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(54) Title: PATHOGEN-RESISTANT TRANSGENIC PLANTS		
(57) Abstract Recombinant pathogen-resistant plants comprise transformed plant cells, with the transformed plant cells containing a he- terologous DNA construct comprising an expression cassette. The construct comprises a promoter, a structural gene positioned downstream from the promoter, and a termination sequence such as the nos terminator positioned downstream from the structural gene. The promoter is one which is activated by a plant pathogen which attacks the plant, such as the RB7 nematode-responsive element. The structural gene encodes a product such a Barnase which is toxic to the plant cells.		

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PATHOGEN-RESISTANT TRANSGENIC PLANTS

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Field of the Invention

This invention relates to methods of controlling plant pathogens in general, and particularly relates to methods of controlling plant-parasitic nematodes.

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Background of the Invention

World-wide, plant-parasitic nematodes are among the most devastating pathogens of life sustaining crops. In 1984, nematodes accounted for more than \$100 billion in economic losses. The United States' portion of this figure is almost \$6 billion. While such monetary figures are staggering, much of this crop destruction occurs in tropical and subtropical regions where agricultural production is often a matter of life and death.

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Genetic resistance to certain nematode species is available in some cultivars, but these are restricted

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in number and the availability of cultivars with both desirable agronomic features and resistance is limited. In addition, traditional methods for plant breeding require 5-10 years to produce a viable cultivar, while
5 the need for new nematode control tools is immediate and critical.

The major means of nematode control has been the application of chemical nematicides. During 1982, in the United States alone over 100 million pounds of
10 nematicide were applied to crops. Chemical nematicides are generally highly toxic compounds known to cause substantial environmental impact. In the past several years, issues such as ground water contamination, mammalian and avian toxicity, and residues in food have
15 caused much tighter restrictions on the use of chemical nematicides. Unfortunately, in many situations there is no alternative available for growers who rely upon nematicides to protect their crop from root-knot and cyst nematodes.

20 Recently, it has become possible to genetically engineer crop plants resistant to particular pests. Perhaps the first example of this approach is that of viral coat protein genes introduced into tobacco. Tobacco plants genetically engineered to carry and
25 express the Tobacco Mosaic Virus coat protein gene were shown to resist systemic infection by the intact virus. Another strategy is to utilize gene sequences that will kill or inhibit the pathogen directly. This approach has been used to produce transgenic plants that express the
30 insect toxin gene from the bacterium *Bacillus thuringiensis* which, when ingested, causes insect gut paralysis. Although this strategy has resulted in crop cultivars resistant to certain pests, there are several disadvantages to the approach. Primarily, the
35 constitutive expression of any "toxin" gene places upon the pest population very strong selective pressure for resistance. Another disadvantage of this approach is the

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negative energy balance the host plant suffers when there is no pest pressure. Finally, the constitutive global expression of toxin genes guarantees that non-target species, including humans, will be exposed to the protein product.

The present invention is based on our work in developing new ways of combatting plant pathogens.

Summary of the Invention

The present approach to imparting pathogen resistance to plants is dramatically different from the foregoing strategies in that it directs a toxic compound to plant cells rather than the pathogen itself. Thus, when a pathogen attempts to infect the plant the infected cells tend to die, thereby both inhibiting the ability of the pathogen to infect the plant and disrupting the pathogen's normal life cycle.

In view of the foregoing, a first aspect of the present invention is a recombinant pathogen-resistant plant comprising transformed plant cells. The transformed plant cells contain a heterologous DNA construct comprising an expression cassette, which construct comprises, in the 5' to 3' direction, a promoter, a structural gene positioned downstream from the promoter and operatively associated therewith, and a termination sequence positioned downstream from the structural gene and operatively associated therewith. The promoter is activated by a plant pathogen which attacks the plant, and the structural gene encodes a product toxic to the plant cells.

A second aspect of the present invention is a crop comprised of a plurality of plants as given above planted together in an agricultural field (i.e., any common environment in which pathogens are shared between plants of the crop, including a greenhouse).

A third aspect of the present invention is a method of combatting a plant pathogen in an agricultural

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field. The method comprises planting the field with a crop of recombinant pathogen-resistant plants as given above.

5 A fourth aspect of the present invention is a method of making a recombinant pathogen-resistant plant. The method comprises providing a plant cell capable of regeneration, then transforming the plant cell with a DNA construct comprising an expression cassette, which
10 construct comprises, in the 5' to 3' direction, a promoter activated by a plant pathogen, a structural gene positioned downstream from said promoter and operatively associated therewith, and a termination sequence positioned downstream from the structural gene and operatively associated therewith. A recombinant
15 pathogen-resistant plant is regenerated from the transformed plant cell.

A fifth aspect of the present invention is a DNA construct comprising an expression cassette, which
20 construct comprises, in the 5' to 3' direction, a promoter activated by a plant pathogen, a structural gene positioned downstream from the promoter and operatively associated therewith, and a termination sequence positioned downstream from the structural gene and operatively associated therewith. The structural gene
25 encodes a product toxic to plant cells.

The foregoing and other objects and aspects of this invention are explained in detail in the drawings herein and the specification set forth below.

Brief Description of the Drawings

30 **Figure 1** shows restriction maps of genomic clones hybridizing to the root-specific cDNA clone TobRB7. Genomic clones were restriction mapped for *Bam*HI (B), *Hind*III (H), *Pst*I (P), *Eco*RI (R), and *Sal*I (S). Regions hybridizing to the root specific cDNA clone RB7
35 are shown under the bars; and

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Figure 2 schematically illustrates the deletion analysis of the genomic RB7 promoter sequence. RB7 flanking regions of various lengths were prepared and coupled to a β -Glucuronidase (GUS) gene, transgenic plants prepared with the construct, and GUS activity assayed in both the roots and the leaves of the transgenic plants. Results are summarized on the right-hand side of the Figure.

Detailed Description of the Invention

Plant pathogens which may be combatted by the method of the present invention include bacteria, viruses, fungi, and nematodes. The pathogens may be those which attack any tissue of the plant, including leaf and root, but the invention is contemplated to be particularly useful for combatting pathogens which attack (or infect) the root. The present invention may be carried out with a variety of plants, both monocots and dicots, preferably dicots.

The invention may be illustrated with respect to nematodes, particularly the root knot nematodes (*Meloidogyne* spp.) and the cyst nematodes (*Globodera* spp. and *Heterodera* spp.), which have similar life cycles. Root-knot nematodes are sedentary endoparasites with an extremely intimate and complex relationship to the host plant. The infective second stage juvenile (J2) is free in the soil. Upon location of a host root, the J2 penetrates the root intercellularly in the region just posterior to the root cap and migrates to the developing vascular cylinder. The nematode then orients itself parallel to the cylinder and injects glandular secretions into the plant cells surrounding its head, resulting in the initiation of nematode feeding cells. These 5-7 cells undergo rapid nuclear divisions, increase tremendously in size, and become filled with pores and cell wall invaginations. The feeding site cells, or "giant cells", function as super transfer cells to

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provide nourishment to the developing nematode. During this time, the nematode loses the ability to move and swells from the normal eel shaped J2 to a large, pear shaped adult female. As the nematode feeds on the giant cells, parthenogenic reproduction results in the the disposition of 300-400 eggs. This entire process occurs over the span of 20-30 days, and root-knot nematodes may complete as many as 7 generations during a cropping season. The life cycle of the cyst nematode is essentially the same, except that its feeding site is referred to as a "syncytia", and it undergoes sexual reproduction. It will be seen that, by causing the plant itself to kill or disable the cells upon which the pathogen must feed, the pathogen will be much less successful at infecting the plant.

The pathogen-inducible promoters (or "pathogen-responsive elements") of two gene types may be employed in the present invention: (a) genes not normally expressed in plant tissues, but expressed in response to pathogen infection; and (b) genes normally expressed in plant tissues whose expression is increased in response to pathogen infection. A variety of screening strategies allow the isolation of genes, and their corresponding pathogen-responsive elements of either type. See, e.g., M. Conkling et al., *Plant Physiol.* **93**, 1203-1211 (1990); S. Gurr et al., *Mol. Gen. Genet.* **226**, 361-366 (1991). Screening may be carried out with the polymerase chain reaction procedure, as described in U.S. Patents Nos. 4,683,185 and 4,683,202, the disclosures of which are to be incorporated herein by reference, or by low stringency hybridization procedures (e.g., hybridization procedures in which probes are capable of hybridizing to sequences to which they are 60% homologous, such as procedures characterized by a wash stringency of 5x SSC, 25% Formamide and 0.1% SDS at 42° C). In general, a cDNA library from the mRNA of a pathogen-infected plant tissue is differentially screened with probes generated from

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5 cDNA obtained from the mRNA of (a) plant tissue (e.g.,
plant root tissue) infected with the pathogen and (b)
corresponding plant tissue not infected with that
pathogen to identify clones of genes which exhibit
greater expression in pathogen-infected plants. The
10 pathogen-responsive elements of these genes are then
identified by deletion analysis. These elements may in
turn be used to screen cDNA libraries of other plants and
other plant tissues at low stringency for homologous
15 pathogen-responsive elements.

Hybridization procedures are available which
allow for the isolation of cDNA clones whose mRNA levels
are as low as about 0.05% of poly(A⁺)RNA. See M. Conkling
et al., *supra*. In brief, cDNA libraries are screened
20 using single-stranded cDNA probes of reverse transcribed
mRNA from plant tissue (i.e., roots and leaves). For
differential screening, a nitrocellulose or nylon
membrane is soaked in 5xSSC, placed in a 96 well suction
manifold, 150 μ L of stationary overnight culture
25 transferred from a master plate to each well, and vacuum
applied until all liquid has passed through the filter.
150 μ L of denaturing solution (0.5M NaOH, 1.5 M NaCl) is
placed in each well using a multiple pipetter and allowed
to sit about 3 minutes. Suction is applied as above and
30 the filter removed and neutralized in 0.5 M Tris-HCl (pH
8.0), 1.5 M NaCl. It is then baked 2 hours *in vacuo* and
incubated with the relevant probes. By using nylon
membrane filters and keeping master plates stored at -
70°C in 7% DMSO, filters may be screened multiple times
with multiple probes and appropriate clones recovered
after several years of storage.

For example, to isolate genes whose expression
is induced or enhanced by nematode infection, a cDNA
library of mRNA isolated from nematode infected tobacco
35 roots is constructed. The roots are staged such that
mRNA is isolated at the time of giant cell initiation.
The library is then screened by the procedures given

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above using single stranded cDNA probes of mRNA isolated from nematode-infected and control roots. Those cDNA clones exhibiting differential expression are then used as probes on tobacco genomic Southern blots (to confirm the cDNA corresponds to tobacco and not nematode transcripts) and Northern blots of root RNA from infected and control tissue (to confirm differential expression). Those clones exhibiting differential expression are then used as probes to screen an existing tobacco genomic library. Essentially the same procedure is carried out with plants other than tobacco and nematodes (or other pathogens) other than root-knot nematodes. The procedure is useful for identifying promoters induced by cyst nematodes, in which case the roots are staged such that mRNA is isolated at the time of syncytia initiation. For example, a potato-cyst nematode (*Globodera* spp.) inducible promoter is isolated from potato plants (*Solanum tuberosum*) in accordance with the foregoing procedures. See, e.g., S. Gurr et al., *supra*.

While a particularly preferred promoter for carrying out the present invention is the nematode-responsive element of the TobRB7 promoter, also useful in the present invention are promoters and pathogen-responsive elements isolated from other tobacco genes, or from plants other than tobacco as set forth below, which are homologous to the TobB7 promoter nematode responsive element and are capable of directing transcription of a downstream structural gene in a plant cell in response to nematode infection. RB7 promoter sequences and their nematode-responsive elements may be obtained from other plant species by using TobRB7 structural gene segments as probes to screen for homologous structural genes in other plants by DNA hybridization under low stringency conditions, as given above. Alternatively, regions of the TobRB7 structural gene which are conserved among species are used as PCR primers to amplify a longer segment from a species other than Tobacco, and that

longer segment used as a hybridization probe (the latter approach permitting higher stringency screening).

Examples of plant species which may be used in accordance with the foregoing procedures to generate additional RB7 sequences include soybean, potato, cotton, sugarbeet, sunflower, carrot, celery, flax, cabbage and other cruciferous plants, pepper, tomato, citrus trees, bean, strawberry, lettuce, maize, alfalfa, oat, wheat, rice, barley, sorghum and canola. RB7 nematode-responsive elements from other plants are generally those which are at least about 75 percent homologous, more particularly at least about 85 percent homologous, and most particularly at least about 90 percent homologous, to a 50 base segment of the Tobacco RB7 promoter capable of directing nematode-responsive expression of a downstream structural gene in a plant cell. By "50 base segment" is meant a continuous portion of the TobRB7 promoter, or the nematode-responsive element thereof, which is 50 nucleotides in length.

Another illustrative promoter, where the pathogen is a geminivirus, is the AL2 promoter of the geminiviruses, which is activated by the geminivirus AL3 protein. Hence, the geminivirus AL2 promoter serves as a geminivirus responsive element responding to AL3.

An advantage of the present invention is that two or more promoters can be "daisy chained" to a single structural gene. Where each promoter is responsive to a different pathogen, the plant is then provided with resistance to a plurality of promoters. For example, a second promoter may be positioned upstream from the structural gene and operatively associated therewith so that the structural gene is associated with a plurality of promoters, with each of the promoters activated by a different plant pathogen. Still more promoters can be included if desired.

The term "operatively associated," as used herein, refers to DNA sequences on a single DNA molecule

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which are associated so that the function of one is affected by the other. Thus, a promoter is operatively associated with a structural gene when it is capable of affecting the expression of that structural gene (i.e., the structural gene is under the transcriptional control of the promoter). The promoter is said to be "upstream" from the structural gene, which is in turn said to be "downstream" from the promoter.

DNA constructs, or "expression cassettes," of the present invention include, 5'-3' in the direction of transcription, a promoter as discussed above, a structural gene operatively associated with the promoter, and, optionally, a termination sequence including stop signal for RNA polymerase and a polyadenylation signal for polyadenylase (e.g., the nos terminator). All of these regulatory regions should be capable of operating in the cells of the tissue to be transformed. The 3' termination region may be derived from the same gene as the transcriptional initiation region or may be derived from a different gene.

Structural genes are those portions of genes which comprise a DNA segment coding for a protein, polypeptide, or portion thereof, possibly including a ribosome binding site and/or a translational start codon, but lacking a promoter. The term can also refer to copies of a structural gene naturally found within a cell but artificially introduced. The structural gene may encode a protein not normally found in the plant cell in which the gene is introduced or in combination with the promoter to which it is operationally associated, in which case it is termed a heterologous structural gene. Genes which may be operationally associated with a promoter of the present invention for expression in a plant species may be derived from a chromosomal gene, cDNA, a synthetic gene, or combinations thereof.

Structural genes employed in carrying out the present invention encode a product which is toxic to

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plant cells. A wide variety of protein or peptide products which are toxic to plant cells can be used, including (but not limited to) enzymes capable of degrading nucleic acids (DNA, RNA) such as nucleases, restriction endonucleases micrococcal nucleas, Rnase A, and barnase; enzymes which attack proteins such as trypsin, pronase A, carboxypeptidase, endoproteinase Asp-N, endoproteinase Glu-C, and endoproteinase Lys-C; ribonucleases such as RNase CL-3 and RNase T₁, toxins from plant pathogenic bacteria such as phaseolotoxin, tabtoxin, and syringotoxin; lipases such as produced from porcine pancrease and *Candida cyclindracea*, membrane channel proteins such as glp F and connexins (gap junction proteins, and antibodies which bind proteins in the cell so that the cell is thereby killed or debilitated. Genes which produce antibodies to plant cell proteins can be produced as described in W. Huse et al., *Science* 246, 1275-1281 (1989). Proteins to which such antibodies can be directed include, but are not limited to, RNA polymerase, respiratory enzymes, cytochrome oxidase, Krebs cycle enzymes, protein kinases, aminocyclopropane-1-carboxylic acid synthase, and enzymes involved in the shikimic acid pathway such as enolpyruvyl shikimic acid-5-phosphate synthase.

Particularly preferred is a structural gene encoding mature *Bacillus amyloliquefaciens* RNase (or Barnase). See, e.g., C. Mariani et al., *Nature* 347, 737-741 (1990); C. Paddon and R. Hartley, *Gene* 40, 231-39 (1985). The toxic product may either kill the plant cell in which it is expressed or simply disable the cell so that it is less capable of supporting the pathogen. It is preferred, particularly where the plant is a food plant, that the plant-toxic product be non-toxic to animals, and particularly be non-toxic to humans.

Where the expression product of the structural gene is to be located in a cellular compartment other than the cytoplasm, the structural gene may be

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constructed to include regions which code for particular amino acid sequences which result in translocation of the product to a particular site, such as the cell plasma membrane, or may be secreted into the periplasmic space or into the external environment of the cell. Various secretory leaders, membrane integration sequences, and translocation sequences for directing the peptide expression product to a particular site are described in the literature. See, for example, Cashmore et al., *Bio/Technology* 3, 803-808 (1985), Wickner and Lodish, *Science* 230, 400-407 (1985).

The expression cassette may be provided in a DNA construct which also has at least one replication system. For convenience, it is common to have a replication system functional in *Escherichia coli*, such as ColE1, pSC101, pACYC184, or the like. In this manner, at each stage after each manipulation, the resulting construct may be cloned, sequenced, and the correctness of the manipulation determined. In addition, or in place of the *E. coli* replication system, a broad host range replication system may be employed, such as the replication systems of the P-1 incompatibility plasmids, e.g., pRK290. In addition to the replication system, there will frequently be at least one marker present, which may be useful in one or more hosts, or different markers for individual hosts. That is, one marker may be employed for selection in a prokaryotic host, while another marker may be employed for selection in a eukaryotic host, particularly the plant host. The markers may be protection against a biocide, such as antibiotics, toxins, heavy metals, or the like; provide complementation, by imparting prototrophy to an auxotrophic host; or provide a visible phenotype through the production of a novel compound in the plant. Exemplary genes which may be employed include neomycin phosphotransferase (NPTII), hygromycin phosphotransferase (HPT), chloramphenicol acetyltransferase (CAT),

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nitrilase, and the gentamicin resistance gene. For plant host selection, non-limiting examples of suitable markers are beta-glucuronidase, providing indigo production, luciferase, providing visible light production, NPTII, providing kanamycin resistance or G418 resistance, HPT, providing hygromycin resistance, and the mutated *aroA* gene, providing glyphosate resistance.

The various fragments comprising the various constructs, expression cassettes, markers, and the like may be introduced consecutively by restriction enzyme cleavage of an appropriate replication system, and insertion of the particular construct or fragment into the available site. After ligation and cloning the DNA construct may be isolated for further manipulation. All of these techniques are amply exemplified in the literature and find particular exemplification in Maniatis et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., 1982.

Vectors which may be used to transform plant tissue with DNA constructs of the present invention include both *Agrobacterium* vectors and ballistic vectors, as well as vectors suitable for DNA-mediated transformation.

Agrobacterium tumefaciens cells containing a DNA construct of the present invention, wherein the DNA construct comprises a Ti plasmid, are useful in methods of making transformed plants. Plant cells are infected with an *Agrobacterium tumefaciens* as described above to produce a transformed plant cell, and then a plant is regenerated from the transformed plant cell.

Numerous *Agrobacterium* vector systems useful in carrying out the present invention are known. For example, U.S. Patent No. 4,459,355 discloses a method for transforming susceptible plants, including dicots, with an *Agrobacterium* strain containing the Ti plasmid. The transformation of woody plants with an *Agrobacterium*

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vector is disclosed in U.S. Patent No. 4,795,855. Further, U.S. Patent No. 4,940,838 to Schilperoort et al. discloses a binary *Agrobacterium* vector (i.e., one in which the *Agrobacterium* contains one plasmid having the vir region of a Ti plasmid but no T region, and a second plasmid having a T region but no vir region) useful in carrying out the present invention.

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Microparticles carrying a DNA construct of the present invention, which microparticle is suitable for the ballistic transformation of a plant cell, are also useful for making transformed plants of the present invention. The microparticle is propelled into a plant cell to produce a transformed plant cell, and a plant is regenerated from the transformed plant cell. Any suitable ballistic cell transformation methodology and apparatus can be used in practicing the present invention. Exemplary apparatus and procedures are disclosed in Sanford and Wolf, U.S. Patent No. 4,945,050, and in Agracetus European Patent Application Publication No. 0 270 356, titled Pollen-mediated Plant Transformation. When using ballistic transformation procedures, the expression cassette may be incorporated into a plasmid capable of replicating in the cell to be transformed. Examples of microparticles suitable for use in such systems include 1 to 5 μm gold spheres. The DNA construct may be deposited on the microparticle by any suitable technique, such as by precipitation.

30
Plant species may be transformed with the DNA construct of the present invention by the DNA-mediated transformation of plant cell protoplasts and subsequent regeneration of the plant from the transformed protoplasts in accordance with procedures well known in the art.

35
Any plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a vector of the present invention. The term "organogenesis," as used herein,

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means a process by which shoots and roots are developed sequentially from meristematic centers; the term "embryogenesis," as used herein, means a process by which shoots and roots develop together in a concerted fashion (not sequentially), whether from somatic cells or gametes. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen, embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristems, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and hypocotyl meristem).

Plants of the present invention may take a variety of forms. The plants may be chimeras of transformed cells and non-transformed cells; the plants may be clonal transformants (e.g., all cells transformed to contain the expression cassette); the plants may comprise grafts of transformed and untransformed tissues (e.g., a transformed root stock grafted to an untransformed scion in citrus species). The transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, first generation (or T1) transformed plants may be selfed to give homozygous second generation (or T2) transformed plants, and the T2 plants further propagated through classical breeding techniques. A dominant selectable marker (such as *npt II*) can be associated with the expression cassette to assist in breeding.

Plants which may be employed in practicing the present invention include (but are not limited to) tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), soybean (*glycine max*), peanuts (*Arachis hypogaea*), cotton (*Gossypium hirsutum*), sweet potato (*Ipomoea batatus*), cassava (*Manihot esculenta*), coffee (*Cofea spp.*), coconut

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(*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), Avocado (*Persea americana*), Fig (*Ficus casica*), Guava (*Psidium guajava*),
5 Mango (*Mangifera indica*), Olive (*Olea europaea*), papaya (*Carica papaya*), Cashew (*Anacardium occidentale*), Macadamia (*Macadamia integrifolia*), Almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), corn (*Zea mays*), wheat, oats, rye, barley, rice, vegetables, ornamentals,
10 and conifers. Vegetables include tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuea sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.) and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C.*
15 *cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petnunias (*Petunia hybrida*),
20 carnation (*dianthus caryophyllus*), poinsettia (*Euphorbia pulcherima*), and chyrsanthemum. Conifers which may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus*
25 *ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*); Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam
30 fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*).

Some plants-parasitic nematodes from which plants may be protected by the present invention, and the
35 corresponding plants, are as follows: Alfalfa: *Ditylenchus dipsaci*, *Meloidogyne hapla*, *Meloidogyne incognita*, *Meloidogyne javanica*, *Pratylenchus* spp.,

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Paratylenchus spp., and *Xiphinema* spp.; Banana:
Radopholus similis, *Helicotylenchus multicinctus*,
Meloidogyne incognita, *M. arenaria*, *M. javanica*,
Pratylenchus coffeae, and *Rotylenchulus reniformis*; Beans
5 & peas: *Meloidogyne* spp., *Heterodera* spp., *Belonolaimus*
spp., *Helicotylenchus* spp., *Rotylenchulus reniformis*,
Paratrichodorus anemones, and *Trichodorus* spp.; cassava:
Rotylenchulus reniformis, *Meloidogyne* spp. cereals:
Anguina tritici (Emmer, rye, spelt wheat), *Biddera avenae*
10 (oat, wheat), *Ditylenchus dipsaci* (rye, oat), *Subanguina*
radicicola (oat, barley, wheat, rye), *Meloidogyne naasi*
(barley, wheat, rye), *Pratylenchus* spp. (oat, wheat,
barley, rye), *Paratylenchus* spp. (wheat),
Tylenchorhynchus spp. (wheat, oat); chickpea:
15 *Heterodera cajani*, *Rotylenchulus reniformis*, *Hoplolaimus*
seinhorsti, *Meloidogyne* spp., *Pratylenchus* spp.; Citrus:
Tylenchulus semipenetrans, *Radopholus similis*, *Radopholus*
citrophilus (Florida only), *Hemicycliophora arenaria*,
Pratylenchus spp., *Meloidogyne* spp., *Bolonolaimus*
20 *longicaudatus* (Florida only), *Trichodorus*,
Paratrichodorus, *Xiphinema* spp.; clover: *Meloidogyne*
spp., *Heterodera trifolii*; coconut: *Rhadinaphelenchus*
cocophilus; coffee: *Meloidogyne incognita* (Most
important in Brazil), *M. exigua* (widespread),
25 *Pratylenchus coffeae*, *Pratylenchus brachyurus*, *Radopholus*
similis, *Rotylenchulus reniformis*, *Helicotylenchus* spp.;
corn: *Pratylenchus* spp., *Paratrichodorus minor*,
Longidorus spp., *Hoplolaimus columbus*; cotton:
Meloidogyne incognita, *Belonolaimus longicaudatus*,
30 *Rotylenchulus reniformis*, *Hoplolaimus galeatus*,
Pratylenchus spp., *Tylenchorhynchus* spp., *Paratrichodorus*
minor; grapes: *Xiphinema* spp., *Pratylenchus vulnus*,
Meloidogyne spp., *Tylenchulus semipenetrans*,
Rotylenchulus reniformis; grasses: *Pratylenchus* spp.,
35 *Longidorus* spp., *Paratrichodorus christiei*, *Xiphinema*
spp., *Ditylenchus* spp.; peanut:

Pratylenchus spp., *Meloidogyne hapla.*, *Meloidogyne arenaria*, *Criconemella* spp., *Belonolaimus longicaudatus* (in Eastern United States); pigeonpea: *Heterodera cajani*, *Rotylenchulus reniformis*, *Hoplolaimus seinhorsti*,
5 *Meloidogyne* spp., *Pratylenchus* spp.; pineapple: *Paratrichodorus christiei*, *Criconemella* spp., *Meloidogyne* spp., *Rotylenchulus reniformis*, *Helicotylenchus* spp., *Pratylenchus* spp., *Paratylenchus* spp.; potato: *Globodera rostochiensis*, *Globodera pallida*, *Meloidogyne* spp.,
10 *Pratylenchus* spp., *Trichodorus primitivus*, *Ditylenchus* spp., *Paratrichodorus* spp., *Nacoabbus aberrans*; rice: *Aphelenchoides besseyi*, *Ditylenchus angustus*, *Hirschmanniella* spp., *Heterodera oryzae*, *Meloidogyne* spp.
small fruits: *Meloidogyne* spp.; *Pratylenchus* spp.,
15 *Xiphinema* spp., *Longidorus* spp., *Paratrichodorus christiei*, *Aphelenchoides* spp. (strawberry); soybean: *Heterodera glycines*, *Meloidogyne incognita*, *Meloidogyne javanica*, *Belonolaimus* spp., *Hoplolaimus columbus*; sugar beet: *Heterodera schachtii*, *Ditylenchus dipsaci*,
20 *Meloidogyne* spp., *Nacobbus aberrans*, *Trichodorus* spp., *Longidorus* spp., *Paratrichodorus* spp.; sugar cane: *Meloidogyne* spp., *Pratylenchus* spp., *Radopholus* spp., *Heterodera* spp., *Hoplolaimus* spp., *Helicotylenchus* spp., *Scutellonema* spp., *Belonolaimus* spp., *Tylenchorhynchus* spp., *Xiphinema* spp., *Longidorus* spp., *Paratrichodorus* spp.; tea: *Meloidogyne* spp., *Pratylenchus* spp., *Radopholus similis*, *Hemicriconemoides kanayaensis*, *Helicotylenchus* spp., *Paratylenchus curvatus*; tobacco:
30 *Meloidogyne* spp., *Pratylenchus* spp., *Tylenchorhynchus claytoni*, *Globodera tabacum*, *Trichodorus* spp., *Xiphinema americanum*, *Ditylenchus dipsaci* (Europe only), *Paratrichodorus* spp.; tomato: *Pratylenchus* spp., *Meloidogyne* spp.; tree fruits: *Pratylenchus* spp. (apple, pear, stone fruits), *Paratylenchus* spp. (apple, pear),
35 *Xiphinema* spp. (pear, cherry, peach), *Cacopaurus pestis* (walnut), *Meloidogyne* spp. (stone fruits, apple, etc.),

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Longidorus spp. (cherry), *Criconebella* spp. (peach), and *Tylenchulus* spp. (olive).

In addition to nematodes, the present invention can be employed to combat plant pathogenic viruses, plant pathogenic bacteria, and plant pathogenic fungi. See generally G. Agrios, *Plant Pathology* (3d Ed., Academic Press, Inc.). Examples of plant viruses which may be combatted by the present invention include single stranded RNA viruses (with and without envelope), double stranded RNA viruses, and single and double stranded DNA viruses such as (but not limited to) tobacco mosaic virus, tobacco rattle virus, pea enation mosaic virus, barley stripe mosaic virus, potato viruses X and Y, carnation latent virus, beet yellows virus, maize chlorotic virus, tobacco necrosis virus, turnip yellow mosaic virus, tomato bushy stunt virus, southern bean mosaic virus, barley yellow dwarf virus, tomato spotted wilt virus, lettuce necrotic yellows virus, wound tumor virus, maize streak virus, and cauliflower mosaic virus. Examples of plant pathogenic bacteria which can be combatted by the present invention include (but are not limited to) *Agrobacterium* spp., *Clavibacter* (or *Corynebacterium*) spp., *Erwinia* spp., *Pseudomonas* spp., *Xanthomonas* spp., *Streptomyces* spp., and *Xylella* spp. Examples of plant pathogenic fungi which can be combatted by the present invention, and some of the plants which can be protected therefrom by the present invention, include (but are not limited to) *Fuligo* spp., *Mucilago* spp., *Physarum* spp., *Plasmodiophora brassicaea* (causes clubroot of crucifers), *Polymyxa graminis* (parasitic in wheat and other cereals), *Spongospora subterranea* (causes powdery scab of potato tubers), *Olpidium brassicae* (parasitic in roots of cabbage), *Physoderma maydis* (causes brown spot of corn), *Sychytrium endobioticum*, *Urophylytis alfalfae*, *Aphanomyces* spp. (causes root rot in many vegetables), *Phytophthora infestans*, *Albugo candida*, *Peronospora nicotianae*, *Bermia lactucae*,

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Sclerospora graminicola, *Pseudoperonospora cubensis*,
Rhizopus spp. (causes soft rot of fruits and vegetables),
Choanephora cucurbitarum, *Saccharomyces cerevisiae*,
Podosphaera leucotricha (causes powdery mildew of apple),
5 *Spaerotheca pannosa* (causes powdery mildew of roses and
peach), *Hypoxyton mammatum* (causes canker of poplars),
Cochliobolus sativus (causes leaf spots and root rots on
grain crops), *Diplocarpon rosae* (causes black spot of
roses), *Lophodermium* spp. (causes pine needle blight),
10 *Diplodia maydis* (causes stalk and ear rot of corn),
Botrytis cinerea (causes gray mold), *Graphium ulmi*
(causes Dutch elm disease; sexual stage is *Ceratocystis*),
Ustilago spp. (causes smut of corn, wheat, barley, etc.),
and *Armillaria mellea* (causes root rots of forest and
15 fruit trees).

Those skilled in the art will appreciate that
the RB7 nematode-responsive elements disclosed herein may
be employed in other strategies, such as in activating
genes which produce an insect toxin such as a *Bacillus*
20 *thuringiensis* toxin. Thus, the present invention
provides recombinant pathogen-resistant plants comprising
transformed plant cells, wherein the transformed plant
cells contain a heterologous DNA construct comprising an
expression cassette, which construct comprises, in the 5'
25 to 3' direction, a promoter, a structural gene positioned
downstream from the promoter and operatively associated
therewith, and a termination sequence positioned
downstream from the structural gene and operatively
associated therewith. The promoter comprises the RB7
30 nematode-responsive element, and the structural gene
encodes a product toxic to the nematode such as a
Bacillus thuringiensis toxin. Such plants can be made
and used essentially as described above.

The examples which follow are set forth to
35 illustrate the present invention, and are not to be
construed as limiting thereof.

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EXAMPLE 1**Isolation and Expression of Genomic****Root-Specific Clone RB7**

Nicotiana tabacum cv Wisconsin 38 was used as
5 the source of material for cloning and gene
characterization. Genomic DNA was partially digested
with *Sau3A* and size-fractionated on 5 to 20% potassium
acetate gradients. Size fractions of 17 to 23 kb were
pooled and ligated into the λ vector, EMBL3b that had
10 been digested with *Bam*HI and *Eco*RI. See A. Frischauf et
al., J. Mol. Biol. 170, 827-842 (1983). A primary
library of approximately 3.5×10^6 recombinants was
screened by plaque hybridization. Positive clones were
plaque purified. Restriction maps of the genomic clones
15 were constructed using the rapid mapping procedure of
Rachwitz et al., Gene 30, 195-200 (1984).

Regions encoding the root-specific clones were
identified by Southern blots. To further define the
transcribed regions, we took advantage of the fact that
20 the genes are expressed at high levels. Thus, probes
made of cDNA of reverse transcribed poly(A+)RNA would
hybridize to Southern blots of restricted genomic clones
in a manner analogous to differential screening
experiments. See F. Kilcherr, Nature 321, 493-499
25 (1986). The clones were digested with the appropriate
restriction enzymes and the fragments separated on
agarose gels. These fragments were then Southern blotted
to nitrocellulose filters and probed with reverse
transcribed root poly(A+)RNA. The probe was primed using
30 random hexanucleotides (Pharmacia Biochemicals, Inc.)
such that the 3' termini of the mRNA molecules would not
be over represented among the probe.

Clones hybridizing to each root-specific cDNA
clone were plaque purified. Preliminary restriction maps
35 of some of the isolated genomic clones are shown in
Figure 1. Comparisons of the restriction maps of the
genomic clones (Fig. 1) with genomic Southern

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hybridization experiments (not shown) reveal a good correlation of the sequences hybridizing to the root-specific cDNA clones. Clones λ 5A and λ 8D appear overlapping and, along with λ 18C, hybridize to the cDNA clone TobRB7. All of the fragments hybridizing strongly to TobRB7 in genomic Southern hybridization experiments may be accounted for by those hybridizing from the genomic clones, suggesting that the genomic sequences encoding this cDNA have been isolated. Note that clone λ 18C, though encoding a different gene from clones λ 5A and λ 8D, shows about 90% nucleotide sequence homology in the first 800 base pairs upstream from the structural gene.

Clone λ 5A was designated as TobRB7-5A (SEQ ID NO: 1) and used to generate the promoter sequences employed in the experiments described below. This clone is hypothesized to code for a cell membrane channel protein (SEQ ID NO: 2).

EXAMPLE 2

Root-Specific Expression of an Exogenous Reporter Gene with the TobRB7 Promoter

The ability of the TobRB7 promoter region of the λ 5A genomic clone to regulate the expression of a heterologous reporter gene was tested by cloning approximately 1.4 kb of 5' flanking sequence into pBI101.2. In brief, a TobRB7 5' flanking region (SEQ ID NO: 3) was isolated from λ 5A and fused with β -glucuronidase in the *Agrobacterium* binary vector, pBI 101.2. This vector contains a β -glucuronidase (GUS) reporter gene and an *nptII* selectable marker flanked by the T-DNA border sequences (R. Jefferson et al., EMBO J. 6, 3901-3907 (1987)). The construction was mobilized into an *Agrobacterium* host that carries a disarmed Ti-plasmid (LBA4404) capable of providing (*in trans*) the *vir* functions required for T-DNA transfer and integration into the plant genome, essentially as described by An et

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al., in S. Belvin and R. Schilperoot, eds., Plant Molecular Biology Manual, Martinus Nijhoff, Dordrecht, The Netherlands, pp A3-1-19 (1988). *Nicotiana tabacum* SR1 leaf discs were infected and transformants selected and regenerated as described by An et al., Plant Physiol. **81**, 301-305 (1986). Whole plants or excised root and leaf tissue were assayed for GUS expression according to Jefferson et al., supra. For histochemical staining, plants were incubated in the 5-bromo-4-chloro-3-indolyl β -D-glucuronide (X-GLUC) at 37°C overnight. Tissues expressing GUS activity cleave this substrate and thereby stain blue. After the incubation the tissues were bleached in 70% ethanol. GUS enzyme activities were measured using the fluorogenic assay described by Jefferson et al.

Table 1 below presents GUS activity measurements of roots and leaves from five independent transformants. Although variable expression levels are observed from transformant to transformant, in all cases GUS activity is root-specific, demonstrating that these sequences are sufficient for regulated gene expression.

TABLE 1
Organ-Specific Expression of GUS
Activity in Transgenic Plants

Transgenic Plant No.	GUS Activity	
	Roots pmol MU/mg	Leaves protein/min
1	100	ND ^a
2	170	ND
3	200	ND
4	100	ND
5	530	ND
Nontransformed	ND	ND

^aNot detectable.

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EXAMPLE 3

Deletion Analysis of the TobRB7 Promoter

5 These experiments were carried out in essentially the same manner as the experiments described in Example 2 above, except that (a) the length of the TobRB7 flanking region employed was varied to explore how various portions of the flanking region affected expression of GUS, and (b) the TobRB7 structural gene was completely removed and the TobRB7 flanking regions fused to the GUS initiating methionene codon.

10 Deletion mutants employed as promoter sequences in these experiments are graphically summarized in Figure 2. These deletion mutants are designated as Δ 1.8 (SEQ ID NO:4), Δ 1.3 (SEQ ID NO: 5), Δ 1.2 (SEQ ID NO: 6), Δ 1.0 (SEQ ID NO: 7), Δ 0.8 (SEQ ID NO: 8), Δ 0.6 (SEQ ID NO:9), and Δ 0.3 (SEQ ID NO:10).

20 The activity of these various mutants is summarized in the right-hand portion of Figure 2. Note that the greatest root-specific expression was obtained with the Δ 0.6 deletion mutant, indicating the presence of an upstream silencer region. GUS activity data is presented in detail in Table 2 below. Note that only Δ 0.3 (SEQ ID NO:10) was inactive as a promoter, indicating that the TobRB7 promoter is found in the region extending about 800 nucleotides upstream from the TobRB7 structural gene. However, the Δ 0.3 deletion mutant contains the RB7 nematode-responsive element, as discussed below.

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TABLE 2
AVERAGE GUS ACTIVITY
(Range of activities)

		No. of Plants	ROOTS	LEAVES	Median Ratio (Roots/Leaves)
	Wild Type	8	4 (1-11)	0.7 (0.17-2.26)	2.8
5	pBI-0.0	21	187 (4-614)	6.9 (0.18-95.7)	19.0
	pBI-0.3	21	160 (1-586)	5.2 (0.8-28.4)	21.1
	pBI-0.6	22	2242 (4-11,540)	24.7 (0.05-217.5)	122.3
	pBI-0.8	17	652 (2-3394)	4.8 (0.03-23.5)	103.2
	pBI-1.0	9	804 (3-2068)	55.7 (1.72-373.4)	97.1
10	pBI-1.2	23	881 (2-4688)	4.3 (0.14-22.4)	113.5
	pBI-1.3	24	1475 (5-14,110)	3.0 (0.14-8.9)	166.4
	pBI-1.8	18	1007 (1-4274)	6.5 (0.3-20.0)	121.3

EXAMPLE 4

Localization of Gene Activation in
Nematode Infected Plants

15

Transgenic tobacco plants prepared as described in Examples 2 and 3 above were infected with tobacco root-knot nematodes (*Meloidogyne incognita*) in accordance with known techniques. See, e.g., C. Opperman et al., *Plant Disease*, 869-871 (October 1988). Roots were stained for GUS activity (blue) and nematodes were stained red at three stages: (a) 24-48 hours post infection; (b) 7-10 days post infection; and (c) 20-25 days post infection. Nematodes were stained after GUS staining by incubating roots in 95% ethanol/glacial acetic acid (1:1) plus five drops of acid fushsin (per 100 mLs) for four hours, then destained in a saturated chloral hydrate solution for twelve hours to overnight.

20

25

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GUS activity was generally found in the elongation zone of the root. At 24-48 hours post infection, second stage juvenile nematodes have penetrated the tobacco roots, are in the corticle tissue and are migrating in search of an appropriate feeding site. Juveniles in the vascular tissue at this stage have already begun to establish feeding sites. At 7-10 days post infection, swollen late second stage juveniles are seen with their heads in the feeding site. At 20-25 days post infection, adult nematodes are seen protruding from galled root tissue, with their head still embedded in the vascular tissue and the posterior exposed to allow egg deposition.

GUS activity in nematode infected root tissue of plants transformed with the various deletion mutants described in Example 3 indicated that the nematode-responsive element of the TobRB7 promoter is located in the $\Delta 0.3$ (SEQ ID NO:10) deletion mutant.

Similar results are obtained with the peanut root-knot nematode (*Meloidogyne arenaria*).

During the foregoing experiments, it was observed that duration of gene expression in nematode-infected plants was much longer than in uninfected plants, and that the regions of gene activity were no longer restricted to the elongation zone of the root. For example, in each location where a nematode was able to establish a feeding site, gene expression continued at that site for as long as 25-30 days (i.e., the duration of the nematode life cycle). In addition, at least one of the deletion constructions ($\Delta 0.3$) exhibited a delay before expression was detected in infected plants. The delay was observed to be 3-6 days after inoculation of the plant with nematodes.

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EXAMPLE 5

Recombinant Nematode-Resistant Tobacco

This example is carried out in essentially the same manner as described in Examples 2 and 4 above, with the TobRB7 Δ 0.3 deletion mutant (the nematode responsive element) as the promoter, and the gene encoding *Bacillus amyloliquefaciens* RNase (barnase), see C. Paddon and R. Hartley, *Gene* **40**, 231-239 (1986), as the structural gene in the expression cassette. Barnase is known to be toxic to plant cells when expressed as a mature protein therein. See C. Mariani et al., *Nature* **347**, 737-741 (1990).

Construction of the expression cassette containing the barnase gene is carried out in the plasmid pUC18 in *Escherichia coli* DH5 α . The *E. coli* is protected from barnase during construction of the cassette essentially as described in R. Hartley, *J. Molec. Biol.* **202**, 913-915 (1988). In brief, the bacteria is modified to include a second plasmid, pSa4, which has a different origin of replication from pUC18 and which expresses Barstar, with the Barstar binding to the Barnase to prevent the Barnase from digesting *E. coli* RNA.

The gene encoding the mature barnase protein (i.e., without the secretory leader sequence) is prepared in the following manner. A 5' synthetic oligonucleotide Barnase PCR primer is produced having, in the 5' to 3' order, a *Bam* HI restriction site, an initiating ATG codon, and 18 bases homologous to the N-terminus of the mature Barnase. A 3' synthetic oligonucleotide Barnase PCR primer is produced having, in the 5' to 3' order, 21 bases homologous to the C-terminus of the mature Barnase and a *Sac* I restriction site. PCR amplification of the Barnase gene with these two PCR primers produces a DNA sequence having, in the 5' to 3' order, a *Bam* HI restriction site, an initiating ATG codon, the entire coding sequence of the mature Barnase protein, and a *Sac* I restriction site. The Barnase gene so prepared is then

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spliced to the 3' end of the TobRB7 Δ0.3 promoter and this sequence is spliced to the 5' end of the termination sequence of the *nos* gene (the *nos* terminator).

5 The cassette (TobRB7 Δ0.3 promoter; ATG; mature Barnase coding sequence; *nos* terminator) produced above is cloned into the *Agrobacterium* binary vector pBin19 in *Agrobacterium tumefaciens* LBA4404, plant leaf discs transformed therewith, and whole plants regenerated as described in Example 2 above.

10 When tobacco plants carrying the foregoing cassette are infected with tobacco root-knot nematodes in the manner described in Example 4 above, the formation of giant cells is found to be hindered, and the life cycle of the nematodes is found to be adversely affected.

15 The foregoing examples are illustrative of the present invention, and are not to be construed as limiting thereof. The invention is defined by the following claims, with equivalents of the claims to be included therein.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Conkling, Mark A.
Opperman, Charles H.
Taylor, Christopher G.
- (ii) TITLE OF INVENTION: Pathogen-Resistant Transgenic Plants
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park and Gibson
 - (B) STREET: Post Office Drawer 34009
 - (C) CITY: Charlotte
 - (D) STATE: North Carolina
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 28234
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Sibley, Kenneth D.
 - (B) REGISTRATION NUMBER: 31,665
 - (C) REFERENCE/DOCKET NUMBER: 5051-166
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 919-881-3140
 - (B) TELEFAX: 919-881-3175
 - (C) TELEX: 575102

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Nicotiana tabacum*

(vii) IMMEDIATE SOURCE:

(B) CLONE: TobRB7-5A

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 1..1877

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: join(1954..2079, 2376..2627, 2913..3284)

(ix) FEATURE:

(A) NAME/KEY: 5'UTR

(B) LOCATION: 1878..1953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GGATCCCCCT CTTTATAAT AGAGGGTCAT TACTTTATTT ACAATAAAAT AATAAAATAA      60
AGCATATAGT GGAGGACCCA TGATGACTTG TTTCTTCCTC GATTTTCGCC GAGATTCTCT      120
CCCATAGTGC GGTTGCAACG GCCCTTGTCT GCGAGCTCGA TACTGGTTCG AGCTCGGCAT      180
TGGACCGAGC CCTCGACCTT GGTCCGAGCT CGATTCTGAC TTGGGGTCTC GGTATTCGGG      240
GTGAGTGTTG GTCGGTCTAT GCATCTTCGA TAATCTCCGT TTTGCCTCGT AGTTCGATTT      300
GGATATGAGC TCGATAATGA TACCGAGCTT GTCATTGATC GGTCTTAGAG CTCGAAGTTC      360
GACGCCTTTA CTTCGGACCT TGACCGAGCT TGTTATGTAG ATATCCTTTG ATCGAAACAT      420
TATCGTTTTG ACCAATCCGT ACGACTGACT CAAATCGATT TGACCGCACA CAAGATTATT      480
TTCGAAAGAC CCTCGACGTC TTGGAGTATA AAATAATTTA GTAAAGAGAG TAATTGTTTCG      540
TTAAAAATCT TGACACCATT CCAAGCATAC CCCTTATTGT ACTTCAATTA ATTATCATT      600
TATCAGCATA AACATTATAA TAAGTTTCTT GCGTGTTGGA ACGTCATTTT AGTTATTCTA      660
AAGAGGAAAT AGTTTCTTTT TTGCTCATGA CATCAGACAT CTGGACTACT AACTGGAGT      720
TTACCTTTTC TTCTCCTCTT TTTCTTATTG TTCCTCTAAA AAAAATTATC ACTTTTTAAA      780
TGCATTAGTT AAACCTATCT CAACAACGTT TAAATTCAT TTCTTGAATG CCCATTACAA      840
TGTAATAGTA TAACTTAATT AGTCGTCTCC ATGAACCATT AATACGTACG GAGTAATATA      900
AAACACCATT GGGGAGTTCA ATTTGCAATA ATTTCTTGCA AAAATGTAAA GTACCTTTTT      960
GTTCTTGCAA AATTTTACAA ATAAAAATTT GCAGCTCTTT TTTTCTCTC TCTCCAAATA     1020

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CTAGCTCAAA ACCCACAAT ATTTTGAAT TTATGGCATA CTTTGAAT GCGTTTGATG	1080
CAACTATTTT CCTTTAGGAA ATATTCACAA CAATCTAAGA CAATCAAAA GTAGAAAATA	1140
GTTTGTA AAA AGGGATGTGG AGGACATCTT AATCAAATAT TTTCAGTTTA AAAGTTGAAA	1200
ATGAAAAAAC ACCCGAAAGG AAATGATTCG TTCTTTAATA TGCCTACAC AATGTGAATT	1260
TGAATTAGTT TGGTCATACG GTATATCATA TGATTATAAA TAAAAAAT TAGCAAAAGA	1320
ATATAATTTA TTAATATTT TACACCATAC CAAACACAAC CGCATTATAT ATAATCTTAA	1380
TTATCATTAT CACCAGCATC AACATTATAA TGATCCCCT ATGCGTTGGA ACGTCATTAT	1440
AGTTATTCTA AACAAGAAAG AAATTTGTTT TGGACATCAG ACATCTAGTA TTATAACTCT	1500
AGTGGAGCTT ACCTTTTCTT TTCCTTCTT TTTTCTTCT TAAAAAATT ATCACTTTTT	1560
AAATCTTGTA TATTAGTTAA GCTTATCTAA ACAAAGTTT AAATTCATTT CTAAACGTC	1620
CATTACAATG TAATATACT TAGTCGTCTC AATTAACCA TTAATGTGAA ATATAAATCA	1680
AAAAAGCCA AAGGGCGGTG GGACGGCGCC AATCATTGT CCTAGTCCAC TCAAATAAGG	1740
CCCATGGTCG GCAAACCAA ACACAAAATG TGTTATTTT AATTTTTTCC TCTTTATTG	1800
TTAAAGTTGC AAAATGTGTT ATTTTGGTA AGACCCTATG GATATATAAA GACAGGTTAT	1860
GTGAAACTTG GAAAACCATC AAGTTTAAAG CAAAACCTC TTAAGAACTT AAATTGAGCT	1920
TCTTTGGGG CATTTTCTA GTGAGAACTA AAA ATG GTG AGG ATT GCC TTT GGT	1974
	Met Val Arg Ile Ala Phe Gly
	1 5
AGC ATT GGT GAC TCT TTT AGT GTT GGA TCA TTG AAG GCC TAT GTA GCT	2022
Ser Ile Gly Asp Ser Phe Ser Val Gly Ser Leu Lys Ala Tyr Val Ala	
	10 15 20
GAG TTT ATT GCT ACT CTT CTC TTT GTG TTT GCT GGG GTT GGG TCT GCT	2070
Glu Phe Ile Ala Thr Leu Leu Phe Val Phe Ala Gly Val Gly Ser Ala	
	25 30 35
ATA GCT TAT AGTAAGTAAC ACTTCTCTAA TTAAGTTGC ATGCTAACAT	2119
Ile Ala Tyr	
	40
AAATACTTAA TCTGCTCTAG CACTAAATAG TAAAAAGAGC AATCAGGTGC ACTAAGGTCC	2179
CATTAATTCG TTATGCACAT GCCACGGAGT CTAGAGAAAG ACTAGACTGG CTCTATCATA	2239
TTCAATTTTA CCTTACATTT TACTAGATGC CGTTTTCTCA ATCCATAACC GAAAACAACA	2299
TAACTTTAC AGTTACACCA AGACTGCCTA ATTAACCTTT TTTTTTTTT TTTTGTCTT	2359

GTGGGGTGAT TTTGTA GAT AAA TTG ACA GCA GAT GCA GCT CTT GAT CCA Asp Lys Leu Thr Ala Asp Ala Ala Leu Asp Pro 45 50	2408
GCT GGT CTA GTA GCA GTA GCT GTG GCT CAT GCA TTT GCA TTG TTT GTT Ala Gly Leu Val Ala Val Ala Val Ala His Ala Phe Ala Leu Phe Val 55 60 65	2456
GGG GTT TCC ATA GCA GCC AAT ATT TCA GGT GGC CAT TTG AAT CCA GCT Gly Val Ser Ile Ala Ala Asn Ile Ser Gly Gly His Leu Asn Pro Ala 70 75 80 85	2504
GTA ACT TTG GGA TTG GCT GTT GGT GGA AAC ATC ACC ATC TTG ACT GGC Val Thr Leu Gly Leu Ala Val Gly Gly Asn Ile Thr Ile Leu Thr Gly 90 95 100	2552
TTC TTC TAC TGG ATT GCC CAA TTG CTT GGC TCC ACA GTT GCT TGC CTC Phe Phe Tyr Trp Ile Ala Gln Leu Leu Gly Ser Thr Val Ala Cys Leu 105 110 115	2600
CTC CTC AAA TAC GTT ACT AAT GGA TTG GTATGTACTG CTATCATTTT Leu Leu Lys Tyr Val Thr Asn Gly Leu 120 125	2647
CAATCCATAT TATATGTCTT TTTATATTTT TCACAACCTC AATAAAAAAA CAACTTTACC	2707
TAAGACCAGC CTAAGCCGTC GTATAGCCGT CCATCCAACC CTTTAAATTA AAAAGAGCCG	2767
GCATAGTCAT AATATATGTA TATTTTCATGT AGAATATTTG TATAATTAGT GTATATTGTA	2827
CGTATATCGA CTAGAAAAAA ATAAATAATG AATATGACTG TTTATTTGTA ATGGAGTTG	2887
GGCCTCATAT GTTGGTTTTT GGCAG GCT GTT CCA ACC CAT GGA GTT GCT GCT Ala Val Pro Thr His Gly Val Ala Ala 130 135	2939
GGG CTC AAT GGA TTA CAA GGA GTG GTG ATG GAG ATA ATC ATA ACC TTT Gly Leu Asn Gly Leu Gln Gly Val Val Met Glu Ile Ile Ile Thr Phe 140 145 150	2987
GCA CTG GTC TAC ACT GTT TAT GCA ACA GCA GCA GAC CCT AAA AAG GGC Ala Leu Val Tyr Thr Val Tyr Ala Thr Ala Ala Asp Pro Lys Lys Gly 155 160 165	3035
TCA CTT GGA ACC ATT GCA CCC ATT GCA ATT GGG TTC ATT GTT GGG GCC Ser Leu Gly Thr Ile Ala Pro Ile Ala Ile Gly Phe Ile Val Gly Ala 170 175 180	3083
AAC ATT TTG GCA GCT GGT CCA TTC AGT GGT GGG TCA ATG AAC CCA GCT Asn Ile Leu Ala Ala Gly Pro Phe Ser Gly Gly Ser Met Asn Pro Ala 185 190 195	3131
CGA TCA TTT GGG CCA GCT GTG GTT GCA GGA GAC TTT TCT CAA AAC TGG Arg Ser Phe Gly Pro Ala Val Val Ala Gly Asp Phe Ser Gln Asn Trp 200 205 210 215	3179

ATC TAT TGG GCC GGC CCA CTC ATT GGT GGA GGA TTA GCT GGG TTT ATT 3227
 Ile Tyr Trp Ala Gly Pro Leu Ile Gly Gly Gly Leu Ala Gly Phe Ile
 220 225 230

TAT GGA GAT GTC TTT ATT GGA TGC CAC ACC CCA CTT CCA ACC TCA GAA 3275
 Tyr Gly Asp Val Phe Ile Gly Cys His Thr Pro Leu Pro Thr Ser Glu
 235 240 245

GAC TAT GCT TAAACTTAA AAGAAGACAA GTCTGTCTTC AATGTTTCTT 3324
 Asp Tyr Ala
 250

TGTGTGTTTT CAAATGCAAT GTTGATTTTT AATTTAAGCT TTGTATATTA TGCTATGCAA 3384

CAAGTTTGTT TCCAATGAAA TATCATGTTT TGGTTTCTTT TG 3426

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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

Ser Leu Lys Ala Tyr Val Ala Glu Phe Ile Ala Thr Leu Leu Phe Val
 20 25 30

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

Ala Ala Leu Asp Pro Ala Gly Leu Val Ala Val Ala Val Ala His Ala
 50 55 60

Phe Ala Leu Phe Val Gly Val Ser Ile Ala Ala Asn Ile Ser Gly Gly
 65 70 75 80

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

Thr Ile Leu Thr Gly Phe Phe Tyr Trp Ile Ala Gln Leu Leu Gly Ser
 100 105 110

Thr Val Ala Cys Leu Leu Leu Lys Tyr Val Thr Asn Gly Leu Ala Val
 115 120 125

Pro Thr His Gly Val Ala Ala Gly Leu Asn Gly Leu Gln Gly Val Val
 130 135 140

Met Glu Ile Ile Ile Thr Phe Ala Leu Val Tyr Thr Val Tyr Ala Thr
 145 150 155 160
 Ala Ala Asp Pro Lys Lys Gly Ser Leu Gly Thr Ile Ala Pro Ile Ala
 165 170 175
 Ile Gly Phe Ile Val Gly Ala Asn Ile Leu Ala Ala Gly Pro Phe Ser
 180 185 190
 Gly Gly Ser Met Asn Pro Ala Arg Ser Phe Gly Pro Ala Val Val Ala
 195 200 205
 Gly Asp Phe Ser Gln Asn Trp Ile Tyr Trp Ala Gly Pro Leu Ile Gly
 210 215 220
 Gly Gly Leu Ala Gly Phe Ile Tyr Gly Asp Val Phe Ile Gly Cys His
 225 230 235 240
 Thr Pro Leu Pro Thr Ser Glu Asp Tyr Ala
 245 250

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1933 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCATATGAA AGACCCTCGA CGTCTTGGAG TATAAAATAA TTTAGTAAAG AGAGTAATTG 60
 TTCGTTAAAA ATCTTGACAC CATTCCAAGC ATACCCCTTA TTGACTTCA ATTAATTATC 120
 ATTATATCAG CATAACATT ATAATAAGTT TCTTGC GTGT TGGAACGTCA TTTTAGTTAT 180
 TCTAAAGAGG AAATAGTTTC TTTTTTGCTC ATGACATCAG ACATCTGGAC TACTATACTG 240
 GAGTTTACCT TTTCTTCTCC TCTTTTTCTT ATTGTTCTC TAAAAAAAT TATCACTTTT 300
 TAAATGCATT AGTTAACTT ATCTCAACAA CGTTTAAAT TCATTTCTTG AATGCCATT 360
 ACAATGTAAT AGTATACTT AATTAGTCGT CTCCATGAAC CATTAAACG TACGGAGTAA 420
 TATAAACAC CATTGGGGAG TTCAATTTGC AATAATTTCT TGCAAAAATG TAAAGTACCT 480
 TTTTGTCTT GCAAATTTT ACAAATAAAA ATTTGCAGCT CTTTTTTTTT TCTCTCTCCA 540
 AATACTAGCT CAAAACCCAC AAATATTTTT GAATTTATGG CATACTTTTA GAATGCGTTT 600
 GATGCAACTA TTTTCTTTA GGAAATATTC ACAACAATCT AAGACAATCA AAAAGTAGAA 660

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AATAGTTTGT AAAAAGGGAT GTGGAGGACA TCTTAATCAA ATATTTTCAG TTTAAACTT	720
GAAAATGAAA AAACACCCGA AAGGAAATGA TTCGTTCTTT AATATGTCCT ACACAATGTG	780
AATTTGAATT AGTTTGGTCA TACGGTATAT CATATGATTA TAAATAAAAA AAATTAGCAA	840
AAGAATATAA TTTATTAAT ATTTTACACC ATACCAAACA CAACCGCATT ATATATAATC	900
TTAATTATCA TTATCACCAG CATCAACATT ATAATGATTC CCCTATGCGT TGGAACGTCA	960
TTATAGTTAT TCTAAACAAG AAAGAAATTT GTTCTTGACA TCAGACATCT AGTATTATAA	1020
CTCTAGTGGA GCTTACCTTT TCTTTTCCTT CTTTTTTTTT TTCTTAAAAA AATTATCACT	1080
TTTTAAATCT TGTATATTAG TTAAGCTTAT CTAACAAAG TTTTAAATTC ATTTCTTAAA	1140
CGTCCATTAC AATGTAATAT AACTTAGTCG TCTCAATTAA ACCATTAATG TGAAATATAA	1200
ATCAAAAAAA GCCAAAGGGC GGTGGGACGG CGCCAATCAT TTGTCCTAGT CCACTCAAAT	1260
AAGGCCCATG GTCGGCAAAA CCAAACACAA AATGTGTTAT TTTTAAATTT TTCCTCTTTT	1320
ATTGTTAAAG TTGCAAAATG TGTTATTTTT GGTAAGACCC TATGGATATA TAAAGACAGG	1380
TTATGTGAAA CTTGGAAAAC CATCAAGTTT TAAGCAAAAC CCTCTTAAGA ACTTAAATTG	1440
AGCTTCTTTT GGGGCATTTT TCTAGTGAGA ACTAAAAATG GTGAGGATTG CCTTTGGTAG	1500
CATTGGTGAC TCTTTTAGTG TTGGATCATT GAAGGCCTAT GTAGCTGAGT TTATTGCTAC	1560
TCTTCTCTTT GTGTTTGCTG GGGTTGGGTC TGCTATAGCT TATAGTAAGT AACACTTCTC	1620
TAATTAAGT TGCATGCTAA CATAAATACT TAATCTGCTC TAGCACTAAA TAGTAAAAAG	1680
AGCAATCAGG TGCACTAAGG TCCCATTAAT TCGTTATGCA CATGCCACGG AGTCTAGAGA	1740
AAGACTAGAC TGGCTCTATC ATATTCAATT TTACCTTACA TTTTACTAGA TGCCGTTTTT	1800
TCAATCCATA ACCGAAAACA ACATAACTTT TACAGTTACA CCAAGACTGC CTAATTAACC	1860
TTTTTTTTTT TTTTTTTTGC TTTGTGGGGT GATTTTGTAG ATAAATTGAC AGCAGATGCA	1920
GCTCTTGATC CAG	1933

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1859 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCCATATTCC TCGATTTTCG CCGAGATTCT CTCCCATAGT GCGGTTGCAA CGGCCCTTGT	60
CTGCGAGCTC GATACTGGTT CGAGCTCGGC ATTGGACCGA GCCCTCGACC TTGGTCCGAG	120
CTCGATTCTG ACTTGGGGTC TCGGTATTCG GGGTGAGTGT TGGTCGGTCT ATGCATCTTC	180
GATAATCTCC GTTTTGCCTC GTAGTTCGAT TTGGATATGA GCTCGATAAT GATACCGAGC	240
TTGTCATTGA TCGGTCTTAG AGCTCGAAGT TCGACGCCTT TACTTCGGAC CTTGACCGAG	300
CTTGTTATGT AGATATCCTT TGATCGAAAC ATTATCGTTT TGACCAATCC GTACGACTGA	360
CTCAAATCGA TTTGACCGCA CACAAGATTA TTTTCGAAAG ACCCTCGACG TCTTGAGTA	420
TAAAATAATT TAGTAAAGAG AGTAATTGTT CGTAAAAAAT CTTGACACCA TTCCAAGCAT	480
ACCCCTTATT GACTTCAAT TAATTATCAT TATATCAGCA TAAACATTAT AATAAGTTTC	540
TTGCGTGTTG GAACGTCATT TTAGTTATTC TAAAGAGGAA ATAGTTTCTT TTTTGCTCAT	600
GACATCAGAC ATCTGGACTA CTATACTGGA GTTTACCTTT TCTTCTCCTC TTTTCTTAT	660
TGTTCTCTA AAAAAAATTA TCACTTTTTA AATGCATTAG TTAAACTTAT CTCAACAACG	720
TTTAAAATTC ATTTCTTGAA TGCCATTAC AATGTAATAG TATAACTTAA TTAGTCGTCT	780
CCATGAACCA TTAATACGTA CGGAGTAATA TAAACACCA TTGGGGAGTT CAATTTGCAA	840
TAATTTCTTG CAAAAATGTA AAGTACCTTT TTGTTCTTGC AAAATTTTAC AAATAAAAAT	900
TTGCAGCTCT TTTTTTCTC TCTCTCCAAA TACTAGCTCA AAACCCACAA ATATTTTTGA	960
ATTTATGGCA TACTTTTAGA ATGCGTTTGA TGCAACTATT TTCCTTTAGG AAATATTCAC	1020
AACAATCTAA GACAATCAAA AAGTAGAAAA TAGTTTGTA AAAGGGATGT GGAGGACATC	1080
TTAATCAAAT ATTTTCAGTT TAAAACCTGA AAATGAAAA ACACCCGAAA GGAAATGATT	1140
CGTTCCTTAA TATGCCTAC ACAATGTGAA TTTGAATTAG TTTGGTCATA CGGTATATCA	1200
TATGATTATA AATAAAAAAA ATTAGCAAAA GAATATAATT TATTAAATAT TTTACACCAT	1260
ACCAAACACA ACCGCATTAT ATATAATCTT AATTATCATT ATCACCAGCA TCAACATTAT	1320
AATGATTCCC CTATGCGTTG GAACGTCATT ATAGTTATTC TAAACAAGAA AGAAATTTGT	1380
TCTTGACATC AGACATCTAG TATTATAACT CTAGTGGAGC TTACCTTTTC TTTTCTTCT	1440
TTTTTTTCTT CTAAAAAAA TTATCACTTT TAAATCTTG TATATTAGTT AAGCTTATCT	1500
AAACAAAGTT TAAATTCAT TTCTTAAACG TCCATTACAA TGTAATATAA CTTAGTCGTC	1560
TCAATTAAC CATTAAATGT AAATATAAAT CAAAAAAGC CAAAGGGCGG TGGGACGGCG	1620

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CCAATCATTT GTCCTAGTCC ACTCAAATAA GGCCCATGGT CGGCAAAACC AAACACAAAA 1680
 TGTGTTATTT TTAATTTTTT CCTCTTTTAT TGTTAAAGTT GCAAATGTG TTATTTTTGG 1740
 TAAGACCCTA TGGATATATA AAGACAGGTT ATGTGAAACT TGGAAAACCA TCAAGTTTTA 1800
 AGCAAAACCC TCTTAAGAAC TTAATTGAG CTTCTTTTGG GGCATTTTTTC TAGTGAGAA 1859

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1385 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCATATCCC CTTATTGTAC TTCAATTAAT TATCATTATA TCAGCATAAA CATTATAATA 60
 AGTTTCTTGC GTGTTGGAAC GTCATTTTAG TTATTCTAAA GAGGAAATAG TTTCTTTTTT 120
 GCTCATGACA TCAGACATCT GGACTACTAT ACTGGAGTTT ACCTTTTCTT CTCCTCTTTT 180
 TCTTATTGTT CCTCTAAAAA AAATTATCAC TTTTAAATG CATTAGTTAA ACTTATCTCA 240
 ACAACGTTTA AAATTCATTT CTTGAATGCC CATTACAATG TAATAGTATA ACTTAATTAG 300
 TCGTCTCCAT GAACCATTAA TACGTACGGA GTAATATAAA ACACCATTGG GGAGTTCAAT 360
 TTGCAATAAT TTCTTGCAAA AATGTAAAGT ACCTTTTTGT TCTTGCAAAA TTTTACAAAT 420
 AAAAAATTTGC AGCTCTTTTT TTTCTCTCTC TCCAAATACT AGCTCAAAAC CCACAAATAT 480
 TTTTGAATTT ATGGCATACT TTTAGAATGC GTTTGATGCA ACTATTTTCC TTTAGGAAAT 540
 ATTCACAACA ATCTAAGACA ATCAAAAAGT AGAAAATAGT TTGTAAAAAG GGATGTGGAG 600
 GACATCTTAA TCAAATATTT TCAGTTTAAA ACTTGAAAAT GAAAAACAC CCGAAAGGAA 660
 ATGATTCGTT CTTAATATG TCCTACACAA TGTGAATTTG AATTAGTTTG GTCATACGGT 720
 ATATCATATG ATTATAAATA AAAAAATTA GCAAAAAGAA ATAATTTATT AAATATTTTA 780
 CACCATACCA AACACAACCG CATTATATAT AATCTTAATT ATCATTATCA CCAGCATCAA 840
 CATTATAATG ATTCCCCTAT GCGTTGGAAC GTCATTATAG TTATTCTAAA CAAGAAAGAA 900
 ATTTGTTCTT GACATCAGAC ATCTAGTATT ATAACCTAG TGGAGCTTAC CTTTTCTTTT 960
 CCTTCTTTTT TTTCTTCTTA AAAAAATTAT CACTTTTTAA ATCTTGATA TTAGTTAAGC 1020

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TTATCTAAAC AAAGTTTTAA ATTCATTCT TAAACGTCCA TTACAATGTA ATATAACTTA 1080
 GTCGTCTCAA TTAACCATT AATGTGAAAT ATAAATCAA AAAAGCCAAA GGGCGGTGGG 1140
 ACGGCGCCAA TCATTTGTCC TAGTCCACTC AAATAAGGCC CATGGTCGGC AAAACCAAAC 1200
 ACAAATGTG TTATTTTTAA TTTTTCCTC TTTTATTGTT AAAGTTGCAA AATGTGTTAT 1260
 TTTTGGTAAG ACCCTATGGA TATATAAGA CAGGTTATGT GAAACTTGA AAACCATCAA 1320
 GTTTAAGCA AAACCCTCTT AAGAACTTAA ATTGAGCTTC TTTTGGGCA TTTTCTAGT 1380
 GAGAA 1385

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1268 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCCATATATG ACATCAGACA TCTGGACTAC TATACTGGAG TTTACCTTTT CTTCTCCTCT 60
 TTTTCTTATT GTTCCTCTAA AAAAAATTAT CACTTTTTAA ATGCATTAGT TAACTTATC 120
 TCAACAACGT TAAAATTCA TTTCTTGAAT GCCCATTACA ATGTAATAGT ATAACTTAAT 180
 TAGTCGTCTC CATGAACCAT TAATACGTAC GGAGTAATAT AAAACACCAT TGGGGAGTTC 240
 AATTTGCAAT AATTTCTTGC AAAAATGTAA AGTACCTTTT TGTTCTTGCA AAATTTTACA 300
 AATAAAAATT TGCAGCTCTT TTTTTCTCT CTCTCAAAT ACTAGCTCAA AACCCACAAA 360
 TATTTTTGAA TTTATGGCAT ACTTTTAGAA TCGTTTTGAT GCAACTATTT TCCTTTAGGA 420
 AATATTCACA ACAATCTAAG ACAATCAAAA AGTAGAAAAT AGTTTGTAAG AAGGGATGTG 480
 GAGGACATCT TAATCAAATA TTTTCAGTTT AAAACTTGAA AATGAAAAAA CACCCGAAAG 540
 GAAATGATTC GTTCTTTAAT ATGTCCTACA CAATGTGAAT TTGAATTAGT TTGGTCATAC 600
 GGTATATCAT ATGATTATAA ATAAAAAAA TTAGCAAAAAG AATATAATTT ATTAATATT 660
 TTACACCATA CCAAACACAA CCGCATTATA TATAATCTTA ATTATCATT TACCAGCAT 720
 CAACATTATA ATGATTCCTC TATGCGTTGG AACGTCATTA TAGTTATTCT AAACAAGAAA 780
 GAAATTTGTT CTTGACATCA GACATCTAGT ATTATAACTC TAGTGGAGCT TACCTTTTCT 840

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TTTCCTTCTT TTTTTTCTTC TTAAAAAAT TATCACTTTT TAAATCTTGT ATATTAGTTA	900
AGCTTATCTA AACAAAGTTT TAAATTCATT TCTTAAACGT CCATTACAAT GTAATATAAC	960
TTAGTCGTCT CAATTAACC ATTAATGTGA AATATAAATC AAAAAAGCC AAAGGGCGGT	1020
GGGACGGCGC CAATCATTTG TCCTAGTCCA CTCAAATAAG GCCCATGGTC GGCAAAACCA	1080
AACACAAAAT GTGTTATTTT TAATTTTTTC CTCTTTTATT GTTAAAGTTG CAAAATGTGT	1140
TATTTTTGGT AAGACCCTAT GGATATATAA AGACAGGTTA TGTGAACTT GGAAAACCAT	1200
CAAGTTTTAA GCAAAACCCT CTTAAGAACT TAAATTGAGC TTCTTTTGGG GCATTTTTCT	1260
AGTGAGAA	1268

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCATATTTA ATTAGTCGTC TCCATGAACC ATTAATACGT ACGGAGTAAT ATAAAACACC	60
ATTGGGGAGT TCAATTTGCA ATAATTTCTT GCAAAAATGT AAAGTACCTT TTTGTTCTTG	120
CAAATTTTA CAAATAAAAA TTTGCAGCTC TTTTTTTCT CTCTCTCAA ATACTAGCTC	180
AAAACCCACA AATATTTTTG AATTTATGGC ATACTTTTAG AATGCGTTTG ATGCAACTAT	240
TTTCCTTTAG GAAATATTCA CAACAATCTA AGACAATCAA AAAGTAGAAA ATAGTTTGTA	300
AAAAGGGATG TGGAGGACAT CTTAATCAAA TATTTTCAGT TAAAACTTG AAAATGAAAA	360
AACACCCGAA AGGAAATGAT TCGTTCCTTA ATATGTCCTA CACAATGTGA ATTTGAATTA	420
GTTTGGTCAT ACGGTATATC ATATGATTAT AAATAAAAA AATTAGCAAA AGAATATAAT	480
TTATTAATA TTTTACACCA TACCAAACAC AACCGCATTA TATATAATCT TAATTATCAT	540
TATCACCAGC ATCAACATTA TAATGATTCC CCTATGCGTT GGAACGTCAT TATAGTTATT	600
CTAAACAAGA AAGAAATTTG TTCTTGACAT CAGACATCTA GTATTATAAC TCTAGTGGAG	660
CTTACCTTTT CTTTTCTTC TTTTTTTCT TCTTAAAAA ATTATCACTT TTAAATCTT	720
GTATATTAGT TAAGCTTATC TAAACAAAGT TTAAATTCA TTTCTTAAAC GTCCATTACA	780

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ATGTAATATA ACTTAGTCGT CTCAATTA	840
CCAAAGGGCG GTGGGACGGC GCCAATCATT	900
TCGGCAAAC CAAACACAAA ATGTGTTATT	960
TGCAAATGT GTTATTTTTG GTAAGACCCT	1020
TTGGAAAACC ATCAAGTTTT AAGCAAACC	1080
GGGCATTTTT CTAGTGAGAA	1100

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 890 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCCATATTAG AATGCGTTTG ATGCAACTAT	60
AGACAATCAA AAAGTAGAAA ATAGTTTGTA	120
TATTTTCAGT TAAAACCTG AAAATGAAAA	180
ATATGTCCTA CACAATGTGA ATTTGAATTA	240
AAATAAAAAA AATTAGCAAA AGAATATAAT	300
AACCGCATT A TATAATCT TAATTATCAT	360
CCTATGCGTT GGAACGTCAT TATAGTTATT	420
CAGACATCTA GTATTATAAC TCTAGTGGAG	480
TCTTAAAAAA ATTATCACTT TTAAATCTT	540
TTTAAATTCA TTTCTTAAAC GTCCATTACA	600
CCATTAATGT GAAATATAAA TCAAAAAAAG	660
TGTCCTAGTC CACTCAAATA AGGCCCATGG	720
TTTAATTTTT TCCTCTTTTA TTGTTAAAGT	780
ATGGATATAT AAAGACAGGT TATGTGAAAC	840
CTCTTAAGAA CTAAATTGA GCTTCTTTTG	890

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(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 713 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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CCCATATGTC CTACACAATG TGAATTTGAA TTAGTTTGGT CATACGGTAT ATCATATGAT      60
TATAAATAAA AAAAATTAGC AAAAGAATAT AATTTATTAA ATATTTTACA CCATACCAAA      120
CACAACCGCA TTATATATAA TCTTAATTAT CATTATCACC AGCATCAACA TTATAATGAT      180
TCCCCTATGC GTTGAACGT CATTATAGTT ATTCTAAACA AGAAAGAAAT TTGTTCTTGA      240
CATCAGACAT CTAGTATTAT AACTCTAGTG GAGCTTACCT TTTCTTTTCC TTCTTTTTTT      300
TCTTCTTAAA AAAATTATCA CTTTTTAAAT CTTGTATATT AGTTAAGCTT ATCTAAACAA      360
AGTTTTAAAT TCATTTCTTA AACGTCCATT ACAATGTAAT ATAACTTAGT CGTCTCAATT      420
AAACCATTAA TGTGAAATAT AAATCAAAAA AAGCCAAAGG GCGGTGGGAC GGCGCCAATC      480
ATTTGTCCTA GTCCACTCAA ATAAGGCCCA TGGTCGGCAA AACCAAACAC AAAATGTGTT      540
ATTTTTAATT TTTTCTCTT TTATTGTTAA AGTTGCAAAA TGTGTTATTT TTGGTAAGAC      600
CCTATGGATA TATAAGACA GGTTATGTGA AACTTGGAAA ACCATCAAGT TTTAAGCAAA      660
ACCCTCTTAA GAACTTAAAT TGAGCTTCTT TTGGGGCATT TTTCTAGTGA GAA          713

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(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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CCCATATAGC TTATCTAAC AAAGTTTTAA ATTCATTTCT TAAACGTCCA TTACAATGTA      60
ATATAACTTA GTCGTCTCAA TTAACCATT AATGTGAAAT ATAAATCAA AAAAGCCAAA      120

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GGGCGGTGGG ACGGCGCCAA TCATTTGTCC TAGTCCACTC AAATAAGGCC CATGGTCGGC	180
AAAACCAAAC ACAAATGTG TTATTTTAA TTTTTCCTC TTTTATTGTT AAAGTTGCAA	240
AATGTGTTAT TTTTGGTAAG ACCCTATGGA TATATAAAGA CAGGTTATGT GAAACTTGGA	300
AAACCATCAA GTTTAAGCA AAACCCTCTT AAGAACTTAA ATTGAGCTTC TTTTGGGGCA	360
TTTTCTAGT GAGAA	375

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THAT WHICH IS CLAIMED IS:

1. A recombinant pathogen-resistant plant comprising transformed plant cells, said transformed plant cells containing a heterologous DNA construct comprising an expression cassette, which construct comprises, in the 5' to 3' direction, a promoter, a structural gene positioned downstream from said promoter and operatively associated therewith, and a termination sequence positioned downstream from said structural gene and operatively associated therewith, wherein said promoter is activated by a plant pathogen which attacks said plant, and wherein said structural gene encodes a product toxic to said plant cells.
2. A recombinant plant according to claim 1, wherein said promoter is activated by a pathogen selected from the group consisting of viruses, bacteria, fungi, and nematodes.
3. A recombinant plant according to claim 1, which promoter is activated by a plant-parasitic nematode.
4. A recombinant plant according to claim 1, which promoter is activated by a nematode selected from the group consisting of root-knot nematodes and cyst nematodes.
5. A recombinant plant according to claim 1, which pathogen attacks a tissue of said plant selected from the group consisting of leaf tissue and root tissue.
6. A recombinant plant according to claim 1, which pathogen attacks the root tissue of said plant.

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7. A recombinant plant according to claim 1, which promoter is an RB7 nematode-responsive element.

8. A recombinant plant according to claim 1, which plant is a monocot.

9. A recombinant plant according to claim 1, which plant is a dicot.

10. A recombinant plant according to claim 1, which plant is a dicot selected from the group consisting of tobacco, potato, soybean, peanuts, pineapple, cotton, and vegetable crops.

11. A recombinant plant according to claim 1, which structural gene encodes an enzyme capable of digesting a nucleic acid selected from the group consisting of DNA and RNA.

12. A recombinant plant according to claim 1, which structural gene encodes *Bacillus amyloliquefaciens* RNase.

13. A recombinant plant according to claim 1, further comprising a second promoter positioned upstream from said structural gene and operatively associated therewith so that said structural gene is associated with a plurality of promoters, wherein each of said promoters is activated by a different plant pathogen.

14. A recombinant nematode-resistant plant comprising:

transformed dicotyledenous plant cells, said transformed dicotyledenous plant cells containing a heterologous DNA construct comprising an expression cassette, which construct comprises, in the 5' to 3'

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direction, a promoter, a structural gene positioned downstream from said promoter and operatively associated therewith, and a termination sequence downstream from said structural gene and operatively associated therewith,

wherein said promoter is activated by a nematode which attacks the roots of said plant,
and wherein said structural gene encodes a product toxic to said plant cells.

15. A recombinant plant according to claim 14, which promoter is activated by a nematode selected from the group consisting of root-knot nematodes and cyst nematodes.

16. A recombinant plant according to claim 14, which promoter is an RB7 nematode-responsive element.

17. A recombinant plant according to claim 14, which plant is a dicot selected from the group consisting of tobacco, potato, soybean, peanuts, pineapple, cotton, and vegetable crops.

18. A recombinant plant according to claim 14, which structural gene encodes an enzyme capable of digesting a nucleic acid selected from the group consisting of DNA and RNA.

19. A recombinant plant according to claim 14, which structural gene encodes *Bacillus amyloliquefaciens* RNase.

20. A recombinant plant according to claim 14, further comprising a second promoter positioned upstream from said structural gene and operatively associated therewith so that said structural gene is

associated with a plurality of promoters, wherein each of said promoters is activated by a different plant pathogen.

21. A crop comprising a plurality of plants according to claims 1 or 14 planted together in an agricultural field.

22. A method of combatting a plant pathogen in an agricultural field, comprising planting the field with a crop of recombinant pathogen-resistant plants comprising transformed plant cells, said transformed plant cells containing a heterologous DNA construct comprising an expression cassette, which construct comprises, in the 5' to 3' direction, a promoter, a structural gene positioned downstream from said promoter and operatively associated therewith, and a termination sequence positioned downstream from said structural gene and operatively associated therewith, wherein said promoter is activated by a plant pathogen which attacks said plant, and wherein said structural gene encodes a product toxic to said plant cells.

23. A method of making a recombinant pathogen-resistant plant, said method comprising:
providing a plant cell capable of
regeneration;

transforming said plant cell with a DNA construct comprising an expression cassette, which construct comprises, in the 5' to 3' direction, a promoter activated by a plant pathogen, a structural gene positioned downstream from said promoter and operatively associated therewith, and a termination sequence positioned downstream from said structural gene and operatively associated therewith, said structural gene encoding a product toxic to plant cells; and then

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regenerating a recombinant pathogen-resistant plant from said transformed plant cell.

24. A method according to claim 23, wherein said plant cell resides in a plant tissue capable of regeneration.

25. A method according to claim 23, wherein said transforming step is carried out by bombarding said plant cell with microparticles carrying said expression cassette.

26. A method according to claim 23, wherein said transforming step is carried out by infecting said cells with an *Agrobacterium tumefaciens* containing a Ti plasmid carrying said expression cassette.

27. A DNA construct comprising an expression cassette, which construct comprises, in the 5' to 3' direction, a promoter activated by a plant pathogen, a structural gene positioned downstream from said promoter and operatively associated therewith, and a termination sequence positioned downstream from said structural gene and operatively associated therewith, said structural gene encoding a product toxic to plant cells.

28. A DNA construct according to claim 27 carried by a plant transformation vector.

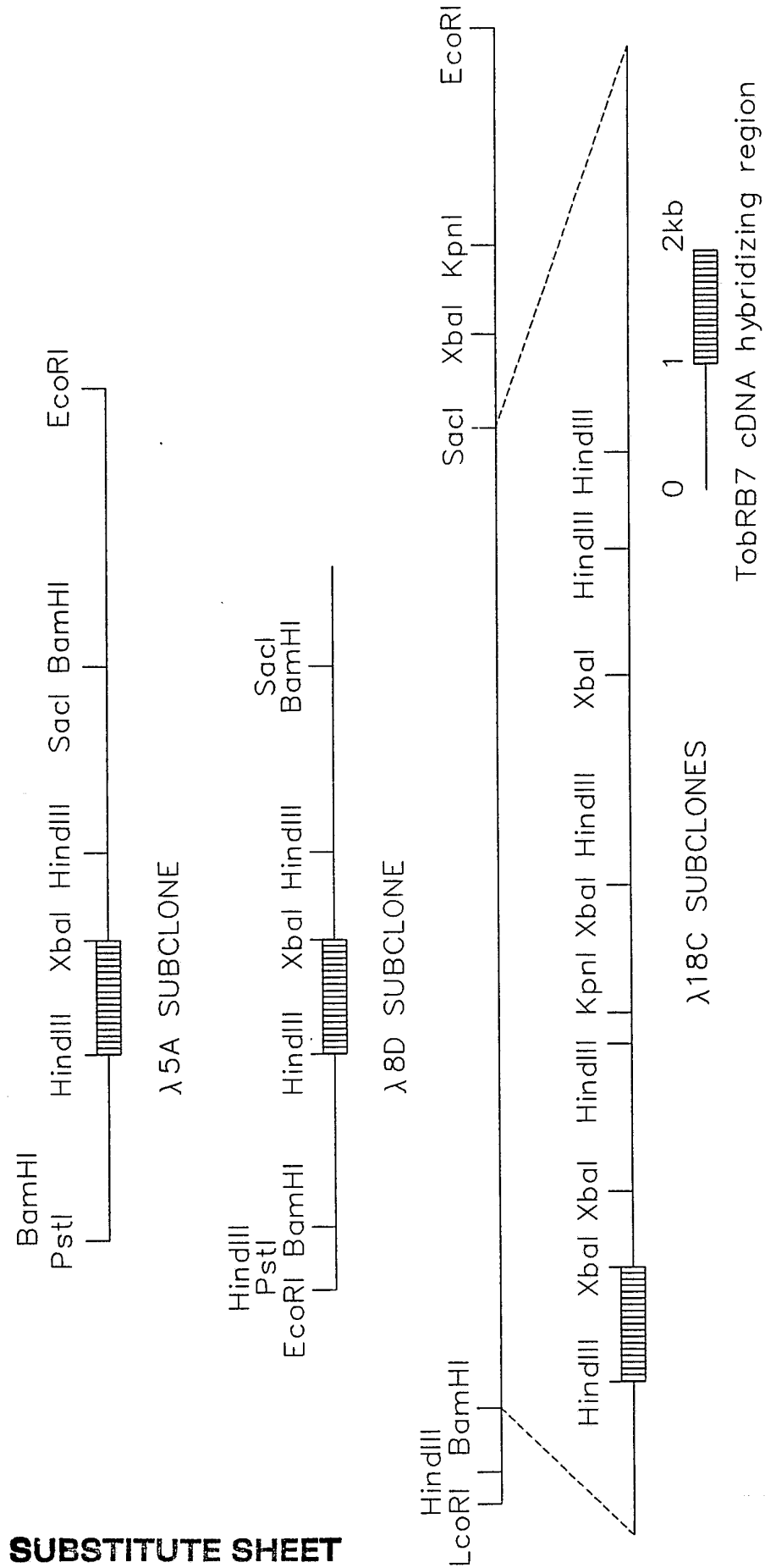


FIG. 1.

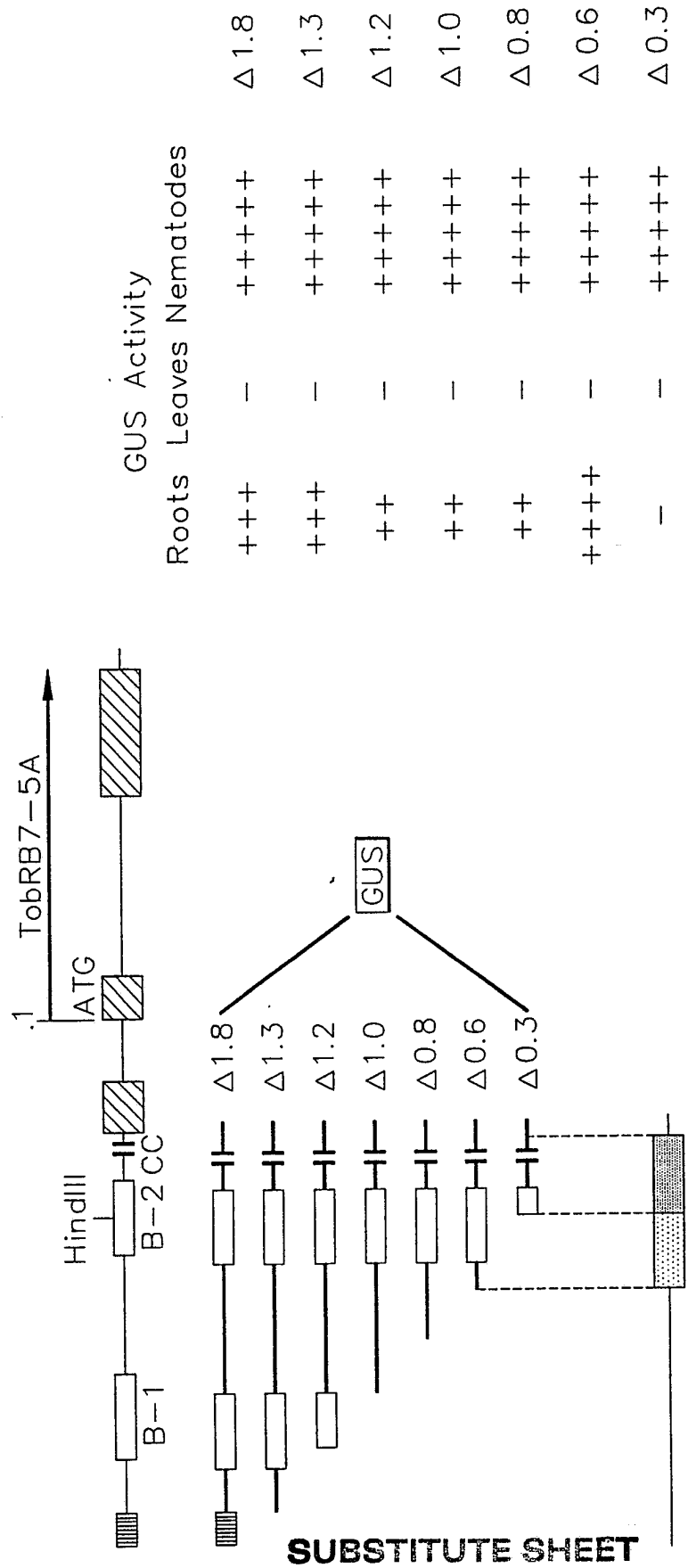


FIG. 2.

SUBSTITUTE SHEET

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US92/08411

A. CLASSIFICATION OF SUBJECT MATTER
 IPC(5) :A01H 1/00, 5/00; C12N 15/00; C07H 15/12, 17/00
 US CL :800/205; 435/172.3, 320.1; 536/27
 According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED
 Minimum documentation searched (classification system followed by classification symbols)
 U.S. : 800/205; 435/172.3, 320.1; 536/27; 935/6, 22, 30, 41

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
 Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US, A, 4,940,840 (Suslow et al.) 10 July 1990, see entire document, especially columns 1, 4, 9, and 15-28	1-28
Y	Annals of Applied Biology, Volume 97, No. 3, issued 1981, M. G. K. Jones et al., "Host Cell Responses to Endoparasitic Nematode Attack: Structure and Function of Giant Cells and Syncytia", pages 353-372, especially pages 353-356.	2-7, 14-21
Y	Journal of Cellular Biochemistry, Supplement 0, Volume 13, Part D, issued 1989, A. Niebel et al., "Molecular Analysis of Nematode-Induced Giant Cells in Potato Roots", see entire abstract.	2-7, 14-21
Y	Biochemical and Biophysical Research Communications, Volume 151, No. 3, issued 30 March 1988, M. S. Chapekar et al., "The Synergistic Cytocidal Effect Produced By Immune Interferon and Tumor Necrosis Factor in HT-29 Cells is Associated with Inhibition of rRNA Processing and (2',5') Oligo(A) Activation of RNase L", pages 1180-1187, especially pages 1181, 1184-1185.	1-28

Further documents are listed in the continuation of Box C. See patent family annex.

* Special categories of cited documents:	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be part of particular relevance	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E" earlier document published on or after the international filing date	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&" document member of the same patent family
"O" document referring to an oral disclosure, use, exhibition or other means	
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search 03 DECEMBER 1992	Date of mailing of the international search report 21 DEC 1992
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Name and mailing address of the ISA/ Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. NOT APPLICABLE	Authorized officer CHARLES C. P. RORIES, PH.D. Telephone No. (703) 308-0196
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US92/08411

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Journal of Molecular Biology, Volume 202, issued 1988, R. W. Hartley, Barnase et al, "Expression of its Cloned Inhibitor Permits Expression of a Cloned Ribonuclease", pages 913-915, especially pages 913-914.	11, 12, 18, 19
Y	Nature, volume 347, issued 25 October 1990, C. Mariani et al., "Induction of Male Sterility in Plants by a Chimaeric Ribonuclease Gene", pages 737-741, especially page 738.	1-28
Y	US, A, 5,015,580 (Christou et al.) 14 May 1991, see entire document, especially columns 3 & 9.	25
Y	Cell, Volume 40, issued April 1985, P. Shaw et al., "The Two Promoters of Mouse α -Amylase Gene <u>Amy-1</u> are Differentially Activated during Parotid Gland Differentiation", pages 907-912. especially pages 907-908.	13, 25