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(54) Titre : PROCEDE DE GENERATION D'UNE RESISTANCE A DES AGENTS PATHOGENES DANS DES PLANTES PAR SILENCAGE DE L'EXPRESSION GENIQUE DE L'OXYDASE NADPH INDUIT PAR ARN DOUBLE BRIN

(54) Title: METHOD FOR OBTAINING PATHOGEN RESISTANCE IN PLANTS BY DOUBLE-STRANDED RNA GENE SILENCING OF NADPH OXIDASE

(57) Abrégé/Abstract:
The invention relates to a method for obtaining or increasing the pathogenic resistance in plants by reducing the expression, activity or the functioning of a NADPH oxidase.

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(54) Title: METHOD FOR OBTAINING THE PATHOGENIC RESISTANCE IN PLANTS

(54) Bezeichnung: VERFAHREN ZUM ERREICHEN EINER PATHOGENRESISTENZ IN PFLANZEN

(57) Abstract: The invention relates to a method for obtaining or increasing the pathogenic resistance in plants by reducing the expression, activity or the functioning of a NADPH oxidase.

(57) Zusammenfassung: Die Erfindung betrifft Verfahren zur Erzeugung oder Erhöhung einer Pathogenresistenz in Pflanzen durch Verminderung der Expression, Aktivität oder Funktion einer NADPH Oxidase.

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METHOD FOR OBTAINING PATHOGEN RESISTANCE IN PLANTS BY DOUBLE-STRANDED RNA GENE SILENCING OF NADPH OXIDASE

The invention relates to methods for generating or increasing a pathogen resistance in plants by reducing the expression, activity or function of an NADPH oxidase.

The aim of plant biotechnology work is the generation of plants with advantageous novel properties, for example for increasing agricultural productivity. The plants' natural defense mechanisms against pathogens are frequently insufficient. Fungal diseases alone result in annual yield losses of many billions of US$. The introduction of foreign genes from plants, animals or microbial sources can increase the defenses. Examples are the protection against feeding damage by insects by expressing *Bacillus thuringiensis* endotoxins (Vaeck et al. (1987) Nature 328:33-37) or the protection against fungal infection by expressing a bean chitinase (Broglie et al. (1991) Science 254:1194-1197). However, most of the approaches described only offer resistance to a single pathogen or a narrow spectrum of pathogens.

Only a few approaches exist which impart a resistance to a broader spectrum of pathogens to plants. Systemic acquired resistance (SAR) - a defense mechanism in a variety of plant/pathogen interactions - can be conferred by the application of endogenous messenger substances such as jasmonic acid (JA) or salicylic acid (SA) (Ward, et al. (1991) Plant Cell 3:1085-1094; Uknes, et al. (1992) Plant Cell 4(6):645-656). Similar effects can also be achieved by synthetic compounds such as 2,6-dichloroisonicotinic acid (INA) or S-methyl benzo(1,2,3)thiadiazole-7-thiocarboxylate (BTH; Bion®) (Friedrich et al. (1996) Plant J 10(1):61-70; Lawton et al. (1996) Plant J. 10:71-82). The expression of pathogenesis-related (PR) proteins, which are upregulated in the case of SAR, may also cause pathogen resistance in some cases.

In barley, the Mlo locus has been described as a negative regulator of the defense against pathogens. The loss of the Mlo gene causes an increased and, above all, race-unspecific resistance against a large number of mildew species (Büschges R et al. (1997) Cell 88:695-705; Jorgensen JH (1977) Euphytica 26:55-62; Lyngkjaer MF et al. (1995) Plant Pathol 44:786-790). Mlo-deficient barley varieties obtained by conventional breeding are already being used in agriculture. Despite intensive cultivation, the resistance has proved to be durable, presumably due to the fact that it is recessive. Mlo-like resistances in other plants,

in particular in cereal species, are not described. The Mlo gene and various homologs from other cereal species have been identified and cloned (Büschges R et al. (1997) Cell 88:695-705; WO 98/04586; Schulze-Lefert P, Vogel J (2000) Trends Plant Sci. 5:343-348). Various methods using these genes for obtaining a pathogen resistance are described (WO 98/04586; WO 00/01722; WO 99/47552). The disadvantage is that the Mlo-mediated defense mechanism comprises a spontaneous die-off of leaf cells (Wolter M et al. (1993) Mol Gen Genet 239:122-128). Another disadvantage is that the Mlo-deficient genotypes show hypersensitivity to hemibiotrophic pathogens such as *Magnaporte grisea* (*M. grisea*) and *Cochliobolus sativus* (*Bipolaris sorokiniana*) (Jarosch B et al. (1999) Mol Plant Microbe Interact 12:508-514; Kumar J et al. (2001) Phytopathology 91:127-133).

The liberation of reactive oxygen species (ROS; for example superoxide (O_2-), hydroxyl radicals and H_2O_2) is ascribed an important protection function in the reaction on plant pathogens (Wojtaszek P (1997) Biochem J 322:681-692). A variety of ways of how a cell can produce ROS are known. In the macrophages of mammals, it is in particular the enzyme NADPH oxidase, which is able to transfer electrons to molecular oxygen, which must be mentioned. Homologous enzymes have also been identified in plants (Lamb & Dixon (1997) Annu Rev Plant Physiol Plant Mol Biol 48:251).

It has been shown that mutations in the catalytic subunit of NADPH oxidase in Arabidopsis thaliana show a reduced accumulation of reactive oxygen intermediates (ROI). With regard to the hypersensitive reaction (HR), the results were heterogeneous: while infection with the aviralulent and bactrium Pseudomonas syringae showed a reduced HR in a double mutant, the virulent oomycete Peronospora parasitica showed an increased HR. Growth - both of virulent and of avirulent P. syringae strains - was not changed in comparison with wild-type plants, however (Torres MA et al. (2002) Proc Natl Acad Sci USA 99:517-522). Likewise, the inhibition of NADPH oxidase by means of the inhibitor diphenyleneiodonium chloride (DPI) - at physiologically relevant concentrations - had no effect on the development of pathogenic fungi (Hückelhoven R & Kogel KH (1998) Mol Plant Microbe Interact 11:292-300). A cDNA fragment of a phagocytic barley NADPH oxidase (*pNAox*, homolog of the large subunit *gp91phox* of a phagocytic NADPH oxidase) is described under the GenBank Acc.-No.: AJ251717).

The present invention aims at providing novel compounds for the defense against pathogens in plants, which compounds bring about an efficient defense against as broad as possible a pathogen spectrum in as many different plant species as possible, prefer-

ably the crop plants used in agriculture. We have found that this object is achieved by the present method.

A first aspect of the invention comprises a method for generating or increasing the resistance to fungi in a monocotyledonous plant, which comprises the following operating steps:

a) reduction of the protein quantity, activity or function of an NADPH oxidase in a plant or a tissue, organ, plant part or cell thereof by introducing a double-stranded NADPH oxidase RNA nucleic acid sequence or (an) expression cassette(s) ensuring its expression; and

b) selection of the plant in which - in contrast or in comparison with the starting plant - the resistance fungi exists or is increased.

Another aspect of the invention comprises a double-stranded RNA molecule for reducing the expression of an NADPH oxidase protein comprising:

a) a sense RNA strand comprising at least one ribonucleotide sequence which has at least 75% identity to at least part of the sense RNA transcript of a nucleic acid sequence encoding an NADPH oxidase; and

b) an antisense RNA strand which has at least 80% identity to a complement of the RNA sense strand of a).

Another aspect of the invention comprises a transgenic expression cassette comprising, in functional linkage with a promoter which is functional in a plant organism, a nucleic acid sequence encoding the double-stranded RNA molecule as defined therein.

Another aspect of the invention comprises a transgenic expression cassette comprising at least a part of a nucleic acid sequence encoding an NADPH oxidase

having at least 70% identity to a sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19 or 21, where said nucleic acid sequence is linked functionally in antisense orientation with a promoter which is functional in a plant organism.

Another aspect of the invention comprises a transgenic vector comprising the expression cassette as defined therein.

Another aspect of the invention comprises a monocotyledonous transgenic plant cell comprising the double-stranded RNA molecule as defined therein, the expression cassette as defined therein or the transgenic vector as defined therein.

A further aspect of the invention comprises a monocotyledonous plant tissue cell, a monocotyledonous plant organ cell or a monocotyledonous plant cell culture comprising:

a) the double-stranded RNA molecule as defined herein;

b) the transgenic expression cassette as defined herein; or

c) the transgenic vector as defined herein,

characterized in that the double-stranded RNA molecule in a), the transgenic expression cassette in b) and the transgenic vector in c) are obtained from the monocotyledonous transgenic plant cell as defined herein.

Surprisingly, the reduction of the expression of a barley NADPH oxidase (pNAox) in the epidermal cell by a sequence-specific RNA interference approach using double-stranded pNAox-dsRNA ("gene silencing") shows a significantly reduced disease level following *Bgh* infection (measured with reference to the formulation of Haustoria). This finding is particularly surprising because the release of reactive oxygen species ("oxidative burst"), which is associated with NADPH oxidase, is generally ascribed a protective function.

Similar to Mlo, the reduction of the NADPH oxidase expression mediates a broad resistance to various isolates of Blumeria graminis f.sp. hordei. In transient gene silencing experiments, the penetration efficiency (development of Haustoria) of Bgh is reduced significantly by more than 35% - an effect which, in its intensity, corresponds to the effect obtained by means of Mlo-dsRNA (Schweizer P et al. (2000) Plant J 24:895-903). In the wild-type barley variety Pallas, approximately 40% of the fungal penetrations result in the development of haustoria, while the penetration rate in the case of reduced NADPH oxidase expression by introduction of a double-stranded RNA of NADPH oxidase (pNAox-dsRNA) only amounts to approximately 25%. The fact that even in pathogen-sensitive wild-type varieties such as Pallas only a penetration rate of approximately 40 to 50% can be observed can be attributed to the basal resistance, which is always present. Owing to these findings, the enzyme NADPH oxidase can be considered a key element for the successful penetration of a pathogen such as Bgh into the plant cell. In addition, the method is superior to all those methods where a pathogen-resistant phenotype is generated by overexpression of a resistance-mediating protein. Switching off a gene can be done without expression of a (foreign) protein. In the ideal case, only the endogenous gene is de-

activated. This has not inconsiderable advantages regarding approval and acceptance by the consumer, who is frequently unsure about plants with foreign proteins. Very especially advantageous in this context is the use of inducible promoters for reducing the NADPH oxidase quantity, activity or function, which, for example in the case of pathogen-inducible promoters, makes possible an expression only when required (i.e. attack by pathogens).

In principle, the method according to the invention can be applied to all plant species, preferably to those in which an NADPH oxidase or a functional equivalent thereof is expressed naturally.

For the purposes of the invention, "plant" means all genera and species of higher and lower plants of the Plant Kingdom. Included in this expression are the mature plants, seed, shoots and seedlings, and parts, propagation material, plant organs, tissues, protoplasts, callus and other cultures, for example cell cultures, derived from them, and all other types of groups of plant cells which give functional or structural units. Mature plants refers to plants at any developmental stage beyond that of the seedling. Seedling means a young, immature plant in an early developmental stage. "Plant" comprises all annual and perennial monocotyledonous and dicotyledonous plants and includes by way of example, but not by limitation, those of the genera Cucurbita, Rosa, Vitis, Juglans, Fragaria, Lotus, Medicago, Onobrychis, Trifolium, Trigonella, Vigna, Citrus, Linum, Geranium, Manihot, Daucus, Arabidopsis, Brassica, Raphanus, Sinapis, Atropa, Capsicum, Datura, Hyoscyamus, Lycopersicon, Nicotiana, Solarium, Petunia, Digitalis, Majorana, Cichorium, Helianthus, Lactuca, Bromus, Asparagus, Antirrhinum, Heterocallis, Nemesis, Pelargonium, Panieum, Pennisetum, Ranunculus, Senecio, Salpiglossis, Cucumis, Browaalia, Glycine, Pisum, Phaseolus, Lolium, Oryza, Zea, Avena, Hordeum, Secale, Triticum, Sorghum, Picea and Populus.

The term "plant" preferably comprises monocotyledonous crop plants, such as, for example, cereal species such as wheat, barley, millet, rye, triticale, maize, rice, sorghum or oats, and sugar cane.

The term furthermore comprises dicotyledonous crop plants such as, for example

- Brassicaceae such as oilseed rape, canola, cress, Arabidopsis, cabbages or canola, Leguminosae such as soybean, alfalfa, pea, beans or peanut

- Solanaceae such as potato, tobacco, tomato, egg plant or paprika, Asteraceae such as sunflower, Tagetes, lettice or Calendula,

- Cucurbitaceae such as melon, pumpkin/squash or zucchini,

and linseed, cotton, hemp, clover, spinach, flax, red pepper, carrot, beet, radish, sugar beet, sweet potato, cucumber, chicory, cauliflower, broccoli, asparagus, onion, garlic, celeriac, strawberry, raspberry, blackberry, pineapple, avocado, and the various tree, bush, nut and vine species. Tree species preferably comprises plum, cherry, peach, nectarine, apricot, banana, paw paw, mango, apple, pear, quince.

Furthermore comprised are ornamental plants, useful or ornamental trees, flowers, cut flowers, shrubs or lawn, by way of example but not by way of limitation, the families of the Rosaceae such as rose, Ericaceae such as rhododendrons and azaleas, Euphorbiaceae such as poinsettias and croton, Caryophyllaceae such as carnations, Solanaceae such as petunias, Gesneriaceae such as African violets, Balsaminaceae such as touch-me-not, Orchidaceae such as orchids, Iridaceae such as gladioli, iris, freesia and crocus, Compositae such as calendula, Geraniaceae such as geraniums, Liliaceae such as dracaena, Moraceae such as ficus, Araceae such as philodendron, and many others.

Preferred for the purposes of the invention are those plants which are employed as food or feedstuff, very especially preferably monocotyledonous genera and species, such as the above-described cereal species.

The method is very especially preferably applied to monocotyledonous plants, most preferably to plants with agricultural importance such as wheat, oats, millet, barley, rye, maize, rice, buckwheat, sorghum, triticale, spelt, linseed or sugar cane.

"Pathogen resistance" denotes the reduction or weakening of disease symptoms of a plant following infection by a pathogen. The symptoms can be manifold, but preferably comprise those which directly or indirectly have an adverse effect on the quality of the plant, the quantity of the yield, the suitability for use as feedstuff or foodstuff, or else which make sowing, planting, harvesting or processing of the crop difficult.

"Conferring", "existing", "generating" or "increasing" a pathogen resistance means that the defense mechanisms of a specific plant species or variety is increasingly resistant to one or more

pathogens due to the use of the method according to the invention in comparison with the wild type of the plant ("original plant"), to which the method according to the invention has not been applied, under otherwise identical conditions (such as, for example, climatic conditions, growing conditions, pathogen species and the like). The increased resistance manifests itself preferably in a reduced manifestation of the disease symptoms, disease symptoms comprising - in addition to the abovementioned adverse effects - for example also the penetration efficiency of a pathogen into the plant or plant cells or the proliferation efficiency in or on the same. In this context, the disease symptoms are preferably reduced by at least 10% or at least 20%, especially preferably by at least 40% or 60%, very especially preferably by at least 70% or 80% and most preferably by at least 90% or 95%.

"Selection" with regard to plants in which - as opposed or as compared to the original plant - resistance to at least one pathogen exists or is increased means all those methods which are suitable for recognizing an existing or increased resistance to pathogens. These may be symptoms of pathogen infection (for example the development of haustoria in the case of fungal infection), but may also comprise the above-described symptoms which relate to the quality of the plant, the quantity of the yield, the suitability for use as feedstuff or foodstuff and the like.

"Pathogen" within the scope of the invention means by way of example but not by limitation viruses or viroids, bacteria, fungi, animal pests such as, for example, insects or nematodes. Especially preferred are fungi, such as mildew. However, it can be assumed that the expression of an NADPH oxidase, its activity or its function also brings about resistance to other pathogens. The following pathogens may be mentioned by way of example but not by limitation:

1. Fungal pathogens and fungus-like pathogens:

Fungal pathogens and fungus-like pathogens (such as, for example, Chromista) are preferably from the group comprising Plasmodiophoramycota, Oomycota, Ascomycota, Chytridiomycetes, Zygomycetes, Basidiomycota and Deuteromycetes (Fungi imperfecti). The pathogens mentioned in Tables 1 and 2 and the diseases with which they are associated may be mentioned by way of example but not by limitation.

Table 1: Fungal plant diseases

Disease	Pathogen
Leaf ruse	Puccinia recondita
Yellow rust	P. striiformis
Powdery mildew	Erysiphe graminis / Blumeria graminis
Glume blotch	Septoria nodorum
Leaf blotch	Septoria tritici
Ear fusarioses	Fusarium spp.
Eyespot	Pseudocercosporella herpotrichoides
Smut	Ustilago spp.
Bunt	Tilletia caries
Take-all	Gaeumannomyces graminis
Anthrocnose leaf blight Anthracnose stalk rot	Colletotrichum graminicola (teleomorph: Glomerella graminicola Politis); Glomerella tucumanensis (anamorph: Glomerella falcatum Went)
Aspergillus ear and kernel rot	Aspergillus flavus
Banded leaf and sheath spot	Rhizoctonia solani Kuhn = Rhizoctonia microsclerotia J. Matz (telomorph: Thanatephorus cucumeris)
Black bundle disease	Acremonium strictum W. Gams = Cephalosporium acremonium Auct. non Corda
Black kernel rot	Lasiodiplodia theobromae = Botryodiplodia theobromae
Borde blanco	Marasmiellus sp.
Brown spot (black spot, stalk rot)	Physoderma maydis
Cephalosporium kernel rot	Acremonium strictum = Cephalosporium acremonium
Charcoal rot	Macrophomina phaseolina
Corticium ear rot	Thanatephorus cucumeris = Corticium sasakii
Curvularia leaf spot	Curvularia clavata, C. eragrostidis = C. maculans (teleomorph: Cochliobolus eragrostidis), Curvularia inaequalis, C. intermedia (teleomorph: Cochliobolus intermedius), Curvularia lunata (teleomorph: Cochliobolus lunatus), Curvularia pallescens (teleomorph: Cochliobolus pallescens), Curvularia senegalensis, C. tuberculata (teleomorph: Cochliobolus tuberculatus)
Didymella leaf spot	Didymella exitalis

Disease	Pathogen
Diplodia ear rot and stalk rot	Diplodia frumenti (teleomorph: Botryosphaeria festucae)
Diplodia ear rot, stalk rot, seed rot and seedling blight	Diplodia maydis = Stenocarpella maydis
Diplodia leaf spot or streak	Stenocarpella macrospora = Diplodialeaf macrospora

Table 2: Downy mildew

Disease	Pathogen
Brown stripe downy mildew	Sclerophthora rayssiae var. zeae
Crazy top downy mildew	Sclerophthora macrospora = Sclerospora macrospora
Green ear downy mildew (graminicola downy mildew)	Sclerospora graminicola
Java downy mildew	Peronosclerospora maydis = Sclerospora maydis
Philippine downy mildew	Peronosclerospora philippinensis = Sclerospora philippinensis
Sorghum downy mildew	Peronosclerospora sorghi = Sclerospora sorghi
Spontaneum downy mildew	Peronosclerospora spontanea = Sclerospora spontanea
Sugarcane downy mildew	Peronosclerospora sacchari = Sclerospora sacchari
Dry ear rot (cob, kernel and stalk rot)	Nigrospora oryzae (teleomorph: Khuskia oryzae)
Ear rots, minor	Alternaria alternata = A. tenuis, Aspergillus glaucus, A. niger, Aspergillus spp., Botrytis cinerea (teleomorph: Botryotinia fuckeliana), Cunninghamella sp., Curvularia pallescens, Doratomyces stemonitis = Cephalotrichum stemonitis, Fusarium culmorum, Gonatobotrys simplex, Pithomyces maydicus, Rhizopus microsporus Tiegh., R. stolonifer = R. nigricans, Scopulariopsis brumptii
Ergot (horse's tooth)	Claviceps gigantea (anamorph: Sphacelia sp.)
Eyespot	Aureobasidium zeae = Kabatiella zeae

Disease	Pathogen
Fusarium ear and stalk rot	Fusarium subglutinans = F. moniliforme var.subglutinans
Fusarium kernel, root and stalk rot, seed rot and seedling blight	Fusarium moniliforme (teleomorph: Gibberella fujikuroi)
Fusarium stalk rot, seedling root rot	Fusarium avenaceum (teleomorph: Gibberella avenacea)
Gibberella ear and stalk rot	Gibberella zeae (anamorph: Fusarium graminearum)
Gray ear rot	Botryosphaeria zeae = Physalospora zeae (anamorph: Macrophoma zeae)
Gray leaf spot (Cercospora leaf spot)	Cercospora sorghi = C. sorghi var. maydis, C. zeae-maydis
Helminthosporium root rot	Exserohilum pedicellatum = Helminthosporium pedicellatum (teleomorph: Setosphaeria pedicellata)
Hormodendrum ear rot (Cladosporium rot)	Cladosporium cladosporioides = Hormodendrum cladosporioides, C. herbarum (teleomorph: Mycosphaerella tassiana)
Hyalothyridium leaf spot	Hyalothyridium maydis
Late wilt	Cephalosporium maydis
Leaf spots, minor	Alternaria alternata, Ascochyta maydis, A. tritici, A. zeicola, Bipolaris victoriae = Helminthosporium victoriae (teleomorph: Cochliobolus victoriae), C. sativus (anamorph: Bipolaris sorokiniana = H. sorokinianum = H. sativum), Epicoccum nigrum, Exserohilum prolatum = Drechslera prolata (teleomorph: Setosphaeria prolata) Graphium penicillioides, Leptosphaeria maydis, Leptothyrium zeae, Ophiosphaerella herpotricha, (anamorph: Scolecosporiella sp.), Paraphaeosphaeria michotii, Phoma sp., Septoria zeae, S. zeicola, S. zeina
Northern corn leaf blight (white blast, crown stalk rot, stripe)	Setosphaeria turcica (anamorph: Exserohilum turcicum = Helminthosporium turcicum)
Northern corn leaf spot Helminthosporium ear rot (race 1)	Cochliobolus carbonum (anamorph: Bipolaris zeicola = Helminthosporium carbonum)
Penicillium ear rot (blue eye, blue mold)	Penicillium spp., P. chrysogenum, P. expansum, P. oxalicum
Phaeocytostroma stalk rot and root rot	Phaeocytostroma ambiguum, = Phaeocytosporella zeae

Disease	Pathogen
Phaeosphaeria leaf spot	Phaeosphaeria maydis = Sphaerulina maydis
Physalospora ear rot (Botryosphaeria ear rot)	Botryosphaeria festucae = Physalospora zeicola (anamorph: Diplodia frumenti)
Purple leaf sheath	Hemiparasitic bacteria and fungi
Pyrenochaeta stalk rot and root rot	Phoma terrestris = Pyrenochaeta terrestris
Pythium root rot	Pythium spp., P. arrhenomanes, P. graminicola
Pythium stalk rot	Pythium aphanidermatum = P. butleri L.
Red kernel disease (ear mold, leaf and seed rot)	Epicoccum nigrum
Rhizoctonia ear rot (sclerotial rot)	Rhizoctonia zeae (teleomorph: Waitea circinata)
Rhizoctonia root rot and stalk rot	Rhizoctonia solani, Rhizoctonia zeae
Root rots, minor	Alternaria alternata, Cercospora sorghi, Dictochaeta fertilis, Fusarium acuminatum (teleomorph: Gibberella acuminata), F. equiseti (teleomorph: G. intricans), F. oxysporum, F. pallidoroseum, F. poae, F. roseum, G. cyanogena, (anamorph: F. sulphureum), Microdochium bolleyi, Mucor sp., Periconia circinata, Phytophthora cactorum, P. drechsleri, P. nicotianae var. parasitica, Rhizopus arrhizus
Rostratum leaf spot (Helminthosporium leaf disease, ear and stalk rot)	Setosphaeria rostrata, (anamorph: Exserohilum rostratum = Helminthosporium rostratum)
Rust, common corn	Puccinia sorghi
Rust, southern corn	Puccinia polysora
Rust, tropical corn	Physopella pallescens, P. zeae = Angiopsora zeae
Sclerotium ear rot (southern blight)	Sclerotium rolfsii Sacc. (teleomorph: Athelia rolfsii)
Seed rot-seedling blight	Bipolaris sorokiniana, B. zeicola = Helminthosporium carbonum, Diplodia maydis, Exserohilum pedicillatum, Exserohilum turcicum = Helminthosporium turcicum, Fusarium avenaceum, F. culmorum, F. moniliforme, Gibberella zeae (anamorph: F. graminearum), Macrophomina phaseolina, Penicillium spp., Phomopsis sp., Pythium spp., Rhizoctonia solani, R. zeae, Sclerotium rolfsii, Spicaria sp.

Disease	Pathogen
Selenophoma leaf spot	Selenophoma sp.
Sheath rot	Gaeumannomyces graminis
Shuck rot	Myrothecium gramineum
Silage mold	Monascus purpureus, M ruber
Smut, common	Ustilago zeae = U. maydis
Smut, false	Ustilaginoidea virens
Smut, head	Sphacelotheca reiliana = Sporisorium holcisorghi
Southern corn leaf blight and stalk rot	Cochliobolus heterostrophus (anamorph: Bipolaris maydis = Helminthosporium maydis)
Southern leaf spot	Stenocarpella macrospora = Diplodia macrospora
Stalk rots, minor	Cercospora sorghi, Fusarium episphaeria, F. merismoides, F. oxysporum Schlechtend, F. poae, F. roseum, F. solani (teleomorph: Nectria haematococca), F. tricinctum, Mariannaea elegans, Mucor sp., Rhopographus zeae, Spicaria sp.
Storage rots	Aspergillus spp., Penicillium spp. and other fungi
Tar spot	Phyllachora maydis
Trichoderma ear rot and root rot	Trichoderma viride = T. lignorum teleomorph: Hypocrea sp.
White ear rot, root and stalk rot	Stenocarpella maydis = Diplodia zeae
Yellow leaf blight	Ascochyta ischaemi, Phyllosticta maydis (teleomorph: Mycosphaerella zeae-maydis)
Zonate leaf spot	Gloeocercospora sorghi

The following are especially preferred

- Plasmodiophoromycota such as Plasmodiophora brassicae (clubroot of crucifers), Spongospora subterranea (powdery scab of potato tubers), Polymyxa graminis (root disease of cereals and grasses),

- Oomycota such as Bremia lactucae (downy mildew of lettuce), Peronospora (downy mildew) in snapdragon (P. antirrhini), onion (P. destructor), spinach (P. effusa), soybean (P. manchurica), tobacco ("blue mold"; P. tabacina), alfalfa and clover (P. trifolium), Pseudoperonospora humuli (downy mildew of hops), Plasmopara (downy mildew in grapevines) (P.

viticola) and sunflower (P. halstedii), Sclerophtohra macrospora (downy mildew in cereals and grasses), Pythium (seed rot, seedling damping-off, and root rot of all types of plants, for example damping-off of Beta beet caused by P. debaryanum), Phytophthora infestans (blight in potato, brown rot in tomato and the like), Albugo spec. (white rust on cruciferous plants).

- Ascomycota such as Microdochium nivale (snow mold of rye and wheat), Fusarium graminearum, Fusarium culmorum (partial ear sterility mainly in wheat), Fusarium oxysporum (Fusarium wilt of tomato), Blumeria graminis (powdery mildew of barley (f.sp. hordei) and wheat (f.sp. tritici)), Erysiphe pisi (powdery mildew of pea), Nectria galligena (Nectria canker of fruit trees), Uncinula necator (powdery mildew of grapevine), Pseudopeziza tracheiphila (red fire disease of grapevine), Claviceps purpurea (ergot on, for example, rye and grasses), Gaeumannomyces graminis (take-all on wheat, rye and other grasses), Magnaporthe grisea (rice blast disease), Pyrenophora graminea (leaf stripe of barley), Pyrenophora teres (net blotch of barley), Pyrenophora tritici-repentis (leaf blight of wheat), Venturia inaequalis (apple scab), Sclerotinia sclerotium (stalk break, stem rot), Pseudopeziza medicaginis (leaf spot of alfalfa, white and red clover).

- Basidiomycetes such as Typhula incarnata (typhula blight on barley, rye, wheat), Ustilago maydis (blister smut on maize), Ustilago nuda (loose smut on barley), Ustilago tritici (loose smut on wheat, spelt), Ustilago avenae (loose smut on oats), Rhizoctonia solani (rhizoctonia root rot of potato), Sphacelotheca spp. (head smut of sorghum), Melampsora lini (rust of flax), Puccinia graminis (stem rust of wheat, barley, rye, oats), Puccinia recondita (leaf rust on wheat), Puccinia dispersa (brown rust on rye), Puccinia hordei (leaf rust of barley), Puccinia coronata (crown rust of oats), Puccinia striiformis (yellow rust of wheat, barley, rye and a large number of grasses), Uromyces appendiculatus (brown rust of bean), Sclerotium rolfsii (root and stem rots of many plants).

- Deuteromycetes (Fungi imperfecti) such as Septoria nodorum (glume blotch) of wheat (Septoria tritici), Pseudocercosporella herpotrichoides (eyespot of wheat, barley, rye), Rynchosporium secalis (leaf spot on rye and barley), Alternaria solani (early blight of potato, tomato), Phoma betae (blackleg on Beta beet), Cercospora beticola (leaf spot on Beta beet), Alternaria brassicae (black spot on

oilseed rape, cabbage and other crucifers), Verticillium dahliae (verticillium wilt), Colletotrichum lindemuthianum (bean anthracnose), Phoma lingam (blackleg of cabbage and oilseed rape), Botrytis cinerea (gray mold of grapevine, strawberry, tomato, hops and the like).

Most preferred are Phytophthora infestans (potato blight, brown rot in tomato and the like), Microdochium nivale (previously Fusarium nivale; snow mold of rye and wheat), Fusarium graminearum, Fusarium culmorum (partial ear sterility of wheat), Fusarium oxysporum (Fusarium wilt of tomato), Blumeria graminis (powdery mildew of barley (f. sp. hordei) and wheat (f. sp. tritici)), Magnaporthe grisea (rice blast disease), Sclerotinia sclerotium (stalk break, stem rot), Septoria nodorum and Septoria tritici (glume blotch of wheat), Alternaria brassicae (black spot of oilseed rape, cabbage and other crucifers), Phoma lingam (blackleg of cabbage and oilseed rape).

2. Bacterial pathogens:

The pathogens and diseases associated with them, all of which are mentioned in table 3, may be mentioned by way of example, but not by limitation.

Table 3: Bacterial diseases

Disease	Pathogen
Bacterial leaf blight and stalk rot	Pseudomonas avenae subsp. avenae
Bacterial leaf spot	Xanthomonas campestris pv. holcicola
Bacterial stalk rot	Enterobacter dissolvens = Erwinia dissolvens
Bacterial stalk and top rot	Erwinia carotovora subsp. carotovora, Erwinia chrysanthemi pv. zeae
Bacterial stripe	Pseudomonas andropogonis
Chocolate spot	Pseudomonas syringae pv. coronafaciens
Goss's bacterial wilt and blight (leaf freckles and wilt)	Clavibacter michiganensis subsp. nebraskensis = Corynebacterium michiganense pv.nebraskense
Holcus spot	Pseudomonas syringae pv. syringae
Purple leaf sheath	Hemiparasitic bacteria
Seed rot-seedling blight	Bacillus subtilis

Stewart's disease (bacterial wilt)	Pantoea stewartii = Erwinia stewartii
Corn stunt (achapparramiento, maize stunt, Mesa Central or Rio Grande maize stunt)	Spiroplasma kunkelii

Very especially preferred are the following pathogenic bacteria: Corynebacterium sepedonicum (potato bacterial ring rot), Erwinia carotovora (potato bacterial soft rot), Erwinia amylovora (fire blight on pear, apple, quince), Streptomyces scabies (potato scab), Pseudomonas syringae pv. tabaci (tobacco black fire), Pseudomonas syringae pv. phaseolicola (bean grease spot), Pseudomonas syringae pv. tomato (tomato bacterial speck), Xanthomonas campestris pv. malvacearum (cotton bacterial blight) and Xanthomonas campestris pv. oryzae (bacterial leaf blight on rice and other grasses).

3. Viral pathogens:

"Viral pathogens" includes all plant viruses such as, for example, tobacco or cucumber mosaic virus, ringspot virus, necroses virus, maize dwarf mosaic virus and the like.

Pathogens and the diseases associated with them may be mentioned in table 4 by way of example, but not by limitation.

Table 4: Viral diseases

Disease	Pathogen
American wheat striate (wheat striate mosaic)	American wheat striate mosaic virus (AWSMV)
Barley stripe mosaic	Barley stripe mosaic virus (BSMV)
Barley yellow dwarf	Barley yellow dwarf virus (BYDV)
Brome mosaic	Brome mosaic virus (BMV)
Cereal chlorotic mottle	Cereal chlorotic mottle virus (CCMV)
Corn chlorotic vein banding (Braizilian maize mosaic)	Corn chlorotic vein banding virus (CCVBV)
Corn lethal necrosis	Virus complex of Maize chlorotic mottle virus (MCMV) and Maize dwarf mosaic virus (MDMV) A or B or Wheat streak mosaic virus(WSMV)
Cucumber mosaic	Cucumber mosaic virus (CMV)
Cynodon chlorotic streak	Cynodon chlorotic streak virus (CCSV)
Johnsongrass mosaic	Johnsongrass mosaic virus (JGMV)

Disease	Pathogen
Maize bushy stunt	Mycoplasma-like organism (MLO) associated
Maize chlorotic dwarf	Maize chlorotic dwarf virus (MCDV)
Maize chlorotic mottle	Maize chlorotic mottle virus (MCMV)
Maize dwarf mosaic	Maize dwarf mosaic virus (MDMV) strains A, D, E and F
Maize leaf fleck	Maize leaf fleck virus (MLFV)
Maize line	Maize line virus (MLV)
Maize mosaic (corn leaf stripe, enanismo rayado)	Maize mosaic virus (MMV)
Maize mottle and chlorotic stunt	Maize mottle and chlorotic stunt virus
Maize pellucid ringspot	Maize pellucid ringspot virus (MPRV)
Maize raya gruesa	Maize raya gruesa virus (MRGV)
maize rayado fino (fine striping disease)	Maize rayado fino virus (MRFV)
Maize red leaf and red stripe	Mollicute
Maize red stripe	Maize red stripe virus (MRSV)
Maize ring mottle	Maize ring mottle virus (MRMV)
Maize rio IV	Maize rio cuarto virus (MRCV)
Maize rough dwarf (nanismo ruvido)	Maize rough dwarf virus (MRDV) (Cereal tillering disease virus)
Maize sterile stunt	Maize sterile stunt virus (strains of barley yellow striate virus)
Maize streak	Maize streak virus (MSV)
Maize stripe (maize chlorotic stripe, maize hoja blanca)	Maize stripe virus
Maize stunting	Maize stunting virus
Maize tassel abortion	Maize tassel abortion virus (MTAV)
Maize vein enation	Maize vein enation virus (MVEV)
Maize wallaby ear	Maize wallaby ear virus (MWEV)
Maize white leaf	Maize white leaf virus
Maize white line mosaic	Maize white line mosaic virus (MWLMV)
Millet red leaf	Millet red leaf virus (MRLV)
Northern cereal mosaic	Northern cereal mosaic virus (NCMV)
Oat pseudorosette (zakuklivanie)	Oat pseudorosette virus
Oat sterile dwarf	Oat sterile dwarf virus (OSDV)
Rice black-streaked dwarf	Rice black-streaked dwarf virus (RBSDV)
Rice stripe	Rice stripe virus (RSV)

Disease	Pathogen
Sorghum mosaic	Sorghum mosaic virus (SrMV) (also: sugarcane mosaic virus (SCMV) strains H, I and M)
Sugarcane Fiji disease	Sugarcane Fiji disease virus (FDV)
Sugarcane mosaic	Sugarcane mosaic virus (SCMV) strains A, B, D, E, SC, BC, Sabi and MB (formerly MDMV-B)
Wheat spot mosaic	Wheat spot mosaic virus (WSMV)

4. Animal pests

4.1 Insect pathogens:

Insects such as, for example, beetles, caterpillars, lice or mites may be mentioned by way of example, but not by limitation. Preferred are insects of the genera Coleoptera, Diptera, Hymenoptera, Lepidoptera, Mallophaga, Homoptera, Hemiptera, Orthoptera, Thysanoptera, Dermaptera, Isoptera, Anoplura, Siphonaptera, Trichoptera, and the like. Especially preferred are Coleoptera and Lepidoptera insects such as, for example, the European corn borer (ECB), Diabrotica barberi ("northern corn rootworm"), Diabrotica undecimpunctata ("southern corn rootworm"), Diabrotica virgifera ("Western corn rootworm"), Agrotis ipsilon ("black cutworm"), Crymodes devastator ("glassy cutworm"), Feltia ducens ("dingy cutworm"), Agrotis gladiaria ("claybacked cutworm"), Melanotus spp., Aeolus mellillus ("wireworm"), Aeolus mancus ("wheat wireworm"), Horistonotus uhlerii ("sand wireworm"), Sphenophorus maidis ("maize billbug"), Sphenophorus zeae ("timothy billbug"), Sphenophorus parvulus ("bluegrass billbug"), Sphenophorus callosus ("southern corn billbug"), Phyllogphaga spp. ("white grubs"), Anuraphis maidiradicis ("corn root aphid"), Delia platura ("seedcorn maggot"), Colaspis brunnea ("grape colaspis"), Stenolophus lecontei ("seedcorn beetle") and Clivinia impressifrons ("lender seedcorn beetle").

Others which may be mentioned are: the cereal leaf beetle (Oulema melanopus), the frit fly (Oscinella frit), wireworms (Agrotis lineatus) and aphids (such as, for example, the oat grain aphid Rhopalosiphum padi, the blackberry aphid Sitobion avenae).

4.2 Nematodes:

Pathogens and the diseases associated with them may be mentioned by way of example, but not by way of limitation, in table 6.

Table 6: Parasitic nematodes

Disease	Pathogenic Nematode
Awl	Dolichodorus spp., D. heterocephalus
Bulb and stem nematode disease; Europe	Ditylenchus dipsaci
Burrowing	Radopholus similis
Cyst nematode disease	Heterodera avenae, H. zeae, Punctodera chalcoensis
Dagger	Xiphinema spp., X. americanum, X. mediterraneum
False root-knot	Nacobbus dorsalis
Lance, Columbia	Hoplolaimus columbus
Lance	Hoplolaimus spp., H. galeatus
Lesion	Pratylenchus spp., P. brachyurus, P. crenatus, P. hexincisus, P. neglectus, P. penetrans, P. scribneri, P. thornei, P. zeae
Needle	Longidorus spp., L. breviannulatus
Ring	Criconemella spp., C. ornata
Root-knot disease	Meloidogyne spp., M. chitwoodi, M. incognita, M. javanica
Spiral	Helicotylenchus spp.
Sting	Belonolaimus spp., B. longicaudatus
Stubby-root	Paratrichodorus spp., P. christiei, P. minor, Quinisulcius acutus, Trichodorus spp.
Stunt	Tylenchorhynchus dubius

Very especially preferred are Globodera rostochiensis and G. pallida (cyst eelworm on potato, tomato and other Solanaceae), Heterodera schachtii (beet eelworm on sugar and fodder beet, oilseed rape, cabbage and the like), Heterodera avenae (cereal cyst nematode on oat and other cereal species), Ditylenchus dipsaci (stem or bulb eelworm, stem eelworm of rye, oats, maize, clover, tobacco, beet), Anguina tritici (ear-cockle nematode, cockle disease of wheat (spelt, rye), Meloidogyne hapla (root-knot nematode of carrot, cucumber, lettuce, tomato, potato, sugar beet, alfalfa).

Examples of fungal or viral pathogens which are preferred for the individual varieties are the following:

1. Barley:

fungal, bacterial and viral pathogens: Puccinia graminis f.sp. hordei (barley stem rust), Blumeria (Erysiphe) graminis f.sp. hordei (Barley Powdery Mildew), barley yellow dwarf virus (BYDV),

Pathogenic insects / nematodes: Ostrinia nubilalis (European corn borer); Agrotis ipsilon (black cutworm); Schizaphis graminum (greenbug); Blissus leucopterus leucopterus (chinch bug); Acrosternum hilare (green stink bug); Euschistus servus (brown stink bug); Deliaplatura (seedcorn maggot); Mayetiola destructor (Hessian fly); Petrobia latens (brown wheat mite).

2. Soybean:

Fungal, bacterial or viral pathogens: Phytophthora megasperma fsp. glycinea, Macrophomina phaseolina, Rhizoctonia solani, Sclerotinia sclerotiorum, Fusarium oxysporum, Diaporthe phaseolorum var. sojae (Phomopsis sojae), Diaporthe phaseolorum var. caulivora, Sclerotium rolfsii, Cercospora kikuchii, Cercospora sojina, Peronospora manchurica, Colletotrichum dematium (Colletotrichum truncatum), Corynespora cassiicola, Septoria glycines, Phyllosticta sojicola, Alternaria alternata, Pseudomonas syringae p.v. glycinea, Xanthomonas campestris p.v. phaseoli, Microsphaera diffussa, Fusarium semitectum, Phialophora gregata, Soybean mosaic virus, Glomerella glycines, Tobacco Ring spot virus, Tobacco Streak virus, Phakopsorapachyrhizi, Pythium aphanidermatum, Pythium ultimum, Pythium debaryanum, Tomato spotted wilt virus, Heterodera glycines, Fusarium solani.

Pathogenic insects / nematodes: Pseudoplusia includens (soybean looper); Anticarsia gemmatalis (velvetbean caterpillar); Plathypena scabra (green cloverworm); Ostrinia nubilalis (European corn borer); Agrotis ipsilon (black cutworm); Spodoptera exigua (beet armyworm); Heliothis virescens (cotton budworm); Helicoverpa zea (cotton bollworm); Epilachna varivestis (Mexican bean beetle); Myzus persicae (green peach aphid); Empoasca fabae (potato leaf hopper); Acrosternum hilare (green stink bug); Melanoplus femurrubrum (redlegged grasshopper); Melanoplus differentialis (differential grasshopper); Hylemya platura (seedcorn maggot); Sericothrips variabilis (soybean thrips); Thrips tabaci (onion thrips); Te-

tranychus turkestani (strawberry spider mite); Tetranychus urticae (two-spotted spider mite).

3. Canola:

Fungal, bacterial or viral pathogens: Albugo candida, Alternaria brassicae, Leptosphaeria maculans, Rhizoctonia solani, Sclerotinia sclerotiorum, Mycosphaerella brassiccola, Pythium ultimum, Peronospora parasitica, Fusarium roseum, Alternaria alternata.

4. Alfalfa:

Fungal, bacterial or viral pathogens: Clavibacter michiganense subsp. insidiosum, Pythium ultimum, Pythium irregulare, Pythium splendens, Pythium debaryanum, Pythium aphanidermatum, Phytophthora megasperma, Peronospora trifoliorum, Phoma medicaginis var. medicaginis, Cercospora medicaginis, Pseudopeziza medicaginis, Leptotrochila medicaginis, Fusarium, Xanthomonas campestris p.v. alfalfae, Aphanomyces euteiches, Stemphylium herbarum, Stemphylium alfalfae.

5. Wheat:

Fungal, bacterial or viral pathogens: Pseudomonas syringae p.v. atrofaciens, Urocystis agropyri, Xanthomonas campestris p.v. translucens, Pseudomonas syringae p.v. syringae, Alternaria alternata, Cladosporium herbarum, Fusarium graminearum, Fusarium avenaceum, Fusarium culmorum, Ustilago tritici, Ascochyta tritici, Cephalosporium gramineum, Collotetrichum graminicola, Erysiphe graminis f.sp. tritici, Puccinia graminis f.sp. tritici, Puccinia recondita f.sp. tritici, Puccinia striiformis, Pyrenophora tritici-repentis, Septoria nodorum, Septoria tritici, Septoria avenae, Pseudocercosporella herpotrichoides, Rhizoctonia solani, Rhizoctonia cerealis, Gaeumannomyces graminis var. tritici, Pythium aphanidermatum, Pythium arrhenomanes, Pythium ultimum, Bipolaris sorokiniana, Barley Yellow Dwarf Virus, Brome Mosaic Virus, Soil-Borne Wheat Mosaic Virus, Wheat Streak Mosaic Virus, Wheat Spindle Streak Virus, American Wheat Striate Virus, Claviceps purpurea, Tilletia tritici, Tilletia laevis, Ustilago tritici, Tilletia indica, Rhizoctonia solani, Pythium arrhenomannes, Pythium gramicola, Pythium aphanidermatum, High Plains Virus, European wheat striate virus, Puccinia graminis f.sp. tritici (Wheat stem rust), Blumeria (Erysiphe) graminis f.sp. tritici (Wheat Powdery Mildew)

Pathogenic insects / nematodes: Pseudaletia unipunctata (army worm); Spodoptera frugiperda (fall armyworm); Elasmopalpus lignosellus (lesser cornstalk borer); Agrotis orthogonia (western cutworm); Elasmopalpus Zignosellus (lesser cornstalk borer); Oulema melanopus (cereal leaf beetle); Hypera punctata (clover leaf weevil); Diabrotica undecimpunctata howardi (southern corn rootworm); Russian wheat aphid; Schizaphis graminum (greenbug); Macrosiphum avenae (English grain aphid); Melanoplus femurrubrum (redlegged grasshopper); Melanoplus differentialis (differential grasshopper); Melanoplus sanguinipes (migratory grasshopper); Mayetiola destructor (Hessian fly); Sitodiplosis mosellana (wheat midge); Meromyza americana (wheat stem maggot); Hylemya coarctata (wheat bulb fly); Frankliniella fusca (tobacco thrips); Cephus cinctus (wheat stem sawfly); Aceria tulipae (wheat curl mite).

6. Sunflower:

Fungal, bacterial or viral pathogens: Plasmophora halstedii, Sclerotinia sclerotiorum, Aster Yellows, Septoria helianthi, Phomopsis helianthi, Alternaria helianthi, Alternaria zinniae, Botrytis cinerea, Phoma macdonaldii, Macrophomina phaseolina, Erysiphe cichoracearum, Rhizopus oryzae, Rhizopus arrhizus, Rhizopus stolonifer, Puccinia helianthi, Verticillium dahliae, Erwinia carotovorum p.v. Carotovora, Cephalosporium acremonium, Phytophthora cryptogea, Albugo tragopogonis.

Pathogenic insects / nematodes: Suleima helianthana (sunflower bud moth); Homoeosoma electellum (sunflower moth); zygogramma exclamationis (sunflower beetle); Bothyrus gibbosus (carrot beetle); Neolasioptera murtfeldtiana (sunflower seed midge).

7. Maize:

Fungal, bacterial or viral pathogens: Fusarium moniliforme var. subglutinans, Erwinia stewartii, Fusarium moniliforme, Gibberella zeae (Fusarium graminearum), Stenocarpella maydi (Diplodia maydis), Pythium irregulare, Pythium debaryanum, Pythium graminicola, Pythium splendens, Pythium ultimum, Pythium aphanidermatum, Aspergillus flavus, Bipolaris maydis 0, T (Cochliobolus heterostrophus), Helminthosporium carbonum I, II & III (Cochliobolus carbonum), Exserohilum turcicum I, II & III, Helminthosporium pedicellatum, Physoderma maydis, Phyllosticta maydis, Kabatiella maydis, Cercospora sorghi, Ustilago maydis, Puccinia sorghi, Puccinia polysora, Macro-

phomina phaseolina, Penicillium oxalicum, Nigrospora oryzae, Cladosporium herbarum, Curvularia lunata, Curvularia inaequalis, Curvularia pallescens, Clavibacter michiganense subsp. nebraskense, Trichoderma viride, Maize Dwarf Mosaic Virus A & B, Wheat Streak Mosaic Virus, Maize Chlorotic Dwarf Virus, Claviceps sorghi, Pseudonomas avenae, Erwinia chrysanthemi p.v. Zea, Erwinia corotovora, Cornstunt spiroplasma, Diplodia macrospora, Sclerophthora macrospora, Peronosclerospora sorghi, Peronosclerospora philippinesis, Peronosclerospora maydis, Peronosclerospora sacchari, Spacelotheca reiliana, Physopella zeae, Cephalosporium maydis, Caphalosporium acremonium, Maize Chlorotic Mottle Virus, High Plains Virus, Maize Mosaic Virus, Maize Rayado Fino Virus, Maize Streak Virus (MSV), Maize Stripe Virus, Maize Rough Dwarf Virus.

Pathogenic insects / nematodes: Ostrinia nubilalis (European corn borer); Agrotis ipsilon (black cutworm); Helicoverpa zea (corn earworm); Spodoptera frugiperda (fall armyworm); Diatraea grandiosella (southwestern corn borer); Elasmopalpus lignosellus (lesser cornstalk borer); Diatraea saccharalis (surgarcane borer); Diabrotica virgifera (western corn rootworm); Diabrotica longicornis barberi (northern corn rootworm); Diabrotica undecimpunctata howardi (southern corn rootworm); Melanotus spp. (wireworms); Cyclocephala borealis (northern masked chafer; white grub); Cyclocephala immaculata (southern masked chafer; white grub); Popillia japonica (Japanese beetle); Chaetocnema pulicaria (corn flea beetle); Sphenophorus maidis (maize billbug); Rhopalosiphum maidis (corn leaf aphid); Anuraphis maidiradicis (corn root aphid); Blissus leucopterus leucopterus (chinch bug); Melanoplus femurrubrum (redlegged grasshopper); Melanoplus sanguinipes (migratory grasshopper); Hylemva platura (seedcorn maggot); Agromyza parvicornis (corn blot leafminer); Anaphothrips obscrurus (grass thrips); Solenopsis milesta (thief ant); Tetranychus urticae (twospotted spider mite).

8. Sorghum:

Fungal, bacterial or viral pathogens: Exserohilum turcicum, Colletotrichum graminicola (Glomerella graminicola), Cercospora sorghi, Gloeocercospora sorghi, Ascochyta sorghina, Pseudomonas syringae p.v. syringae, Xanthomonas campestris p.v. holcicola, Pseudomonas andropogonis, Puccinia purpurea, Macrophomina phaseolina, Perconia circinata, Fusarium moniliforme, Alternaria alternata, Bipolaris sorghicola, Helminthosporium sorghicola, Curvularia lunata, Phoma insidiosa, Pseudomonas avenae (Pseudomonas alboprecipitans), Ramulispora

sorghi, Ramulispora sorghicola, Phyllachara sacchari, Sporisorium reilianum (Sphacelotheca reiliana), Sphacelotheca cruenta, Sporisorium sorghi, Sugarcane mosaic H, Maize Dwarf Mosaic Virus A & B, Claviceps sorghi, Rhizoctonia solani, Acremonium strictum, Sclerophthona macrospora, Peronosclerospora sorghi, Peronosclerospora philippinensis, Sclerospora graminicola, Fusarium graminearum, Fusarium oxysporum, Pythium arrhenomanes, Pythium graminicola.

Pathogenic insects / nematodes: Chilo partellus (sorghum borer); Spodoptera frugiperda (fall armyworm); Helicoverpa zea (corn earworm); Elasmopalpus lignosellus (lesser cornstalk borer); Feltia subterranea (granulate cutworm); Phyllophaga crinita (white grub); Eleodes, Conoderus and Aeolus spp. (wireworm); Oulema melanopus (cereal leaf beetle); Chaetocnema pulicaria (corn flea beetle); Sphenophorus maidis (maize billbug); Rhopalosiphum maidis (corn leaf aphid); Siphaflava (yellow sugarcane aphid); Blissus leucopterus leucopterus (chinch bug); Contarinia sorghicola (sorghum midge); Tetranychus cinnabarinus (carmine spider mite); Tetranychus urticae (two-spotted spider mite).

9. Cotton:

Pathogenic insects / nematodes: Heliothis virescens (cotton budworm); Helicoverpa zea (cotton bollworm); Spodoptera exigua (beet armyworm); Pectinophora gossypiella (pink bollworm); Anthonomus grandis grandis (boll weevil); Aphis gossypii (cotton aphid); Pseudatomoscelis seriatus (cotton fleahopper); Trialeurodes abutilonea (bandedwinged whitefly); Lygus lineolaris (tarnished plant bug); Melanoplus femurrubrum (redlegged grasshopper); Melanoplus differentialis (differential grasshopper); Thrips tabaci (onion thrips); Frankliniella fusca (tobacco thrips); Tetranychus cinnabarinus (carmine spider mite); Tetranychus urticae (twospotted spider mite).

10. Rice:

Pathogenic insects / nematodes: Diatraea saccharalis (sugarcane borer); Spodoptera frugiperda (fall armyworm); Helicoverpa zea (corn earworm); Colaspis brunnea (grape colaspis); Lissorhoptrus oryzophilus (rice water weevil); Sitophilus oryzae (rice weevil); Nephotettix nigropictus (rice leafhopper); Blissus leucopterus leucopterus (chinch bug); Acrosternum hilare (green stink bug).

11. Oilseed rape:

Pathogenic insects / nematodes: Brevicoryne brassicae (cabbage aphid); Phyilotreta cruciferae (Flea beetle); Mamestra conjugrata (Bertha armyworm); Plutella xylostella (Diamondback moth); Delia ssp. (Root maggots).

For the purposes of the invention, "NADPH oxidase" means all those enzymes whose essential characteristic is that they are capable, by means of a single electron transfer, of converting molecular oxygen (O_2) into superoxide (O_{2-}). Preferred are those enzymes which are described by the EC class E.C.1.23.45.3. In this context, the NADPH oxidases can consist of one or more polypeptides which may be identical or different.

Preferably, the NADPH oxidase is a flavocytochrome protein and comprises, as prosthetic groups, a cytochrome b and/or an FAD unit. The NADPH oxidase may consist of an $\alpha 1 \beta 1$ heterodimer, the β subunit being the functional subunit of the flavocytochrome, which may comprise, as glycoprotein, the electron transport components (a hydrophilic, cytosolic, C-terminal domain, comprising NADPH and FAD, and 4 to 6 N-terminal, putative transmembrane α-helices, comprising two histidine-complexed prosthetic heme groups). The α-subunit may comprise a C-terminal, prolin-rich sequence which is capable of binding potential cytosolic, activating factors of the NADPH oxidase. Activation may take place by binding the cytosolic phox proteins (for example p47-phox, p67-phox, p40-phox) and p21rac, a GTP-binding protein.

The skilled worker is familiar with a large number of NADPH oxidases from plant organisms (Torres MA et al. (1998) Plant J 14: 365-370, inter alia). Sequences which may be mentioned by way of example, but not by limitation, are those with the following GenBank Acc. Nos.: AJ251717 (Hordeum vulgare), AP003560 (Oryza sativa var. japonica), AJ320505 (Nicotiana tabacum), AB050660 (Solanum tuberosum), AF088276 (Lycopersicon esculentum), AB008111 (Arabidopsis thaliana; Atrboh F), AF055357 (Arabidopsis thaliana; RbohD), AJ309006 (Nicotiana tabacum; rboh), AP003271 (Oryza sativa cv. japonica), AF055355 (Arabidopsis thaliana; RbohC), AF055353 (Arabidopsis thaliana; RbohA). Especially preferred are the NADPH oxidases which comprise a sequence as shown in SEQ ID: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 or 22.

The sequences from other plants which are homologous to the NADPH oxidase sequences disclosed within the present invention can be found readily for example by database search or by screening genetic libraries using the NADPH oxidase sequences as search se-

quence or probe. Examples which may be mentioned are sequences with the following GenBank Acc. Nos.: CAC51517.1, AJ251717, T03973, BAB68079.1, AP003560, T02024, CAC87256.1, AJ320505, BAB70750.1, AB050660, AF088276_1, NP_564821.1, NM_105079, T00265 AC007764_16, NP_192862.1, NM_117194, AF147783_1, AAM28891.1, AF506374, CAC84140.1, AJ309006, T51804, NP_199602.1, NM_124165, BAB89740.1, AP003271, AAC39477.1, AF055355, NP_199919.1, NM_124485, AAC39475.1, AF055353, NP_196356.1, NM_120821, NP_194239.1, NM_118641, BAB08369.1, AB015475, AAC39478.1, AF055356, AC069143_9, NP_173357.1, NM_101781, NP_172383.1, NM_100780, AAB70398.1, AC000106, AAC39476.1, AF055354, BAB70751.1, AB050661, BAB63664.1, AP003275, AAD24966.1, AF109150.

The polypeptide sequence of the NADPH oxidase especially preferably comprises at least one sequence motif selected from the group of sequence motifs consisting of

i) AL(K/R)GL(K/R)
ii) DK(N/D)XDG(R/K)(I/L/V)(T/N)E
iii) LSASAN
iv) IMEELDP
v) K(F/L)NMA(I/L)(I/V)LXPVCRN
vi) (E/Q)WHPFSIT
vii) S(A/S)PXDD(Q/Y)(L/I)S(I/V)H(V/I/L)R
viii) DGPYG(S/A)PAGDY
ix) L(I/V)GLGIGATP
x) FYWVTREQGSF
xi) GVFYCG

The peptide sequence very especially preferably comprises at least 2 or 3, very especially preferably at least 4 or 5, most preferably all of the sequence motifs selected from the group of the sequence motifs i), ii), iii), iv), v), vi), vii), viii), ix) x) and xi). (Letters in brackets mean alternative amino acids which are possible at this position, for example (V/I) means that valine or isoleucine are possible at this position).

NADPH oxidase may also mean any other unit of an NADPH oxidase enzyme complex which is essential for activity of the NADPH oxidase.

"Protein quantity" means the amount of a NADPH oxidase polypeptide in an organism, a tissue, a cell or a cell compartment. "Reduction" of the protein quantity means the quantitative reduction of the amount of an NADPH oxidase in an organism, a tissue, a cell or a cell compartment - for example by one of the methods described hereinbelow - in comparison with the wild-type of the

same genus and species to which this method has not been applied, under otherwise identical conditions (such as, for example, culture conditions, age of the plants and the like). In this context, the reduction amounts to at least 10%, preferably at least 10% or at least 20%, especially preferably by at least 40% or 60%, very especially preferably by at least 70% or 80%, most preferably by at least 90% or 95%.

"Activity" means the ability of an NADPH oxidase of converting molecular oxygen (O_2) into superoxide (O_{2-}). "Reduction" of the activity means the reduction of the total activity of an NADPH oxidase protein in an organism, a tissue, a cell or a cell compartment - for example by one of the methods described hereinbelow - in comparison with the wild type of the same genus and species, to which this method has not been applied, under otherwise identical conditions (such as, for example, culture conditions, age of the plants and the like). In this context, the reduction amounts to at least 10%, preferably at least 10% or at least 20%, especially preferably to at least 40% or 60%, very especially preferably to at least 70% or 80%, most preferably to at least 90% or 95%.

"Function" preferably means the substrate binding capacity of an NADPH oxidase in an organism, a tissue, a cell or a cell compartment. Suitable substrates are low-molecular-weight compounds such as NADPH or FAD, but also the protein interaction partners of an NADPH oxidase.

"Reduction" of the function means, for example, the quantitative reduction of the binding capacity or binding strength of an NADPH oxidase for at least one substrate in an organism, a tissue, a cell or a cell compartment - for example by one of the methods described hereinbelow - in comparison with the wild-type of the same genus and species to which this method has not been applied, under otherwise identical conditions (such as, for example, culture conditions, age of the plants and the like). "Reduction" is also understood as meaning the change in substrate specificity as expressed, for example, by the kcat/Km value. In this context, the reduction amounts to at least 10%, preferably at least 10% or at least 20%, especially preferably to at least 40% or 60%, very especially preferably to at least 70% or 80%, most preferably to at least 90% or 95%. Binding partners for NADPH oxidase can be identified for example by the yeast-2-hybrid system in the manner with which the skilled worker is familiar.

Methods for determining the protein quantity, the activity of NADPH oxidases or the substrate binding capacity are known to the skilled worker. For example, it is possible to measure the NADPH-dependent O_2^- or H_2O_2 production which can be inhibited by DPI (for example via Nitro Blue Tetrazolium [NBT] or cytochrome c reduction). The protein quantity can be determined for example immunologically, using suitable antibodies. Suitable methods are described (Yu L et al. (1999) Blood 94(7):2497-504; Doke N (1983a) Physiol Plant Pathol 23:345-357; Levine A et al. (1994) Cell 79:583-593; Tenhaken R et al. (1995) Proc Nat Acad Sci USA 92: 4158-4163; Sagi M & Fluhr R. (2001) Plant Physiol 126(3):1281-90; Hückelhoven R & Kogel KH (1998) Mol Plant Microbe Interact 11:292-300; and references cited in the above papers).

"Functional equivalents" of an NADPH oxidase protein preferably means those sequences which are derived from an NADPH oxidase comprising a polypeptide sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 or 22 or which are homologous with the former and which have the same essential characteristics.

In this context, the efficiency of the pathogen resistance may deviate both upwards and downwards in comparison with a value obtained when reducing one of the NADPH oxidases comprising a polypeptide sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 or 22. Preferred functional equivalents are those where the efficiency of the pathogen resistance - measured for example with the aid of the penetration efficiency of a pathogen (development of haustora) - differs by not more than 50%, preferably 25%, especially preferably 10%, from a comparative value obtained by reducing an NADPH oxidase comprising a polypeptide sequence as described in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 or 22. Especially preferred are those sequences whose reduction has the result that the efficiency of the pathogen resistance quantitatively exceeds a comparative value obtained by reducing one of the NAPDH oxidases comprising a polypeptide sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 or 22 by more than 50%, preferably 100%, especially preferably 500%, very especially preferably 1000%.

The comparison is preferably carried out under analogous conditions. "Analogous conditions" means that all framework conditions such as, for example, culture or growth conditions, assay conditions (such as buffer, temperature, substrates, pathogen concentration and the like) between the experiments to be compared are kept identical and that the set-ups differ only by the sequence of the NAPDH oxidases to be compared, their organism of origin and, if appropriate, the pathogen. When selecting the

pathogen for the comparison, the pathogen to be selected for the comparison is that which is most similar to the corresponding other pathogen, taking into consideration the species specificity.

In particular, "functional equivalents" means natural or artificial mutations of the NADPH oxidases comprising a polypeptide sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 or 22 and homologous polypeptides from other plants which continue to have essentially identical characteristics. Homologous polypeptides from the above-described preferred plants are preferred. The sequences from other plants (for example Arabidopsis thaliana) which are homologous to the NAPDH oxidase sequences disclosed within the scope of the present invention can be found readily for example by database search or screening genetic libraries, using the NADPH oxidase sequences as search sequence or probe. Such sequences are detailed above by way of example together with their GenBank Acc No.

Mutations comprise substitutions, additions, deletions, inversions or insertions of one or more amino acid residues. Thus, the present invention also comprises for example those polypeptides which are obtained by modification of a polypeptide comprising a polypeptide sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 or 22.

Homology between two nucleic acid sequences is understood as meaning the identity of the two nucleic acid sequences over in each case the entire sequence length which is calculated by comparison with the aid of the program algorithm GAP (Wisconsin Package Version 10.0, University of Wisconsin, Genetics Computer Group (GCG), Madison, USA), setting the following parameters:

Gap weight: 50	Length weight: 3
Average match: 10	Average mismatch: 0

For example a sequence which has at least 80% homology with sequence SEQ ID NO: 1 at the nucleic acid level is understood as meaning a sequence which, upon comparison with the sequence SEQ ID NO: 1 by the above program algorithm with the above parameter set, has at least 80% homology.

Homology between two polypeptides is understood as meaning the identity of the two nucleic acid sequences over in each case the entire sequence length which is calculated by comparison with the aid of the program algorithm GAP (Wisconsin Package Version 10.0,

University of Wisconsin, Genetics Computer Group (GCG), Madison, USA; Altschul et al. (1997) Nucleic Acids Res. 25:3389 et seq.), setting the following parameters:

Gap weight: 8 Length weight: 2

Average match: 2,912 Average mismatch: -2,003

For example a sequence which has at least 80% homology with sequence SEQ ID NO: 2 at the protein level is understood as meaning a sequence which, upon comparison with the sequence SEQ ID NO: 2 by the above program algorithm with the above parameter set, has at least 80% homology.

Functional equivalents derived from an NADPH oxidase comprising a polypeptide sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 or 22 by substitution, insertion or deletion have at least 50%, preferably at least 70%, by preference at least 90%, especially preferably at least 95%, very especially preferably at least 98% homology with a polypeptide comprising a polypeptide sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 or 22 and are distinguished by identical essential characteristics as the former.

Functional equivalents derived from an NAPDH oxidase nucleic acid sequence comprising a sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19 or 21 by substitution, insertion or deletion, have at least 50%, preferably at least 70%, by preference at least 90%, especially preferably at least 95%, very especially preferably at least 98% homology with one of the polypeptides according to the invention as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19 or 21 and encode polypeptides with the same essential characteristics as a polypeptide comprising a sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 or 22.

Also, screening cDNA libraries or genomic libraries of other organisms, preferably of the plant species which are mentioned further below as being suitable hosts for the transformation, using the nucleic acid sequences described under SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19 or 21 or parts of these as probe, is a method known to the skilled worker for identifying homologs in other species. In this context, the probes derived from the nucleic acid sequences as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19 or 21 have a length of at least 20 bp, preferably at least 50 bp, especially preferably at least 100 bp, very especially preferably at least 200 bp, most preferably at least 400 bp. A DNA strand which is complementary to the sequences de-

scribed under SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19 or 21 may also be employed for screening the libraries.

Functional equivalents comprises DNA sequences which hybridize under standard conditions with the NAPDH oxidase nucleic acid sequences described under SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19 or 21, the nucleic acid sequence complementary thereto or parts of the above and which, as complete sequences, encode proteins which have the same essential characteristics as a polypeptide comprising a sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 or 22.

"Standard hybridization conditions" is to be understood in the broad sense and means stringent or else less stringent hybridization conditions. Such hybridization conditions are described, inter alia, by Sambrook J, Fritsch EF, Maniatis T et al., in Molecular Cloning (A Laboratory Manual), 2nd Edition, Cold Spring Harbor Laboratory Press, 1989, pages 9.31-9.57 or in Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6.

For example, the conditions during the wash step can be selected from the range of conditions delimited by low-stringency conditions (approximately 2X SSC at 50°C) and high-stringency conditions (approximately 0.2X SSC at 50°C, preferably at 65°C) (20X SSC: 0.3M sodium citrate, 3M NaCl, pH 7.0). In addition, the temperature during the wash step can be raised from low-stringency conditions at room temperature, approximately 22°C, to higher-stringency conditions at approximately 65°C. Both of the parameters, salt concentration and temperature, can be varied simultaneously, or else one of the two parameters can be kept constant while only the other is varied. Denaturants, for example formamide or SDS, may also be employed during the hybridization. In the presence of 50% formamide, hybridization is preferably effected at 42°C. Some examples of conditions for hybridization and wash step are shown hereinbelow:

(1) Hybridization conditions can be selected, for example, from the following conditions:

a) 4X SSC at 65°C (with - optionally - 100 µg/ml denatured fragmented fish sperm DNA)

b) 6X SSC at 45°C (with - optionally - 100 µg/ml denatured fragmented fish sperm DNA),

c) 6X SSC, 0.5% SDS, 50% formamide at 42°C (with - optionally - 100 µg/ml denatured fragmented fish sperm DNA)

d) 4X SSC, 50% formamide at 42°C (with - optionally - 100 µg/ml denatured fragmented fish sperm DNA)
e) 2X or 4X SSC at 50°C (low-stringency condition),
f) 30 to 40% formamide, 2X or 4X SSC at 42°C (low-stringency condition).

(2) Wash steps can be selected, for example, from the following conditions:

a) 0.015 M NaCl/0.0015 M sodium citrate/0.1% SDS at 50°C.
b) 0.1X SSC at 65°C.
c) 0.1X SSC, 0.5% SDS at 68°C.
d) 0.1X SSC, 0.5% SDS, 50% formamide at 42°C.
e) 0.2X SSC, 0.1% SDS at 42°C.
f) 2X SSC at 65°C (low-stringency condition).

The reduction of the expression of an NADPH oxidase protein, the NADPH oxidase activity or the NADPH oxidase function can be performed in many ways.

"Reduction" or "to reduce" in connection with an NADPH oxidase, an NADPH oxidase activity or NADPH oxidase function is to be interpreted in the broad sense and comprises the partial or essentially complete prevention or blocking (due to a variety of cell-biological mechanisms) of the functionality of an NAPDH oxidase in a plant or a part, tissue, organ, cells or seed derived therefrom. A reduction for the purposes of the invention also comprises a quantitative reduction of an NADPH oxidase down to an essentially complete absence of the NAPDH oxidase (i.e. lack of detectability of NADPH oxidase activity or NADPH oxidase function, or lack of immunological detectability of the NADPH oxidase protein). In this context, one or more essential units of the NADPH oxidase can be reduced. In this context, the expression of a certain NADPH oxidase or the NADPH oxidase activity or NADPH oxidase function in a cell or an organism is reduced by preferably more than 50%, especially preferably more than 80%, very especially preferably more than 90%.

A variety of strategies for reducing the expression of an NADPH oxidase protein, the NADPH oxidase activity or NADPH oxidase function are comprised in accordance with the invention. Strategies which may be mentioned by way of example, but not by limitation, are:

a) Introducing a double-stranded NADPH oxidase RNA nucleic acid sequence (NAox-dsRNA) or (an) expression cassette(s) ensuring its expression;

b) Introducing an NADPH oxidase antisense nucleic acid sequence or an expression cassette ensuring its expression. Comprised are those methods in which the antisense nucleic acid sequence is directed against an NADPH oxidase gene (that is to say, genomic DNA sequences) or an NADPH oxidase gene transcript (that is to say, RNA sequences). Also comprised are α-anomeric nucleic acid sequences.

c) Introducing an NADPH oxidase antisense nucleic acid sequence in combination with a ribozyme or an expression cassette ensuring its expression

d) Introducing NADPH oxidase sense nucleic acid sequences for inducing a cosuppression or an expression cassette ensuring their expression

e) Introducing DNA- or protein-binding factors against NADPH oxidase genes, RNAs or proteins or an expression cassette ensuring their expression

f) Introducing viral nucleic acid sequences and expression constructs bringing about the degradation of NADPH oxidase RNA, or an expression cassette ensuring their expression

g) Introducing constructs for inducing a homologous recombination at endogenous NADPH oxidase genes, for example for the generation of knock-out mutants.

h) Introducing mutations into endogenous NADPH oxidase genes for generating a loss of function (for example generation of stop codons, reading frame shifts and the like)

Here, each and every one of these methods can bring about a reduction of the NADPH oxidase expression, NADPH oxidase activity or NADPH oxidase function in the sense of the invention. A combined use is also feasible. Further methods are known to the skilled worker and can comprise hindering or preventing the processing of the NADPH oxidase protein, the transport of the NADPH oxidase protein or its mRNA, inhibition of the attachment of ribosomes, inhibition of RNA splicing, induction of an NADPH oxidase RNA degrading enzyme and/or inhibition of the translational elongation or termination.

The individual methods which are preferred shall be described briefly hereinbelow:

a) Introducing a double-stranded NADPH oxidase RNA nucleic acid sequence (NAox-dsRNA)

The method of regulating genes by means of double-stranded RNA (double-stranded RNA interference; dsRNAi) has been described many times in animal and plant organisms (for example Matzke MA et al. (2000) Plant Mol Biol 43:401-415; Fire A. et al (1998) Nature 391:806-811; WO 99/32619; WO 99/53050; WO 00/68374; WO 00/44914; WO 00/44895; WO 00/49035; WO 00/63364). The processes and methods described in the abovementioned references are expressly referred to. Efficient gene suppression can also be shown in the case of transient expression or after transient expression, for example as the result of a biolistic transformation (Schweizer P et al. (2000) Plant J 2000 24:895-903). dsRNAi methods are based on the phenomenon that the simultaneous introduction of complementary strand and counterstrand of a gene transcript brings about a highly-efficient suppression of the expression of the gene in question. The phenotype which results is very similar to a corresponding knock-out mutant (Waterhouse PM et al. (1998) Proc Natl Acad Sci USA 95:13959-64).

The dsRNAi method has proved to be particularly efficient and advantageous when reducing the NADPH oxidase expression. As described in WO 99/32619, inter alia, dsRNAi approaches are markedly superior to traditional antisense approaches.

A further aspect of the invention therefore relates to double-stranded RNA molecules (dsRNA molecules) which, when introduced into a plant (or a cell, tissue, organ or seed derived therefrom), bring about the reduction of an NADPH oxidase.

The double-stranded RNA molecule for reducing the expression of an NADPH oxidase protein comprises

a) a sense RNA strand comprising at least one ribonucleotide sequence which is essentially identical to at least part of an NADPH oxidase nucleic acid sequence, and

b) an antisense RNA strand which is essentially - preferably completely - complementary to the RNA sense strand of a).

In a furthermore preferred embodiment, the double-stranded RNA molecule for reducing the expression of an NADPH oxidase protein comprises

a) a sense RNA strand comprising at least one ribonucleotide sequence which is essentially identical to at least part of the sense RNA transcript of a nucleic acid sequence encoding an NADPH oxidase protein, and

b) an antisense RNA strand which is essentially - preferably completely - complementary to the RNA sense strand of a).

With regard to the double-stranded RNA molecules, NADPH oxidase nucleic acid sequence preferably means a sequence comprising a sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19 or 21.

"Essentially identical" means that the dsRNA sequence may also have insertions, deletions and individual point mutations in comparison with the NADPH oxidase target sequence or a functional equivalent target sequence while still bringing about an efficient reduction of the expression. Preferably, the homology as defined above between the sense strand of an inhibitory dsRNA and at least part of the sense RNA transcript of a nucleic acid sequence encoding an NAPDH oxidase protein or functional equivalent thereof (or between the antisense strand of the complementary strand of a nucleic acid sequence encoding an NAPDH oxidase protein or a functional equivalent thereof) amounts to at least 75%, preferably at least 80%, very especially preferably at least 90% most preferably 100%.

The length of the part-segment amounts to at least 10 bases, preferably at least 25 bases, especially preferably at least 50 bases, very especially preferably at least 100 bases, most preferably at least 200 bases or at least 300 bases.

Alternatively, an "essentially identical" dsRNA may also be defined as a nucleic acid sequence which is capable of hybridizing with a part of a storage protein gene transcript (for example in 400 mM NaCl, 40 mM PIPES pH 6.4, 1 mM EDTA at 50°C or 70°C for 12 to 16 h).

"Essentially complementary" means that the antisense RNA strand may also have insertions, deletions and individual point mutations in comparison with the complement of the sense RNA strand. Preferably, the homology between the antisense RNA strand and the complement of the sense RNA strand amounts to at least 80%, pre-

ferably at least 90%, very especially preferably at least 95%, most preferably 100%.

"Part of the sense RNA transcript" of a nucleic acid sequence encoding an NADPH oxidase protein or a functional equivalent thereof means fragments of an RNA or mRNA transcribed from a nucleic acid sequence encoding an NADPH oxidase protein or a functional equivalent thereof, preferably an NADPH oxidase gene. Here, the fragments preferably have a sequence length of at least 20 bases, preferably at least 50 bases, especially preferably at least 100 bases, very especially preferably at least 200 bases, most preferably at least 500 bases. Also comprised is the complete transcribed RNA or mRNA.

Also comprised is the use of the dsRNA molecules according to the invention in the methods according to the invention for generating a pathogen resistance in plants.

The dsRNA can consist of one or more strands of polymerized ribonucleotides. Furthermore, modifications both of the sugar-phosphate skeleton and of the nucleosides may be present. For example, the phosphodiester bonds of the natural RNA can be modified in such a way that they comprise at least one nitrogen or sulfur heteroatom. Bases can be modified in such a way that the activity of, for example, adenosine deaminase is limited. These and further modifications are described hereinbelow in the methods for stabilizing antisense RNA.

To achieve the same purpose it is, of course, also possible to introduce, into the cell or the organism, a plurality of individual dsRNA molecules, each of which comprises one of the above-defined ribonucleotide sequence segments.

The dsRNA can be produced enzymatically or, fully or in parts, by chemical synthesis.

The double-stranded dsRNA structure can be formed starting from two complementary, separate RNA strands or - preferably - starting from a single, autocomplementary RNA strand.

In the case of a single, autocomplementary strand, sense and antisense sequence can be linked by a linking sequence (linker) and form for example a hairpin structure. Preferably, the linking sequence may be an intron, which is spliced out after the dsRNA has been synthesized.

The nucleic acid sequence encoding a dsRNA may comprise further elements such as, for example transcription termination signals or polyadenylation signals.

If the two strands of the dsRNA are to be combined in a cell or plant, this may take place in various ways, for example:

a) transformation of the cell or plant with a vector which comprises both expression cassettes,

b) cotransformation of the cell or plant with two vectors, where one comprises the expression cassettes with the sense strand and the other comprises the expression cassettes with the antisense strand,

c) hybridizing two plants, each of which has been transformed with a vector, where one comprises the expression cassettes with the sense strand and the other comprises the expression cassettes with the antisense strand.

The formation of the RNA duplex can be initiated either outside the cell or within the same. As in WO 99/53050, the dsRNA may also comprise a hairpin structure by linking sense and antisense strand by a linker (for example an intron). The autocomplementary dsRNA structures are preferred since they merely require the expression of a construct and comprise the complementary strands always in an equimolar ratio.

The expression cassettes encoding the antisense or sense strand of a dsRNA or the autocomplementary strand of the dsRNA are preferably inserted into a vector and, using the methods described hereinbelow, stably (for example using selection markers) inserted into the genome of a plant in order to ensure durable expression of the dsRNA.

The dsRNA can be introduced using such an amount that at least one copy per cell is made possible. Larger amounts (for example at least 5, 10, 100, 500 or 1000 copies per cell) may, if appropriate, bring about a more efficient reduction.

As already described, 100% sequence identity between dsRNA and an NADPH oxidase gene transcript or the gene transcript of a functionally equivalent gene is not necessarily required in order to bring about an efficient reduction of the NADPH oxidase expression. Accordingly, there is the advantage that the method tolerates sequence deviations, as may be present as the result of genetic mutations, polymorphisms or evolutionary divergences. Using

the dsRNA which has been generated starting from the NADPH oxidase sequence of an organism, it is thus, for example, possible to suppress the NAPDH oxidase expression in another organism. The high degree of sequence homology between the NADPH oxidase sequences from rice, maize and barley allows the conclusion that this protein is highly conserved within plants, so that the expression of a dsRNA derived from one of the NADPH oxidase sequences comprising a sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19 or 21 probably also has an advantageous effect in other plant species.

Owing to the high degree of homology between the individual NADPH oxidase proteins and their functional equivalents, it is also possible to suppress the expression of further homologous NAPDH oxidase proteins and/or their functional equivalents of the same organism or else the expression of NAPDH oxidase proteins in other related species, using a single dsRNA which has been generated starting from a specific NADPH oxidase sequence of an organism. For this purpose, the dsRNA preferably comprises sequence regions of NADPH oxidase gene transcripts which correspond to conserved regions. Said conserved regions can be deduced readily from sequence alignments.

The dsRNA can be synthesized either in vivo or in vitro. To this end, a DNA sequence encoding a dsRNA can be introduced into an expression cassette under the control of at least one genetic control element (such as, for example, promoter, enhancer, silencer, splice donor or acceptor, polyadenylation signal). Suitable advantageous constructions are described hereinbelow. A polyadenylation is not necessary, nor do elements for initiating a translation have to be present.

A dsRNA can be synthesized chemically or enzymatically. To this end, cellular RNA polymerases or bacteriophage RNA polymerases (such as, for example, T3, T7 or SP6 RNA polymerase) can be used. Such methods for the in-vitro expression of RNA are described (WO 97/32016; US 5,593,874; US 5,698,425, US 5,712,135, US 5,789,214, US 5,804,693). A dsRNA which has been synthesized in vitro, either chemically or enzymatically, can be isolated fully or in part from the reaction mixture, for example by extraction, precipitation, electrophoresis, chromatography or combination of these methods, before it is introduced into a cell, tissue or organism. The dsRNA can be introduced directly into the cell or else by applied extracellularly (for example into the interstitial space).

However, the plant is preferably transformed stably using an expression construct which brings about the expression of the dsRNA. Suitable methods are described hereinbelow.

b) Introduction of an NADPH oxidase antisense nucleic acid sequence

Methods for suppressing a particular protein by preventing the accumulation of its mRNA by antisense technology have been described many times, also in plants (Sheehy et al. (1988) Proc Natl Acad Sci USA 85: 8805-8809; US 4,801,340; Mol JN et al. (1990) FEBS Lett 268(2):427-430). The antisense nucleic acid molecule hybridized with, or binds to, the cellular mRNA and/or genomic DNA encoding the NADPH oxidase target protein to be suppressed, which suppresses the transcription and/or translation of the target protein. The hybridization can be brought about in the traditional manner via the formation of a stable duplex or - in the case of genomic DNA - by binding the antisense nucleic acid molecule with the duplex of the genomic DNA by specific interaction in the large groove of the DNA helix.

An antisense nucleic acid sequence suitable for reducing an NADPH oxidase protein can be derived using the nucleic acid sequence which encodes this protein, for example the nucleic acid sequence comprising a sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19 or 21, following the Watson-Crick base pair rules. The antisense nucleic acid sequence can be complementary to all of the transcribed mRNA of said protein, may be limited to the coding region or may consist of one oligonucleotide only, which is complementary to part of the coding or noncoding sequence of the mRNA. Thus, the oligonucleotide may, for example, be complementary to the region which comprises the translation start for said protein. Antisense nucleic acid sequences can have a length of, for example, 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides, but may also be longer and comprise at least 100, 200, 500, 1000, 2000 or 5000 nucleotides. Antisense nucleic acid sequences can be expressed recombinantly or synthetized chemically or enzymatically using methods known to the skilled worker. In the case of chemical synthesis, natural or modified nucleotides may be used. Modified nucleotides can impart an increased biochemical stability to the antisense nucleic acid sequence and may lead to an increased physical stability of the duplex formed of antisense nucleic acid sequence and sense target sequence. Nucleotides which can be used are, for example, phosphorothioate derivatives and acridine-substituted nucleotides such as 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthin, xanthin, 4-acetylcytosine, 5-(carboxyhydroxylmethyl)uracil,

5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, β-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, β-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methyl ester, uracil-5-oxyacetic acid, 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl)uracil and 2,6-diaminopurine.

In a further preferred embodiment, the expression of an NADPH oxidase protein can be inhibited by nucleotide sequences which are complementary to the regulatory region of an NADPH oxidase gene (for example an NADPH oxidase promoter and/or enhancer) and form triple-helical structures with the DNA double helix therein, so that the transcription of the NADPH oxidase gene is reduced. Suitable methods are described (Helene C (1991) Anticancer Drug Res 6(6):569-84; Helene C et al. (1992) Ann NY Acad Sci 660:27-36; Maher LJ (1992) Bioassays 14(12):807-815).

In a further embodiment, the antisense nucleic acid molecule can be an α-anomeric nucleic acid. Such α-anomeric nucleic acid molecules form specific double-stranded hybrids with complementary RNA in which - in contrast to the conventional β-nucleic acids - the two strands are parallel to one another (Gautier C et al. (1987) Nucleic Acids Res 15:6625-6641). The antisense nucleic acid molecule can furthermore also comprise 2'-O-methylribonucleotides (Inoue et al. (1987) Nucleic Acids Res 15:6131-6148) or chimeric RNA-DNA analogs (Inoue et al. (1987) FEBS Lett 215:327-330).

c) Introduction of an NADPH oxidase antisense nucleic acid sequence in combination with a ribozyme

The above-described antisense strategy can advantageously be coupled with a ribozyme method. Catalytic RNA molecules or ribozymes can be adapted to any target RNA and cleave the phosphodiester backbone at specific positions, whereby the target DNA is functionally deactivated (Tanner NK (1999) FEMS Microbiol Rev 23(3):257-275). The ribozyme itself is not modified thereby, but is capable of cleaving further target RNA molecules in an analogous manner, whereby it gains the properties of an enzyme. The incorporation of ribozyme sequences into antisense RNAs imparts to these antisense-RNAs this enzyme-like, RNA-cleaving property

and thus increases their efficiency in the inactivation of the target RNA. The preparation and use of suitable ribozyme antisense RNA molecules is described for example by Haseloff et al. (1988) Nature 334:585-591.

In this manner, ribozymes (for example Hammerhead ribozymes; Haselhoff and Gerlach (1988) Nature 334:585-591) can be used for catalytically cleaving the mRNA of an enzyme to be suppressed - for example NADPH oxidase - and for preventing translation. The ribozyme technology can increase the efficiency of an antisense strategy. Methods for the expression of ribozymes for reducing certain proteins are described in (EP 0 291 533, EP 0 321 201, EP 0 360 257). Ribozyme expression in plant cells is also described (Steinecke P et al. (1992) EMBO J 11(4):1525-1530; de Feyter R et al. (1996) Mol Gen Genet. 250(3):329-338). Suitable target sequences and ribozymes can be determined for example as described by "Steinecke P, Ribozymes, Methods in Cell Biology 50, Galbraith et al. eds, Academic Press, Inc. (1995), pp. 449-460", by calculating the secondary structure of ribozyme RNA and target RNA, and by their interaction (Bayley CC et al. (1992) Plant Mol Biol. 18(2):353-361; Lloyd AM and Davis RW et al. (1994) Mol Gen Genet. 242(6):653-657). For example, it is possible to construct derivatives of the Tetrahymena L-19 IVS RNA, which have complementary regions to the mRNA of the NADPH oxidase protein to be suppressed (see also US 4,987,071 and US 5,116,742). Alternatively, such ribozymes can also be identified from a library of diverse ribozymes, using a selection process (Bartel D and Szostak JW (1993) Science 261:1411-1418).

d) Introducing an NADPH oxidase sense nucleic acid sequence for inducing a cosuppression

The expression of an NADPH oxidase nucleic acid sequence in sense orientation can lead to a cosuppression of the corresponding homologous, endogenous gene. The expression of sense RNA with homology to an endogenous gene can reduce or switch off the expression of same, similarly to what has been described for antisense approaches (Jorgensen et al. (1996) Plant Mol Biol 31(5):957-973; Goring et al. (1991) Proc Natl Acad Sci USA 88:1770-1774; Smith et al. (1990) Mol Gen Genet 224:447-481; Napoli et al. (1990) Plant Cell 2:279-289; Van der Krol et al. (1990) Plant Cell 2:291-99). Here, the introduced construct can fully or only partly represent the homologous gene to be reduced. The possibility of translation is not required. The application of this technology to plants is described for example by Napoli et al. (1990) The Plant Cell 2: 279-289 and in US 5,034,323.

Preferably, cosuppression is carried out using a sequence which is essentially identical to at least a part of the nucleic acid sequence encoding an NADPH oxidase protein or a functional equivalent thereof, for example the nucleic acid sequence comprising a sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19 or 21.

e) Introducing DNA- or protein-binding factors against NADPH oxidase genes, RNAs or proteins

A reduction of an NADPH oxidase gene expression is also possible using specific DNA-binding factors, for example with factors of the zinc finger transcription factor type. These factors anneal with the genomic sequence of the endogenous target gene, preferably in the regulatory regions, and bring about a repression of the endogenous gene. The use of such a method makes it possible to reduce the expression of an endogenous NADPH oxidase gene without it being necessary to recombinantly manipulate the sequence of the latter. Suitable methods for the generation of suitable factors are described (Dreier B et al. (2001) J Biol Chem 276(31):29466-78; Dreier B et al. (2000) J Mol Biol 303(4):489-502; Beerli RR et al. (2000) Proc Natl Acad Sci USA 97 (4):1495-1500; Beerli RR et al. (2000) J Biol Chem 275(42):32617-32627; Segal DJ and Barbas CF 3rd. (2000) Curr Opin Chem Biol 4(1):34-39; Kang JS and Kim JS (2000) J Biol Chem 275(12):8742-8748; Beerli RR et al. (1998) Proc Natl Acad Sci USA 95(25):14628-14633; Kim JS et al. (1997) Proc Natl Acad Sci USA 94(8):3616-3620; Klug A (1999) J Mol Biol 293(2):215-218; Tsai SY et al. (1998) Adv Drug Deliv Rev 30(1-3):23-31; Mapp AK et al. (2000) Proc Natl Acad Sci USA 97(8):3930-3935; Sharrocks AD et al. (1997) Int J Biochem Cell Biol 29(12):1371-1387; Zhang L et al. (2000) J Biol Chem 275(43):33850-33860).

These factors may be selected using any desired portion of an NADPH oxidase gene. Preferably, this segment is located within the promoter region. For gene suppression, however, it may also be located in the region of the coding exons or introns. The corresponding segments are obtainable for the skilled worker by means of database search from the genetic library or - starting from an NADPH oxidase cDNA whose gene is not present in the genetic library, by screening a genomic library for corresponding genomic clones. The methods required for this purpose are known to the skilled worker.

Furthermore, it is possible to introduce, into a cell, factors which inhibit the NADPH oxidase target protein itself. The protein-binding factors may be for example aptamers (Famulok M and

Mayer G (1999) Curr Top Microbiol Immunol 243:123-36) or antibodies or antibody fragments or single-chain antibodies. The way in which these factors are obtained is described and known to the skilled worker. For example, a cytoplasmic scFv antibody has been employed for modulating the activity of the phytochrome A protein in genetically modified tobacco plants (Owen M et al. (1992) Biotechnology (N Y) 10(7):790-794; Franken E et al. (1997) Curr Opin Biotechnol 8(4):411-416; Whitelam (1996) Trend Plant Sci 1:286-272).

Gene expression can also be suppressed by tailor-made low-molecular-weight synthetic compounds, for example of the polyamide type (Dervan PB and Bürli RW (1999) Current Opinion in Chemical Biology 3:688-693; Gottesfeld JM et al. (2000) Gene Expr 9(1-2):77-91). These oligomers consist of the units 3-(dimethylamino)propylamine, N-methyl-3-hydroxypyrrole, N-methylimidazole and N-methylpyrrole and can be adapted to any portion of double-stranded DNA in such a way that they bind sequence-specifically in the large groove and block the expression of the gene sequences which are located therein. Suitable methods are described (see, inter alia, Bremer RE et al. (2001) Bioorg Med Chem. 9(8):2093-103; Ansari AZ et al. (2001) Chem Biol. 8(6):583-92; Gottesfeld JM et al. (2001) J Mol Biol. 309(3):615-29; Wurtz NR et al. (2001) Org Lett 3(8):1201-3; Wang CC et al. (2001) Bioorg Med Chem 9(3):653-7; Urbach AR and Dervan PB (2001) Proc Natl Acad Sci USA 98(8):4343-8; Chiang SY et al. (2000) J Biol Chem. 275(32):24246-54).

f) Introducing viral nucleic acid sequences and expression constructs which bring about the degradation of NADPH oxidase RNA

NADPH oxidase expression can also be brought about efficiently by inducing the specific NADPH oxidase RNA degradation by the plant with the aid of a viral expression system (amplicon) (Angell, SM et al. (1999) Plant J. 20(3):357-362). These systems - also referred to as "VIGS" (viral induced gene silencing) - introduce nucleic acid sequences with homology to the transcripts to be suppressed into the plant, using viral vectors. Then, transcription is switched off, probably mediated by plant defense mechanisms against viruses. Suitable techniques and methods are described (Ratcliff F et al. (2001) Plant J 25(2):237-45; Fagard M and Vaucheret H (2000) Plant Mol Biol 43(2-3):285-93; Anandalakshmi R et al. (1998) Proc Natl Acad Sci USA 95(22):13079-84; Ruiz MT (1998) Plant Cell 10(6): 937-46).

g) Introducing constructs for the induction of a homologous recombination on endogenous NADPH oxidase genes, for example for the generation of knock-out mutants.

To generate a homologously recombinant organism with reduced NADPH oxidase activity, for example a nucleic acid construct is used which comprises at least a part of the endogenous NADPH oxidase gene which is modified by a deletion, addition or substitution of at least one nucleotide in such a way that the functionality is reduced or nullified completely. The modification may also affect the regulatory elements (for example the promoter) of the gene, so that the coding sequence remains unaltered, but expression (transcription and/or translation) does not take place and is reduced.

In the case of conventional homologous recombination, the modified region is flanked at its 5′ and 3′ end by further nucleic acid sequences which must have a sufficient length for making possible the recombination. The length is, as a rule, in the range of from several hundred bases to several kilobases (Thomas KR and Capecchi MR (1987) Cell 51:503; Strepp et al. (1998) Proc Natl Acad Sci USA 95(8):4368-4373). For the homologous recombination, the host organism - for example a plant - is transformed with the recombination construct using the methods described hereinbelow, and clones which have undergone successful recombination are selected using, for example, an antibiotic or herbicide resistance.

Homologous recombination is a relatively rare event in higher eukaryotes, especially in plants. Random integrations into the host genome predominate. A possibility of removing the randomly integrated sequences and thus of enriching cell clones with a correct homologous recombination consists in using a sequence-specific recombination system as described in US 6,110,736, by which unspecifically integrated sequences can be deleted, which facilitates the selection of events which have integrated successfully via homologous recombination. A multiplicity of sequence-specific recombination systems can be used, examples which may be mentioned being the Cre/lox system of the bacteriophage P1, the FLP/FRT system of yeast, the Gin recombinase of the phage Mu, the Pin recombinase from E. coli and the R/RS system of the plasmid pSR1. Preferred are the bacteriophage P1 Cre/lox and the yeast FLP/FRT system. The FLP/FRT and cre/lox recombinase system has already been employed in plant systems (Odell et al. (1990) Mol Gen Genet 223: 369-378)

h) Introducing mutations into endogenous NADPH oxidase genes for generating a loss of function (for example generation of stop codons, reading frame shifts and the like)

Further suitable methods for reducing the NADPH oxidase activity are the introduction of nonsense mutations into endogenous NADPH oxidase genes, for example by means of introducing RNA/DNA oligonucleotides into the plant (Zhu et al. (2000) Nat Biotechnol 18(5):555-558), and the generation of knockout mutants with the aid of, for example, T-DNA mutagenesis (Koncz et al. (1992) Plant Mol Biol 20(5):963-976), ENU (N-ethyl-N-nitrosourea) mutagenesis or homologous recombination (Hohn B and Puchta (1999) H Proc Natl Acad Sci USA 96:8321-8323). Point mutations can also be generated by means of DNA-RNA hybrids, which are also known as chimeraplasty (Cole-Strauss et al. (1999) Nucl Acids Res 27(5):1323-1330; Kmiec (1999) Gene Therapy American Scientist 87(3):240-247).

The methods of dsRNAi, cosuppression by means of sense RNA and VIGS (virus-induced gene silencing) are also referred to as post-transcriptional gene silencing (PTGS). PTGS methods, including the reduction of the NADPH oxidase function or activity with dominant-negative NADPH oxidase variants are especially advantageous since the requirements to the homology between the endogenous gene to be suppressed and the transgenically expressed sense or dsRNA nucleic acid sequence (or between the endogeous gene and its dominant-negative variant, respectively) are lower than, for example in the case of a traditional antisense approach. Suitable homology criteria are mentioned in the description of the dsRNAi method and applied generally to PTGS methods or dominant-negative approaches. Owing to the high degree of homology between the NADPH oxidase proteins from maize, rice and barley, a high degree of conservation of these protein in plants can be deduced. Thus, using the NADPH oxidase nucleic acid sequences from barley, maize or rice, it is probably also possible efficiently to suppress the expression of homologous NADPH oxidase proteins in other species, without the isolation and structural elucidation of the NADPH oxidase homologs in these species being necessarily required. This substantially reduces the labor involved. Analogously, using dominant-negative variants of an NADPH oxidase protein from rice, maize or barley, it is presumably also possible efficiently to reduce or suppress the function/activity of its homolog in other plant species.

All substances and compounds which directly or indirectly bring about a reduction of the protein quantity, RNA quantity, gene activity or protein activity of an NADPH oxidase protein, shall hereinbelow be grouped together under the term "anti-NADPH oxi-

dase" compounds. The term "anti-NADPH oxidase" compound explicitly includes the nucleic acid sequences, peptides, proteins or other factors employed in the above-described methods.

For the purposes of the invention, "introduction" comprises all those methods which are suitable for introducing an anti-NAPDH oxidase compound directly or indirectly into a plant or a cell, compartment, tissue, organ or seed thereof, or generating it therein. Direct and indirect methods are comprised. The introduction can lead to a transient presence of an anti-NADPH-oxidase compound (for example a dsRNA) or else to a stable presence.

In accordance with the different nature of the above-described approaches, the anti-NADPH-oxidase compound can exert its function directly (for example by insertion into an endogenous NADPH oxidase gene). However, the function can also be exerted indirectly after transcription into an RNA (for example in the case of antisense approaches) or after transcription and translation into a protein (for example binding factors). Both directly and indirectly acting anti-NADPH-oxidase compounds are comprised in accordance with the invention.

"Introducing" comprises for example methods such as transfection, transduction or transformation.

Thus, for example, anti-NADPH-oxidase compounds also comprise recombinant expression constructs which bring about an expression (i.e. transcription and, if appropriate, translation) of, for example, an NADPH oxidase dsRNA or an NADPH oxidase antisense RNA - preferably in a plant or a part, tissue, organ or seed thereof.

In said expression constructs, a nucleic acid molecule whose expression (transcription and, if appropriate, translation) generates an anti-NADPH-oxidase compound, is preferably in functional linkage with at least one genetic control element (for example a promoter) which ensures expression in an organism, preferably in plants. If the expression construct is to be introduced directly into the plant and the anti-NADPH-oxidase compound (for example the NADPH oxidase dsRNA) is to be generated therein *in plantae*, then plant-specific genetic control elements (for example promoters) are preferred. However, the anti-NADPH-oxidase compound can also be generated in other organisms or *in vitro* and then be introduced into the plant (as described in Example 6 and 7). Here, preferred control elements are all those prokaryotic or eukaryotic genetic control elements (for example promoters) which

permit the expression in the organism selected in each case for the production.

Functional linkage is to be understood as meaning, for example, the sequential arrangement of a promoter with the nucleic acid sequence to be expressed (for example an anti-NAox compound) and, if appropriate, further regulatory elements such as, for example, a terminator in such a way that each of the regulatory elements can fulfill its function when the nucleic acid sequence is expressed recombinantly depending on the arrangement of the nucleic acids into sense on antisense RNA. To this end, direct linkage in the chemical sense is not necessarily required. Genetic control sequences such as, for example, enhancer sequences, can also exert their function on the target sequence from positions which are further away, or indeed from other DNA molecules. Preferred arrangements are those in which the nucleic acid sequence to be expressed recombinantly is positioned behind the sequence acting as promoter, so that the two sequences are linked covalently to each other.

Here, the distance between the promoter sequence and the nucleic acid sequence to be expressed recombinantly is less than 200 base pairs, especially preferably less than 100 base pairs, very especially preferably less than 50 base pairs.

Functional linkage, and an expression cassette, can be generated by means of customary recombination and cloning techniques as are described, for example, in Maniatis T, Fritsch EF and Sambrook J (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor (NY), in Silhavy TJ, Berman ML and Enquist LW (1984) Experiments with Gene Fusions, Cold Spring Harbor Laboratory, Cold Spring Harbor (NY), in Ausubel FM et al. (1987) Current Protocols in Molecular Biology, Greene Publishing Assoc. and Wiley Interscience and in Gelvin et al. (1990) In: Plant Molecular Biology Manual. However, further sequences which, for example, act as a linker with specific cleavage sites for restriction enzymes or as a signal peptide, may also be positioned between the two sequences. The insertion of sequences may also lead to the expression of fusion proteins. Preferably, the expression cassette, consisting of a linkage of promoter and nucleic acid sequence to be expressed, can exist in a vector-integrated form and be inserted into a plant genome, for example by transformation.

However, an expression cassette also denotes those constructions in which a promoter is placed behind an endogenous NADPH oxidase gene - for example by a homologous recombination - and the

reduction according to the invention, of an NADPH oxidase protein, is brought about by expressing an antisense NADPH oxidase RNA. Analogously, an anti-NADPH-oxidase compound (for example a nucleic acid compound encoding an NADPH oxidase dsRNA or an NADPH oxidase antisense RNA) can be placed behind an endogenous promoter in such a way that the same effect occurs. Both approaches lead to expression cassettes in the sense of the invention.

The term plant-specific promoters is understood as meaning, in principle, any promoter which is capable of governing the expression of genes, in particular foreign genes, in plants or plant parts, plant cells, plant tissues, or plant cultures. Here, expression may be, for example, constitutive, inducible or development-dependent.

The following are preferred:

a) Constitutive promoters

Preferred vectors are those which make possible a constitutive expression in plants (Benfey et al.(1989) EMBO J 8:2195-2202). "Constitutive" promoter is understood as meaning those promoters which ensure expression in a large number of, preferably all, tissues over a substantial period of plant development, preferably at all stages of plant development. In particular a plant promoter or a promoter derived from a plant virus are preferably used. Particularly preferred is the promoter of the CaMV cauliflower mosaic virus 35S transcript (Franck et al. (1980) Cell 21:285-294; Odell et al. (1985) Nature 313:810-812; Shewmaker et al. (1985) Virology 140:281-288; Gardner et al. (1986) Plant Mol Biol 6:221-228) or the 19S CaMV promoter (US 5,352,605; WO 84/02913; Benfey et al. (1989) EMBO J 8:2195-2202). Another suitable constitutive promoter is the Rubisco small subunit (SSU) promoter (US 4,962,028), the leguminB promoter (GenBank Acc. No. X03677), the Agrobacterium nopaline synthase promoter, the TR dual promoter, the Agrobacterium OCS (octopine synthase) promoter, the ubiquitin promoter (Holtorf S et al. (1995) Plant Mol Biol 29:637-649), the ubiquitin 1 promoter (Christensen et al. (1992) Plant Mol Biol 18:675-689; Bruce et al. (1989) Proc Natl Acad Sci USA 86:9692-9696), the Smas promoter, the cinnamyl alcohol dehydrogenase promoter (US 5,683,439), the promoters of the ATPase subunits or the promoter of a proline-rich protein from wheat (WO 91/13991), and further promoters of genes whose constitutive expression in plants is known to the skilled worker. Especially preferred as constitutive promoter is the promoter of the nitrilase-1 (nit1)

gene from A. thaliana (GenBank Acc. No.: Y07648.2, Nucleotide 2456-4340, Hillebrand et al. (1996) Gene 170:197-200).

b) Tissue-specific promoters

Preferred are furthermore promoters with specificity for the anthers, ovaries, flower, leaves, stems, roots and seeds.

Seed-specific promoters comprise, for example, the phaseolin promoter (US 5,504,200; Bustos MM et al. (1989) Plant Cell 1(9):839-53), the 2S albumin promoter (Joseffson LG et al. (1987) J Biol Chem 262:12196-12201), the legumin promoter (Shirsat A et al. (1989) Mol Gen Genet 215(2): 326-331), the USP (unknown seed protein) promoter (Bäumlein H et al. (1991) Mol Gen Genet 225(3):459-467, the napin promoter (US 5,608,152; Stalberg K et al. (1996) L Planta 199:515-519), the sucrose binding protein promoter (WO 00/26388), the legumin B4 promoter (LeB4; Bäumlein H et al. (1991) Mol Gen Genet 225: 121-128; Bäumlein H et al. (1992) Plant J 2(2):233-239; Fiedler U et al. (1995) Biotechnology (NY) 13(10):1090f), the Arabidopsis oleosin promoter (WO 98/45461), the Brassica Bce4 promoter (WO 91/13980). Further suitable seed-specific promoters are those of the genes encoding the high-molecular-weight glutenin (HMWG), gliadin, branching enzyme, ADP glucose pyrophosphatase (AGPase) or starch synthase. Furthermore preferred promoters are those which permit seed-specific expression in monocots such as maize, barley, wheat, rye, rice and the like. The following can be employed advantageously: the promoter of the lpt2 or lpt1 gene (WO 95/15389, WO 95/23230) or the promoters described in WO 99/16890 (promoters of the hordein gene, the glutelin gene, the oryzin gene, the prolamin gene, the gliadin gene, the glutelin gene, the zein gene, the kasirin gene, or the secalin gene).

Tuber-, storage-root- or root-specific promoters comprise, for example, the class I patatin promoter (B33), the potato cathepsin D inhibitor promoter.

Leaf-specific promoters comprise the potato cytosolic FBPase promoter (WO 97/05900), the Rubisco (ribulose-1,5-bisphosphate carboxylase) SSU (small subunit) promoter or the ST-LSI promoter from potato (Stockhaus et al. (1989) EMBO J 8:2445-2451). Very especially preferred are epidermis-specific promoters such as, for example, the OXLP gene (oxalate-oxidase-like protein) promoter (Wei et al. (1998) Plant Mol Biol 36:101-112).

Flower-specific promoters comprise, for example, the phytoene synthase promoter (WO 92/16635) or the promoter of the P-rr gene (WO 98/22593).

Anther-specific promoters comprise, for example, the 5126 promoter (US 5,689,049, US 5,689,051), the glob-1 promoter and the γ-zein promoter.

c) Chemically inducible promoters

The expression cassettes can also comprise a chemically inducible promoter (review article: Gatz et al. (1997) Annu Rev Plant Physiol Plant Mol Biol 48:89-108), by which the expression of the exogenous gene in the plant at a particular point in time can be controlled. Examples which may be mentioned are the PRP1 promoter (Ward et al. (1993) Plant Mol Biol 22:361-366), a salicylic-acid-inducible promoter (WO 95/19443), a benzenesulfonamide-inducible promoter (EP 0 388 186), a tetracyclin-inducible promoter (Gatz et al. (1992) Plant J 2:397-404), an abscisic-acid-inducible promoter (EP 0 335 528) or an ethanol- or cyclohexanone-inducible promoter (WO 93/21334).

d) Stress- or pathogen-inducible promoters

Further preferred promoters are those which are induced by biotic or abiotic stress such as, for example, the pathogen-inducible promoter of the PRP1 gene (or gst1 promotor), for example from potato (WO 96/28561; Ward et al. (1993) Plant Mol Biol 22:361-366), the tomato high-temperature-inducible hsp70 or hsp80 promoter (US 5,187,267), the potato low-temperature-inducible alpha-amylase promoter (WO 96/12814) or the light-inducible PPDK promoter. Further pathogen-inducible promoters comprise the flax *Fis1* promoter (WO 96/34949), the Vst1 promoter (Schubert et al. (1997) Plant Mol Biol 34:417-426) and the tobacco EAS4 sesquiterpene cyclase promoter (US 6,100,451).

Pathogen-inducible promoters furthermore comprise the promoters of genes which are induced as a consequence of infection by pathogens, such as, for example, genes of PR proteins, SAR proteins, β-1,3-glucanase, chitinase and the like (for example Redolfi et al. (1983) Neth J Plant Pathol 89:245-254; Uknes et al. (1992) Plant Cell 4:645-656; Van Loon (1985) Plant Mol Viral 4:111-116; Marineau et al. (1987) Plant Mol Biol 9:335-342; Matton et al. (1987) Molecular Plant-Microbe Interactions 2:325-342; Somssich et al. (1986) Proc Natl Acad Sci USA 83:2427-2430; Somssich et al. (1988) Mol Gen Genetics 2:93-98; Chen et al. (1996) Plant J 10:955-966; Zhang and Sing (1994) Proc

Natl Acad Sci USA 91:2507-2511; Warner, et al. (1993) Plant J 3:191-201; Siebertz et al. (1989) Plant Cell 1:961-968(1989).

Also comprised are wounding-inducible promoters such as that of the pinII gene (EP-A 0 375 091; Ryan (1990) Ann Rev Phytopath 28:425-449; Duan et al. (1996) Nat Biotech 14:494-498), of the wun1 and wun2 gene (US 5,428,148), of the win1 and win2 gene (Stanford et al. (1989) Mol Gen Genet 215:200-208), of the systemin gene (McGurl et al. (1992) Science 225:1570-1573), of the WIP1 gene (Rohmeier et al. (1993) Plant Mol Biol 22:783-792; Eckelkamp et al. (1993) FEBS Letters 323:73-76), of the MPI gene (Corderok et al. (1994) Plant J 6(2):141-150) and the like.

A source of further pathogen-inducible promoters is the PR gene family. A series of elements in these promoters has proved to be advantageous. Thus, the region -364 to -288 in the promoter of PR-2d mediates salicylate specificity (Buchel et al. (1996) Plant Mol Biol 30, 493-504). The sequence 5'-TCATCTTCTT-3' occurs repeatedly in the promoter of the barley β-1,3-glucanase and in more than 30 further stress-induced genes. In tobacco, this region binds a nuclear protein whose abundance is increased by salicylate. The PR-1 promoters from tobacco and Arabidopsis (EP-A 0 332 104, WO 98/03536) are likewise suitable as pathogen-inducible promoters. Preferred, since especially specifically pathogen-induced, are the acidic *PR-5* (aPR5) promoters from barley (Schweizer et al. (1997) Plant Physiol 114:79-88) and wheat (Rebmann et al. (1991) Plant Mol Biol 16:329-331). aPR5 proteins accumulate in approximately 4 to 6 hours after pathogen attack and show only very little background expression (WO 99/66057). An approach for achieving an increased pathogen-induced specificity is the generation of synthetic promoters from combinations of known pathogen-responsive elements (Rushton et al. (2002) Plant Cell 14, 749-762; WO 00/01830; WO 99/66057). Further pathogen-inducible promoters from different species are known to the skilled worker (EP-A 1 165 794; EP-A 1 062 356; EP-A 1 041 148; EP-A 1 032 684).

e) Development-dependent promoters

Further suitable promoters are, for example, fruit-maturation-specific promoters such as, for example, the tomato fruit-maturation-specific promoter (WO 94/21794, EP 409 625). Development-dependent promoters comprise partly the tissue-specific promoters since individual tissues develop by nature in a development-dependent fashion.

Especially preferred are constitutive promoters and also leaf- and/or stem-specific, pathogen-inducible and epidermis-specific promoters, with pathogen-inducible and epidermis-specific promoters being most preferred.

Furthermore, further promoters may be linked functionally to the nucleic acid sequence to be expressed, which promoters make possible an expression in further plant tissues or in other organisms, such as, for example, *E. coli* bacteria. Suitable plant promoters are, in principle, all of the above-described promoters.

The nucleic acid sequences present in the expression cassettes according to the invention can be linked operably to further genetic control sequences in addition to a promoter. The term "genetic control sequences" is to be understood in the broad sense and refers to all those sequences which have an effect on the generation or the function of the expression cassette according to the invention. For example, genetic control sequences modify the transcription and translation in prokaryotic or eukaryotic organisms. Preferably, the expression cassette according to the invention comprise the promoter with specificity for the embryonal epidermis and/or the flower 5'-upstream of the nucleic acid sequence in question to be expressed recombinantly, and 3'-downstream a terminator sequence as additional genetic control sequence and, if appropriate, further customary regulatory elements, in each case linked functionally to the nucleic acid sequence to be expressed recombinantly.

Genetic control sequences also comprise further promoters, promoter elements or minimal promoters, all of which can modify the expression-governing properties. Thus, for example, the tissue-specific expression may additionally depend on certain stress factors, owing to genetic control sequences. Such elements have been described, for example, for water stress, abscisic acid (Lam E and Chua NH (1991) J Biol Chem 266(26): 17131-17135) and heat stress (Schoffl F et al. (1989) Mol Gen Genetics 217(2-3):246-53).

In principle, all natural promoters together with their regulatory sequences such as those mentioned above may be used for the method according to the invention. In addition, synthetic promoters may also be used advantageously.

Genetic control sequences furthermore also comprise the 5'-untranslated regions, introns or noncoding 3'-region of genes, such as, for example, the actin-1 intron, or the Adh1-S introns

1, 2 and 6 (general reference: The Maize Handbook, Chapter 116, Freeling and Walbot, Eds., Springer, New York (1994)). It has been demonstrated that they may play a significant role in the regulation of gene expression. Thus, it has been demonstrated that 5'-untranslated sequences can enhance the transient expression of heterologous genes. Examples of translation enhancers which may be mentioned are the tobacco mosaic virus 5' leader sequence (Gallie et al. (1987) Nucl Acids Res 15:8693-8711) and the like. Furthermore, they may promote tissue specificity (Rouster J et al. (1998) Plant J 15:435-440).

The expression cassette may advantageously comprise one or more of what are known as enhancer sequences, linked functionally to the promoter, which make possible an increased recombinant expression of the nucleic acid sequence. Additional advantageous sequences, such as further regulatory elements or terminators, may also be inserted at the 3' end of the nucleic acid sequences to be expressed recombinantly. One or more copies of the nucleic acid sequences to be expressed recombinantly may be present in the gene construct.

Polyadenylation signals which are suitable as control sequences are plant polyadenylation signals, preferably those which essentially correspond to T-DNA polyadenylation signals from *Agrobacterium tumefaciens*, in particular to gene 3 of the T-DNA (octopine synthase) of the Ti plasmid pTiACHS (Gielen et al. (1984) EMBO J 3:835 et seq.) or functional equivalents thereof. Examples of terminator sequences which are especially suitable are the OCS (octopine synthase) terminator and the NOS (nopaline synthase) terminator.

Control sequences are furthermore to be understood as those which make possible homologous recombination or insertion into the genome of a host organism or which permit removal from the genome. Upon homologous recombination, for example the natural promoter of a particular gene can be exchanged to a promoter with specificity for the embryonal epidermis and/or the flower. Methods such as the cre/lox technology permit a tissue-specific, if appropriate inducible, removal of the expression cassette from the genome of the host organism (Sauer B (1998) Methods. 14(4):381-92). Here, certain flanking sequences (lox sequences), which later make possible a removal by means of the cre recombinase, are added to the target gene.

An expression cassette and vectors derived therefrom may comprise further functional elements. The term functional element is to be understood in the broad sense and refers to all those elements

which have an effect on the generation, amplification or function of the expression cassettes, vectors or transgenic organisms according to the invention. The following may be mentioned by way of example, but not by limitation:

a) Selection markers which confer a resistance to metabolism inhibitors (such as 2-deoxyglucose-6-phosphate (WO 98/45456)), antibiotics or biocides, preferably herbicides, such as, for example, kanamycin, G 418, bleomycin, hygromycin or phosphinothricin etc. Especially preferred selection markers are those which confer resistance to herbicides. Examples which may be mentioned are: DNA sequences which encode phosphinothricin acetyl transferases (PAT) and which inactivate glutamin synthase inhibitors (bar and pat genes), 5-enolpyruvylshikimate-3-phosphate synthase genes (EPSP synthase genes), which confer resistance to Glyphosate® (N-(phosphonomethyl)glycine), the gox gene, which encodes Glyphosate®-degrading enzymes (glyphosate oxidoreductase), the deh gene (encoding a dehalogenase which inactivates Dalapon), sulfonylurea- and imidazolinone-inactivating acetolactate synthases, and bxn genes, which encode bromoxynil-degrading nitrilase enzymes, the aasa gene, which confers resistance to the antibiotic apectinomycin, the streptomycin phosphotransferase (spt) gene, which allows resistance to streptomycin, the neomycin phosphotransferase (nptII) gene, which confers resistance to kanamycin or geneticin, the hygromycin phosphotransferase (hpt) gene, which mediates resistance to hygromycin, the acetolactate synthase gene (ALS), which confers resistance to sulfonylurea herbicides (for example mutated ALS variants with, for example, the S4 and/or Hra mutation).

b) Reporter genes which encode readily quantifiable proteins and, via their color or enzyme activity, make possible an assessment of the transformation efficacy, the site of expression or the time of expression. Very especially preferred in this context are reporter proteins (Schenborn E, Groskreutz D. Mol Biotechnol. 1999; 13(1):29-44) such as the green fluorescent protein (GFP) (Sheen et al. (1995) Plant Journal 8(5):777-784; Haseloff et al. (1997) Proc Natl Acad Sci USA 94(6):2122-2127; Reichel et al. (1996) Proc Natl Acad Sci USA 93(12):5888-5893; Tian et al. (1997) Plant Cell Rep 16:267-271; WO 97/41228; Chui WL et al. (1996) Curr Biol 6:325-330; Leffel SM et al. (1997) Biotechniques. 23(5):912-8), chloramphenicol transferase, a luciferase (Ow et al. (1986) Science 234:856-859; Millar et al. (1992) Plant Mol Biol Rep 10:324-414), the aequoringen (Prasher et al.

(1985) Biochem Biophys Res Commun 126(3):1259-1268), β-galactosidase, R-locus gene (encode a protein which regulates the production of anthocyanin pigments (red coloration) in plant tissue and thus makes possible a direct analysis of the promoter activity without addition of extra adjuvants or chromogenic substrates; Dellaporta et al., In: Chromosome Structure and Function: Impact of New Concepts, 18th Stadler Genetics Symposium, 11:263-282, 1988), with β-glucuronidase being very especially preferred (Jefferson et al., EMBO J. 1987, 6, 3901-3907).

c) Origins of replication, which ensure amplification of the expression cassettes or vectors according to the invention in, for example, E. coli. Examples which may be mentioned are ORI (origin of DNA replication) the pBR322 ori or the P15A ori (Sambrook et al.: Molecular Cloning. A Laboratory Manual, 2nd ed. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

d) Elements which are necessary for Agrobacterium-mediated plant transformation, such as, for example, the right or left border of the T-DNA or the vir region.

The introduction of an expression cassette according to the invention into an organism or cells, tissues, organs, parts or seeds thereof (preferably into plants or plant cells, tissue, organs, parts or seeds) can be effected advantageously using vectors which comprise the expression cassettes. The expression cassette can be introduced into the vector (for example a plasmid vector) via a suitable restriction cleavage site. The plasmid formed is first introduced into E. coli. Correctly transformed E. coli are selected, grown, and the recombinant plasmid is obtained by the methods familiar to the skilled worker. Restriction analysis and sequencing may serve to verify the cloning step.

Examples of vectors may be plasmids, cosmids, phages, viruses or else agrobacteria. In an advantageous embodiment, the expression cassette is introduced by means of plasmid vectors. Preferred vectors are those which make possible a stable integration of the expression cassette into the host genome.

The generation of a transformed organism (or of a transformed cell or tissue) requires that the DNA, RNA or protein in question is introduced into the corresponding host cell.

A multiplicity of methods are available for this procedure, which is termed transformation (or transduction or transfection) (Keown et al. (1990) Methods in Enzymology 185:527-537). For example, the DNA or RNA can be introduced directly by microinjection or by bombardment with DNA-coated microparticles. Also, the cell can be permeabilized chemically, for example using polyethylene glycol, so that the DNA can enter the cell by diffusion. The DNA can also be introduced by protoplast fusion with other DNA-containing units such as minicells, cells, lysosomes or liposomes. Another suitable method of introducing DNA is electroporation, where the cells are permeabilized reversibly by an electrical pulse. Suitable methods have been described (for example by Bilang et al. (1991) Gene 100:247-250; Scheid et al. (1991) Mol Gen Genet 228:104-112; Guerche et al. (1987) Plant Science 52:111-116; Neuhause et al. (1987) Theor Appl Genet 75:30-36; Klein et al. (1987) Nature 327:70-73; Howell et al. (1980) Science 208:1265; Horsch et al.(1985) Science 227:1229-1231; DeBlock et al. (1989) Plant Physiology 91:694-701; Methods for Plant Molecular Biology (Weissbach and Weissbach, eds.) Academic Press Inc. (1988); and Methods in Plant Molecular Biology (Schuler and Zielinski, eds.) Academic Press Inc. (1989)).

In plants, the above-described methods of transforming and regenerating plants from plant tissues or plant cells are exploited for transient or stable transformation. Suitable methods are especially protoplast transformation by polyethylene-glycol-induced DNA uptake, the biolistic method with the gene gun, what is known as the particle bombardment method, electroporation, incubation of dry embryos in DNA-containing solution, and microinjection.

In addition to these "direct" transformation techniques, transformation can also be effected by bacterial infection by means of Agrobacterium tumefaciens or Agrobacterium rhizogenes. The Agrobacterium-mediated transformation is best suited to dicotyledonous plant cells. The methods are described, for example, by Horsch RB et al. (1985) Science 225: 1229f.

When agrobacteria are used, the expression cassette must be integrated into specific plasmids, either into a shuttle or intermediate vector, or into a binary vector. If a Ti or Ri plasmid is to be used for the transformation, at least the right border, but in most cases the right and left border, of the Ti or Ri plasmid T-DNA is linked to the transgenic expression construct to be introduced in the form of a flanking region.

Binary vectors are preferably used. Binary vectors are capable of replication both in E. coli and in Agrobacterium. As a rule, they comprise a selection marker gene for the selection of transformed plants (see above) and a linker or polylinker flanked by the right and left T-DNA border sequence. They can be transformed directly into Agrobacterium (Holsters et al. (1978) Mol Gen Genet 163:181-187). Apart from the T-DNA region, they can additionally comprise elements such as a selection marker gene for the selection of transformed E. coli or agrobacteria (e.g. the nptIII gene). The Agrobacterium which acts as host organism in this case should already contain a plasmid with the vir region. The latter is required for transferring the T-DNA to the plant cell. An Agrobacterium transformed in this way can be used for transforming plant cells. The use of T-DNA for transforming plant cells has been studied and described intensively (EP 120 516; Hoekema, In: The Binary Plant Vector System, Offsetdrukkerij Kanters B.V., Alblasserdam, Chapter V; An et al. (1985) EMBO J 4:277-287). Various binary vectors are known, some of which are commercially available such as, for example, pBI101.2 or pBIN19 (Clontech Laboratories, Inc. USA).

Further promoters which are suitable for expression in plants are described (Rogers et al. (1987) Meth in Enzymol 153:253-277; Schardl et al. (1987) Gene 61:1-11; Berger et al. (1989) Proc Natl Acad Sci USA 86:8402-8406).

Direct transformation techniques are suitable for any organism and cell type.

The plasmid used need not meet any particular requirements in the case of the injection or electroporation of DNA or RNA into plant cells. Simple plasmids such as those of the pUC series can be used. If complete plants are to be regenerated from the transformed cells, it is advantageous for an additional selectable marker gene to be located on the plasmid.

Stably transformed cells, i.e. those which contain the introduced DNA integrated into the DNA of the host cell, can be selected from untransformed cells when a selectable marker is part of the DNA introduced. Examples of genes which can act as markers are all those which are capable of conferring resistance to a biocide (for example an antibiotic, herbicide or a metabolism inhibitor such as 2-deoxyglucose-6-phosphate WO 98/45456) (see above). Transformed cells which express such marker genes are capable of surviving in the presence of concentrations of a corresponding antibiotic or herbicide which kill an untransformed wild type. Examples are mentioned above and preferably comprise the bar

gene, which confers resistance to the herbicide phosphinothricin (Rathore KS et al. (1993) Plant Mol Biol 21(5):871-884), the nptII gene, which confers resistance to kanamycin, the hpt gene, which confers resistance to hygromycin, or the EPSP gene, which confers resistance to the herbicide glyphosate. The selection marker permits the selection of transformed cells from untransformed cells (McCormick et al. (1986) Plant Cell Reports 5:81-84). The resulting plants can be bred and hybridized in the customary fashion. Two or more generations should be grown in order to ensure that the genomic integration is stable and hereditary.

The abovementioned methods are described, for example, in Jenes B et al.(1993) Techniques for Gene Transfer, in: Transgenic Plants, Vol. 1, Engineering and Utilization, edited by SD Kung and R Wu, Academic Press, pp. 128-143 and in Potrykus (1991) Annu Rev Plant Physiol Plant Molec Biol 42:205-225. The construct to be expressed is preferably cloned into a vector which is suitable for the transformation of Agrobacterium tumefaciens, for example pBin19 (Bevan et al. (1984) Nucl Acids Res 12:8711f).

As soon as a transformed plant cell has been generated, a complete plant can be obtained using methods known to the skilled worker. For example, callus cultures are used as starting material. The development of shoot and root can be induced from this as yet undifferentiated cell biomass in a known fashion. The shoots obtained can be planted out and bred.

The skilled worker is familiar with such methods of regenerating intact plants from plant cells and plant parts. Methods to do so are described, for example, by Fennell et al. (1992) Plant Cell Rep. 11: 567-570; Stoeger et al (1995) Plant Cell Rep. 14:273-278; Jahne et al. (1994) Theor Appl Genet 89:525-533.

The method according to the invention can advantageously be combined with further methods which bring about a pathogen resistance (for example against insects, fungi, bacteria, nematodes and the like), stress resistance or another improvement of the plant's properties. Examples are mentioned in Dunwell JM, Transgenic approaches to crop improvement, J Exp Bot. 2000;51 Spec No; pages 487-96, inter alia.

With regard to, for example, a nucleic acid sequence, an expression cassette or a vector comprising said nucleic acid sequence or an organism transformed with said nucleic acid sequence, expression cassette or vector, "transgenic" means all those

constructs which have been generated by recombinant methods in which either

a) the NADPH oxidase nucleic acid sequence, or

b) a genetic control sequence which is functionally linked with the NADPH oxidase nucleic acid sequence, for example a promoter, or

c) (a) and (b)

are not located in their natural genetic environment or have been modified by recombinant methods, an example of a modification being a substitution, addition, deletion, inversion or insertion of one or more nucleotide residues. Natural genetic environment refers to the natural chromosomal locus in the source organism, or to the presence in a genomic library. In the case of a genomic library, the natural genetic environment of the nucleic acid sequence is preferably at least partially retained. The environment flanks the nucleic acid sequence at at least one side and has a sequence length of at least 50 bp, preferably at least 500 bp, especially preferably at least 1000 bp, very especially preferably at least 5000 bp. A naturally occurring expression cassette - for example the naturally occurring combination of the NADPH oxidase promoter and the corresponding NADPH oxidase gene - becomes a transgenic expression cassette when the latter is modified by nonnatural, synthetic ("artificial") methods such as, for example, mutagenization. Suitable methods are described (US 5,565,350; WO 00/15815; see also above).

Another aspect of the invention relates to transgenic organisms transformed with at least one nucleic acid sequence, expression cassette or vector according to the invention, and to cells, cell cultures, tissues, parts - such as, for example in the case of plant organisms, leaves, roots and the like - or propagation material derived from such organisms. Organism is to be understood in the broad sense and means prokaryotic and eukaryotic organisms, preferably bacteria, yeasts, fungi, animal and plant organisms.

The following are preferred:

a) fungi such as Aspergillus, Eremothecium, Trichoderma, Ashbya, Neurospora, Fusarium, Beauveria or further fungi described in Indian Chem Eng. Section B. Vol 37, No 1,2 (1995) on page 15,

table 6. Especially preferred is the filamentous Hemiascomycete Ashbya gossypii or Eremothecium ashbyii,

b) yeasts such as Candida, Saccharomyces, Hansenula or Pichia, with Saccharomyces cerevisiae or Pichia pastoris (ATCC Accession No. 201178) being especially preferred,

c) plants in accordance with the abovementioned definition for "plants",

d) vertebrates and invertebrates. Especially preferred vertebrates are nonhuman mammals such as dogs, cats, sheep, goats, chickens, mice, rats, cattle or horses. Preferred animal cells comprise CHO, COS, HEK293 cells. Preferred invertebrates comprise insect cells such as Drosophila S2 and Spodoptera Sf9 or Sf21 cells,

e) prokaryotic organisms such as Gram-positive or Gram-negative bacteria such as Acetobacter, Gluconobacter, Corynebacterium, Brevibacterium, Bacillus, Clostridium, Cyanobacter, Escherichia (especially Escherichia coli), Serratia, Staphylococcus, Aerobacter, Alcaligenes, Penicillium or Klebsiella.

Host or starting organisms which are preferred as transgenic organisms are especially plants in accordance with the abovementioned definition. Included within the scope of the invention are all genera and species of higher and lower plants of the Plant Kingdom. Furthermore included are the mature plants, seeds, shoots and seedlings, and parts, propagation materials and culture derived from them, for example cell cultures. Mature plants means plants at any developmental stage beyond the seedling stage. Seedling means a young immature plant in an early developmental stage. Plants which are especially preferred as host organisms are plants to which the method according to the invention for obtaining a pathogen resistance in accordance with the abovementioned criteria can be applied. Very especially preferred are monocotyledonous plants such as wheat, oats, millet, barley, rye, maize, rice, buckwheat, sorghum, triticale, spelt, linseed, sugar cane, and dicotyledonous crop plants such as oilseed rape, canola, cress, Arabidopsis, cabbages, soybeans, alfalfa, pea, bean plants, peanut, potato, tobacco, tomato, egg plant, capsicum, sunflower, tagetes, lettuce, Calendula, melon, pumpkin/squash or zucchini.

The transgenic organisms can be generated with the above-described methods for the transformation or transfection of organisms.

A further aspect of the invention relates to the use of transgenic organisms according to the invention and of the cells, cell cultures, parts - such as for example in the case of transgenic plant organisms roots, leaves and the like - and transgenic propagation material such as seeds or fruits derived from these organisms for the production of foodstuffs, feedstuffs, pharmaceuticals or fine chemicals.

Furthermore preferred is a method for the recombinant production of pharmaceuticals or fine chemicals in host organisms, where a host organism is transformed with one of the above-described expression cassettes and this expression cassette comprises one or more structural genes which encode the desired fine chemical or catalyze the biosynthesis of the desired fine chemical, the transformed host organism is cultured, and the desired fine chemical is isolated from the culture medium. This method can be applied widely for fine chemicals such as enzymes, vitamins, amino acids, sugars, fatty acids, natural and synthetic flavorings, aroma substances and colorants. Especially preferred is the production of tocopherols and tocotrienols and of carotenoids. Culturing the transformed host organisms, and the isolation from the host organisms or from the culture medium, are carried out with methods known to the skilled worker. The production of pharmaceuticals, such as, for example, antibodies or vaccines, is described by Hood EE, Jilka JM (1999) Curr Opin Biotechnol 10(4):382-6; Ma JK, Vine ND (1999) Curr Top Microbiol Immunol 236:275-92.

Sequences

1. SEQ ID NO: 1 nucleic acid sequence encoding a barley (Hordeum vulgare) NADPH oxidase.

2. SEQ ID NO: 2 amino acid sequence encoding a barley (Hordeum vulgare) NADPH oxidase.

3. SEQ ID NO: 3 nucleic acid sequence encoding a rice (Oryza sativa var. japonica) NADPH oxidase

4. SEQ ID NO: 4 amino acid sequence encoding a rice (Oryza sativa var. japonica) NADPH oxidase

5. SEQ ID NO: 5 nucleic acid sequence encoding a Nicotiana tabacum NADPH oxidase

6. SEQ ID NO: 6 amino acid sequence encoding a Nicotiana tabacum NADPH oxidase

7. SEQ ID NO: 7 nucleic acid sequence encoding a potato (Solanum tuberosum) NADPH oxidase

8. SEQ ID NO: 8 amino acid sequence encoding a potato (Solanum tuberosum) NADPH oxidase

9. SEQ ID NO: 9 nucleic acid sequence encoding a tomato (Lycopersicon esculentum) NADPH oxidase

10. SEQ ID NO: 10 amino acid sequence encoding a tomato (Lycopersicon esculentum) NADPH oxidase

11. SEQ ID NO: 11 nucleic acid sequence encoding a NADPH oxidase aus Arabidopsis thaliana (RbohF)

12. SEQ ID NO: 12 amino acid sequence encoding a NADPH oxidase aus NADPH oxidase Arabidopsis thaliana (RbohF)

13. SEQ ID NO: 13 nucleic acid sequence encoding an Arabidopsis thaliana (RbohD) NADPH oxidase

14. SEQ ID NO: 14 amino acid sequence encoding an Arabidopsis thaliana (RbohD) NADPH oxidase

15. SEQ ID NO: 15 nucleic acid sequence encoding a Nicotiana tabacum (rboh) NADPH oxidase

16. SEQ ID NO: 16 amino acid sequence encoding a Nicotiana tabacum (rboh) NADPH oxidase

17. SEQ ID NO: 17 nucleic acid sequence encoding a rice (Oryza sativa var. japonica) NADPH oxidase

18. SEQ ID NO: 18 amino acid sequence encoding a rice (Oryza sativa var. japonica) NADPH oxidase

19. SEQ ID NO: 19 nucleic acid sequence encoding an Arabidopsis thaliana (RbohC) NADPH oxidase

20. SEQ ID NO: 20 amino acid sequence encoding an Arabidopsis thaliana (RbohC) NADPH oxidase

21. SEQ ID NO: 21 nucleic acid sequence encoding an Arabidopsis thaliana (RbohA) NADPH oxidase

22. SEQ ID NO: 22 amino acid sequence encoding an Arabidopsis thaliana (RbohA) NADPH oxidase

23. SEQ ID NO: 23 oligonucleotide primer 5' NAOX 5'-GARCAAGGCTCTTTTGATTG-3'

24. SEQ ID NO: 24 oligonucleotide primer 3' Naox 5'-GAAATGCTCCTTATGGAATTC-3'

Figures

Fig. 1: RNA interference with *pNAox*-dsRNA reduces the penetration efficiency of powdery mildew of barley BghA6 in barley.

The relative penetration efficiency (RPE) was determined in five individual experiments with inoculation with *Bgh* from barley cv Pallas. The RPE is calculated as the difference between the penetration efficiency of pNAox-dsRNA-transformed cells and the penetration efficiency of control-dsRNA-transformed cells (here: average penetration efficiency 38.74%). The percent RPE (% RPE) is calculated from the RPE minus 1, multiplied by 100.

$$\text{RPE} = \frac{\text{[PE in pNAox-dsRNA-transformed cells]}}{\text{[PE in control-dsRNA transformed cells]}}$$

$$\%\ \text{RPE} = 100 * (\text{RPE}-1)$$

The columns (1) to (5) represent the % RPE (i.e. the deviation of the penetration efficiency from the average of the penetration efficiency of the control) when evaluating at least 100 interac-

tion sites for in each case one independent experiment. The column (m) represents the average % RPE of the experiments. The error bar indicates the standard error.

"Control dsRNA" represents the parallel experiments with a control dsRNA. "pNAox" dsRNA represents the experiments with the dsRNA of the barley NADPH oxidase.

In cells which have been bombarded with pNAox-dsRNA, the % RPE was markedly (significance p=0.0054) reduced in comparison with cells bombarded with a control dsRNA (*TR*: human thyroid receptor dsRNA).

Examples

General methods:

The chemical synthesis of oligonucleotides can be effected for example in the known manner by the phosphoamidite method (Voet, Voet, 2nd edition, Wiley Press New York, pages 896-897). The cloning steps carried out within the scope of the present invention, such as, for example, restriction cleavages, agarose gel electrophoresis, purification of DNA fragments, transfer of nucleic acids to nitrocellulose and nylon membranes, linking DNA fragments, transformation of E. coli cells, bacterial cultures, phage multiplication and sequence analysis of recombinant DNA, are carried out as described by Sambrook et al. (1989) Cold Spring Harbor Laboratory Press; ISBN 0-87969-309-6. Recombinant DNA molecules are sequenced with a laser fluorescence DNA sequencer from MWG Licor following the method of Sanger (Sanger et al. (1977) Proc Natl Acad Sci USA 74:5463-5467).

Example 1: Plants, pathogens and inoculation

The variety Pallas was provided by Lisa Munk, Department of Plant Pathology, Royal Veterinary and Agricultural University, Copenhagen, Denmark. Its production is described (Kølster P et al. (1986) Crop Sci 26: 903-907).

Unless otherwise described, the seed, which had been pregerminated for 12 to 36 hours in the dark on damp filter paper, was placed at a rate of 5 kernels along the edge of a square pot (8 × 8 cm) in Fruhstorfer soil, type P, covered with soil and watered regularly with tap water. All plants were grown in controlled-environment cabinets or chambers at 16 to 18°C, 50 to 60% relative atmospheric humidity and a 16-hour-light/8-hour-dark photoperiod at 3000 or 5000 lux (photon flux density 50 or

60 µmols^{-1}m^{-2}) for 5 to 8 days and used in the experiments during the seedling stage. In experiments in which primary leaves were treated, the latter were fully developed.

Prior to carrying out the transient transfection experiments, the plants were grown in controlled environment cabinets or chambers at 24°C daytime temperature, 20°C nighttime temperature, 50 to 60% relative atmospheric humidity and a 16-hour-light/8-hour-dark photoperiod at 30 000 lux.

Powdery mildew of barley *Blumeria graminis* (DC) Speer f.sp. *hordei* Em. Marchal race A6 (Wiberg A (1974) Hereditas 77: 89-148) (BghA6) was used for the inoculation of barley plants. The fungus was provided from the Department of Biometry, JLU Gießen. The inoculum was propagated in controlled-environment chambers under identical conditions as described above for the plants by transferring the conidia of infected material to regularly grown 7-day-old barley plants cv. Golden Promise at a density of 100 conidia/mm^2.

The inoculation with BghA6 was carried out using 7-day-old seedlings by shaking off the conidia from infected plants in an inoculation tower at approximately 100 conidia/mm^2 (unless otherwise specified).

Example 2: Cloning of the barley pNAox cDNA sequence

The cDNA fragments required for the isolation of the HvpNAox cDNA, its cloning, sequencing and generation of probes were obtained by RT-PCR using the "One Step RT-PCR Kit" (Life Technologies, Karlsruhe, Germany, or Qiagen, Hilden, Germany). To this end, a total RNA from barley seedlings was used as template. The RNA was isolated from Pallas 3, 5 and 7 days after germination. In addition, RNA was isolated from Pallas and from the backcrossed lines with *mlo5*, *Mlg* or *Mla12* 1, 2 and 5 days after inoculation with *Bgh*A6 on day 7 after germination. The RT-PCR was carried out using primers which are derived from conserved regions of the gp91phox homologs from rice and Arabidopsis thaliana (GenBank Acc. No.: X93301 and AB008111):

5' NAOX: 5'-GARCAAGGCTCTTTTGATTG-3' (SEQ ID NO: 23) and

3' Naox: 5' GAAATGCTCCTTATGGAATTC 3'(SEQ ID NO: 24)

In each case 1000 ng of total DNA, 0.4 mM dNTPs, in each case 0.6 mM OPN-1 and OPN-2 primer, 10 µl of RNase inhibitor and 1 µl of enzyme mix in 1x RT buffer (*one step RT-PCR Kit*, Qiagen, Hilden) were employed for the reaction.

The following temperature program is used (PTC-100TM model 96V; MJ Research, Inc., Watertown, Massachussetts):

1	cycle of 30 minutes at 50°C
1	cycle of 150 seconds at 94°C
30	cycles of 94°C for 45 seconds, 55°C for 1 minute and 72°C for 2 minutes
1	cycle of 72°C for 7 minutes

The PCR products were separated by means of 2% w/v agarose gel electrophoresis. This gave a 378 bp RT-PCR product (SEQ ID NO: 1) which encodes a part of the open reading frame of the barley NADPH oxidase. The corresponding cDNA was isolated from an agarose gel and cloned in the pGEM-T vector (Promega, Mannheim, Germany) by means of T-overhang ligation. The cDNAs were sequenced starting from the plasmid DNA using the "Thermo Sequenase Fluorescent Labeled Primer Cycle Sequencing Kit" (Amersham, Freiburg, Germany). The construct was named pGEM-T-pNAox.

Example 3: In-vitro synthesis of the pNAox dsRNA

The plasmid, which had been employed for the in-vitro RNA transcription, comprises the T7 and SP6 promoters at the respective ends of the inserted nucleic acid sequence, which makes possible the synthesis of sense RNA and antisense RNA. The plasmid can be linearized with suitable restriction enzymes (ApaI for SP6 polymerase and PstI for T7 polymerase) in order to ensure correct transcription of the inserted nucleic acid sequence and to prevent read-through into vectorial sequences. To this end, in each case 10 µg of pGEM-T-pNAox plasmid DNA were cut with ApaI for SP6 polymerase and with and PstI for T7 polymerase. The cut plasmids are extracted in 200 µl of water with the same volume phenol/chloroform/isoamyl alcohol, transferred into a fresh Eppendorf vessel (RNAse-free) and centrifuged for 5 minutes at 20 000 g. 180 µl of the plasmid solution were treated with 420 µl of ethanol, placed on ice and subsequently precipitated by centrifugation for 30 minutes at 20 000 g and -4°C. The precipitate was taken up in 10 µl of TE buffer. The preparations in question were employed directly in an in-vitro transcription with T7-RNA polymerase and with SP6-RNA polymerase, respectively. RNA polymerases were obtaied from Roche Molecular Biology, Mannheim, Germany.

Each transcription mixture contained the following in a volume of 40 µl:

2 µl linearized plasmid DNA (1 ∝g)
2 µl NTPs (25 mM) (1.25 mM of each NTP)
4 µl 10x reaction buffer (Roche Molecular Biology),
1 µl RNAsin RNAsin (27 units; Roche Molecular Biology),
2 µl RNA polymerase (40 units)
29 µl DEPC water

After 2 hours of incubation at 37°C, in each case some of the reaction mixtures from the transcription of the sense and antisense strands were mixed, denatured for 5 minutes at 95°C and thereafter hybridized with one another (annealed) by cooling over 30 minutes to a final temperature of 37°C. As an alternative, the mixture of sense and antisense strand can also be cooled for 30 minutes at -20°C after the denaturation. The protein precipitate which formed during denaturation and hybridization was removed by briefly centrifuging at 20 800 g, and the supernatant was used directly for coating tungsten particles (see hereinbelow). For the analysis, in each case 1 µl of each RNA strand and of the dsRNA were separated on a non-denaturing agarose gel. Successful hybridization is evident by a band shift towards higher molecular weight in comparison with the individual strands.

4 µl of the dsRNA were precipitated with ethanol (by addition of 6 µl of water, 1 µl of 3M sodium acetate solution and 25 µl of ethanol, and centrifugation for at least 5 minutes at 20 000 g and 4°C) and resuspended in 500 µl of water. The absorption spectrum between 230 and 300 nm was measured or the absorption at 280 and 260 nm was determined to determine the purity and the concentration of the dsRNA. As a rule, 80 to 100 µg of dsRNA with an OD_{260}/OD_{280} ratio of 1.80 to 1.95 were obtained. If desired, a digestion with DNase I may be carried out, but this has no substantial effect on subsequent results.

The dsRNA of the human thyroid receptor (starting vector pT7beta-Sal (Norman C et al. (1988) Cell 55(6):989-1003), provided by Dr. Baniahmad, Department of Genetics, Gießen, Germany; the sequence of the insert is described under the GenBank Acc. No.: NM_000461) acted as control dsRNA. The plasmid was digested with PvuII to generate the sense RNA and with HindIII to generate the antisense RNA, and the RNA was then transcribed using T7 or SP6 RNA polymerase. The individual process steps for the generation of the control dsRNA are carried out analogously to those described above for the pNAox-dsRNA.

Example 4: Transient transformation, RNAi and evaluation of the development of the fungal pathogen

Barley cv Pallas leaf segments were transformed with a *pNAox* dsRNA together with a GFP expression vector. Thereafer the leaves were inoculated with Bgh and the result was analyzed after 48 h by means of light and fluorescence microscopy. The penetration into GFP-expressing cells was assessed by detecting haustoria in live cells and by assessing the fungal development in precisely those cells. In all five experiments, the bombardment of barley cv Pallas with *pNAox* dsRNA resulted in a reduced number of cells which were successfully penetrated by Bgh in comparison with cells which had been bombarded with foreign control dsRNA (human thyroid hormone receptor dsRNA, TR). The resistance-inducing effect of the *pNAox* dsRNA resulted in an average reduction of the Bgh penetration efficiency by 35% (Fig. 4).

A method which had already been described for the biolistic introduction of dsRNA into epidermal cells of barley leaves was employed for the transient transformation (Schweizer P et al. (1999) Mol Plant Microbe Interact 12:647-54; Schweizer P et al. (2000) Plant J 2000 24: 895-903). Tungsten particles 1.1 µm in diameter (particle density 25 mg/ml) were coated with dsRNA (preparation see above) together with plasmid DNA of the vector *pGFP* (GFP under the control of the CaMV 35S promoters) as transformation marker. To this end, the following amounts of dsRNA and reporter plasmid were used for the coating per shot: 1 µg pGFP and 2 µg dsRNA. Double-stranded RNA was synthesized by annealing sense and antisense RNA *in vitro* (see above).

To prepare microcarriers, 55 mg of tungsten particles (M 17, diameter 1.1 µm; Bio-Rad, Munich) were washed twice with 1 ml of autoclave-distilled water and once with 1 ml of absolute ethanol, dried and taken up in 1 ml of 50% strength glycerol (approximately 50 mg/ml stock solution). The solution was diluted with 50% glycerol to 25 mg/ml, mixed thoroughly prior to use and suspended in an ultrasonic bath. To coat microcarriers, 1 µg of plasmid, 2 µg of dsRNA (1 µl), 12.5 µl of tungsten particle suspension (25 mg/ml), 12.5 µl of 1 M $Ca(NO_3)_2$ solution (pH 10) per shot were combined dropwise with constant mixing, left to stand for 10 minutes at RT, centrifuged briefly, and 20 µl of the supernatant were removed. The remainder with the tungsten particles is resuspended (ultrasonic bath) and employed in the experiment.

Barley primary leaf segments approximately 4 cm in length were used. The tissues were placed on 0.5% Phytagar (GibcoBRL™ Life Technologies™, Karlsruhe) supplemented with 20 µg/ml benzimida-

zole in Petri dishes (diameter 6.5 cm) and, immediately before the particle bombardment, the edges were covered with a stencil with a rectangular opening of dimensions 2.2 cm × 2.3 cm. One after the other, the dishes were placed on the bottom of the vacuum chamber (Schweizer P et al. (1999) Mol Plant Microbe Interact 12:647-54) over which a nylon mesh (mesh size 0.2 mm, Millipore, Eschborn) had been inserted on a perforated sheet to act as diffusor (5 cm above the bottom, 11 cm underneath the macrocarriers, see hereinbelow) in order to diffuse particle clumps and to slow down the particle stream. The macrocarrier attached at the top of the chamber (plastic sterile filter holder, 13 mm, Gelman Sciences, Swinney, UK) was loaded with 5.8 µl of DNA-coated tungsten particles per shot (microcarriers, see hereinbelow). Using a diaphragm vacuum pump (Vacuubrand, Wertheim), the pressure in the chamber was reduced by 0.9 bar, and the tungsten particles were fired at the surface of the plant tissue at a helium-gas pressure of 9 bar. Immediately thereafter, the chamber was aerated. To label transformed cells, the leaves were bombarded with the plasmid (pGFP; vector on pUC18-basis, CaMV 35S promoter/terminator cassette with inserted GFP gene; Schweizer P et al. (1999) Mol Plant Microbe Interact 12:647-54; provided by Dr. P. Schweizer, Department of Plant Genetics IPK, Gatersleben, Germany). Each time a different plasmid was used for the bombardments, the macrocarrier was cleaned thoroughly with water beforehand. After incubation for four hours after the bombardment with slightly open Petri dishes at RT and with daylight, the leaves were incubated with 100 conidia/mm^2 of powdery mildew of barley (race A6) and incubated under identical conditions for a further 40 to 48 hours.

Leaf segments were bombarded with the coated particles using a particle inflow gun. For each shot, 312 µg of tungsten particles were applied. 4 hours after the bombardment, the leaves were inoculated with *Blumeria graminis f.sp. hordei* mildew (race A6) and, after a further 40 hours, evaluated for symptoms of infection. The result (for example the penetration efficiency, defined as percentage of attacked cells with a mature haustorium and a secondary elongating hypha were analyzed by means of fluorescence and light microscopy. An inoculation with 100 conidia/mm^2 results in an infection frequency of approximately 50% of the transformed cells. A minimum of 100 interaction sites was evaluated for each individual experiment. Transformed (GFP-expressing) cells were identified under excitation with blue light. Three different categories of transformed cells were distinguished:

1. Penetrated cells containing a readily recognizable haustorium. A cell with more than one haustorium was considered as one cell.

2. Cells which, while attacked by a fungal appressorium, contain no haustorium. A cell which has been attacked more than once by Bgh, but which contains no haustorium, was considered as one cell.

3. Cells which are not infected by Bgh.

Stomatal cells and guard cells were excluded from the assessment. Surface structures of Bgh were analyzed by means of light microscopy or fluorescence staining of the fungus with 0.1% Calcofluor (w/v in water) for 30 seconds. The fungal development can be evaluated readily by fluorescence microscopy following staining with Calcofluor. In pNAox-dsRNA-transformed cells, the fungus develops a primary and apressorial germ tube, but no haustorium. The development of a haustorium is a condition for the development of a secondary hypha.

The relative penetration efficiency (RPE) is calculated as the difference between the penetration efficiency of transformed cells (transformation with pNAox or control dsRNA) and the penetration efficiency of untransformed cells (here: average penetration efficiency 38.74%). The percent RPE (% RPE) is calculated from the RPE minus 1, multiplied by 100.

$$RPE = \frac{[PE \text{ in pNAox-dsRNA-transformed cells}]}{[PE \text{ in control-dsRNA transformed cells}]}$$

$$\% \text{ RPE} = 100 * (RPE-1)$$

The % RPE value (deviation of the average penetration efficiency of the control) is used to determine the susceptibility of cells transfected with pNAox-dsRNA (fig. 4).

In the case of the control dsRNA, five different experiments reveal no difference between the transfection with the control dsRNA and water with regard to the penetration efficiency of *Bgh*.

To rule out an effect of the dsRNA and the transformation rate or survival rate of the attacked cells, the number of GFP-expressing cells in control experiments and *pNAox*-dsRNA experiments was compared. The *pNAox*-dsRNA had no effect on the total number or the number of the attacked GFP-expressing cells.

Example 5: NADPH oxidase inhibition with diphenyleneiodonium chloride

The results were supported by further experiments with the NADPH oxidase inhibitor diphenyleneiodonium chloride (DPI; table 1). In general, the experiments were carried out as described by Hückelhoven and Kogel, 1998.

Tab. 1: Effect of DPI on the defense against pathogens in Pallas[a]

Type of interaction	Interactions (% ± standard error)	
	Control[b]	200 µM DPI[c]
Penetration	68.25 ± 9.9	16.25 ± 0.5
Nonpenetration	24.25 ± 6.3	67.5 ± 9.5
HR (Hypersensitive response)	7.5 ± 3.7	16.25 ± 9.3

a The DPI treatment was carried out 12 hours after inoculation with the pathogen and the evaluation 36 hours after inoculation.

b Controll with 10 mM potassium phosphate buffer, pH 7.8, with DMSO content as in the DPI treatment.

c DPI dissolved in 10 mM potassium phosphate buffer, pH 7.8, starting from a 10 mg/ml DPI stock solution in DMSO.

SEQUENCE LISTING

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<120> Method for obtaining the pathogenic resistance in plants

<130> 003230-3323

<140> 2.492.784
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Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr
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gcc aag ata gga gtg ttc tat tgc gga gct cca gtt ctg gcg cag gaa   289
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                85                  90                  95
cta agc aac ctt tgc cat gag ttc aat ggc aaa tgc acg aca aaa ttc   337
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ccg tcg atc cgg agg agc tcg tcg cac cgg ctg ctg cag ttc tcg cag   336
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Ser Asp Phe Ala Glu Cys Ile Gly Met Thr Glu Ser Lys Glu Phe Ala
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ctc gag ctg ttc gac acg ctg agc cgg cga cga cag atg aag gtg gac   720
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225                 230                 235                 240
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Asn Ala Asp Gly Arg Ile Thr Glu Ala Glu Val Lys Glu Ile Ile Met
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Tyr Ile Glu Leu Trp Gln Leu Glu Thr Leu Leu Leu Gln Lys Asp Thr
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385                 390                 395                 400
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Met Gln Tyr Arg Asn Arg Tyr Val Phe Asp Val Met Gly Tyr Cys Val
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His Leu Val Cys Asp Phe Pro Arg Leu Ile Lys Ser Ser Asp Glu Lys
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Pro Thr Phe Arg Tyr Lys Ser Gly Gln Tyr Met Phe Val Gln Cys Pro
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Gly Asp Asp Tyr Leu Ser Ile His Val Arg Gln Leu Gly Asp Trp Thr
        675                 680                 685
cga gaa ctc aag aga gta ttt gct gca gct tgt gag ccc cca gcg ggt   2112
Arg Glu Leu Lys Arg Val Phe Ala Ala Ala Cys Glu Pro Pro Ala Gly
    690                 695                 700
ggt aaa agc ggc ctt ctt agg gca gat gag aca act aag aaa atc tta   2160
Gly Lys Ser Gly Leu Leu Arg Ala Asp Glu Thr Thr Lys Lys Ile Leu
705                 710                 715                 720
ccc aag ctt ctg att gat gga ccg tat ggt tct cct gct cag gat tac   2208
Pro Lys Leu Leu Ile Asp Gly Pro Tyr Gly Ser Pro Ala Gln Asp Tyr
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agc aag tat gat gtt tta tta ctt gtt gga tta gga att ggt gcg aca   2256
Ser Lys Tyr Asp Val Leu Leu Leu Val Gly Leu Gly Ile Gly Ala Thr
            740                 745                 750
ccc ttt att agc ata tta aaa gat ctt ctg aat aac atc atc aaa atg   2304
Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Asn Asn Ile Ile Lys Met
        755                 760                 765
gag gaa gag gag gat gct tct act gat ctt tat cca cca atg ggt cgg   2352
Glu Glu Glu Glu Asp Ala Ser Thr Asp Leu Tyr Pro Pro Met Gly Arg
    770                 775                 780
aat aag cca cat gtt gat ctg ggc aca ctt atg acg att acc tca aga   2400
Asn Lys Pro His Val Asp Leu Gly Thr Leu Met Thr Ile Thr Ser Arg
785                 790                 795                 800
cca aag aag atc ttg aag acc aca aat gct tac ttt tac tgg gtg aca   2448
Pro Lys Lys Ile Leu Lys Thr Thr Asn Ala Tyr Phe Tyr Trp Val Thr
                805                 810                 815
cgt gag caa ggc tct ttt gat tgg ttc aaa gga gtc atg aat gaa att   2496
Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly Val Met Asn Glu Ile
            820                 825                 830
gct gac ttg gat caa agg aat atc att gag atg cac aac tac cta aca   2544
Ala Asp Leu Asp Gln Arg Asn Ile Ile Glu Met His Asn Tyr Leu Thr
        835                 840                 845
agc gtc tat gag gag ggg gat gcc agg tca gca ctc atc acc atg ctc   2592
Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu
    850                 855                 860
caa gct ctg aac cat gcc aag aat gga gtt gat att gtc tct ggg aca   2640
Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr
865                 870                 875                 880
aaa gtc cgg aca cat ttt gca cga cca aat tgg aga aag gtc ctt tct   2688
Lys Val Arg Thr His Phe Ala Arg Pro Asn Trp Arg Lys Val Leu Ser
                885                 890                 895
aaa att tcc tcc aag cat cca tat gcc aaa ata ggt gta ttc tac tgt   2736
Lys Ile Ser Ser Lys His Pro Tyr Ala Lys Ile Gly Val Phe Tyr Cys
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gga gct cca gtc ctg gca caa gaa cta agc aaa ctt tgc cat gaa ttc   2784
Gly Ala Pro Val Leu Ala Gln Glu Leu Ser Lys Leu Cys His Glu Phe
        915                 920                 925
aac ggg aaa tgc aca acg aag ttc gaa ttc cat aag gag cat ttc tga   2832
Asn Gly Lys Cys Thr Thr Lys Phe Glu Phe His Lys Glu His Phe
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Asp Arg Ser Ser Asp Asp Gly Glu Glu Leu Val Glu Val Thr Leu Asp
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Leu Gln Asp Asp Asp Thr Ile Val Leu Arg Ser Val Glu Pro Ala Ala
    50                  55                  60
Ala Ala Ala Ala Gly Val Gly Ala Gly Ala Gly Ala Ala Ser Ala Arg
65                  70                  75                  80
Gly Glu Leu Thr Gly Gly Pro Ser Ser Ser Ser Ser Arg Ser Arg Ser
                85                  90                  95
Pro Ser Ile Arg Arg Ser Ser Ser His Arg Leu Leu Gln Phe Ser Gln
            100                 105                 110
Glu Leu Lys Ala Glu Ala Met Ala Arg Ala Arg Gln Phe Ser Gln Asp
        115                 120                 125
Leu Thr Lys Arg Phe Gly Arg Ser His Ser Arg Ser Glu Ala Gln Ala
    130                 135                 140
Pro Ser Gly Leu Glu Ser Ala Leu Ala Ala Arg Ala Ala Arg Arg Gln
145                 150                 155                 160
Arg Ala Gln Leu Asp Arg Thr Arg Ser Gly Ala His Lys Ala Leu Arg
                165                 170                 175
Gly Leu Arg Phe Ile Ser Ser Asn Lys Ala Asn Asn Ala Trp Met Glu
            180                 185                 190
Val Gln Ala Asn Phe Asp Arg Leu Ala Arg Asp Gly Tyr Leu Ser Arg
        195                 200                 205
Ser Asp Phe Ala Glu Cys Ile Gly Met Thr Glu Ser Lys Glu Phe Ala
    210                 215                 220
Leu Glu Leu Phe Asp Thr Leu Ser Arg Arg Arg Gln Met Lys Val Asp
225                 230                 235                 240
Thr Ile Asn Lys Asp Glu Leu Arg Glu Ile Trp Gln Gln Ile Thr Asp
                245                 250                 255
Asn Ser Phe Asp Ser Arg Leu Gln Ile Phe Phe Glu Met Val Asp Lys
            260                 265                 270
Asn Ala Asp Gly Arg Ile Thr Glu Ala Glu Val Lys Glu Ile Ile Met
        275                 280                 285
Leu Ser Ala Ser Ala Asn Lys Leu Ser Arg Leu Lys Glu Gln Ala Glu
    290                 295                 300
Glu Tyr Ala Ala Leu Ile Met Glu Glu Leu Asp Pro Glu Gly Leu Gly
305                 310                 315                 320
Tyr Ile Glu Leu Trp Gln Leu Glu Thr Leu Leu Leu Gln Lys Asp Thr
                325                 330                 335
Tyr Met Asn Tyr Ser Gln Ala Leu Ser Tyr Thr Ser Gln Ala Leu Ser
            340                 345                 350
Gln Asn Leu Ala Gly Leu Arg Lys Lys Ser Ser Ile Arg Lys Ile Ser
        355                 360                 365
Thr Ser Leu Ser Tyr Tyr Phe Glu Asp Asn Trp Lys Arg Leu Trp Val
    370                 375                 380
Leu Ala Leu Trp Ile Gly Ile Met Ala Gly Leu Phe Thr Trp Lys Phe
385                 390                 395                 400
Met Gln Tyr Arg Asn Arg Tyr Val Phe Asp Val Met Gly Tyr Cys Val
                405                 410                 415
Thr Thr Ala Lys Gly Ala Ala Glu Thr Leu Lys Leu Asn Met Ala Ile
            420                 425                 430
Ile Leu Leu Pro Val Cys Arg Asn Thr Ile Thr Trp Leu Arg Ser Thr
        435                 440                 445
Arg Ala Ala Arg Ala Leu Pro Phe Asp Asp Asn Ile Asn Phe His Lys
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Thr Ile Ala Ala Ala Ile Val Val Gly Ile Ile Leu His Ala Gly Asn
465                 470                 475                 480
His Leu Val Cys Asp Phe Pro Arg Leu Ile Lys Ser Ser Asp Glu Lys
                485                 490                 495
Tyr Ala Pro Leu Gly Gln Tyr Phe Gly Glu Ile Lys Pro Thr Tyr Phe
            500                 505                 510
Thr Leu Val Lys Gly Val Glu Gly Ile Thr Gly Val Ile Met Val Val
        515                 520                 525
Cys Met Ile Ile Ala Phe Thr Leu Ala Thr Arg Trp Phe Arg Arg Ser
    530                 535                 540
Leu Val Lys Leu Pro Arg Pro Phe Asp Lys Leu Thr Gly Phe Asn Ala
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545 550 555 560
Phe Trp Tyr Ser His His Leu Phe Ile Ile Val Tyr Ile Ala Leu Ile
565 570 575
Val His Gly Glu Cys Leu Tyr Leu Ile His Val Trp Tyr Arg Arg Thr
580 585 590
Thr Trp Met Tyr Leu Ser Val Pro Val Cys Leu Tyr Val Gly Glu Arg
595 600 605
Ile Leu Arg Phe Phe Arg Ser Gly Ser Tyr Ser Val Arg Leu Leu Lys
610 615 620
Val Ala Ile Tyr Pro Gly Asn Val Leu Thr Leu Gln Met Ser Lys Pro
625 630 635 640
Pro Thr Phe Arg Tyr Lys Ser Gly Gln Tyr Met Phe Val Gln Cys Pro
645 650 655
Ala Val Ser Pro Phe Glu Trp His Pro Phe Ser Ile Thr Ser Ala Pro
660 665 670
Gly Asp Asp Tyr Leu Ser Ile His Val Arg Gln Leu Gly Asp Trp Thr
675 680 685
Arg Glu Leu Lys Arg Val Phe Ala Ala Ala Cys Glu Pro Pro Ala Gly
690 695 700
Gly Lys Ser Gly Leu Leu Arg Ala Asp Glu Thr Thr Lys Lys Ile Leu
705 710 715 720
Pro Lys Leu Leu Ile Asp Gly Pro Tyr Gly Ser Pro Ala Gln Asp Tyr
725 730 735
Ser Lys Tyr Asp Val Leu Leu Leu Val Gly Leu Gly Ile Gly Ala Thr
740 745 750
Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Asn Asn Ile Ile Lys Met
755 760 765
Glu Glu Glu Glu Asp Ala Ser Thr Asp Leu Tyr Pro Pro Met Gly Arg
770 775 780
Asn Lys Pro His Val Asp Leu Gly Thr Leu Met Thr Ile Thr Ser Arg
785 790 795 800
Pro Lys Lys Ile Leu Lys Thr Thr Asn Ala Tyr Phe Tyr Trp Val Thr
805 810 815
Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly Val Met Asn Glu Ile
820 825 830
Ala Asp Leu Asp Gln Arg Asn Ile Ile Glu Met His Asn Tyr Leu Thr
835 840 845
Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu
850 855 860
Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr
865 870 875 880
Lys Val Arg Thr His Phe Ala Arg Pro Asn Trp Arg Lys Val Leu Ser
885 890 895
Lys Ile Ser Ser Lys His Pro Tyr Ala Lys Ile Gly Val Phe Tyr Cys
900 905 910
Gly Ala Pro Val Leu Ala Gln Glu Leu Ser Lys Leu Cys His Glu Phe
915 920 925
Asn Gly Lys Cys Thr Thr Lys Phe Glu Phe His Lys Glu His Phe
930 935 940

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Ser Ser Asp Lys Asp Phe Ser Gly Glu Leu Ser Pro Gly Ala Asp Ser
20 25 30
ggc tat aat tcc ggt ttt gct tcc gag gag ttt gtt gaa gtc acg ctt 144

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Gly Tyr Asn Ser Gly Phe Ala Ser Glu Glu Phe Val Glu Val Thr Leu
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gat ctt cag gat gat gat acc att att cta cgg agc gtt gaa ccg gct   192
Asp Leu Gln Asp Asp Asp Thr Ile Ile Leu Arg Ser Val Glu Pro Ala
      50                  55                  60
act gtg att aac att gac gct cct gat ctt ccc gcc gga gtc ggt att   240
Thr Val Ile Asn Ile Asp Ala Pro Asp Leu Pro Ala Gly Val Gly Ile
 65                  70                  75                  80
tcc gga gtt tca att gaa act ccg acg tca gca tcg gtg tcg gaa tct   288
Ser Gly Val Ser Ile Glu Thr Pro Thr Ser Ala Ser Val Ser Glu Ser
                 85                  90                  95
cga tcg ccg acg atc cgc cgg agt tca tct agt aaa ctt cgt cag ttt   336
Arg Ser Pro Thr Ile Arg Arg Ser Ser Ser Ser Lys Leu Arg Gln Phe
            100                 105                 110
tca cag gag ttg aaa gct gag gcg gtt gcg aaa gcg agg cag ttt tca   384
Ser Gln Glu Leu Lys Ala Glu Ala Val Ala Lys Ala Arg Gln Phe Ser
        115                 120                 125
caa gag ctg aag gcg gag tta agg aga ttc tca tgg agc cat ggg cat   432
Gln Glu Leu Lys Ala Glu Leu Arg Arg Phe Ser Trp Ser His Gly His
    130                 135                 140
gcg tct cgc gcg ttt tcg ccc tcg tcg ttt ttt caa aac gcc gtc gtt   480
Ala Ser Arg Ala Phe Ser Pro Ser Ser Phe Phe Gln Asn Ala Val Val
145                 150                 155                 160
gga aca ggt aac ggc gtg gac tcg gct tta gcg gca cgt gca tta cgt   528
Gly Thr Gly Asn Gly Val Asp Ser Ala Leu Ala Ala Arg Ala Leu Arg
                165                 170                 175
cgg caa cgc gcg cag ctt gat cgg act cgt tcc agc gcc cat aga gct   576
Arg Gln Arg Ala Gln Leu Asp Arg Thr Arg Ser Ser Ala His Arg Ala
            180                 185                 190
ctt cgt aga ctc aaa ttc att agc aat aac aaa acc aat gga tgg aat   624
Leu Arg Arg Leu Lys Phe Ile Ser Asn Asn Lys Thr Asn Gly Trp Asn
        195                 200                 205
gaa gtt gaa aac aat ttc tca aag ctc gct aaa gac ggt tat ctt tac   672
Glu Val Glu Asn Asn Phe Ser Lys Leu Ala Lys Asp Gly Tyr Leu Tyr
    210                 215                 220
cgt tcc gat ttc gca caa tgc ata ggt atg aag gat tcg aag gaa ttt   720
Arg Ser Asp Phe Ala Gln Cys Ile Gly Met Lys Asp Ser Lys Glu Phe
225                 230                 235                 240
gca ttg gaa tta ttt gat gct ttg agt aga aga aga aga tta aag gtt   768
Ala Leu Glu Leu Phe Asp Ala Leu Ser Arg Arg Arg Arg Leu Lys Val
                245                 250                 255
gat aaa att agc aag gag gaa ttg tat gag tac tgg tct caa atc acc   816
Asp Lys Ile Ser Lys Glu Glu Leu Tyr Glu Tyr Trp Ser Gln Ile Thr
            260                 265                 270
gat cag agt ttc gat tct cgg ctt cag atc tcc ttc gac atg gtg gac   864
Asp Gln Ser Phe Asp Ser Arg Leu Gln Ile Ser Phe Asp Met Val Asp
        275                 280                 285
aag aat gaa gat ggt cga att gct gaa gag gaa gta aaa gag atc atc   912
Lys Asn Glu Asp Gly Arg Ile Ala Glu Glu Glu Val Lys Glu Ile Ile
    290                 295                 300
atg cta agt gca tct gca aac aag tta tca aga tta aaa gaa caa gca   960
Met Leu Ser Ala Ser Ala Asn Lys Leu Ser Arg Leu Lys Glu Gln Ala
305                 310                 315                 320
gag gag tat gca gct tta atc atg gaa gaa tta gat cct gaa aga ctc  1008
Glu Glu Tyr Ala Ala Leu Ile Met Glu Glu Leu Asp Pro Glu Arg Leu
                325                 330                 335
ggc tac att gag cta tgg cag ctg gaa aca ctt ctc ctc caa aag gac  1056
Gly Tyr Ile Glu Leu Trp Gln Leu Glu Thr Leu Leu Leu Gln Lys Asp
            340                 345                 350
act tac ctc aac tac agt caa gca cta agt tac acg agc caa gcc ttg  1104
Thr Tyr Leu Asn Tyr Ser Gln Ala Leu Ser Tyr Thr Ser Gln Ala Leu
        355                 360                 365
agc caa aac ctt cac gga tta agg aag aaa agc cca ata aaa aga atg  1152
Ser Gln Asn Leu His Gly Leu Arg Lys Lys Ser Pro Ile Lys Arg Met
    370                 375                 380
agc aca aaa ctt gtc tat tca ttg caa gaa aac tgg aag aga att tgg  1200
Ser Thr Lys Leu Val Tyr Ser Leu Gln Glu Asn Trp Lys Arg Ile Trp
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gtt ctc act tta tgg att ttg ata atg att ggg ctt ttt ctt tgg aag  1248
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Val Leu Thr Leu Trp Ile Leu Ile Met Ile Gly Leu Phe Leu Trp Lys
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ttc tat cag tac aaa aac aag agt gca ttc cgt gtc atg ggt tat tgc   1296
Phe Tyr Gln Tyr Lys Asn Lys Ser Ala Phe Arg Val Met Gly Tyr Cys
            420                 425                 430
ctt gtc acg gct aag ggc gct gct gag act ctc aag ttc aac atg gct   1344
Leu Val Thr Ala Lys Gly Ala Ala Glu Thr Leu Lys Phe Asn Met Ala
        435                 440                 445
ctt ata tta ttg cca gta tgc aga aac act att aca tgg ctc agg tcc   1392
Leu Ile Leu Leu Pro Val Cys Arg Asn Thr Ile Thr Trp Leu Arg Ser
    450                 455                 460
acc aag ttg agc cat ttt gta ccc ttt gac gac aac atc aac ttt cac   1440
Thr Lys Leu Ser His Phe Val Pro Phe Asp Asp Asn Ile Asn Phe His
465                 470                 475                 480
aag act gtc gct gca gcc att gtc act ggt atc ata ctc cat gct ggt   1488
Lys Thr Val Ala Ala Ala Ile Val Thr Gly Ile Ile Leu His Ala Gly
                485                 490                 495
aac cat ctt gta tgt gat ttc cca agg ctt ata cat gca gat gat caa   1536
Asn His Leu Val Cys Asp Phe Pro Arg Leu Ile His Ala Asp Asp Gln
            500                 505                 510
gat tat caa agt ttt ttg tcg aat gat ttt ggc caa agt aag cct gga   1584
Asp Tyr Gln Ser Phe Leu Ser Asn Asp Phe Gly Gln Ser Lys Pro Gly
        515                 520                 525
tac ata gac ctt gtt aaa gga gtt gag ggt gtg acg gga ata ata atg   1632
Tyr Ile Asp Leu Val Lys Gly Val Glu Gly Val Thr Gly Ile Ile Met
    530                 535                 540
gta atc ctt atg gcc att gct ttc act ctt gct aca cga tgg ttt aga   1680
Val Ile Leu Met Ala Ile Ala Phe Thr Leu Ala Thr Arg Trp Phe Arg
545                 550                 555                 560
cgg agc ctc att aag ttg ccc aaa cct ttt gat aga ctc act ggc ttc   1728
Arg Ser Leu Ile Lys Leu Pro Lys Pro Phe Asp Arg Leu Thr Gly Phe
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aat gca ttc tgg tat tca cac cac ctt ctt gtc att gtc tac atc cta   1776
Asn Ala Phe Trp Tyr Ser His His Leu Leu Val Ile Val Tyr Ile Leu
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ctg atc atc cat ggc acg ttc ctc ttc ctt gtg cat aaa tgg tac tcc   1824
Leu Ile Ile His Gly Thr Phe Leu Phe Leu Val His Lys Trp Tyr Ser
        595                 600                 605
aag acg acg tgg atg tat cta gca gtt cct gtg ctt ctc tac gca ggg   1872
Lys Thr Thr Trp Met Tyr Leu Ala Val Pro Val Leu Leu Tyr Ala Gly
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gaa aga act ctt aga ttc ttc cgg tca ggc ttg tac act gtc cgg ctt   1920
Glu Arg Thr Leu Arg Phe Phe Arg Ser Gly Leu Tyr Thr Val Arg Leu
625                 630                 635                 640
ctg aaa gta gca ata tat cct gga aat gtc ctc act cta caa atg tct   1968
Leu Lys Val Ala Ile Tyr Pro Gly Asn Val Leu Thr Leu Gln Met Ser
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Cys Pro Ala Val Ser Pro Phe Glu Trp His Pro Phe Ser Ile Thr Ser
        675                 680                 685
gct cct ggg gat gac tac ttg agc att cac atc cgg caa ctt ggt gac   2112
Ala Pro Gly Asp Asp Tyr Leu Ser Ile His Ile Arg Gln Leu Gly Asp
    690                 695                 700
tgg act caa gaa ctc aag cgg gtc ttt tct gag gct tgc gag cgg cca   2160
Trp Thr Gln Glu Leu Lys Arg Val Phe Ser Glu Ala Cys Glu Arg Pro
705                 710                 715                 720
gag gct gga aag agt ggc ctg ctc aga gct gac gaa aac act aag aaa   2208
Glu Ala Gly Lys Ser Gly Leu Leu Arg Ala Asp Glu Asn Thr Lys Lys
                725                 730                 735
agt ttg cca aag cta tta ata gat gga cct tac gga gct cca gca caa   2256
Ser Leu Pro Lys Leu Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln
            740                 745                 750
gat tac cga aaa tat gat gtc ttg ctg ctt gtt ggt ctt ggc att gga   2304
Asp Tyr Arg Lys Tyr Asp Val Leu Leu Leu Val Gly Leu Gly Ile Gly
        755                 760                 765
gca acg ccg ttc ata agt atc ctg aaa gac ttg ctc gtt aac atc gtg   2352
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Ala Thr Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Val Asn Ile Val
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aaa atg gag gag caa gca gat tta gcc tca gat ttc agt ggg aac tca   2400
Lys Met Glu Glu Gln Ala Asp Leu Ala Ser Asp Phe Ser Gly Asn Ser
785                 790                 795                 800
gac atg agc gtt gcg aca agt gaa caa cca gct ctc aac aag att tct   2448
Asp Met Ser Val Ala Thr Ser Glu Gln Pro Ala Leu Asn Lys Ile Ser
                805                 810                 815
ctg aaa agg aga aag agc act cta aga acc aca aat gca tat ttt tat   2496
Leu Lys Arg Arg Lys Ser Thr Leu Arg Thr Thr Asn Ala Tyr Phe Tyr
            820                 825                 830
tgg gtg acc cgg gag caa gga tca ttt gat tgg ttc aaa ggc gtt atg   2544
Trp Val Thr Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly Val Met
        835                 840                 845
aac gaa gtg gct gaa ctt gat caa agg ggg gtc atc gag atg cat aac   2592
Asn Glu Val Ala Glu Leu Asp Gln Arg Gly Val Ile Glu Met His Asn
    850                 855                 860
tac ttg acg agt gtt tat gag gaa ggg gat gct cgt tca gct ctc att   2640
Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile
865                 870                 875                 880
acc atg gtc cag gca ctt aac cat gct aag aat ggg gtt gat att gta   2688
Thr Met Val Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val
                885                 890                 895
tca ggc acc agg gtg agg aca cat ttt gct agg cca aat tgg aag aaa   2736
Ser Gly Thr Arg Val Arg Thr His Phe Ala Arg Pro Asn Trp Lys Lys
            900                 905                 910
gta ttt tcc aag acc tta acc aag cat gca aat gca aga ata ggg gtt   2784
Val Phe Ser Lys Thr Leu Thr Lys His Ala Asn Ala Arg Ile Gly Val
        915                 920                 925
ttc tac tgt ggt gca ccc gta tta gca aaa gaa ctc agc aaa ctc tgc   2832
Phe Tyr Cys Gly Ala Pro Val Leu Ala Lys Glu Leu Ser Lys Leu Cys
    930                 935                 940
aaa gag tat aat caa aag ggt gca aca aag ttc gag ttt cac aaa gaa   2880
Lys Glu Tyr Asn Gln Lys Gly Ala Thr Lys Phe Glu Phe His Lys Glu
945                 950                 955                 960
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His Phe
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             20                  25                  30
Gly Tyr Asn Ser Gly Phe Ala Ser Glu Glu Phe Val Glu Val Thr Leu
         35                  40                  45
Asp Leu Gln Asp Asp Asp Thr Ile Ile Leu Arg Ser Val Glu Pro Ala
     50                  55                  60
Thr Val Ile Asn Ile Asp Ala Pro Asp Leu Pro Ala Gly Val Gly Ile
 65                  70                  75                  80
Ser Gly Val Ser Ile Glu Thr Pro Thr Ser Ala Ser Val Ser Glu Ser
                 85                  90                  95
Arg Ser Pro Thr Ile Arg Arg Ser Ser Ser Ser Lys Leu Arg Gln Phe
            100                 105                 110
Ser Gln Glu Leu Lys Ala Glu Ala Val Ala Lys Ala Arg Gln Phe Ser
        115                 120                 125
Gln Glu Leu Lys Ala Glu Leu Arg Arg Phe Ser Trp Ser His Gly His
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Ala Ser Arg Ala Phe Ser Pro Ser Ser Phe Phe Gln Asn Ala Val Val
145                 150                 155                 160
Gly Thr Gly Asn Gly Val Asp Ser Ala Leu Ala Ala Arg Ala Leu Arg
                165                 170                 175
Arg Gln Arg Ala Gln Leu Asp Arg Thr Arg Ser Ser Ala His Arg Ala
            180                 185                 190
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210 215 220
Arg Ser Asp Phe Ala Gln Cys Ile Gly Met Lys Asp Ser Lys Glu Phe
225 230 235 240
Ala Leu Glu Leu Phe Asp Ala Leu Ser Arg Arg Arg Arg Leu Lys Val
245 250 255
Asp Lys Ile Ser Lys Glu Glu Leu Tyr Glu Tyr Trp Ser Gln Ile Thr
260 265 270
Asp Gln Ser Phe Asp Ser Arg Leu Gln Ile Ser Phe Asp Met Val Asp
275 280 285
Lys Asn Glu Asp Gly Arg Ile Ala Glu Glu Glu Val Lys Glu Ile Ile
290 295 300
Met Leu Ser Ala Ser Ala Asn Lys Leu Ser Arg Leu Lys Glu Gln Ala
305 310 315 320
Glu Glu Tyr Ala Ala Leu Ile Met Glu Glu Leu Asp Pro Glu Arg Leu
325 330 335
Gly Tyr Ile Glu Leu Trp Gln Leu Glu Thr Leu Leu Leu Gln Lys Asp
340 345 350
Thr Tyr Leu Asn Tyr Ser Gln Ala Leu Ser Tyr Thr Ser Gln Ala Leu
355 360 365
Ser Gln Asn Leu His Gly Leu Arg Lys Lys Ser Pro Ile Lys Arg Met
370 375 380
Ser Thr Lys Leu Val Tyr Ser Leu Gln Glu Asn Trp Lys Arg Ile Trp
385 390 395 400
Val Leu Thr Leu Trp Ile Leu Ile Met Ile Gly Leu Phe Leu Trp Lys
405 410 415
Phe Tyr Gln Tyr Lys Asn Lys Ser Ala Phe Arg Val Met Gly Tyr Cys
420 425 430
Leu Val Thr Ala Lys Gly Ala Ala Glu Thr Leu Lys Phe Asn Met Ala
435 440 445
Leu Ile Leu Leu Pro Val Cys Arg Asn Thr Ile Thr Trp Leu Arg Ser
450 455 460
Thr Lys Leu Ser His Phe Val Pro Phe Asp Asp Asn Ile Asn Phe His
465 470 475 480
Lys Thr Val Ala Ala Ala Ile Val Thr Gly Ile Ile Leu His Ala Gly
485 490 495
Asn His Leu Val Cys Asp Phe Pro Arg Leu Ile His Ala Asp Asp Gln
500 505 510
Asp Tyr Gln Ser Phe Leu Ser Asn Asp Phe Gly Gln Ser Lys Pro Gly
515 520 525
Tyr Ile Asp Leu Val Lys Gly Val Glu Gly Val Thr Gly Ile Ile Met
530 535 540
Val Ile Leu Met Ala Ile Ala Phe Thr Leu Ala Thr Arg Trp Phe Arg
545 550 555 560
Arg Ser Leu Ile Lys Leu Pro Lys Pro Phe Asp Arg Leu Thr Gly Phe
565 570 575
Asn Ala Phe Trp Tyr Ser His His Leu Leu Val Ile Val Tyr Ile Leu
580 585 590
Leu Ile Ile His Gly Thr Phe Leu Phe Leu Val His Lys Trp Tyr Ser
595 600 605
Lys Thr Thr Trp Met Tyr Leu Ala Val Pro Val Leu Leu Tyr Ala Gly
610 615 620
Glu Arg Thr Leu Arg Phe Phe Arg Ser Gly Leu Tyr Thr Val Arg Leu
625 630 635 640
Leu Lys Val Ala Ile Tyr Pro Gly Asn Val Leu Thr Leu Gln Met Ser
645 650 655
Lys Pro Pro Gln Phe Arg Tyr Lys Ser Gly Gln Tyr Met Phe Val Gln
660 665 670
Cys Pro Ala Val Ser Pro Phe Glu Trp His Pro Phe Ser Ile Thr Ser
675 680 685
Ala Pro Gly Asp Asp Tyr Leu Ser Ile His Ile Arg Gln Leu Gly Asp
690 695 700
Trp Thr Gln Glu Leu Lys Arg Val Phe Ser Glu Ala Cys Glu Arg Pro
705 710 715 720
Glu Ala Gly Lys Ser Gly Leu Leu Arg Ala Asp Glu Asn Thr Lys Lys
725 730 735
Ser Leu Pro Lys Leu Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln

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                740                 745                 750
Asp Tyr Arg Lys Tyr Asp Val Leu Leu Leu Val Gly Leu Gly Ile Gly
            755                 760                 765
Ala Thr Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Val Asn Ile Val
        770                 775                 780
Lys Met Glu Glu Gln Ala Asp Leu Ala Ser Asp Phe Ser Gly Asn Ser
785                 790                 795                 800
Asp Met Ser Val Ala Thr Ser Glu Gln Pro Ala Leu Asn Lys Ile Ser
                805                 810                 815
Leu Lys Arg Arg Lys Ser Thr Leu Arg Thr Thr Asn Ala Tyr Phe Tyr
            820                 825                 830
Trp Val Thr Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly Val Met
            835                 840                 845
Asn Glu Val Ala Glu Leu Asp Gln Arg Gly Val Ile Glu Met His Asn
        850                 855                 860
Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile
865                 870                 875                 880
Thr Met Val Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val
                885                 890                 895
Ser Gly Thr Arg Val Arg Thr His Phe Ala Arg Pro Asn Trp Lys Lys
            900                 905                 910
Val Phe Ser Lys Thr Leu Thr Lys His Ala Asn Ala Arg Ile Gly Val
            915                 920                 925
Phe Tyr Cys Gly Ala Pro Val Leu Ala Lys Glu Leu Ser Lys Leu Cys
        930                 935                 940
Lys Glu Tyr Asn Gln Lys Gly Ala Thr Lys Phe Glu Phe His Lys Glu
945                 950                 955                 960
His Phe
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<210> 7
<211> 3733
<212> DNA
<213> Solanum tuberosum

<220>
<221> CDS
<222> (92)..(2980)
<223> coding for NADPH oxidase

<400> 7

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tatttattta ttgtgctttg atttgggaca a atg agg ggt tta cct ggg cat    112
                                    Met Arg Gly Leu Pro Gly His
                                      1               5
gaa cgc cgg tgg acg tcg gat acg gta tct tcc ggc aag gat tta agt   160
Glu Arg Arg Trp Thr Ser Asp Thr Val Ser Ser Gly Lys Asp Leu Ser
          10                  15                  20
ggt gag tca tcg ccg gga act gat tcc ggg aat att tcc ggt ttt gct   208
Gly Glu Ser Ser Pro Gly Thr Asp Ser Gly Asn Ile Ser Gly Phe Ala
      25                  30                  35
tcc gag gag ttt gtt gaa gtt ata ctt gat ctt cag gat gat gat acg   256
Ser Glu Glu Phe Val Glu Val Ile Leu Asp Leu Gln Asp Asp Asp Thr
  40                  45                  50                  55
att att cta cgg agc gtt gaa ccg gct act gta atc aac att gat gct   304
Ile Ile Leu Arg Ser Val Glu Pro Ala Thr Val Ile Asn Ile Asp Ala
                  60                  65                  70
tct gat cct gct acc gga gtc ggt att ggt gga gta tcg att gaa act   352
Ser Asp Pro Ala Thr Gly Val Gly Ile Gly Gly Val Ser Ile Glu Thr
              75                  80                  85
ccg gcg tcg ctg act tcg acg tcg gga act cga tcg ccg acg atg cgt   400
Pro Ala Ser Leu Thr Ser Thr Ser Gly Thr Arg Ser Pro Thr Met Arg
          90                  95                  100
cgg agt aca tcg aat aaa tta cgt cag ttt tca cag gag ttg aaa gct   448
Arg Ser Thr Ser Asn Lys Leu Arg Gln Phe Ser Gln Glu Leu Lys Ala
      105                 110                 115
gag gct gtc gcg aaa gcg aag cat ttc tcg caa gag ctt aaa gcg gag   496
Glu Ala Val Ala Lys Ala Lys His Phe Ser Gln Glu Leu Lys Ala Glu
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120                 125                 130                 135
cta agg aga ttc tca tgg agc cat gga cat gcg tct cgc act ttt tcg   544
Leu Arg Arg Phe Ser Trp Ser His Gly His Ala Ser Arg Thr Phe Ser
                140                 145                 150
ccg gcg tcg ttt ttc caa aac gcc gtc gtc ggt aca ggc aac ggt gta   592
Pro Ala Ser Phe Phe Gln Asn Ala Val Val Gly Thr Gly Asn Gly Val
            155                 160                 165
gat tcg gct tta gca gct cga gca tta cga cgg cag cgc gct cag ctc   640
Asp Ser Ala Leu Ala Ala Arg Ala Leu Arg Arg Gln Arg Ala Gln Leu
        170                 175                 180
gat cgg act cgt tcc agc gct cac aag gct ctt cgt gga ctc aaa ttc   688
Asp Arg Thr Arg Ser Ser Ala His Lys Ala Leu Arg Gly Leu Lys Phe
    185                 190                 195
atc agc aat aac aaa act aac gga tgg aat gaa gtt gaa aac aat ttt   736
Ile Ser Asn Asn Lys Thr Asn Gly Trp Asn Glu Val Glu Asn Asn Phe
200                 205                 210                 215
gct aag ctc gct aaa gac ggt tac ctt tat cgc tcc gat ttc gca caa   784
Ala Lys Leu Ala Lys Asp Gly Tyr Leu Tyr Arg Ser Asp Phe Ala Gln
                220                 225                 230
tgc atc ggt atg aag gat tca aag gaa ttt gca ttg gaa ttg ttt gat   832
Cys Ile Gly Met Lys Asp Ser Lys Glu Phe Ala Leu Glu Leu Phe Asp
            235                 240                 245
gct ttg agt aga aga aga aga ttg aag gtt gat aag att agc aaa gag   880
Ala Leu Ser Arg Arg Arg Arg Leu Lys Val Asp Lys Ile Ser Lys Glu
        250                 255                 260
gaa ttg tat gag tat tgg tct caa atc acc gat cag agt ttc gat tct   928
Glu Leu Tyr Glu Tyr Trp Ser Gln Ile Thr Asp Gln Ser Phe Asp Ser
    265                 270                 275
cgg ctt cag atc ttc ttc gac atg gtg gac aag aat gaa gat ggt cga   976
Arg Leu Gln Ile Phe Phe Asp Met Val Asp Lys Asn Glu Asp Gly Arg
280                 285                 290                 295
att ggt gaa gaa gaa gta aaa gag atc atc atg cta agt gcc tct gca  1024
Ile Gly Glu Glu Glu Val Lys Glu Ile Ile Met Leu Ser Ala Ser Ala
                300                 305                 310
aac aaa tta tca aga tta aaa gaa caa gca gag gag tat gca gct ctg  1072
Asn Lys Leu Ser Arg Leu Lys Glu Gln Ala Glu Glu Tyr Ala Ala Leu
            315                 320                 325
atc atg gaa gaa tta gat cct gaa aga ctt ggc tac att gag cta tgg  1120
Ile Met Glu Glu Leu Asp Pro Glu Arg Leu Gly Tyr Ile Glu Leu Trp
        330                 335                 340
cag ctg gaa acg ctt ctc ctc caa aag gac act tac ctc aac tac agt  1168
Gln Leu Glu Thr Leu Leu Leu Gln Lys Asp Thr Tyr Leu Asn Tyr Ser
    345                 350                 355
caa gca cta agc tac aca agc caa gct ttg agc caa aac ctg caa ggg  1216
Gln Ala Leu Ser Tyr Thr Ser Gln Ala Leu Ser Gln Asn Leu Gln Gly
360                 365                 370                 375
ttg agg aag aga agc cca ata aga aga atg agc aca aaa ctt gtc tat  1264
Leu Arg Lys Arg Ser Pro Ile Arg Arg Met Ser Thr Lys Leu Val Tyr
                380                 385                 390
tca ctg caa gag aat tgg aag aga att tgg gtt ctg gtc ttg tgg att  1312
Ser Leu Gln Glu Asn Trp Lys Arg Ile Trp Val Leu Val Leu Trp Ile
            395                 400                 405
ttg ata atg att gga ctt ttt ctt tgg aag ttc tat ctg tac aaa cag  1360
Leu Ile Met Ile Gly Leu Phe Leu Trp Lys Phe Tyr Leu Tyr Lys Gln
        410                 415                 420
aaa agt gca ttt caa gtt atg ggt tat tgc ctt cta aca gct aag ggt  1408
Lys Ser Ala Phe Gln Val Met Gly Tyr Cys Leu Leu Thr Ala Lys Gly
    425                 430                 435
gct gct gag act cta aag ttc aac atg gct ttg ata ttg ttg cca gtt  1456
Ala Ala Glu Thr Leu Lys Phe Asn Met Ala Leu Ile Leu Leu Pro Val
440                 445                 450                 455
tgc agg aac acc att aca ttc ctc agg tct act aaa ttg agt tgt ttt  1504
Cys Arg Asn Thr Ile Thr Phe Leu Arg Ser Thr Lys Leu Ser Cys Phe
                460                 465                 470
gta ccc ttt gat gac aac atc aac ttc cac aag act gtt gct gca gcc  1552
Val Pro Phe Asp Asp Asn Ile Asn Phe His Lys Thr Val Ala Ala Ala
            475                 480                 485
att gtt act ggt atc ata ctc cat gcc ggt aat cat ctt gta tgt gat  1600
Ile Val Thr Gly Ile Ile Leu His Ala Gly Asn His Leu Val Cys Asp
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          490                 495                 500
ttc cca aag ctt ata cat gca aat aat acg aat tat cag aaa tat ttg   1648
Phe Pro Lys Leu Ile His Ala Asn Asn Thr Asn Tyr Gln Lys Tyr Leu
    505                 510                 515
gtg aat gat ttt ggc cca agc cag cct cag tac ata gat ctt gtt aaa   1696
Val Asn Asp Phe Gly Pro Ser Gln Pro Gln Tyr Ile Asp Leu Val Lys
520                 525                 530                 535
gga gtg gag ggt gtg aca gga ata ata atg gta atc ctc atg gcc att   1744
Gly Val Glu Gly Val Thr Gly Ile Ile Met Val Ile Leu Met Ala Ile
                540                 545                 550
gct ttc act ctt gca acg cga tgg ttt agg cgg agc ctc att aag ttt   1792
Ala Phe Thr Leu Ala Thr Arg Trp Phe Arg Arg Ser Leu Ile Lys Phe
            555                 560                 565
ccc aaa cct ttt gat aga ctc act ggt ttc aat gcg ttc tgg tac tcg   1840
Pro Lys Pro Phe Asp Arg Leu Thr Gly Phe Asn Ala Phe Trp Tyr Ser
        570                 575                 580
cac cac ctt ctc atc att gtc tac atc gta ctg atc atc cat ggc aca   1888
His His Leu Leu Ile Ile Val Tyr Ile Val Leu Ile Ile His Gly Thr
    585                 590                 595
ttc ctc tac ctt gtg cat aac tgg tac tcc aaa acg aca tgg atg tat   1936
Phe Leu Tyr Leu Val His Asn Trp Tyr Ser Lys Thr Thr Trp Met Tyr
600                 605                 610                 615
cta gca gtt cct gta ctt ctc tac gca ggg gaa aga act ctt aga ttc   1984
Leu Ala Val Pro Val Leu Leu Tyr Ala Gly Glu Arg Thr Leu Arg Phe
                620                 625                 630
ttc cga tca ggc tta tat aca gtc cgg ctt cta aaa gta gca ata tat   2032
Phe Arg Ser Gly Leu Tyr Thr Val Arg Leu Leu Lys Val Ala Ile Tyr
            635                 640                 645
cct gga aat gtc ctt act ctg caa atg tct aag cct ccg caa ttt cga   2080
Pro Gly Asn Val Leu Thr Leu Gln Met Ser Lys Pro Pro Gln Phe Arg
        650                 655                 660
tac aag agt gga caa tat atg ttt gtc cag tgt cca gct gtt tct cca   2128
Tyr Lys Ser Gly Gln Tyr Met Phe Val Gln Cys Pro Ala Val Ser Pro
    665                 670                 675
ttc gag tgg cat cca ttt tcc att act tca gct cct ggg gat gac tac   2176
Phe Glu Trp His Pro Phe Ser Ile Thr Ser Ala Pro Gly Asp Asp Tyr
680                 685                 690                 695
ttg agc att cat atc cga caa ctt ggt gac tgg act caa gaa ctc aag   2224
Leu Ser Ile His Ile Arg Gln Leu Gly Asp Trp Thr Gln Glu Leu Lys
                700                 705                 710
cgg gtg ttt tcc gag gct tgc gag cag cca gag gct gga aag agt ggc   2272
Arg Val Phe Ser Glu Ala Cys Glu Gln Pro Glu Ala Gly Lys Ser Gly
            715                 720                 725
ctg ctc aga gct gac gaa aac acc aaa aca agt ttg cca aag cta ttg   2320
Leu Leu Arg Ala Asp Glu Asn Thr Lys Thr Ser Leu Pro Lys Leu Leu
        730                 735                 740
ata gat gga cct tat gga gct cca gca caa gat tac cga aag tat gat   2368
Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln Asp Tyr Arg Lys Tyr Asp
    745                 750                 755
gtc tta ctg ctt gtt ggt ctt ggc att gga gca act ccc ttt ata agt   2416
Val Leu Leu Leu Val Gly Leu Gly Ile Gly Ala Thr Pro Phe Ile Ser
760                 765                 770                 775
atc ctg aaa gac ttg ctc aaa aac atc gtc aca atg gag gag caa gca   2464
Ile Leu Lys Asp Leu Leu Lys Asn Ile Val Thr Met Glu Glu Gln Ala
                780                 785                 790
gat tta gtc tcg gat ttt tca ggg aac tca gac atg agc gct gca aca   2512
Asp Leu Val Ser Asp Phe Ser Gly Asn Ser Asp Met Ser Ala Ala Thr
            795                 800                 805
agt gaa caa cca gct ctc aac aag att tct cca aaa aag aga aag agt   2560
Ser Glu Gln Pro Ala Leu Asn Lys Ile Ser Pro Lys Lys Arg Lys Ser
        810                 815                 820
act cta aaa acc aca aat gca tat ttt tat tgg gtg acc cgg gag caa   2608
Thr Leu Lys Thr Thr Asn Ala Tyr Phe Tyr Trp Val Thr Arg Glu Gln
    825                 830                 835
gga tca ttt gat tgg ttc aaa ggt gtt atg aac gaa gtg gct gaa ctt   2656
Gly Ser Phe Asp Trp Phe Lys Gly Val Met Asn Glu Val Ala Glu Leu
840                 845                 850                 855
gat caa agg ggg gtc atc gag atg cat aac tac tta acg agt gtt tat   2704
Asp Gln Arg Gly Val Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr
```

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                    860                 865                 870
gag gaa ggg gat gca cgt tca gct ctc att acc atg gtc cag gcg ctt   2752
Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Val Gln Ala Leu
            875                 880                 885
aac cat gct aag aat ggg gtt gat att gta tca ggc acc agt gtg agg   2800
Asn His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr Ser Val Arg
        890                 895                 900
aca cat ttt gcc aga ccg aat tgg agg aaa gta ttt tcc aag acc tta   2848
Thr His Phe Ala Arg Pro Asn Trp Arg Lys Val Phe Ser Lys Thr Leu
    905                 910                 915
acc aag cat gca aat gca aga ata gga gtt ttc tac tgc ggt gca ccc   2896
Thr Lys His Ala Asn Ala Arg Ile Gly Val Phe Tyr Cys Gly Ala Pro
920                 925                 930                 935
ata tta gct aaa gaa ctc agc aaa ctc tgc aaa gag ttt aac caa aag   2944
Ile Leu Ala Lys Glu Leu Ser Lys Leu Cys Lys Glu Phe Asn Gln Lys
                940                 945                 950
ggc aca acg aag ttc gag ttt cac aaa gaa cat ttt tagaaggccc        2990
Gly Thr Thr Lys Phe Glu Phe His Lys Glu His Phe
            955                 960
tggagtacaa ttaatcttgc atcaacggta cacacatcgg taaaccagta tttaccacat 3050
ctatctttgg tacctgattt gatgattcta ctgaagacat aacattagta aggaataagt 3110
cagagacaaa ttgtacataa taggaggaag cacatttaca gagaaaatac ataccaatat 3170
gatatgtgta taggttttgt atattcagtc atctgttatc acataccaaa cttcagaact 3230
ccaaaaggga gactctgctt tggtctgatg gcttagaata tgggagggaa aaaaagacga 3290
caattgaatg gtcacgatac acatgaagaa tgagaatatt gggaaacagc taataagaag 3350
ttgaccttct tgataaagaa acactatgaa aatggcaagc atgaaaggac agacaatcat 3410
ggcttggatg gggaaaacaa aatacaattt tgaaagaaga agataatatt agtaggagta 3470
gtgggggact gatagctttg ttggtggaac ttataatggg gctaagggaa tccttccaaa 3530
aaatgtctat gtagtaacta ctttttcttt tgctttgtga gtatttttg gggtatttta 3590
atatactact tattagataa gaggatagaa aatacgtgta tatgcaattc ttattagtaa 3650
agtttatctg tagtagttct ttaatctgga gaaaggtact atcaaaggaa atatctcatc 3710
gaaaaaaaaa aaaaaaaaaa aaa                                        3733
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<210> 8
<211> 963
<212> PRT
<213> Solanum tuberosum

<400> 8

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            20                  25                  30
Gly Asn Ile Ser Gly Phe Ala Ser Glu Glu Phe Val Glu Val Ile Leu
        35                  40                  45
Asp Leu Gln Asp Asp Asp Thr Ile Ile Leu Arg Ser Val Glu Pro Ala
    50                  55                  60
Thr Val Ile Asn Ile Asp Ala Ser Asp Pro Ala Thr Gly Val Gly Ile
65                  70                  75                  80
Gly Gly Val Ser Ile Glu Thr Pro Ala Ser Leu Thr Ser Thr Ser Gly
                85                  90                  95
Thr Arg Ser Pro Thr Met Arg Arg Ser Thr Ser Asn Lys Leu Arg Gln
            100                 105                 110
Phe Ser Gln Glu Leu Lys Ala Glu Ala Val Ala Lys Ala Lys His Phe
        115                 120                 125
Ser Gln Glu Leu Lys Ala Glu Leu Arg Arg Phe Ser Trp Ser His Gly
    130                 135                 140
His Ala Ser Arg Thr Phe Ser Pro Ala Ser Phe Phe Gln Asn Ala Val
145                 150                 155                 160
Val Gly Thr Gly Asn Gly Val Asp Ser Ala Leu Ala Ala Arg Ala Leu
                165                 170                 175
Arg Arg Gln Arg Ala Gln Leu Asp Arg Thr Arg Ser Ser Ala His Lys
            180                 185                 190
Ala Leu Arg Gly Leu Lys Phe Ile Ser Asn Asn Lys Thr Asn Gly Trp
        195                 200                 205
Asn Glu Val Glu Asn Asn Phe Ala Lys Leu Ala Lys Asp Gly Tyr Leu
    210                 215                 220
Tyr Arg Ser Asp Phe Ala Gln Cys Ile Gly Met Lys Asp Ser Lys Glu
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225 230 235 240
Phe Ala Leu Glu Leu Phe Asp Ala Leu Ser Arg Arg Arg Arg Leu Lys
245 250 255
Val Asp Lys Ile Ser Lys Glu Glu Leu Tyr Glu Tyr Trp Ser Gln Ile
260 265 270
Thr Asp Gln Ser Phe Asp Ser Arg Leu Gln Ile Phe Phe Asp Met Val
275 280 285
Asp Lys Asn Glu Asp Gly Arg Ile Gly Glu Glu Glu Val Lys Glu Ile
290 295 300
Ile Met Leu Ser Ala Ser Ala Asn Lys Leu Ser Arg Leu Lys Glu Gln
305 310 315 320
Ala Glu Glu Tyr Ala Ala Leu Ile Met Glu Glu Leu Asp Pro Glu Arg
325 330 335
Leu Gly Tyr Ile Glu Leu Trp Gln Leu Glu Thr Leu Leu Leu Gln Lys
340 345 350
Asp Thr Tyr Leu Asn Tyr Ser Gln Ala Leu Ser Tyr Thr Ser Gln Ala
355 360 365
Leu Ser Gln Asn Leu Gln Gly Leu Arg Lys Arg Ser Pro Ile Arg Arg
370 375 380
Met Ser Thr Lys Leu Val Tyr Ser Leu Gln Glu Asn Trp Lys Arg Ile
385 390 395 400
Trp Val Leu Val Leu Trp Ile Leu Ile Met Ile Gly Leu Phe Leu Trp
405 410 415
Lys Phe Tyr Leu Tyr Lys Gln Lys Ser Ala Phe Gln Val Met Gly Tyr
420 425 430
Cys Leu Leu Thr Ala Lys Gly Ala Ala Glu Thr Leu Lys Phe Asn Met
435 440 445
Ala Leu Ile Leu Leu Pro Val Cys Arg Asn Thr Ile Thr Phe Leu Arg
450 455 460
Ser Thr Lys Leu Ser Cys Phe Val Pro Phe Asp Asp Asn Ile Asn Phe
465 470 475 480
His Lys Thr Val Ala Ala Ala Ile Val Thr Gly Ile Ile Leu His Ala
485 490 495
Gly Asn His Leu Val Cys Asp Phe Pro Lys Leu Ile His Ala Asn Asn
500 505 510
Thr Asn Tyr Gln Lys Tyr Leu Val Asn Asp Phe Gly Pro Ser Gln Pro
515 520 525
Gln Tyr Ile Asp Leu Val Lys Gly Val Glu Gly Val Thr Gly Ile Ile
530 535 540
Met Val Ile Leu Met Ala Ile Ala Phe Thr Leu Ala Thr Arg Trp Phe
545 550 555 560
Arg Arg Ser Leu Ile Lys Phe Pro Lys Pro Phe Asp Arg Leu Thr Gly
565 570 575
Phe Asn Ala Phe Trp Tyr Ser His His Leu Leu Ile Ile Val Tyr Ile
580 585 590
Val Leu Ile Ile His Gly Thr Phe Leu Tyr Leu Val His Asn Trp Tyr
595 600 605
Ser Lys Thr Thr Trp Met Tyr Leu Ala Val Pro Val Leu Leu Tyr Ala
610 615 620
Gly Glu Arg Thr Leu Arg Phe Phe Arg Ser Gly Leu Tyr Thr Val Arg
625 630 635 640
Leu Leu Lys Val Ala Ile Tyr Pro Gly Asn Val Leu Thr Leu Gln Met
645 650 655
Ser Lys Pro Pro Gln Phe Arg Tyr Lys Ser Gly Gln Tyr Met Phe Val
660 665 670
Gln Cys Pro Ala Val Ser Pro Phe Glu Trp His Pro Phe Ser Ile Thr
675 680 685
Ser Ala Pro Gly Asp Asp Tyr Leu Ser Ile His Ile Arg Gln Leu Gly
690 695 700
Asp Trp Thr Gln Glu Leu Lys Arg Val Phe Ser Glu Ala Cys Glu Gln
705 710 715 720
Pro Glu Ala Gly Lys Ser Gly Leu Leu Arg Ala Asp Glu Asn Thr Lys
725 730 735
Thr Ser Leu Pro Lys Leu Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala
740 745 750
Gln Asp Tyr Arg Lys Tyr Asp Val Leu Leu Leu Val Gly Leu Gly Ile
755 760 765
Gly Ala Thr Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Lys Asn Ile
770 775 780

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Val Thr Met Glu Glu Gln Ala Asp Leu Val Ser Asp Phe Ser Gly Asn
785                 790                 795                 800
Ser Asp Met Ser Ala Ala Thr Ser Glu Gln Pro Ala Leu Asn Lys Ile
                805                 810                 815
Ser Pro Lys Lys Arg Lys Ser Thr Leu Lys Thr Thr Asn Ala Tyr Phe
            820                 825                 830
Tyr Trp Val Thr Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly Val
        835                 840                 845
Met Asn Glu Val Ala Glu Leu Asp Gln Arg Gly Val Ile Glu Met His
    850                 855                 860
Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu
865                 870                 875                 880
Ile Thr Met Val Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile
                885                 890                 895
Val Ser Gly Thr Ser Val Arg Thr His Phe Ala Arg Pro Asn Trp Arg
            900                 905                 910
Lys Val Phe Ser Lys Thr Leu Thr Lys His Ala Asn Ala Arg Ile Gly
        915                 920                 925
Val Phe Tyr Cys Gly Ala Pro Ile Leu Ala Lys Glu Leu Ser Lys Leu
    930                 935                 940
Cys Lys Glu Phe Asn Gln Lys Gly Thr Thr Lys Phe Glu Phe His Lys
945                 950                 955                 960
Glu His Phe
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<210> 9
<211> 3316
<212> DNA
<213> Lycopersicon esculentum

<220>
<221> CDS
<222> (146)..(3112)
<223> coding for NADPH oxidase

<400> 9

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tttattgtca tttgatttgg gacag atg agg ggt tta cct ggg cat gaa cgc   172
                          Met Arg Gly Leu Pro Gly His Glu Arg
                            1               5
cgg tgg acg tcg gat acg gtg tct tcc ggg aag gat tta agt ggt gag   220
Arg Trp Thr Ser Asp Thr Val Ser Ser Gly Lys Asp Leu Ser Gly Glu
 10                  15                  20                  25
tca tcg ccg gga act gat tcc ggg aat att tcc ggt ttt gct tcg gag   268
Ser Ser Pro Gly Thr Asp Ser Gly Asn Ile Ser Gly Phe Ala Ser Glu
                30                  35                  40
gag ttt gtt gaa gtt ata ctt gat ctt cag gat gat gat acg att att   316
Glu Phe Val Glu Val Ile Leu Asp Leu Gln Asp Asp Asp Thr Ile Ile
            45                  50                  55
tta cgg agc gtt gaa ccg gct act gta atc aac att gat ggt tct gat   364
Leu Arg Ser Val Glu Pro Ala Thr Val Ile Asn Ile Asp Gly Ser Asp
        60                  65                  70
cct gct tcc gga gtc ggt att ggt gga gca tcg att gaa act ccg gcg   412
Pro Ala Ser Gly Val Gly Ile Gly Gly Ala Ser Ile Glu Thr Pro Ala
    75                  80                  85
tcg gtg acg tcg acg tcg gaa act cga tcg ccg atg atg cgt cgg agt   460
Ser Val Thr Ser Thr Ser Glu Thr Arg Ser Pro Met Met Arg Arg Ser
 90                  95                  100                 105
aca tct aat aag ttt cgt cag ttt tca cag gag ttg aaa gct gag gct   508
Thr Ser Asn Lys Phe Arg Gln Phe Ser Gln Glu Leu Lys Ala Glu Ala
                110                 115                 120
gtt gcg aaa gcg aag cat ttc tcg caa gag ctt aaa gcg gag cta agg   556
Val Ala Lys Ala Lys His Phe Ser Gln Glu Leu Lys Ala Glu Leu Arg
            125                 130                 135
aga ttc tca tgg agc cat gga cat gcg tct cgt gct ttt tcg ccg gcg   604
Arg Phe Ser Trp Ser His Gly His Ala Ser Arg Ala Phe Ser Pro Ala
        140                 145                 150
```

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tcg ttt ttc caa aac gct gtc gtc gga aca ggc aac ggt gta gac tcg   652
Ser Phe Phe Gln Asn Ala Val Val Gly Thr Gly Asn Gly Val Asp Ser
    155                 160                 165
gct tta gcg gct cga gca tta cgt cgg cag cgt gct cag ctc gac cgg   700
Ala Leu Ala Ala Arg Ala Leu Arg Arg Gln Arg Ala Gln Leu Asp Arg
170                 175                 180                 185
act cgt tcc agc gca cac aag gct ctt cgt gga ctc aaa ttc atc agc   748
Thr Arg Ser Ser Ala His Lys Ala Leu Arg Gly Leu Lys Phe Ile Ser
                190                 195                 200
aat aac aaa act aac gga tgg aat gaa gtt gaa aac aat ttc gct aag   796
Asn Asn Lys Thr Asn Gly Trp Asn Glu Val Glu Asn Asn Phe Ala Lys
            205                 210                 215
ctc gct aaa gac ggt tac ctt tat cgt tcc gat ttc gca caa tgc atc   844
Leu Ala Lys Asp Gly Tyr Leu Tyr Arg Ser Asp Phe Ala Gln Cys Ile
        220                 225                 230
ggt cag tac tca cgc cgg cga tca cta cag ttt aat tat aga tta att   892
Gly Gln Tyr Ser Arg Arg Arg Ser Leu Gln Phe Asn Tyr Arg Leu Ile
    235                 240                 245
aca tta att ttg att aat tat ttg gtt aaa ggt atg aag gat tca aag   940
Thr Leu Ile Leu Ile Asn Tyr Leu Val Lys Gly Met Lys Asp Ser Lys
250                 255                 260                 265
gaa ttt gcg ttg gaa ttg ttt gat gct tta agt aga aga aga aga ttg   988
Glu Phe Ala Leu Glu Leu Phe Asp Ala Leu Ser Arg Arg Arg Arg Leu
                270                 275                 280
aag gtt gat aag att agc caa gag gaa ttg tat gag tat tgg tct caa  1036
Lys Val Asp Lys Ile Ser Gln Glu Glu Leu Tyr Glu Tyr Trp Ser Gln
            285                 290                 295
atc acc gat cag agt ttc gat tct cgg ctt cag atc ttc ttc gac atg  1084
Ile Thr Asp Gln Ser Phe Asp Ser Arg Leu Gln Ile Phe Phe Asp Met
        300                 305                 310
gtg gac aag aat gaa gat ggt cga att ggt gaa gaa gaa gta aaa gag  1132
Val Asp Lys Asn Glu Asp Gly Arg Ile Gly Glu Glu Glu Val Lys Glu
    315                 320                 325
atc atc atg cta agt gcc tct gca aac aaa tta tca aga tta aaa gaa  1180
Ile Ile Met Leu Ser Ala Ser Ala Asn Lys Leu Ser Arg Leu Lys Glu
330                 335                 340                 345
caa gca gag gag tat gca gct ctg atc atg gaa gaa tta gat cct gaa  1228
Gln Ala Glu Glu Tyr Ala Ala Leu Ile Met Glu Glu Leu Asp Pro Glu
                350                 355                 360
aga ctt ggc tac att gag cta tgg cag ctg gaa aca ctt ctc ctc caa  1276
Arg Leu Gly Tyr Ile Glu Leu Trp Gln Leu Glu Thr Leu Leu Leu Gln
            365                 370                 375
aag gac act tac ctc aac tac agt caa gca cta agc tac aca agc caa  1324
Lys Asp Thr Tyr Leu Asn Tyr Ser Gln Ala Leu Ser Tyr Thr Ser Gln
        380                 385                 390
gct ttg agc caa aat ctg caa ggg ttg agg aag aga agc cca ata aga  1372
Ala Leu Ser Gln Asn Leu Gln Gly Leu Arg Lys Arg Ser Pro Ile Arg
    395                 400                 405
aga atg agc aca aaa ctt gtc tat tca ctg caa gag aat tgg aag aga  1420
Arg Met Ser Thr Lys Leu Val Tyr Ser Leu Gln Glu Asn Trp Lys Arg
410                 415                 420                 425
att tgg gtt ctg gtc ttg tgg att ttg ata atg att gga ctt ttt ctt  1468
Ile Trp Val Leu Val Leu Trp Ile Leu Ile Met Ile Gly Leu Phe Leu
                430                 435                 440
tgg aag ttc tat cag tac aaa cag aaa agt gca ttt caa gtc atg ggt  1516
Trp Lys Phe Tyr Gln Tyr Lys Gln Lys Ser Ala Phe Gln Val Met Gly
            445                 450                 455
tat tgc ctt cta aca gct aag ggt gct gct gag act ctc aag ttc aac  1564
Tyr Cys Leu Leu Thr Ala Lys Gly Ala Ala Glu Thr Leu Lys Phe Asn
        460                 465                 470
atg gct tta ata ttg ttg cca gta tgc agg aac acc att aca ttc ctc  1612
Met Ala Leu Ile Leu Leu Pro Val Cys Arg Asn Thr Ile Thr Phe Leu
    475                 480                 485
agg tct act aaa ttg agc tgt ttt gta ccc ttt gat gac aac ata aac  1660
Arg Ser Thr Lys Leu Ser Cys Phe Val Pro Phe Asp Asp Asn Ile Asn
490                 495                 500                 505
ttt cac aag act gtt gct gca gcc att gtc act ggt atc ata ctc cat  1708
Phe His Lys Thr Val Ala Ala Ala Ile Val Thr Gly Ile Ile Leu His
                510                 515                 520
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gcc ggt aat cac ctt gta tgt gat ttc cca aag ctt ata cat gca aat   1756
Ala Gly Asn His Leu Val Cys Asp Phe Pro Lys Leu Ile His Ala Asn
                525                 530                 535
agt acg aat tat cag aaa tat ttg gtg aat gat ttt ggc cca agc cag   1804
Ser Thr Asn Tyr Gln Lys Tyr Leu Val Asn Asp Phe Gly Pro Ser Gln
        540                 545                 550
cct cag tac ata gat ctt gtt aaa gga gtg gag ggt gtg act gga ata   1852
Pro Gln Tyr Ile Asp Leu Val Lys Gly Val Glu Gly Val Thr Gly Ile
    555                 560                 565
gtt atg gta atc ctc atg gcc att gct ttc act ctt gca acg cga tgg   1900
Val Met Val Ile Leu Met Ala Ile Ala Phe Thr Leu Ala Thr Arg Trp
570                 575                 580                 585
ttt agg cgg agc ctc att aag tta ccc aaa cct ttt gat aga ctc act   1948
Phe Arg Arg Ser Leu Ile Lys Leu Pro Lys Pro Phe Asp Arg Leu Thr
                590                 595                 600
ggt ttc aat gcg ttc tgg tac tcg cac cac ctt ctc atc att gtc tac   1996
Gly Phe Asn Ala Phe Trp Tyr Ser His His Leu Leu Ile Ile Val Tyr
                605                 610                 615
atc gta ctg atc atc cat ggc aca ttc ctc tac ctt gtg cat aac tgg   2044
Ile Val Leu Ile Ile His Gly Thr Phe Leu Tyr Leu Val His Asn Trp
        620                 625                 630
tac tcc aaa acg aca tgg atg tat ata gca gtt cct gta ctt ctt tac   2092
Tyr Ser Lys Thr Thr Trp Met Tyr Ile Ala Val Pro Val Leu Leu Tyr
    635                 640                 645
gca ggg gaa aga act ctt aga ttc ttc cga tca ggc tta tac agt gtc   2140
Ala Gly Glu Arg Thr Leu Arg Phe Phe Arg Ser Gly Leu Tyr Ser Val
650                 655                 660                 665
cgg ctt cta aaa gta gca ata tat cct gga aat gtc ctt act ctg caa   2188
Arg Leu Leu Lys Val Ala Ile Tyr Pro Gly Asn Val Leu Thr Leu Gln
                670                 675                 680
atg tct aag cct ccg caa ttt cga tac aag agt gga cag tat atg ttt   2236
Met Ser Lys Pro Pro Gln Phe Arg Tyr Lys Ser Gly Gln Tyr Met Phe
                685                 690                 695
gtc cag tgt cca gct gtt tct cca ttc gag tgg cat cca ttt tcc att   2284
Val Gln Cys Pro Ala Val Ser Pro Phe Glu Trp His Pro Phe Ser Ile
        700                 705                 710
act tca gct cct ggg gat gac tac ttg agc att cat atc cga caa ctt   2332
Thr Ser Ala Pro Gly Asp Asp Tyr Leu Ser Ile His Ile Arg Gln Leu
    715                 720                 725
ggt gac tgg act caa gaa ctc aag cga gtg ttt tcc gag gct tgc gag   2380
Gly Asp Trp Thr Gln Glu Leu Lys Arg Val Phe Ser Glu Ala Cys Glu
730                 735                 740                 745
cag cca gag gct gga aag agt ggc ctg ctc aga gct gac gaa aac acc   2428
Gln Pro Glu Ala Gly Lys Ser Gly Leu Leu Arg Ala Asp Glu Asn Thr
                750                 755                 760
aaa aca agt ttg cca aag cta tta ata gat gga cct tat gga gct cca   2476
Lys Thr Ser Leu Pro Lys Leu Leu Ile Asp Gly Pro Tyr Gly Ala Pro
                765                 770                 775
gca caa gat tac cgg aag tat gat gtc tta ctg ctt gtt ggt ctt ggc   2524
Ala Gln Asp Tyr Arg Lys Tyr Asp Val Leu Leu Leu Val Gly Leu Gly
        780                 785                 790
att gga gca act ccc ttt ata agt atc ctg aaa gac ttg ctc aaa aac   2572
Ile Gly Ala Thr Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Lys Asn
    795                 800                 805
atc gtc gca atg gag gag caa gca gat tta gtc tcg gat ttc agt gga   2620
Ile Val Ala Met Glu Glu Gln Ala Asp Leu Val Ser Asp Phe Ser Gly
810                 815                 820                 825
aac tcg gac atg agt gct gca aca agt gaa caa cca gct ctc aac aag   2668
Asn Ser Asp Met Ser Ala Ala Thr Ser Glu Gln Pro Ala Leu Asn Lys
                830                 835                 840
att tct cca aaa aag aga aag agt act cta aaa acc aca aat gca tat   2716
Ile Ser Pro Lys Lys Arg Lys Ser Thr Leu Lys Thr Thr Asn Ala Tyr
                845                 850                 855
ttt tat tgg gtg acc cgg gag caa gga tca ttt gat tgg ttc aaa ggt   2764
Phe Tyr Trp Val Thr Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly
        860                 865                 870
gtt atg aat gaa gtg gct gaa ctt gat caa agg ggt gtc atc gag atg   2812
Val Met Asn Glu Val Ala Glu Leu Asp Gln Arg Gly Val Ile Glu Met
    875                 880                 885
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cat aac tac ttg acg agt gtt tat gag gaa ggg gat gca cgt tca gct   2860
His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala
890                 895                 900                 905
ctc att acc atg gtc cag gca ctt aac cat gct aag aat ggg gtt gat   2908
Leu Ile Thr Met Val Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp
                910                 915                 920
att gta tca ggc acc agt gtg agg aca cat ttc gcc agg ccg aat tgg   2956
Ile Val Ser Gly Thr Ser Val Arg Thr His Phe Ala Arg Pro Asn Trp
            925                 930                 935
agg aaa gta ttt tcc aag acc tta acc aag cat gca aat gca aga ata   3004
Arg Lys Val Phe Ser Lys Thr Leu Thr Lys His Ala Asn Ala Arg Ile
        940                 945                 950
gga gtt ttc tac tgt ggt gca ccc ata tta gct aaa gaa ctc agc caa   3052
Gly Val Phe Tyr Cys Gly Ala Pro Ile Leu Ala Lys Glu Leu Ser Gln
    955                 960                 965
ctc tgc aaa gag ttt aac caa aag ggc aca aca aag ttc gag ttt cac   3100
Leu Cys Lys Glu Phe Asn Gln Lys Gly Thr Thr Lys Phe Glu Phe His
970                 975                 980                 985
aaa gaa cat ttt tagaagggcc tggagtatga ttaatcttgc atcaacggta       3152
Lys Glu His Phe
cacacatcta tcttcggtac cttatttgat tattctactg aagagataac attagtaagg 3212
aataagtcag agataaattg tacataatag ggaagaagac tatttcaaga gaaaatacat 3272
accaataaga tgtgaaaaaa aaaaaaaaaa aaaaactcgt gccg                  3316
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<210> 10
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<212> PRT
<213> Lycopersicon esculentum

<400> 10

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Ser Ser Gly Lys Asp Leu Ser Gly Glu Ser Ser Pro Gly Thr Asp Ser
             20                  25                  30
Gly Asn Ile Ser Gly Phe Ala Ser Glu Glu Phe Val Glu Val Ile Leu
         35                  40                  45
Asp Leu Gln Asp Asp Asp Thr Ile Ile Leu Arg Ser Val Glu Pro Ala
     50                  55                  60
Thr Val Ile Asn Ile Asp Gly Ser Asp Pro Ala Ser Gly Val Gly Ile
 65                  70                  75                  80
Gly Gly Ala Ser Ile Glu Thr Pro Ala Ser Val Thr Ser Thr Ser Glu
                 85                  90                  95
Thr Arg Ser Pro Met Met Arg Arg Ser Thr Ser Asn Lys Phe Arg Gln
            100                 105                 110
Phe Ser Gln Glu Leu Lys Ala Glu Ala Val Ala Lys Ala Lys His Phe
        115                 120                 125
Ser Gln Glu Leu Lys Ala Glu Leu Arg Arg Phe Ser Trp Ser His Gly
    130                 135                 140
His Ala Ser Arg Ala Phe Ser Pro Ala Ser Phe Phe Gln Asn Ala Val
145                 150                 155                 160
Val Gly Thr Gly Asn Gly Val Asp Ser Ala Leu Ala Ala Arg Ala Leu
                165                 170                 175
Arg Arg Gln Arg Ala Gln Leu Asp Arg Thr Arg Ser Ser Ala His Lys
            180                 185                 190
Ala Leu Arg Gly Leu Lys Phe Ile Ser Asn Asn Lys Thr Asn Gly Trp
        195                 200                 205
Asn Glu Val Glu Asn Asn Phe Ala Lys Leu Ala Lys Asp Gly Tyr Leu
    210                 215                 220
Tyr Arg Ser Asp Phe Ala Gln Cys Ile Gly Gln Tyr Ser Arg Arg Arg
225                 230                 235                 240
Ser Leu Gln Phe Asn Tyr Arg Leu Ile Thr Leu Ile Leu Ile Asn Tyr
                245                 250                 255
Leu Val Lys Gly Met Lys Asp Ser Lys Glu Phe Ala Leu Glu Leu Phe
            260                 265                 270
Asp Ala Leu Ser Arg Arg Arg Arg Leu Lys Val Asp Lys Ile Ser Gln
        275                 280                 285
Glu Glu Leu Tyr Glu Tyr Trp Ser Gln Ile Thr Asp Gln Ser Phe Asp
    290                 295                 300
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Ser Arg Leu Gln Ile Phe Phe Asp Met Val Asp Lys Asn Glu Asp Gly
305 310 315 320
Arg Ile Gly Glu Glu Glu Val Lys Glu Ile Ile Met Leu Ser Ala Ser
325 330 335
Ala Asn Lys Leu Ser Arg Leu Lys Glu Gln Ala Glu Glu Tyr Ala Ala
340 345 350
Leu Ile Met Glu Glu Leu Asp Pro Glu Arg Leu Gly Tyr Ile Glu Leu
355 360 365
Trp Gln Leu Glu Thr Leu Leu Leu Gln Lys Asp Thr Tyr Leu Asn Tyr
370 375 380
Ser Gln Ala Leu Ser Tyr Thr Ser Gln Ala Leu Ser Gln Asn Leu Gln
385 390 395 400
Gly Leu Arg Lys Arg Ser Pro Ile Arg Arg Met Ser Thr Lys Leu Val
405 410 415
Tyr Ser Leu Gln Glu Asn Trp Lys Arg Ile Trp Val Leu Val Leu Trp
420 425 430
Ile Leu Ile Met Ile Gly Leu Phe Leu Trp Lys Phe Tyr Gln Tyr Lys
435 440 445
Gln Lys Ser Ala Phe Gln Val Met Gly Tyr Cys Leu Leu Thr Ala Lys
450 455 460
Gly Ala Ala Glu Thr Leu Lys Phe Asn Met Ala Leu Ile Leu Leu Pro
465 470 475 480
Val Cys Arg Asn Thr Ile Thr Phe Leu Arg Ser Thr Lys Leu Ser Cys
485 490 495
Phe Val Pro Phe Asp Asp Asn Ile Asn Phe His Lys Thr Val Ala Ala
500 505 510
Ala Ile Val Thr Gly Ile Ile Leu His Ala Gly Asn His Leu Val Cys
515 520 525
Asp Phe Pro Lys Leu Ile His Ala Asn Ser Thr Asn Tyr Gln Lys Tyr
530 535 540
Leu Val Asn Asp Phe Gly Pro Ser Gln Pro Gln Tyr Ile Asp Leu Val
545 550 555 560
Lys Gly Val Glu Gly Val Thr Gly Ile Val Met Val Ile Leu Met Ala
565 570 575
Ile Ala Phe Thr Leu Ala Thr Arg Trp Phe Arg Arg Ser Leu Ile Lys
580 585 590
Leu Pro Lys Pro Phe Asp Arg Leu Thr Gly Phe Asn Ala Phe Trp Tyr
595 600 605
Ser His His Leu Leu Ile Ile Val Tyr Ile Val Leu Ile Ile His Gly
610 615 620
Thr Phe Leu Tyr Leu Val His Asn Trp Tyr Ser Lys Thr Thr Trp Met
625 630 635 640
Tyr Ile Ala Val Pro Val Leu Leu Tyr Ala Gly Glu Arg Thr Leu Arg
645 650 655
Phe Phe Arg Ser Gly Leu Tyr Ser Val Arg Leu Leu Lys Val Ala Ile
660 665 670
Tyr Pro Gly Asn Val Leu Thr Leu Gln Met Ser Lys Pro Pro Gln Phe
675 680 685
Arg Tyr Lys Ser Gly Gln Tyr Met Phe Val Gln Cys Pro Ala Val Ser
690 695 700
Pro Phe Glu Trp His Pro Phe Ser Ile Thr Ser Ala Pro Gly Asp Asp
705 710 715 720
Tyr Leu Ser Ile His Ile Arg Gln Leu Gly Asp Trp Thr Gln Glu Leu
725 730 735
Lys Arg Val Phe Ser Glu Ala Cys Glu Gln Pro Glu Ala Gly Lys Ser
740 745 750
Gly Leu Leu Arg Ala Asp Glu Asn Thr Lys Thr Ser Leu Pro Lys Leu
755 760 765
Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln Asp Tyr Arg Lys Tyr
770 775 780
Asp Val Leu Leu Leu Val Gly Leu Gly Ile Gly Ala Thr Pro Phe Ile
785 790 795 800
Ser Ile Leu Lys Asp Leu Leu Lys Asn Ile Val Ala Met Glu Glu Gln
805 810 815
Ala Asp Leu Val Ser Asp Phe Ser Gly Asn Ser Asp Met Ser Ala Ala
820 825 830
Thr Ser Glu Gln Pro Ala Leu Asn Lys Ile Ser Pro Lys Lys Arg Lys
835 840 845
Ser Thr Leu Lys Thr Thr Asn Ala Tyr Phe Tyr Trp Val Thr Arg Glu

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    850                 855                 860
Gln Gly Ser Phe Asp Trp Phe Lys Gly Val Met Asn Glu Val Ala Glu
865                 870                 875                 880
Leu Asp Gln Arg Gly Val Ile Glu Met His Asn Tyr Leu Thr Ser Val
                885                 890                 895
Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Val Gln Ala
            900                 905                 910
Leu Asn His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr Ser Val
        915                 920                 925
Arg Thr His Phe Ala Arg Pro Asn Trp Arg Lys Val Phe Ser Lys Thr
    930                 935                 940
Leu Thr Lys His Ala Asn Ala Arg Ile Gly Val Phe Tyr Cys Gly Ala
945                 950                 955                 960
Pro Ile Leu Ala Lys Glu Leu Ser Gln Leu Cys Lys Glu Phe Asn Gln
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Lys Gly Thr Thr Lys Phe Glu Phe His Lys Glu His Phe
            980                 985
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<220>
<221> CDS
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<223> coding for NADPH oxidase

<400> 11

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               Met Lys Pro Phe Ser Lys Asn Asp Arg Arg Arg Trp
                 1               5                  10
tca ttt gat tca gtt tcc gcc gga aaa acc gcc gtc gga agt gca tca   98
Ser Phe Asp Ser Val Ser Ala Gly Lys Thr Ala Val Gly Ser Ala Ser
            15                  20                  25
act tca ccg gga act gaa tac tcc att aac ggt gat caa gag ttc gtt   146
Thr Ser Pro Gly Thr Glu Tyr Ser Ile Asn Gly Asp Gln Glu Phe Val
        30                  35                  40
gaa gtc aca atc gat ctt caa gac gat gac aca atc gtt ctt cgt agc   194
Glu Val Thr Ile Asp Leu Gln Asp Asp Asp Thr Ile Val Leu Arg Ser
    45                  50                  55                  60
gtc gag cca gca acc gcc att aat gtc atc gga gat atc tcc gac gac   242
Val Glu Pro Ala Thr Ala Ile Asn Val Ile Gly Asp Ile Ser Asp Asp
                65                  70                  75
aac acc gga ata atg act ccg gtt tcg att tcg aga tct ccg acg atg   290
Asn Thr Gly Ile Met Thr Pro Val Ser Ile Ser Arg Ser Pro Thr Met
            80                  85                  90
aaa cga act tca tct aat cgg ttc cga caa ttc tca caa gag ctt aaa   338
Lys Arg Thr Ser Ser Asn Arg Phe Arg Gln Phe Ser Gln Glu Leu Lys
        95                  100                 105
gcc gaa gct gtg gcg aaa gcg aaa cag tta tct cag gag ttg aaa cga   386
Ala Glu Ala Val Ala Lys Ala Lys Gln Leu Ser Gln Glu Leu Lys Arg
    110                 115                 120
ttc tca tgg tct cgt tct ttc tca ggt aac tta acc act act agt acc   434
Phe Ser Trp Ser Arg Ser Phe Ser Gly Asn Leu Thr Thr Thr Ser Thr
125                 130                 135                 140
gcc gct aat caa agc ggc ggt gct ggt ggt ggt ttg gtg aac tcg gct   482
Ala Ala Asn Gln Ser Gly Gly Ala Gly Gly Gly Leu Val Asn Ser Ala
                145                 150                 155
tta gaa gcg cga gcg ttg cga aag caa cgt gct cag tta gat cgg act   530
Leu Glu Ala Arg Ala Leu Arg Lys Gln Arg Ala Gln Leu Asp Arg Thr
            160                 165                 170
cgg tct agt gct caa aga gct ctt cgt ggt ttg aga ttc att agc aat   578
Arg Ser Ser Ala Gln Arg Ala Leu Arg Gly Leu Arg Phe Ile Ser Asn
        175                 180                 185
aag caa aag aac gtt gat ggt tgg aac gat gtt caa tca aat ttc gaa   626
Lys Gln Lys Asn Val Asp Gly Trp Asn Asp Val Gln Ser Asn Phe Glu
    190                 195                 200
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aaa ttc gaa aaa aat ggt tac atc tat cgc tcc gat ttc gct caa tgc   674
Lys Phe Glu Lys Asn Gly Tyr Ile Tyr Arg Ser Asp Phe Ala Gln Cys
205                 210                 215                 220
ata gga atg aaa gat tcg aaa gaa ttt gca ttg gaa ctg ttc gat gca   722
Ile Gly Met Lys Asp Ser Lys Glu Phe Ala Leu Glu Leu Phe Asp Ala
                225                 230                 235
ttg agt aga aga aga aga tta aaa gta gag aaa atc aat cac gat gag   770
Leu Ser Arg Arg Arg Arg Leu Lys Val Glu Lys Ile Asn His Asp Glu
            240                 245                 250
ctt tat gag tat tgg tca caa atc aac gac gag agt ttt gat tct cgt   818
Leu Tyr Glu Tyr Trp Ser Gln Ile Asn Asp Glu Ser Phe Asp Ser Arg
        255                 260                 265
ctc cag atc ttc ttc gac ata gtg gac aag aat gaa gat ggg aga att   866
Leu Gln Ile Phe Phe Asp Ile Val Asp Lys Asn Glu Asp Gly Arg Ile
    270                 275                 280
aca gaa gag gaa gta aaa gag ata ata atg ttg agt gca tct gca aat   914
Thr Glu Glu Glu Val Lys Glu Ile Ile Met Leu Ser Ala Ser Ala Asn
285                 290                 295                 300
aag cta tca aga tta aag gaa caa gca gag gaa tat gca gct ttg att   962
Lys Leu Ser Arg Leu Lys Glu Gln Ala Glu Glu Tyr Ala Ala Leu Ile
                305                 310                 315
atg gaa gag tta gat cct gaa aga ctt ggc tac ata gag cta tgg caa  1010
Met Glu Glu Leu Asp Pro Glu Arg Leu Gly Tyr Ile Glu Leu Trp Gln
            320                 325                 330
cta gag act ttg ctt cta caa aaa gac aca tac ctc aat tac agt caa  1058
Leu Glu Thr Leu Leu Leu Gln Lys Asp Thr Tyr Leu Asn Tyr Ser Gln
        335                 340                 345
gca ttg agc tat acg agc caa gca ttg agc caa aac ctt caa ggg tta  1106
Ala Leu Ser Tyr Thr Ser Gln Ala Leu Ser Gln Asn Leu Gln Gly Leu
    350                 355                 360
agg gga aag agt cga ata cat aga atg agt tcg gat ttc gtc tac att  1154
Arg Gly Lys Ser Arg Ile His Arg Met Ser Ser Asp Phe Val Tyr Ile
365                 370                 375                 380
atg caa gag aat tgg aaa agg ata tgg gtt tta tcc tta tgg atc atg  1202
Met Gln Glu Asn Trp Lys Arg Ile Trp Val Leu Ser Leu Trp Ile Met
                385                 390                 395
atc atg atc gga tta ttc ttg tgg aaa ttc ttc caa tac aag caa aaa  1250
Ile Met Ile Gly Leu Phe Leu Trp Lys Phe Phe Gln Tyr Lys Gln Lys
            400                 405                 410
gat gca ttt cat gtg atg gga tat tgt tta ctc aca gcc aaa gga gca  1298
Asp Ala Phe His Val Met Gly Tyr Cys Leu Leu Thr Ala Lys Gly Ala
        415                 420                 425
gct gaa aca ctt aaa ttc aac atg gct cta ata ctt ttc cca gtt tgc  1346
Ala Glu Thr Leu Lys Phe Asn Met Ala Leu Ile Leu Phe Pro Val Cys
    430                 435                 440
aga aac acc att act tgg ctt aga tcc aca aga ctc tct tac ttc gtt  1394
Arg Asn Thr Ile Thr Trp Leu Arg Ser Thr Arg Leu Ser Tyr Phe Val
445                 450                 455                 460
cct ttt gat gat aat atc aac ttc cac aag aca att gct gga gcc att  1442
Pro Phe Asp Asp Asn Ile Asn Phe His Lys Thr Ile Ala Gly Ala Ile
                465                 470                 475
gta gta gct gtg atc ctt cat att gga gac cat ctt gct tgt gat ttc  1490
Val Val Ala Val Ile Leu His Ile Gly Asp His Leu Ala Cys Asp Phe
            480                 485                 490
cct aga att gtt aga gcc acc gaa tac gat tac aat cgg tat ctg ttt  1538
Pro Arg Ile Val Arg Ala Thr Glu Tyr Asp Tyr Asn Arg Tyr Leu Phe
        495                 500                 505
cat tac ttt caa aca aaa cag cca aca tac ttc gac ctc gtt aag gga  1586
His Tyr Phe Gln Thr Lys Gln Pro Thr Tyr Phe Asp Leu Val Lys Gly
    510                 515                 520
cct gaa gga atc act ggg att tta atg gtc att ttg atg att att tca  1634
Pro Glu Gly Ile Thr Gly Ile Leu Met Val Ile Leu Met Ile Ile Ser
525                 530                 535                 540
ttc aca tta gca aca aga tgg ttt agg cgt aac cta gtc aag ctt cct  1682
Phe Thr Leu Ala Thr Arg Trp Phe Arg Arg Asn Leu Val Lys Leu Pro
                545                 550                 555
aag cca ttt gat cga cta acc ggt ttt aac gcc ttt tgg tat tcg cat  1730
Lys Pro Phe Asp Arg Leu Thr Gly Phe Asn Ala Phe Trp Tyr Ser His
            560                 565                 570
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cat ttg ttc gtc att gtt tat atc ttg ctt att ctt cat ggt atc ttc   1778
His Leu Phe Val Ile Val Tyr Ile Leu Leu Ile Leu His Gly Ile Phe
        575                 580                 585
ctc tat ttc gcc aag cct tgg tat gtt cgt acg aca tgg atg tat ctt   1826
Leu Tyr Phe Ala Lys Pro Trp Tyr Val Arg Thr Thr Trp Met Tyr Leu
    590                 595                 600
gca gta cca gtt tta ctc tat ggt gga gaa aga aca ctt agg tac ttc   1874
Ala Val Pro Val Leu Leu Tyr Gly Gly Glu Arg Thr Leu Arg Tyr Phe
605                 610                 615                 620
cgt tct ggt tct tat tcg gtt cga ctg ctt aag gtt gct ata tat cct   1922
Arg Ser Gly Ser Tyr Ser Val Arg Leu Leu Lys Val Ala Ile Tyr Pro
                625                 630                 635
ggt aat gtt cta acg cta caa atg tcg aaa cca act caa ttt cgt tac   1970
Gly Asn Val Leu Thr Leu Gln Met Ser Lys Pro Thr Gln Phe Arg Tyr
            640                 645                 650
aaa agc gga caa tac atg ttt gtc caa tgt cct gcg gtt tcg cca ttc   2018
Lys Ser Gly Gln Tyr Met Phe Val Gln Cys Pro Ala Val Ser Pro Phe
        655                 660                 665
gag tgg cat cca ttc tca att act tcc gca cct gaa gat gat tat atc   2066
Glu Trp His Pro Phe Ser Ile Thr Ser Ala Pro Glu Asp Asp Tyr Ile
    670                 675                 680
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Ser Ile His Ile Arg Gln Leu Gly Asp Trp Thr Gln Glu Leu Lys Arg
685                 690                 695                 700
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Val Phe Ser Glu Val Cys Glu Pro Pro Val Gly Gly Lys Ser Gly Leu
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ctc aga gcc gac gaa aca aca aag aaa agt ttg cca aag cta ttg ata   2210
Leu Arg Ala Asp Glu Thr Thr Lys Lys Ser Leu Pro Lys Leu Leu Ile
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gat gga ccg tac ggt gca cca gca caa gat tat agg aaa tat gat gtt   2258
Asp Gly Pro Tyr Gly Ala Pro Ala Gln Asp Tyr Arg Lys Tyr Asp Val
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ctc tta tta gtt ggt ctt ggc att ggt gca act cca ttt atc agt atc   2306
Leu Leu Leu Val Gly Leu Gly Ile Gly Ala Thr Pro Phe Ile Ser Ile
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765                 770                 775                 780
tcg atc tcg gat ttc agt aga tca tca gaa tac agc aca gga agc aac   2402
Ser Ile Ser Asp Phe Ser Arg Ser Ser Glu Tyr Ser Thr Gly Ser Asn
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ggt gac acg cca aga cga aag aga ata cta aaa acc aca aat gct tat   2450
Gly Asp Thr Pro Arg Arg Lys Arg Ile Leu Lys Thr Thr Asn Ala Tyr
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Phe Tyr Trp Val Thr Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly
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gtc atg aac gaa gtt gca gaa ctt gac caa cgg ggt gtg ata gag atg   2546
Val Met Asn Glu Val Ala Glu Leu Asp Gln Arg Gly Val Ile Glu Met
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ctc att aca atg gtt caa gct ctt aat cat gcc aaa aat ggt gtc gac   2642
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Ile Val Ser Gly Thr Arg Val Arg Thr His Phe Ala Arg Pro Asn Trp
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Lys Lys Val Leu Thr Lys Leu Ser Ser Lys His Cys Asn Ala Arg Thr
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gga gtg ttt tat tgc gga gta ccg gtt tta ggg aag gag ctt agc aaa   2786
Gly Val Phe Tyr Cys Gly Val Pro Val Leu Gly Lys Glu Leu Ser Lys
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cta tgc aac aca ttc aat caa aaa ggt tca acc aag ttt gaa ttt cac   2834
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Thr Ala Ile Asn Val Ile Gly Asp Ile Ser Asp Asp Asn Thr Gly Ile
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Ser Gly Gly Ala Gly Gly Gly Leu Val Asn Ser Ala Leu Glu Ala Arg
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Gln Arg Ala Leu Arg Gly Leu Arg Phe Ile Ser Asn Lys Gln Lys Asn
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Val Asp Gly Trp Asn Asp Val Gln Ser Asn Phe Glu Lys Phe Glu Lys
195 200 205
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Asp Ser Lys Glu Phe Ala Leu Glu Leu Phe Asp Ala Leu Ser Arg Arg
225 230 235 240
Arg Arg Leu Lys Val Glu Lys Ile Asn His Asp Glu Leu Tyr Glu Tyr
245 250 255
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Phe Asp Ile Val Asp Lys Asn Glu Asp Gly Arg Ile Thr Glu Glu Glu
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325 330 335
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340 345 350
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Arg Ile His Arg Met Ser Ser Asp Phe Val Tyr Ile Met Gln Glu Asn
370 375 380
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Glu Thr Thr Lys Lys Ser Leu Pro Lys Leu Leu Ile Asp Gly Pro Tyr
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Gly Ala Pro Ala Gln Asp Tyr Arg Lys Tyr Asp Val Leu Leu Leu Val
            740                 745                 750
Gly Leu Gly Ile Gly Ala Thr Pro Phe Ile Ser Ile Leu Lys Asp Leu
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785                 790                 795                 800
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Val Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val Ser Gly
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Thr Lys Leu Ser Ser Lys His Cys Asn Ala Arg Thr Gly Val Phe Tyr
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Cys Gly Val Pro Val Leu Gly Lys Glu Leu Ser Lys Leu Cys Asn Thr
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tctcgaattc g atg aaa atg aga cga ggc aat tca agt aac gac cat gaa 170
Met Lys Met Arg Arg Gly Asn Ser Ser Asn Asp His Glu
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ctt ggg att cta cga gga gct aac tcg gac acc aac tcg gac acg gag 218
Leu Gly Ile Leu Arg Gly Ala Asn Ser Asp Thr Asn Ser Asp Thr Glu
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agc atc gct agc gac cgt ggt gcc ttt agc ggt ccg ctt ggc cgg cct 266
Ser Ile Ala Ser Asp Arg Gly Ala Phe Ser Gly Pro Leu Gly Arg Pro
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aaa cgt gcg tcc aag aaa aac gca aga ttc gcc gac gat ctt ccc aag 314
Lys Arg Ala Ser Lys Lys Asn Ala Arg Phe Ala Asp Asp Leu Pro Lys
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Arg Ser Asn Ser Val Ala Gly Gly Arg Gly Asp Asp Asp Glu Tyr Val
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Glu Ile Thr Leu Asp Ile Arg Asp Asp Ser Val Ala Val His Ser Val
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Gln Gln Ala Ala Gly Gly Gly Gly His Leu Glu Asp Pro Glu Leu Ala
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gag ctc cgc cgc gtg ttc tct aga cgt ccc tcc ccg gcc gtg cgg cgg 602
Glu Leu Arg Arg Val Phe Ser Arg Arg Pro Ser Pro Ala Val Arg Arg
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225 230 235
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Asp Gly Arg Val Thr Glu Glu Glu Val Ala Glu Ile Ile Ser Leu Ser
270 275 280 285
gct tct gca aac aag ctc tca aat att caa aag caa gcc aaa gaa tat 1034
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Val Arg Met Gly Asp Ser Arg Ile Leu Ser Gln Met Leu Ser Gln Lys
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ctt aga ccg gca aaa gag agc aac cct tta ttg aga tgg tcg gag aaa   1226
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Tyr Lys Asn Lys Ala Ala Tyr Gly Val Met Gly Tyr Cys Val Cys Val
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gcc aaa gga ggc gcc gag act ctc aaa ttc aac atg gct ctc ata ttg   1418
Ala Lys Gly Gly Ala Glu Thr Leu Lys Phe Asn Met Ala Leu Ile Leu
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Ser Val Ala Gly Gly Arg Gly Asp Asp Asp Glu Tyr Val Glu Ile Thr
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Phe Arg Ser Ser Ile Lys Pro Val Lys Met Ile Lys Val Ala Val Tyr
610 615 620
Pro Gly Asn Val Leu Ser Leu His Met Thr Lys Pro Gln Gly Phe Lys
625 630 635 640
Tyr Lys Ser Gly Gln Phe Met Leu Val Asn Cys Arg Ala Val Ser Pro
645 650 655

Phe Glu Trp His Pro Phe Ser Ile Thr Ser Ala Pro Gly Asp Asp Tyr
660 665 670
Leu Ser Val His Ile Arg Thr Leu Gly Asp Trp Thr Arg Lys Leu Arg
675 680 685
Thr Val Phe Ser Glu Val Cys Lys Pro Pro Thr Ala Gly Lys Ser Gly
690 695 700
Leu Leu Arg Ala Asp Gly Gly Asp Gly Asn Leu Pro Phe Pro Lys Val
705 710 715 720
Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln Asp Tyr Lys Lys Tyr
725 730 735
Asp Val Val Leu Leu Val Gly Leu Gly Ile Gly Ala Thr Pro Met Ile
740 745 750
Ser Ile Leu Lys Asp Ile Ile Asn Asn Met Lys Gly Pro Asp Arg Asp
755 760 765
Ser Asp Ile Glu Asn Asn Asn Ser Asn Asn Asn Ser Lys Gly Phe Lys
770 775 780
Thr Arg Lys Ala Tyr Phe Tyr Trp Val Thr Arg Glu Gln Gly Ser Phe
785 790 795 800
Glu Trp Phe Lys Gly Ile Met Asp Glu Ile Ser Glu Leu Asp Glu Glu
805 810 815
Gly Ile Ile Glu Leu His Asn Tyr Cys Thr Ser Val Tyr Glu Glu Gly
820 825 830
Asp Ala Arg Val Ala Leu Ile Ala Met Leu Gln Ser Leu Gln His Ala
835 840 845
Lys Asn Gly Val Asp Val Val Ser Gly Thr Arg Val Lys Ser His Phe
850 855 860
Ala Lys Pro Asn Trp Arg Gln Val Tyr Lys Lys Ile Ala Val Gln His
865 870 875 880
Pro Gly Lys Arg Ile Gly Val Phe Tyr Cys Gly Met Pro Gly Met Ile
885 890 895
Lys Glu Leu Lys Asn Leu Ala Leu Asp Phe Ser Arg Lys Thr Thr Thr
900 905 910
Lys Phe Asp Phe His Lys Glu Asn Phe
915 920

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<223> coding for NADPH oxidase

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ataccaatta ttaatctttt gtcatctttt tccttctcgc gttcatatat actggaatat 180
acatcttttt ttcaacctat cttctttcat tttcaagaat tcgggttcca taaatagtag 240
gttcactact tttatttcaa cctccttaaa gtttattcat tcatattttt tctcaaagaa 300
aaaactatag aa atg caa aat tcg gaa aat cat cat ccg cac cac cag cac 351
Met Gln Asn Ser Glu Asn His His Pro His His Gln His
1 5 10
cac cat tcg gac aca gag ata att gga aat gat aga gcg tcg tac agt 399
His His Ser Asp Thr Glu Ile Ile Gly Asn Asp Arg Ala Ser Tyr Ser
15 20 25
ggt ccg tta agc gga ccg tta aac aaa cga ggc ggc aaa aag agt gcg 447
Gly Pro Leu Ser Gly Pro Leu Asn Lys Arg Gly Gly Lys Lys Ser Ala
30 35 40 45
aga ttt aac att cct gaa tct acc gac atc gga acc agt gtc gga acc 495
Arg Phe Asn Ile Pro Glu Ser Thr Asp Ile Gly Thr Ser Val Gly Thr
50 55 60
ggc ggc aag tcc aat gat gat gcg tac gtt gaa atc act ctc gat gtc 543
Gly Gly Lys Ser Asn Asp Asp Ala Tyr Val Glu Ile Thr Leu Asp Val
65 70 75
cgc gaa gat tcc gtc gct gtc cac agt gtc aaa act gcc ggc ggt gat 591
Arg Glu Asp Ser Val Ala Val His Ser Val Lys Thr Ala Gly Gly Asp

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          80                  85                  90
gac gtg gaa gat ccc gag ctg gct tta ttg gct aaa ggc tta gag aag   639
Asp Val Glu Asp Pro Glu Leu Ala Leu Leu Ala Lys Gly Leu Glu Lys
     95                 100                 105
aag tcc act tta gga tct tca ctt gtt cga aat gct tcg tct aga att   687
Lys Ser Thr Leu Gly Ser Ser Leu Val Arg Asn Ala Ser Ser Arg Ile
110                 115                 120                 125
cgg caa gtg tca caa gag ctc agg cgt ttg gct tcc tta aat aaa cgc   735
Arg Gln Val Ser Gln Glu Leu Arg Arg Leu Ala Ser Leu Asn Lys Arg
                130                 135                 140
cca att cct act gga agg ttc gac agg aat aaa tca gct gct gct cat   783
Pro Ile Pro Thr Gly Arg Phe Asp Arg Asn Lys Ser Ala Ala Ala His
            145                 150                 155
gct ctt aaa ggt ctc aag ttt att agt aag acc gac ggc ggc gct ggt   831
Ala Leu Lys Gly Leu Lys Phe Ile Ser Lys Thr Asp Gly Gly Ala Gly
        160                 165                 170
tgg gcc gcc gtc gag aag cgg ttc gat gag att act gct tct act act   879
Trp Ala Ala Val Glu Lys Arg Phe Asp Glu Ile Thr Ala Ser Thr Thr
    175                 180                 185
ggt ttg ctt cct cgt gcc aaa ttt gga gaa tgt ata ggt atg aat aag   927
Gly Leu Leu Pro Arg Ala Lys Phe Gly Glu Cys Ile Gly Met Asn Lys
190                 195                 200                 205
gag tct aag gaa ttt gct gtt gag cta tat gat gcg cta gct cgg agg   975
Glu Ser Lys Glu Phe Ala Val Glu Leu Tyr Asp Ala Leu Ala Arg Arg
                210                 215                 220
aga aac att aca act gat tcc att aac aaa gca cag ctc aaa gag ttc  1023
Arg Asn Ile Thr Thr Asp Ser Ile Asn Lys Ala Gln Leu Lys Glu Phe
            225                 230                 235
tgg gac caa gtg gct gac caa agt ttt gat tct cgc ctt caa aca ttt  1071
Trp Asp Gln Val Ala Asp Gln Ser Phe Asp Ser Arg Leu Gln Thr Phe
        240                 245                 250
ttt gac atg gtt gat aaa gat gct gat ggt aga att aca gaa gaa gaa  1119
Phe Asp Met Val Asp Lys Asp Ala Asp Gly Arg Ile Thr Glu Glu Glu
    255                 260                 265
gtc aga gag att ata ggc ctt agc gcg tcg gcc aac agg ctg tca aca  1167
Val Arg Glu Ile Ile Gly Leu Ser Ala Ser Ala Asn Arg Leu Ser Thr
270                 275                 280                 285
atc cag aaa caa gct gat gaa tac gca gca atg atc atg gaa gag ttg  1215
Ile Gln Lys Gln Ala Asp Glu Tyr Ala Ala Met Ile Met Glu Glu Leu
                290                 295                 300
gat cct aac aac ctc gga tac att atg att gag aac ttg gaa atg ctt  1263
Asp Pro Asn Asn Leu Gly Tyr Ile Met Ile Glu Asn Leu Glu Met Leu
            305                 310                 315
tta ctg caa gca cca aat caa tca gtg caa aga gga ggc gaa agt cgg  1311
Leu Leu Gln Ala Pro Asn Gln Ser Val Gln Arg Gly Gly Glu Ser Arg
        320                 325                 330
aac ttg agt caa atg cta agt caa aaa cta aag cat aca caa gag aga  1359
Asn Leu Ser Gln Met Leu Ser Gln Lys Leu Lys His Thr Gln Glu Arg
    335                 340                 345
aat cca ata gta aga tgg tac aag agt ttc atg tac ttt ttg ctg gat  1407
Asn Pro Ile Val Arg Trp Tyr Lys Ser Phe Met Tyr Phe Leu Leu Asp
350                 355                 360                 365
aat tgg caa aga gtt tgg gta ttg tta ctg tgg att gga att atg gct  1455
Asn Trp Gln Arg Val Trp Val Leu Leu Leu Trp Ile Gly Ile Met Ala
                370                 375                 380
ggt cta ttt aca tgg aaa tat ata cag tat aaa gaa aaa gct gca tat  1503
Gly Leu Phe Thr Trp Lys Tyr Ile Gln Tyr Lys Glu Lys Ala Ala Tyr
            385                 390                 395
aaa gtc atg ggt ccc tgt gtg tgt ttt gcc aaa ggt gct gct gaa aca  1551
Lys Val Met Gly Pro Cys Val Cys Phe Ala Lys Gly Ala Ala Glu Thr
        400                 405                 410
ctc aag ctc aac atg gca att att tta ttt ccg gtt tgc aga aac acg  1599
Leu Lys Leu Asn Met Ala Ile Ile Leu Phe Pro Val Cys Arg Asn Thr
    415                 420                 425
atc aca tgg ctt cga aat aag acc aga tta ggt gct gct gtt cct ttt  1647
Ile Thr Trp Leu Arg Asn Lys Thr Arg Leu Gly Ala Ala Val Pro Phe
430                 435                 440                 445
gat gat aac ctt aat ttt cac aaa gtg ata gca gtg gca att gct ctt  1695
Asp Asp Asn Leu Asn Phe His Lys Val Ile Ala Val Ala Ile Ala Leu
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                    450                 455                 460
ggg gtt gga ata cac gga cta tct cac ttg aca tgt gat ttt cct cgg   1743
Gly Val Gly Ile His Gly Leu Ser His Leu Thr Cys Asp Phe Pro Arg
                465                 470                 475
ctt tta aat gct agt gaa gaa gaa tat gaa cca atg aag tac tat ttt   1791
Leu Leu Asn Ala Ser Glu Glu Glu Tyr Glu Pro Met Lys Tyr Tyr Phe
            480                 485                 490
gga gat cag cca gaa agc tat tgg tgg ttt ata aaa gga gta gaa ggg   1839
Gly Asp Gln Pro Glu Ser Tyr Trp Trp Phe Ile Lys Gly Val Glu Gly
        495                 500                 505
gta act gga att ata atg gtg gtt tta atg gca ata gca ttt act cta   1887
Val Thr Gly Ile Ile Met Val Val Leu Met Ala Ile Ala Phe Thr Leu
510                 515                 520                 525
gca acc cca tgg ttt aga agg aat aga gtt agt ttg cca aaa cca ttt   1935
Ala Thr Pro Trp Phe Arg Arg Asn Arg Val Ser Leu Pro Lys Pro Phe
                530                 535                 540
cac aaa ctc act gga tnt aat gcc ttt tgg tac tct cac cat ctc ttt   1983
His Lys Leu Thr Gly Xaa Asn Ala Phe Trp Tyr Ser His His Leu Phe
            545                 550                 555
gtt atc gtc tac act ctg ttc att gtg cat ggt gaa aag cta tac att   2031
Val Ile Val Tyr Thr Leu Phe Ile Val His Gly Glu Lys Leu Tyr Ile
        560                 565                 570
acc aaa gat tgg tac aag aga acc gac atg gat gta ctt tta act atc   2079
Thr Lys Asp Trp Tyr Lys Arg Thr Asp Met Asp Val Leu Leu Thr Ile
    575                 580                 585
cca atc ata ctc tat gct agt gaa agg ttg att agg gca ttc agg tca   2127
Pro Ile Ile Leu Tyr Ala Ser Glu Arg Leu Ile Arg Ala Phe Arg Ser
590                 595                 600                 605
agc att aaa gct gtt aag att ttg aag gtg gca gta tat cca gga aat   2175
Ser Ile Lys Ala Val Lys Ile Leu Lys Val Ala Val Tyr Pro Gly Asn
                610                 615                 620
gtg ttg gca ctt cac atg tca aaa cca cag ggc tac aaa tac aaa agt   2223
Val Leu Ala Leu His Met Ser Lys Pro Gln Gly Tyr Lys Tyr Lys Ser
            625                 630                 635
ggg caa tac atg ttt gtc aac tgt gct gca gtt tct cca ttt gag tgg   2271
Gly Gln Tyr Met Phe Val Asn Cys Ala Ala Val Ser Pro Phe Glu Trp
        640                 645                 650
cat cca ttt tca att act tcg gcc cca gga gat gac tat ctc agt gtc   2319
His Pro Phe Ser Ile Thr Ser Ala Pro Gly Asp Asp Tyr Leu Ser Val
    655                 660                 665
cat att cga act ctt ggt gat tgg acc agg caa ctt aaa act gtt ttc   2367
His Ile Arg Thr Leu Gly Asp Trp Thr Arg Gln Leu Lys Thr Val Phe
670                 675                 680                 685
tcc gag gtt tgc cag cca cca cct aat gga aaa agt gga ctc ctc aga   2415
Ser Glu Val Cys Gln Pro Pro Pro Asn Gly Lys Ser Gly Leu Leu Arg
                690                 695                 700
gct gac tac ttg caa gga gag aat aat cct aat ttc cca agg gtg tta   2463
Ala Asp Tyr Leu Gln Gly Glu Asn Asn Pro Asn Phe Pro Arg Val Leu
            705                 710                 715
ata gat gga cca tat gga gca cca gca caa gac tac aag aaa tat gag   2511
Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln Asp Tyr Lys Lys Tyr Glu
        720                 725                 730
gtg gtt ttg ttg gta ggt ctt gga att gga gct aca cca atg atc agt   2559
Val Val Leu Leu Val Gly Leu Gly Ile Gly Ala Thr Pro Met Ile Ser
    735                 740                 745
att gtt aaa gac att gtc aac aac atg aag gca atg gac gaa gaa gaa   2607
Ile Val Lys Asp Ile Val Asn Asn Met Lys Ala Met Asp Glu Glu Glu
750                 755                 760                 765
aat tcc ttg gaa gat gga cac aat aat aat atg gca cca aat tct agc   2655
Asn Ser Leu Glu Asp Gly His Asn Asn Asn Met Ala Pro Asn Ser Ser
                770                 775                 780
ccc aat att gca aaa aat aag ggt aat aaa tca ggt tca gca agt gga   2703
Pro Asn Ile Ala Lys Asn Lys Gly Asn Lys Ser Gly Ser Ala Ser Gly
            785                 790                 795
gga aat aat ttc aat aca agg aga gca tat ttc tat tgg gtt act aga   2751
Gly Asn Asn Phe Asn Thr Arg Arg Ala Tyr Phe Tyr Trp Val Thr Arg
        800                 805                 810
gaa caa ggt tca ttt gat tgg ttc aaa ggt ata atg aat gaa gct gct   2799
Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly Ile Met Asn Glu Ala Ala
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    815                 820                 825
gaa atg gac cat aag gga gta att gaa atg cat aat tat tgt act agt   2847
Glu Met Asp His Lys Gly Val Ile Glu Met His Asn Tyr Cys Thr Ser
830                 835                 840                 845
gtt tat gaa gaa ggt gat gct cgt tct gct ctt att act atg ctt cag   2895
Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu Gln
                850                 855                 860
tct ctt cac cat gcc aaa aat ggt gtt gac att gtc tct ggc acc aga   2943
Ser Leu His His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr Arg
            865                 870                 875
gtt aag tca cat ttt gct aaa cct aat tgg cgt aat gtc tac aaa cgc   2991
Val Lys Ser His Phe Ala Lys Pro Asn Trp Arg Asn Val Tyr Lys Arg
        880                 885                 890
att gct ctc aac cac cct gag gct aaa gtt ggg gtc ttc tat tgt ggg   3039
Ile Ala Leu Asn His Pro Glu Ala Lys Val Gly Val Phe Tyr Cys Gly
    895                 900                 905
gca cca gca ctg acc aaa gaa cta aga caa cac gcc ttg gat ttt tca   3087
Ala Pro Ala Leu Thr Lys Glu Leu Arg Gln His Ala Leu Asp Phe Ser
910                 915                 920                 925
cac aag aca tct acc aag ttt gat ttc cat aaa gaa aat ttt           3129
His Lys Thr Ser Thr Lys Phe Asp Phe His Lys Glu Asn Phe
                930                 935
tgagcaaaga atagaccatt aagcagagca ttaaaatttc atcaaaacag ctaaggacac 3189
aggttgtttt atagaagtct accaactctc cctattgtgt acagataatg ttgcacttca 3249
agttgatata tagttgtggt tgtgatgcta gtatattaca aaataataag attatttta 3309
tttgtagtaa aaaaaaaaaa aaaaaaaaa                                   3338
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<213> Nicotiana tabacum

<400> 16

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            20                  25                  30
Ser Gly Pro Leu Asn Lys Arg Gly Gly Lys Lys Ser Ala Arg Phe Asn
        35                  40                  45
Ile Pro Glu Ser Thr Asp Ile Gly Thr Ser Val Gly Thr Gly Gly Lys
    50                  55                  60
Ser Asn Asp Asp Ala Tyr Val Glu Ile Thr Leu Asp Val Arg Glu Asp
65                  70                  75                  80
Ser Val Ala Val His Ser Val Lys Thr Ala Gly Gly Asp Asp Val Glu
                85                  90                  95
Asp Pro Glu Leu Ala Leu Leu Ala Lys Gly Leu Glu Lys Lys Ser Thr
            100                 105                 110
Leu Gly Ser Ser Leu Val Arg Asn Ala Ser Ser Arg Ile Arg Gln Val
        115                 120                 125
Ser Gln Glu Leu Arg Arg Leu Ala Ser Leu Asn Lys Arg Pro Ile Pro
    130                 135                 140
Thr Gly Arg Phe Asp Arg Asn Lys Ser Ala Ala Ala His Ala Leu Lys
145                 150                 155                 160
Gly Leu Lys Phe Ile Ser Lys Thr Asp Gly Gly Ala Gly Trp Ala Ala
                165                 170                 175
Val Glu Lys Arg Phe Asp Glu Ile Thr Ala Ser Thr Thr Gly Leu Leu
            180                 185                 190
Pro Arg Ala Lys Phe Gly Glu Cys Ile Gly Met Asn Lys Glu Ser Lys
        195                 200                 205
Glu Phe Ala Val Glu Leu Tyr Asp Ala Leu Ala Arg Arg Arg Asn Ile
    210                 215                 220
Thr Thr Asp Ser Ile Asn Lys Ala Gln Leu Lys Glu Phe Trp Asp Gln
225                 230                 235                 240
Val Ala Asp Gln Ser Phe Asp Ser Arg Leu Gln Thr Phe Phe Asp Met
                245                 250                 255
Val Asp Lys Asp Ala Asp Gly Arg Ile Thr Glu Glu Glu Val Arg Glu
            260                 265                 270
Ile Ile Gly Leu Ser Ala Ser Ala Asn Arg Leu Ser Thr Ile Gln Lys
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          275                 280                 285
Gln Ala Asp Glu Tyr Ala Ala Met Ile Met Glu Glu Leu Asp Pro Asn
    290                 295                 300
Asn Leu Gly Tyr Ile Met Ile Glu Asn Leu Glu Met Leu Leu Leu Gln
305                 310                 315                 320
Ala Pro Asn Gln Ser Val Gln Arg Gly Gly Glu Ser Arg Asn Leu Ser
                325                 330                 335
Gln Met Leu Ser Gln Lys Leu Lys His Thr Gln Glu Arg Asn Pro Ile
            340                 345                 350
Val Arg Trp Tyr Lys Ser Phe Met Tyr Phe Leu Leu Asp Asn Trp Gln
        355                 360                 365
Arg Val Trp Val Leu Leu Leu Trp Ile Gly Ile Met Ala Gly Leu Phe
    370                 375                 380
Thr Trp Lys Tyr Ile Gln Tyr Lys Glu Lys Ala Ala Tyr Lys Val Met
385                 390                 395                 400
Gly Pro Cys Val Cys Phe Ala Lys Gly Ala Ala Glu Thr Leu Lys Leu
                405                 410                 415
Asn Met Ala Ile Ile Leu Phe Pro Val Cys Arg Asn Thr Ile Thr Trp
            420                 425                 430
Leu Arg Asn Lys Thr Arg Leu Gly Ala Ala Val Pro Phe Asp Asp Asn
        435                 440                 445
Leu Asn Phe His Lys Val Ile Ala Val Ala Ile Ala Leu Gly Val Gly
    450                 455                 460
Ile His Gly Leu Ser His Leu Thr Cys Asp Phe Pro Arg Leu Leu Asn
465                 470                 475                 480
Ala Ser Glu Glu Glu Tyr Glu Pro Met Lys Tyr Tyr Phe Gly Asp Gln
                485                 490                 495
Pro Glu Ser Tyr Trp Trp Phe Ile Lys Gly Val Glu Gly Val Thr Gly
            500                 505                 510
Ile Ile Met Val Val Leu Met Ala Ile Ala Phe Thr Leu Ala Thr Pro
        515                 520                 525
Trp Phe Arg Arg Asn Arg Val Ser Leu Pro Lys Pro Phe His Lys Leu
    530                 535                 540
Thr Gly Xaa Asn Ala Phe Trp Tyr Ser His His Leu Phe Val Ile Val
545                 550                 555                 560
Tyr Thr Leu Phe Ile Val His Gly Glu Lys Leu Tyr Ile Thr Lys Asp
                565                 570                 575
Trp Tyr Lys Arg Thr Asp Met Asp Val Leu Leu Thr Ile Pro Ile Ile
            580                 585                 590
Leu Tyr Ala Ser Glu Arg Leu Ile Arg Ala Phe Arg Ser Ser Ile Lys
        595                 600                 605
Ala Val Lys Ile Leu Lys Val Ala Val Tyr Pro Gly Asn Val Leu Ala
    610                 615                 620
Leu His Met Ser Lys Pro Gln Gly Tyr Lys Tyr Lys Ser Gly Gln Tyr
625                 630                 635                 640
Met Phe Val Asn Cys Ala Ala Val Ser Pro Phe Glu Trp His Pro Phe
                645                 650                 655
Ser Ile Thr Ser Ala Pro Gly Asp Asp Tyr Leu Ser Val His Ile Arg
            660                 665                 670
Thr Leu Gly Asp Trp Thr Arg Gln Leu Lys Thr Val Phe Ser Glu Val
        675                 680                 685
Cys Gln Pro Pro Pro Asn Gly Lys Ser Gly Leu Leu Arg Ala Asp Tyr
    690                 695                 700
Leu Gln Gly Glu Asn Asn Pro Asn Phe Pro Arg Val Leu Ile Asp Gly
705                 710                 715                 720
Pro Tyr Gly Ala Pro Ala Gln Asp Tyr Lys Lys Tyr Glu Val Val Leu
                725                 730                 735
Leu Val Gly Leu Gly Ile Gly Ala Thr Pro Met Ile Ser Ile Val Lys
            740                 745                 750
Asp Ile Val Asn Asn Met Lys Ala Met Asp Glu Glu Glu Asn Ser Leu
        755                 760                 765
Glu Asp Gly His Asn Asn Asn Met Ala Pro Asn Ser Ser Pro Asn Ile
    770                 775                 780
Ala Lys Asn Lys Gly Asn Lys Ser Gly Ser Ala Ser Gly Gly Asn Asn
785                 790                 795                 800
Phe Asn Thr Arg Arg Ala Tyr Phe Tyr Trp Val Thr Arg Glu Gln Gly
                805                 810                 815
Ser Phe Asp Trp Phe Lys Gly Ile Met Asn Glu Ala Ala Glu Met Asp
            820                 825                 830
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His Lys Gly Val Ile Glu Met His Asn Tyr Cys Thr Ser Val Tyr Glu
835 840 845
Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu Gln Ser Leu His
850 855 860
His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr Arg Val Lys Ser
865 870 875 880
His Phe Ala Lys Pro Asn Trp Arg Asn Val Tyr Lys Arg Ile Ala Leu
885 890 895
Asn His Pro Glu Ala Lys Val Gly Val Phe Tyr Cys Gly Ala Pro Ala
900 905 910
Leu Thr Lys Glu Leu Arg Gln His Ala Leu Asp Phe Ser His Lys Thr
915 920 925
Ser Thr Lys Phe Asp Phe His Lys Glu Asn Phe
930 935

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<223> coding for NADPH oxidase

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Met Ala Ser Pro Tyr Asp His Gln Ser Pro His Ala Gln His Pro Ser
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ggg ttg ccg agg ccg ccg ggg gcg ggg gcg ggt gcg gcg gcg ggc ggg 96
Gly Leu Pro Arg Pro Pro Gly Ala Gly Ala Gly Ala Ala Ala Gly Gly
20 25 30
ttc gcg cgg ggg ctg atg aag cag ccg tcg cgg ctg gcg tcc ggg gtg 144
Phe Ala Arg Gly Leu Met Lys Gln Pro Ser Arg Leu Ala Ser Gly Val
35 40 45
agg cag ttc gcg tcg agg gtg tcg atg aag gtg ccg gag ggg gtg ggg 192
Arg Gln Phe Ala Ser Arg Val Ser Met Lys Val Pro Glu Gly Val Gly
50 55 60
ggg atg cgg ccc ggt ggc ggg agg atg acg cgg atg cag tcc agc gcg 240
Gly Met Arg Pro Gly Gly Gly Arg Met Thr Arg Met Gln Ser Ser Ala
65 70 75 80
cag gtg ggg ctc cgg ggg ctc cgc ttc ctc gac aag acg tcc ggc ggg 288
Gln Val Gly Leu Arg Gly Leu Arg Phe Leu Asp Lys Thr Ser Gly Gly
85 90 95
aag gag ggg tgg aag tcc gtc gag cgc cgc ttc gac gag atg aac cgc 336
Lys Glu Gly Trp Lys Ser Val Glu Arg Arg Phe Asp Glu Met Asn Arg
100 105 110
aac ggc cgc ctc ccc aag gag agc ttc ggc aag tgc atc ggc atg ggg 384
Asn Gly Arg Leu Pro Lys Glu Ser Phe Gly Lys Cys Ile Gly Met Gly
115 120 125
gac tcc aag gag ttc gcc ggc gag ctg ttc gtg gcg ctg gcg cgg cgg 432
Asp Ser Lys Glu Phe Ala Gly Glu Leu Phe Val Ala Leu Ala Arg Arg
130 135 140
agg aac ctg gag ccg gag gac ggc atc acc aag gag cag ctc aag gag 480
Arg Asn Leu Glu Pro Glu Asp Gly Ile Thr Lys Glu Gln Leu Lys Glu
145 150 155 160
ttc tgg gag gag atg acc gac cag aac ttc gac tcg cgg ctt cgc att 528
Phe Trp Glu Glu Met Thr Asp Gln Asn Phe Asp Ser Arg Leu Arg Ile
165 170 175
ttc ttt gac atg tgc gac aag aat ggc gat ggg atg ctc acg gaa gat 576
Phe Phe Asp Met Cys Asp Lys Asn Gly Asp Gly Met Leu Thr Glu Asp
180 185 190
gag gtc aag gag gtt att ata ctg agt gcg tcg gcg aac aag ctg gcg 624
Glu Val Lys Glu Val Ile Ile Leu Ser Ala Ser Ala Asn Lys Leu Ala
195 200 205
aag ctg aag gga cac gcg gcg acg tac gcg tcg ctg atc atg gag gag 672
Lys Leu Lys Gly His Ala Ala Thr Tyr Ala Ser Leu Ile Met Glu Glu
210 215 220

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ctg gac ccg gac gac cgc ggg tac atc gag atc tgg cag ctg gag acg   720
Leu Asp Pro Asp Asp Arg Gly Tyr Ile Glu Ile Trp Gln Leu Glu Thr
225                 230                 235                 240
ctg ctg cgc ggc atg gtg agc gcg cag gcg gcg ccg gag aag atg aag   768
Leu Leu Arg Gly Met Val Ser Ala Gln Ala Ala Pro Glu Lys Met Lys
                245                 250                 255
cgg acg acg tcg agc ctc gcg agg acg atg atc ccg tcg cgg tac cgg   816
Arg Thr Thr Ser Ser Leu Ala Arg Thr Met Ile Pro Ser Arg Tyr Arg
            260                 265                 270
agc ccg ctg aag cgg cac gtg tcc agg acg gtg gac ttc gtg cac gag   864
Ser Pro Leu Lys Arg His Val Ser Arg Thr Val Asp Phe Val His Glu
        275                 280                 285
aac tgg aag cgg atc tgg ctc gtc gcg ctg tgg ctc gcc gtc aac gtc   912
Asn Trp Lys Arg Ile Trp Leu Val Ala Leu Trp Leu Ala Val Asn Val
    290                 295                 300
ggc ctc ttc gcc tac aag ttc gag cag tac gag cgg cgc gcc gcg ttc   960
Gly Leu Phe Ala Tyr Lys Phe Glu Gln Tyr Glu Arg Arg Ala Ala Phe
305                 310                 315                 320
cag gtg atg ggc cac tgc gtg tgc gtg gcc aag ggc gcc gcc gag gtg   1008
Gln Val Met Gly His Cys Val Cys Val Ala Lys Gly Ala Ala Glu Val
                325                 330                 335
ctc aag ctc aac atg gcg ctc atc ctc ctc ccc gtg tgc cgg aac acg   1056
Leu Lys Leu Asn Met Ala Leu Ile Leu Leu Pro Val Cys Arg Asn Thr
            340                 345                 350
ctc acc acg ctc agg tcc acg gcg ctc agc cac gtc atc ccc ttc gac   1104
Leu Thr Thr Leu Arg Ser Thr Ala Leu Ser His Val Ile Pro Phe Asp
        355                 360                 365
gac aac atc aac ttc cac aag gtg atc gcg gcg acc atc gcc gcc gcc   1152
Asp Asn Ile Asn Phe His Lys Val Ile Ala Ala Thr Ile Ala Ala Ala
    370                 375                 380
acc gcc gtc cac acg ctg gcg cac gtc acc tgc gac ttc ccg agg ctg   1200
Thr Ala Val His Thr Leu Ala His Val Thr Cys Asp Phe Pro Arg Leu
385                 390                 395                 400
atc aac tgc ccc agc gac aag ttc atg gcg acg ctg ggg ccg aac ttc   1248
Ile Asn Cys Pro Ser Asp Lys Phe Met Ala Thr Leu Gly Pro Asn Phe
                405                 410                 415
ggg tac agg cag ccg acg tac gcc gac ctg ctg gag agc gcc ccc ggc   1296
Gly Tyr Arg Gln Pro Thr Tyr Ala Asp Leu Leu Glu Ser Ala Pro Gly
            420                 425                 430
gtc acc ggc atc ctc atg atc atc atc atg tcc ttc tcc ttc acg ctg   1344
Val Thr Gly Ile Leu Met Ile Ile Ile Met Ser Phe Ser Phe Thr Leu
        435                 440                 445
gcc acg cac tcc ttc cgc cgg agc gtc gtc aag ctg ccg tcg ccg ctg   1392
Ala Thr His Ser Phe Arg Arg Ser Val Val Lys Leu Pro Ser Pro Leu
    450                 455                 460
cac cac ctc gcc ggc ttc aac gcc ttc tgg tac gcg cac cac ctc ctg   1440
His His Leu Ala Gly Phe Asn Ala Phe Trp Tyr Ala His His Leu Leu
465                 470                 475                 480
gtg ctc gcc tac gtc ctc ctc gtc gtg cac tcc tac ttc ata ttc ctc   1488
Val Leu Ala Tyr Val Leu Leu Val Val His Ser Tyr Phe Ile Phe Leu
                485                 490                 495
acc agg gag tgg tac aag aaa acg aca tgg atg tac ctg ata gtc cca   1536
Thr Arg Glu Trp Tyr Lys Lys Thr Thr Trp Met Tyr Leu Ile Val Pro
            500                 505                 510
gtg ctc ttc tat gca tgc gag aga acg atc aga aaa gtt cga gag aac   1584
Val Leu Phe Tyr Ala Cys Glu Arg Thr Ile Arg Lys Val Arg Glu Asn
        515                 520                 525
aac tac cgc gtg agc atc gtc aag gca gcg att tac cca gga aat gtg   1632
Asn Tyr Arg Val Ser Ile Val Lys Ala Ala Ile Tyr Pro Gly Asn Val
    530                 535                 540
ctc tct ctt cac atg aag aag ccg ccg ggt ttc aag tac aag agc ggg   1680
Leu Ser Leu His Met Lys Lys Pro Pro Gly Phe Lys Tyr Lys Ser Gly
545                 550                 555                 560
atg tac ctg ttt gtg aag tgc cct gat gtc tct cct ttc gaa tgg cat   1728
Met Tyr Leu Phe Val Lys Cys Pro Asp Val Ser Pro Phe Glu Trp His
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ccc ttc tcc atc act tct gca cct gga gat gac tac ctg agt gtg cat   1776
Pro Phe Ser Ile Thr Ser Ala Pro Gly Asp Asp Tyr Leu Ser Val His
            580                 585                 590
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Ile Arg Thr Leu Gly Asp Trp Thr Thr Glu Leu Arg Asn Leu Phe Gly
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aag gct tgc gag gca cag gtt act tct aag aag gct acc ctt tca aga   1872
Lys Ala Cys Glu Ala Gln Val Thr Ser Lys Lys Ala Thr Leu Ser Arg
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ctt gaa act aca gtt gtg gcg gac gct cag aca gag gat act agg ttt   1920
Leu Glu Thr Thr Val Val Ala Asp Ala Gln Thr Glu Asp Thr Arg Phe
625                 630                 635                 640
cct aag gtc ctt att gat ggg ccc tat ggt gca ccg gcg caa aac tac   1968
Pro Lys Val Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln Asn Tyr
                645                 650                 655
aag aag tat gac att ctt ttg ctt att ggt ctt gga att ggt gct act   2016
Lys Lys Tyr Asp Ile Leu Leu Leu Ile Gly Leu Gly Ile Gly Ala Thr
            660                 665                 670
cct ttc atc agc att ctg aag gat ctg ttg aac aac att aaa tcc aac   2064
Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Asn Asn Ile Lys Ser Asn
        675                 680                 685
gaa gag gtg gaa agc ata cat ggt tct gag ata ggc agc ttc aag aac   2112
Glu Glu Val Glu Ser Ile His Gly Ser Glu Ile Gly Ser Phe Lys Asn
    690                 695                 700
aat ggg cca gga aga gct tac ttc tac tgg gtg acc aga gag caa ggg   2160
Asn Gly Pro Gly Arg Ala Tyr Phe Tyr Trp Val Thr Arg Glu Gln Gly
705                 710                 715                 720
tcc ttc gag tgg ttt aaa gga gtc atg aac gat gtc gct gaa agt gat   2208
Ser Phe Glu Trp Phe Lys Gly Val Met Asn Asp Val Ala Glu Ser Asp
                725                 730                 735
cac aat aat att ata gag atg cac aat tac ctg acc agc gtg tat gaa   2256
His Asn Asn Ile Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu
            740                 745                 750
gaa ggc gac gca agg tca gct ttg att gcc atg gtt cag tca ctt caa   2304
Glu Gly Asp Ala Arg Ser Ala Leu Ile Ala Met Val Gln Ser Leu Gln
        755                 760                 765
cat gcc aaa aat ggt gtg gat atc gtc tcc ggc agc agg att cgc aca   2352
His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Ser Arg Ile Arg Thr
    770                 775                 780
cat ttt gcg agg cct aac tgg aga aag gtg ttc tct gac ttg gcg aat   2400
His Phe Ala Arg Pro Asn Trp Arg Lys Val Phe Ser Asp Leu Ala Asn
785                 790                 795                 800
gcc cac aaa aac tca cgc ata ggt gtt ttc tat tgt gga tcc cct aca   2448
Ala His Lys Asn Ser Arg Ile Gly Val Phe Tyr Cys Gly Ser Pro Thr
                805                 810                 815
ctc acg aaa caa ctc aag gat ctt tca aaa gaa ttc agc cag aca acc   2496
Leu Thr Lys Gln Leu Lys Asp Leu Ser Lys Glu Phe Ser Gln Thr Thr
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Phe Ala Arg Gly Leu Met Lys Gln Pro Ser Arg Leu Ala Ser Gly Val
        35                  40                  45
Arg Gln Phe Ala Ser Arg Val Ser Met Lys Val Pro Glu Gly Val Gly
    50                  55                  60
Gly Met Arg Pro Gly Gly Gly Arg Met Thr Arg Met Gln Ser Ser Ala
65                  70                  75                  80
Gln Val Gly Leu Arg Gly Leu Arg Phe Leu Asp Lys Thr Ser Gly Gly
                85                  90                  95
Lys Glu Gly Trp Lys Ser Val Glu Arg Arg Phe Asp Glu Met Asn Arg
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Asn Gly Arg Leu Pro Lys Glu Ser Phe Gly Lys Cys Ile Gly Met Gly
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Asp Ser Lys Glu Phe Ala Gly Glu Leu Phe Val Ala Leu Ala Arg Arg
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Arg Asn Leu Glu Pro Glu Asp Gly Ile Thr Lys Glu Gln Leu Lys Glu
145 150 155 160
Phe Trp Glu Glu Met Thr Asp Gln Asn Phe Asp Ser Arg Leu Arg Ile
165 170 175
Phe Phe Asp Met Cys Asp Lys Asn Gly Asp Gly Met Leu Thr Glu Asp
180 185 190
Glu Val Lys Glu Val Ile Ile Leu Ser Ala Ser Ala Asn Lys Leu Ala
195 200 205
Lys Leu Lys Gly His Ala Ala Thr Tyr Ala Ser Leu Ile Met Glu Glu
210 215 220
Leu Asp Pro Asp Asp Arg Gly Tyr Ile Glu Ile Trp Gln Leu Glu Thr
225 230 235 240
Leu Leu Arg Gly Met Val Ser Ala Gln Ala Ala Pro Glu Lys Met Lys
245 250 255
Arg Thr Thr Ser Ser Leu Ala Arg Thr Met Ile Pro Ser Arg Tyr Arg
260 265 270
Ser Pro Leu Lys Arg His Val Ser Arg Thr Val Asp Phe Val His Glu
275 280 285
Asn Trp Lys Arg Ile Trp Leu Val Ala Leu Trp Leu Ala Val Asn Val
290 295 300
Gly Leu Phe Ala Tyr Lys Phe Glu Gln Tyr Glu Arg Arg Ala Ala Phe
305 310 315 320
Gln Val Met Gly His Cys Val Cys Val Ala Lys Gly Ala Ala Glu Val
325 330 335
Leu Lys Leu Asn Met Ala Leu Ile Leu Leu Pro Val Cys Arg Asn Thr
340 345 350
Leu Thr Thr Leu Arg Ser Thr Ala Leu Ser His Val Ile Pro Phe Asp
355 360 365
Asp Asn Ile Asn Phe His Lys Val Ile Ala Ala Thr Ile Ala Ala Ala
370 375 380
Thr Ala Val His Thr Leu Ala His Val Thr Cys Asp Phe Pro Arg Leu
385 390 395 400
Ile Asn Cys Pro Ser Asp Lys Phe Met Ala Thr Leu Gly Pro Asn Phe
405 410 415
Gly Tyr Arg Gln Pro Thr Tyr Ala Asp Leu Leu Glu Ser Ala Pro Gly
420 425 430
Val Thr Gly Ile Leu Met Ile Ile Ile Met Ser Phe Ser Phe Thr Leu
435 440 445
Ala Thr His Ser Phe Arg Arg Ser Val Val Lys Leu Pro Ser Pro Leu
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His His Leu Ala Gly Phe Asn Ala Phe Trp Tyr Ala His His Leu Leu
465 470 475 480
Val Leu Ala Tyr Val Leu Leu Val Val His Ser Tyr Phe Ile Phe Leu
485 490 495
Thr Arg Glu Trp Tyr Lys Lys Thr Thr Trp Met Tyr Leu Ile Val Pro
500 505 510
Val Leu Phe Tyr Ala Cys Glu Arg Thr Ile Arg Lys Val Arg Glu Asn
515 520 525
Asn Tyr Arg Val Ser Ile Val Lys Ala Ala Ile Tyr Pro Gly Asn Val
530 535 540
Leu Ser Leu His Met Lys Lys Pro Pro Gly Phe Lys Tyr Lys Ser Gly
545 550 555 560
Met Tyr Leu Phe Val Lys Cys Pro Asp Val Ser Pro Phe Glu Trp His
565 570 575
Pro Phe Ser Ile Thr Ser Ala Pro Gly Asp Asp Tyr Leu Ser Val His
580 585 590
Ile Arg Thr Leu Gly Asp Trp Thr Thr Glu Leu Arg Asn Leu Phe Gly
595 600 605
Lys Ala Cys Glu Ala Gln Val Thr Ser Lys Lys Ala Thr Leu Ser Arg
610 615 620
Leu Glu Thr Thr Val Val Ala Asp Ala Gln Thr Glu Asp Thr Arg Phe
625 630 635 640
Pro Lys Val Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln Asn Tyr
645 650 655

Lys Lys Tyr Asp Ile Leu Leu Leu Ile Gly Leu Gly Ile Gly Ala Thr
660 665 670
Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Asn Asn Ile Lys Ser Asn
675 680 685
Glu Glu Val Glu Ser Ile His Gly Ser Glu Ile Gly Ser Phe Lys Asn
690 695 700
Asn Gly Pro Gly Arg Ala Tyr Phe Tyr Trp Val Thr Arg Glu Gln Gly
705 710 715 720
Ser Phe Glu Trp Phe Lys Gly Val Met Asn Asp Val Ala Glu Ser Asp
725 730 735
His Asn Asn Ile Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu
740 745 750
Glu Gly Asp Ala Arg Ser Ala Leu Ile Ala Met Val Gln Ser Leu Gln
755 760 765
His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Ser Arg Ile Arg Thr
770 775 780
His Phe Ala Arg Pro Asn Trp Arg Lys Val Phe Ser Asp Leu Ala Asn
785 790 795 800
Ala His Lys Asn Ser Arg Ile Gly Val Phe Tyr Cys Gly Ser Pro Thr
805 810 815
Leu Thr Lys Gln Leu Lys Asp Leu Ser Lys Glu Phe Ser Gln Thr Thr
820 825 830
Thr Thr Arg Phe His Phe His Lys Glu Asn Phe
835 840

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gaa gcc gga aac agc gga cca atg agc ggt ggt caa tta cca ccg atc 96
Glu Ala Gly Asn Ser Gly Pro Met Ser Gly Gly Gln Leu Pro Pro Ile
20 25 30
tat aaa aaa ccg ggg aac tcc aga ttc act gct gag aac agt cag aga 144
Tyr Lys Lys Pro Gly Asn Ser Arg Phe Thr Ala Glu Asn Ser Gln Arg
35 40 45
aca cgt acg gca cca tac gtg gac ctc acg gta gat gta caa gac gat 192
Thr Arg Thr Ala Pro Tyr Val Asp Leu Thr Val Asp Val Gln Asp Asp
50 55 60
aca gtc tct gta cat agc ttg aaa atg gaa ggt gga tct agc gtt gaa 240
Thr Val Ser Val His Ser Leu Lys Met Glu Gly Gly Ser Ser Val Glu
65 70 75 80
gag agt ccg gag ctt act ttg ctg aaa cga aac cgt ctt gag aag aaa 288
Glu Ser Pro Glu Leu Thr Leu Leu Lys Arg Asn Arg Leu Glu Lys Lys
85 90 95
aca acg gtg gtg aaa cgt ttg gcg tct gtt tct cac gag ctt aag cgt 336
Thr Thr Val Val Lys Arg Leu Ala Ser Val Ser His Glu Leu Lys Arg
100 105 110
ttg aca tct gtt tct ggt ggt att ggt gga aga aag ccg cct cga ccg 384
Leu Thr Ser Val Ser Gly Gly Ile Gly Gly Arg Lys Pro Pro Arg Pro
115 120 125
gct aag tta gac cgg act aaa tcc gcc gcg agt caa gcg ttg aag gga 432
Ala Lys Leu Asp Arg Thr Lys Ser Ala Ala Ser Gln Ala Leu Lys Gly
130 135 140
ctt aag ttc att agt aaa acc gac ggt ggc gcc ggt tgg tct gcc gtg 480
Leu Lys Phe Ile Ser Lys Thr Asp Gly Gly Ala Gly Trp Ser Ala Val
145 150 155 160
gag aag cgg ttt aat cag att acc gcg act acc ggt gga cta ctt ctt 528
Glu Lys Arg Phe Asn Gln Ile Thr Ala Thr Thr Gly Gly Leu Leu Leu

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                    165                 170                 175
cgg aca aag ttc ggt gaa tgc ata gga atg act tca aag gat ttt gct   576
Arg Thr Lys Phe Gly Glu Cys Ile Gly Met Thr Ser Lys Asp Phe Ala
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ttg gaa ctg ttt gat gca ttg gct aga aga agg aat ata aca ggg gaa   624
Leu Glu Leu Phe Asp Ala Leu Ala Arg Arg Arg Asn Ile Thr Gly Glu
            195                 200                 205
gtg att gat gga gat caa cta aag gag ttt tgg gaa caa att aat gat   672
Val Ile Asp Gly Asp Gln Leu Lys Glu Phe Trp Glu Gln Ile Asn Asp
        210                 215                 220
caa agt ttt gat tct cgg ctt aag aca ttc ttt gac atg gtg gat aaa   720
Gln Ser Phe Asp Ser Arg Leu Lys Thr Phe Phe Asp Met Val Asp Lys
225                 230                 235                 240
gat gct gat ggt aga ctt aca gaa gac gaa gtt aga gag ttg gag agt   768
Asp Ala Asp Gly Arg Leu Thr Glu Asp Glu Val Arg Glu Leu Glu Ser
                245                 250                 255
ctt gag act ctg ctt ttg caa gcg gca aca cag tct gtg ata aca agt   816
Leu Glu Thr Leu Leu Leu Gln Ala Ala Thr Gln Ser Val Ile Thr Ser
            260                 265                 270
act ggg gag aga aag aat ctg agt cat atg atg agt cag agg ctt aag   864
Thr Gly Glu Arg Lys Asn Leu Ser His Met Met Ser Gln Arg Leu Lys
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cct acg ttt aac cgc aac ccg ttg aag cga tgg tac cgt ggt ctt aga   912
Pro Thr Phe Asn Arg Asn Pro Leu Lys Arg Trp Tyr Arg Gly Leu Arg
    290                 295                 300
ttc ttc ttg tta gac aac tgg caa aga tgt tgg gtt ata gtg cta tgg   960
Phe Phe Leu Leu Asp Asn Trp Gln Arg Cys Trp Val Ile Val Leu Trp
305                 310                 315                 320
ttc ata gtt atg gct ata ctc ttc acc tac aaa tat atc caa tac agg  1008
Phe Ile Val Met Ala Ile Leu Phe Thr Tyr Lys Tyr Ile Gln Tyr Arg
                325                 330                 335
cgt agc cct gtg tat cca gtg atg ggt gat tgt gtg tgc atg gct aaa  1056
Arg Ser Pro Val Tyr Pro Val Met Gly Asp Cys Val Cys Met Ala Lys
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ggt gct gca gaa aca gtg aag ctg aac atg gct ttg att ctc tta cct  1104
Gly Ala Ala Glu Thr Val Lys Leu Asn Met Ala Leu Ile Leu Leu Pro
        355                 360                 365
gtt tgt aga aac acc atc aca tgg ctt aga aat aag acc agg ttg ggt  1152
Val Cys Arg Asn Thr Ile Thr Trp Leu Arg Asn Lys Thr Arg Leu Gly
    370                 375                 380
cgt gtt gtc cca ttt gat gac aat ctc aac ttc cac aag gtt ata gcg  1200
Arg Val Val Pro Phe Asp Asp Asn Leu Asn Phe His Lys Val Ile Ala
385                 390                 395                 400
gtg ggg att ata gtt gga gta acg atg cac gcc ggg gca cat tta gcg  1248
Val Gly Ile Ile Val Gly Val Thr Met His Ala Gly Ala His Leu Ala
                405                 410                 415
tgt gat ttc ccg cgg tta cta cat gca act cca gag gca tat agg cct  1296
Cys Asp Phe Pro Arg Leu Leu His Ala Thr Pro Glu Ala Tyr Arg Pro
            420                 425                 430
tta aga cag ttt ttt ggg gat gag caa cca aag agc tac tgg cat ttt  1344
Leu Arg Gln Phe Phe Gly Asp Glu Gln Pro Lys Ser Tyr Trp His Phe
        435                 440                 445
gta aac tcg gta gaa ggt ata acc gga ctt gtg atg gtt ttg tta atg  1392
Val Asn Ser Val Glu Gly Ile Thr Gly Leu Val Met Val Leu Leu Met
    450                 455                 460
gcg att gca ttc aca cta gcc acg cct tgg ttc aga aga ggg aag cta  1440
Ala Ile Ala Phe Thr Leu Ala Thr Pro Trp Phe Arg Arg Gly Lys Leu
465                 470                 475                 480
aac tat ctt cca gga cca tta aag aaa cta gct agc ttc aat gcc ttc  1488
Asn Tyr Leu Pro Gly Pro Leu Lys Lys Leu Ala Ser Phe Asn Ala Phe
                485                 490                 495
tgg tac act cat cat ttg ttt gtc ata gtc tac att ctt ctt gtt gct  1536
Trp Tyr Thr His His Leu Phe Val Ile Val Tyr Ile Leu Leu Val Ala
            500                 505                 510
cat gga tac tac ttg tat ctc acc aga gac tgg cac aat aaa acg act  1584
His Gly Tyr Tyr Leu Tyr Leu Thr Arg Asp Trp His Asn Lys Thr Thr
        515                 520                 525
tgg atg tat ttg gtg gta cca gtg gtt cta tac gcg tgt gaa agg ttg  1632
Trp Met Tyr Leu Val Val Pro Val Val Leu Tyr Ala Cys Glu Arg Leu
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    530                 535                 540
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Ala Val Tyr Pro Gly Asn Val Leu Ala Ile His Leu Ser Arg Pro Gln
                565                 570                 575
aac ttc aaa tac aag agt ggt caa tac atg ttt gtt aac tgt gct gct   1776
Asn Phe Lys Tyr Lys Ser Gly Gln Tyr Met Phe Val Asn Cys Ala Ala
            580                 585                 590
gtt tct cca ttt gaa tgg cat cca ttt tca atc aca tct gca cca caa   1824
Val Ser Pro Phe Glu Trp His Pro Phe Ser Ile Thr Ser Ala Pro Gln
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gat gat tac cta agt gtt cac att aga gtt ctt ggg gat tgg aca cga   1872
Asp Asp Tyr Leu Ser Val His Ile Arg Val Leu Gly Asp Trp Thr Arg
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gct ctc aaa gga gtc ttc tct gag gtg tgt aag cca cca ccg gca gga   1920
Ala Leu Lys Gly Val Phe Ser Glu Val Cys Lys Pro Pro Pro Ala Gly
625                 630                 635                 640
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Asp Tyr Lys Lys Tyr Glu Val Val Leu Leu Val Gly Leu Gly Ile Gly
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gcc aca cca atg atc agt atc gtc aaa gac att gtt aat aac atc aag   2112
Ala Thr Pro Met Ile Ser Ile Val Lys Asp Ile Val Asn Asn Ile Lys
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gcc aag gaa caa gcc caa cta aac cga atg gag aat gga aca agc gaa   2160
Ala Lys Glu Gln Ala Gln Leu Asn Arg Met Glu Asn Gly Thr Ser Glu
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cca caa cga agt aag aaa gag agt ttc agg acc cgt aga gct tac ttc   2208
Pro Gln Arg Ser Lys Lys Glu Ser Phe Arg Thr Arg Arg Ala Tyr Phe
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atg aac gaa gtc gcg gaa cga gat gcc aac cgc gtc atc gaa atg cat   2304
Met Asn Glu Val Ala Glu Arg Asp Ala Asn Arg Val Ile Glu Met His
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aac tat tgt aca agt gtc tat gaa gaa ggt gac gct cgt tcc gca ctt   2352
Asn Tyr Cys Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu
    770                 775                 780
ata cat atg ctt caa tca cta aac cat gca aag aac ggc gtc gac att   2400
Ile His Met Leu Gln Ser Leu Asn His Ala Lys Asn Gly Val Asp Ile
785                 790                 795                 800
gtc tct gga aca aga gtt atg tcc cat ttc gct aaa cct aat tgg aga   2448
Val Ser Gly Thr Arg Val Met Ser His Phe Ala Lys Pro Asn Trp Arg
                805                 810                 815
aat gtt tac aag cgt ata gct atg gat cat cct aac acc aaa gtt gga   2496
Asn Val Tyr Lys Arg Ile Ala Met Asp His Pro Asn Thr Lys Val Gly
            820                 825                 830
gtg ttt tac tgt gga gca cca gca ttg aca aag gag cta agg cat cta   2544
Val Phe Tyr Cys Gly Ala Pro Ala Leu Thr Lys Glu Leu Arg His Leu
        835                 840                 845
gct tta gat ttc acc cac aaa aca agc acc aga ttc tcc ttc cac aaa   2592
Ala Leu Asp Phe Thr His Lys Thr Ser Thr Arg Phe Ser Phe His Lys
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         35                  40                  45
Thr Arg Thr Ala Pro Tyr Val Asp Leu Thr Val Asp Val Gln Asp Asp
     50                  55                  60
Thr Val Ser Val His Ser Leu Lys Met Glu Gly Gly Ser Ser Val Glu
 65                  70                  75                  80
Glu Ser Pro Glu Leu Thr Leu Leu Lys Arg Asn Arg Leu Glu Lys Lys
                 85                  90                  95
Thr Thr Val Val Lys Arg Leu Ala Ser Val Ser His Glu Leu Lys Arg
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Leu Thr Ser Val Ser Gly Gly Ile Gly Gly Arg Lys Pro Pro Arg Pro
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Ala Lys Leu Asp Arg Thr Lys Ser Ala Ala Ser Gln Ala Leu Lys Gly
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Leu Lys Phe Ile Ser Lys Thr Asp Gly Gly Ala Gly Trp Ser Ala Val
145                 150                 155                 160
Glu Lys Arg Phe Asn Gln Ile Thr Ala Thr Thr Gly Gly Leu Leu Leu
                165                 170                 175
Arg Thr Lys Phe Gly Glu Cys Ile Gly Met Thr Ser Lys Asp Phe Ala
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Leu Glu Leu Phe Asp Ala Leu Ala Arg Arg Arg Asn Ile Thr Gly Glu
        195                 200                 205
Val Ile Asp Gly Asp Gln Leu Lys Glu Phe Trp Glu Gln Ile Asn Asp
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Gln Ser Phe Asp Ser Arg Leu Lys Thr Phe Phe Asp Met Val Asp Lys
225                 230                 235                 240
Asp Ala Asp Gly Arg Leu Thr Glu Asp Glu Val Arg Glu Leu Glu Ser
                245                 250                 255
Leu Glu Thr Leu Leu Leu Gln Ala Ala Thr Gln Ser Val Ile Thr Ser
            260                 265                 270
Thr Gly Glu Arg Lys Asn Leu Ser His Met Met Ser Gln Arg Leu Lys
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Pro Thr Phe Asn Arg Asn Pro Leu Lys Arg Trp Tyr Arg Gly Leu Arg
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Phe Phe Leu Leu Asp Asn Trp Gln Arg Cys Trp Val Ile Val Leu Trp
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Phe Ile Val Met Ala Ile Leu Phe Thr Tyr Lys Tyr Ile Gln Tyr Arg
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Arg Ser Pro Val Tyr Pro Val Met Gly Asp Cys Val Cys Met Ala Lys
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Gly Ala Ala Glu Thr Val Lys Leu Asn Met Ala Leu Ile Leu Leu Pro
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Val Cys Arg Asn Thr Ile Thr Trp Leu Arg Asn Lys Thr Arg Leu Gly
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Arg Val Val Pro Phe Asp Asp Asn Leu Asn Phe His Lys Val Ile Ala
385                 390                 395                 400
Val Gly Ile Ile Val Gly Val Thr Met His Ala Gly Ala His Leu Ala
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Cys Asp Phe Pro Arg Leu Leu His Ala Thr Pro Glu Ala Tyr Arg Pro
            420                 425                 430
Leu Arg Gln Phe Phe Gly Asp Glu Gln Pro Lys Ser Tyr Trp His Phe
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Val Asn Ser Val Glu Gly Ile Thr Gly Leu Val Met Val Leu Leu Met
    450                 455                 460
Ala Ile Ala Phe Thr Leu Ala Thr Pro Trp Phe Arg Arg Gly Lys Leu
465                 470                 475                 480
Asn Tyr Leu Pro Gly Pro Leu Lys Lys Leu Ala Ser Phe Asn Ala Phe
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Trp Tyr Thr His His Leu Phe Val Ile Val Tyr Ile Leu Leu Val Ala
            500                 505                 510
His Gly Tyr Tyr Leu Tyr Leu Thr Arg Asp Trp His Asn Lys Thr Thr
        515                 520                 525
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Arg Gln Gly Arg Ser Gly Arg Ser Asn Ser Val Leu Lys Arg Leu Ala
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Ser Ser Val Ser Thr Gly Ile Thr Arg Val Ala Ser Ser Val Ser Ser
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Ser Ser Ala Arg Lys Pro Pro Arg Pro Gln Leu Ala Lys Leu Arg Arg
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Ser Lys Ser Arg Ala Glu Leu Ala Leu Lys Gly Leu Lys Phe Ile Thr
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WHAT IS CLAIMED IS:

1. A method for generating or increasing the resistance to fungi in a monocotyledonous plant, which comprises the following operating steps:

a) reduction of the protein quantity, activity or function of an NADPH oxidase in a plant or a tissue, organ, plant part or cell thereof by introducing a double-stranded NADPH oxidase RNA nucleic acid sequence or (an) expression cassette(s) ensuring its expression; and

b) selection of the plant in which - in contrast or in comparison with the starting plant - the resistance fungi exists or is increased.

2. The method according to claim 1, wherein the NADPH oxidase is encoded by:

a) polypeptide sequence comprising a sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 or 22; or

b) polypeptide sequence having at least 50% identity to the sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 or 22, and wherein the polypeptide has a NADPH oxidase activity.

3. The method according to claim 2, wherein the polypeptide in b) has at least 70% identity to the sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 or 22, and wherein the polypeptide has a NADPH oxidase activity.

4. The method according to any one of claims 1 to 3, comprising:

(i) the stable transformation of a plant cell with a recombinant expression cassette comprising, in functional linkage with a promoter which is active in plants, a nucleic acid sequence encoding a double-stranded NADPH oxidase RNA ribonucleic acid sequence;

(ii) regeneration of the plant from the plant cell; and

(iii) expression of said nucleic acid sequence in such a quantity and for such a time as suffices for generating or increasing a pathogen resistance in said plant.

5. The method according to any one of claims 1 to 4, wherein the fungi is Plasmodiophoramycota, Oomycota, Ascomycota, Chytridiomycetes, Zygomycetes, Basidiomycota or Deuteromyceten.

6. The method according to any one of claims 1 to 5, wherein the plant is wheat, oats, millet, barley, rye, maize, rice, sorghum, triticale, spelt or sugar cane.

7. A double-stranded RNA molecule for reducing the expression of an NADPH oxidase protein comprising:

a) a sense RNA strand comprising at least one ribonucleotide sequence which has at least 75% identity to at least part of the sense RNA transcript of a nucleic acid sequence encoding an NADPH oxidase; and

b) an antisense RNA strand which has at least 80% identity to a complement of the RNA sense strand of a).

8. The double-stranded RNA molecule according to claim 7, wherein the two RNA strands of the double-stranded RNA are bonded covalently with one another.

9. The double-stranded RNA molecule according to claim 7 or 8, wherein one of the two RNA strands is encoded by at least a part of the nucleic acid sequence encoding an NADPH oxidase sequence having at least 70% identity to a sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19 or 21.

10. A transgenic expression cassette comprising, in functional linkage with a promoter which is functional in a plant organism, a nucleic acid sequence encoding the double-stranded RNA molecule according to any one of claims 7 to 9.

11. A transgenic expression cassette comprising at least a part of a nucleic acid sequence encoding an NADPH oxidase having at least 70% identity to a sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19 or 21, where said nucleic acid sequence is linked functionally in antisense orientation with a promoter which is functional in a plant organism.

12. The transgenic expression cassette according to claim 10 or 11, wherein the promoter which is functional in the plant organism is a pathogen-inducible promoter.

13. A transgenic vector comprising the expression cassette according to any one of claims 10 to 12.

14. A monocotyledonous transgenic plant cell comprising the double-stranded RNA molecule according to any one of claims 7 to 9, the expression cassette according to any one of claims 10 to 12 or the transgenic vector according to claim 13.

15. The monocotyledonous transgenic plant cell according to claim 14, wherein the plant cell is a wheat, oat, millet, barley, rye, maize, rice, sorghum, triticale, spelt or sugar cane cell.

16. A monocotyledonous plant tissue cell, a monocotyledonous plant organ cell or a monocotyledonous plant cell culture comprising:

a) the double-stranded RNA molecule according to any one of claims 7 to 9;

b) the transgenic expression cassette according to any one of claims 10 to 12; or

c) the transgenic vector according to claim 13,

characterized in that the double-stranded RNA molecule in a), the transgenic expression cassette in b) and the transgenic vector in c) are obtained from the monocotyledonous transgenic plant cell according to claim 15.

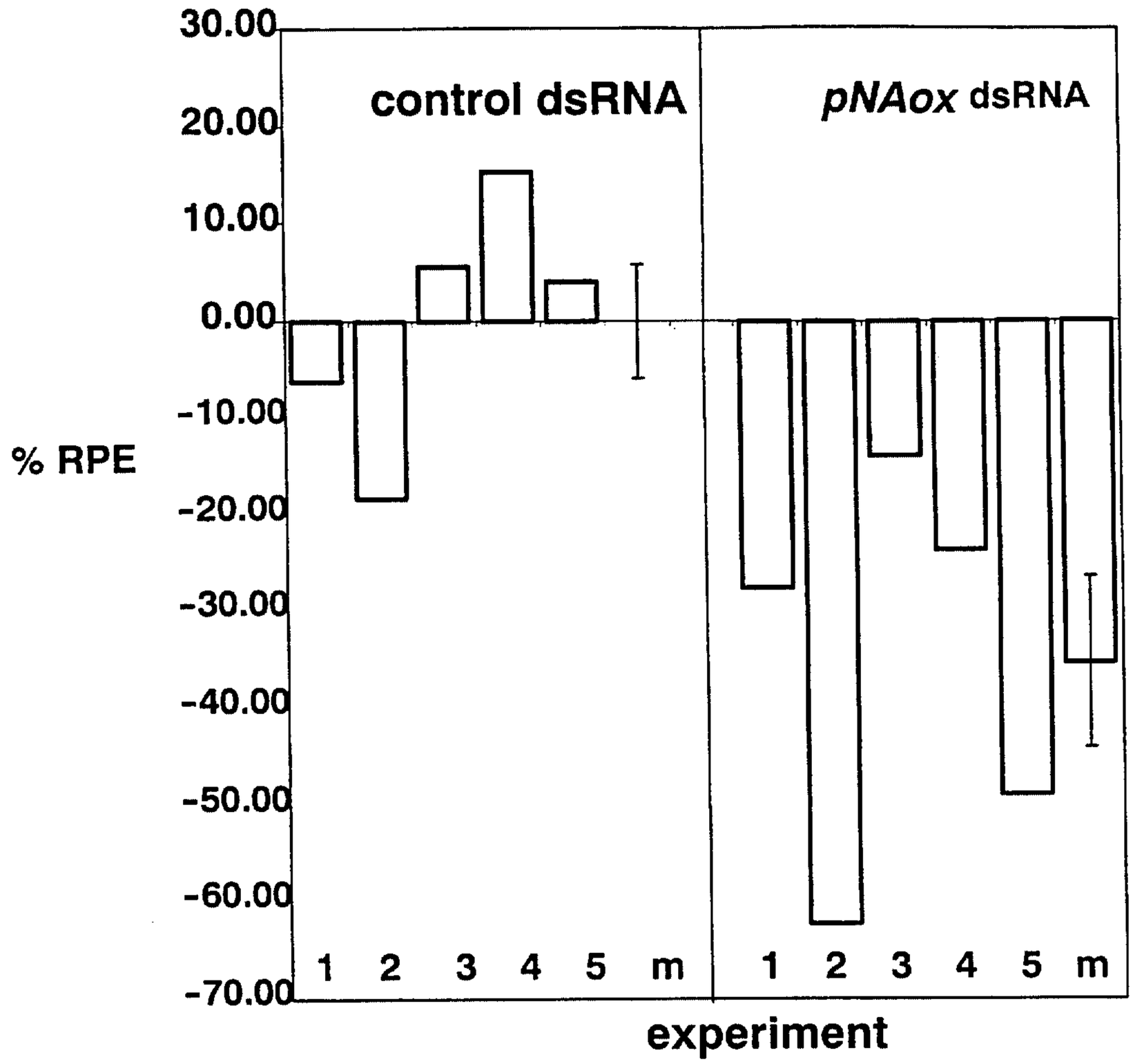

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experiment

Fig. 1