), conditions being optimal for stolonization. All plants used for experimental procedures were obtained by fixation of mother seedling stolons (asexual propagation) in sterile substrate under axenic conditions and then further grown under the same growth conditions. Once rooted, around two weeks later, new seedlings were separated from the mother plant and set to grow for another 12- 14 weeks. That is, mother seedlings are grown up to they are overall 14 to 16 weeks old, having at least four fully expanded leaves, representing a relatively early growth stage for the seedling. During this period, seedlings were watered only with distilled water twice a week and did not receive preventive application of fungicides or fertilizers.

A. strictum SS71 /*C. acutatum* M11 cross-protection system response was assessed in cultivar Pájaro, wherein it was defined and characterized.

An ecotype from *Fragaria vesca* wild strawberry was used in all the assays as a strain virulence positive control because of its extreme susceptibility to the strain SS71 of *A. strictum*. This genotype was also used as inactivation control for *A. strictum* SS71 in the fractions derived from such strain to demonstrate that they do not produce any disease, which serves for substantiating the applicability of this biocontrol methodology in the field.

Arabidopsis Plants

Arabidopsis thaliana wild type (ecotype Columbia) seeds were germinated on MS medium (½ diluted) supplemented with 1% sucrose and 0.8% agar. When having two leaves, seedlings were transplanted to a sterile substrate, and were kept in growth chambers under optimal growing conditions (22°C, 70% humidity, 12h of light) until 4 weeks old.

Cell cultures in suspension

Cells cultured in suspension (*Solanum lycopersicon* cv. Money Maker®; line Msk8) were grown at 24 °C in the dark at 125 rpm in MS medium (Duchefa, Haarlem, The Netherlands) supplemented with NAA 5.4 µM, 6-benzyladenine 1 µM and vitamins (Duchefa) as described previously (Felix *et al.*, 1991. Plant Physiol. 97, 19-25).

Fungi:

The following strains were used: SS71 of *Acremonium strictum* of the invention and strain M11 of *Colletotrichum acutatum* for infection. These strains were used in the *A. strictum*/*C. acutatum* cross-protection system defined in cv. Pájaro. In this system, strain SS71 produces the compound with defence elicitory activity, and strain M11 is the virulent strain against cv. Pájaro used for the assessment of the inducing activity exhibited by the increased resistance to anthracnose (produced by M11) in plants previously treated with strain SS71.

To study the protecting elicitory activity against anthracnose in other strawberry cultivars, other strains of *Colletotrichum acutatum* (e.g. MP3, LCF1) were used, having virulent behaviour against the respective cultivars.

Culture media

Avirulent pathogen strains of *A. strictum* of the invention were cultured in agar-potatoe-glucose medium with 1.5% agar (APG 1.5%). After being melt, the medium is cooled to 45-50°C and distributed in sterile Petri plates (15 ml per box), after adding Streptomycin Sulphate (Richet) to a final concentration of 300 µg/ ml. The liquid culture of the strain SS71 of *A. strictum* was carried out in potatoe-glucose (PG) medium which exhibits equal composition as the APG medium without adding agar and is obtained by the identical procedure.

Culture conditions

Strains were kept in conidial suspensions (10^7 - 10^8 conidia/ml) in 50% glycerol and kept frozen at -70°C.

Solid cultures

Cultures of the different strains in solid medium were obtained by seeding mycelium on APG 1.5% medium or by seeding conidia kept in glycerol, and then incubation for 10 days under optimal growth (28°C) and esporulation (continuous white light) conditions.

Liquid cultures

Cultures in liquid medium for the strain of *A. strictum* of the invention were obtained inoculating 40 ml of (PG) culture medium, contained in 100 ml capacity glass containers, with such volume of aqueous conidial suspension to obtain a final concentration of 10^6 conidia/ml culture medium. The conidial suspension was prepared on the assay day from a new plate culture (see “Conidial Suspension Preparation” below). Then, the inoculated liquid medium was incubated under optimal and favourable conditions for sporulation, i.e. 28°C with continuous white light and without stirring up to stationary growing phase (21 days). This culture was called SN.

Cultures were followed by macroscopic and microscopic observations. Macroscopic observation is qualitative, observing: formation of mycelial film on top, colour, turbidity or opacity, compaction degree and solidity. Microscopic observations consisted in observing at 40X magnification, a wet preparation (between slide and cover slip) to assess culture purity and uniformity and the lack of spurious cells indicating any contamination.

Example 2

Conidial Suspension Preparation

The suspension was prepared under sterile conditions from new cultures of strain *A. strictum* SS71 or M11, grown on APG medium at 1.5%. Conidia were collected scratching the colony surface with a sterile loop or spatula. Then, conidia were resuspended in a certain volume of sterile distilled water (5 or 15 ml). Conidia were mixed by vortex for 1 minute and filtered through some lint with a sterile syringe. Conidia were counted in a Neubauer chamber and then depending on the use

intended for the suspension, two different procedures were performed.

As for assays wherein the live conidial suspension of strain SS71 of *A. strictum* or M11 of *C. acutatum* was used to inoculate the plants, the suspension was adjusted by dilution with sterile distilled water, to a conidial concentration of 1.5×10^6 conidia/ml. Finally, Tween® 20 was added to the suspension at 0.1% v/v final concentration, as a tensioactive agent.

As for inoculation assays wherein the strain SS71 of *A. strictum* was used inactivated (see “Phytopathological Assays” below), the avirulent pathogen conidia were inactivated before the dilution performed to adjust the concentration to the desired value. In these cases Tween® 20 was not used so as to avoid a possible interaction between this tensioactive agent and the active compound.

Example 3

Method for obtaining the conidial extract (CE)

The concentrated conidial suspension of avirulent *Acremonium strictum* SS71 of the invention (at 10^8 conidia/ml concentration) was fractioned in 1.5 ml aliquots in 2 ml tubes. Each aliquot was treated by ultrasound until the typical opalescence of the suspension disappeared, obtaining a translucent liquid. For such purpose, the suspension was subjected to sonication for 15 minutes, with intermittent pulses (each sonication cycle was 20 seconds long, separated by 10 seconds rest periods) at 60% intensity and 40W power in ice bath. Brandon Sonifier Tune 40 titanium-tip equipment was used. The tube containing the conidial suspension was kept in an ice bath (0-4°C) to avoid overheating.

After sonicating the sample, a wet preparation was subjected to microscopic observation (40X) to determine the conidial destruction degree as compared to the starting concentration, so as to estimate cell lysis efficiency by the sonication method. Then, the sonication product was filtered through a membrane (Millipore® GV in PVDF) 0.45 µm pore-diameter, so as to remove cell remains and conidia not destroyed during the treatment. Protein concentration was also determined, giving values around 1.5 µg protein/ ml. The treated suspension was then diluted by sterile distilled water to reach a concentration equivalent to 1.5×10^6 conidia/ml based on the

starting conidia count, amounting to 0.12 µg protein/ml final concentration. This fraction is herein referred to as CE.

Suspension volumes and sonication times and cycles were standardized in order to optimize cell lysis.

Example 4

Obtaining the liquid culture supernatant (SN)

The starting cultures were two equal liquid cultures (PG medium) of *A. strictum* SS71, 40 ml each, which were inoculated and incubated and explained above. Upon completing the growing stage, each culture was centrifuged at 10,400g for 20 min at 4°C, removing the pellet and recovering the supernatant. Then, the supernatants of both cultures were collected and centrifuged again at 10,400g for 30 minutes at 4°C the residual sediment. Subsequently, the recovered supernatant was subjected to subsequent filtrations under sterile conditions to remove resuspended conidia. First it was filtered through a Whatman® No. 2 filter paper, then by Millipore® cellulose nitrate membrane filter 0,8 µm pore-diameter and finally by Millipore® cellulose nitrate membrane filter 0,45 µm pore-diameter. The axenic filtrate is the cell-free liquid culture supernatant (SN). In this case, a 25 ml volume was recovered, which was determined to have 8.43 µg de protein/ ml protein concentration.

The two culture fractions of *A. strictum* SS71, both the cell-free extract (CE) and the liquid culture supernatant (SN) were subjected to a sterile control consisting in striation of the filtrated product in 1.5% APG sterile fresh medium followed by plate incubation for 48 h at 28°C and under continuous white light. The absence of fungal growth confirmed the absence of viable cells in the filtrate, either vegetative cells in the extracts or reproductive structures (conidia) in the filtrates.

Example 5

Characterization of the elicitor present in the SN produced from *Acremonium strictum* of the invention.

Thermal stability determination

To determine the active compound thermal stability two thermal treatments of different severity were used. For such purpose, a volume of 25 ml SS71 liquid culture cell-free supernatant, which retains the capacity to provide protection against the stain of *C. acutatum* causing anthracnose, was subjected to:

A- Heating by boiling in a water bath (100-95°C for 15 min, at atmospheric pressure) (Product SN1).

B- Autoclaved (121°C for 15 min at overpressure 1 atm) (Product SN2).

The protein content in the samples corresponding to both treatments was below the detection limit of the method employed.

C- Proteolysis with Proteinase K (SIGMA): to a solution containing elicitory activity (10 µg protein /ml) the enzyme was added at 100 µg proteinase/ml final concentration and it was incubated at 50°C for 1 hour (this extract is referred to as SNA) or overnight (12 h, this extract was referred to as SNB).

The products obtained after each inactivation treatment (CE and SN products and derivatives thereof: 1, 2, A, B) were used to spray plants in the pre-treatment prior to inoculation (see “Phytopathological Assays: double-treatment system”).

Example 6: Phytopathological Assays: double-treatment system

The experimental designed used to assess the cross-protection consists in the double-treatment strategy detailed below:

1) First Treatment: INDUCTION: it consisted in spraying the aerial parts of the plant (petioles and leaf sheets) to dripping point, with one of the fractions from the different treatments of strain SS71 of *A. strictum* (CE and SN fractions). A 5ml volume is considered sufficient to wet the complete foliage of a 3-month-old seedling (4 fully expanded leaves).

2) Upon completion of the first treatment, plants were transferred to a monitoring chamber, where they were grown under controlled humidity (70%), temperature (28°C) and photoperiod (16 h light) conditions for 72 h (or 7 days in certain cases). Note: The time period between the first and the second treatment is mainly aimed at allowing the activation of plant defence mechanisms by the elicitor action.

3) Second treatment: INOCULATION: After the established period had been completed (3-7 days), aerial parts (petioles and sheets) of the plants that had received the first treatment were sprayed again with spray to dripping point, but this time with a 1.5×10^6 conidia/ml suspension of isolate M11 of *C. acutatum*, highly virulent for cv. Pájaro. Note: In this stage a live conidial suspension of this strain was always used to trigger a compatible-like interaction (disease control) against the strawberry variety used in the assay (cv. Pájaro) so as to assess the protection degree acquired by the plants against anthracnose disease.

4) Immediately after the second inoculation, plants were taken into a stress chamber (darkness, 100% humidity, 30-32°C) and kept for 24 h to produce the stomatal opening and favour the germination of virulent pathogen conidia and the penetration of infective hyphae by plant stomas and trichomas.

5) Finally, plants were transferred into the monitoring chamber under conditions that favour the fungal pathogen development, aside from allowing plant growth. Plants were kept under these conditions for 40 days in order to assess the plant symptoms after infection. In this stage, it was determined whether anthracnose disease occurred or not, depending on the protection level accomplished by the different treatments.

The controls used in the assays performed were as follows:

1) Plant sanity control: a lot of cv. Pájaro plants received the identical treatment as the assayed plants but using sterile distilled water in both sprays. Under these conditions, plants should not exhibit disease symptoms.

2) Cross-protection control (control of the inducing capacity of the strain SS71 of *A. strictum*): a lot of cv. Pájaro plants received a first inoculation with a live conidial suspension of the avirulent strain *A. strictum* SS71, at 1.5×10^6 conidia/ml concentration, and after 72 h (the first 24 h under stress conditions), a second inoculation with live conidia of virulent isolate *C. acutatum* M11 at the same concentration. This experiment was used to control that the avirulent pathogen did not lose the “elicitory” defence response capacity in cv. Pájaro, so that plants do not present disease symptoms.

3) Positive control of *Colletotrichum acutatum* virulence (Control isolate

M11 used in the second inoculation): a lot of cv. Pájaro plants received identical treatment as the assayed plants but using sterile distilled water. In this case, plants should develop the disease and wilt within a maximum period of 21 days.

4) Vehicle (liquid culture medium) inactivity positive control (absence of active compounds): to verify that the effect produced by the supernatant used in the assays results from the presence of active compounds exclusively derived from fungal growth and not from the liquid culture medium used, a lot of cv. Pájaro plants received identical treatment as the assayed lot but the first treatment was replaced by spraying with PG medium. The expected results from such treatment was plants developing disease and wilt within a maximum period of 21 days.

5) Positive control of *Acremonium strictum* (strain SS71 producing the elicitor and used in the first inoculation of the cross-protection system): To verify that strain SS71 of *A. strictum* is active and can trigger the disease in genotypes susceptible to the same pathogen, a lot of *F. vesca* wild strawberry plants (highly sensitive) received a single inoculation with a live conidial suspension of such strain at 1.5×10^6 conidia/ ml concentration, which is the same than the one used to get the cross-protection response in cv. Pájaro. Plants develop disease and die around 7 days after inoculation.

6) Innocuity positive control of fractions derived from such strain containing the elicitor or not, if any: in order to verify that extracts and supernatants are free from agents that are phytotoxic or pathogenic for strawberry culture and, therefore, are innocuous and capable of being applied in the field, a lot of *F. vesca* wild strawberry plants highly susceptible to *A. strictum* SS71, was inoculated with each of the fractions from this pathogen cultures (CE, SN or purification subfractions) at the same concentration as the one used to assess the resistance induced in cv. Pájaro. Plants should not exhibit disease symptoms.

Experiments were performed three times and each phytopathological assay was carried out at random with 4 plants per experimental lot and 4 plants per each control. The results shown correspond to the measure (ξ) of one of the repetitions since the variance (s^2) between both repetitions was practically null. Table 2 summarizes the experiments performed and the controls used in this Example.

Table 2: Resistance induction protocol for fractions of cell extract and supernatant

No. of plants – strawberry genotype		First Treatment		Second Treatment
Phytopathological Assay		4 cv. Pájaro plants	CE SN Purified Frac } of <i>A. strictum</i>	Live conidia of <i>C. acutatum</i>
Controls	Plant Sanity	4 cv. Pájaro plants	Sterile distilled H ₂ O	Sterile distilled H ₂ O
	Cross-protection (CP)	4 cv. Pájaro plants	Live conidia of <i>A. strictum</i>	Live conidia of <i>C. acutatum</i>
	Virulence	4 <i>F. vesca</i> plants	Live conidia of <i>A. strictum</i>	—
		4 cv. Pájaro plants	Sterile distilled H ₂ O	Live conidia of <i>C. acutatum</i>
	Inactivity	4 cv. Pájaro plants	Medio PG	Live conidia of <i>C. acutatum</i>
	Innocuity	4 <i>F. vesca</i> plants	Product derived from <i>A. strictum</i> (CE, SN, Purified Frac.)	—

Data Statistical Analysis

Statistix software (1996 Windows Analytical software) was used. DSR arithmetic mean was studied as position measurement. The software calculated the arithmetic mean of DSR values (average of each repetition four experimental units) corresponding to the forth assessment date (40 days) for each phytopathogenic assay, which were performed with the cultures fractions of *A. strictum* obtained by different treatments. Ctr-PC means Cross-Protection control and Ctr-Ca means positive control of infection of live conidia of *C. acutatum*. The comparison between the different assay means was made by “LSD Test” and “Tukey Test”, with 5% significance degree ($\alpha = 0.05$) in both cases. To study data dispersion as compared to mean values an Analysis of Variance (ANOVA) was carried out.

Example 6

Elicitor purification

The elicitor of the present invention was purified from a 21-day culture supernatant of strain SS71 of *A strictum* grown at 28° C under continuous white light in PG medium without stirring (SN fraction). After 21 days of culture, the supernatant was collected by centrifugation at 10,000g (30 min, 4°C) and filtered through diathomea earth and then through 0.22 µm diameter Millipore® membrane. The axenic supernatant was frozen and concentrated 10 times under vacuum (liophilization).

The extract then went through a dialysis tube (12 kDa cut-off) and was further concentrated 4 times by a dehydration treatment using PEG (MW 15000-20000; Sigma) at 4°C. The concentrated extract was subjected to ultrafiltration under nitrogen gas pressure through a molecular filter (30 kDa cut-off; AMICON). The remaining fraction on the membrane was recovered rinsing the membrane surface with Tris-HCl buffer 20 mM (pH 7.5). Elicitor activity was assayed in the retentate and in the filtrate, confirming that all the activity was recovered in the fraction with heavier molecular weight retained by the membrane. The extract containing the active elicitor polypeptide was subjected to two chromatographical separation steps by FPLC: anion exchange and hydrophobic interaction.

In the first chromatography, a Q Sepharose® Fast Flow column (Pharmacia-FPLC) was used and in the second a Phenyl Superose® HP column (GE-FPLC), both adapted to a FPLC system, monitored at $\lambda = 280$ nm. Q Sepharose® matrix was balanced with Tris HCl 20 mM (pH 7.5) and eluted by increased ionic strength with a discontinuous NaCl gradient in three steps: 0.24 M (8 min), 0.38 M (8 min) and 1 M (10 min); flux rate 1 ml/min. The fraction with elicitory activity corresponding to the column wash (fraction eluted without salt) was collected and subjected to a new chromatography using Phenyl Superose® HP column (GE-FPLC) balanced with buffer A: Tris HCl 50 mM (pH 7.5), EDTA (1 mM) and (NH₄)₂SO₄ (1.5M). Elution buffer B has the same composition as buffer A but without adding (NH₄)₂SO₄. The samples were eluted by decreased ionic strength with a discontinuous gradient of (NH₄)₂SO₄ salt divided into 8 steps: 22% B (5min), 30% B (7min), 40% (7min), 50% (7min), 70% (5min), 80% (5min), 90% (5min), 100% (10min); flux rate= 1 ml/min. The activity of

all the fractions was tested by two parallel procedures, analyzing ROS production and the plant protection against pathogen *C. acutatum* M11.

The fraction eluted at 0.5 M of $(\text{NH}_4)_2\text{SO}_4$ was visualized as a single peak (peak 7, Fig 6) and showed both activities analyzed. This peak was collected and desalted twice; first by dialysis with bidistilled water and then by running through an ultra-thin Sephadex® G25 column (SIGMA). In each purification step, total proteins were quantified and separated by SDS-PAGE in polyacrylamide gels (12%), dyed with Coomassie® Brilliant Blue and/or silver dyeing (Sambrook. *et. al*, 1989. Molecular cloning, a laboratory manual. Second edition). The desalted fraction eluted from HP column (peak 7) showed a 34kDa single band on a SDS-PAGE (10%).

Total protein determination: Bradford Method

Total protein content in water soluble samples were determined using “Bio-Rad® Protein Assay Kit II” based on the Bradford Method (Bradford, 1976. Anal. Biochem. 72, 248-254). The products obtained up to this step were used in the first treatment of Induced Resistance phytopathological assays.

Example 7: Assessment of elicitory activity in each purification step

Elicitory activity in each purification step was assessed in strawberry plants analyzing the accumulation of ROS (e.g. H_2O_2 , and O_2^-) and the protection against anthracnose. In this last case, it was determined by phytopathological assays of the capacity of the different fractions and the purified protein to protect the plant against virulent pathogens. The methodology used for phytopathological assays was explained hereinabove.

Oxidative burst assessment:

H_2O_2 accumulation was detected by histochemical dyeing with DAB (in strawberry) or by DCFH-DA fluorescent probe (in *Arabidopsis*) and O_2^- accumulation was detected by histochemical dyeing with NBT (in both species).

To assess the evolution of the oxidative burst, the generation of hydrogen

peroxide and radical superoxide was followed at different time points. For this purpose, strawberry plants (cv. Pájaro) were treated with the elicitor at 10 µg/ml concentration and at different time points, ranging from 0 to 12 hours after treatment (hpt) with the elicitor, 10 proximal or distal leaflets were cut and incubated in a solution containing 0.1 % (w/v) DAB, 10 mM MES, pH 3.8 (for peroxide detection) or 0.1 % (w/v) NBT, 10 mM sodium azide, 10 mM potassium phosphate (pH 7.8), without adding NADPH (for superoxide detection). Leaves were then incubated from 2 to 8 h in the dark under nitrogen gas pressure. After incubation, the tissue was fixed and bleached by heating in 95% ethanol (w/v), clarified with lactic acid /glycerol/H₂O [3:3:4] for 24 h and mounted on a microscopic slide with 60% glycerol. Histochemical dyeing was observed and documented with an Olympus® BH-2 microscope with a digital camera. Plants treated with water and sterile PG medium were used as negative controls.

Hydrogen peroxide intracellular detection in *Arabidopsis* foliar tissue was performed by DCFH-DA fluorescent probe. A stock solution was prepared at 10 mM concentration in DMSO and working solution was prepared at 40 µM concentration in 10mM phosphate buffer (pH 7.4). Harvested leaves at different times after elicitor treatment were incubated in DCFH-DA solution in the dark under nitrogen gas pressure for 15 minutes and immediately observed in the fluorescence microscope. For fluorescence detection, microscopic observations and photographing an Olympus® BXS1 model microscope, equipped with an U-LH 100HG-like epifluorescence system, a U-MWB2 excitation filter and a digital camera was used. O₂⁻ anion detection was performed by histochemical dyeing with NBT as described hereinabove for strawberries.

Quantification of NO and ROS production in tomato cells (*Solanum lycopersicon*) cultured in suspension by fluorescence:

Four to 5-days-old tomato suspension cell cultures were exposed to different treatments in microtiter plates (for fluorescence measurements). ROS (H₂O₂) detection in cells was carried out using the H₂DCF diacetate (2',7'-

difluorodihydrofluorescein diacetate) fluorescent probe (Molecular Probes). The latter, originally described for phagocytic cells, was adapted and modified to measure the oxidative burst reaction of elicitor-induced cell cultures in suspension by assays in a microplate multichannel automatic fluorescence system. Nitric oxide (NO) quantification in cells was carried out using a DAF-FM diacetate (4-amino-5-methylamino-2',7'-difluorofluorescein diacetate) fluorescent probe (Molecular Probes).

Ninety μl of cell culture suspension was carefully aliquoted by micropipetting into the wells of a 96-well microtiter plate (Greiner) containing 0.025 μM H2DCF-DA or 0.5 μM DAF-FM-DA and 10 μl elicitor at different concentrations (5 or 10 $\mu\text{g}/\text{ml}$ final concentration, respectively). The microplate was immediately transferred to the fluorometer to perform measurements. The fluorescence resulting from the oxidative burst reaction produced by the cells was continuously monitored during 30 minutes in a Fluoroskan AscentTM microplate fluorometer (Termo Electron Company, Vantaa, Finland) using Chroma[®] D480-40 and D525-30 filters (Chroma Technology Corp, Rockingham, VT, AS) using $\lambda_{\text{ex}} = 480 \text{ nm}$ and $\lambda_{\text{em}} = 525 \text{ nm}$.

The fluorescence in each individual well was measured every 20 milliseconds during 2 minutes at 25 °C. Between measurements cell suspensions were agitated at 120 RPM with 1 cm rotation at 25°C. All the experiments were performed in triplicate. The resulting fluorescence was expressed as relative ROS production. Control cells were treated with 20 μl pre-incubation medium instead of the elicitor. Xylanase derived from *Trichoderma viride* was used as ROS and NO induction control at 10 and 100 $\mu\text{g}/\text{ml}$ concentration, respectively. Control experiments were also carried out with NO scavengers (cPTIO: 2-(4-carboxyphenyl)-4,4,5,5-tetramethylimidazoline-1-oxyl-3-oxide potassium salt) and inhibitors of nitric oxide synthase enzyme (Arginine competitors), of NADPH oxidase (Apocinine) and of both enzymes (DPI: diphenyliodonium) to reduce the source of fluorescent species. The treatments with inhibitors were performed incubating cells 30 minutes before the treatment.

Callose deposition analysis:

To observe the accumulation of callose, strawberry leaves were treated and dyed. Plants were sprayed with the purified elicitor protein (10 µg/ml) or with water. Leaves were collected 7 days after having been treated with the elicitor (7dpi). For a positive control, callose deposition was assessed in plants that had been infected with virulent isolate M11 of *C. acutatum* 7 days post-treatment. In this case, leaves were analyzed 48 hours post-inoculation with M11 and thereafter the tissue was clarified and dehydrated with 100% EtOH overnight. Clarified tissue was sequentially transferred into decreasing ethanol solutions in 67 mM K₂HPO₄ buffer (pH 12), from 100% to 0% (e.g. 100%, 75%, 50%, 25% and 0%), and then dyed for 1 hour at room temperature with 0.01% blue aniline in 67 mM K₂HPO₄ (pH 12). The dyed material was then put in 30% glycerol and examined using ultraviolet epifluorescence in the Olympus® BXS1 model microscope, mentioned above.

Determination of salicylic acid:

Salicylic acid (SA) was determined in the phloem exudate of leaves from Cv. Pájaro plants sprayed with the elicitor (15 µg/ml). After spraying leaves were harvested at different time points to extract phloem fluid. Experiment controls consisted in plants treated with water (negative), BTH and the virulent isolate M11 of *C. acutatum* as positive controls. At different time points after treatment, phloem exudate was collected by using a micropipette from the petioles of fully expanded leaves of two plants and put together in a single sample. SA concentration was determined for each time point. The exudates were put in cold acidified 100% ethanol (pH 2.5) to pellet proteins and other high molecular weight compounds.

After removing insoluble materials by centrifugation (12,000g for 15 minutes at 4°C), ethanolic extracts were transferred into previously weighed microcentrifuge tubes and concentrated to dryness under vacuum using a SVC 200 SpeedVac Sample Concentrator (Savant Instrumentos Co., Farmingale, NY). Once dried, tubes were weighted to calculate the dry weight and samples were resuspended in 250 µl of 30% methanol.

SA separation was performed by HPLC using a C18 reversed phase column (Phenomenex- CV=3.4ml) balanced in 30% methanol. Runs were performed at 0.5

ml/min mobile phase flow rate and with linear gradient elution with methanol (0-100% in 15 minutes) and then kept in 100% for 20 minutes. SA was spectrophotometrically detected at 280 nm using an UV detector and the SA peak eluted with 100% methanol under the conditions applied. Quantitative analysis was performed by fluorescence using an ISS-PC1 photon counting spectrofluorometer. Salicylic acid concentration was determined in each collected fraction by HPLC (λ_{ex} = 296 nm, λ_{em} = 408 nm). Each punctual data was determined as the average between two replicas of a representative experiment performed in duplicate. Data was expressed as total SA per gram dried weight of exudate.

Self- fluorescence detection:

Since it was reported that the defense response development can be associated to the accumulation of self-fluorescent compounds, the presence of self-fluorescent compounds in strawberry leaves after being treated with extracts containing the elicitor was studied, with the pure protein and other solutions used as controls. Treatment was performed by infiltration through the leaflet abaxial side, with a volume of around 50 μ l of water or of elicitor (10 μ g/ml) using a needleless syringe and the reaction was followed for 96 h by UV epifluorescence (329 nm). Microphotographies were taken with a BH-2 Olympus® microscope.

Example 8: Elicitor molecular characterization

Microsequencing, finding similarities and alignments

The elicitor polypeptide purified by hydrophobic interaction chromatography by a FPLC system was separated on 12% polyacrylamide gel under denaturalizing conditions using a Tris-Glycine buffer system with SDS and then electro-transferred to an Immobilon-PSQ membrane 0.1 μ m pore-diameter in 10 mM CAPS buffer (pH 11).

The band corresponding to the polypeptide was extracted from the gel and subjected to microsequencing by Edman degradation reaction with an 476 Applied Biosystems gas-phase sequencer. The amino acid sequences obtained were compared to known sequences stored in the databases using the BLAST software and the DNAMAN software (version 4-03).

Building an expression library of the elicitor (SS71) producing isolate:

In order to obtain the complete sequence of the elicitor polypeptide, the cDNA transcript was cloned. An expression library was built from the fungal mycelium of a SS71 culture grown in liquid PG medium to stationary phase.

Total RNA from the fungal mycelium of SS71 strain was isolated as follows: each sample (approximately 1,2 grams) was grounded using a mortar and a pestle with liquid N₂ and homogenized with 8 ml of extraction buffer preheated to 65 °C.

The composition of the extraction buffer used for RNA isolation was the following: Tris-HCl, 100 mM (pH 8), EDTA, 25 mM (pH 8); NaCl, 2.5 M; CTA, 2% PVP, 2%; Spermidine, 0.5 g / l, β-mercaptoethanol, 2%. Once homogenised, the mixture was incubated at 65°C for 30 min with vigorous stirring every 5 min. After centrifugation at 5,000g for 10 min at 4 °C, the supernatant was filtered through a column QIAshredder™ (Qiagen) and incubated on ice for one hour. Subsequently, it was further centrifuged at 14,000g for 10 min at 4°C to remove any remaining plant material in suspension. The supernatant was purified by two extractions with equal volume of chloroform / isoamyl alcohol (24:1) followed by centrifugation at 14,000g for 5 min at 4°C. The purified solution was then precipitated with 1/4 volume 10 M LiCl and incubated at 4°C overnight. The following day the precipitate was centrifuged at 14,000g for 45 min at 4°C and the pellet washed with 70% ethanol and resuspended in 100 µl of bidistilled water treated with DEPC (diethyl pyrocarbonate) 0.1% v/v. Finally, a final cleaning was performed and treatment with "on-column" DNase by using RNeasy® MiniKit and RNase-Free DNase Set (Qiagen) kits, respectively, following the manufacturer's instructions. The concentration and purity of the total RNA samples were determined spectrophotometrically by assessing the absorbances at 260, 230 and 280 nm. The total RNA concentration was calculated using the following formula:

$$\text{ARN [ng/}\mu\text{l]} = A_{260} \times \text{Dilution Factor} \times \text{FC}$$

wherein FC is the conversion factor (ng/μl): 1 unit of absorbance is around 40 ng/μl for RNA.

The purity with respect to contamination with protein and carbohydrate/polyphenols was estimated by A_{260}/A_{280} and A_{260}/A_{230} relations (both should be ≥ 2).

Once quantified, samples were immediately used in reverse transcription reactions or stored at -80°C precipitated with 1/10 volume sodium acetate and 2 volumes of ethanol until used. The corresponding cDNA library was used for PCR amplification reactions.

Isolation of the elicitor polypeptide coding sequence by PCR using degenerate primers:

Semi-degenerate primers were used to amplify DNA sequences encoding the elicitor protein from *A. strictum*.

Internal and amino terminal sequenced peptides of the elicitor protein were used to design oligonucleotide primers with the lowest possible degree of degeneration (nucleotide variations by position). For such purpose, the regions containing amino acids with less genetic code multiplicity (Example: tryptophan) were used as template thereof, as well as the less conserved amino acid regions in order to avoid obtaining a cDNA coding for a protein homologous to the protein of interest with disease defense elicitory activity.

In the design of the primers the following criteria were taken into account: (1) the most frequently used codons in the species *Acremonium strictum* and other species of *Acremonium spp.*, and (2) the codons found in proteins with high sequence identity (obtained from the search performed by BLAST) that belong to other species..

The semi-degenerate primers used were:

NH2 F1 (N1): 5'-GCNTAYACNACNCARGCNT-3' (SEQ ID N° 3)

NH2 F2 (N2): 5'-CAGGCBWSBGCBCCBTGG- 3' (SEQ ID N° 4)

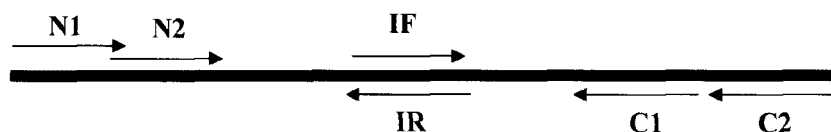
Internal F (IF): 5'-ATYATYGCYGGYATYAACTAYG- 3' (SEQ ID N° 5)

InternalR (IR): 5'-CRTAGTTRATRCCRGCRAT-3' (SEQ ID N° 6)

COOH R1 (C1): 5'-RATVACRCCVGTGTVGCRAT-3' (SEQ ID N° 7)

COOH R2 (C2): 5'-GTTVGGVGTRCCVWSVGGR-3' (SEQ ID N° 8)

With the aim of selectively isolating the sequence corresponding to the elicitor protein protein , three consecutive amplifications were performed using different combinations of degenerate primers.



The protocol used for PCR amplification was as follows:

1: An initial amplification was performed to enrich the sample in the product of interest, using the outermost sense and antisense primers (N1 and C2). Twenty ng of cDNA from the expression library was used as template for the PCR reaction.

2: A second Nested PCR type amplification was performed using as template the amplification product obtained from the first PCR diluted 125 times in the reaction mixture (2 µl of dilution 1/10 in 25 µl final volume). In this amplification, the most internal sense and antisense primers were used (N2 and C1). 1.5% agarose gel was used to visualize the amplified product. Candidate bands were selected according to their size in the gel, excised from the gel and purified by a band purification kit.

3: Then, two independent PCR reactions were performed using as template the nucleic acid solution purified in the previous step (4 µl), derived from a single band of 800 bp amplified by Nested PCR. For each amplification reaction internal primer (IF or IR) was used in combination with the amino-terminal primer N2 (N2/IR) or in combination with the carboxy-terminal primer (C1/IF).

The sum of the band sizes obtained with N2/IR and C1/IF should be equal to the weight of the band from which it is derived (~ 800bp). Combining primers N2/IR a single band of appropriate intensity of 350 bp is obtained, and with C1/IF a single band of around 500pb is obtained.

The reactions were carried out in a final reaction volume of 25 µl containing 50 mM KCl, 20 mM Tris-HCl (pH 8.4), 1.5 mM MgCl₂, 2 µM of each primer (sense and antisense), 0, 2 mM of each dNTP and 0.75 U of Taq DNA polymerase (Invitrogen).

The PCR reaction conditions included an initial denaturation of 10 min at 94°C, followed by 40 consecutive cycles of 45 sec at 94°C (denaturation), 30 sec at 55°C (primer hybridization) and 1.5 min at 72°C (primer elongation). Finally, a final elongation period was added for 10 min at 72°C.

Optimal temperatures for primer hybridization were determined after testing at different temperatures, ranging from 45°C to 55°C. In addition, different concentrations of MgCl₂, concentration of genomic DNA and for each of the primers were tested to optimize reaction conditions. Amplification reactions were performed in a PTC-100 thermocycler from MJ Research Inc.

Separation and purification of PCR products:

40 µl of the total reaction volume were grown in TBE/1.5% agarose gels and the amplification products were separated by electrophoresis at 90 V for 1 hour, then dyed with ethidium bromide and visualized with a UV transilluminator (320 nm).

In the second and third amplification step wherein bands with appropriate intensity and size were observed, bands were excised from the gel, purified as explained below and concentrated eluting them in 20 µl volume. A 5 µl aliquot of the purified fragments was used to reamplified them by PCR using the same conditions and the same primers used in the initial amplification. Finally, the presence of the amplicon was verified by electrophoresis.

Cloning and sequencing of PCR products:

In all cases, PCR products were directly cloned into cloning vector pCR[®]2.1 (Invitrogen). The pCR[®]2.1 vector contains the promoters of the RNA polymerases of T7 and T3 bacteriophages, flanking a multiple cloning region within the coding region of the enzyme β-galactosidase (lac Z). Cloned fragments were sequenced using

sequencing primers located upstreams and downstreams of the bacteriophage promoters in accordance with the manufacturer's instructions.

Obtention of competent *E. coli* cells:

An aliquot of 100 µl of a pure culture of *Escherichia coli* DH5α in exponential growth phase was inoculated into 40 ml fresh medium and grown at 37°C and 250 rpm to optical density of 0.6 (OD at 550nm). The culture obtained under these conditions was kept in an ice bath for 10 min and then centrifuged at 4°C for 10 min at 7,000 rpm. The supernatant was removed and cells were resuspended in 5 ml of sterile 0.1 M CaCl₂. Resuspended cells were left on ice for 20 min, centrifuged as indicated above and after aseptically discarding the supernatant, cells were carefully resuspended in 500 µL of 0.1 M CaCl₂ precooled at 4°C. The cell suspension was stored in a refrigerator at 4°C overnight.

Transformation:

The transformation of competent cells was performed by thermal shock in accordance with Sambrook *et al.* (Sambrook *et al.*, 1989. Molecular cloning, a laboratory manual. Second edition).

Verification of inserts and sequencing:

For each cloning event, 10 white colonies were selected for further analysis, and grown o/n on LB agar plates supplemented with ampicillin 100 µg/ml. From these colonies, liquid cultures were produced in 8 to 10 mL of LB medium with ampicillin (100 µg/ml). Plasmids were then extracted and purified according to Sambrook *et al.* (Sambrook *et al.*, 1989. Molecular cloning, a laboratory manual. Second edition).

Plasmids were eluted in 100 µl of sterile bidistilled water and the integrity and amount of DNA was verified as described in section 2.3. Identification of positive clones (verification of inserts) was conducted by PCR technique using T3 (5'-ATTAACCCTCACTAAAGGGA-3') (SEQ ID N° 9) and T7 (5'-TAATACGACTCACTATAGGG-3') (SEQ ID N° 10) universal primers in a

reaction volume of 20 µL containing 1X Taq polymerase buffer without Mg, 2mM MgCl₂, 0.5 µM of each primer, 0.2 mM of each dNTP, 1 U of Taq DNA polymerase (Promega) and 50 ng of plasmid DNA. Reaction conditions were: denaturation for 2 min at 95°C, 30 cycles of 30 sec at 95°C, 30 sec at 52°C and 1 min at 72°C followed by a final extension of 5 min at 72°C. PCR products were separated on 1% agarose gels in 0.5 X TBE, dyed with ethidium bromide and visualized by UV light. The same primers used for insert verification were used to sequence each insert in both directions.

Sequence editing and DNA-protein homology search

The sequences obtained were initially analyzed with the VecScreen® and ORF Finder algorithms (<https://www.ncbi.nlm.nih.gov/tools/vecscreen/>) in order to remove vector sequences and to identify potential open reading frames, respectively. DNAMAN software version 5.2.2 (Lynnon Biosoft, Quebec, Canada) was used for assemblies of nucleotide sequences and obtention of the deduced amino acid sequences. The nucleotide and amino acid sequences were compared with sequences deposited in the GenBank NR database using Blast X and Blast P heuristic algorithms. The expected threshold value was set at 0.0001 (e-value), which is a value empirically determined to filter expected alignments at random due to the size of the search space. By CDSearch (NCBI), SMART 5 and Pfam (Sanger Institute) programs the presence of structural motifs and/or conserved domains was determined.

Specific primer design

To confirm the sequence corresponding to the mature cDNA transcript of the elicitor protein, specific primers were designed from the consensus nucleotide sequence obtained from the 10 selected clones. In addition, less conserved regions of the subtilisin family, which did not contain variable nucleotides among the sequences of the different clones, were also selected. Primers were designed using the software DNAMAN version 5.2.2 program.

GSPvar-F: 5'-GGCCCAACTGGCTACACC-3' (SEQ ID N° 11)

GSPvar-R: 5'-ATGGCGACGATGCGGTTG-3' (SEQ ID N° 12)

Complete sequencing of the cDNA using RACE-PCR methodology

The complete sequence of the complementary DNA (cDNA) transcribed or the mature transcript corresponding to the elicitor protein was obtained by the RACE technique (Rapid Amplification of cDNA Ends) according to Frohman *et al.* (Frohman *et al.*, 1988. Proc. Natl. Acad. Sci. USA. 85, 8998-9002).

A GeneRacer™ system by Invitrogen was used, which is based on a technique that uses RNA ligase (RLM-RACE: “RNA ligase-mediated Rapid Amplification of cDNA Ends”), following the manufacture’s instructions.

A RACE-like expression library of the elicitor-producing pathogenic isolate *A. strictum* SS71, comprised of the first strands of the cDNA with annealing sites for GeneRacer™ primers of the 5' and 3' ends was obtained. Briefly, the GeneRacer™ technology system is based on the treatment of isolated mRNA with a phosphatase (CIP) which removes the phosphate groups present at the 5' end of the partially degraded messengers, so that only those with complete sequence and protected by cap or a "Cap" structure can continue with the cloning protocol. Then, the mRNA is treated with a pyrophosphatase (TAP), which removes this "cap" from the undegraded mRNA leaving a phosphate group in the 5' position which can be bound by a RNA oligonucleotide with a specific sequence which will be used for the amplification process typical of the RACE technique.

Design of specific primers for RACE

The design of gene-specific primers (GSP”), that anneal to the 5' and 3' ends of the gene fragment of interest, was carried out using the DNAMAN program version 5.2.2 (Lynnon Biosoft, Québec, Canada) following the criteria below:

- High temperature annealing (> 72°C) which was achieved by the length of the primers (24-28 nucleotides) and high GC content (50-70%).
- Low GC content to the 3' end of the primers (no more than two G or C residues in the last 5 bases)
- Absence of self-complementarity within the primer and absence of complementary sequences to the GeneRacer™ primers used.

- Design of nested primers (Nested RACE) located within the first amplified sequence in order to increase specificity by using nested PCR technique, which consists in a second amplification using as template the product of the first amplification. These internal primers characteristics should be similar to those mentioned above.

To obtain the nucleotide sequence of 5' and 3' ends of the mature transcript corresponding to the elicitor protein using RACE-like technology, specific primers were designed according to the requirements described hereinabove from the sequence confirmed by cloning with GSPvar-F and GSPvar-R primers.

The primers used to obtain the 5' end were:

GSP RACE-R (GSP-5): 5'-GATGTTGTTGTCGATCAAGGACTTGG-3' (SEQ ID N° 13)

GSP RACE Nested-R (GSPN-5): 5'-TGCCTTGGTAGGAGACAAGCTGGAA-3' (SEQ ID N° 14)

The primers used to obtain the 3' end were:

GSP RACE -F (GSP-3): 5'-AGCTTGTCCTCTACCAAGGCAGCAA-3' (SEQ ID N° 15)

GSP RACE Nested-F (GSPN-3): 5'-GGCCAAGTCCTTGATCGACAACAAC-3' (SEQ ID N° 16)

The primers provided by RACE kit are as follows:

GeneRacer™ 5' (R-5): 5'-CGACTGGAGCACGAGGACACTGA-3' (SEQ ID N° 17)

GeneRacer™ 5' Nested (RN-5): 5'-GGACACTGACATGGACTGAAGGAGTA-3' (SEQ ID N° 18)

GeneRacer™ 3' (R-3): 5'-GCTGTCAACGATACGCTACGTAACG-3' (SEQ ID N° 19)

GeneRacer™ 3' Nested (RN-3): 5'-CGCTACGTAACGGCATGACAGTG-3' (SEQ ID N° 20)

The following is a scheme with the relative location of all primers described in the RACE-PCR procedure outlined above.:



Amplifications by PCR

In order to minimize non-specific primer annealing ("misspriming") for the amplification reactions Platinum® Taq DNA Polymerase High Fidelity enzyme (Invitrogen) was used in accordance to the manufacturer's instructions.

Reactions were carried out in a final volume of 50 µl containing 1X PCR buffer, 0.2 mM of each dNTP, 2 mM MgSO₄, 0.6 µM of 5' or 3' GeneRacer® primer, 0.2 µM of 5' or 3' specific primer (GSP-5 or GSP-3 respectively), 2.5 U of Platinum® Taq DNA Polymerase and 1 µl of a 1/5 dilution of the product of reverse transcription of the RACE expression library constructed from the isolated producer SS71. The thermocycler program used to apply the technique of "touch-down" was:

- Initial denaturation: 94°C for 2 minutes
- 5 cycles of 94°C for 30 seg and 72°C for 4 min (1 min/kb DNA)
- 5 cycles of 94°C for 30 seg and 70°C for 4 min
- 25 cycles of 94°C for 30 seg, 66°C for 30 seg and 68°C for 4 min
- Final extension: 68°C for 10 min

PCR products were separated and visualized on 1% agarose gels as described in 2.4.

Nested PCR

Amplifications were performed by nested PCR from the first amplification product. The reactions were carried out in a final volume of 50 µl containing 1X PCR buffer, 0.2 mM of each dNTP, 2 mM MgSO₄, 0.2 µM of 5' or 3' GeneRacer® Nested Primer, 0.2 µM of 5' or 3' of the specific primer (GSPN-5 or GSPN-3, respectively), 1 U de Platinum® Taq DNA Polymerase and 1 µl of a 1/10 dilution of initial PCR product. The PCR program used was:

- Initial denaturation: 94°C for 2 minutes
- 25 cycles of 94°C for 30 seg, 66°C for 30 seg and 68°C for 4 min
- Final extension: 68°C for 10 min

PCR products were separated and visualized on 1% agarose gels. If there was more than one band, each of these was separated from the gel, purified and cloned as described above. Finally, 3 recombinant clones were selected for each amplification/transformation event, which were purified and sequenced in both directions using T3 and T7 universal primers as described above.

Example 9: Determination of subtilisin-like proteolytic activity

Since the analysis of nucleotide and amino acid sequences suggested that the protein might be a subtilisin-like protease, assays were conducted to determine proteolytic activity *in vitro*. For such purpose, the ability to hydrolyze the chromogenic peptide substrate N-Suc-Ala-Ala-Pro-Phe-pNA, specific for trypsin/subtilisin, was assessed. The proteolytic cleavage causes the release of p-nitroanilide that absorbs at $\lambda = 405\text{nm}$ (Moallaei *et al.*, 2006. Mycopathologia 161, 369-375). Optimal conditions for the enzymatic activity of the elicitor protein were first determined (temperature, pH). To further characterize and confirm the protease function, the effect of specific inhibitors for various proteases on the proteolytic activity of the elicitor of the invention derived from SS71 was also studied.

Example 10: Treatment of strawberry plants with conidia of the strain SS71 of *A. strictum*

Conidia of the strain SS71 of *A. strictum* were resuspended as shown in Example 2. They were sprayed on strawberry plants of cultivars Pájaro, Chandler, Milsei, Camarosa and Sweet Charlie at a concentration of 10^5 , 10^6 and 10^7 conidia/ml. Induction of the defense response in plants was assessed by monitoring oxidative burst by measuring accumulation of H_2O_2 y O_2^- , determine SA increase, production of PR-proteins, plant cell wall thickening, translocation of the signal from a leaf to the rest of the plant (systemic response), protection against different virulent isolates of the genus *Colletotrichum spp.* causing anthracnose and other strawberry pathogens (*Botrytis cinerea*, *Xanthomonas fragariae*), resistance to subsequent infections with virulent isolates and long-term response over time (durability or persistence over time).

Example 11: Plant treatment with CE extract of the strain SS71 of *A. strictum*

Conidial extract (CE) was obtained by sonication of conidia from the strain SS71 of *A. strictum* as shown in Example 3. The aerial parts of strawberry plants were sprayed with CE at a concentration of $1.5\ \mu\text{g protein/ml}$. Interestingly, CE

retains its activity when diluted 12 times reaching a final concentration of 0.12 µg/ml protein.

Induction of plant defense responses in strawberries was assessed by protection against different virulent isolates of the genus *Colletotrichum spp.* causing anthracnose in different strawberry genotypes (Pájaro, Chandler Milsei and Camarosa) and other strawberry pathogens (*B. cinerea* and *X. fragariae*). In addition, ROS production (H_2O_2 y O_2^-) was observed when strawberry plants were treated with CE at a concentration 0.12 µg/ml.

Example 12: Plant treatment with SN extract of the strain SS71 of *A. strictum*

The cell-free supernatant (SN) was recovered from a culture of isolate SS71 of *A. strictum* grown at 28°C, without stirring at continuous white light until reaching stationary phase (21 days) as shown in Example 4. Aerial parts of strawberry plants were sprayed with 1X SN (undiluted) corresponding to a total concentration of 8.43 µg protein/ml. SN retained its elicitory activity when diluted about 21 times reaching a final concentration of only 0.4 µg protein/ml.

The induction of plant defense responses in strawberries was assessed by disease resistance, evaluated by the protection against different virulent isolates of the genus *Colletotrichum spp.* causing anthracnose in different strawberry genotypes (Pájaro, Chandler Milsei and Camarosa) and other strawberry pathogens (*B. cinerea* and *X. fragariae*) in cv. Pájaro. Anthracnose resistance is obtained by treating a single leaf of the plant, generating a systemic protective response.

When cv. Pájaro strawberry plants were treated with SN 1X (8.43 µg protein/ml) accumulation of ROS (H_2O_2 y O_2^-) and microscopic HR was observed not only in treated tissue but also in untreated leaves (micro bursts and micro systemic HR). Other defense responses observed were SA increase, plant cell wall thickening due to accumulation of lignin and accumulation of self-fluorescent species resulting from accumulation of compounds of the phenylpropanoid pathway. These responses are also observed when performing the application of axenic SN diluted 5 times (~ 2 µg protein/ml). When tomato cell cultures (*Solanum lycopersicon*) were treated with SN 1X (8.43 µg protein/ml) exacerbated accumulation of ROS and NO

was observed. In addition, SN 1X (8.43 µg protein/ml) resulted in deposition of callose in cell wall and accumulation of ROS (H_2O_2 y O_2^-) in plants of *A. thaliana*.

Example 13: Plant treatment with the purified elicitor polypeptide of the strain SS71 of *A. strictum*

The subtilisin-like elicitor polypeptide was purified from the cell-free supernatant (SN) of a culture of the isolate SS71 of *A. strictum* as shown in Example 7. Aerial parts of strawberry plants were sprayed with such elicitor polypeptide at varying concentrations between 2.5 to 15 µg/ml of polypeptide, depending on the studied defense response.

The induction of plant defense responses was assessed by disease resistance when the polypeptide was applied at a minimum concentration of 2.5 µg/ml and an optimal concentration of 10 µg/ml. The protection against different virulent isolates of *Colletotrichum spp.* causing anthracnose in different strawberry genotypes (broad spectrum response) and against other strawberry pathogens (*Botrytis cinerea*, *X. fragariae*) in cv. Pájaro was observed. Anthracnose resistance in particular is achieved by treating a single leaf of the plant with the elicitor polypeptide at a concentration 5 µg/ml, which is a systemic protective response.

When strawberry plants of cv. Pájaro were treated with the elicitor polypeptide at a concentration of 10 µg/ml, accumulation of ROS (H_2O_2 y O_2^-) was observed and microscopic HR including in untreated foliar tissue (micro bursts and micro systemic HR), plant cell wall thickening due to accumulation of callose and lignin; accumulation of self-fluorescent species derived from the phenylpropanoid pathway and induction of PR protein encoding genes (chitinases, glucanases). Treatment with the elicitor polypeptide at a concentration of 15 µg/ml induced SA accumulation. On the other hand, exacerbated accumulation of ROS and NO was observed in cell cultures of tomato (*Solanum lycopersicon*) treated with the elicitor polypeptide at a final concentration of 10 and 5 µg/ml, respectively. In addition, elicitor polypeptide at a concentration of 10 µg/ml is capable of inducing callose accumulation in the plant cell wall and oxidative burst (H_2O_2 y O_2^-) in plants of *A. thaliana*.

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CLAIMS

1. A polypeptide which is a subtilisin from a strain of *Acremonium strictum*, which comprises the amino acid sequence SEQ ID NO: 2, wherein such polypeptide induces resistance of a plant to stress caused by pathogens.
2. The polypeptide according to claim 1, wherein the strain of *Acremonium strictum* is the strain SS71 of *Acremonium strictum* deposited in the German Deposit Centre DSMZ under access code DSM 24396.
3. The polypeptide according to any one of claims 1 or 2, which is encoded by the nucleotide sequence SEQ ID NO: 1 or a sequence at least 90% identical thereto.
4. A microorganism which expresses a polypeptide having an amino acid sequence SEQ ID NO: 2, which is the strain *Acremonium strictum* SS71 deposited in the German deposit center DSMZ under access code DSM 24396.
5. A composition for inducing plant resistance to stress caused by pathogens, wherein said pathogens are selected from the group consisting of *Colletotrichum spp.*, *Botrytis cinera* and *Xanthomonas fragariae*, the composition comprising the polypeptide according to any one of claims 1 to 3, and excipients.
6. The composition according to claim 5, wherein the composition comprises between 2.5 and 15 µg/ml of the polypeptide according to any one of claims 1 to 3, and excipients.
7. A process for obtaining and purifying the polypeptide according to any one of claims 1 to 3, wherein the process comprises the following steps:
 - a. culturing a strain of *Acremonium strictum*, which is the strain SS71 of *Acremonium strictum* deposited in the German deposit center DSMZ under access code DSM 24396, in a liquid culture medium;
 - b. recovering the supernatant from the culture of step a);
 - c. concentrating the supernatant recovered in step b); and

d. ultrafiltrating the concentrated supernatant obtained in step c);

thus obtaining a purified polypeptide according to any one of claims 1 to 3.

8. The process according to claim 7, further comprising a chromatographic purification step by anion exchange chromatography after step d).

9. The process according to claim 8, further comprising a purification step by hydrophobic interaction chromatography.

10. A method for inducing plant resistance to stress caused by pathogens in a plant, said pathogens being selected from the group consisting of *Colletotrichum spp.*, *Botrytis cinera* and *Xanthomonas fragariae*, wherein the method comprises applying to such plant a composition according to any one of claims 5 and 6.

11. The method according to claim 10, wherein the pathogen is *Colletotrichum spp.*

12. The method according to any one of claims 10 to 11, wherein the plant is a dicotyledon.

13. The method according to claim 12, wherein the plant is selected from the group consisting of strawberry (*Fragaria x ananassa*), tomato (*Solanum lycopersicon*) and *Arabidopsis thaliana*.

14. The method according to any one of claims 10 to 13, wherein the composition is applied to the plant by spraying, infiltration or irrigation.

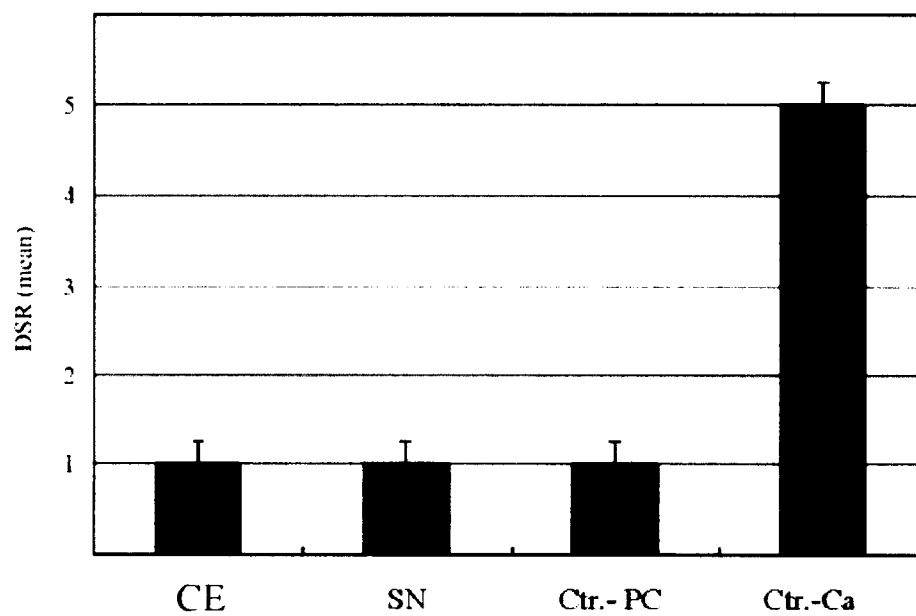


FIGURE 1

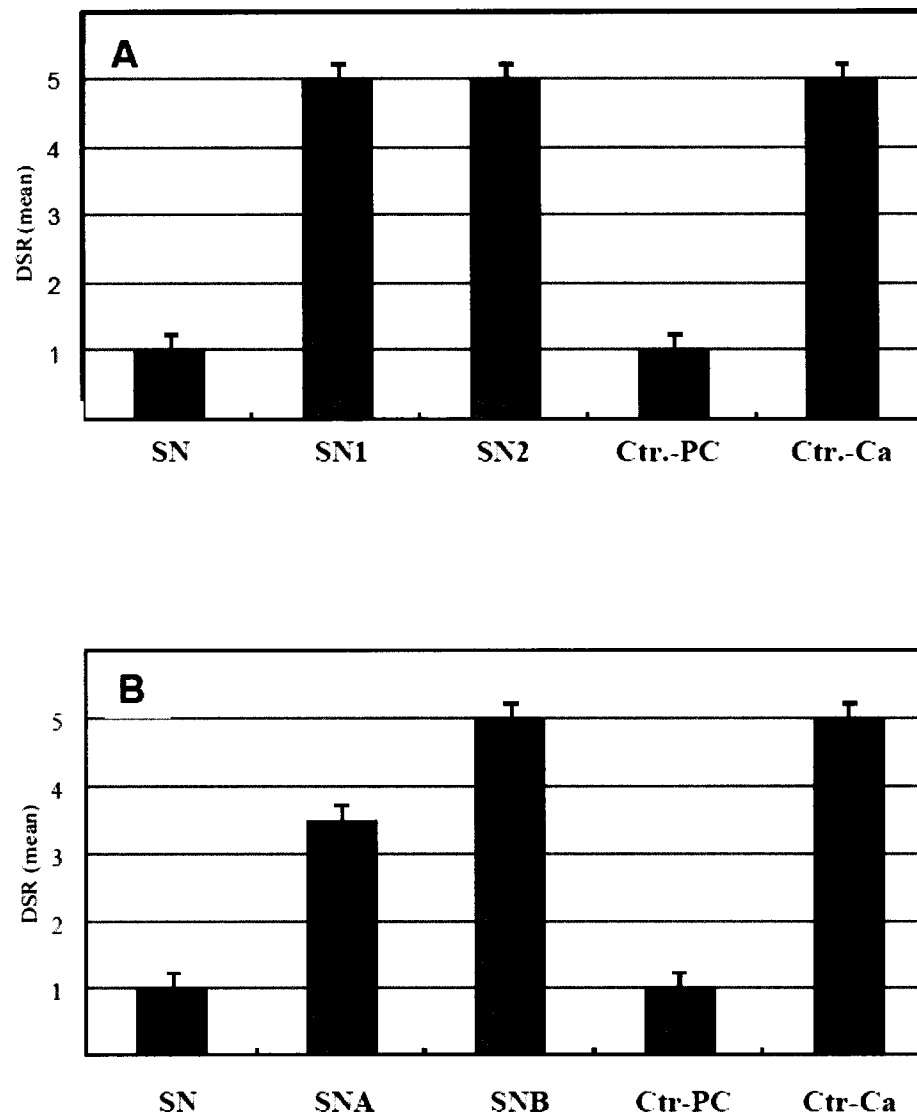


FIGURE 2

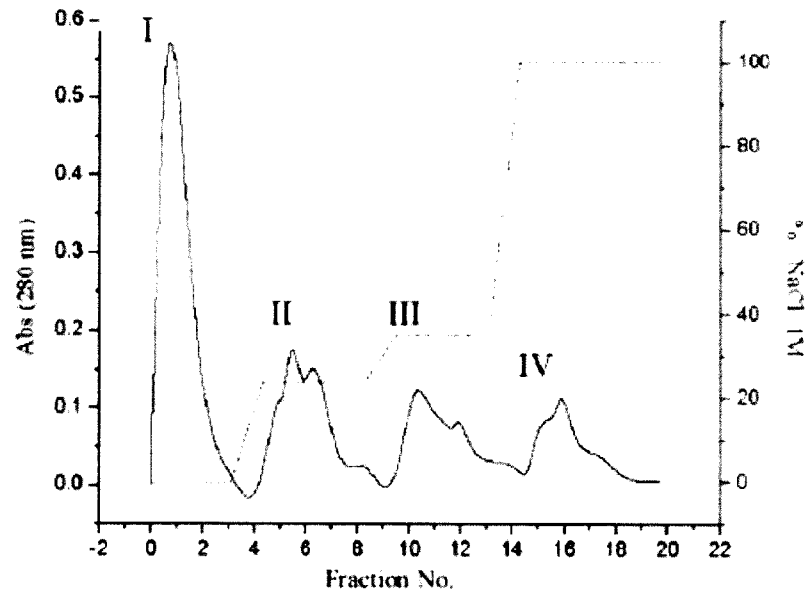


FIGURE 3

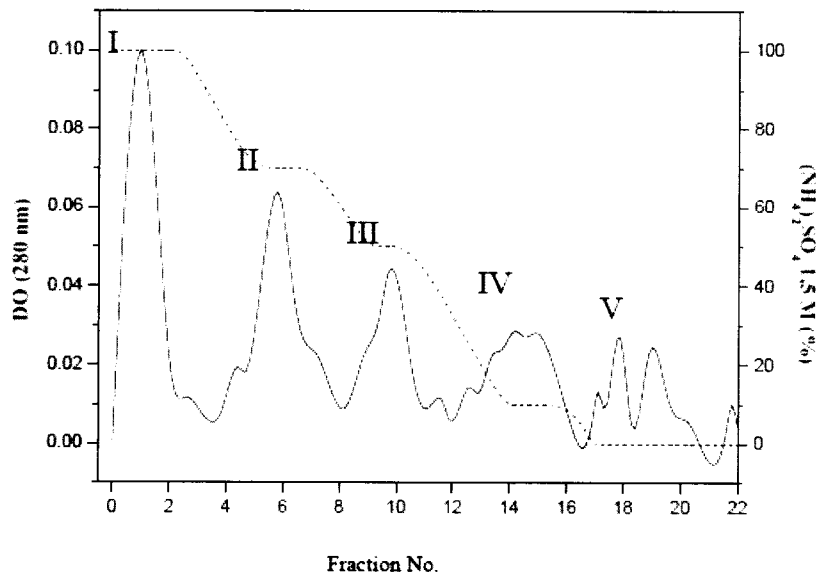


FIGURE 4

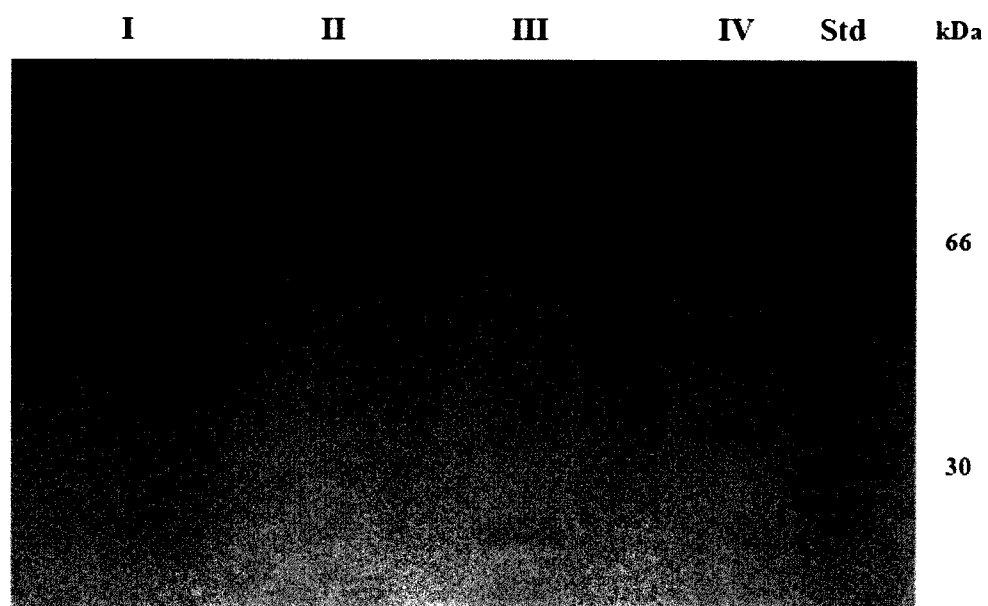


FIGURE 5

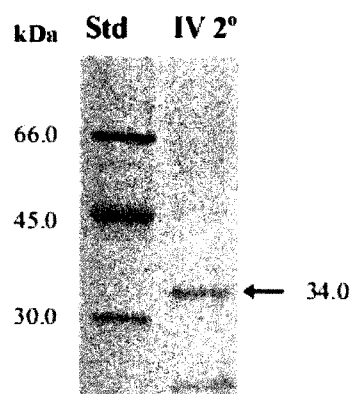


FIGURE 6



FIGURE 7



FIGURE 8



FIGURE 9

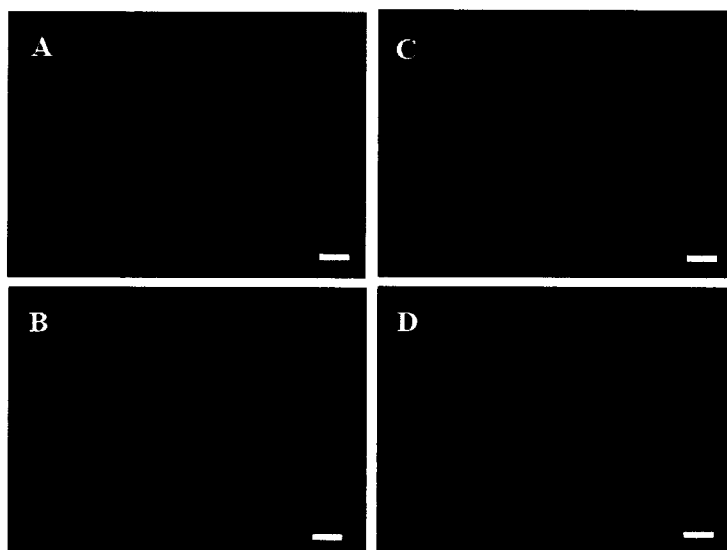


FIGURE 10

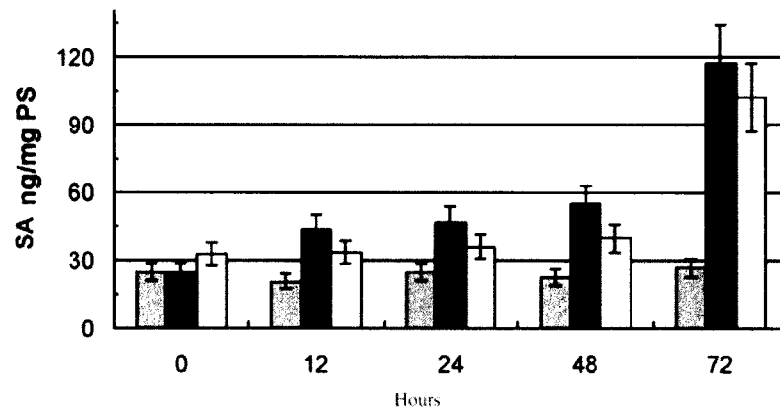


FIGURE 11

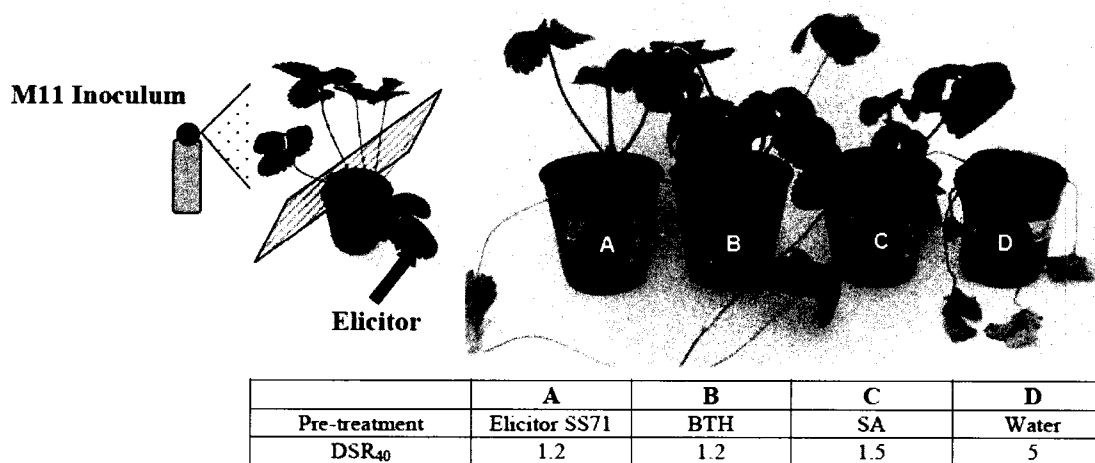


FIGURE 12

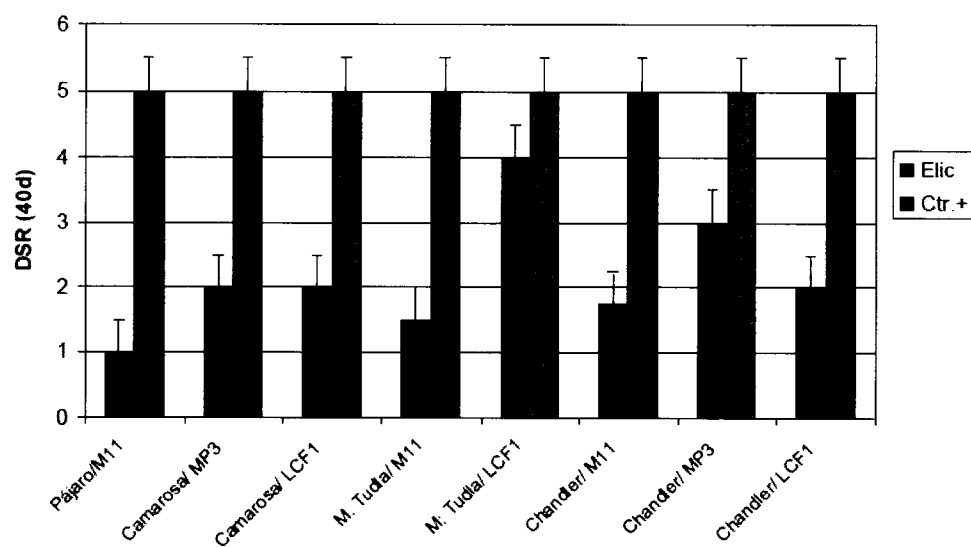


FIGURE 13

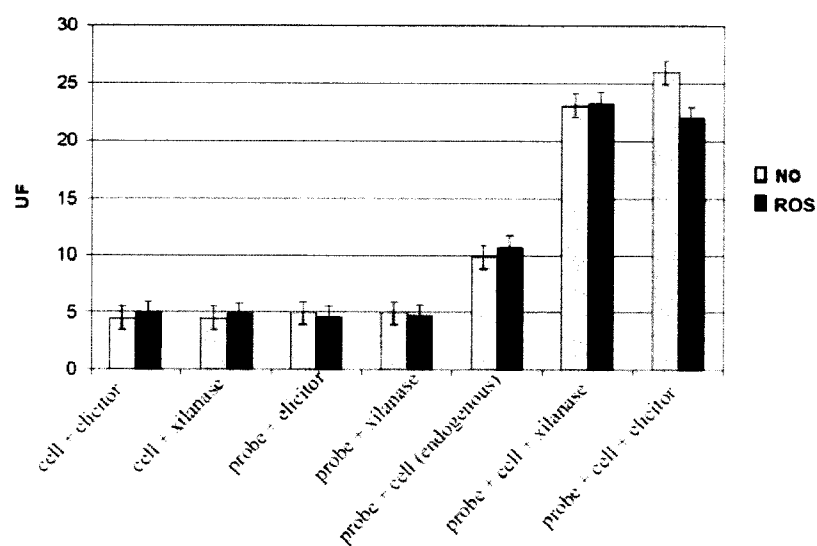


FIGURE 14

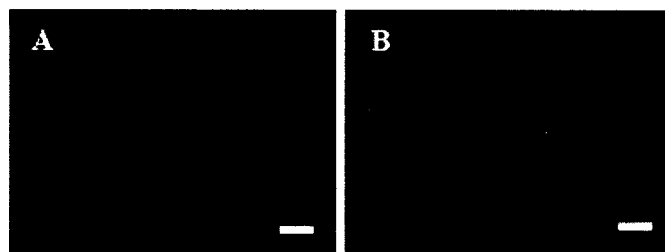


FIGURE 15

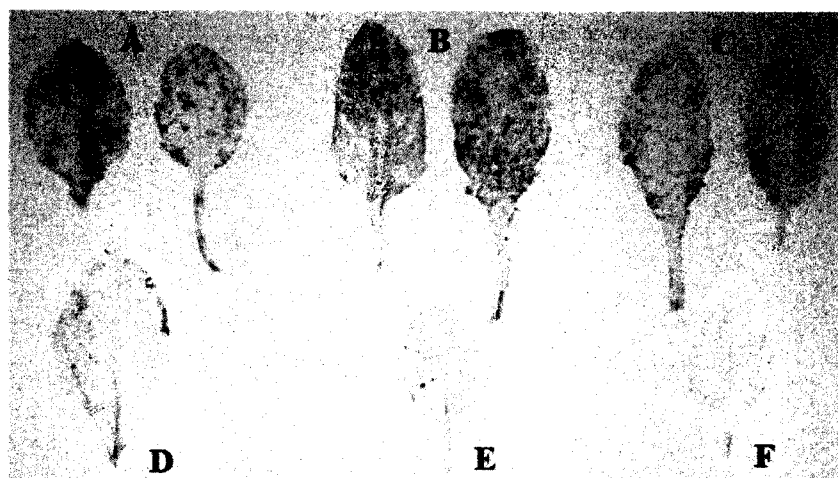


FIGURE 16

N-terminal: msms 1095.19 msms 2441.2 msms 1938.1	A-Y-T-T-Q-A-S-A-P-W (residues 108-118 relative position with respect to the reference sequence of <i>Trichoderma koningii</i>). See FIGURE 19C. V-L-S-D-S-G-S-G-S-T-S-G-I-I-A-G-I-N-Y-V-V-S-D-S-R (residues 204-229 relative position with respect to the reference sequence of <i>Trichoderma koningii</i>). See FIGURE 19C. I-V-A-I-A-T-T-G-V-I-K-G-I-P-S-G-T-P- N- R (residues 362-381 relative position with respect to the reference sequence of <i>Trichoderma koningii</i>). See FIGURE 19C.
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FIGURE 17

A (SEQ ID N° 1)

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1      GCGTACACCA CCCAGGCCAG TGCCCCCTGG GGTCTTGCCC GTATCTCTAC TCGTCAGCGT
61     GGCCCAACTG GCTACACCTA CGACGACAGC GCCGGGCGCAG GAACCTGCTC CTACATCATT
121    GACACCGGCA TCCAGGCTAA CCACCCCAAC TTCGGTGGCC GTGCTTTCCA GCTTGTCTCC
181    TACCAAGGCA GCAACGCCGA CGGTAATGGC CACGGCACTC ACGTTGCCGG TACCATCGGT
241    TCTACCACCT ACGGTGTGCG CAAGCGCACC ACCCTCCTCG GCGTCAAGGT CCTCAGCGAC
301    TCCGGCTCCG GTTCCACCTC CGGTATCATC GCCGGCATCA ACTACGTCGT CAGCGACTCT
361    CGTCCCGCA GCTGCCCAA CGGTTCCGTC GCCAACATGT CGCTCGGCGG AGGCTACTCT
421    GCTTCGCTCA ACAGCGCGGC CAAGTCCTTG ATCGACAACA ACATCTTCCT TGCCGTTGCT
481    GCCGGTAACG AGAACCAGAA CGCCGCCAAT GTCTCCCCTG CTTCTGAGCC GACTGTCTGC
541    ACTGTTGGTG CGACCACTTC TGCCGACGCC AAGGCTTCTT TCTCCAATA CGGCTCCGGT
601    GTCGACATCT TCGTCTCTGG TCAGACATT CTATCCACTT GGATTGGCAG CAGCACCAAC
661    ACCATCTCTG GCACCTCCAT GGCTTCTCCC CACATCGCCG GTCTTGCTGC TTACCTTGCT
721    GGTCTTGAGG GCTTCCCGG TGCCAGGCC CTGTGCAACC GCATCGTCGC CCTCGCTACC
781    ACTGGTGTC TACCGGTCT GCCAGCGGT ACCCCCAACC GCCTTGCTT CAACGGCAAC
841    CCCTCTGGTT AAA

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B

Accession	Description	Max score	Total score	Query coverage	E value	Max ident
ABN04079.1	SprT [Hvooorea koninui]	298	298	99%	4e-79	58%
3F7Q-A	Chain A, Crystal Structure Of Cuticle-Degradng Protease From Pae	296	296	99%	2e-78	57%
ABC22256.1	subtilisin-like serine protease precursor [Paecilomyces lilacinus]	296	296	99%	2e-78	57%
AA491584.1	serine protease [Paecilomyces lilacinus]	296	296	99%	2e-78	57%
CAB64346.1	subtilisin-like protease PR11 [Metarhizium anisopliae var. anisopliae]	288	288	99%	4e-76	55%
CAC95043.1	subtilisin-like protease PR11 [Metarhizium anisopliae var. anisopliae]	285	285	98%	3e-75	54%
ABQ51089.1	serine protease [Hirsutella minnesotensis]	281	281	99%	5e-74	55%
XP_364121.1	hypothetical protein MGG_08966 [Magnaporthe oryzae 70-15] >gb E	281	281	99%	5e-74	57%
CAB95012.1	subtilisin-like protease PR1B [Metarhizium anisopliae var. anisopliae]	280	280	98%	2e-73	53%
AAC49831.1	subtilisin-like protease Pr1B [Metarhizium anisopliae]	280	280	98%	2e-73	53%
ABX79999.1	serine protease [Ophiocordyceps sinensis]	279	279	99%	3e-73	54%
ABD96101.1	alkaline serine protease [Hirsutella rhossiliensis]	278	278	98%	3e-73	54%
XP_957384.1	proteinase T precursor [Neurospora crassa OR74A] >gb EAA28148.	278	278	97%	3e-73	56%
XP_001224513.1	hypothetical protein CHGG_06857 [Chaetomium oboosum CBS 146]	278	278	99%	5e-73	55%
ACT66136.1	subtilisin-like serine protease PR1A [Metarhizium anisopliae]	277	277	99%	1e-72	53%
XP_001903167.1	unnamed protein product [Podospore anserina] >emb CAP60959.11	275	275	98%	3e-72	57%
CAC95049.1	subtilisin-like serine protease PR1A [Metarhizium anisopliae var. anisopliae]	274	274	99%	9e-72	53%
P29138.1	ReName: Full=Cuticle-degrading protease; AltName: Full=PR1; Alt	274	274	99%	9e-72	53%
BAE70705.1	elastase-like serine protease [Metarhizium anisopliae]	274	274	99%	9e-72	53%
CAC95042.1	subtilisin-like protease PR1A [Metarhizium anisopliae var. anisopliae]	272	272	99%	3e-71	53%
ACT66138.1	subtilisin-like serine protease PR1A [Metarhizium flavoviride var. m]	271	271	98%	6e-71	53%
ACB56624.1	insect cuticle degrading enzyme [Metarhizium anisopliae]	271	271	98%	6e-71	53%
AA_797788.1	subtilisin-like protein PR1A [Metarhizium acridum]	271	271	98%	6e-71	53%
CAC95045.1	subtilisin-like protease PR1A [Metarhizium anisopliae var. acridum]	271	271	98%	7e-71	53%
CAB63911.1	Subtilisin-like serine protease PR1A [Metarhizium anisopliae var. ac]	271	271	98%	7e-71	53%
ABX79998.1	serine protease [Ophiocordyceps sinensis]	270	270	97%	1e-70	52%
CAC95044.1	subtilisin-like protease PR1B [Metarhizium anisopliae var. anisopliae]	270	270	98%	1e-70	52%
ACT66134.1	subtilisin-like serine protease PR1A [Metarhizium anisopliae]	269	269	99%	2e-70	52%
ABR20899.1	subtilisin-like protein PR1A [Metarhizium acridum]	269	269	98%	2e-70	53%
AAR_5024.1	subtilisin-like serine protease PR1A [Metarhizium anisopliae]	269	269	86%	2e-70	58%
BAE70704.1	elastase-like serine protease [Metarhizium anisopliae] >db BAE707	269	269	99%	2e-70	52%
ACT66135.1	subtilisin-like serine protease PR1A [Metarhizium anisopliae]	268	268	99%	6e-70	52%
AAR26021.1	subtilisin-like serine protease PR1A [Metarhizium anisopliae]	268	268	86%	6e-70	58%
AAR26027.1	subtilisin-like serine protease PR1A [Metarhizium anisopliae]	267	267	86%	8e-70	58%
ABK27198.1	subtilisin-like protease [Neotyphodium lolii]	267	267	98%	1e-69	54%
ABK27194.1	subtilisin-like protease [Epichloe festucae]	267	267	98%	1e-69	53%
AAR26029.1	subtilisin-like serine protease PR1A [Metarhizium anisopliae]	267	267	86%	1e-69	57%
BAE70707.1	elastase-like serine protease [Metarhizium anisopliae]	266	266	99%	1e-69	52%

FIGURE 18

A (SEQ ID N° 2)

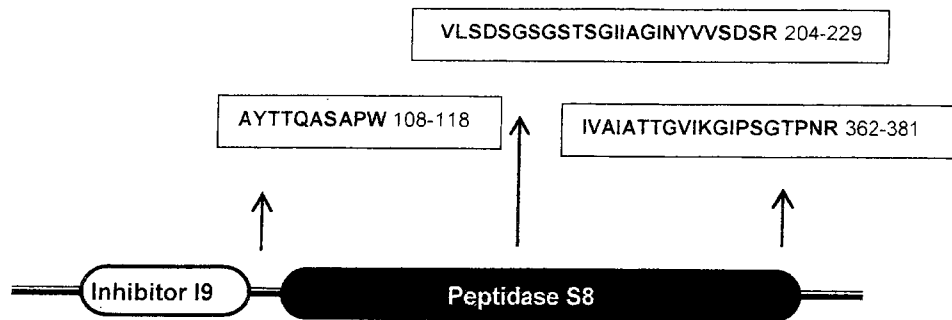
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1      AYTQTASAPW GLARISTRQR GPTGYTYDDS AGAGTCSYII DTGIQANHPN FGGRAFLQVS
61     YQGSNADGNG HGTHVAGTIG STTYGVAKRT TLLGVKVLSD SGSGSTSGII AGINYVVSIDS
121    RSRSCPNGSV ANMSLGGGYS ASLNSAAKSL IDNNIFLAVA AGNENQNAAN VSPASEPTVC
181    TVGATTSADA KASFSNYGSG VDIFAPGQSI LSTWIGSSTN TISGTSMASP HIAGLAAYLA
241    GLEGFPGAQA LCNRIVALAT TGVITGLPSG TPNRLAFNGN PSG
  
```

B

Accession	Description	Max score	Total score	Query coverage	E value
AFN04079.1	Sort (Hydrocra koninoid)	374	374	99%	4e-102
CAB64346.1	subtilisin-like protease PR11 (Metarhizium anisopliae var. anisopli)	373	370	99%	1e-100
CAC95043.1	subtilisin-like protease PR11 (Metarhizium anisopliae var. anisopli)	369	369	99%	2e-100
ABO32356.1	subtilisin-like serine protease precursor (Paecilomyces lilacinus)	366	360	99%	7e-98
AAA91584.1	serine protease (Paecilomyces lilacinus)	365	359	99%	2e-97
3F70-A	Chain A, Crystal Structure Of Cuticle-Degrading Protease From F	359	359	99%	2e-97
ACT66136.1	subtilisin-like serine protease PR1A (Metarhizium anisopliae)	358	358	98%	3e-97
BAE70795.1	elastase-like serine protease (Metarhizium anisopliae)	357	357	98%	5e-97
ABX79936.1	serine protease (Ophiocordyceps sinensis)	357	357	100%	5e-97
ABO51085.1	serine protease (Hirsutiella minnesotensis)	357	357	99%	1e-96
CAI29042.1	subtilisin-like protease PR1A (Metarhizium anisopliae var. anisopli)	355	355	98%	2e-96
CAC95049.1	subtilisin-like serine protease PR1A (Metarhizium anisopliae var. anisopli)	355	355	98%	3e-96
AAC39831.1	subtilisin-like protease PR1B (Metarhizium anisopliae)	353	353	99%	1e-95
ABD96101.1	alkaline serine protease (Hirsutiella rhossiliensis)	351	351	100%	5e-95
AAW55381.1	alkaline serine protease (Lecanicillium osaliotae)	350	350	99%	7e-95
ACT66138.1	subtilisin-like serine protease PR1A (Metarhizium flavoviride var. RecName: Full=Cuticle-degrading protease; AltName: Full=PR1;	350	350	98%	9e-95
P39138.1	subtilisin-like protease PR1B (Metarhizium anisopliae var. anisopli)	349	349	99%	2e-94
CAB95012.1	subtilisin-like protein PR1A (Metarhizium acridum)	349	349	98%	2e-94
AA197738.1	Subtilisin-like serine protease PR1A (Metarhizium anisopliae var. insect cuticle degrading enzyme (Metarhizium anisopliae)	348	348	98%	3e-94
CAC95045.1	subtilisin-like protease PR1A (Metarhizium anisopliae var. acridur	348	348	98%	4e-94
Q66GV9.1	RecName: Full=Alkaline serine protease ver112; Flags: Precurs	348	348	99%	4e-94
3F7M-A	Chain A, Crystal Structure Of Apo Cuticle-Degrading Protease (v	347	347	98%	1e-93
ABR20899.1	subtilisin-like protein PR1A (Metarhizium acridum)	347	347	98%	1e-93
ABX79938.1	serine protease (Ophiocordyceps sinensis)	344	344	99%	6e-93
CAC95044.1	subtilisin-like protease PR1B (Metarhizium anisopliae var. anisopli)	343	343	99%	1e-92
BAE70794.1	elastase-like serine protease (Metarhizium anisopliae) >dbiBAB	340	340	98%	1e-91
ACT66134.1	subtilisin-like serine protease PR1A (Metarhizium anisopliae)	338	338	98%	3e-91
AAR39852.1	secreted protein 2 (Leptosphaeria maculans)	338	338	99%	4e-91
ACT66135.1	subtilisin-like serine protease PR1A (Metarhizium anisopliae)	337	337	98%	8e-91
BAE70797.1	elastase-like serine protease (Metarhizium anisopliae)	337	337	98%	1e-90
ACT66137.1	subtilisin-like serine protease PR1A (Metarhizium anisopliae)	336	336	98%	2e-90
AAR26024.1	subtilisin-like serine protease PR1A (Metarhizium anisopliae)	335	335	86%	2e-90
AAR26031.1	subtilisin-like serine protease PR1A (Metarhizium anisopliae)	333	333	86%	8e-90
AAR26027.1	subtilisin-like serine protease PR1A (Metarhizium anisopliae)	333	333	86%	1e-89

FIGURE 19 A and B



Source	Domain	Start	End
PfamA	Inhibitor I9	40	107
PfamA	Peptidase S8	124	368

FIGURE 19 C

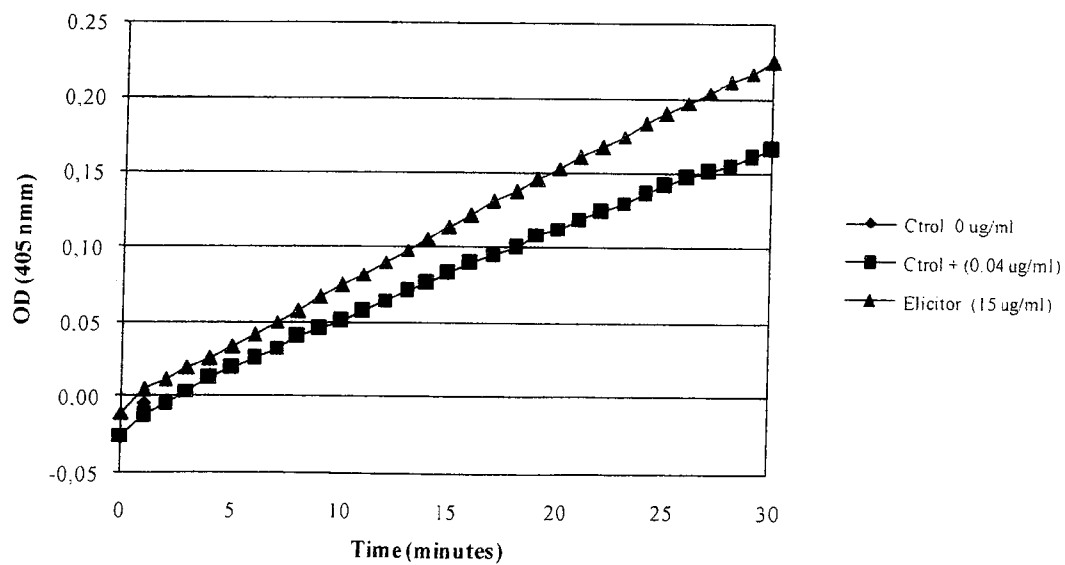


FIGURE 20