The invention relates to a method for creating resistance to Oomycetes in plants. In particular, the invention relates to a method for creating resistance to Phytophthora cactorum in plants of the family Rosaceae, in particular in the genus Fragaria.
Plant resistance genes

FIELD OF THE INVENTION

The invention relates to a method for creating resistance to Oomycetes in plants. In particular the invention relates to a method for creating resistance to Phytophthora cactorum in plants of the family Rosaceae, in particular in the genus Fragaria.

BACKGROUND OF THE INVENTION

Plant diseases, which are caused by various pathogens, such as viruses, bacteria and fungi, may lead to significant crop failure in the cultivation of cultivated plants, resulting in economic consequences and in threatening human food supply.

Since the last century, chemical fungicides have been utilised for controlling fungal diseases. Using these substances has reduced the extent of plant diseases, however, it cannot be excluded to this day that these compounds have adverse effects on humans, animals and the environment. In order to reduce the usage of conventional pesticides to a minimum in the long run, it is important to examine the natural pathogen defence of various plants towards different pathogens and to use the same specifically for the production of pathogen-resistant plants by gene technological manipulation, e.g. by means of introducing external resistance genes or by means of the manipulation of the endogenous gene expression of the plants.

Resistance is the ability of a plant to inhibit any infestation or population of a pest or at least to limit the same. The plants have a certain degree of natural resistance which is imparted by the formation of specific defence substances, such as isoprenoids, flavonoids, enzymes and reactive oxygen species.

One approach for producing resistant plants is the expression of a plant transgene in said plants, resulting in the formation of said specific defence substances. In this way, chitinase (WO 92/17591) and pathogenesis-related genes (WO 92/20800) as well as genes for various oxidizing enzymes, such as glucose oxidase (WO 95/21924) and
oxalate oxidase (WO 99/04013), have already been overexpressed in plants, thus creating plants having increased fungal resistance.

To date, resistance strategies against all fungal pathogens are not available. This is particularly serious, since virtually every agricultural crop may be attacked by a plurality of pathogenic fungi. Thus, there is an urgent need for strategies to confer resistance to a plant against a plurality of potential pathogenic fungi at the same time.

_Fragaria_ is an important soft fruit genus, primarily due to the cultivation of the genetically complex garden strawberry (_Fragaria xananassa_ Duch; 2n = 8x = 56). The world production of strawberries exceeded 5 million tons in 2012 and the crop was valued in excess of US$10 billion (FAO 2014). The strawberry is, however, also a host plant for a wide range of disease-causing pathogens of significant economic impact, including the oomycete _Phytophthora cactorum_ (Lebert & Cohn) J.Schrot. which causes crown rot.

_P. cactorum_ has been known since 1952 as the causal organism of crown rot (Deutschmann 1954). Crown rot in strawberry is characterized by a sudden wilt of the younger leaves followed by the plant collapsing within a few days (Deutschmann 1954). The disease can cause severe damage for the growers and plant losses of up to 40% have been reported (Stensvand et al. 1999).

The most important short-term inoculum source for _P. cactorum_ is sporangia, which contains motile zoospores. However, this pathogen is homothallic and consequently produces resting spores (oospores) which can survive for many years in the soil even in the absence of a host plant. There are few means of eliminating this pathogen once a field is infected. Even with fumigation, the pathogen is rarely eliminated and once a nursery is infected there is a significant risk of rapid spread of the disease (Fennimore et al. 2008). Thus, the use of resistant cultivars to the disease is essential to maintain sustainable cultivation of the species.
The cultivar Senga Sengana has been known to show high levels of resistance to crown rot, while the majority of later releases adapted to the Nordic growing season appear highly susceptible (Eikemo et al. 2003). Two French cultivars, Cirafine and Cireine, are considered to harbor resistance comparable to that found in Senga Sengana (Schafleitner et al. 2013). While these cultivars provide valuable resources for breeding, they are, however, not adapted to the Nordic growing conditions.

Consequently, very few commercially acceptable varieties that are robust to the pathogen exist at the moment.

The genome of the commercially important *F. xananassa* strawberry is complex with a likely contribution from up to four diploid ancestors (Rousseau-Gueutin et al. 2009). The most accepted cytological model is that of Bringhurst (1990), who suggested the conformation AAA'A'BBB'B' indicating that the genome of the octoploid *Fragaria* has undergone diploidisation and that the inheritance is predominantly disomic, a hypothesis that was confirmed by linkage mapping evidence presented by Sargent et al. (2012) and van Dijk et al. (2014).

The polyploid constitution and high level of heterozygosity of the *F. xananassa* genome have made genetic analyses of quantitative traits and development of markers for molecular assisted selection challenging. Using the diploid *F. vesca* for genetic studies of *Phytophthora* resistance is an attractive approach to circumvent the complex genetics of the garden strawberry. The colinearity and high degree of macro-synteny between the diploid and the octoploid species (Sargent et al. 2012; van Dijk et al. 2014), ensures transferability between the species. Moreover, variability in the resistance response has been demonstrated (Eikemo et al. 2010).

The present invention is centered on delineating genetic markers and providing new genes that can be used as tools in the amelioration of resistant strawberry cultivars and/or to develop more effective control measures for disease management. Infection experiments were performed with a sparse diallel cross and an F₂ mapping population.
derived from two grandparents diverging in crown rot resistance. In addition, the mapping results are supported by microarray expression data.

The inventors have identified 16 genes that co-segregate with resistance to *Phytophthora cactorum* and that also are upregulated

It is thus an object of the present invention to provide a method for producing genetically modified plants having resistance to fungal pathogens, in particular Oomycetes. In particular the invention relates to a method for creating resistance to *Phytophthora cactorum* in plants of the genus *Fragaria*.

### BRIEF DESCRIPTION OF THE INVENTION

One aspect of the present invention relates to a method for producing a genetically modified plant cell, a plant or a part thereof with increased tolerance and/or resistance to Oomycetes as compared to a corresponding non-modified wild type plant cell, a plant or a part thereof, wherein the expression and/or activity of at least one polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to a polypeptide sequence selected from the group consisting of SEQ ID No.1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27, is increased or generated as compared to a corresponding non-modified wild type plant cell, a plant or a part thereof.

Another aspect of the present invention relates to a method for producing a genetically modified plant cell, a plant or a part thereof with increased tolerance and/or resistance to Oomycetes as compared to a corresponding non-modified wild type plant cell, a plant or a part thereof, wherein the expression of at least one polynucleotide comprising a polynucleotide having at least 80% identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule selected from the group consisting of SEQ ID No.2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26 and 28, or the corresponding complementary sequence thereof, is increased or generated as compared to a corresponding non-modified wild type plant cell, a plant or a part thereof.
A third aspect relates to isolated nucleic acids comprising a polynucleotide having at least 80% identity to a continuous stretch of at least 15 nt, preferably 20, 30, 50, 100, 200 or 500 nt of a nucleic acid molecule selected from the group consisting of SEQ ID No.2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26 and 28.

A fourth aspect of the invention relates to a transgenic plant cell, a plant tissue, a propagation material, a plant or a part thereof with increased tolerance and/or resistance to Oomycetes as compared to a corresponding non-transformed wild type plant cell, plant tissue, propagation material, plant or a part thereof produced by a the above methods wherein the transgenic plant cell, a plant or a part thereof is derived from a monocotyledonous or a dicotyledonous plant, preferably from a dicotyledonous plant, more preferably from a plant belonging to the genus *Fragaria*.

A fifth aspect relates to the use of at least one nucleic acid molecule having at least 80% identity to a continuous stretch of at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21 or 22 nt, within the nucleic acid molecule sequence of a polynucleotide comprising a nucleic acid molecule selected from the group consisting of SEQ ID No.2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26 and 28, in a method of measuring gene expression in plant offspring to control breeding success.

A sixth aspect relates to a plant of the genus *Fragaria*, obtained by crossing a plant selected from the group consisting of F. vesca (cvs 'Bukammen', 'NCGR1603'), and F × ananassa (cvs 'Korona','Polka','Senga Sengana', 'Sonata', 'Elsanta', 'Florence', 'Nobel', and 'Saga'), preferably wherein the plant or a part thereof has increased tolerance and/or resistance to Oomycetes as compared to a corresponding wild type F × ananassa (cvs 'Korona', 'Polka', 'Senga Sengana', 'Sonata', 'Elsanta', 'Florence', 'Nobel', and 'Saga') plant.

**BRIEF DESCRIPTION OF DRAWINGS**

*Fig. 1*. New resistance genes identified by crossing and microarray experiments as detailed below and corresponding SEQ ID numbers for mRNAs and polypeptides.
Fig. 2 New resistance genes identified by crossing and microarray experiments as detailed below and corresponding SEQ ID numbers for mRNAs and polypeptides.

Fig 3. Box-plots of the disease scores in the parents Bukammen and Haugast0l 3, the F1 hybrid and the F2-population divided into susceptible (F2_Susc) and resistant (F2_Res) genotypes.

Fig 4. The SNP-based linkage maps of the Bukammen x Haugast0l 3 mapping progeny based on 151 SNP markers generated by Genotyping-By-Sequencing (GBS).

Fig 5. The QTL analysis of Linkage Group 6 (LG6) of the Bukammen x Haugast0l 3 linkage map performed using interval mapping showing a major QTL between markers S6_5591260 (mapped at 0.0 cM) and S6_5569517 (mapped at 8.6 cM) with a LOD of 26.61 that explained a total of 74.4 % of the phenotypic variance (marker means AA=1.29 AB=1.29 BB=5.36 var=0.46).

Fig 6. Genetic data for Linkage Group 6 (LG6) of the Bukammen x Haugast0l 3 linkage map detailing the genetic position of the RPc-1 locus when scored as a dominant major gene in the 90 progeny. A indicates a homozygous genotype the same as that of the resistant parent, H indicates a heterozygous genotype, and B indicates a homozygous genotype the same as the susceptible parent. A score of S (susceptible) for the observed phenotype indicates a disease score higher than 2, whilst R (resistant) indicates a score below 2.

Fig 7. Box-plots representing log2 gene expression scores of the LOC101290881 gene in two genotypes, the susceptible CFRA1218 (1218) and the resistant CFRA1603 (1603), wounded (W) and inoculated (P) with Phytophthora cactorum. Samples were collected at 0 h (00), 24 h (24), and 72h (72) post inoculation. The LOC101290881 gene encodes a putative receptor-like protein-12.

Fig. 8. Experimental set-up of the microarray experiment. Each experimental cell has three biological replicates.
Fig. 9. Disease scores in a 6 x 6 sparse *Fragaria vesca* diallel artificially infected with *Phytophthora cactorum* and scored according to the method detailed in Eikemo *et al.*, 2000.

Fig. 10. A description of the seven linkage groups of the 'Bukammen x Haugastol 3' linkage map detailing the number of mapping bins and markers contained on each group, the total linkage group length and the marker density.

Fig. 11 Sixty-eight putative resistance genes found in the 3.3Mb QTL-region on LG6.

Fig. 12 Genes that are upregulated in the resistant genotype NCGR1603 and not regulated in the susceptible genotype NCGR1218 during the first 24 hours post infection with *Phytophthora cactorum*

**DETAILED DESCRIPTION OF THE INVENTION**

Plant pathogens such as Oomycetes are a constant threat to the cultivation and production of plants and their use as a source of food, fibre, medicaments and the like. Using the woodland strawberry *Fragaria vesca* as a model organism, the present inventors have identified a novel group of genes and corresponding polypeptides that play a role in resistance to Oomycetes, in particular to *Phytophthora cactorum*. These genes are (gene symbol given in brackets):

- receptor-like protein 12-like (LOC 101290881);
- receptor-like protein 12 (LOC 105352099);
- acid phosphatase 1-like (LOC 101300261);
- abscisic acid receptor PYL4-like (LOC 101304013);
- ammonium transporter 2-like (LOC 1013 12841);
- L-type lectin-domain containing receptor kinase S.4-like (LOC 101309756);
- serine/threonine-protein kinase AtPK2/AtPK19-like (LOC 1013 12550);
- uncharacterized protein Atlg04910-like [Pyrus x bretschneideri] (LOC 101298447);
- beta-galactosidase 13-like [Prunus mume] (LOC 1013 13427);
- nodulation- signaling pathway 2 protein-like (LOC 101309570);
ferritin-1, chloroplastic-like (LOC101293015);
L-type lectin-domain containing receptor kinase IV.l-like (LOC10130048); Uncharacterized in Fragaria; receptor-like protein 12 [Pyrus x bretschneideri] (LOC101305388); and
protein SRGI-like (LOC10129612)

SEQ ID Nos for the respective polypeptides and coding regions of these genes are depicted in Figures 1 and 2.

The expression of the above genes has been found to be upregulated upon infection of *F. vesca* plants with *Phytophthora cactorum* and these genes also show increased expression when comparing *P. cactorum* resistant plants which susceptible plants.

Thus, tolerance/resistance to Oomycetes, and particularly, *Phytophthora cactorum* and in general in plants thus appears to be linked to the generation and/or increase of expression of gene products, that is, polypeptides and/or RNA species, encoded by the genes of the invention.

For purposes of this specification, the term "gene" or "genes" is used to mean nucleic acid sequences (including both RNA or DNA) that encode genetic information for the synthesis of a whole RNA, a whole polypeptide, or any portion of such whole RNA or whole polypeptide. The term "coding region" refers to a nucleic acid sequence comprising, containing and preferably consisting of the genetic information for the synthesis of a whole RNA, a whole polypeptide, or any portion of such whole RNA or whole polypeptide. The term "gene products" refers to RNAs or proteins that are encoded by the gene.

Thus, it is an objective of the present invention to increase tolerance/resistance to Oomycetes in plants by generating and/or increasing expression of gene products, that is, RNA species and, optionally, polypeptides.
In a first aspect the invention thus provides a method for producing a genetically modified plant cell, a plant or a part thereof with increased tolerance and/or resistance to Oomycetes as compared to a corresponding non-modified wild type plant cell, a plant or a part thereof, wherein the expression and/or activity of at least one polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to a polypeptide sequence selected from the group consisting of SEQ ID No.1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27, is increased or generated as compared to a corresponding non-modified wild type plant cell, a plant or a part thereof.

In a preferred embodiment the polypeptide comprises a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to a polypeptide sequence of SEQ ID No.1.

As laid out above, also increasing the expression of gene products other than polypeptides is desirable in an effort to provide genetically modified plants with increased resistance to Oomycetes, as for example, the observed role of the genes of the invention might rely on the increased expression of RNA species.

In a second aspect the invention thus provides a method for producing a genetically modified plant cell, a plant or a part thereof with increased tolerance and/or resistance to Oomycetes as compared to a corresponding non-modified wild type plant cell, a plant or a part thereof, wherein the expression of at least one polynucleotide comprising a nucleic acid molecule having at least 80% identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule selected from the group consisting of SEQ ID No.2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26 and 28, or a corresponding complementary sequence thereof,
is increased or generated as compared to a corresponding non-modified wild type plant
cell, a plant or a part thereof.

In a preferred embodiment the at least one polynucleotide comprises a nucleic acid
molecule having at least 80% identity to a continuous stretch of at least 15 nt, preferably
20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt to a nucleic acid molecule of SEQ ID No.2 or
a corresponding complementary sequence thereof.

The term "nucleic acid molecule" refers to the genes (or corresponding coding regions)
of the inventions, or parts thereof, as defined herein. As laid out above it is an objective
of the present invention to increase tolerance/resistance to Oomycetes in plants by
generating and/or increasing expression of gene products of the genes of the invention,
that is, RNA species and, optionally, polypeptides, The term "expression of at least one
nucleic acid molecule" and "expression of at least one polynucleotide" are used
interchangeably and both refer to the generation of RNA species from a gene as defined
herein, preferably, a nucleic acid molecule having at least 80 % identity to a continuous
stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt to a
nucleic acid molecule selected from the group consisting of SEQ ID No.2, 4, 6, 8, 10, 12,
14, 16, 18, 20, 22, 24, 26 and 28, or a corresponding complementary sequence thereof.

The term "polynucleotide(s)" refers to RNA species which are encoded and/or
expressed from a gene as defined herein, e.g. by transcription. RNA species such as
ribosomal RNA (rRNA); short hairpin RNA (shRNA); small interfering RNA (siRNA);
microRNA (miRNA); messenger RNA (mRNA), or combinations thereof are
contemplated. RNA species have the nucleotide sequence as per SED ID Nos. 2, 4, 6, 8,
10, 12, 14, 16, 18, 20, 22, 24, 26 and 28, or a corresponding complementary sequence
thereof. The skilled person is aware of the concept of "base complementarity" in nucleic
acid sequences, as the bases Adenine (A) and Thymine (T), and Guanine (G) and
Cytosine (C) may hybridize due to hydrogen bonds between complementary bases. By
specifying a certain nucleic acid sequence the skilled person is thus automatically given
the necessary information to determine the complementary sequence.
The term "expression of at least one polynucleotide" refers to the generation of RNA species from a gene as defined herein.

The term "expression" with respect to polypeptides refers to the generation of polypeptide molecules e.g. by translation from a RNA species, e.g. an mRNA.

As used herein, the terms "peptide", "oligopeptide", "polypeptide" and "protein" may be used interchangeably. Peptides may contain non-natural amino acids and may be joined to linker elements known to the skilled person. Peptides may also be monomeric or multimeric.

The term "expression is increased or generated" means that expression of polypeptides and/or expression of at least one nucleic acid molecule, as defined herein, is increased, when compared to the expression level of the non-modified plant as defined herein, or is generated if such expression is not detectable in the non-modified wild type plant cell, a plant or a part thereof.

The term "activity" with respect to polypeptides refers to an enzymatic activity of the respective polypeptide, e.g kinase activity. The skilled person is aware of a plurality of assays and test methods to test such activities. The level of expression of polypeptides can be measured as a function of their enzymatic activity, as defined above. Preferably, the enzymatic activity is increased by at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 140, 160, 180, 200, 300, 400, 500, 600, or 700% compared to the corresponding non-modified wild type plant cell, a plant or a part thereof.

Alternatively, protein expression can be measured by antibody-staining and detection as for example, with enzyme linked immunosorbent assays (ELISAs), e.g. in the form of a dot blot, slot blot etc. Quantitative methods employing bioluminescence, chemoluminescence etc. and high-resolution imaging e.g. with CCD cameras allow for quantitative determination of proteins in cell extracts ate. Preferably, the expression of the at least one polypeptide is increased by at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 140, 160, 180, 200, 300, 400, 500, 600, or 700% compared to the
corresponding non-modified wild type plant cell, a plant or a part thereof.

The expression level of the at least one polynucleotide, that is, RNA species, can be determined by standard methods in the field, for example based on polymerase chain reaction-protocols, e.g. Real time quantitative PCR (RT-qPCR) employing proprietary methodology such as Lightcycler technology etc. Preferably, the expression of the at least one polynucleotide is increased by at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 140, 160, 180, 200, 300, 400, 500, 600, or 700% compared to the corresponding non-modified wild type plant cell, a plant or a part thereof. Alternatively, microarray-technology can be employed to measure abundance of RNA species in a sample, wherein RNA samples are reverse transcribed and labelled with fluorescent dyes and then hybridised onto microarrays containing immobilised DNA probes, and analysis of fluorescent signals is then performed. Data can be expressed e.g. as fold logarithmic changes (e.g. natural logarithm, In) over control samples. Preferably, the expression of the at least one polynucleotide, that is, the RNA species, preferably mRNA, as defined herein, is increased by a fold change in \( \ln \) of at least 1.0; 1.1; 1.2; 1.5; 1.7; 2.0; 2.5; 3.0; 3.5; 4.0; 4.5; 5.0; 6; 7; 8; 9; or 10 compared to the corresponding non-modified wild type plant cell, a plant or a part thereof.

In the context of the invention, the term "genetically modified" encompasses methods and protocols to influence the expression of a gene and thus inducing the synthesis of a whole RNA, a whole polypeptide, or any portion of such whole RNA or whole polypeptide or a part thereof in a plant cell, plant or part thereof. In particular, the term "genetically modified" also explicitly refers to the generation of transgenic plants by introducing into a plant at least one heterologous nucleic acid sequence or gene.

In a preferred embodiment of the methods for producing a genetically modified plant cell, a plant or a part thereof in accordance with the first two aspects, the expression and/or activity of at least one polypeptide as identified above, and/or of the nucleic acid as identified above is increased or generated by introduction of at least one heterologous nucleic acid into a plant cell, or, in other words, the production of a transgenic plant.
As used herein, "heterologous nucleic acid" refer to DNA or RNA that does not occur naturally as part of the plant genome in which it is present or which is found in a location or locations in the genome that differ from that in which it occurs in nature. Thus, heterologous or foreign DNA or RNA is nucleic acid that is not normally found in the host genome in an identical context. It is DNA or RNA that is not endogenous to the cell and has been exogenously introduced into the cell. In one aspect, heterologous DNA may be the same as the host DNA but modified by methods known in the art, where the modifications include, but are not limited to, insertion in a vector, linked to a foreign promoter and/or other regulatory elements, or repeated at multiple copies. In another aspect, heterologous DNA may be from a different organism, a different species, a different genus or a different kingdom, as the host DNA. Further, the heterologous DNA may be a transgene. As used herein, "transgene" refers to a segment of DNA containing a gene, which gene is not present in the host plant.

In a preferred embodiment the transgene is a gene as defined herein, having a sequence that has been isolated from one organism and is then introduced into a different organism. For example, a gene or a part thereof as defined herein, e.g. a polynucleotide comprising a polynucleotide having at least 80% identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt to a nucleic acid molecule selected from the group consisting of SEQ ID No.2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26 and 28, or a corresponding complementary sequence thereof, is introduced into an organism different from Fragaria vesca, e.g. into Fragaria x ananassa.

Also, activation of a host gene by genetic modification as defined herein is specifically contemplated, e.g. increasing or generating expression of an RNA species and/or increasing or generating expression or activity of a polypeptide by activating transcription from a host gene.

The term "host gene" and "endogenous gene" are used interchangeably. Methods to increase endogenous gene expression are known to the skilled person. Site directed introduction of a constitutive promoter active in plants (e.g. 35S CaMV) into a desired locus can be performed, e.g. by Cre-lox mediated insertion, bringing an endogenous
gene under the control of a strong promoter. Alternatively, also an endogenous gene or nucleic acid sequence, e.g. a copy of the coding region, can be operably linked to a promoter functional in plants, or the host gene can be employed, e.g. inserted into an expression vector, cosmid, phage, etc. and used for transforming the plant cell, plant or parts thereof, and regeneration of plants. Regarding the instant genes, this would mean to increase expression of *F. vesca* genes in a genetically modified *F.vesca* plant cell, plant or part thereof etc.

As described herein the 14 genes identified in the invention play a role in pathogen resistance, and, clearly also combinations of such genes, or nucleic acid molecules, can be employed in the methods of the invention.

In a preferred embodiment of the method of the first aspect the expression and/or activity of at least one polypeptide comprises a polypeptide selected from the group consisting of:

(i) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No.1, and/or

(ii) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No.3, and/or

(iii) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No.5, and/or

(iv) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No.7, and/or

(v) a polypeptide comprising a polypeptide having at least 80% identity to a
continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No. 9, and/or

(vi) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No. 11, and/or

(vii) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No. 13, and/or

(viii) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No. 15, and/or

(ix) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No. 17, and/or

(x) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No. 19, and/or

(xi) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No. 21, and/or

(xii) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No. 23, and/or

(xiii)a polypeptide comprising a polypeptide having at least 80% identity to a
continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No. 25, and/or
(xiv) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No. 27,
is increased or generated as compared to a corresponding non-modified wild type plant cell, a plant or a part thereof.

Any combination of the polypeptides of the invention and derivatives, as defined above, is contemplated, e.g. further preferred embodiment relates to a genetically modified plant cell, plant or part thereof according to the first aspect, expressing polypeptides according to SEQ ID Nos 1 and 3 and derivatives thereof, as defined herein. Another preferred embodiment refers to polypeptides according to SEQ ID Nos 1 and 5, and derivatives thereof as defined herein; or to polypeptides according to SEQ ID Nos 1 and 7, and derivatives thereof as defined herein; or to polypeptides according to SEQ ID Nos 1 and 9, and derivatives thereof as defined herein; or to polypeptides according to SEQ ID Nos 1 and 11, and derivatives thereof as defined herein; or to polypeptides according to SEQ ID Nos 1 and 13, and derivatives thereof as defined herein; or to polypeptides according to SEQ ID Nos 1 and 15, and derivatives thereof as defined herein; or to polypeptides according to SEQ ID Nos 1 and 17, and derivatives thereof as defined herein; or to polypeptides according to SEQ ID Nos 1 and 19, and derivatives thereof as defined herein; or to polypeptides according to SEQ ID Nos 1 and 21, and derivatives thereof as defined herein; or to polypeptides according to SEQ ID Nos 1 and 23, and derivatives thereof as defined herein; or to polypeptides according to SEQ ID Nos 1 and 25, and derivatives thereof as defined herein; or to polypeptides according to SEQ ID Nos 1 and 27. Similar combinations starting from SEQ ID Nos 3, 5, 7 etc. are contemplated.

In a preferred embodiment of the method of the first and second aspect the expression of at least one polynucleotide comprising a nucleic acid molecule selected from the
group consisting of:

a) a nucleic acid molecule encoding a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to a polypeptide selected from the group consisting of of SEQ ID No.1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide selected from the group consisting of SEQ ID No.1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27;

b) a nucleic acid molecule having at least 80% identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of a nucleic acid molecule selected from the group consisting of SEQ ID No.2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26 and 28, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide selected from the group consisting of SEQ ID No.1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27;

c) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence selected from the group consisting of SEQ ID No.1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide selected from the group consisting of SEQ ID No.1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27;

d) a nucleic acid molecule which hybridizes with a nucleic acid molecule of a) to c) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide selected from the group consisting of SEQ ID No.1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27;

e) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of a) to e) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in a) to d) and preferably encoding a polypeptide having the activity represented by a
protein comprising a polypeptide selected from the group consisting SEQ ID No.1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27, is increased or generated as compared to a corresponding non-modified wild type plant cell, a plant or a part thereof.

In a preferred embodiment of the method of the first and second aspect the expression of at least one polynucleotide comprising a nucleic acid molecule selected from the group consisting of:

a) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.1 and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1,

b) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.2, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1,

c) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 1, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1,

d) a nucleic acid molecule which hybridizes with a nucleic acid molecule of a) to c) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1,

e) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of a) to d) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized...
in al) to a4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1, and/or

bl) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.3, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.3,

b2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.4, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.3,

b3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 3, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.3,

b4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of bl) to b3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.3,

b5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of bl) to b4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in bl) to b5) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.3, and/or

c1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.5, and
preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.5,
c2) a nucleic acid molecule having at least 80% identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule
sequence of the nucleic acid molecule of SEQ ID No.6, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.5,
c3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No.5, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.5,
c4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of c1) to c3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.5,
c5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of c1) to c4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in c1) to c4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.5, and/or
d1) a nucleic acid molecule encoding a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.7, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.7,
d2) a nucleic acid molecule having at least 80% identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.8, or a corresponding
complementary sequence thereof, and preferably encoding a polypeptide having the
activity represented by a protein comprising a polypeptide of SEQ ID No.7,
d3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code,
can be derived from a polypeptide sequence of SEQ ID No. 7, and preferably encoding
a polypeptide having the activity represented by a protein comprising a polypeptide of
SEQ ID No.7,
d4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of d1) to d3)
under stringent hybridization conditions, and preferably encoding a polypeptide having
the activity represented by a protein comprising a polypeptide of SEQ ID No.7,
d5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid
library under stringent hybridization conditions with a probe comprising a
complementary sequence of a nucleic acid molecule of d1) to d4) or with a fragment
thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a
nucleic acid molecule complementary to a nucleic acid molecule sequence characterized
in d1) to d4) and preferably encoding a polypeptide having the activity represented by a
protein comprising a polypeptide of SEQ ID No.7, and/or

e1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a
continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140,
160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.9, and
preferably encoding a polypeptide having the activity represented by a protein
comprising a polypeptide of SEQ ID No.9,
e2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least
15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid
molecule
sequence of the nucleic acid molecule of SEQ ID No.10, or a corresponding
complementary sequence thereof, and preferably encoding a polypeptide having the
activity represented by a protein comprising a polypeptide of SEQ ID No.9,
e3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code,
can be derived from a polypeptide sequence of SEQ ID No. 9, and preferably encoding
a polypeptide having the activity represented by a protein comprising a polypeptide of
SEQ ID No.9,
e4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of e1) to e3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 9,
e5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of e1) to e5) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in e1) to e5) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 9, and/or
f1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 11, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 11,
f2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No. 12, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 11,
f3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 11, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 11,
f4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of f1) to f3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 11,
f5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of f1) to f4) or with a fragment
thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in f1) to f4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1, and/or

5 g1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.13, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.13,

g2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt , preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.14, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.13,

g3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No.13, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.13,

g4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of g1) to g3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.13,

g5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of g1) to g4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in g1) to g4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.13, and/or

hi) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a
continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 15, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 15,

h2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No. 16, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 15,

h3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 15, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 15,

h4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of hi) to h3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 15,

h5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of hi) to h4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in hi) to h4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 15, and/or

11) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 17, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17,

12) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid
molecule

sequence of the nucleic acid molecule of SEQ ID No. 18, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17,

13) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 17, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17,

14) a nucleic acid molecule which hybridizes with a nucleic acid molecule of il) to i3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17,

15) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of il) to i4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in il) to i4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17, and/or

j1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 19, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 19,

j2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.20, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 19,

j3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 19, and preferably encoding
a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.19,
j4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of j1) to j3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.19,
j5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of j1) to j4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in j1) to j5) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.19, and/or

kl) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.21, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.21,
k2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.22, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.21,
k3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 21, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.21,
k4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of kl) to k3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.21,
k5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid
library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of k1) to k4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in k1) to k4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.23, and/or

11) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.23, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.23,

12) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.24, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.23,

13) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 23, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.23,

14) a nucleic acid molecule which hybridizes with a nucleic acid molecule of 11) to 13) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.23,

15) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of 11) to 14) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in 11) to 14) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.23, and/or
a nucleic acid molecule encoding a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 25, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.25,
m2) a nucleic acid molecule having at least 80% identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid sequence of the nucleic acid molecule of SEQ ID No.26, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.25,
m3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 25, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.25,
m4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of m1) to m3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.25,
m5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of m1) to m4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in m1) to m4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.25, and/or

a nucleic acid molecule encoding a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.27, and preferably encoding a polypeptide having the activity represented by a protein
comprising a polypeptide of SEQ ID No.27,

n2) a nucleic acid molecule having at least 80% identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.28, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.27,

n3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 27, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.27,

n4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of nl) to n3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.27,

n5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of nl) to n4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in nl) to n4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.27,

is increased or generated as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

In addition to the contemplated combination relating to combinations of polypeptides as defined above, also any combination of the nucleic acid molecules of the invention and derivatives, as defined above, is contemplated. Thus further preferred embodiment relate to a genetically modified plant cell, plant or part thereof according to the first or second aspect, expressing nucleic acid molecules according to SEQ ID Nos 2 and 4 and derivatives thereof, as defined herein. Another preferred embodiment refers nucleic acid molecules according to SEQ ID Nos 2 and 6, and derivatives thereof as defined
herein; or to nucleic acid molecules according to SEQ ID Nos 2 and 8, and derivatives thereof as defined herein; or to nucleic acid molecules according to SEQ ID Nos 2 and 10, and derivatives thereof as defined herein; or to nucleic acid molecules according to SEQ ID Nos 2 and 12, and derivatives thereof as defined herein; or to nucleic acid molecules according to SEQ ID Nos 2 and 14, and derivatives thereof as defined herein; or to nucleic acid molecules according to SEQ ID Nos 1 and 16, and derivatives thereof as defined herein; or to nucleic acid molecules according to SEQ ID Nos 2 and 18, and derivatives thereof as defined herein; or to nucleic acid molecules according to SEQ ID Nos 2 and 20, and derivatives thereof as defined herein; or to nucleic acid molecules according to SEQ ID Nos 2 and 22, and derivatives thereof as defined herein; or to nucleic acid molecules according to SEQ ID Nos 2 and 24, and derivatives thereof as defined herein; or to nucleic acid molecules according to SEQ ID Nos 2 and 26, and derivatives thereof as defined herein; or nucleic acid molecules according to SEQ ID Nos 2 and 28. Similar combinations starting from SEQ ID Nos 4, 6, 8 etc. are contemplated.

In a third aspect the invention provides an isolated nucleic acid molecule comprising a nucleic acid molecule selected from the group consisting of

a) a nucleic acid molecule encoding a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.1 and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1,

a2) a nucleic acid molecule having at least 80% identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.2, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1,

a3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 1, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of
SEQ ID No.1,

a4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of al) to a3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1,

a5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of al) to a4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in al) to a4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1, and/or

b1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.3, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.3,

b2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt , preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.4, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.3,

b3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 3, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.3,

b4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of bl) to b3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.3,

b5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a
complementary sequence of a nucleic acid molecule of bl) to b4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in bl) to b5) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.3, and/or

c1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.5, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.5,  
c2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt , preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule  
sequence of the nucleic acid molecule of SEQ ID No.6, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.5,  
c3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 5, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.5,  
c4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of c1) to c3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.5,  
c5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of c1) to c4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in c1) to c4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.5, and/or
dl) a nucleic acid molecule encoding a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.7, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.7,

d2) a nucleic acid molecule having at least 80% identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.8, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.7,

d3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No.7, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.7,

d4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of dl) to d3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.7,

d5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of dl) to d4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in dl) to d4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.7, and/or

el) a nucleic acid molecule encoding a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.9, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.9,

e2) a nucleic acid molecule having at least 80% identity to a continuous stretch of at least
15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No. 10, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 9,

e3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 9, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 9,

e4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of e1) to e3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 9,

e5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of e1) to e5) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in e1) to e5) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 9, and/or

f1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 11, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 11,

f2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No. 12, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 11,

f3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code,
can be derived from a polypeptide sequence of SEQ ID No. 11, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 11,

f4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of f1) to f3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1 1,

f5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of f1) to f4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in f1) to f4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1 1, and/or

g1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 13, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 13,

g2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt , preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.1 4, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 13,

g3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 13, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.13,

g4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of g1) to g3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 13,
g5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of g1) to g4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in g1) to g4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 13, and/or

h1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 15, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 15.

h2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No. 16, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 15.

h3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 15, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 15.

h4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of h1) to h3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 15.

h5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of h1) to h4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in h1) to h4) and preferably encoding a polypeptide having the activity represented by a
protein comprising a polypeptide of SEQ ID No. 15, and/or

11) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 17, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17.

12) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid sequence of the nucleic acid molecule of SEQ ID No. 18, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17.

13) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 17, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17.

14) a nucleic acid molecule which hybridizes with a nucleic acid molecule of i) to i3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17.

15) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of i) to i4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in i) to i4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17, and/or

16) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 19, and preferably encoding a polypeptide having the activity represented by a protein
comprising a polypeptide of SEQ ID No. 19,
j2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least
15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid
sequence of the nucleic acid molecule of SEQ ID No. 20, or a corresponding
complementary sequence thereof, and preferably encoding a polypeptide having the
activity represented by a protein comprising a polypeptide of SEQ ID No. 19,
j3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code,
can be derived from a polypeptide sequence of SEQ ID No. 19, and preferably encoding
a polypeptide having the activity represented by a protein comprising a polypeptide of
SEQ ID No. 19,
j4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of j1) to j3)
under stringent hybridization conditions, and preferably encoding a polypeptide having
the activity represented by a protein comprising a polypeptide of SEQ ID No. 19,
j5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid
library under stringent hybridization conditions with a probe comprising a
complementary sequence of a nucleic acid molecule of j1) to j4) or with a fragment
thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a
nucleic acid molecule complementary to a nucleic acid molecule sequence characterized
in j1) to j5) and preferably encoding a polypeptide having the activity represented by a
protein comprising a polypeptide of SEQ ID No. 19, and/or
kl) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a
continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140,
160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 21, and
preferably encoding a polypeptide having the activity represented by a protein
comprising a polypeptide of SEQ ID No. 21,
k2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least
15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid
sequence of the nucleic acid molecule of SEQ ID No. 22, or a corresponding
complementary sequence thereof, and preferably encoding a polypeptide having the
activity represented by a protein comprising a polypeptide of SEQ ID No.21,
k3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 21, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.21,
k4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of k1) to k3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.21,
k5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of k1) to k4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in k1) to k4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.21, and/or
11) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.23, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.23,
12) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt , preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule
sequence of the nucleic acid molecule of SEQ ID No.24, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.23,
13) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 23, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.23,
14) a nucleic acid molecule which hybridizes with a nucleic acid molecule of 11) to 13)
under stringent hybridization conditions, and preferably encoding a polypeptide having
the activity represented by a protein comprising a polypeptide of SEQ ID No.23,
15) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid
library under stringent hybridization conditions with a probe comprising a
complementary sequence of a nucleic acid molecule of 11) to 14) or with a fragment
thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a
nucleic acid molecule complementary to a nucleic acid molecule sequence characterized
in 11) to 14) and preferably encoding a polypeptide having the activity represented by a
protein comprising a polypeptide of SEQ ID No.23, and/or
ml) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a
continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140,
160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.25, and
preferably encoding a polypeptide having the activity represented by a protein
comprising a polypeptide of SEQ ID No.25,
m2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at
least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid
molecule sequence of the nucleic acid molecule of SEQ ID No.26, or a corresponding
complementary sequence thereof, and preferably encoding a polypeptide having the
activity represented by a protein comprising a polypeptide of SEQ ID No.25,
m3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code,
can be derived from a polypeptide sequence of SEQ ID No. 25, and preferably encoding
a polypeptide having the activity represented by a protein comprising a polypeptide of
SEQ ID No.25,
m4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of ml) to
m3)
under stringent hybridization conditions, and preferably encoding a polypeptide having
the activity represented by a protein comprising a polypeptide of SEQ ID No.25,
m5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid
library under stringent hybridization conditions with a probe comprising a
complementary sequence of a nucleic acid molecule of ml) to m4) or with a fragment
thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a
nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in ml) to m4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.25, and/or

nl) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.27, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.27,

n2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.28, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.27,

n3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 27, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.27,

n4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of nl) to n3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.27,

n5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of nl) to n4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in nl) to n4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.27.

With respect to similarities in macromolecules (nucleic acids, polypeptides) the term "identity" refers to sequence identity. As used herein, "sequence identity" and "%" (or
percent) sequence identity" is determined by comparing two optimally aligned sequences over a comparison window, where the fragment of the nucleic acid sequence in the comparison window may comprise additions or deletions (e.g., gaps or overhangs) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the comparison window and multiplying the result by 100 to provide the percentage of sequence identity. Algorithms to align sequences are known in the art. Exemplary algorithms include, but are not limited to, the local homology algorithm of Smith and Waterman (Add APL Math, 2: 482, 1981); the homology alignment algorithm of Needleman and Wunsch (J Mol Biol, 48: 443, 1970); the search for similarity method of Pearson and Lipman (Proc Natl Acad Sci USA, 85: 2444, 1988); and computerized implementations of these algorithms (GAP, BESTFIT, BLAST, PASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, Wis.). In one aspect, two sequences may be aligned using the "Blast 2 Sequences" tool at the NCBI website at default settings (Tatusova and Madden. FEMS Microbiol Lett, 174: 247-250, 1999). Alternatively, nucleic acids sequences may be aligned by human inspection.

Preferred polypeptides comprise a contiguous span of at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to a polypeptide sequence selected from the group consisting of SEQ ID No.1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27. Preferably the identity is at least 85, 86, 87, 88, 89, 90, 91, 92, 93 94, 95, 96, 97, 98, 99% or is a 100%.

In an even more preferred embodiment the polypeptide comprise a contiguous span of at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to a polypeptide sequence of SEQ ID No.1.
In an even more preferred embodiment the polypeptide comprise a contiguous span of at least 85% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to a polypeptide sequence of SEQ ID No.1.

In a preferred embodiment the polypeptide comprise a contiguous span of at least 90% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to a polypeptide sequence of SEQ ID No.1.

In a preferred embodiment the polypeptide comprise a contiguous span of at least 95%, at least 96, 97, 98 or 99% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to a polypeptide sequence of SEQ ID No.1.

Another preferred embodiment of the invention refers to a recombinant nucleic acid molecule which confers the expression of at least one polynucleotide and/or at least one nucleic acid molecule as defined above, wherein the recombinant nucleic acid molecule additionally comprises one or more regulatory elements, optionally operably linked to the at least one nucleic acid molecule, whereby expression of the at least one nucleic acid in a host cell results in increased tolerance and/or resistance to Oomycetes as compared to a corresponding non-modified wild type plant cell, a plant or a part thereof.

The recombinant nucleic acid molecule may be a linear or circular, single-stranded or double-stranded DNA or RNA molecule, that can confer expression of the nucleic acid molecules and/or polypeptides, as defined above, in a host cell.

As used herein, "operably-linked" refers to two nucleic acid sequences that are related physically or functionally. For example, a regulatory element is said to be "operably linked to" a coding sequence if the two sequences are situated such that the regulatory DNA sequence affects expression of the coding DNA sequence. Coding sequences may be operably-linked to regulatory sequences in sense or antisense orientation.
As used herein, "regulatory element" refers to nucleic acid sequences that affect the expression of a coding sequence or gene, as defined above. Regulatory elements are known in the art and include, but are not limited to, promoters, enhancers, transcription terminators, polyadenylation sites, matrix attachment regions and/or other elements that regulate expression of a coding sequence.

As used herein, a "promoter" refers to a nucleotide sequence that directs the initiation and rate of transcription of a coding sequence. The promoter contains the site at which RNA polymerase binds and also contains sites for the binding of other regulatory elements (such as transcription factors). Promoters may be naturally occurring or synthetic. Further, promoters may be species specific (for example, active only in B. napus); tissue specific (for example, the Brassica napin or cruciferin seed specific promoters, the soybean glycinin or conglycinin promoters); developmentally specific (for example, active only during embryogenesis); constitutive (for example, Nopaline synthase, Beta actin, ubiquitin, CsVMV and CaMV 35S promoters); or inducible (for example the stilbene synthase promoter). A promoter includes a minimal promoter that is a short DNA sequence comprised of a TATA box or an Inr element, and other sequences that serve to specify the site of transcription initiation, to which regulatory elements are added for control of expression. A promoter may also refer to a nucleotide sequence that includes a minimal promoter plus DNA elements that regulates the expression of a coding sequence, such as enhancers and silencers. For example, plant cells may be modified by transformation with a nucleic acid construct under the control of a heterologous promoter.

Another preferred embodiment of the invention refers to a vector comprising at least one nucleic acid molecule as defined above, or comprising at least one recombinant nucleic acid molecule as defined above whereby expression of said at least one nucleic acid in a host cell results in increased tolerance and/or resistance to Oomycetes as compared to a corresponding non-modified wild type plant cell, a plant or a part thereof.

The terms "vector" and "nucleic acid construct" are used interchangeably and refer to
all plasmids, cosmids, viruses and other means to introduce and propagate nucleic acid molecules in(to) plants. Vectors for cloning and/or for expression of nucleic acids in plants are well known in the art.

In preparation for the introduction of the at least one gene of the invention, or derivatives thereof, as defined above, into higher plants or their cells, a large number of cloning vectors are available which contain a replication signal for E. coli and a marker gene for selecting transformed bacterial cells. Examples of such vectors are pBR322, pUC series, M13 mp series, pACYC184 etc. The desired sequence can be introduced at a suitable restriction site in the vector. The obtained plasmid is used for transformation of E. coli cells. The plasmid is recovered. The analytical methods for the characterization of the obtained plasmid DNA can comprise restriction analysis, gel electrophoresis and other biochemical-molecular biological methods that are generally used. After each manipulation the plasmid DNA can be cleaved and the obtained DNA fragments may be linked to other DNA sequences. Each plasmid DNA sequence can be cloned in the same or other plasmids. Standard methods for cloning can Sambrook et al, 2001 (Molecular Cloning: A Laboratory Manual, 3rd edition, Cold Spring Harbor Laboratory Press).

The vectors that are used for expression of the nucleic acid molecules and/or the polypeptides as defined above, may contain in addition to the nucleic acid sequence, as defined above, or the recombinant nucleic acid as defined above, to be transmitted, further regulatory elements.

What specific regulatory elements these vectors must contain, in each case depends on the method that should be carried out with these vectors.

for producing transgenic plants in which the at least one gene and/or polypeptide is expressed. Typically, vectors are employed containing regulatory elements that convey transcription and, if desired, translation of nucleic acid molecules and/or genes, as defined above, in the plant cell. Enhancer elements, resistance genes, replication signals and other DNA regions which allow for propagation of the vectors in bacteria such as E.
coli are contemplated. The regulatory elements include sequences which bring about a stabilization of the vectors in the host cells. In particular, regulatory elements include those sequences which allow a stable integration of the vector into the host genome of the plant or an autonomous replication of the vector in the plant cells. Such regulatory elements are known in the art.

Another preferred embodiment of the invention refers to a composition comprising the nucleic acid molecule, the recombinant nucleic acid molecule, or the vector as described above, and optionally an agricultural acceptable carrier.

Another preferred embodiment of the first and second aspects and embodiments thereof as defined above invention refers to a method for producing a genetically modified plant cell, a plant or a part thereof with increased tolerance and/or resistance to Oomycetes as compared to a corresponding non-modified wild type plant cell, a plant or a part thereof, comprising:

a) transforming a plant cell, or a part of a plant with a vector as defined above and/or a composition as defined above, and

b) generating from the plant cell or the part of a plant a transgenic plant.

Preferably, the carrier is an *Agrobacterium tumefaciens* vector.


The introduction of DNA into plant cells by Agrobacterium mediated transfer is well known to those skilled in the art. Virulent strains of Agrobacterium contain a large plasmid DNA known as a Ti-plasmid that contains genes required for DNA transfer (vir genes), replication and a T-DNA region that is transferred to plant cells. The T-DNA region is bordered by T-DNA border sequences that are essential to the DNA transfer process. These T-DNA border sequences are recognized by the vir genes. The two primary types of Agrobacterium-based plant transformation systems include binary [see for example U.S. 4,940,838] and co-integrate [see for example Fraley et al. Biotechnology, 3: 629-635, 1985] methods. In both systems, the T-DNA border repeats are maintained and the natural DNA transfer process is used to transfer the DNA fragment located between the T-DNA borders into the plant cell genome.

Another method for introducing DNA into plant cells is by biolistics. This method involves the bombardment of plant cells with microscopic particles (such as gold or tungsten particles) coated with DNA. The particles are rapidly accelerated, typically by gas or electrical discharge, through the cell wall and membranes, whereby the DNA is released into the cell and incorporated into the genome of the cell. This method is used for transformation of many crops, including corn, wheat, barley, rice, woody tree species and others. Biolistic bombardment has been proven effective in transfecting a wide variety of animal tissues as well as in both eukaryotic and prokaryotic microbes, mitochondria, and microbial and plant chloroplasts (Johnston. Nature, 346: 776-777, 1990; Klein et al. Bio/Technol, 10: 286-291, 1992; Pecorino and Lo. Curr Biol, 2:30-32, 1992; Jiao et al, Bio/Technol, 11: 497-502, 1993).

Another method for introducing DNA into plant cells is by electroporation. This method involves a pulse of high voltage applied to protoplasts/cells/tissues resulting in transient pores in the plasma membrane which facilitates the uptake of foreign DNA.
The foreign DNA enter through the holes into the cytoplasm and then to the nucleus.

Plant cells may be transformed by liposome mediated gene transfer. This method refers to the use of liposomes, which are circular lipid molecules with an aqueous interior, to deliver nucleic acids into cells. Liposomes encapsulate DNA fragments and then adhere to and fuse with the cell membranes resulting in the transfer of DNA. The DNA enters the cell and then to the nucleus.

Nucleic acid constructs of the present invention may be introduced into plant protoplasts. Plant protoplasts are cells in which its cell wall is completely or partially removed using either mechanical or enzymatic means, and may be transformed with known methods including, calcium phosphate based precipitation, polyethylene glycol treatment and electroporation (see for example Potrykus et al., Mol. Gen. Genet., 199: 183, 1985; Marcotte et al., Nature, 335: 454, 1988). Polyethylene glycol (PEG) is a polymer of ethylene oxide. It is widely used as a polymeric gene carrier to induce DNA uptake into plant protoplasts. PEG may be used in combination with divalent cations to precipitate DNA and effect cellular uptake. Alternatively, PEG may be complexed with other polymers, such as poly(ethylene imine) and poly L lysine.

Plant cell culture techniques are known in the art (see for example Fischer et al. Biotechnol Appl Biochem, 30: 109-11 2, 1999; Doran. Current Opinions in Biotechnology, 11: 199-204, 2000). The skilled person would appreciate that the composition of the culture media, its pH and the incubating conditions, such as temperatures, aeration, C02 levels, and light cycles, may vary depending on the type of cells.

After transformation, plant cells may be sub-cloned to obtain clonal populations of cells. Methods of sub-cloning cells are known in the art and include, but are not limited to, limiting dilution of the pool of transformed cells. The transformed cells may also be grown under selective pressure to identify those that contain and/or express the gene product associated with plant fatty acid metabolism. In this regard, the nucleic acid construct encodes a selectable marker. Selectable markers may be used to select for
plants or plant cells that contain the exogenous genetic material. The exogenous genetic material may include, but is not limited to, an enzyme that confers resistance to an agent such as a herbicide or an antibiotic, or a protein that reports the presence of the construct.

Examples of a selectable marker include, but are not limited to, a neo gene, which codes for kanamycin resistance and can be selected for using kanamycin, Rptl, G418, hpt etc.; an amp resistance gene for selection with the antibiotic ampicillin; an hygromycinR gene for hygromycin resistance; a BAR gene (encoding phosphinothricin acetyl transferase) which codes for bialaphos resistance; a mutant EPSP synthase gene, aadA, which encodes glyphosate resistance; a nitrilase gene, which confers resistance to bromoxynil; a mutant acetolactate synthase gene (ALS), which confers imidazolinone or sulphphonylurea resistance, ALS, and a methotrexate resistant DHFR gene. Other non-selectable but screenable markers include: a beta-glucuronidase or uidA gene (GUS), which encodes an enzyme for which various chromogenic substrates are known, green fluorescent protein (GFP), and luciferase (LUX).

A nucleic acid construct of the present invention may encode a gene conferring resistance to bialaphos (also known as bilanafos or PPT; commercialized under the trade-marks Basta(R), Buster(R) and Liberty(R)) which is converted to the phytotoxic agent phosphinothricin in plant cells. In one aspect, the bialaphos resistance gene is a BAR gene. In another aspect, multiple copies of the glutamine synthetase gene confer resistance to bialaphos.

After preparing clonal populations of transgenic plant cells, the cells may be characterized and selected based on analysis at the level of DNA, RNA and protein. Preferably, transgenic plant cells in which the nucleic acid construct is stably integrated into DNA are selected. As used herein, "stably integrated" refers to the integration of genetic material into the genome of the transgenic plant cell and remains part of the plant cell genome over time and passage number.

Stable integration of nucleic acid constructs may be influenced by a number of factors
including, but not limited to, the transformation method used and the vector containing
the gene of interest. The transformation method determines which cell type can be
targeted for stable integration. The type of vector used for stable integration defines the
integration mechanism, the regulation of transgene expression and the selection
conditions for stably expressing cells. After integration, the level and time of
expression of the gene of interest may depend on the linked promoter and on the
particular integration site.

The site of integration may affect the transcription rate of the gene of interest. Usually
an expression plasmid is integrated into the genome of the target cell randomly.
Integration into inactive heterochromatin results in little or no transgene expression,
whereas integration into active euchromatin often allows transgene expression.

A fourth aspect of the present invention refers to a transgenic plant cell, a plant tissue, a
propagation material, a plant or a part thereof with increased tolerance and/or resistance
to Oomycetes as compared to a corresponding non-transformed wild type plant cell,
plant tissue, propagation material, plant or a part thereof produced by a method as
defined above, wherein the transgenic plant cell, a plant or a part thereof is derived
from a monocotyledonous or a dicotyledonous plant, preferably from a dicotyledonous
plant, more preferably from a plant belonging to the genus Fragaria.

A preferred embodiment of the fourth aspect refers to a seed produced by a transgenic
plant as defined above, wherein the seed is genetically homozygous for at least one
transgene comprising at least one nucleic acid sequence as per al) through n5) as
defined above, conferring increased tolerance and/or resistance to Oomycetes as
compared to a corresponding non-transformed wild type plant cell, a plant or a part
thereof.

A fifth aspect of the invention refers to the use of at least one nucleic acid molecule as
declared herein for producing a transgenic plant cell, plant or a part thereof with
increased tolerance and/or resistance to Oomycetes compared to a corresponding non
transformed wild type plant cell, a plant or a part thereof.
In the context of the present invention, "plant" refers to a eukaryotic species that contains, in addition to a nucleus and mitochondria, chloroplasts capable of carrying out photosynthesis. A plant may be unicellular, multi-cellular or comprised of numerous tissues or organs. Plants may reproduce sexually or asexually and may be perennial or annual in growth habit. Plants may be terrestrial or aquatic. As used herein, a plant encompasses a plant cell, plant organ or plant tissue, or other parts of a whole plant such as shoot vegetative organs/structures (e.g. leaves, stems and tubers), roots, flowers and floral organs/structures (e.g. bracts, sepals, petals, stamens, carpels, anthers and ovules), seeds (including embryo, endosperm, and seed coat) and fruits (the mature ovary), plant tissues (e.g. vascular tissue, ground tissue, and the like) and cells (e.g. guard cells, egg cells, trichomes and the like), and progeny of the same.

As used herein, "transgenic plant" refers to a plant, plant cell culture, plant cell line, plant tissue culture, or progeny of a transformed plant cell or protoplast wherein foreign genetic material has been introduced into the genome of the plant cell. The terms "transgenic plant" and "transformed plant" are used synonymously to refer to a plant whose genome contains exogenous genetic material.

As used herein, "plant cell culture" refers to plant cells maintained in media and separated from their original tissue source. Plant cell cultures are typically grown as cell suspension cultures in liquid medium or as callus cultures on solid medium.

In a preferred embodiment the transgenic plant produced by the methods of the invention is a monotypeledonous plant, belonging to the genera Avena (oat), Triticum (wheat), Secale (rye), Hordeum (barley), Oryza (rice), Panicum, Pennisetum, Setaria, Sorghum (millet), or Zea (maize).

In yet another preferred embodiment, the plant is a dicotyledonous plant, selected from cotton, legumes such as pulses and in particular alfalfa, soyben, oilseed rape, canola, tomato, sugar beet, potato, sunflower, tobacco, ornamentals and trees.
In yet another preferred embodiment the dicotyledonous plant is a plant of the family *Rosaceae*, preferably the plant is selected from apples, pears, quinces, apricots, plums, cherries, peaches, raspberries, loquats, and strawberries, almonds, ornamental trees and roses, meadowsweets, photinias, firethorns, rowans, and hawthorns.

In an even more preferred embodiment the plant belongs to the genus *Fragaria*, and is preferably selected from the group consisting of *Fragaria bucharica* *Fragaria daltoniana*; *Fragaria gracilis*; *Fragaria iinumae*; *Fragaria nilgerrensis*; *Fragaria nipponica*; *Fragaria nubicola*; *Fragaria pentaphylla*; *Fragaria rubicola*; *Fragaria vesca*; *Fragaria viridis*; *Fragaria yezoensis*; *Fragaria x bifera*; *Fragaria moupinensis*; *Fragaria orientalis*; *Fragaria x bringhurstii*; *Fragaria moschata*; *Fragaria x ananassa*; *Fragaria chiloensis*; *Fragaria iturupensis*; *Fragaria virginiana*; *Fragaria cascadensis*.

In a very preferred embodiment the plant is *F. vesca*, or *F x ananassa*.

In the most preferred embodiment the plant is *F x ananassa*.

According to the present invention the term "increased tolerance" and/or "increased resistance" to Oomycete infection relates to a reduction in signs and symptoms of infection of plants, as defined above, with Oomycetes, in particular the genus *Phytophthora*. Preferably, but not necessarily, increased tolerance and/or resistance to Oomycetes leads to an improved survival and growth of the genetically modified plants.

In a preferred embodiment of the genetically modified plants of the invention, the plant survives for at least one, two, three, four, five, six, seven, eight, nine, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 weeks post-infection with an Oomycete.

However, depending on the severity of the pathogen-induced symptoms, also more subtle effects than survival vs. death can be effected by expression of the polypeptides and/or nucleic acids as defined herein. In a preferred embodiment the genetically modified plants of the invention produce at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100,
110, 120, 140, 160, 180, 200, 300, 400, 500, 600, or 700% more biomass than the non-modified plants, upon inoculation and/or infection with the Oomycete

In a preferred embodiment of the invention the genetically modified plants of the invention display increased tolerance and/or resistance towards Oomycetes.

In another preferred embodiment of the invention plants show increased tolerance and/or resistance towards Oomycetes of the genus *Phytophthora*, preferably at least one species selected from the group consisting of *Phytophthora alni*, *Phytophthora botryose*, *Phytophthora cactorum*, *Phytophthora cajani*, *Phytophthora cambivora*, *Phytophthora capsici*, *Phytophthora cinnamomi*, *Phytophthora citricola*, *Phytophthora citrophthora*, *Phytophthora clandestine*, *Phytophthora colacasiae*, *Phytophthora cryptogea*, *Phytophthora drechslera*, *Phytophthora erythroseptica*, *Phytophthora fragariae*, *Phytophthora gonapodyides*, *Phytophthora heveae*, *Phytophthora humicola*, *Phytophthora idaei*, *Phytophthora ilicis*, *Phytophthora infestans*, *Phytophthora inflata*, *Phytophthora iranica*, *Phytophthora katsurae*, *Phytophthora lateralis*, *Phytophthora medicagnis*, *Phytophthora megakarya*, *Phytophthora megasperma*, *Phytophthora melonis*, *Phytophthora mirabilis*, *Phytophthora multivesiculata*, *Phytophthora nicotianae*, *Phytophthora palmivora*, *Phytophthora phaseoli*, *Phytophthora porri*, *Phytophthora primulae*, *Phytophthora pseudotsugae*, *Phytophthora quercina*, *Phytophthora ramorum*, *Phytophthora sinensis*, *Phytophthora sojae*, *Phytophthora syringae*, *Phytophthora tentaculata*, *Phytophthora trifolii*, *Phytophthora vignae*

In a very preferred embodiment of the invention the genetically modified plants of the invention display increased tolerance and/or resistance towards *Phytophthora cactorum*.

For *Phytophthora cactorum* a previously described method for scoring of the disease can be performed (Eikemo H, Stensvand A, Tronsmo AM (2000) Evaluation of methods of screening strawberry cultivars for resistance to crown rot caused by *Phytophthora cactorum*. Ann appl Biol 137: 237-244). Briefly, plants are inoculated
with *Phytophthora cactorum* and are monitored in the following weeks for symptoms and survival, and scores are given on a scale from 1 to 8 as follows: The plants that die during the first, second, third, or fourth week after inoculation are given the scores 8, 7, 6, or 5, respectively. After 4 weeks, the remaining plants are bisected longitudinally and scored 1 to 4 based on the degree of necrosis in the crown: 1 = no symptoms, 2 = a few brown/dark speckles, 3 = small patches of necrosis, and 4 = more than 50% of the crown necrotic.

Thus in most preferred embodiment the genetically modified plants of the invention display increased tolerance and/or resistance towards *Phytophthora cactorum*, wherein the mean disease score, as defined above, is at least 1.0; 1.1; 1.2; 1.3; 1.4; 1.5; 1.6; 1.7; 1.8; 1.9; 2.0; 2.1; 2.2; 2.3; 2.4; 2.5; 2.6; 2.7; 2.8; 2.9; 3.0; 3.1; 3.2; 3.3; 3.4; 3.5; 3.6; 3.7; 3.8; or 3.9.

As detailed above the genes of the invention as defined herein play a role in pathogen resistance to Oomycetes. Thus, their expression level is most likely connected to the resistance/tolerance of a given plant towards Oomycetes, e.g. such of the genus *Phytophthora*.

Thus, another aspect of the invention refers to the use of at least one nucleic acid molecule having at least 80% identity to a continuous stretch of at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21 or 22 nt, within the nucleic acid molecule sequence of a nucleic acid molecule selected from the group consisting of SEQ ID No.2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26 and 28, or a corresponding complementary sequence thereof, in a method of measuring gene expression in plant offspring to control breeding success.

Alternatively, the activity and/or expression of polypeptides as defined herein can be measured in a method of controlling breeding success.

The above method thus allows to assay/screen any given plant, preferably from the genus *Fragaria* as defined above by measuring/determining the activity and/or
expression of polypeptides and/or expression of at least one nucleic acid molecule, as defined herein.

The term "activity" with respect to polypeptides refers to an enzymatic activity of the respective polypeptide, e.g. kinase activity. The skilled person is aware of a plurality of assays and test methods to test such activities. The level of expression of polypeptides can be measured as a function of their enzymatic activity, as defined above. Preferably, the enzymatic activity is increased by at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 140, 160, 180, 200, 300, 400, 500, 600, or 700% compared to the corresponding non-modified wild type plant cell, a plant or a part thereof.

Alternatively, protein expression can be measured by antibody-staining and detection as for example, with enzyme linked immunosorbent assays (ELISAs), e.g. in the form of a dot blot, slot blot etc. Quantitative methods employing bioluminescence, chemoluminescence etc. and high-resolution imaging e.g. with CCD cameras allow for quantitative determination of proteins in cell extracts. Preferably, the expression of the at least one polypeptide is increased by at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 140, 160, 180, 200, 300, 400, 500, 600, or 700% compared to the corresponding non-modified wild type plant cell, a plant or a part thereof.

The expression level of the at least one polynucleotide, that is, RNA species, can be determined by standard methods in the field, for example based on polymerase chain reaction-protocols, e.g. Real time quantitative PCR (RT-qPCR) employing proprietary methodology such as Lightcycler technology etc. Preferably, the expression of the at least one polynucleotide is increased by at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 140, 160, 180, 200, 300, 400, 500, 600, or 700% compared to the corresponding non-modified wild type plant cell, a plant or a part thereof. Alternatively, microarray-technology can be employed to measure abundance of RNA species in a sample, wherein RNA samples are reverse transcribed and labelled with fluorescent dyes and then hybridised onto microarrays containing immobilised DNA probes, and analysis of fluorescent signals is then performed. Data can be expressed e.g. as fold logarithmic changes (e.g. natural logarithm, ln) over control samples. Preferably, the
expression of the at least one polynucleotide, that is, the RNA species, preferably mRNA, as defined herein, is increased by a fold change in \( \ln \) of at least 1.0; 1.1; 1.2; 1.5; 1.7; 2.0; 2.5; 3.0; 3.5; 4.0; 4.5; 5.0; 6; 7; 8; 9; or 10 compared to the corresponding non-modified wild type plant cell, a plant or a part thereof.

As laid out below, resistant F. vesca variants have been employed in isolating the new resistance genes of the invention. The offspring of a crossing between F. vesca plants resistant to Oomycetes, in particular \( P. cactorum \), and \( F \times ananassa \) plants, that is, \( F \times ananassa \) plants with increased tolerance and/or resistance to Oomycetes is also contemplated.

A sixth aspect thus relates to a plant of the genus \( Fragaria \), obtained by crossing a plant selected from the group consisting of F. vesca (cvs 'Bukammen', 'NCGR1603') and \( F \times ananassa \) (cvs 'Korona', 'Polka', 'Senga Sengana', 'Sonata', 'Elsanta', 'Florence', 'Nobel', and 'Saga'), preferably wherein the plant or a part thereof has increased tolerance and/or resistance to Oomycetes as compared to a corresponding wild type \( F \times ananassa \) (cvs 'Korona', 'Polka', 'Senga Sengana', 'Sonata', 'Elsanta', 'Florence', 'Nobel', and 'Saga') plant.

A seventh aspect relates to a plant of the genus \( Fragaria \), obtained by crossing two plants selected from the group consisting of F. vesca (cvs 'Bukammen', 'NCGR1603', Alta, Haugast0l 3, CFRA1428, CFRA1603, CFRA1848) wherein the plant or a part of the plant comprises in its genome at least one allele conferring increased tolerance and/or resistance to Oomycetes as compared to a corresponding wild type F. vesca plant.

In one embodiment said plant or the part of the plant the at least said allele is in the RPc-1 locus.
EXAMPLES

Plant material development

Sparse diallel development: Based on previous work (Eikemo et al. 2010) a sparse diallel cross between four *P. cactorum* susceptible and four resistant *F. vesca* genotypes was made. The four susceptible genotypes were FDP821 (*F. vesca* ssp. *americana*), CFRA0424 (*F. vesca* ssp *bracteata*), Haugastol3 (*F. vesca* ssp. *vesca*), and CFRA1428 (*F. vesca* ssp. *vesca*), while the resistant genotypes were Alta, Bukammen, CFRA1603, and CFRA1848 (all *F. vesca* ssp. *vesca*). One confirmed hybrid from each attempted cross combination was propagated and tested for *P. cactorum* susceptibility.

F₂ mapping population development: Three hybrid plants from the Bukammen (♀) × Haugastol3 (♂) cross were selfed using bagging. They all produced ample amounts of F₂ seed and one of these batches were chosen at random for mapping and QTL identification purposes.

The hybrid nature in three F₁ progeny from each cross in the sparse diallel was confirmed using the microsatellites CFVCT011 (Monfort et al. 2006), UDF 006 (Cipriani et al. 2006), EMFvi3, and EMFvi7 (James et al. 2003) labelled on the forward primer with either 6-FAM, VIC, NED, or PET fluorescent dyes (Applied Biosystems, Forster City, CA, USA). DNA was extracted using DNeasy Plant Mini Kit (Qiagen). Amplification was performed in a final volume of 25 µL, containing 10 ng genomic DNA, 1x PCR buffer (Invitrogen), 1.5 mM MgCl₂, 0.2 mM each dNTP, 0.2 µM each primer, and 0.5 U Taq polymerase. The 'touch-down' PCR conditions of Sargent et al. (2003) were used: an initial denaturation step of 94 °C (2 min), then 10 cycles of 94 °C (30 s), 60-55 °C annealing temperature decreasing by 0.5 °C per cycle (45 s) and 72 °C (1 min), followed by 25 cycles of 94 °C (30 s), 55 °C (45 s) and 72 °C (1 min), and a final elongation step of 72 °C (5 min). The PCR products were separated by capillary electrophoresis through a 3730 genetic analyser against the 600LIZ size standard (Applied Biosystems) and the data generated were analysed and alleles were sized using the GENEMAPPER software (Applied Biosystems).

Plant propagation
The parents and one hybrid plant from each realized cross in the sparse diallel were multiplied by runner plants. From the Bukammen × Haugastøl 3 mapping population the selected F₂ seed batch was germinated and propagated together with the grand-parental and the parental Fi genotypes. Runner plants from each of the grand-parents, the Fi hybrid and 93 F₂ plants from the mapping population, as well as the parents and the hybrids from the sparse diallel, were collected and transplanted to flats in a greenhouse with 16 h day/20 °C and 8 h night/14 °C. Artificial light was provided by high-pressure sodium lamps (SON/T, 120 µE·s⁻¹·m⁻²) in periods of less than 16 h of natural light. After establishment, the plants were grown for an additional two weeks before pathogen inoculation and tissue sampling.

**Preparation of inoculum, inoculation and disease scoring**

Nine equal-sized plants from each of the 96 genotypes in the F₂ mapping population and from one hybrid and the parents in the sparse diallel cross were selected for the infection experiment. The infection experiment was established in a completely randomized design and plants were grown under the same conditions as during the pre-inoculation. The plants were inoculated with a suspension of zoospores (2 x 10⁵ spores/plant) of *P. cactorum* (Bioforsk isolate ID 10300) after gently wounding the rhizome with a scalpel, as described by Eikemo et al. (2010).

The scoring of disease symptoms was done according to Eikemo et al. (2000) and Simpson et al. (1994). Plants that died during the first, second, third, or fourth week after inoculation were given the scores 8, 7, 6, 5, respectively. After 4 weeks, the remaining plants were bisected longitudinally and scored 1 to 4 based on the degree of necrosis in the crown: 1 = no symptoms, 2 = a few brown/dark speckles, 3 = small patches of necrosis, and 4 = more than 50 % of the crown necrotic.

**DNA extraction and genotyping**

Young leaf tissue from one representative of each of 93 progeny plants, the grand-parental and Fi parental genotypes was flash frozen in liquid nitrogen and lyophilized prior to infection for DNA extraction. DNA was extracted from the leaf tissue using the DNeasy plant miniprep kit (Qiagen) according to the manufacturer's protocol and subsequently shipped to the Institute for Genomic Diversity (IGD; Cornell University, Ithaca, NY) for genotyping-by-sequencing (GBS). The standard procedure for GBS described by Elshire et al. (2011) was followed, but the restriction enzyme *Pst*I was
used in place of ApelKI and a total of 96 bar-coded adaptors were used to genotype the progeny. The data were processed at IGD using TASSEL-GBS (Glaubitz et al. 2014) and the generated HapMap format files were filtered on 'missingness' to include only loci for which there were data for more than 80 % of the progeny.

**Linkage map construction and QTL analysis**

Data produced by TASSEL-GBS were coded as an F2 segregating population using the genotypes of the grand-parental accessions to correctly phase the markers. Re-coded data were analysed using JoinMap 4.1 (Kyazma, NL). Marker placement was determined using a minimum logarithm of odds (LOD) score threshold of 3.0, a recombination fraction threshold of 0.35, ripple value of 1.0, jump threshold of 3.0 and a triplet threshold of 5.0, and mapping distances were calculated using the Kosambi mapping function. Linkage groups were identified and named according to the pseudo-chromosomes to which the mapped markers were associated in the v1.1 *F. vesca* genome sequence (Sargent et al. 2011; Shulaev et al. 2011) following analysis with TASSEL-GBS. The linkage maps presented were plotted using MapChart 2.1 (Voorrips 2002).

QTL analyses were conducted using MapQTL 6.0 (Kyasma) by performing interval mapping (IM), following which markers most significantly associated with *Phytophthora* resistance were selected for use as co-factors and the multiple QTL method (MQM) was implemented to look for additional minor QTL. A 95 % genome wide LODs threshold for *Phytophthora* resistance was calculated using 1,000-permutation test using the average disease score for the nine replicates of each genotype scored. A step size of 1 cM was used in both the IM and MQM analyses.

**Mapping of Phytophthora resistance as a major gene**

Following QTL analysis and scrutiny of the segregation distortion on LG6 of the Bukammen x Haugastøl 3 linkage map, the data suggested that *Phytophthora* resistance segregated as a single dominant gene that governed resistance, with possible additional, undetected loci controlling symptom severity. Resistance data were recoded as resistant (dominant to susceptible and therefore coded 'D' for mapping in JoinMap 4.1) or susceptible (recessive and thus coded 'B' since resistance was conferred by the female grand-parental genotype), and resistance was included as a single gene character for linkage group construction as described above.
Analysis of gene expression in resistant and susceptible cultivars following pathogen challenge

A microarray experiment was performed using a susceptible (CFRA1218) and a resistant (CFRA1603) *F. vesca* accession (Eikemo et al. 2010). The plants were inoculated as described above and sampled according to Figure 8. Five clonal plants of each genotype were pooled into each of three biological replicates within each experimental cell. Crowns were split in half and a 2 - 3 cm long section of the pith was cut out with a scalpel, flash frozen and stored at -80 °C. RNA was extracted using the Spectrum™ Plant Total RNA Kit. The resultant 30 RNA samples were subsequently prepared and hybridized to a customized *Fragaria* microarray with 43,723 unique 60 mer probes as described by Rohloff et al. (2010) and Koehler et al. (2012a). The Limma (Linear Models for Microarray Data) package (version 3.18.13) (Smyth 2005) and R version 3.0.3 were used for statistical analysis and identification of significant differentially expressed genes. Single color feature expression files from the microarray scans were generated with Feature Extraction Software version 9.5.1 (Agilent Technologies, Inc). Median signal intensities were used and weak or not detected spots were given reduced weight, using the limma weight function. The data were normalized using the quantile method, no background subtraction was performed. A design matrix was created and pair-wise comparisons between the samples were performed. The method of Benjamini and Hochberg (1995) was used to estimate the false discovery rate. The log2 expression data were filtered to fit the profile 'up-regulated in CFRA1603 (R) and not upregulated in CFRA1218 (S)' after inoculation. A gene was considered up-regulated when the adj.P.Val < 0.01 and the logFC > 1. An additional candidate gene list was generated using the 'decideTests' tool provided in limma and the resulting probe lists from the two approaches were merged.

Identification of candidate genes for Phytophthora resistance from the *F. vesca* genome sequence

The *F. vesca*-accession 'Hawaii 4' genome sequence annotation for the genomic region surrounding the *Phytophthora* resistance gene locus identified in this experiment was downloaded from the Genome Database for Rosaceae (GDR) (Jung et al. 2013). Gene IDs were retrieved from the annotation, and the corresponding mRNA sequences were used as blastn queries at the NCBI nucleotide repository. Function for all genes
contained in the interval was inferred from the best hits recovered with a functional annotation. Following the identification of a candidate gene through the mapping and gene expression experiments, the structure and function of the candidate gene was predicted using Phyre2 (Kelley and Sternberg 2009).

Results

**Symptom expression and disease scoring in the sparse diallel cross**

The results shown in Figure 9 thus include crosses between *F. vesca* subsp. *vesca* accessions. While the results from the current scores on the parental material are consistent with the scores in previous studies (Eikemo et al. 2010), hybrid material has to our knowledge not been reported previously. In cases where a resistant genotype was crossed with a susceptible genotype, or the reciprocal cross was performed, the F1 hybrid showed resistance on the same level as the resistant parent, indicating that no maternal effects were present. Despite only one F1 hybrid genotype representing each cross combination was tested, the results were consistent across all combinations. This demonstrates that resistance to *P. cactorum* in *F. vesca* is under nuclear control and that the resistance is dominant. However, the Haugast01 3 x CFRA1428 and the CFRA1603 x CFRA1428 hybrids, say, indicate that the dominance may not be absolute in all cases and that modifying genes might be present.

**Symptom expression and disease scoring in mapping population**

Disease was scored on a scale from 1 to 8 (Eikemo H, Stensvand A, Tronsmo AM (2000) Evaluation of methods of screening strawberry cultivars for resistance to crown rot caused by *Phytophthora cactorum*. Ann appl Biol 137: 237-244). The plants that died during the first, second, third, or fourth week after inoculation were given the scores 8, 7, 6, or 5, respectively. After 4 weeks, the remaining plants were bisected longitudinally and scored 1 to 4 based on the degree of necrosis in the crown: 1 = no symptoms, 2 = a few brown/dark speckles, 3 = small patches of necrosis, and 4 = more than 50% of the crown necrotic. For the purpose of the genetic analyses the F2 genotypes were classified as resistant if their score average was below 2 - meaning that symptoms in the resistant genotypes were hardly detected in the tissues even after dissection of the crown. As seen in Fig 3 there is large variation within the five groups at the single plant level, in particular the variation seem to increase as the average disease scores increase. This was very pronounced in the susceptible F2 genotypes and
also in the susceptible grandparental genotype Haugast0l 3. Variation in expression of symptoms is well known for this disease, and has also been shown in earlier studies where variation within cultivars has been reported (Gooding et al. 1981; Pettitt and Pegg 1994).

The results showed significant differences between individual F₂ progeny (p < 0.0001). Fifty-six F₂ progenies had the same level of resistance as the resistant grand parent, Bukammen. Whilst only two progenies were scored equally susceptible to the other grand parent Haugast0l 3, an additional 14 F₂ genotypes were classified as susceptible. Thus, the distribution of disease scores was skewed towards the resistant side of the distribution (figure not shown). The hypothesis of a 3:1 segregation based on phenotypic classification alone was rejected (χ² = 4.28, p<0.05).

**Genotyping-by-sequencing data analysis and linkage map construction**

Following analysis of data obtained using the GBS protocol of Elshire et al. (2011) with TASSEL-GBS (Glaubitz et al. 2014) a total of 830 SNPs, for which less than 20% missing data were recovered. The segregating SNPs were recoded corresponding to an F₂ population using the grand-parental and Fi scores for each SNP and all non-segregating SNPs (those for which less than three genotypes were observed in the progeny) were removed, leaving a total of 218 segregating SNPs.

The segregating SNPs were used for linkage map construction using JoinMap 4.1 (Kyazma, NL) and a total of 136 unique mapping bins containing 151 SNPs coalesced into the seven expected linkage groups for a diploid F₂ linkage map, spanning a total of 416.2 cM. The longest linkage group was LG3, spanning 89.5 cM and containing 48 SNPs. The shortest was LG4, containing 8 SNPs and covering a total of 24.2 cM. The average marker density across the map was one SNP per 2.76 cM. Significant segregation distortion was observed for SNP markers mapping to LG5 (75 % mapped markers), LG6 (75 % mapped markers) and LG7 (69 % mapped markers). The number of SNPs contained on each of the seven linkage groups and the respective lengths and marker densities of each linkage group are given in Figure 10. Fig 4 shows the linkage map developed and the genetic positions of all 151 SNPs mapped in the progeny.

**QTL mapping**

A single major QTL, with a LOD of 26.61 that explained a total of 74.4% of the phenotypic variance (marker means AA=1.29 AB=1.29 BB=5.36 var=0.46) was
identified on LG6 of the Bukammen x Haugast0l 3 linkage map following analysis using IM. The QTL was identified between markers S6_5591260 (mapped at 0.0 cM) and S6_5569517 (mapped at 8.6 cM) (Fig 5). Marker S6_5569517 was most significantly associated with Phytophthora resistance (LOD=25.18 PVE=72.4%; marker means AA=1.23 AB=1.29 BB=4.52 var=0.50) and thus it was selected as a co-factor for MQM analysis. Following MQM analysis, no additional QTL were identified associated with Phytophthora resistance.

**Mapping Phytophthora resistance as a single genetic locus**

Following scoring of Phytophthora disease symptoms as a single major gene (A0 x A0), the locus mapped to LG6 in an interval between markers S6_5569517 and S6_8871004. Resistance data for the genotypes fit the SNP genotype data well in all but one case. For seedling_232, heterozygous genotypes were returned for all SNPs mapped, despite phenotypic data suggesting it was a susceptible seedling (Figure 6), and thus this seedling may have displayed phenotype-genotype incongruence (Padmarasu et al. 2014). Since the genetic data for resistance we report here fitted well to a single dominant gene hypothesis, we propose the name RPc-1 (Resistance to Phytophthora cactorum 1) for the locus.

**Identification of candidate genes for Phytophthora resistance from the Fragaria vesca genome sequence**

The interval to which Phytophthora resistance mapped spanned a total of 3.3 Mb of the F. vesca Hawaii 4 vl.1 genome sequence. Within this region, 801 gene predictions were recovered from the GDR. Following analysis with blastn a total of 645 genes returned a significant match to genes with predicted function in the EMBL nucleotide database. Of these genes, 68 had a putative role in plant disease resistance and could be divided into 15 classes. In summary these 68 returned matches to genes with the following known or predicted function: ABC transporter, calcium binding protein, calcium-dependent protein kinase, L-type lectin domain-containing protein kinases, non-specific lipid transfer proteins, MLO proteins, cyclic nucleotide-gated ion channel proteins, resistance gene analogues, receptor-like proteins, protein kinases, receptor protein kinases, serine-threonine kinases, WRKY transcription factors, and a homologue of phenylalanine ammonia lyase. Figure 11 lists the 68 putative resistance genes in the region to which
RPc-1 was mapped, the gene's known or predicted function to which they were most significantly associated, and their putative roles in disease resistance.

Identification of candidate genes for Phytophthora resistance from microarray experiment

A microarray experiment was performed with two other genotypes than the ones that were used in the QTL analysis - the susceptible CFRA1218 and the resistant CFRA1603 identified by Eikemo et al. (2010). The filtering of the expression data revealed 14 genes (Figures 1, 2 and 12) within the S6_5569517 - S6_8871004 interval that were up-regulated in the resistant genotype, CFRA1603, following infection with P. cactorum, while not regulated in CFRA1218.

The most significantly up-regulated gene associated with disease resistance found in this study within the LG6 mapping interval was a receptor-like protein 12 (LOC101290881). In the control plants (not wounded and not inoculated), the expression of LOC101290881 was 3.6-fold higher in the resistant genotype than in the susceptible (Figure 7). At 24 hs post inoculation, expression of LOC101290881 was more than 17-fold higher in the inoculated resistant genotype than in the resistant control (not wounded and not inoculated). The level of expression in the susceptible genotype remained at the level observed in the control. The 17-fold response coincided with a B-statistic of 22.3 provided by the limma package, indicating a high probability of this gene being differentially expressed in the two genotypes.

At 72 hs post inoculation, expression of LOC101290881 in the resistant genotype remained high compared to the control (19-fold rise) but still had not changed in the susceptible genotype. Expression of LOC101290881 in resistant control plants that had been wounded but not inoculated, was also significantly higher than in the untreated control plants (4.6-fold increase). However, expression levels were 4-fold lower than in the wounded, inoculated plants (Fig. 7).

The predicted mRNA corresponding to Frag005689 (LOC101290881) is encoding a predicted receptor-like protein-12 in F. vesca. Analysis of the protein structure and function using Phyre2 (Kelley and Sternberg 2009) identified this protein with 100 % confidence (32 % identity) as belonging to the family of leucine-rich repeat, receptor-like protein kinases, LRR-RLP (PLN00113, E-value = 3.37e-55) with roles as pattern-recognition receptors perceiving pathogen-associated molecular patterns (Zipfel 2014).
Other genes associated with disease resistance from the LG6 resistance QTL region were also up-regulated (Figure 12). The gene represented by probe Frag005693 has not been predicted in Fragaria (NCBI). However, it also represents a receptor-like protein-12 gene which was identified in Pyrus x bretschneideri. The genes represented by probes Frag032073 (LOC101313427) and Frag032074 (gene symbol not available in Fragaria NCBI), are genes coding for dehydration-responsive element-binding protein 2A (DREB2A) which is a key transcription factor involved in the network that controls the plant's response to dehydration and heat stress (Shinozaki and Yamaguchi-Shinozaki 1996); LOC101309570 codes in Arabidopsis for a DELLA (RGA-like) protein which are known to be involved in the regulation of the jasmonate signaling pathway; and finally, LOC101303588, represents a leucine-rich repeat receptor-like protein kinase. These genes were all significantly differentially expressed according to their B-values, but none were as highly up-regulated or were up-regulated at the same level of significance as LOC101290881 in the resistant genotype (Figure 12).
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1. A method for producing a genetically modified plant cell, a plant or a part thereof with 
increased tolerance and/or resistance to Oomycetes as compared to a corresponding 
non-modified wild type plant cell, a plant or a part thereof, wherein the expression 
and/or activity of at least one polypeptide comprising a polypeptide having at least 80% identity 
to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 
200 amino acids according to a polypeptide sequence selected from the group consisting of SEQ ID No.1, 
3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27, is increased or generated as compared to a corresponding 
non-modified wild type plant cell, a plant or a part thereof.

2. A method for producing a genetically modified plant cell, a plant or a part thereof with 
increased tolerance and/or resistance to Oomycetes as compared to a corresponding 
non-modified wild type plant cell, a plant or a part thereof, wherein the expression of at least one polynucleotide comprising a nucleic acid 
molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 
20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule selected from the 
group consisting of SEQ ID No.2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26 and 28, or a 
corresponding complementary sequence thereof, is increased or generated as compared to a corresponding 
non-modified wild type plant cell, a plant or a part thereof.

3. A method according to claim 1, wherein the expression and/or activity of at least one 
polypeptide comprises a polypeptide selected from the group consisting of:

   (i) a polypeptide comprising a polypeptide having at least 80% identity to a 
   continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 
   100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide
sequence of SEQ ID No.1, and/or

(ii) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No.3, and/or

(iii) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No.5, and/or

(iv) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No.7, and/or

(v) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No.9, and/or

(vi) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No.11, and/or

(vii) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No.13, and/or

(viii) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No.15, and/or

(ix) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide
sequence of SEQ ID No. 17, and/or
(x) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No. 19, and/or

(xi) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No. 21, and/or

(xii) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No. 23, and/or

(xiii) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No. 25, and/or

(xiv) a polypeptide comprising a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide sequence of SEQ ID No. 27,
is increased or generated as compared to a corresponding non-modified wild type plant cell, a plant or a part thereof.

4. A method according to claims 1 to 3,
wherein the expression of at least one polynucleotide comprising a nucleic acid molecule selected from the group consisting of:
a) a nucleic acid molecule encoding a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to a polypeptide selected from the group consisting of of SEQ ID No. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27, and
preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide selected from the group consisting of SEQ ID No.1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27,
b) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of a nucleic acid molecule selected from the group consisting of SEQ ID No.2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26 and 28, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide selected from the group consisting of SEQ ID No.1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27,
c) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence selected from the group consisting of SEQ ID No.1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide selected from the group consisting of SEQ ID No.1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27,
d) a nucleic acid molecule which hybridizes with a nucleic acid molecule of a) to c) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide selected from the group consisting of SEQ ID No.1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27,
e) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of a) to e) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in a) to d) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide selected from the group consisting SEQ ID No.1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27,
is increased or generated as compared to a corresponding non-modified wild type plant cell, a plant or a part thereof.
5. A method according to claims 1 to 4, wherein the expression of at least one polynucleotide comprising a nucleic acid molecule selected from the group consisting of:

- **a1)** a nucleic acid molecule encoding a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.1 and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1,

- **a2)** a nucleic acid molecule having at least 80% identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.2, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1,

- **a3)** a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No.1, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1,

- **a4)** a nucleic acid molecule which hybridizes with a nucleic acid molecule of a1) to a3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1,

- **a5)** a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of a1) to a4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in a1) to a4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1, and/or

- **b1)** a nucleic acid molecule encoding a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140,
160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.3, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.3,
b2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule
sequence of the nucleic acid molecule of SEQ ID No.4, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.3,
b3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 3, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.3,
b4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of b1) to b3)
under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.3,
b5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of b1) to b4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in b1) to b5) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.3, and/or
c1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.5, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.5,
c2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule
sequence of the nucleic acid molecule of SEQ ID No. 6, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.5, c3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 5, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.5, c4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of cl) to c3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.5, c5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of cl) to c4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in cl) to c4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.5, and/or
d1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.7, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.7, d2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.8, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.7, d3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 7, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of
SEQ ID No.7,

d4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of d1) to d3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.7,

d5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of d1) to d4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in d1) to d4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.7, and/or

el) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.9, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.9,

e2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.10, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.9,

e3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 9, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.9,

e4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of el) to e3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.9,

e5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a
complementary sequence of a nucleic acid molecule of el) to e5) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in el) to e5) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.11, and/or

fl) a nucleic acid molecule encoding a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.11, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.11,

f2) a nucleic acid molecule having at least 80% identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.12, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.11,

D) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No.11, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.11,

f4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of fl) to f3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.11,

f5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of fl) to f4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in fl) to f4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.11, and/or
gl) a nucleic acid molecule encoding a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 13, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 13,

g2) a nucleic acid molecule having at least 80% identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No. 14, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 13,

g3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 13, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.13,

g4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of gl) to g3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 13,

g5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of gl) to g4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in gl) to g4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 13, and/or

hi) a nucleic acid molecule encoding a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 15, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 15,

h2) a nucleic acid molecule having at least 80% identity to a continuous stretch of at least
15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No. 16, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 15.

h3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 15, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 15.

h4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of hi) to h3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 15.

h5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of hi) to h4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in hi) to h4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 15, and/or

11) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 17, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17.

12) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No. 18, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17.

13) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code,
can be derived from a polypeptide sequence of SEQ ID No. 17, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17.

14) a nucleic acid molecule which hybridizes with a nucleic acid molecule of il) to i3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17,

15) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of il) to i4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in il) to i4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17, and/or

j1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 19, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 19,

j2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule
sequence of the nucleic acid molecule of SEQ ID No.20, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 19.

j3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 19, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 19,

j4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of j1) to j3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 19,
j5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of j1) to j4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in j1) to j5) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 19, and/or

k1) a nucleic acid molecule encoding a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 21, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 21,
k2) a nucleic acid molecule having at least 80% identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No. 22, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 21,
k3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 21, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 21,
k4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of k1) to k3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 21,
k5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of k1) to k4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in k1) to k4) and preferably encoding a polypeptide having the activity represented by a
protein comprising a polypeptide of SEQ ID No.21, and/or

11) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.23, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.23,

12) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid sequence of the nucleic acid molecule of SEQ ID No.24, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.23,

13) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 23, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.23,

14) a nucleic acid molecule which hybridizes with a nucleic acid molecule of 11) to 13) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.23,

15) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of 11) to 14) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in 11) to 14) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.23, and/or

16) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.25, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.25,
m2) a nucleic acid molecule having at least 80% identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No. 26, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.25.

m3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 25, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.25.

m4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of m1) to m3)

under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.25.

m5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of m1) to m4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in m1) to m4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.25, and/or

n1) a nucleic acid molecule encoding a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.27, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.27.

n2) a nucleic acid molecule having at least 80% identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.28, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the
activity represented by a protein comprising a polypeptide of SEQ ID No.27,
n3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code,
can be derived from a polypeptide sequence of SEQ ID No. 27, and preferably encoding
a polypeptide having the activity represented by a protein comprising a polypeptide of
SEQ ID No.27,

n4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of nl) to n3)
under stringent hybridization conditions, and preferably encoding a polypeptide having
the activity represented by a protein comprising a polypeptide of SEQ ID No.27,

n5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid
library under stringent hybridization conditions with a probe comprising a
complementary sequence of a nucleic acid molecule of nl) to n4) or with a fragment
thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a
nucleic acid molecule complementary to a nucleic acid molecule sequence characterized
in nl) to n4) and preferably encoding a polypeptide having the activity represented by a
protein comprising a polypeptide of SEQ ID No.27,

is increased or generated as compared to a corresponding non-transformed wild type
plant cell, a plant or a part thereof.

6.

An isolated nucleic acid molecule comprising a nucleic acid molecule selected from the

article consisting of:

a1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a
continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140,
160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.1 and
preferably encoding a polypeptide having the activity represented by a protein
comprising a polypeptide of SEQ ID No.1,

a2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least
15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid
molecule

sequence of the nucleic acid molecule of SEQ ID No.2, or a corresponding
complementary sequence thereof, and preferably encoding a polypeptide having the
activity represented by a protein comprising a polypeptide of SEQ ID No.1,
a3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 1, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1,
a4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of al) to a3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1,
a5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of al) to a4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in al) to a4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.1, and/or
bl) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.3, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.3,
b2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.4 or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.3,
b3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 3, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.3,
b4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of bl) to b3)
under stringent hybridization conditions, and preferably encoding a polypeptide having
the activity represented by a protein comprising a polypeptide of SEQ ID No.3,

b5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid
library under stringent hybridization conditions with a probe comprising a
complementary sequence of a nucleic acid molecule of b1) to b4) or with a fragment
thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a
nucleic acid molecule complementary to a nucleic acid molecule sequence characterized
in b1) to b5) and preferably encoding a polypeptide having the activity represented by a
protein comprising a polypeptide of SEQ ID No.3, and/or

cl) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a
continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140,
160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.5, and
preferably encoding a polypeptide having the activity represented by a protein
comprising a polypeptide of SEQ ID No.5,

c2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least
15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid
molecule
sequence of the nucleic acid molecule of SEQ ID No.6, or a corresponding
complementary sequence thereof, and preferably encoding a polypeptide having the
activity represented by a protein comprising a polypeptide of SEQ ID No.5,

c3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code,
can be derived from a polypeptide sequence of SEQ ID No. 5, and preferably encoding
a polypeptide having the activity represented by a protein comprising a polypeptide of
SEQ ID No.5,

c4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of cl) to c3)
under stringent hybridization conditions, and preferably encoding a polypeptide having
the activity represented by a protein comprising a polypeptide of SEQ ID No.5,

c5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid
library under stringent hybridization conditions with a probe comprising a
complementary sequence of a nucleic acid molecule of cl) to c4) or with a fragment
thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a
nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in cl) to c4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.5, and/or

d1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.7, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.7,

d2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.8, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.7,

d3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 7, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.7,

d4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of d1) to d3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.7,

d5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of d1) to d4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in d1) to d4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.7, and/or

e1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140,
160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.9, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.9, 
e2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule 
sequence of the nucleic acid molecule of SEQ ID No.10, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.9, 
e3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 9, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.9, 
e4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of el) to e3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.9, 
e5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of el) to e5) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in el) to e5) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.9, and/or 

f1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.11, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.11, 
f2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule
sequence of the nucleic acid molecule of SEQ ID No. 12, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 11.

D) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 11, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 11,

f4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of f1) to f3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 11,

f5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of f1) to f4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in f1) to f4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 11, and/or

g1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 13, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 13,

g2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No. 14, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 13,

g3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 13, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of
SEQ ID No.13,  
g4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of g1) to g3)  
under stringent hybridization conditions, and preferably encoding a polypeptide having  
the activity represented by a protein comprising a polypeptide of SEQ ID No. 13,  
g5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid  
library under stringent hybridization conditions with a probe comprising a  
complementary sequence of a nucleic acid molecule of g1) to g4) or with a fragment  
thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a  
nucleic acid molecule complementary to a nucleic acid molecule sequence characterized  
in g1) to g4) and preferably encoding a polypeptide having the activity represented by a  
protein comprising a polypeptide of SEQ ID No. 13, and/or  

h1) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a  
continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140,  
160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 15, and  
preferably encoding a polypeptide having the activity represented by a protein  
comprising a polypeptide of SEQ ID No. 15,  
h2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least  
15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid  
molecule  
sequence of the nucleic acid molecule of SEQ ID No. 16, or a corresponding  
complementary sequence thereof, and preferably encoding a polypeptide having the  
activity represented by a protein comprising a polypeptide of SEQ ID No. 15,  
h3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code,  
can be derived from a polypeptide sequence of SEQ ID No. 15, and preferably encoding  
a polypeptide having the activity represented by a protein comprising a polypeptide of  
SEQ ID No. 15,  
h4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of hi) to h3)  
under stringent hybridization conditions, and preferably encoding a polypeptide having  
the activity represented by a protein comprising a polypeptide of SEQ ID No. 15,  
h5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid  
library under stringent hybridization conditions with a probe comprising a
complementary sequence of a nucleic acid molecule of h1) to h4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in h1) to h4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 15, and/or

11) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 17, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17,

12) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No. 18, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17,

13) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 17, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17,

14) a nucleic acid molecule which hybridizes with a nucleic acid molecule of i1) to i3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17,

15) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of i1) to i4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in i1) to i4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 17, and/or
jl) a nucleic acid molecule encoding a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.19, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.19,

j2) a nucleic acid molecule having at least 80% identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.20, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.19,

j3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 19, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.19,

j4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of jl) to j3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.19,

j5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of jl) to j4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in jl) to j5) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.19, and/or

kl) a nucleic acid molecule encoding a polypeptide having at least 80% identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.21, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.21,

k2) a nucleic acid molecule having at least 80% identity to a continuous stretch of at least
15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No. 22, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 21,  

k3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 21, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 21,  

k4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of k1) to k3) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 21,  

k5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of k1) to k4) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in k1) to k4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 21, and/or  

11) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 23, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 23,  

12) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No. 24, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No. 23,  

13) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code,
can be derived from a polypeptide sequence of SEQ ID No. 23, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.23,

14) a nucleic acid molecule which hybridizes with a nucleic acid molecule of 11) to 13) under stringent hybridization conditions, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.23,

15) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of 11) to 14) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in 11) to 14) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.23, and/or

ml) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180 or 200 amino acids according to the polypeptide of SEQ ID No.25, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.25,

m2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid molecule sequence of the nucleic acid molecule of SEQ ID No.26, or a corresponding complementary sequence thereof, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.25,

m3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence of SEQ ID No. 25, and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.25,

m4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of ml) to m3)

under stringent hybridization conditions, and preferably encoding a polypeptide having
the activity represented by a protein comprising a polypeptide of SEQ ID No. 25,

m5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid
library under stringent hybridization conditions with a probe comprising a
complementary sequence of a nucleic acid molecule of m1) to m4) or with a fragment
thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a
nucleic acid molecule complementary to a nucleic acid molecule sequence characterized

preferably

n5) in m1) to m4) and preferably encoding a polypeptide having the activity represented by
a protein comprising a polypeptide of SEQ ID No. 25, and/or

nl) a nucleic acid molecule encoding a polypeptide having at least 80 % identity to a
continuous stretch of at least 15, preferably 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140,
160, 180 or 200 amino acids according to the polypeptide of SEQ ID No. 27, and
preferably encoding a polypeptide having the activity represented by a protein
comprising a polypeptide of SEQ ID No. 27,

n2) a nucleic acid molecule having at least 80 % identity to a continuous stretch of at least
15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt within the nucleic acid
molecule

sequence of the nucleic acid molecule of SEQ ID No. 28, or a corresponding
complementary sequence thereof, and preferably encoding a polypeptide having the
activity represented by a protein comprising a polypeptide of SEQ ID No. 27,

n3) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code,
can be derived from a polypeptide sequence of SEQ ID No. 27, and preferably encoding
a polypeptide having the activity represented by a protein comprising a polypeptide of
SEQ ID No. 27,

n4) a nucleic acid molecule which hybridizes with a nucleic acid molecule of n1) to n3)
under stringent hybridization conditions, and preferably encoding a polypeptide having
the activity represented by a protein comprising a polypeptide of SEQ ID No. 27,

n5) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid
library under stringent hybridization conditions with a probe comprising a
complementary sequence of a nucleic acid molecule of n1) to n4) or with a fragment
thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a
nucleic acid molecule complementary to a nucleic acid molecule sequence characterized
in n1) to n4) and preferably encoding a polypeptide having the activity represented by a protein comprising a polypeptide of SEQ ID No.27.

7. A recombinant nucleic acid molecule which confers the expression of at least one nucleic acid molecule according to claim 6, wherein the recombinant nucleic acid molecule additionally comprises one or more regulatory elements, whereby expression of the at least one nucleic acid in a host cell results in increased tolerance and/or resistance to Oomycetes as compared to a corresponding non-modified wild type plant cell, a plant or a part thereof.

8. A vector comprising at least one nucleic acid molecule according to claim 6 or comprising at least one recombinant nucleic acid molecule according to claim 7, whereby expression of said at least one nucleic acid in a host cell results in increased tolerance and/or resistance to Oomycetes as compared to a corresponding non-modified wild type plant cell, a plant or a part thereof.

9. A composition comprising the nucleic acid molecule of claim 6, the recombinant nucleic acid molecule of claim 7, or the vector of claim 8, and optionally an agricultural acceptable carrier.

10. The method of claims 1 to 5, comprising
   a) transforming a plant cell, or a part of a plant with a vector according to claim 8 and/or a composition according to claim 9, and
   b) generating from the plant cell or the part of a plant a transgenic plant.
11. A transgenic plant cell, a plant tissue, a propagation material, a plant or a part thereof with increased tolerance and/or resistance to Oomycetes as compared to a corresponding non-transformed wild type plant cell, plant tissue, propagation material, plant or a part thereof produced by a method according to claim 10, wherein the transgenic plant cell, a plant or a part thereof is derived from a monocotyledonous or a dicotyledonous plant, preferably from a dicotyledonous plant, more preferably from a plant belonging to the genus *Fragaria*.

12. A seed produced by a transgenic plant of claim 11, wherein the seed is genetically homozygous for at least one transgene comprising at least one nucleic acid sequence as per al) through n5), conferring increased tolerance and/or resistance to Oomycetes as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

13. Use of at least one nucleic acid molecule according to any of claims 5 through 7 or a vector according to claim 8 for producing a transgenic plant cell, plant or a part thereof with increased tolerance and/or resistance to Oomycetes compared to a corresponding non transformed wild type plant cell, a plant or a part thereof.

14. Use of at least one nucleic acid molecule having at least 80 % identity to a continuous stretch of at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 ,21 or 22 nt, within the nucleic acid molecule sequence of a nucleic acid molecule selected from the group consisting of SEQ ID No.2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26 and 28, or a corresponding complementary sequence thereof, in a method of measuring gene expression in plant offspring to control breeding success.
15. A plant of the genus *Fragaria*, obtained by crossing a plant selected from the group consisting of F. vesca (cvs 'Bukammen', 'NCGR1603') and F x ananassa (cvs 'Korona', 'Polka', 'Senga Sengana', 'Sonata', 'Elsanta', 'Florence', 'Nobel', and 'Saga'), preferably wherein the plant or a part thereof has increased tolerance and/or resistance to Oomycetes as compared to a corresponding wild type F x ananassa (cvs 'Korona', 'Polka', 'Senga Sengana', 'Sonata', 'Elsanta', 'Florence', 'Nobel', and 'Saga') plant.

16. A plant of the genus *Fragaria*, obtained by crossing two plants selected from the group consisting of F. vesca (cvs 'Bukammen', 'NCGR1603', Alta, Haugastol 3, CFRA1428, CFRA1603, CFRA1848) wherein the plant or a part of the plant comprises in its genome at least one allele conferring increased tolerance and/or resistance to Oomycetes as compared to a corresponding wild type F. vesca plant.

17. A plant or a part of the plant according to claim 16, wherein said at least one allele is in the RPc-1 locus.
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<th>ProbeName</th>
<th>Predicted function in Fragaria [or in Rosaceae]</th>
<th>mRNA/Polypeptide</th>
<th>SEQ ID No.</th>
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Figure 3

Phenotypic responses

Disease score

Population

Bukammen  F1_hybrid  F2_Res  F2_Susc  Haugastøl3
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<th>Market</th>
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Figure 6
**Figure 8**

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<td>Control</td>
<td>CFRA1603 (R)</td>
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<td>Wounded, not infected</td>
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<td>Wounded and infected</td>
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**Figure 9**

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<th>Maternal parents</th>
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<th>Previous score&lt;sup&gt;1&lt;/sup&gt;</th>
<th>Current score</th>
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<th>Buka</th>
<th>Haug3</th>
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<sup>1</sup> from Eikemo et al (2010)

<sup>2</sup> selves were not realized
Figure 10

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<th>Linkage group</th>
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<th>No. of markers</th>
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<th>Marker density</th>
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Figure 11

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<th>Position</th>
<th>BLAST hit</th>
<th>E-value</th>
<th>Percentage identity</th>
<th>Putative role in disease resistance</th>
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<td>101291075</td>
<td>5151532</td>
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<td>0.00E+00</td>
<td>97.00 %</td>
<td>Calmodulin binding proteins implicated in defense responses</td>
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<td>Negative regulators of defense against pathogens</td>
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<td>6602065</td>
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<td>6606639</td>
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<td>Sensory role in plant defense</td>
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</table>
**Figure 11 (cont.)**

| gene09653 | 101305865 | 8563501 | F. vesca mlo-like protein 6-like mRNA | 0.00E+00 | 86.40% | Sensory role in plant defense |
| gene09712 | 101309855 | 8692030 | F. vesca serine threonine-protein kinase-like mRNA | 0.00E+00 | 89.00% | Roles in signalling during pathogen recognition |
| gene09743 | 101310249 | 8858411 | F. vesca BTB POZ domain-containing protein at5g03250-like mRNA | 0.00E+00 | 85.20% | Negative regulators of defense against pathogens |
| gene09753 | 101315259 | 8934129 | F. vesca phenylalanine ammonia-lyase 1-like mRNA | 0.00E+00 | 87.80% | Precursor to products involved in plant defense |
| gene09601 | 101297170 | 9201791 | F. vesca ABC transporter B family member 1-like mRNA | 0.00E+00 | 90.60% | Possible role in pathogen resistance |

**Figure 12**

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<th>ProbeName</th>
<th>Predicted function in Fragaria [or in the Rosaceae]</th>
<th>Predicted in other species</th>
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<th>B[2]</th>
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<td>Protein Description</td>
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<td>6976612</td>
<td>Uncharacterized in Fragaria; receptor-like protein 12 [Pyrus x bretschnederi]</td>
<td>Leucine-rich repeat family protein (AT4G13880.1)</td>
<td>1,2</td>
<td>5,1</td>
</tr>
<tr>
<td>gene18341</td>
<td>101296212</td>
<td>101296212</td>
<td>6816171</td>
<td>protein SRG1-like</td>
<td>Leucoanthocyanidin dioxygenase, putative [Ricinus communis] (EEF28746.1)</td>
<td>3,2</td>
<td>4,6</td>
</tr>
<tr>
<td>gene13775</td>
<td>101293015</td>
<td>101293015</td>
<td>7132040</td>
<td>ferritin-1, chloroplastic-like</td>
<td>Ferritin [Jatropha curcas] (ACS32300.1) expect=4.00E-09; similar to ATFER4</td>
<td>3,7</td>
<td>4,6</td>
</tr>
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<td>gene18341</td>
<td>101296212</td>
<td>6816171</td>
<td>Frag032118</td>
<td>protein SRG1-like</td>
<td>Leucoanthocyanidin dioxygenase, putative [Ricinus communis] (E0F28746.1)</td>
<td>3.3</td>
<td>3.6</td>
</tr>
</tbody>
</table>

1) log Fold Change

2) The B-statistic is the log-odds that the gene is differentially expressed, e.g., a B=1.5 gives the odds that differential expression of exp(1.5) = 4.48 and the corresponding probability that the gene is DE is 4.48/(1+4.48) = 0.82.
INTERNATIONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER

INV. A01H1/04 A01H5/08

ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

A01H

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

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal

C. DOCUMENTS CONSIDERED TO BE RELEVANT

<table>
<thead>
<tr>
<th>Category</th>
<th>Citation of document, with indication, where appropriate, of the relevant passages</th>
<th>Relevant to claim No.</th>
</tr>
</thead>
</table>

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

Date of the actual completion of the international search: 1 June 2016

Date of mailing of the international search report: 15/06/2016

Name and mailing address of the ISA:
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016

Authorized officer: Kriiger, Julia

Form PCT/ISA/210 (second sheet) (April 2005)
<table>
<thead>
<tr>
<th>Category</th>
<th>Citation of document, with indication, where appropriate, of the relevant passages</th>
<th>Relevant to claim No.</th>
</tr>
</thead>
<tbody>
<tr>
<td>X</td>
<td>El Kemo H; Brurberg MB; Davik J: &quot;Resistance to Phytophthora cactorum in diploid Fragaria species&quot;, Hortic Science, vol. 45, 2010, pages 193-197, XP002758216, cited in the application abstract; figure 1; table 1</td>
<td>15-17</td>
</tr>
<tr>
<td>A</td>
<td>Zorilla-Fontanesi Y; Cabeza A; Dominguez P; Medina JJ; Valpuesta V; Oyes-Rothan B; Sanchez-Sevilla LF; Amaya I: &quot;Quantitative trait loci and underlying candidate genes controlling agronomic and fruit quality traits in octoploid strawberry (Fragaria x ananassa)&quot;, Theor Appl Genet, vol. 123, 2011, pages 755-778, XP19939054, cited in the application</td>
<td>15-17</td>
</tr>
</tbody>
</table>
**INTERNATIONAL SEARCH REPORT**

**Box No. II  Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)**

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. **□** claims Nos.: 15-17 (partially) because they relate to subject matter not required to be searched by this Authority, namely:

A meaningful search is not possible on the basis of claims 15-17 because said claims are directed to Plant variety which are exempt from patentability under Rule 39.1(ii) PCT

2. **X** claims Nos.: 1-14 (completely); 15-17 (partially) because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

see FURTHER INFORMATION sheet PCT/ISA/210

3. **□** Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box No. III  Observations where unity of invention is lacking (Continuation of item 3 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

1. **□** As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. **□** As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.

3. **□** As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: 

4. **□** No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 

**Remark on Protest**

- **□** The additional search fees were accompanied by the applicant’s protest and, where applicable, the payment of a protest fee.

- **□** The additional search fees were accompanied by the applicant’s protest but the applicable protest fee was not paid within the time limit specified in the invitation.

- **□** No protest accompanied the payment of additional search fees.
Continent on of Box II.1

Claims Nos.: 15-17 (partly)

A meaningful search is not possible on the basis of claims 15-17 because said claims are directed to Plant variety which are exempt from patentability under Rule 39.1(ii) PCT.

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Continent on of Box II.2

Claims Nos.: 1-14 (completely); 15-17 (partly)

Claims 1-14 of present application have, according to Rule 13ter 1(d) PCT, not been searched since the sequences disclosed in present application do not comply with WIPO standard ST.25 as prescribed under Rule 5.2 PCT. A Standard-compliant sequence listing has not been furnished in text (TXT) format and the applicant has not remedied the deficiencies within the time limit fixed in the invitation pursuant to Rule 13ter 1(a) PCT (see Guidelines for Search and Examination at the EPO as PCT Authority, B-VIII, 3).