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(54) Title: METHOD FOR IMPROVED UTILIZATION OF THE PRODUCTION POTENTIAL OF TRANSGENIC PLANTS

(57) Abstract: The invention relates to a method for improving the utilization of the production potential of transgenic plants by treating the plant with an effective amount of at least one compound of the formula (I) as described herein.



Method for improved utilization of the production potential of transgenic plants

[0001] The invention relates to a method for improving the utilization of the production potential of transgenic plants and for controlling pests such as insects and/or nematodes.

5 [0002] In recent years, there has been a marked increase in the proportion of transgenic plants in agriculture.

[0003] Transgenic plants are employed mainly to utilize the production potential of respective plant varieties in the most favourable manner, at the lowest possible input of production means. The aim of the genetic modification of the plants is in particular the generation of resistance in the plants to certain pests or harmful organisms or else herbicides and also to abiotic stress (for example drought, heat or elevated salt levels). It is also possible to modify a plant genetically to increase certain quality or product features, such as, for example, the content of selected vitamins or oils, or to improve certain fibre properties.

10 [0004] Herbicide resistance or tolerance can be achieved, for example, by incorporating genes into the useful plant for expressing enzymes to detoxify certain herbicides, so that a relatively unimpeded growth of these plants is possible even in the presence of these herbicides for controlling broad-leaved weeds and weed grasses. Examples which may be mentioned are cotton varieties or maize varieties which tolerate the herbicidally active compound glyphosate (Roundup®), (Roundup Ready®, Monsanto) or the herbicides glufosinate or oxylin.

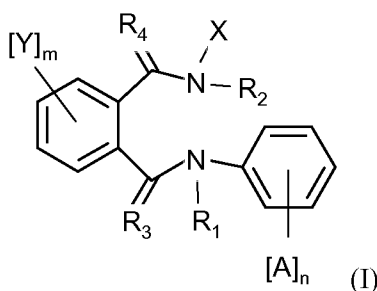
[0005] There has also been the development of useful plants comprising two or more genetic modifications ("stacked transgenic plants" or multiply transgenic crops). Thus, for example, Monsanto has developed multiply transgenic maize varieties which are resistant to the European corn borer (*Ostrinia nubilalis*) and the Western corn rootworm (*Diabrotica virgifera*). Also known are maize and cotton crops which are both resistant to the Western corn rootworm and the cotton bollworm and tolerant to the herbicide Roundup®.

25 [0006] It has now been found that the utilization of the production potential of transgenic useful plants can be improved even more by treating the plants with one or more compounds of the formula (I) defined below. Here, the term "treatment" includes all measures resulting in a contact between these active compounds and at least one plant part. "Plant parts" are to be understood as meaning all above-ground and below-ground parts and organs of plants, such as shoot, leaf, flower and root, by way of example leaves, needles, stalks, stems, flowers, fruit bodies, fruits and seed, and also roots, tubers and rhizomes.

30 The plant parts also include harvested material and also vegetative and generative propagation material, for example cuttings, tubers, rhizomes, slips and seed.

Summary of the invention

[0007] One aspect refers to a method for improving the utilization of the production potential of a transgenic plant and/or for controlling/combating/treating pests, characterized in that the plant is treated with an effective amount of at least one compound of the formula (I)



wherein

A represents individually halogen, cyano, nitro, hydroxyl, amino, C₁-C₈ alkyl group, substituted C₁-C₈ alkyl group having at least one substituent elected from the group consisting of halogen, hydroxy, cyano, nitro, amino, halo C₁-C₃ alkyl group, C₁-C₃ alkoxy group, halo C₁-C₃ alkoxy group, C₁-C₃ alkylthio group, halo C₁-C₃ alkylthio group, C₁-C₃ alkylsulfinyl group, halo C₁-C₃ alkylsulfinyl group, C₁-C₃ alkylsulfonyl group, halo C₁-C₃ alkylsulfonyl group and C₁-C₃ alkylthio, C₁-C₃ alkyl group; further, an arbitrary saturated carbon atom in said optionally substituted C₁-C₈ alkyl group;

n represents 0, 1, 2, 3 or 4, preferably 0, 1 or 2;

R₁ represents hydrogen, halogen, cyano C₁-C₈ alkyl or C₁-C₈ haloalkyl;

R₂ represents hydrogen, halogen, cyano C₁-C₈ alkyl or C₁-C₈ haloalkyl;

R₃ represents O or S;

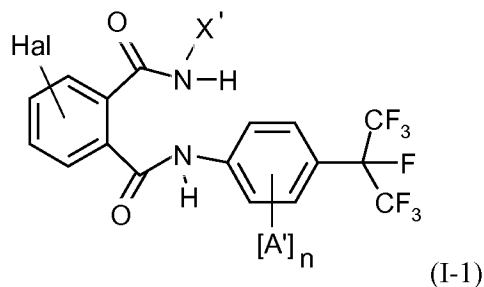
R₄ represents O or S;

Y represents individually hydrogen, halogen, cyano, nitro, C₁-C₆ alkyl group, halo C₁-C₆ alkyl group, C₂-C₆ alkenyl group, halo C₂-C₆ alkenyl group, C₂-C₆ alkynyl group, halo C₂-C₆ alkynyl group, C₃-C₆ cycloalkyl group, halo C₃-C₆ cycloalkyl group, C₁-C₆ alkoxy group, halo C₁-C₆ alkoxy group, C₁-C₆ alkylthio group, halo C₁-C₆ alkylthio group, C₁-C₆ alkylsulfinyl group, halo C₁-C₆ alkylsulfinyl group, C₁-C₆ alkylsulfonyl group, or halo C₁-C₆ alkylsulfonyl group;

m represents 0, 1, 2, 3, or 4;

X represents a C₁-C₈ alkyl group or a substituted C₁-C₈ alkyl group having at least one substituent selected from the group consisting of halogen, hydroxy, cyano, nitro, amino, halo C₁-C₃ alkyl group, C₁-C₃ alkoxy group, halo C₁-C₃ alkoxy group

[0008] One preferred embodiment refers to the method described above, characterized in that the compound of the formula (I) is formula (I-1):



wherein

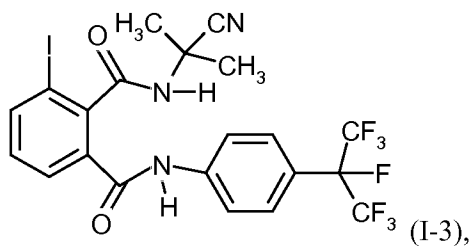
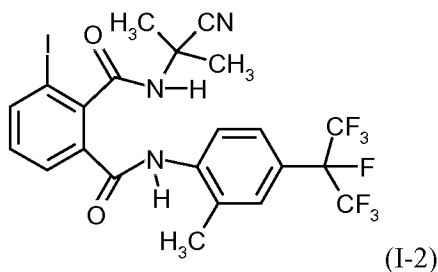
5 Hal represents F, Cl, I or Br; and

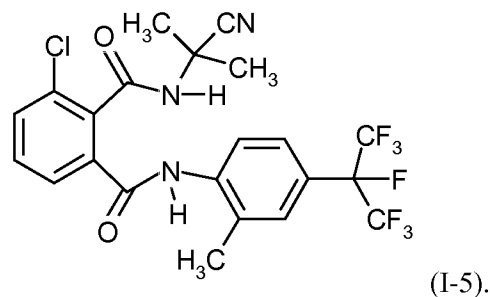
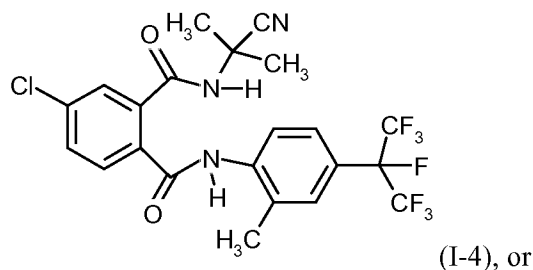
 X' represents C₁-C₆ alkyl or substituted C₁-C₆ alkyl having at least one substituent selected from the group consisting of halogen, hydroxy, cyano, nitro, amino, halo C₁-C₃ alkyl group, preferably a C₁-C₆ cyanoalkyl;

10 A' represents C₁-C₃ alkyl, C₁-C₃ haloalkyl, halogen, preferably methyl, halomethyl, ethyl or haloethyl, more preferably methyl or ethyl;

 n represents 0, 1, 2, 3 or 4, preferably 0, 1 or 2, more preferably 1.

[0009] One preferred embodiment refers to the method described above, characterized in that the compound of the formula (I) is selected from the group consisting of compound (I-2), (I-3), (I-4) or (I-5):





[0010] One preferred embodiment refers to the method described above, characterized in that the compound of the formula (I) is compound (I-5).

[0011] Further preferred embodiments refer to the method described above, characterized in that the plant has at least one genetically modified structure or a tolerance according to Table A or Table B or Table C.

[0012] Further preferred embodiments refer to the method described above, characterized in that the transgenic plant contains at least one cry-gene or a cry-gene fragment coding for a Bt toxin.

[0013] One preferred embodiment refers to the method described above, characterized in that the transgenic plant is a vegetable plant, maize plant, soya bean plant, cotton plant, tobacco plant, rice plant, sugar beet plant, oilseed rape plant or potato plant.

[0014] One preferred embodiment refers to the method described above, characterized in that the use form of the compound of the formula (I) is present in a mixture with at least one mixing partner.

[0015] One preferred embodiment refers to the method described above, characterized in that the Bt toxin of a Bt-plant is encoded by a bt-gene or fragment thereof comprising event MON87701.

[0016] Another aspect refers to a synergistic composition comprising a Bt toxin and a compound of formula (I) as described above.

[0017] One preferred embodiment refers to said synergistic composition, characterized in that the Bt toxin is encoded by a cry gene or a cry-gene fragment selected from the group consisting of cry1, cry2, cry3, cry5 and cry9.

5 [0018] One preferred embodiment refers to said synergistic composition, characterized in that the Bt toxin is encoded by a cry gene or a cry-gene fragment selected from the group consisting of especially preferred are cry1Ab, cry1Ac, cry3A, cry3B and cry9C.

[0019] One preferred embodiment refers to said synergistic composition, characterized in that the Bt toxin is encoded by a cry gene or a cry-gene fragment selected from the subgroup cry1A, preferably cry1Aa, cry1Ab, cry1Ac or a hybrid thereof (e.g., a hybrid of cry1Ac and cry1Ab).

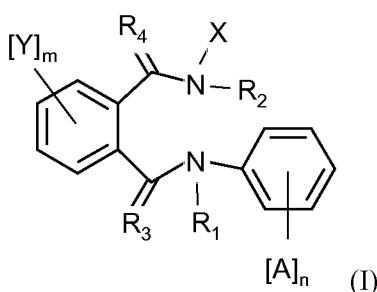
10 [0020] One preferred embodiment refers to said synergistic composition, characterized in that the Bt toxin is encoded by a bt-gene or fragment thereof comprising event MON87701.

[0021] A Bt plant, preferably a Bt-soybean plant comprising event MON87701 or a Bt-soybean plant comprising event MON87701 and MON89788, characterized in that at least 0.00001 g of a compound of formula (I) is attached to it.

15 [0022] The preferred embodiments may be combined as long as such a combination would not contravene existing natural laws.

Detailed description

[0023] Compounds of the formula (I)



20 wherein

A represents individually halogen, cyano, nitro, hydroxyl, amino, C₁-C₈ alkyl group, substituted C₁-C₈ alkyl group having at least one substituent elected from the group consisting of halogen, hydroxy, cyano, nitro, amino, halo C₁-C₃ alkyl group, C₁-C₃ alkoxy group, halo C₁-C₃ alkoxy group, C₁-C₃ alkylthio group, halo C₁-C₃ alkylthio group, C₁-C₃ alkylsulfinyl group, halo C₁-C₃ alkylsulfinyl group, C₁-C₃ alkylsulfonyl group, halo C₁-C₃ alkylsulfonyl group and C₁-C₃ alkylthio, C₁-C₃ alkyl group; further, an
 25 arbitrary saturated carbon atom in said optionally substituted C₁-C₈ alkyl group;

n represents 0, 1, 2, 3 or 4, preferably 0, 1 or 2;

R₁ represents hydrogen, halogen, cyano C₁-C₈ alkyl or C₁-C₈ haloalkyl;

R₂ represents hydrogen, halogen, cyano C₁-C₈ alkyl or C₁-C₈ haloalkyl;

R₃ represents O or S;

5 R₄ represents O or S;

Y represents individually hydrogen, halogen, cyano, nitro, C₁-C₆ alkyl group, halo C₁-C₆ alkyl group, C₂-C₆ alkenyl group, halo C₂-C₆ alkenyl group, C₂-C₆ alkynyl group, halo C₂-C₆ alkynyl group, C₃-C₆ cycloalkyl group, halo C₃-C₆ cycloalkyl group, C₁-C₆ alkoxy group, halo C₁-C₆ alkoxy group, C₁-C₆ alkylthio group, halo C₁-C₆ alkylthio group, C₁-C₆ alkylsulfinyl group, halo C₁-C₆ alkylsulfinyl group,
 10 C₁-C₆ alkylsulfonyl group, or halo C₁-C₆ alkylsulfonyl group;

m represents 0, 1, 2, 3, or 4;

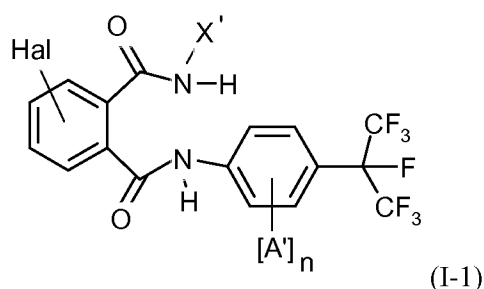
X represents a C₁-C₈ alkyl group or a substituted C₁-C₈ alkyl group having at least one substituent selected from the group consisting of halogen, hydroxy, cyano, nitro, amino, halo C₁-C₃ alkyl group, C₁-C₃ alkoxy group, halo C₁-C₃ alkoxy group

15 and their insecticidal action are known from the prior art (see, e.g., EP 0 919 542, W0 2004/018410, W0 2010/012442 or WO 2012/034472).

[0024] From these documents, the person skilled in the art will be familiar with processes for preparing and methods for using compounds of the formula (I) and with the action of compounds of the formula (I).

[0025] Preferred sub-groups and compounds of formula (I) mentioned above are listed below.

20 [0026] In a preferred embodiment of the present invention, the compounds of the general formula (I) is represented by compounds of formula (I-1):



wherein

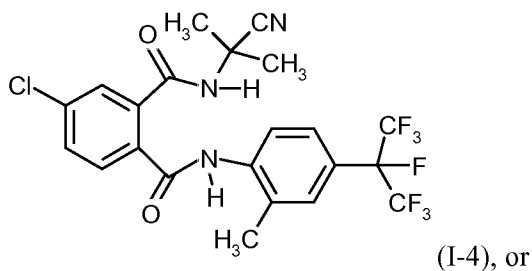
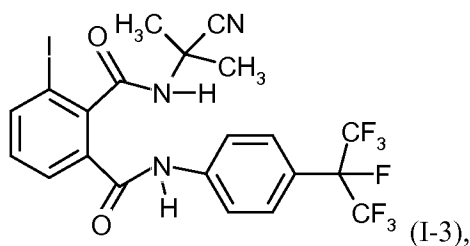
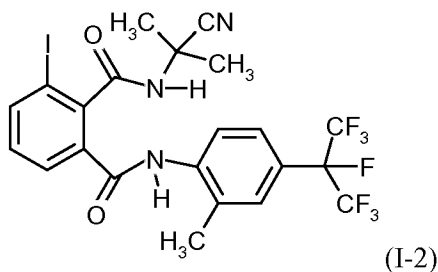
Hal represents F, Cl, I or Br; and

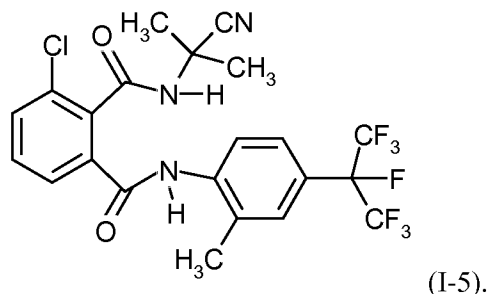
X' represents C₁-C₆ alkyl or substituted C₁-C₆ alkyl having at least one substituent selected from the group consisting of halogen, hydroxy, cyano, nitro, amino, halo C₁-C₃ alkyl group, preferably a C₁-C₆ cyanoalkyl;

A' represents C₁-C₃ alkyl, C₁-C₃ haloalkyl, halogen, preferably methyl, halomethyl, ethyl or haloethyl, more preferably methyl or ethyl;

n represents 0, 1, 2, 3 or 4, preferably 0, 1 or 2, more preferably 1.

[0027] In a more preferred embodiment of the present invention, a composition comprises at least one compound of the general formula (I) selected from the group consisting of compound (I-2), (I-3), (I-4) or (I-5):





[0028] Even more preferably, a compound of formula (I) is selected from the group consisting of compound (I-2) or compound (I-5).

[0029] In one preferred embodiment, the compound of formula (I) is compound (I-5).

5 [0030] According to the invention, "alkyl" represents straight-chain or branched aliphatic hydrocarbons having 1 to 8, preferably 1 to 6, more preferably 1 to 3, carbon atoms. Suitable alkyl groups are, for example, methyl, ethyl, *n*-propyl, *i*-propyl, *n*-, *iso*-, *sec*- or *tert*-butyl, pentyl or hexyl. The alkyl group may be unsubstituted or is substituted by at least one of the substituents mentioned here.

10 [0031] According to the invention, "halogen" or "Hal" represents fluorine, chlorine, bromine or iodine, preferably fluorine, chlorine or bromine.

[0032] According to the invention, "haloalkyl" represents alkyl groups having up to 8 carbon atoms in which at least one hydrogen atom has been replaced by a halogen. Suitable haloalkyl groups are, for example, CH₂F, CHF₂, CF₃, CF₂Cl, CFCF₂, CCl₃, CF₂Br, CF₂CF₃, CFHCF₃, CH₂CF₃, CH₂CH₂F, CH₂CHF₂, CFCF₂CF₃, CCl₂CF₃, CF₂CH₃, CF₂CH₂F, CF₂CHF₂, CF₂CF₂Cl, CF₂CF₂Br, CFHCH₃,
 15 CFHCHF₂, CHFCF₃, CHFCF₂Cl, CHFCF₂Br, CFCF₂CF₃, CCl₂CF₃, CF₂CF₂CF₃, CH₂CH₂CH₂F, CH₂CHFCH₃, CH₂CF₂CF₃, CF₂CH₂CF₃, CF₂CF₂CH₃, CHFCF₂CF₃, CF₂CHFCF₃, CF₂CF₂CHF₂, CF₂CF₂CH₂F, CF₂CF₂CF₂Cl, CF₂CF₂CF₂Br, 1,2,2,2-tetrafluoro-1-(trifluoromethyl)ethyl, 2,2,2-trifluoro-1-(trifluoromethyl)ethyl, pentafluoroethyl, 1-(difluoromethyl)-1,2,2,2-tetrafluoroethyl, 2-bromo-1,2,2-trifluoro-1-(trifluoromethyl)ethyl, 1-(difluoromethyl)-2,2,2-trifluoroethyl. The haloalkyl group may be
 20 unsubstituted or is substituted by at least one of the substituents mentioned here.

[0033] "Production potential" as used herein refers to the yield of a transgenic plant under specific conditions. "Improving the utilization of the production potential of transgenic plants" thus refers to an increase of yield under unfavorable environmental conditions such as use of herbicides, drought stress, cold stress, stress induced by insects, nematodes, or fungi etc. compared to the yield of such plants
 25 under the same conditions without the use of the compounds of formula (I) as described herein.

[0034] The method can also be used for an increased control/an increased treatment of pests such as insects and/or nematodes. Thus, the combination of a transgenic plant such as a Bt-plant and a compound

of formula (I) can show better treatment/control/combating of insects and/or nematodes compared to the expected effect.

[0035] According to the method proposed according to the invention, transgenic plants, in particular useful plants, are treated with compounds of the formula (I) to increase agricultural productivity and/or to control and/or to combat pests, especially nematodes and insects. Preferably, the invention refers to a method for combating pests by treating transgenic plants, preferably insect-resistant transgenic plant such as Bt-plants or Vip-plants with a compound of formula (I), preferably with a compound of formula (I-5).

[0036] For the purpose of the invention, genetically modified organisms (GMOs), e.g. plants or seeds, are genetically modified plants (or transgenic plants) are plants of which a heterologous gene has been stably integrated into genome. The expression "heterologous gene" essentially means a gene which is provided or assembled outside the plant and when introduced in the nuclear, chloroplastic or mitochondrial genome gives the transformed plant new or improved agronomic or other properties by expressing a protein or polypeptide of interest or by downregulating or silencing other gene(s) which are present in the plant (using for example, antisense technology, cosuppression technology, RNA interference – RNAi – technology or microRNA – miRNA - technology). A heterologous gene that is located in the genome is also called a transgene. A transgene that is defined by its particular location in the plant genome is called a transformation or transgenic event.

[0037] Depending on the plant species or plant cultivars, their location and growth conditions (soils, climate, vegetation period, diet), the treatment according to the invention may also result in superadditive ("synergistic") effects. Thus, for example, reduced application rates and/or a widening of the activity spectrum and/or an increase in the activity of the active compounds and compositions which can be used according to the invention, better plant growth, increased tolerance to high or low temperatures, increased tolerance to drought or to water or soil salt content, increased flowering performance, easier harvesting, accelerated maturation, higher harvest yields, bigger fruits, larger plant height, greener leaf color, earlier flowering, higher quality and/or a higher nutritional value of the harvested products, higher sugar concentration within the fruits, better storage stability, increased combating of pests, especially nematodes and insects and/or processability of the harvested products are possible, which exceed the effects which were actually to be expected.

[0038] At certain application rates, the active compound combinations according to the invention may also have a strengthening effect in plants. Accordingly, they are also suitable for mobilizing the defense system of the plant against attack by unwanted microorganisms. This may, if appropriate, be one of the reasons of the enhanced activity of the combinations according to the invention, for example against fungi. Plant-strengthening (resistance-inducing) substances are to be understood as meaning, in the present context, those substances or combinations of substances which are capable of stimulating the defense system of plants in such a way that, when subsequently inoculated with unwanted

microorganisms, the treated plants display a substantial degree of resistance to these microorganisms. In the present case, unwanted microorganisms are to be understood as meaning phytopathogenic fungi, bacteria and viruses. Thus, the substances according to the invention can be employed for protecting plants against attack by the abovementioned pathogens within a certain period of time after the treatment.

- 5 The period of time within which protection is effected generally extends from 1 to 10 days, preferably 1 to 7 days, after the treatment of the plants with the active compounds.

[0039] Plants and plant cultivars which are preferably to be treated according to the invention include all plants which have genetic modified material which impart particularly advantageous, useful traits to these plants (whether obtained by breeding and/or biotechnological means).

- 10 [0040] Plants and plant cultivars which are also preferably to be treated according to the invention are resistant against one or more biotic stresses, i.e. said plants show a better defense against animal and microbial pests, such as against nematodes, insects, mites, phytopathogenic fungi, bacteria, viruses and/or viroids.

- [0041] Examples of nematode or insect resistant plants are described in e.g. U.S. Patent Applications
15 11/765,491, 11/765,494, 10/926,819, 10/782,020, 12/032,479, 10/783,417, 10/782,096, 11/657,964, 12/192,904, 11/396,808, 12/166,253, 12/166,239, 12/166,124, 12/166,209, 11/762,886, 12/364,335, 11/763,947, 12/252,453, 12/209,354, 12/491,396, 12/497,221, 12/644,632, 12/646,004, 12/701,058, 12/718,059, 12/721,595, 12/638,591, and in WO 11/002992, WO 11/014749, WO 11/103247, WO 11/103248, WO 12/135436, WO 12/135501.

- 20 [0042] Examples of plants resistant to other types of pathogens are described in e.g. WO13/050410.

- [0043] Plants and plant cultivars which may also be treated according to the invention are those plants which are resistant to one or more abiotic stresses. Abiotic stress conditions may include, for example, drought, cold temperature exposure, heat exposure, osmotic stress, flooding, increased soil salinity, increased mineral exposure, ozone exposure, high light exposure, limited availability of nitrogen
25 nutrients, limited availability of phosphorus nutrients, shade avoidance.

- [0044] Plants and plant cultivars which may also be treated according to the invention, are those plants characterized by enhanced yield characteristics. Increased yield in said plants can be the result of, for example, improved plant physiology, growth and development, such as water use efficiency, water retention efficiency, improved nitrogen use, enhanced carbon assimilation, improved photosynthesis,
30 increased germination efficiency, improved combating of insects and accelerated maturation. Yield can furthermore be affected by improved plant architecture (under stress and non-stress conditions), including but not limited to, early flowering, flowering control for hybrid seed production, seedling vigor, plant size, internode number and distance, root growth, seed size, fruit size, pod size, pod or ear number, seed number per pod or ear, seed mass, enhanced seed filling, reduced seed dispersal, reduced pod dehiscence

and lodging resistance. Further yield traits include seed composition, such as carbohydrate content, protein content, oil content and composition, nutritional value, reduction in anti-nutritional compounds, improved processability and better storage stability.

[0045] Examples of plants with the above-mentioned traits are non-exhaustively listed in Table A.

5 Table A:

Event	Company	Description	Crop	Patent Ref
ASR368	Scotts Seeds	Glyphosate tolerance derived by inserting a modified 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) encoding gene from <i>Agrobacterium tumefaciens</i> , parent line B99061	<i>Agrostis stolonifera</i> <i>Creeping Bentgrass</i>	US 2006-162007
GT200	Monsanto Company	Glyphosate herbicide tolerant canola produced by inserting genes encoding the enzymes 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) from the CP4 strain of <i>Agrobacterium tumefaciens</i> and glyphosate oxidase from <i>Ochrobactrum anthropi</i> .	<i>Brassica napus</i> (Argentine Canola)	
B, Da, F	Zeneca Seeds	Delayed softening tomatoes produced by inserting a truncated version of the polygalacturonase (PG) encoding gene in the sense or anti-sense orientation in order to reduce expression of the endogenous PG gene, and thus reduce pectin degradation.	<i>Lycopersicon esculentum</i> (Tomato)	
FLAVR SAVR	Calgene Inc.	Delayed softening tomatoes produced by inserting an additional copy of the polygalacturonase (PG) encoding gene in the anti-sense orientation in order to reduce expression of the endogenous PG gene and thus reduce pectin degradation.	<i>Lycopersicon esculentum</i> (Tomato)	
J101, J163	Monsanto Company and Forage Genetics International	Glyphosate herbicide tolerant alfalfa (lucerne) produced by inserting a gene encoding the enzyme 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) from the CP4 strain of <i>Agrobacterium tumefaciens</i> .	<i>Medicago sativa</i> (Alfalfa)	
C/F/93/08-02	Societe National d'Exploitation des Tabacs et Allumettes	Tolerance to the herbicides bromoxynil and ioxynil by incorporation of the nitrilase gene from <i>Klebsiella pneumoniae</i> .	<i>Nicotiana tabacum</i> L. (Tobacco)	
Vector 21-41	Vector Tobacco Inc.	Reduced nicotine content through introduction of a second copy of the tobacco quinolinic acid phosphoribosyltransferase (QTPase) in the antisense orientation. The NPTII encoding gene from <i>E. coli</i> was introduced as a selectable marker to identify transformants.	<i>Nicotiana tabacum</i> L. (Tobacco)	

CL121, CL141, CFX51	BASF Inc.	Tolerance to the imidazolinone herbicide, imazethapyr, induced by chemical mutagenesis of the acetolactate synthase (ALS) enzyme using ethyl methanesulfonate (EMS).	<i>Oryza sativa</i> (Rice)	
GAT-OS2	AVENTIS CROPSCIENCE NV	Glufosinate tolerance; WO 01/83818	<i>Oryza sativa</i> (Rice)	WO 01/83818
GAT-OS3	BAYER BIOSCIENCE NV [BE]	Glufosinate tolerance; US 2008-289060	<i>Oryza sativa</i> (Rice)	US 2008-289060
IMINT A-1, IMINT A-4	BASF Inc.	Tolerance to imidazolinone herbicides induced by chemical mutagenesis of the acetolactate synthase (ALS) enzyme using sodium azide.	<i>Oryza sativa</i> (Rice)	
LLRIC E06, LLRIC E62	Aventis CropScience	Glufosinate ammonium herbicide tolerant rice produced by inserting a modified phosphinothricin acetyltransferase (PAT) encoding gene from the soil bacterium <i>Streptomyces hygroscopicus</i>).	<i>Oryza sativa</i> (Rice)	
GT73, RT73	Monsanto Company	Glyphosate herbicide tolerant canola produced by inserting genes encoding the enzymes 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) from the CP4 strain of <i>Agrobacterium tumefaciens</i> and glyphosate oxidase from <i>Ochrobactrum anthropi</i> .	<i>Brassica napus</i> (Argentine Canola)	
LLRIC E601	Bayer CropScience (Aventis CropScience(AgrEvo))	Glufosinate ammonium herbicide tolerant rice produced by inserting a modified phosphinothricin acetyltransferase (PAT) encoding gene from the soil bacterium <i>Streptomyces hygroscopicus</i>).	<i>Oryza sativa</i> (Rice)	
PE-7	MAHARASHTRA HYBRID SEEDS COMPA	Insect resistance (Cry1Ac); WO 2008/114282	<i>Oryza sativa</i> (Rice)	WO 2008/114282
PWC16	BASF Inc.	Tolerance to the imidazolinone herbicide, imazethapyr, induced by chemical mutagenesis of the acetolactate synthase (ALS) enzyme using ethyl methanesulfonate (EMS).	<i>Oryza sativa</i> (Rice)	
TT51	ZHEJIANG UNIVERSITY	Insect resistance (Cry1Ab/Cry1Ac); CN1840655	<i>Oryza sativa</i> (Rice)	CN1840655

C5	United States Department of Agriculture - Agricultural Research Service	Plum pox virus (PPV) resistant plum tree produced through <i>Agrobacterium</i> -mediated transformation with a coat protein (CP) gene from the virus.	<i>Prunus domestica</i> (Plum)	
ATBT04-6, ATBT04-27, ATBT04-30, ATBT04-31, ATBT04-36, SPBT02-5, SPBT02-7	Monsanto Company	Colorado potato beetle resistant potatoes produced by inserting the cry3A gene from <i>Bacillus thuringiensis</i> (subsp. Tenebrionis).	<i>Solanum tuberosum</i> L. (Potato)	
BT6, BT10, BT12, BT16, BT17, BT18, BT23	Monsanto Company	Colorado potato beetle resistant potatoes produced by inserting the cry3A gene from <i>Bacillus thuringiensis</i> (subsp. Tenebrionis).	<i>Solanum tuberosum</i> L. (Potato)	
RBMT15-101, SEMT15-02, SEMT15-15	Monsanto Company	Colorado potato beetle and potato virus Y (PVY) resistant potatoes produced by inserting the cry3A gene from <i>Bacillus thuringiensis</i> (subsp. Tenebrionis) and the coat protein encoding gene from PVY.	<i>Solanum tuberosum</i> L. (Potato)	
RBMT21-129, RBMT21-350, RBMT22-082	Monsanto Company	Colorado potato beetle and potato leafroll virus (PLRV) resistant potatoes produced by inserting the cry3A gene from <i>Bacillus thuringiensis</i> (subsp. Tenebrionis) and the replicase encoding gene from PLRV.	<i>Solanum tuberosum</i> L. (Potato)	
HCN10	Aventis CropScience	Introduction of the PPT-acetyltransferase (PAT) encoding gene from <i>Streptomyces viridochromogenes</i> , an aerobic soil bacteria. PPT normally acts to inhibit glutamine synthetase, causing a fatal accumulation of ammonia. Acetylated PPT is inactive.	<i>Brassica napus</i> (Argentine Canola)	
AP205 CL	BASF Inc.	Selection for a mutagenized version of the enzyme acetohydroxyacid synthase (AHAS), also known as acetolactate synthase (ALS) or acetolactate pyruvate- lyase.	<i>Triticum aestivum</i> (Wheat)	

AP602 CL	BASF Inc.	Selection for a mutagenized version of the enzyme acetohydroxyacid synthase (AHAS), also known as acetolactate synthase (ALS) or acetolactate pyruvate- lyase.	<i>Triticum aestivum</i> (Wheat)	
BW255-2, BW238-3	BASF Inc.	Selection for a mutagenized version of the enzyme acetohydroxyacid synthase (AHAS), also known as acetolactate synthase (ALS) or acetolactate pyruvate- lyase.	<i>Triticum aestivum</i> (Wheat)	
BW7	BASF Inc.	Tolerance to imidazolinone herbicides induced by chemical mutagenesis of the acetohydroxyacid synthase (AHAS) gene using sodium azide.	<i>Triticum aestivum</i> (Wheat)	
Event 1	Syngenta Participations AG	Fusarium resistance (trichothecene 3-O-acetyltransferase); CA 2561992	<i>Triticum aestivum</i> (Wheat)	CA 2561992
JOPLI N1	Syngenta Participations AG	disease (fungal) resistance (trichothecene 3-O-acetyltransferase); US 2008064032	<i>Triticum aestivum</i> (Wheat)	US 2008064032
MON7 1800	Monsanto Company	Glyphosate tolerant wheat variety produced by inserting a modified 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) encoding gene from the soil bacterium <i>Agrobacterium tumefaciens</i> , strain CP4.	<i>Triticum aestivum</i> (Wheat)	
SWP96 5001	Cyanamid Crop Protection	Selection for a mutagenized version of the enzyme acetohydroxyacid synthase (AHAS), also known as acetolactate synthase (ALS) or acetolactate pyruvate- lyase.	<i>Triticum aestivum</i> (Wheat)	
Teal 11A	BASF Inc.	Selection for a mutagenized version of the enzyme acetohydroxyacid synthase (AHAS), also known as acetolactate synthase (ALS) or acetolactate pyruvate- lyase.	<i>Triticum aestivum</i> (Wheat)	
176	Syngenta Seeds, Inc.	Insect-resistant maize produced by inserting the cry1Ab gene from <i>Bacillus thuringiensis</i> subsp. <i>kurstaki</i> . The genetic modification affords resistance to attack by the European corn borer (ECB).	<i>Zea mays</i> L. (Maize)	
HCN92	Bayer CropScience (Aventis CropScience(AgrEvo))	Introduction of the PPT-acetyltransferase (PAT) encoding gene from <i>Streptomyces viridochromogenes</i> , an aerobic soil bacteria. PPT normally acts to inhibit glutamine synthetase, causing a fatal accumulation of ammonia. Acetylated PPT is inactive.	<i>Brassica napus</i> (Argentine Canola)	
3272	Syngenta Participations AG	Self processing corn (alpha-amylase); US 2006-230473	<i>Zea mays</i> L. (Maize)	US 2006-230473, US2010063265
3751IR	Pioneer Hi-Bred International Inc.	Selection of somaclonal variants by culture of embryos on imidazolinone containing media.	<i>Zea mays</i> L. (Maize)	

676, 678, 680	Pioneer Hi-Bred Internation al Inc.	Male-sterile and glufosinate ammonium herbicide tolerant maize produced by inserting genes encoding DNA adenine methylase and phosphinothricin acetyltransferase (PAT) from <i>Escherichia coli</i> and <i>Streptomyces viridochromogenes</i> , respectively.	<i>Zea mays</i> L. (Maize)	
ACS- ZM00 3-2 x MON- 00810 -6	Bayer CropScien ce (Aventis CropScien ce(AgrEvo))	Stacked insect resistant and herbicide tolerant corn hybrid derived from conventional cross-breeding of the parental lines T25 (OECD identifier: ACS-ZM003-2) and MON810 (OECD identifier: MON-00810-6).	<i>Zea mays</i> L. (Maize)	
B16	DEKALB GENETIC S CORP	Glufosinate resistance; US 2003-126634	<i>Zea mays</i> L. (Maize)	US 2003- 126634
B16 (DLL25)	Dekalb Genetics Corporatio n	Glufosinate ammonium herbicide tolerant maize produced by inserting the gene encoding phosphinothricin acetyltransferase (PAT) from <i>Streptomyces hygroscopicus</i> .	<i>Zea mays</i> L. (Maize)	
BT11 (X4334 CBR, X4734 CBR)	Syngenta Seeds, Inc.	Insect-resistant and herbicide tolerant maize produced by inserting the <i>cry1Ab</i> gene from <i>Bacillus thuringiensis</i> subsp. <i>kurstaki</i> , and the phosphinothricin N-acetyltransferase (PAT) encoding gene from <i>S. viridochromogenes</i> .	<i>Zea mays</i> L. (Maize)	WO 2010148268
BT11 x GA21	Syngenta Seeds, Inc.	Stacked insect resistant and herbicide tolerant maize produced by conventional cross breeding of parental lines BT11 (OECD unique identifier: SYN-BT011-1) and GA21 (OECD unique identifier: MON-00021-9).	<i>Zea mays</i> L. (Maize)	
BT11 x MIR16 2	Syngenta Seeds, Inc.	Stacked insect resistant and herbicide tolerant maize produced by conventional cross breeding of parental lines BT11 (OECD unique identifier: SYN-BT011-1) and MIR162 (OECD unique identifier: SYN-IR162-4). Resistance to the European Corn Borer and tolerance to the herbicide glufosinate ammonium (Liberty) is derived from BT11, which contains the <i>cry1Ab</i> gene from <i>Bacillus thuringiensis</i> subsp. <i>kurstaki</i> , and the phosphinothricin N-acetyltransferase (PAT) encoding gene from <i>S. viridochromogenes</i> . Resistance to other lepidopteran pests, including <i>H. zea</i> , <i>S. frugiperda</i> , <i>A. ipsilon</i> , and <i>S. albicosta</i> , is derived from MIR162, which contains the <i>vip3Aa</i> gene from <i>Bacillus thuringiensis</i> strain AB88.	<i>Zea mays</i> L. (Maize)	

BT11 x MIR16 2 x MIR60 4	Syngenta Seeds, Inc.	<i>Bacillus thuringiensis</i> Cry1Ab delta-endotoxin protein and the genetic material necessary for its production (via elements of vector pZO1502) in Event Bt11 corn (OECD Unique Identifier: SYN-BTØ11-1) x <i>Bacillus thuringiensis</i> Vip3Aa20 insecticidal protein and the genetic material necessary for its production (via elements of vector pNOV1300) in Event MIR162 maize (OECD Unique Identifier: SYN-IR162-4) x modified Cry3A protein and the genetic material necessary for its production (via elements of vector pZM26) in Event MIR604 corn (OECD Unique Identifier: SYN-IR6Ø4-5).	<i>Zea mays</i> L. (Maize)	
MS1, RF1 =>PGS 1	Aventis CropScience (formerly Plant Genetic Systems)	Male-sterility, fertility restoration, pollination control system displaying glufosinate herbicide tolerance. MS lines contained the barnase gene from <i>Bacillus amyloliquefaciens</i> , RF lines contained the barstar gene from the same bacteria, and both lines contained the phosphinothricin N-acetyltransferase (PAT) encoding gene from <i>Streptomyces hygroscopicus</i> .	<i>Brassica napus</i> (Argentine Canola)	
BT11 x MIR60 4	Syngenta Seeds, Inc.	Stacked insect resistant and herbicide tolerant maize produced by conventional cross breeding of parental lines BT11 (OECD unique identifier: SYN-BTØ11-1) and MIR604 (OECD unique identifier: SYN-IR6Ø5-5). Resistance to the European Corn Borer and tolerance to the herbicide glufosinate ammonium (Liberty) is derived from BT11, which contains the cry1Ab gene from <i>Bacillus thuringiensis</i> subsp. <i>kurstaki</i> , and the phosphinothricin N-acetyltransferase (PAT) encoding gene from <i>S. viridochromogenes</i> . Corn rootworm-resistance is derived from MIR604 which contains the mcry3A gene from <i>Bacillus thuringiensis</i> .	<i>Zea mays</i> L. (Maize)	

BT11 x MIR60 4 x GA21	Syngenta Seeds, Inc.	Stacked insect resistant and herbicide tolerant maize produced by conventional cross breeding of parental lines BT11 (OECD unique identifier: SYN-BT011-1), MIR604 (OECD unique identifier: SYN-IR605-5) and GA21 (OECD unique identifier: MON-00021-9). Resistance to the European Corn Borer and tolerance to the herbicide glufosinate ammonium (Liberty) is derived from BT11, which contains the cry1Ab gene from <i>Bacillus thuringiensis</i> subsp. <i>kurstaki</i> , and the phosphinothricin N-acetyltransferase (PAT) encoding gene from <i>S. viridochromogenes</i> . Corn rootworm-resistance is derived from MIR604 which contains the mcr3A gene from <i>Bacillus thuringiensis</i> . Tolerance to glyphosate herbicide is derived from GA21 which contains a modified EPSPS gene from maize.	<i>Zea mays</i> L. (Maize)	
CBH-351	Aventis CropScience	Insect-resistant and glufosinate ammonium herbicide tolerant maize developed by inserting genes encoding Cry9C protein from <i>Bacillus thuringiensis</i> subsp. <i>tolworthi</i> and phosphinothricin acetyltransferase (PAT) from <i>Streptomyces hygroscopicus</i> .	<i>Zea mays</i> L. (Maize)	
DAS-06275-8	DOW AgroSciences LLC	Lepidopteran insect resistant and glufosinate ammonium herbicide-tolerant maize variety produced by inserting the cry1F gene from <i>Bacillus thuringiensis</i> var. <i>aizawai</i> and the phosphinothricin acetyltransferase (PAT) from <i>Streptomyces hygroscopicus</i> .	<i>Zea mays</i> L. (Maize)	
DAS-59122-7	DOW AgroSciences LLC and Pioneer Hi-Bred International Inc.	Corn rootworm-resistant maize produced by inserting the cry34Ab1 and cry35Ab1 genes from <i>Bacillus thuringiensis</i> strain PS149B1. The PAT encoding gene from <i>Streptomyces viridochromogenes</i> was introduced as a selectable marker; US 2006-070139	<i>Zea mays</i> L. (Maize)	US 2006-070139, US 2011030086
DAS-59122-7 x NK603	DOW AgroSciences LLC and Pioneer Hi-Bred International Inc.	Stacked insect resistant and herbicide tolerant maize produced by conventional cross breeding of parental lines DAS-59122-7 (OECD unique identifier: DAS-59122-7) with NK603 (OECD unique identifier: MON-00603-6). Corn rootworm-resistance is derived from DAS-59122-7 which contains the cry34Ab1 and cry35Ab1 genes from <i>Bacillus thuringiensis</i> strain PS149B1. Tolerance to glyphosate herbicide is derived from NK603.	<i>Zea mays</i> L. (Maize)	

DAS-59122-7 x TC1507 x NK603	DOW AgroSciences LLC and Pioneer Hi-Bred International Inc.	Stacked insect resistant and herbicide tolerant maize produced by conventional cross breeding of parental lines DAS-59122-7 (OECD unique identifier: DAS-59122-7) and TC1507 (OECD unique identifier: DAS-Ø15Ø7-1) with NK603 (OECD unique identifier: MON-ØØ6Ø3-6). Corn rootworm-resistance is derived from DAS-59122-7 which contains the cry34Ab1 and cry35Ab1 genes from <i>Bacillus thuringiensis</i> strain PS149B1. Lepidopteran resistance and tolerance to glufosinate ammonium herbicide is derived from TC1507. Tolerance to glyphosate herbicide is derived from NK603.	<i>Zea mays</i> L. (Maize)	
DAS-Ø15Ø7-1 x MON-ØØ6Ø3-6	DOW AgroSciences LLC	Stacked insect resistant and herbicide tolerant corn hybrid derived from conventional cross-breeding of the parental lines 1507 (OECD identifier: DAS-Ø15Ø7-1) and NK603 (OECD identifier: MON-ØØ6Ø3-6).	<i>Zea mays</i> L. (Maize)	
DBT418	Dekalb Genetics Corporation	Insect-resistant and glufosinate ammonium herbicide tolerant maize developed by inserting genes encoding Cry1AC protein from <i>Bacillus thuringiensis</i> subsp kurstaki and phosphinothricin acetyltransferase (PAT) from <i>Streptomyces hygroscopicus</i>	<i>Zea mays</i> L. (Maize)	
DK404 SR	BASF Inc.	Somaclonal variants with a modified acetyl-CoA-carboxylase (ACCase) were selected by culture of embryos on sethoxydim enriched medium.	<i>Zea mays</i> L. (Maize)	
MS1, RF2 =>PGS2	Aventis CropScience (formerly Plant Genetic Systems)	Male-sterility, fertility restoration, pollination control system displaying glufosinate herbicide tolerance. MS lines contained the barnase gene from <i>Bacillus amyloliquefaciens</i> , RF lines contained the barstar gene from the same bacteria, and both lines contained the phosphinothricin N-acetyltransferase (PAT) encoding gene from <i>Streptomyces hygroscopicus</i> .	<i>Brassica napus</i> (Argentine Canola)	
DP-Ø9814 Ø-6 (Event 98140)	Pioneer Hi-Bred International Inc.	Corn line 98140 was genetically engineered to express the GAT4621 (glyphosate acetyltransferase) and ZM-HRA (modified version of a maize acetolactate synthase) proteins. The GAT4621 protein, encoded by the gat4621 gene, confers tolerance to glyphosate-containing herbicides by acetylating glyphosate and thereby rendering it non-phytotoxic. The ZM-HRA protein, encoded by the zm-hra gene, confers tolerance to the ALS-inhibiting class of herbicides.	<i>Zea mays</i> L. (Maize)	-

Event 3272	Syngenta Seeds, Inc.	Maize line expressing a heat stable alpha-amylase gene amy797E for use in the dry-grind ethanol process. The phosphomannose isomerase gene from E.coli was used as a selectable marker.	<i>Zea mays</i> L. (Maize)	
Event 98140	Pioneer Hi-Bred International Inc.	Maize event expressing tolerance to glyphosate herbicide, via expression of a modified bacterial glyphosate N-acetyltransferase, and ALS-inhibiting herbicides, vial expression of a modified form of the maize acetolactate synthase enzyme.	<i>Zea mays</i> L. (Maize)	
EXP19 10IT	Syngenta Seeds, Inc. (formerly Zeneca Seeds)	Tolerance to the imidazolinone herbicide, imazethapyr, induced by chemical mutagenesis of the acetolactate synthase (ALS) enzyme using ethyl methanesulfonate (EMS).	<i>Zea mays</i> L. (Maize)	
FI117		Glyphosate resistance; US 6,040,497	<i>Zea mays</i> L. (Maize)	
GA21	Monsanto Company	Introduction, by particle bombardment, of a modified 5-enolpyruvyl shikimate-3-phosphate synthase (EPSPS), an enzyme involved in the shikimate biochemical pathway for the production of the aromatic amino acids; US 6,040,497	<i>Zea mays</i> L. (Maize)	US 6,040,497
GA21 x MON8 10	Monsanto Company	Stacked insect resistant and herbicide tolerant corn hybrid derived from conventional cross-breeding of the parental lines GA21 (OECD identifier: MON-00021-9) and MON810 (OECD identifier: MON-00810-6).	<i>Zea mays</i> L. (Maize)	US 6,040,497
GAT-ZM1	AVENTIS CROPSCIENCE NV	Glufosinate tolerance; WO 01/51654	<i>Zea mays</i> L. (Maize)	
GG25	DEKALB GENETICS CORP	Glyphosate resistance; US 6,040,497	<i>Zea mays</i> L. (Maize)	WO 01/51654
MS8xR F3	Bayer CropScience (Aventis CropScience(AgrEvo))	Male-sterility, fertility restoration, pollination control system displaying glufosinate herbicide tolerance. MS lines contained the barnase gene from <i>Bacillus amyloliquefaciens</i> , RF lines contained the barstar gene from the same bacteria, and both lines contained the phosphinothricin N-acetyltransferase (PAT) encoding gene from <i>Streptomyces hygroscopicus</i> .	<i>Brassica napus</i> (Argentine Canola)	US 6,040,497
GJ11	DEKALB GENETICS CORP	Glyphosate resistance; US 6,040,497	<i>Zea mays</i> L. (Maize)	
IT	Pioneer Hi-Bred International Inc.	Tolerance to the imidazolinone herbicide, imazethapyr, was obtained by in vitro selection of somaclonal variants.	<i>Zea mays</i> L. (Maize)	US 6,040,497

LY038	Monsanto Company	Altered amino acid composition, specifically elevated levels of lysine, through the introduction of the cordapA gene, derived from Corynebacterium glutamicum, encoding the enzyme dihydrodipicolinate synthase (cDHDPS) ; US 7,157,281	<i>Zea mays</i> L. (Maize)	
MIR162		Insect resistance; WO 2007142840	<i>Zea mays</i> L. (Maize)	US 7,157,281, US2010212051
MIR604	Syngenta Seeds, Inc.	Corn rootworm resistant maize produced by transformation with a modified cry3A gene. The phosphomannose isomerase gene from E.coli was used as a selectable marker; (Cry3a055); EP 1 737 290	<i>Zea mays</i> L. (Maize)	WO 2007142840
MIR604 x GA21	Syngenta Seeds, Inc.	Stacked insect resistant and herbicide tolerant maize produced by conventional cross breeding of parental lines MIR604 (OECD unique identifier: SYN-IR605-5) and GA21 (OECD unique identifier: MON-00021-9). Corn rootworm-resistance is derived from MIR604 which contains the mcr3A gene from Bacillus thuringiensis. Tolerance to glyphosate herbicide is derived from GA21.	<i>Zea mays</i> L. (Maize)	EP 1 737 290
MON80100	Monsanto Company	Insect-resistant maize produced by inserting the cry1Ab gene from Bacillus thuringiensis subsp. kurstaki. The genetic modification affords resistance to attack by the European corn borer (ECB).	<i>Zea mays</i> L. (Maize)	
MON802	Monsanto Company	Insect-resistant and glyphosate herbicide tolerant maize produced by inserting the genes encoding the Cry1Ab protein from Bacillus thuringiensis and the 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) from A. tumefaciens strain CP4.	<i>Zea mays</i> L. (Maize)	
MON809	Pioneer Hi-Bred International Inc.	Resistance to European corn borer (Ostrinia nubilalis) by introduction of a synthetic cry1Ab gene. Glyphosate resistance via introduction of the bacterial version of a plant enzyme, 5-enolpyruvyl shikimate-3-phosphate synthase (EPSPS).	<i>Zea mays</i> L. (Maize)	
MON810	Monsanto Company	Insect-resistant maize produced by inserting a truncated form of the cry1Ab gene from Bacillus thuringiensis subsp. kurstaki HD-1. The genetic modification affords resistance to attack by the European corn borer (ECB); US 2004-180373	<i>Zea mays</i> L. (Maize)	
MS-B2	AVENTIS CROPSCIENCE NV	Male sterility; WO 01/31042	Brassica napus (Argentine Canola)	US 2004-180373

MON8 10 x MON8 8017	Monsanto Company	Stacked insect resistant and glyphosate tolerant maize derived from conventional cross-breeding of the parental lines MON810 (OECD identifier: MON-ØØ81Ø-6) and MON88017 (OECD identifier: MON-88Ø17-3). European corn borer (ECB) resistance is derived from a truncated form of the cry1Ab gene from <i>Bacillus thuringiensis</i> subsp. <i>kurstaki</i> HD-1 present in MON810. Corn rootworm resistance is derived from the cry3Bb1 gene from <i>Bacillus thuringiensis</i> subspecies <i>kumamotoensis</i> strain EG4691 present in MON88017. Glyphosate tolerance is derived from a 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) encoding gene from <i>Agrobacterium tumefaciens</i> strain CP4 present in MON88017.	<i>Zea mays</i> L. (Maize)	WO 01/31042
MON8 32	Monsanto Company	Introduction, by particle bombardment, of glyphosate oxidase (GOX) and a modified 5-enolpyruvyl shikimate-3-phosphate synthase (EPSPS), an enzyme involved in the shikimate biochemical pathway for the production of the aromatic amino acids.	<i>Zea mays</i> L. (Maize)	
MON8 63	Monsanto Company	Corn root worm resistant maize produced by inserting the cry3Bb1 gene from <i>Bacillus thuringiensis</i> subsp. <i>kumamotoensis</i> .	<i>Zea mays</i> L. (Maize)	
MON8 63 x MON8 10	Monsanto Company	Stacked insect resistant corn hybrid derived from conventional cross-breeding of the parental lines MON863 (OECD identifier: MON-ØØ863-5) and MON810 (OECD identifier: MON-ØØ81Ø-6)	<i>Zea mays</i> L. (Maize)	
MON8 63 x MON8 10 x NK603	Monsanto Company	Stacked insect resistant and herbicide tolerant corn hybrid derived from conventional cross-breeding of the stacked hybrid MON-ØØ863-5 x MON-ØØ81Ø-6 and NK603 (OECD identifier: MON-ØØ6Ø3-6).	<i>Zea mays</i> L. (Maize)	
MON8 63 x NK603	Monsanto Company	Stacked insect resistant and herbicide tolerant corn hybrid derived from conventional cross-breeding of the parental lines MON863 (OECD identifier: MON-ØØ863-5) and NK603 (OECD identifier: MON-ØØ6Ø3-6).	<i>Zea mays</i> L. (Maize)	
MON8 7460	MONSANTO TECHNO LOGY LLC	Drought tolerance; Water deficit tolerance; WO 2009/111263	<i>Zea mays</i> L. (Maize)	

MON8 8017	Monsanto Company	Corn rootworm-resistant maize produced by inserting the cry3Bb1 gene from <i>Bacillus thuringiensis</i> subspecies <i>kumamotoensis</i> strain EG4691. Glyphosate tolerance derived by inserting a 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) encoding gene from <i>Agrobacterium tumefaciens</i> strain CP4; WO2005059103	<i>Zea mays</i> L. (Maize)	WO 2009111263
MON8 9034	Monsanto Company	Maize event expressing two different insecticidal proteins from <i>Bacillus thuringiensis</i> providing resistance to number of lepidopteran pests; insect resistance (Lepidoptera –Cry1A.105- Cry2Ab); WO 2007140256	<i>Zea mays</i> L. (Maize)	WO 2005/059103
MON8 9034 x MON8 8017	Monsanto Company	Stacked insect resistant and glyphosate tolerant maize derived from conventional cross-breeding of the parental lines MON89034 (OECD identifier: MON-89034-3) and MON88017 (OECD identifier: MON-88017-3). Resistance to Lepidopteran insects is derived from two cry genes present in MON89043. Corn rootworm resistance is derived from a single cry gene and glyphosate tolerance is derived from the 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) encoding gene from <i>Agrobacterium tumefaciens</i> present in MON88017.	<i>Zea mays</i> L. (Maize)	WO 2007140256
MS-BN1/R F-BN1	AVENTIS CROPSCIENCE NV	Male sterility/restoration; WO 01/41558	Brassica napus (Argentine Canola)	
<u>MON8 9034 x NK603</u>	Monsanto Company	Stacked insect resistant and herbicide tolerant maize produced by conventional cross breeding of parental lines MON89034 (OECD identifier: MON-89034-3) with NK603 (OECD unique identifier: MON-00603-6). Resistance to Lepidopteran insects is derived from two cry genes present in MON89043. Tolerance to glyphosate herbicide is derived from NK603.	<i>Zea mays</i> L. (Maize)	WO 01/41558
<u>MON8 9034 x TC1507</u> <u>x</u> <u>MON8 8017 x DAS-59122-7</u>	Monsanto Company	Stacked insect resistant and herbicide tolerant maize produced by conventional cross breeding of parental lines: MON89034, TC1507, MON88017, and DAS-59122. Resistance to the above-ground and below-ground insect pests and tolerance to glyphosate and glufosinate-ammonium containing herbicides.	<i>Zea mays</i> L. (Maize)	
MON-00603-6 x MON-00810-6	Monsanto Company	Stacked insect resistant and herbicide tolerant corn hybrid derived from conventional cross-breeding of the parental lines NK603 (OECD identifier: MON-00603-6) and MON810 (OECD identifier: MON-00810-6).	<i>Zea mays</i> L. (Maize)	

MON- ØØ81Ø -6 x LY038	Monsanto Company	Stacked insect resistant and enhanced lysine content maize derived from conventional cross-breeding of the parental lines MON810 (OECD identifier: MON-ØØ81Ø-6) and LY038 (OECD identifier: REN-ØØØ38-3).	<i>Zea mays</i> L. (Maize)	
MON- ØØ863- 5 x MON- ØØ6Ø3 -6	Monsanto Company	Stacked insect resistant and herbicide tolerant corn hybrid derived from conventional cross-breeding of the parental lines MON863 (OECD identifier: MON-ØØ863-5) and NK603 (OECD identifier: MON-ØØ6Ø3-6).	<i>Zea mays</i> L. (Maize)	
MON- ØØ863- 5 x MON- ØØ81Ø -6	Monsanto Company	Stacked insect resistant corn hybrid derived from conventional cross-breeding of the parental lines MON863 (OECD identifier: MON-ØØ863-5) and MON810 (OECD identifier: MON-ØØ81Ø-6)	<i>Zea mays</i> L. (Maize)	
MON- ØØ863- 5 x MON- ØØ81Ø -6 x MON- ØØ6Ø3 -6	Monsanto Company	Stacked insect resistant and herbicide tolerant corn hybrid derived from conventional cross-breeding of the stacked hybrid MON-ØØ863-5 x MON-ØØ81Ø-6 and NK603 (OECD identifier: MON-ØØ6Ø3-6).	<i>Zea mays</i> L. (Maize)	
MON- ØØØ21 -9 x MON- ØØ81Ø -6	Monsanto Company	Stacked insect resistant and herbicide tolerant corn hybrid derived from conventional cross-breeding of the parental lines GA21 (OECD identifier: MON-ØØØ21-9) and MON810 (OECD identifier: MON-ØØ81Ø-6).	<i>Zea mays</i> L. (Maize)	
MS3	Bayer CropScien ce (Aventis CropScien ce(AgrEvo))	Male sterility caused by expression of the barnase ribonuclease gene from <i>Bacillus amyloliquefaciens</i> ; PPT resistance was via PPT-acetyltransferase (PAT).	<i>Zea mays</i> L. (Maize)	
MS6	Bayer CropScien ce (Aventis CropScien ce(AgrEvo))	Male sterility caused by expression of the barnase ribonuclease gene from <i>Bacillus amyloliquefaciens</i> ; PPT resistance was via PPT-acetyltransferase (PAT).	<i>Zea mays</i> L. (Maize)	
NS738, NS1471 , NS1473	Pioneer Hi-Bred Internation al Inc.	Selection of somaclonal variants with altered acetolactate synthase (ALS) enzymes, following chemical mutagenesis. Two lines (P1,P2) were initially selected with modifications at different unlinked loci. NS738 contains the P2 mutation only.	<i>Brassica napus</i> (Argent ine Canola)	

NK603	Monsanto Company	Introduction, by particle bombardment, of a modified 5-enolpyruvyl shikimate-3-phosphate synthase (EPSPS), an enzyme involved in the shikimate biochemical pathway for the production of the aromatic amino acids.	<i>Zea mays</i> L. (Maize)	
NK603 x MON810	Monsanto Company	Stacked insect resistant and herbicide tolerant corn hybrid derived from conventional cross-breeding of the parental lines NK603 (OECD identifier: MON-ØØ6Ø3-6) and MON810 (OECD identifier: MON-ØØ81Ø-6).	<i>Zea mays</i> L. (Maize)	
NK603 x T25	Monsanto Company	Stacked glufosinate ammonium and glyphosate herbicide tolerant maize hybrid derived from conventional cross-breeding of the parental lines NK603 (OECD identifier: MON-ØØ6Ø3-6) and T25 (OECD identifier: ACS-ZM003-2).	<i>Zea mays</i> L. (Maize)	
PV-ZMGT 32 (NK603)	MONSANTO TECHNOLOGY LLC	Glyphosate tolerance; US 2007-056056	<i>Zea mays</i> L. (Maize)	
PV-ZMGT 32(nk603)	MONSANTO TECHNOLOGY LLC	Glyphosate tolerance; US 2007292854	<i>Zea mays</i> L. (Maize)	US 2007-056056
PV-ZMIR1 3 (MON863)	MONSANTO TECHNOLOGY LLC	Insect resistance (Cry3Bb); US 2006-095986	<i>Zea mays</i> L. (Maize)	US 2007292854
SYN-BTØ11-1 x MON-ØØØ21-9	Syngenta Seeds, Inc.	Stacked insect resistant and herbicide tolerant maize produced by conventional cross breeding of parental lines BT11 (OECD unique identifier: SYN-BTØ11-1) and GA21 (OECD unique identifier: MON-ØØØ21-9).	<i>Zea mays</i> L. (Maize)	US 2006-095986
T14	Bayer CropScience (Aventis CropScience(AgrEvo))	Glufosinate herbicide tolerant maize produced by inserting the phosphinothricin N-acetyltransferase (PAT) encoding gene from the aerobic actinomycete <i>Streptomyces viridochromogenes</i> .	<i>Zea mays</i> L. (Maize)	
T14, T25	Bayer CropScience (Aventis CropScience(AgrEvo))	Glufosinate herbicide tolerant maize produced by inserting the phosphinothricin N-acetyltransferase (PAT) encoding gene from the aerobic actinomycete <i>Streptomyces viridochromogenes</i> .	<i>Zea mays</i> L. (Maize)	

T25 x MON810	Bayer CropScience (Aventis CropScience(AgrEvo))	Stacked insect resistant and herbicide tolerant corn hybrid derived from conventional cross-breeding of the parental lines T25 (OECD identifier: ACS-ZMØØ3-2) and MON810 (OECD identifier: MON-ØØ81Ø-6).	<i>Zea mays</i> L. (Maize)	
OXY-235	Aventis CropScience (formerly Rhône Poulenc Inc.)	Tolerance to the herbicides bromoxynil and ioxynil by incorporation of the nitrilase gene from <i>Klebsiella pneumoniae</i> .	<i>Brassica napus</i> (Argentine Canola)	-
TC1507	Mycogen (c/o Dow AgroSciences); Pioneer (c/o Dupont)	Insect-resistant and glufosinate ammonium herbicide tolerant maize produced by inserting the cry1F gene from <i>Bacillus thuringiensis</i> var. aizawai and the phosphinothricin N-acetyltransferase encoding gene from <i>Streptomyces viridochromogenes</i> ; Insect resistance (Cry1F); US 7,435,807	<i>Zea mays</i> L. (Maize)	
TC1507 x DAS-59122-7	DOW AgroSciences LLC and Pioneer Hi-Bred International Inc.	Stacked insect resistant and herbicide tolerant maize produced by conventional cross breeding of parental lines TC1507 (OECD unique identifier: DAS-Ø15Ø7-1) with DAS-59122-7 (OECD unique identifier: DAS-59122-7). Resistance to lepidopteran insects is derived from TC1507 due the presence of the cry1F gene from <i>Bacillus thuringiensis</i> var. aizawai. Corn rootworm-resistance is derived from DAS-59122-7 which contains the cry34Ab1 and cry35Ab1 genes from <i>Bacillus thuringiensis</i> strain PS149B1. Tolerance to glufosinate ammonium herbicide is derived from TC1507 from the phosphinothricin N-acetyltransferase encoding gene from <i>Streptomyces viridochromogenes</i> .	<i>Zea mays</i> L. (Maize)	US 7,435,807
VIP1034	Syngenta Participations AG	Insect resistance; WO 03/052073	<i>Zea mays</i> L. (Maize)	
EH92-527	BASF Plant Science	Crop composition; Amflora; Unique EU identifier: BPS-25271-9		WO 03/052073
PHY14, PHY35	Aventis CropScience (formerly Plant Genetic Systems)	Male sterility was via insertion of the barnase ribonuclease gene from <i>Bacillus amyloliquefaciens</i> ; fertility restoration by insertion of the barstar RNase inhibitor; PPT resistance was via PPT-acetyltransferase (PAT) from <i>Streptomyces hygroscopicus</i> .	<i>Brassica napus</i> (Argentine Canola)	

PHY36	Aventis CropScience (formerly Plant Genetic Systems)	Male sterility was via insertion of the barnase ribonuclease gene from <i>Bacillus amyloliquefaciens</i> ; fertility restoration by insertion of the barstar RNase inhibitor; PPT resistance was via PPT-acetyltransferase (PAT) from <i>Streptomyces hygroscopicus</i> .	<i>Brassica napus</i> (Argentine Canola)	
RT73	MONSANTO TECHNOLOGY LLC	Glyphosate resistance; WO 02/36831	<i>Brassica napus</i> (Argentine Canola)	
T45 (HCN28)	Bayer CropScience (Aventis CropScience(AgrEvo))	Introduction of the PPT-acetyltransferase (PAT) encoding gene from <i>Streptomyces viridochromogenes</i> , an aerobic soil bacteria. PPT normally acts to inhibit glutamine synthetase, causing a fatal accumulation of ammonia. Acetylated PPT is inactive.	<i>Brassica napus</i> (Argentine Canola)	WO 02/36831
HCR-1	Bayer CropScience (Aventis CropScience(AgrEvo))	Introduction of the glufosinate ammonium herbicide tolerance trait from transgenic <i>B. napus</i> line T45. This trait is mediated by the phosphinothricin acetyltransferase (PAT) encoding gene from <i>S. viridochromogenes</i> .	<i>Brassica rapa</i> (Polish Canola)	
ZSR500/502	Monsanto Company	Introduction of a modified 5-enol-pyruvylshikimate-3-phosphate synthase (EPSPS) and a gene from <i>Achromobacter</i> sp that degrades glyphosate by conversion to aminomethylphosphonic acid (AMPA) and glyoxylate by interspecific crossing with GT73.	<i>Brassica rapa</i> (Polish Canola)	
EE-1	MAHARASHTRA HYBRID SEEDS COMPANY	Insect resistance (Cry1Ac); WO 2007/091277	Brinjal	
55-1/63-1	Cornell University	Papaya ringspot virus (PRSV) resistant papaya produced by inserting the coat protein (CP) encoding sequences from this plant potyvirus.	<i>Carica papaya</i> (Papaya)	WO 2007/091277
X17-2	University of Florida	Papaya ringspot virus (PRSV) resistant papaya produced by inserting the coat protein (CP) encoding sequences from PRSV isolate H1K with a thymidine inserted after the initiation codon to yield a frameshift. Also contains <i>nptII</i> as a selectable marker.	<i>Carica papaya</i> (Papaya)	
H7-1	Monsanto Company	Glyphosate herbicide tolerant sugar beet produced by inserting a gene encoding the enzyme 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) from the CP4 strain of <i>Agrobacterium tumefaciens</i> ; WO 2004-074492	<i>Beta vulgaris</i> (sugar beet)	

RM3-3, RM3-4, RM3-6	Bejo Zaden BV	Male sterility was via insertion of the barnase ribonuclease gene from <i>Bacillus amyloliquefaciens</i> ; PPT resistance was via the bar gene from <i>S. hygrosopicus</i> , which encodes the PAT enzyme.	<i>Cichorium intybus</i> (Chicory)	WO 2004-074492
DP-098140-6	PIONEER HI-BRED INTERNATIONAL INC, E.I DU PONT DE NEMOURS AND COMPANY	Glyphosate tolerance / ALS inhibitor tolerance	<i>Zea mays</i> L. (Maize)	
A, B	Agrotepe Inc.	Reduced accumulation of S-adenosylmethionine (SAM), and consequently reduced ethylene synthesis, by introduction of the gene encoding S-adenosylmethionine hydrolase.	<i>Cucumis melo</i> (Melon)	WO 2008/112019, US2010240059
CZW-3	Asgrow (USA); Seminis Vegetable Inc. (Canada)	Cucumber mosaic virus (CMV), zucchini yellows mosaic (ZYMV) and watermelon mosaic virus (WMV) 2 resistant squash (<i>Cucurbita pepo</i>) produced by inserting the coat protein (CP) encoding sequences from each of these plant viruses into the host genome.	<i>Cucurbita pepo</i> (Squash)	
ZW20	Upjohn (USA); Seminis Vegetable Inc. (Canada)	Zucchini yellows mosaic (ZYMV) and watermelon mosaic virus (WMV) 2 resistant squash (<i>Cucurbita pepo</i>) produced by inserting the coat protein (CP) encoding sequences from each of these plant potyviruses into the host genome.	<i>Cucurbita pepo</i> (Squash)	
66	Florigene Pty Ltd.	Delayed senescence and sulfonylurea herbicide tolerant carnations produced by inserting a truncated copy of the carnation aminocyclopropane cyclase (ACC) synthase encoding gene in order to suppress expression of the endogenous unmodified gene, which is required for normal ethylene biosynthesis. Tolerance to sulfonyl urea herbicides was via the introduction of a chlorsulfuron tolerant version of the acetolactate synthase (ALS) encoding gene from tobacco.	<i>Dianthus caryophyllus</i> (Carnation)	
4, 11, 15, 16	Florigene Pty Ltd.	Modified colour and sulfonylurea herbicide tolerant carnations produced by inserting two anthocyanin biosynthetic genes whose expression results in a violet/mauve colouration. Tolerance to sulfonyl urea herbicides was via the introduction of a chlorsulfuron tolerant version of the acetolactate synthase (ALS) encoding gene from tobacco.	<i>Dianthus caryophyllus</i> (Carnation)	

959A, 988A, 1226A, 1351A, 1363A, 1400A	Florigene Pty Ltd.	Introduction of two anthocyanin biosynthetic genes to result in a violet/mauve colouration; Introduction of a variant form of acetolactate synthase (ALS).	<i>Dianthus caryophyllus</i> (Carnation)	
3560.4.3.5	Pioneer Hi-Bred International Inc.	Glyphosate/ALS inhibitor-tolerance; WO 2008002872	Glycine max L. (Soybean)	
A2704-12, A2704-21	Bayer CropScience (Aventis CropScience(AgrEvo))	Glufosinate ammonium herbicide tolerant soybean produced by inserting a modified phosphinothricin acetyltransferase (PAT) encoding gene from the soil bacterium <i>Streptomyces viridochromogenes</i> .; WO 2006/108674	Glycine max L. (Soybean)	WO 2008002872
T120-7	Bayer CropScience (Aventis CropScience(AgrEvo))	Introduction of the PPT-acetyltransferase (PAT) encoding gene from <i>Streptomyces viridochromogenes</i> , an aerobic soil bacteria. PPT normally acts to inhibit glutamine synthetase, causing a fatal accumulation of ammonia. Acetylated PPT is inactive.	<i>Beta vulgaris</i> (sugar beet)	WO 2006/108674
A5547-127	Bayer CropScience (Aventis CropScience(AgrEvo))	Glufosinate ammonium herbicide tolerant soybean produced by inserting a modified phosphinothricin acetyltransferase (PAT) encoding gene from the soil bacterium <i>Streptomyces viridochromogenes</i> .	<i>Glycine max</i> L. (Soybean)	
A5547-35	Bayer CropScience (Aventis CropScience(AgrEvo))	Glufosinate tolerance; WO 2006/108675	Glycine max L. (Soybean)	
DP-305423-1	Pioneer Hi-Bred International Inc.	High oleic acid / ALS inhibitor tolerance; WO 2008/054747	Glycine max L. (Soybean)	WO 2006/108675
DP356043	Pioneer Hi-Bred International Inc.	Soybean event with two herbicide tolerance genes: glyphosate N-acetyltransferase, which detoxifies glyphosate, and a modified acetolactate synthase (A	<i>Glycine max</i> L. (Soybean)	WO 2008/054747
G94-1, G94-19, G168	DuPont Canada Agricultural Products	High oleic acid soybean produced by inserting a second copy of the fatty acid desaturase (GmFad2-1) encoding gene from soybean, which resulted in "silencing" of the endogenous host gene.	<i>Glycine max</i> L. (Soybean)	

GTS 40-3-2	Monsanto Company	Glyphosate tolerant soybean variety produced by inserting a modified 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) encoding gene from the soil bacterium <i>Agrobacterium tumefaciens</i> .	<i>Glycine max</i> L. (Soybean)	
GU262	Bayer CropScience (Aventis CropScience(AgrEvo))	Glufosinate ammonium herbicide tolerant soybean produced by inserting a modified phosphinothricin acetyltransferase (PAT) encoding gene from the soil bacterium <i>Streptomyces viridochromogenes</i> .	<i>Glycine max</i> L. (Soybean)	
MON8 7701	Monsanto Company	insect resistance (CryIac); WO 2009064652	<i>Glycine max</i> L. (Soybean)	
MON8 7705	Monsanto Company	altered fatty acid levels (mid-oleic and low saturate); WO 2010037016	<i>Glycine max</i> L. (Soybean)	WO 2009064652
MON8 7754	Monsanto Company	increased oil content; WO 2010024976	<i>Glycine max</i> L. (Soybean)	WO 2010037016
GTSB7 7	Novartis Seeds; Monsanto Company	Glyphosate herbicide tolerant sugar beet produced by inserting a gene encoding the enzyme 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) from the CP4 strain of <i>Agrobacterium tumefaciens</i> .	<i>Beta vulgaris</i> (sugar beet)	WO 2010024976
MON8 7769	Monsanto Company	stearidonic acid (SDA) comprising oil ; WO 2009102873	<i>Glycine max</i> L. (Soybean)	
MON8 9788, MON1 9788	Monsanto Company	Glyphosate-tolerant soybean produced by inserting a modified 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) encoding <i>aroA</i> (<i>epsps</i>) gene from <i>Agrobacterium tumefaciens</i> CP4; WO2006130436	<i>Glycine max</i> L. (Soybean)	WO 2009102873
OT96-15	Agriculture & Agri-Food Canada	Low linolenic acid soybean produced through traditional cross-breeding to incorporate the novel trait from a naturally occurring <i>fan1</i> gene mutant that was selected for low linolenic acid.	<i>Glycine max</i> L. (Soybean)	-
W62, W98	Bayer CropScience (Aventis CropScience(AgrEvo))	Glufosinate ammonium herbicide tolerant soybean produced by inserting a modified phosphinothricin acetyltransferase (PAT) encoding gene from the soil bacterium <i>Streptomyces hygroscopicus</i> .	<i>Glycine max</i> L. (Soybean)	
15985	Monsanto Company	Insect resistant cotton derived by transformation of the DP50B parent variety, which contained event 531 (expressing Cry1Ac protein), with purified plasmid DNA containing the <i>cry2Ab</i> gene from <i>B. thuringiensis</i> subsp. <i>kurstaki</i> .	<i>Gossypium hirsutum</i> L. (Cotton)	
1143-14A	Syngenta Participations AG	Insect resistance (Cry1Ab); WO 2006/128569	<i>Gossypium hirsutum</i> L. (Cotton)	
1143-51B	Syngenta Participations AG	Insect resistance (Cry1Ab); WO 2006/128570	<i>Gossypium hirsutum</i> L. (Cotton)	WO 2006/128569

19-51A	DuPont Canada Agricultural Products	Introduction of a variant form of acetolactate synthase (ALS).	<i>Gossypium hirsutum</i> L. (Cotton)	WO 2006/128570
281-24-236	DOW AgroSciences LLC	Insect-resistant cotton produced by inserting the cry1F gene from <i>Bacillus thuringiensis</i> var. aizawai. The PAT encoding gene from <i>Streptomyces viridochromogenes</i> was introduced as a selectable marker.	<i>Gossypium hirsutum</i> L. (Cotton)	
T227-1	SES EUROPE N.V./S.A	Glyphosate tolerance; US 2004-117870	<i>Beta vulgaris</i> (sugar beet)	
3006-210-23	DOW AgroSciences LLC	Insect-resistant cotton produced by inserting the cry1Ac gene from <i>Bacillus thuringiensis</i> subsp. kurstaki. The PAT encoding gene from <i>Streptomyces viridochromogenes</i> was introduced as a selectable marker.	<i>Gossypium hirsutum</i> L. (Cotton)	US 2004-117870
31807/31808	Calgene Inc.	Insect-resistant and bromoxynil herbicide tolerant cotton produced by inserting the cry1Ac gene from <i>Bacillus thuringiensis</i> and a nitrilase encoding gene from <i>Klebsiella pneumoniae</i> .	<i>Gossypium hirsutum</i> L. (Cotton)	
BXN	Calgene Inc.	Bromoxynil herbicide tolerant cotton produced by inserting a nitrilase encoding gene from <i>Klebsiella pneumoniae</i> .	<i>Gossypium hirsutum</i> L. (Cotton)	
CE43-67B	Syngenta Participations AG	Insect resistance (Cry1Ab); WO 2006/128573	<i>Gossypium hirsutum</i> L. (Cotton)	
CE44-69D	Syngenta Participations AG	Insect resistance (Cry1Ab); WO 2006/128571	<i>Gossypium hirsutum</i> L. (Cotton)	WO 2006/128573, US 2011020828
CE46-02A	Syngenta Participations AG	Insect resistance (Cry1Ab); WO 2006/128572	<i>Gossypium hirsutum</i> L. (Cotton)	WO 2006/128571
Cot102	Syngenta Seeds, Inc.	Insect-resistant cotton produced by inserting the vip3A(a) gene from <i>Bacillus thuringiensis</i> AB88. The APH4 encoding gene from <i>E. coli</i> was introduced as a selectable marker.; US 2006-130175	<i>Gossypium hirsutum</i> L. (Cotton)	WO 2006/128572
COT202	Syngenta Seeds, Inc.	Insect resistance (VIP3A); US2009181399	<i>Gossypium hirsutum</i> L. (Cotton)	US 2006-130175, WO2004039986, US 2010298553
Cot67B	Syngenta Seeds, Inc.	Insect-resistant cotton produced by inserting a full-length <i>cry1Ab</i> gene from <i>Bacillus thuringiensis</i> . The APH4 encoding gene from <i>E. coli</i> was introduced as a selectable marker.	<i>Gossypium hirsutum</i> L. (Cotton)	-

23-18-17, 23-198	Monsanto Company (formerly Calgene)	High laurate (12:0) and myristate (14:0) canola produced by inserting a thioesterase encoding gene from the California bay laurel (<i>Umbellularia californica</i>).	<i>Brassica napus</i> (Argentine Canola)	
DAS-21023-5 x DAS-24236-5	DOW AgroSciences LLC	WideStrike™, a stacked insect-resistant cotton derived from conventional cross-breeding of parental lines 3006-210-23 (OECD identifier: DAS-21023-5) and 281-24-236 (OECD identifier: DAS-24236-5).	<i>Gossypium hirsutum</i> L. (Cotton)	
DAS-21023-5 x DAS-24236-5 x MON88913	DOW AgroSciences LLC and Pioneer Hi-Bred International Inc.	Stacked insect-resistant and glyphosate-tolerant cotton derived from conventional cross-breeding of WideStrike cotton (OECD identifier: DAS-21023-5 x DAS-24236-5) with MON88913, known as RoundupReady Flex (OECD identifier: MON-88913-8).	<i>Gossypium hirsutum</i> L. (Cotton)	
DAS-21023-5 x DAS-24236-5 x MON-01445-2	DOW AgroSciences LLC	WideStrike™/Roundup Ready® cotton, a stacked insect-resistant and glyphosate-tolerant cotton derived from conventional cross-breeding of WideStrike cotton (OECD identifier: DAS-21023-5 x DAS-24236-5) with MON1445 (OECD identifier: MON-01445-2).	<i>Gossypium hirsutum</i> L. (Cotton)	
EE-GH3	BAYER BIOSCIENCE NV	Glyphosate tolerance; WO 2007/017186	<i>Gossypium hirsutum</i> L. (Cotton)	
EE-GH5	BAYER BIOSCIENCE NV	Insect resistance (Cry1Ab); WO 2008/122406	<i>Gossypium hirsutum</i> L. (Cotton)	WO 2007/017186
EE-GH6	BAYER BIOSCIENCE NV	Insect resistance (cry2Ae); WO2008151780	<i>Gossypium hirsutum</i> L. (Cotton)	WO 2008/122406
event 281-24-236	DOW AgroSciences LLC	Insect resistance (Cry1F); WO 2005/103266	<i>Gossypium hirsutum</i> L. (Cotton)	WO2008151780, US2010218281
Event-1	JK Agri Genetics Ltd (India)	Insect-resistant cotton produced by inserting the <i>cry1Ac</i> gene from <i>Bacillus thuringiensis</i> subsp. <i>kurstaki</i> HD-73 (B.t.k.).	<i>Gossypium hirsutum</i> L. (Cotton)	WO 2005/103266
event3006-210-23	DOW AgroSciences LLC	Insect resistance (Cry1Ac); WO 2005/103266	<i>Gossypium hirsutum</i> L. (Cotton)	
GBH614	Bayer CropScience (Aventis CropScience(AgrEvo))	Glyphosate herbicide tolerant cotton produced by inserting 2mepsps gene into variety Coker312 by Agrobacterium under the control of Ph4a748At and TPotpC	<i>Gossypium hirsutum</i> L. (Cotton)	WO 2005/103266

45A37, 46A40	Pioneer Hi-Bred Internation al Inc.	High oleic acid and low linolenic acid canola produced through a combination of chemical mutagenesis to select for a fatty acid desaturase mutant with elevated oleic acid, and traditional back-crossing to introduce the low linolenic acid trait.	<i>Brassica napus</i> (Argentine Canola)	
LLCotton25	Bayer CropScience (Aventis CropScience(AgrEvo))	Glufosinate ammonium herbicide tolerant cotton produced by inserting a modified phosphinothricin acetyltransferase (PAT) encoding gene from the soil bacterium <i>Streptomyces hygroscopicus</i> ; WO 2003013224, WO 2007/017186	<i>Gossypium hirsutum</i> L. (Cotton)	
LLCotton25 x MON15985	Bayer CropScience (Aventis CropScience(AgrEvo))	Stacked herbicide tolerant and insect resistant cotton combining tolerance to glufosinate ammonium herbicide from LLCotton25 (OECD identifier: ACS-GHØØ1-3) with resistance to insects from MON15985 (OECD identifier: MON-15985-7)	<i>Gossypium hirsutum</i> L. (Cotton)	WO 2003013224, WO 2007/017186
MON15985	MONSANTO TECHNOLOGY LLC	Insect resistance (Cry1A/Cry2Ab); US 2004-250317	<i>Gossypium hirsutum</i> L. (Cotton)	
MON1445/1698	Monsanto Company	Glyphosate herbicide tolerant cotton produced by inserting a naturally glyphosate tolerant form of the enzyme 5-enolpyruvyl shikimate-3-phosphate synthase (EPSPS) from <i>A. tumefaciens</i> strain CP4.	<i>Gossypium hirsutum</i> L. (Cotton)	US 2004-250317
MON15985 x MON88913	Monsanto Company	Stacked insect resistant and glyphosate tolerant cotton produced by conventional cross-breeding of the parental lines MON88913 (OECD identifier: MON-88913-8) and 15985 (OECD identifier: MON-15985-7). Glyphosate tolerance is derived from MON88913 which contains two genes encoding the enzyme 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) from the CP4 strain of <i>Agrobacterium tumefaciens</i> . Insect resistance is derived MON15985 which was produced by transformation of the DP50B parent variety, which contained event 531 (expressing Cry1Ac protein), with purified plasmid DNA containing the cry2Ab gene from <i>B. thuringiensis</i> subsp. <i>kurstaki</i> .	<i>Gossypium hirsutum</i> L. (Cotton)	
MON-15985-7 x MON-Ø1445-2	Monsanto Company	Stacked insect resistant and herbicide tolerant cotton derived from conventional cross-breeding of the parental lines 15985 (OECD identifier: MON-15985-7) and MON1445 (OECD identifier: MON-Ø1445-2).	<i>Gossypium hirsutum</i> L. (Cotton)	
MON531/757/1076	Monsanto Company	Insect-resistant cotton produced by inserting the cry1Ac gene from <i>Bacillus thuringiensis</i> subsp. <i>kurstaki</i> HD-73 (B.t.k.).	<i>Gossypium hirsutum</i> L. (Cotton)	

MON8 8913	Monsanto Company	Glyphosate herbicide tolerant cotton produced by inserting two genes encoding the enzyme 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) from the CP4 strain of <i>Agrobacterium tumefaciens</i> , ; WO 2004/072235	<i>Gossypium hirsutum</i> L. (Cotton)	-
MON-ØØ531-6 x MON-Ø1445-2	Monsanto Company	Stacked insect resistant and herbicide tolerant cotton derived from conventional cross-breeding of the parental lines MON531 (OECD identifier: MON-ØØ531-6) and MON1445 (OECD identifier: MON-Ø1445-2).	<i>Gossypium hirsutum</i> L. (Cotton)	WO 2004/072235
46A12, 46A16	Pioneer Hi-Bred International Inc.	Combination of chemical mutagenesis, to achieve the high oleic acid trait, and traditional breeding with registered canola varieties.	<i>Brassica napus</i> (Argentine Canola)	
PV-GHGT07 (1445)	MONSANTO TECHNOLOGY LLC	Glyphosate tolerance; US 2004-148666	<i>Gossypium hirsutum</i> L. (Cotton)	
T304-40	BAYER BIOSCIENCE NV	Insect-resistance (Cry1Ab); WO2008/122406	<i>Gossypium hirsutum</i> L. (Cotton)	US 2004-148666
T342-142	Syngenta Participations AG	Insect resistance (Cry1Ab); WO 2006/128568	<i>Gossypium hirsutum</i> L. (Cotton)	WO2008/122406, US2010077501
X81359	BASF Inc.	Tolerance to imidazolinone herbicides by selection of a naturally occurring mutant.	<i>Helianthus annuus</i> (Sunflower)	WO 2006/128568
RH44	BASF Inc.	Selection for a mutagenized version of the enzyme acetohydroxyacid synthase (AHAS), also known as acetolactate synthase (ALS) or acetolactate pyruvate- lyase.	<i>Lens culinaris</i> (Lentil)	
FP967	University of Saskatchewan, Crop Dev. Centre	A variant form of acetolactate synthase (ALS) was obtained from a chlorsulfuron tolerant line of <i>A. thaliana</i> and used to transform flax.	<i>Linum usitatissimum</i> L. (Flax, Linseed)	
5345	Monsanto Company	Resistance to lepidopteran pests through the introduction of the cry1Ac gene from <i>Bacillus thuringiensis</i> subsp. Kurstaki.	<i>Lycopersicon esculentum</i> (Tomato)	
8338	Monsanto Company	Introduction of a gene sequence encoding the enzyme 1-amino-cyclopropane-1-carboxylic acid deaminase (ACCd) that metabolizes the precursor of the fruit ripening hormone ethylene.	<i>Lycopersicon esculentum</i> (Tomato)	
1345-4	DNA Plant Technology Corporation	Delayed ripening tomatoes produced by inserting an additional copy of a truncated gene encoding 1-aminocyclopropane-1-carboxylic acid (ACC) synthase, which resulted in downregulation of the endogenous ACC synthase and reduced ethylene accumulation.	<i>Lycopersicon esculentum</i> (Tomato)	

35 1 N	Agritope Inc.	Introduction of a gene sequence encoding the enzyme S-adenosylmethionine hydrolase that metabolizes the precursor of the fruit ripening hormone ethylene	<i>Lycopersicon esculentum</i> (Tomato)	
127	BASF AGROCHEMICAL PRODUCTS B.V.	ALS/AHAS inhibitor-tolerance	Glycine max L. (Soybean)	
5307	Syngenta Participations AG	Insect (corn rootworm) resistance (FR8a)	Zea mays L. (Maize)	WO2010080829
17053	MONSANTO TECHNOLOGY LLC	Glyphosate tolerance	Oryza sativa (Rice)	WO2010077816
17314	BAYER BIOSCIENCE NV	Glyphosate tolerance	Oryza sativa (Rice)	WO2010117737
3560.4.3.5	Pioneer Hi-Bred International Inc.	Glyphosate/ALS inhibitor-tolerance	Glycine max L. (Soybean)	WO2010117735
A2704-12	BAYER BIOSCIENCE NV	Glufosinate tolerance	Glycine max L. (Soybean)	WO 2008002872, US2010184079
A5547-35	BAYER BIOSCIENCE NV	Glufosinate tolerance	Glycine max L. (Soybean)	WO 2006/108674
GM RZ13	Syngenta Participations AG	Beet Necrotic Yellow Vein Virus (BNYVV) resistance	<i>Beta vulgaris</i> (sugar beet)	WO 2006/108675
JOPLIN1	Syngenta Participations AG	disease (fungal) resistance (trichothecene 3-O-acetyltransferase)	Wheat	WO2010076212
LLcotton25	BAYER BIOSCIENCE NV	Glufosinate resistance	Gossypium hirsutum L. (Cotton)	US 2008064032
MS-B2	AVENTIS CROPS SCIENCE N.V.	Male sterility	Brassica (A genome)	WO 2003013224
MS-BN1/R F-BN1	AVENTIS CROPS SCIENCE N.V.	Male sterility/restoration	Brassica (napus)	WO 01/31042
RT73	MONSANTO TECHNOLOGY LLC	Glyphosate resistance	Brassica (napus)	WO 01/41558

Kefeng No. 6	CHINA NAT RICE RES INST	Transgenic rice Kefeng 6 is a transformation event containing two insect-resistant genes, cry1Ac and SCK (modified CpTI gene) in China.	Oryza sativa (Rice)	WO 02/36831
E6611.32.1.38 / DP-32138-1 / 32138	Pioneer Hi-Bred International Inc.	1) MS45: anther-specific 5126 (Zea mays) promoter > fertility restoration Ms45 (Zea mays) coding sequence > fertility restoration Ms45 (Zea mays) 3'-untranslated region 2) ZM-AA1: polygalacturonase 47 (Zea mays) promoter > brittle-1 (Zea mays) chloroplast transit peptide > alpha-amylase-1 (Zea mays) truncated coding sequence > >In2-1 (Zea mays) 3'-untranslated region 3) DSRED2: 35S (Cauliflower Mosaic Virus) enhancer > lipid transfer protein-2 (Hordeum vulgare) promoter > red fluorescent protein (Dicosoma sp.) variant coding sequence > protein inhibitor II (Solanum tuberosum) 3'-untranslated region	zea mays L. (Maize)	CN 101824411
DAS-40278-9	DOW AgroSciences LLC	RB7 MARv3>zmUbiquitin 1 promoter>aad1>zmPER5 3'UTR>RB 7 MARv4. The aad-1 gene confers tolerance to 2,4- dichlorophenoxyacetic acid and aryloxyphenoxypropionate (commonly referred to as "fop" herbicides such as quizalofop) herbicides	Zea mays L. (Maize)	WO 2009103049, MX 2010008977
MIR604	Syngenta Participations AG	1) CRY3A: metallotionin-like gene (Zea mays) promoter > delta-endotoxin cry3a (Bacillus thuringiensis subsp. tenebrionis) coding sequence, modified to include a cathepsin-G protease recognition site and maize codon optimized > nopaline synthase (Agrobacterium tumefaciens) 3'-untranslated region 2) PMI: polyubiquitin (Zea mays) promoter (incl. first intron) > mannose-6-phosphate isomerase (Escherichia coli) coding sequence > nopaline synthase (Agrobacterium tumefaciens) 3'-untranslated region	Zea mays L. (Maize)	WO 2011022469
MON 87708	MONSANTO TECHNOLOGY LLC	Dicamba herbicide tolerance, transformation vector PV- GMHT4355 1) DMO: full length transcript (Peanut Chlorotic Streak Virus) promoter > tobacco Etch Virus leader > ribulose 1,5-biphosphate carboxylase small subunit (Pisum sativum) chloroplast transit peptide > dicamba mono-oxygenase (Stenotrophomonas maltophilia) coding sequence > ribulose-1,5-bisphosphate carboxylase small subunit E9 (Pisum sativum) 3'-untranslated region. A CP4 epsps chimeric gene contained within a second T-DNA on the transformation vector used was segregated away.	Glycine max L. (Soybean)	US 2005216970, US 2008167456, US 2011111420

MON 87427	MONSANTO TECHNOLOGY LLC	The transgene insert and expression cassette of MON 87427 comprises the promoter and leader from the cauliflower mosaic virus (CaMV) 35 S containing a duplicated enhancer region (P-e35S); operably linked to a DNA leader derived from the first intron from the maize heat shock protein 70 gene (I- HSP70); operably linked to a DNA molecule encoding an N-terminal chloroplast transit peptide from the shkG gene from Arabidopsis thaliana EPSPS (Ts-CTP2); operably linked to a DNA molecule derived from the aroA gene from the Agrobacterium sp. strain CP4 and encoding the CP4 EPSPS protein; operably linked to a 3' UTR DNA molecule derived from the nopaline synthase (T-NOS) gene from Agrobacterium tumefaciens .	Zea mays L. (Maize)	WO 201103470 4
EE- GM3 / FG72	BAYER BIOSCIENCE NV [BE]; MS TECHNOLOGIES LLC [US]	1) Ph4a748 ABBC: sequence including the promoter region of the histone H4 gene of Arabidopsis thaliana, containing an internal duplication>5'tev: sequence including the leader sequence of the tobacco etch virus>TPotp Y: coding sequence of an optimized transit peptide derivative (position 55 changed into Tyrosine), containing sequence of the RuBisCO small subunit genes of Zea mays (corn) and Helianthus annuus (sunflower)>hppdPf W336: the coding sequence of the 4-hydroxyphenylpyruvate dioxygenase of Pseudomonas fluorescens strain A32 modified by the replacement of the amino acid Glycine 336 with a Tryptophane>3'nos: sequence including the 3' untranslated region of the nopaline synthase gene from the T-DNA of pTiT37 of Agrobacterium tumefaciens. 2) Ph4a748: sequence including the promoter region of the histone H4 gene of Arabidopsis thaliana>intron1 h3At: first intron of gene II of the histone H3.III variant of Arabidopsis thaliana >TPotp C: coding sequence of the optimized transit peptide, containing sequence of the RuBisCO small subunit genes of Zea mays (corn) and Helianthus annuus (sunflower)>2mepsps: the coding sequence of the double-mutant 5-enol-pyruvylshikimate-3-phosphate synthase gene of Zea mays>3'histonAt: sequence including the 3' untranslated region of the histone H4 gene of Arabidopsis thaliana	Glycine max L. (Soybean)	WO 2011062904

416 / pDAB4 468- 0416	DOW AGROSCI ENCES LLC	A novel aad-12 transformation event for herbicide tolerance in soybean plants - referred to herein as pDAB4468-0416. The aad-12 gene (originally from Delftia acidovorans) encodes the aryloxyalkanoate dioxygenase (AAD-12) protein. The trait confers tolerance to 2,4-dichlorophenoxyacetic acid, for example, and to pyridyloxyacetate herbicides. The aad-12 gene, itself, for herbicide tolerance in plants was first disclosed in WO 2007/053482.	Glycine max L. (Soybean)	WO 201106341 1
DP- 004114 -3	Pioneer Hi-Bred Internation al Inc.	cry1F, cry34Ab1, cry35Ab1, and pat: resistance to certain lepidopteran and coleopteran pests, as well as tolerance to phosphinothricin.	Zea mays L. (Maize)	<u>WO</u> <u>2011066384</u>
DP- 032316 -8	Pioneer Hi-Bred Internation al Inc.	Cry1F, cry34Ab1, cry35Ab1, pat: resistance to certain lepidopteran and coleopteran pests, as well as tolerance to phosphinothricin	Zea mays L. (Maize)	US 201115452 3
DP- 040416 -8 a	Pioneer Hi-Bred Internation al Inc.	Cry1F, cry34Ab1, cry35Ab1, pat: resistance to certain lepidopteran and coleopteran pests, as well as tolerance to phosphinothricin	Zea mays L. (Maize)	US 201115452 4
DP- 043A47 -3	Pioneer Hi-Bred Internation al Inc.	Cry1F, cry34Ab1, cry35Ab1, pat: resistance to certain lepidopteran and coleopteran pests, as well as tolerance to phosphinothricin	Zea mays L. (Maize)	US2011015452 5 US2011015452 6
DP- 004114 -3	PIONEER HI-BRED INTERNA TIONAL, INC. / E.I. DU PONT DE NEMOUR S AND COMPAN Y	The invention provides DNA compositions that relate to transgenic insect resistant maize plants. Also provided are assays for detecting the presence of the maize DP-004114-3 event based on the DNA sequence of the recombinant construct inserted into the maize genome and the DNA sequences flanking the insertion site. Kits and conditions useful in conducting the assays are provided.	maize	WO2011/08462 1A1
DP- 032316 -8	PIONEER HI-BRED INTERNA TIONAL, INC. / E.I. DU PONT DE NEMOUR S AND COMPAN Y	The invention provides DNA compositions that relate to transgenic insect resistant maize plants. Also provided are assays for detecting the presence of the maize DP-032316-8 event based on the DNA sequence of the recombinant construct inserted into the maize genome and the DNA sequences flanking the insertion site. Kits and conditions useful in conducting the assays are provided.	maize	WO2011/08463 2

MON-88302-9	MONSANTO TECHNOLOGY LLC	The invention provides plants comprising transgenic event MON 88302 that exhibit tolerance to glyphosate herbicide. The invention also provides seeds, plant parts, cells, commodity products, and methods related to the event. The invention also provides DNA molecules that are unique to the event and were created by the insertion of transgenic DNA into the genome of a <i>Brassica napus</i> plant.	brassica	WO2011/153186
SYN-000H2-5	SYNGENTA PARTICIPATIONS AG	Soybean plants comprising event SYHT0H2, methods of detecting and using the same, and soybean plants comprising a heterologous insert at the same site as SYHT0H2.	soybean	WO2012/082548A2
DAS-14536-7	DOW AGROSCIENCES LLC; MS TECHNOLOGIES LLC	This invention relates to soybean event pDAB8291.45.36.2, which includes a novel expression cassette comprising multiple traits conferring resistance to glyphosate, aryloxyalkanoate, and glufosinate herbicides. This invention also relates in part to methods of controlling resistant weeds, plant breeding, and herbicide tolerant plants. In some embodiments, the event sequence can be "stacked" with other traits, including, for example, other herbicide tolerance gene(s) and/or insect-inhibitory proteins. This invention further relates in part to detection methods, including endpoint TaqMan PCR assays, for the detection of Event pDAB8291.45.36.2 in soybeans and related plant material. Some embodiments can perform high throughput zygoty analysis of plant material and other embodiments can be used to uniquely identify the zygoty of and breed soybean lines comprising the event of the subject invention. Kits and conditions useful in conducting these assays are also provided.	soybean	WO2012/075429A1

DAS-44406-6	DOW AGROSCIENCES LLC; MS TECHNOLOGIES LLC	This invention relates in part to soybean event pDAB8264.44.06.1 and includes a novel expression cassettes and transgenic inserts comprising multiple traits conferring resistance to glyphosate, aryloxyalkanoate, and glufosinate herbicides. This invention also relates in part to methods of controlling resistant weeds, plant breeding and herbicide tolerant plants. In some embodiments, the event sequence can be "stacked" with other traits, including, for example, other herbicide tolerance gene(s) and/or insect-inhibitory proteins. This invention further relates in part to endpoint TaqMan PCR assays for the detection of Event pDAB8264.44.06.1 in soybeans and related plant material. Some embodiments can perform high throughput zygosity analysis of plant material and other embodiments can be used to uniquely identify the zygosity of and breed soybean lines comprising the event of the subject invention. Kits and conditions useful in conducting these assays are also provided.	soybean	WO2012/07542 6A1
MON-87712-4	MONSANTO TECHNOLOGY LLC	The present invention provides a transgenic soybean comprising event MON87712 that exhibits increased yield. The invention also provides cells, plant parts, seeds, plants, commodity products related to the event, and DNA molecules that are unique to the event and were created by the insertion of transgenic DNA into the genome of a soybean plant. The invention further provides methods for detecting the presence of said soybean event nucleotide sequences in a sample, probes and primers for use in detecting nucleotide sequences that are diagnostic for the presence of said soybean event.	soybean	WO2012/05119 9A2
DAS-21606-3	DOW AGROSCIENCES LLC	This invention relates to soybean event pDAB4472-1606 (Event 1606). This invention includes a novel aad-12 transformation event in soybean plants comprising a polynucleotide sequence, as described herein, inserted into a specific site within the genome of a soybean cell. This invention also relates in part to plant breeding and herbicide tolerant plants. In some embodiments, said event / polynucleotide sequence can be "stacked" with other traits, including, for example, other herbicide tolerance gene(s) and/or insect-inhibitory proteins.	soybean	WO2012/03379 4A2

DP-061061-7	PIONEER HI-BRED INTERNATIONAL INC.	Compositions and methods related to transgenic glyphosate tolerant Brassica plants are provided. Specifically, the present invention provides Brassica plants having a DP-061061-7 event which imparts tolerance to glyphosate. The Brassica plant harboring the DP-061061-7 event at the recited chromosomal location comprises genomic/transgene junctions within SEQ ID NO: 2 or with genomic/transgene junctions as set forth in SEQ ID NO: 12 and/or 13. The characterization of the genomic insertion site of events provides for an enhanced breeding efficiency and enables the use of molecular markers to track the transgene insert in the breeding populations and progeny thereof. Various methods and compositions for the identification, detection, and use of the events are provided.	Brassica	WO2012049268A1
DP-073496-4	PIONEER HI-BRED INTERNATIONAL INC.	Compositions and methods related to transgenic glyphosate tolerant Brassica plants are provided. Specifically, the present invention provides Brassica plants having a DP-073496-4 event which imparts tolerance to glyphosate. The Brassica plant harboring the DP-073496-4 event at the recited chromosomal location comprises genomic/transgene junctions within SEQ ID NO: 2 or with genomic/transgene junctions as set forth in SEQ ID NO: 12 and/or 13. The characterization of the genomic insertion site of the event provides for an enhanced breeding efficiency and enables the use of molecular markers to track the transgene insert in the breeding populations and progeny thereof. Various methods and compositions for the identification, detection, and use of the event are provided.	Brassica	WO2012049661A1

8264.44 .06.1	DOW AGROSCI ENCES LLC; MS TECHNO LOGIES LLC	This invention relates in part to soybean event pDAB8264.44.06.1 and includes a novel expression cassettes and transgenic inserts comprising multiple traits conferring resistance to glyphosate, aryloxyalkanoate, and glufosinate herbicides. This invention also relates in part to methods of controlling resistant weeds, plant breeding and herbicide tolerant plants. In some embodiments, the event sequence can be "stacked" with other traits, including, for example, other herbicide tolerance gene(s) and/or insect-inhibitory proteins. This invention further relates in part to endpoint TaqMan PCR assays for the detection of Event pDAB8264.44.06.1 in soybeans and related plant material. Some embodiments can perform high throughput zygosity analysis of plant material and other embodiments can be used to uniquely identify the zygosity of and breed soybean lines comprising the event of the subject invention. Kits and conditions useful in conducting these assays are also provided.	Soybean	WO201205246 8A2
8291.45 .36.2	DOW AGROSCI ENCES LLC; MS TECHNO LOGIES LLC	This invention relates to soybean event pDAB8291.45.36.2, which includes a novel expression cassette comprising multiple traits conferring resistance to glyphosate, aryloxyalkanoate, and glufosinate herbicides. This invention also relates in part to methods of controlling resistant weeds, plant breeding, and herbicide tolerant plants. In some embodiments, the event sequence can be "stacked" with other traits, including, for example, other herbicide tolerance gene(s) and/or insect-inhibitory proteins. This invention further relates in part to detection methods, including endpoint TaqMan PCR assays, for the detection of Event pDAB8291.45.36.2 in soybeans and related plant material. Some embodiments can perform high throughput zygosity analysis of plant material and other embodiments can be used to uniquely identify the zygosity of and breed soybean lines comprising the event of the subject invention. Kits and conditions useful in conducting these assays are also provided.	Soybean	WO201205598 2A2
SYHT0 H2	SYNGEN TA PARTICIP ATIONS AG	Soybean plants comprising event SYHT0H2, methods of detecting and using the same, and soybean plants comprising a heterologous insert at the same site as SYHT0H2.	soybean	WO2012/08254 8A2

MON8 8701	MONSANTO TECHNOLOGY LLC	The invention provides cotton event MON 88701, and plants, plant cells, seeds, plant parts, and commodity products comprising event MON 88701. The invention also provides polynucleotides specific for event MON 88701 and plants, plant cells, seeds, plant parts, and commodity products comprising polynucleotides specific for event MON 88701. The invention also provides methods related to event MON 88701.	cotton	WO2012/13480 8A1
KK179- 2	MONSANTO TECHNOLOGY LLC ; FORAGE GENETICS INTERNATIONAL LLC	The present invention provides a transgenic alfalfa event KK179-2. The invention also provides cells, plant parts, seeds, plants, commodity products related to the event, and DNA molecules that are unique to the event and were created by the insertion of transgenic DNA into the genome of a alfalfa plant. The invention further provides methods for detecting the presence of said alfalfa event nucleotide sequences in a sample, probes and primers for use in detecting nucleotide sequences that are diagnostic for the presence of said alfalfa event.	alfalfa	WO201300355 8A1
pDAB8 264.42. 32.1	DOW AGROSCIENCE LLC ; MS TECHNOLOGIES LLC	This invention relates to soybean event pDAB8264.42.32.1 and includes novel expression cassettes and transgenic inserts comprising multiple traits conferring resistance to glyphosate, aryloxyalkanoate, and glufosinate herbicides. This invention also relates in part to methods of controlling resistant weeds, plant breeding and herbicide tolerant plants. In some embodiments, the event sequence can be "stacked" with other traits, including, for example, other herbicide tolerance gene(s) and/or insect-inhibitory proteins. This invention further relates in part to endpoint TAQMAN PCR assays for the detection of Event pDAB8264.42.32.1 in soybeans and related plant material. Some embodiments can perform high throughput zygosity analysis of plant material and other embodiments can be used to uniquely identify the zygosity of and breed soybean lines comprising the event of the subject invention. Kits and conditions useful in conducting these assays are also provided.	soybean	WO201301009 4A1

MZDT09Y	SYNGENTA PARTICIPATIONS AG	A transgenic corn event designated MZDT09Y is disclosed. The invention relates to nucleic acids that are unique to event MZDT09Y and to methods of detecting the presence of event MZDT09Y based on DNA sequences of the recombinant constructs inserted into the corn genome that resulted in the MZDT09Y event and of genomic sequences flanking the insertion site. The invention further relates to corn plants comprising the transgenic genotype of event MZDT09Y and to methods for producing a corn plant by crossing a corn plant comprising the MZDT09Y genotype with itself or another corn variety. Seeds of corn plants comprising the MZDT09Y genotype are also objects of the invention.	maize	WO2013012775A1
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[0046] Plants that may be treated according to the invention are hybrid plants that already express the characteristic of heterosis or hybrid vigor which results in generally higher yield, vigor, health and resistance towards biotic and abiotic stresses). Such plants are typically made by crossing an inbred male-sterile parent line (the female parent) with another inbred male-fertile parent line (the male parent). Hybrid seed is typically harvested from the male sterile plants and sold to growers. Male sterile plants can sometimes (e.g. in corn) be produced by detasseling, i.e. the mechanical removal of the male reproductive organs (or males flowers) but, more typically, male sterility is the result of genetic determinants in the plant genome. In that case, and especially when seed is the desired product to be harvested from the hybrid plants it is typically useful to ensure that male fertility in the hybrid plants is fully restored. This can be accomplished by ensuring that the male parents have appropriate fertility restorer genes which are capable of restoring the male fertility in hybrid plants that contain the genetic determinants responsible for male-sterility. Genetic determinants for male sterility may be located in the cytoplasm. Examples of cytoplasmic male sterility (CMS) were for instance described in *Brassica* species (WO 92/05251, WO 95/09910, WO 98/27806, WO 05/002324, WO 06/021972 and US 6,229,072). However, genetic determinants for male sterility can also be located in the nuclear genome. Male sterile plants can also be obtained by plant biotechnology methods such as genetic engineering. A particularly useful means of obtaining male-sterile plants is described in WO 89/10396 in which, for example, a ribonuclease such as barnase is selectively expressed in the tapetum cells in the stamens. Fertility can then be restored by expression in the tapetum cells of a ribonuclease inhibitor such as barstar (e.g. WO 91/02069).

[0047] Plants or plant cultivars (obtained by plant biotechnology methods such as genetic engineering) which may be treated according to the invention are herbicide-tolerant plants, i.e. plants made tolerant to one or more given herbicides. Such plants can be obtained either by genetic transformation, or by selection of plants containing a mutation imparting such herbicide tolerance.

[0048] Herbicide-resistant plants are for example glyphosate-tolerant plants, i.e. plants made tolerant to the herbicide glyphosate or salts thereof. Plants can be made tolerant to glyphosate through different means. For example, glyphosate-tolerant plants can be obtained by transforming the plant with a gene encoding the enzyme 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS). Examples of such EPSPS genes are the AroA gene (mutant CT7) of the bacterium *Salmonella typhimurium* (*Science* **1983**, 221, 370-371), the CP4 gene of the bacterium *Agrobacterium sp.* (*Curr. Topics Plant Physiol.* **1992**, 7, 139-145), the genes encoding a Petunia EPSPS (*Science* **1986**, 233, 478-481), a Tomato EPSPS (*J. Biol. Chem.* **1988**, 263, 4280-4289), or an Eleusine EPSPS (WO 01/66704). It can also be a mutated EPSPS as described in for example EP 0837944, WO 00/66746, WO 00/66747 or WO 02/26995, WO 11/000498.

Glyphosate-tolerant plants can also be obtained by expressing a gene that encodes a glyphosate oxidoreductase enzyme as described in US 5,776,760 and US 5,463,175. Glyphosate-tolerant plants can also be obtained by expressing a gene that encodes a glyphosate acetyl transferase enzyme as described in for example WO 02/036782, WO 03/092360, WO 05/012515 and WO 07/024782. Glyphosate-tolerant plants can also be obtained by selecting plants containing naturally-occurring mutations of the above-mentioned genes, as described in for example WO 01/024615 or WO 03/013226. Plants expressing EPSPS genes that confer glyphosate tolerance are described in e.g. U.S. Patent Applications 11/517,991, 10/739,610, 12/139,408, 12/352,532, 11/312,866, 11/315,678, 12/421,292, 11/400,598, 11/651,752, 11/681,285, 11/605,824, 12/468,205, 11/760,570, 11/762,526, 11/769,327, 11/769,255, 11/943801 or 12/362,774. Plants comprising other genes that confer glyphosate tolerance, such as decarboxylase genes, are described in e.g. U.S. Patent Applications 11/588,811, 11/185,342, 12/364,724, 11/185,560 or 12/423,926.

[0049] Other herbicide resistant plants are for example plants that are made tolerant to herbicides inhibiting the enzyme glutamine synthase, such as bialaphos, phosphinothricin or glufosinate. Such plants can be obtained by expressing an enzyme detoxifying the herbicide or a mutant glutamine synthase enzyme that is resistant to inhibition, e.g. described in U.S. Patent Application 11/760,602. One such efficient detoxifying enzyme is an enzyme encoding a phosphinothricin acetyltransferase (such as the bar or pat protein from *Streptomyces* species). Plants expressing an exogenous phosphinothricin acetyltransferase are for example described in U.S. Patents 5,561,236; 5,648,477; 5,646,024; 5,273,894; 5,637,489; 5,276,268; 5,739,082; 5,908,810 and 7,112,665.

[0050] Further herbicide-tolerant plants are also plants that are made tolerant to the herbicides inhibiting the enzyme hydroxyphenylpyruvatedioxygenase (HPPD). HPPD is an enzyme that catalyze the reaction in which para-hydroxyphenylpyruvate (HPP) is transformed into homogentisate. Plants tolerant to HPPD-inhibitors can be transformed with a gene encoding a naturally-occurring resistant HPPD enzyme, or a gene encoding a mutated or chimeric HPPD enzyme as described in WO 96/38567, WO 99/24585, WO 99/24586, WO 09/144079, WO 02/046387, US 6,768,044, WO 11/076877, WO 11/076882, WO 11/076885, WO 11/076889, WO 11/076892, WO13/026740, WO13/092552, WO13/092551 or

WO12/092555. Tolerance to HPPD-inhibitors can also be obtained by transforming plants with genes encoding certain enzymes enabling the formation of homogentisate despite the inhibition of the native HPPD enzyme by the HPPD-inhibitor. Such plants and genes are described in WO 99/34008 and WO 02/36787. Tolerance of plants to HPPD inhibitors can also be improved by transforming plants with a gene encoding an enzyme having prephenate deshydrogenase (PDH) activity in addition to a gene encoding an HPPD-tolerant enzyme, as described in WO 04/024928. Further, plants can be made more tolerant to HPPD-inhibitor herbicides by adding into their genome a gene encoding an enzyme capable of metabolizing or degrading HPPD inhibitors, such as the CYP450 enzymes shown in WO 07/103567 and WO 08/150473.

10 [0051] Still further herbicide resistant plants are plants that are made tolerant to acetolactate synthase (ALS) inhibitors. Known ALS-inhibitors include, for example, sulfonylurea, imidazolinone, triazolo-pyrimidines, pyrimidinyoxy(thio)benzoates, and/or sulfonylaminocarbonyltriazolinone herbicides. Different mutations in the ALS enzyme (also known as acetohydroxyacid synthase, AHAS) are known to confer tolerance to different herbicides and groups of herbicides, as described for example in Tranel and
15 Wright (*Weed Science* **2002**, 50, 700-712), but also, in U.S. Patents 5,605,011, 5,378,824, 5,141,870, and 5,013,659. The production of sulfonylurea-tolerant plants and imidazolinone-tolerant plants is described in U.S. Patents 5,605,011; 5,013,659; 5,141,870; 5,767,361; 5,731,180; 5,304,732; 4,761,373; 5,331,107; 5,928,937; and 5,378,824; and WO 96/33270. Other imidazolinone-tolerant plants are also described in for example WO 04/040012, WO 04/106529, WO 05/020673, WO 05/093093, WO 06/007373,
20 WO 06/015376, WO 06/024351, and WO 06/060634. Further sulfonylurea- and imidazolinone-tolerant plants are also described in for example WO 07/024782, WO 2011/076345, WO 2012058223, WO 2012150335 and U.S. Patent Application 61/288958.

[0052] Other plants tolerant to imidazolinone and/or sulfonylurea can be obtained by induced mutagenesis, selection in cell cultures in the presence of the herbicide or mutation breeding as described
25 for example for soybeans in US 5,084,082, for rice in WO 97/41218, for sugar beet in US 5,773,702 and WO 99/057965, for lettuce in US 5,198,599, or for sunflower in WO 01/065922.

[0053] Plants tolerant to 2,4 D or dicamba are for example described in US6153401.

[0054] Plants or plant cultivars (obtained by plant biotechnology methods such as genetic engineering) which may also be treated according to the invention are insect-resistant transgenic plants, i.e. plants
30 made resistant to attack by certain target insects. Such plants can be obtained by genetic transformation, or by selection of plants containing a mutation imparting such insect resistance.

[0055] An "insect-resistant transgenic plant", as used herein, includes any plant containing at least one transgene comprising a coding sequence encoding:

- 1) an insecticidal crystal protein from *Bacillus thuringiensis* or an insecticidal portion thereof, such as the insecticidal crystal proteins listed by Crickmore et al. (*Microbiology and Molecular Biology Reviews* **1998**, 62, 807-813), updated by Crickmore et al. (2005) at the *Bacillus thuringiensis* toxin nomenclature, online at: http://www.lifesci.sussex.ac.uk/Home/Neil_Crickmore/Bt/), or insecticidal portions thereof, e.g., proteins of the Cry protein classes Cry1Ab, Cry1Ac, Cry1B, Cry1C, Cry1D, Cry1F, Cry2Ab, Cry3Aa, or Cry3Bb or insecticidal portions thereof (e.g. EP-A 1 999 141 and WO 07/107302), or such proteins encoded by synthetic genes as e.g. described in and U.S. Patent Application 12/249,016 ; or
- 2) a crystal protein from *Bacillus thuringiensis* or a portion thereof which is insecticidal in the presence of a second other crystal protein from *Bacillus thuringiensis* or a portion thereof, such as the binary toxin made up of the Cry34 and Cry35 crystal proteins (*Nat. Biotechnol.* **2001**, 19, 668-72; *Applied Environm. Microbiol.* **2006**, 71, 1765-1774) or the binary toxin made up of the Cry1A or Cry1F proteins and the Cry2Aa or Cry2Ab or Cry2Ae proteins (U.S. Patent Application 12/214,022 and EP-A 2 300 618); or
- 3) a hybrid insecticidal protein comprising parts of different insecticidal crystal proteins from *Bacillus thuringiensis*, such as a hybrid of the proteins of 1) above or a hybrid of the proteins of 2) above, e.g., the Cry1A.105 protein produced by corn event MON89034 (WO 07/027777); or
- 4) a protein of any one of 1) to 3) above wherein some, particularly 1 to 10, amino acids have been replaced by another amino acid to obtain a higher insecticidal activity to a target insect species, and/or to expand the range of target insect species affected, and/or because of changes introduced into the encoding DNA during cloning or transformation, such as the Cry3Bb1 protein in corn events MON863 or MON88017, or the Cry3A protein in corn event MIR604; or
- 5) an insecticidal secreted protein from *Bacillus thuringiensis* or *Bacillus cereus*, or an insecticidal portion thereof, such as the vegetative insecticidal (VIP) proteins listed at:
http://www.lifesci.sussex.ac.uk/home/Neil_Crickmore/Bt/vip.html, e.g., proteins from the VIP3Aa protein class; or
- 6) a secreted protein from *Bacillus thuringiensis* or *Bacillus cereus* which is insecticidal in the presence of a second secreted protein from *Bacillus thuringiensis* or *B. cereus*, such as the binary toxin made up of the VIP1A and VIP2A proteins (WO 94/21795); or
- 7) a hybrid insecticidal protein comprising parts from different secreted proteins from *Bacillus thuringiensis* or *Bacillus cereus*, such as a hybrid of the proteins in 1) above or a hybrid of the proteins in 2) above; or

- 8) a protein of any one of 5) to 7) above wherein some, particularly 1 to 10, amino acids have been replaced by another amino acid to obtain a higher insecticidal activity to a target insect species, and/or to expand the range of target insect species affected, and/or because of changes introduced into the encoding DNA during cloning or transformation (while still encoding an insecticidal protein), such as the VIP3Aa protein in cotton event COT102; or
- 9) a secreted protein from *Bacillus thuringiensis* or *Bacillus cereus* which is insecticidal in the presence of a crystal protein from *Bacillus thuringiensis*, such as the binary toxin made up of VIP3 and Cry1A or Cry1F (U.S. Patent Applications 61/126083 and 61/195019), or the binary toxin made up of the VIP3 protein and the Cry2Aa or Cry2Ab or Cry2Ae proteins (U.S. Patent Application 12/214,022 and EP-A 2 300 618).
- 10) a protein of 9) above wherein some, particularly 1 to 10, amino acids have been replaced by another amino acid to obtain a higher insecticidal activity to a target insect species, and/or to expand the range of target insect species affected, and/or because of changes introduced into the encoding DNA during cloning or transformation (while still encoding an insecticidal protein)

[0056] Of course, an insect-resistant transgenic plant, as used herein, also includes any plant comprising a combination of genes encoding the proteins of any one of the above classes 1 to 10. In one embodiment, an insect-resistant plant contains more than one transgene encoding a protein of any one of the above classes 1 to 10, to expand the range of target insect species affected when using different proteins directed at different target insect species, or to delay insect resistance development to the plants by using different proteins insecticidal to the same target insect species but having a different mode of action, such as binding to different receptor binding sites in the insect.

[0057] An “insect-resistant transgenic plant”, as used herein, further includes any plant containing at least one transgene comprising a sequence producing upon expression a double-stranded RNA which upon ingestion by a plant insect pest inhibits the growth of this insect pest, as described e.g. in WO 07/080126, WO 06/129204, WO 07/074405, WO 07/080127 and WO 07/035650.

[0058] Plants or plant cultivars (obtained by plant biotechnology methods such as genetic engineering) which may also be treated according to the invention are tolerant to abiotic stresses. Such plants can be obtained by genetic transformation, or by selection of plants containing a mutation imparting such stress resistance. Particularly useful stress tolerance plants include:

- 1) plants which contain a transgene capable of reducing the expression and/or the activity of poly(ADP-ribose) polymerase (PARP) gene in the plant cells or plants as described in WO 00/04173, WO 06/045633, EP-A 1 807 519, or EP-A 2 018 431.

- 2) plants which contain a stress tolerance enhancing transgene capable of reducing the expression and/or the activity of the PARG encoding genes of the plants or plants cells, as described e.g. in WO 04/090140.
- 3) plants which contain a stress tolerance enhancing transgene coding for a plant-functional enzyme of the nicotineamide adenine dinucleotide salvage synthesis pathway including nicotinamidase, nicotinate phosphoribosyltransferase, nicotinic acid mononucleotide adenyl transferase, nicotinamide adenine dinucleotide synthetase or nicotine amide phosphorybosyltransferase as described e.g. in EP-A 1 794 306, WO 06/133827, WO 07/107326, EP-A 1 999 263, or WO 07/107326.

[0059] Plants or plant cultivars (obtained by plant biotechnology methods such as genetic engineering) which may also be treated according to the invention show altered quantity, quality and/or storage-stability of the harvested product and/or altered properties of specific ingredients of the harvested product such as:

- 1) transgenic plants which synthesize a modified starch, which in its physical-chemical characteristics, in particular the amylose content or the amylose/amylopectin ratio, the degree of branching, the average chain length, the side chain distribution, the viscosity behaviour, the gelling strength, the starch grain size and/or the starch grain morphology, is changed in comparison with the synthesised starch in wild type plant cells or plants, so that this is better suited for special applications. Said transgenic plants synthesizing a modified starch are disclosed, for example, in EP-A 0 571 427, WO 95/04826, EP-A 0 719 338, WO 96/15248, WO 96/19581, WO 96/27674, WO 97/11188, WO 97/26362, WO 97/32985, WO 97/42328, WO 97/44472, WO 97/45545, WO 98/27212, WO 98/40503, WO 99/58688, WO 99/58690, WO 99/58654, WO 00/08184, WO 00/08185, WO 00/08175, WO 00/28052, WO 00/77229, WO 01/12782, WO 01/12826, WO 02/101059, WO 03/071860, WO 04/056999, WO 05/030942, WO 05/030941, WO 05/095632, WO 05/095617, WO 05/095619, WO 2005/095618, WO 05/123927, WO 06/018319, WO 06/103107, WO 06/108702, WO 07/009823, WO 00/22140, WO 06/063862, WO 06/072603, WO 02/034923, WO 08/017518, WO 08/080630, WO 08/080631, WO 08/090008, WO 01/14569, WO 02/79410, WO 03/33540, WO 04/078983, WO 01/19975, WO 95/26407, WO 96/34968, WO 98/20145, WO 99/12950, WO 99/66050, WO 99/53072, US 6,734,341, WO 00/11192, WO 98/22604, WO 98/32326, WO 01/98509, WO 01/98509, WO 05/002359, US 5,824,790, US 6,013,861, WO 94/04693, WO 94/09144, WO 94/11520, WO 95/35026, WO 97/20936, WO 10/012796, WO 10/003701, WO 13/053729, WO 13/053730,
- 2) transgenic plants which synthesize non starch carbohydrate polymers or which synthesize non starch carbohydrate polymers with altered properties in comparison to wild type plants without genetic modification. Examples are plants producing polyfructose, especially of the inulin and levan-type, as disclosed in EP-A 0 663 956, WO 96/01904, WO 96/21023, WO 98/39460, and WO 99/24593,

plants producing alpha-1,4-glucans as disclosed in WO 95/31553, US 2002031826, US 6,284,479, US 5,712,107, WO 97/47806, WO 97/47807, WO 97/47808 and WO 00/14249, plants producing alpha-1,6 branched alpha-1,4-glucans, as disclosed in WO 00/73422, plants producing alternan, as disclosed in e.g. WO 00/47727, WO 00/73422, US 5,908,975 and EP-A 0 728 213,

5 3) transgenic plants which produce hyaluronan, as for example disclosed in WO 06/032538, WO 07/039314, WO 07/039315, WO 07/039316, JP-A 2006-304779, and WO 05/012529.

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

10 5) Transgenic plants displaying an increase yield as for example disclosed in WO 11/095528

[0060] Plants or plant cultivars (that can be obtained by plant biotechnology methods such as genetic engineering) which may also be treated according to the invention are plants, such as cotton plants, with altered fiber characteristics. Such plants can be obtained by genetic transformation, or by selection of plants contain a mutation imparting such altered fiber characteristics and include:

- 15 a) Plants, such as cotton plants, containing an altered form of cellulose synthase genes as described in WO 98/00549.
- b) Plants, such as cotton plants, containing an altered form of rsw2 or rsw3 homologous nucleic acids as described in WO 04/053219.
- 20 c) Plants, such as cotton plants, with increased expression of sucrose phosphate synthase as described in WO 01/17333.
- d) Plants, such as cotton plants, with increased expression of sucrose synthase as described in WO 02/45485.
- 25 e) Plants, such as cotton plants, wherein the timing of the plasmodesmatal gating at the basis of the fiber cell is altered, e.g. through downregulation of fiber-selective β -1,3-glucanase as described in WO 05/017157, or as described in WO 09/143995.
- f) Plants, such as cotton plants, having fibers with altered reactivity, e.g. through the expression of N-acetylglucosaminetransferase gene including nodC and chitin synthase genes as described in WO 06/136351, WO 11/089021, WO 11/089021, WO 12/074868.

[0061] Plants or plant cultivars (that can be obtained by plant biotechnology methods such as genetic engineering) which may also be treated according to the invention are plants, such as oilseed rape or related Brassica plants, with altered oil profile characteristics. Such plants can be obtained by genetic transformation, or by selection of plants contain a mutation imparting such altered oil profile characteristics and include:

- a) Plants, such as oilseed rape plants, producing oil having a high oleic acid content as described e.g. in US 5,969,169, US 5,840,946 or US 6,323,392 or US 6,063,947
- b) Plants such as oilseed rape plants, producing oil having a low linolenic acid content as described in US 6,270,828, US 6,169,190, US 5,965,755 or WO 11/060946
- c) Plant such as oilseed rape plants, producing oil having a low level of saturated fatty acids as described e.g. in US 5,434,283 or U.S. Patent Application 12/668303
- d) Plants such as oilseed rape plants, producing oil having an alter glucosinolate content as described in WO 2012075426.

[0062] Plants or plant cultivars (that can be obtained by plant biotechnology methods such as genetic engineering) which may also be treated according to the invention are plants, such as oilseed rape or related Brassica plants, with altered seed shattering characteristics. Such plants can be obtained by genetic transformation, or by selection of plants contain a mutation imparting such altered seed shattering characteristics and include plants such as oilseed rape plants with delayed or reduced seed shattering as described in WO 2009/068313 and WO 2010/006732, WO 2012090499.

[0063] Plants or plant cultivars (that can be obtained by plant biotechnology methods such as genetic engineering) which may also be treated according to the invention are plants, such as Tobacco plants, with altered post-translational protein modification patterns, for example as described in WO 10/121818 and WO 10/145846.

[0064] Particularly useful transgenic plants which may be treated according to the invention are plants containing transformation events, or combination of transformation events, that are the subject of petitions for non-regulated status, in the United States of America, to the Animal and Plant Health Inspection Service (APHIS) of the United States Department of Agriculture (USDA) whether such petitions are granted or are still pending. At any time this information is readily available from APHIS (4700 River Road, Riverdale, MD 20737, USA), for instance on its internet site (URL http://www.aphis.usda.gov/brs/not_reg.html). On the filing date of this application the petitions for nonregulated status that were pending with APHIS or granted by APHIS were those listed in Table B which contains the following information:

- Petition: the identification number of the petition. Technical descriptions of the transformation events can be found in the individual petition documents which are obtainable from APHIS, for example on the APHIS website, by reference to this petition number. These descriptions are herein incorporated by reference.
- 5 – Extension of Petition: reference to a previous petition for which an extension is requested.
- Institution: the name of the entity submitting the petition.
- Regulated article: the plant species concerned.
- Transgenic phenotype: the trait conferred to the plants by the transformation event.
- Transformation event or line: the name of the event or events (sometimes also designated as lines or
10 lines) for which nonregulated status is requested.
- APHIS documents: various documents published by APHIS in relation to the Petition and which can be requested with APHIS.

Table B

Petition No.	Applicant	Crop	Phenotype/Event
11-342-01p	Genective	Corn	Glyphosate Tolerant/ VCO-Ø1981-5
11-234-01p	Dow	Soybean	2, 4-D, Glyphosate and Glufosinate Tolerant/ DAS-444Ø6-6
11-202-01p	Monsanto	Soybean	Increased Yield/ MON 87712
11-188-01p	Monsanto	Canola	Glyphosate Tolerant/ MON 88302
11-063-01p	Pioneer	Canola	Glyphosate Tolerant/73496
10-281-01p	Monsanto	Corn	Male Sterile/ MON 87427
10-188-01p	Monsanto	Soybean	Dicamba Tolerant/ MON 87708
10-161-01p	Okanagan	Apple	Non-Browning/ GD743, GS784
09-015-01p	BASF	Soybean	Imadazolinone Tolerant/ BPS-CV127-9
The following pending petitions will proceed with the previous process for soliciting public input (simultaneous notice of availability of the petition and decisionmaking documents).			

Petition No.	Applicant	Crop	Phenotype/Event
12-033-01p Extension of 08-340-01p	Bayer	Cotton	Glufosinate Tolerant, Lepidopteran Resistant/ T303-3
11-244-01p	Pioneer	Corn	Insect Resistant and Glufosinate Tolerant/ DP-004114-3
10-336-01p	Syngenta	Corn	Rootworm Resistant/ 5307
09-349-01p	Dow	Soybean	2,4-D and Glufosinate Tolerant/ DAS-68416-4
09-328-01p	Bayer	Soybean	Glyphosate and Isoxaflutole Tolerant/ FG72
09-233-01p	Dow	Corn	2,4-D and ACCase-Inhibitor Tolerant/ DAS-40278-9
03-104-01p	Scotts	Creeping Bentgrass	Glyphosate Tolerant/ ASR368

Determinations of Nonregulated
Status

Petition No.	Applicant	Crop	Phenotype/Event
09-201-01p	Monsanto	Soybean	Improved Fatty Acid Profile/ MON 87705
09-183-01p	Monsanto	Soybean	Stearidonic Acid Produced/ MON 87769
09-082-01p	Monsanto	Soybean	Insect Resistant/ MON 87701
09-055-01p	Monsanto	Corn	Drought Tolerant/ MON 87460
08-340-01p	Bayer	Cotton	Glufosinate Tolerant, Lepidopteran Resistant/ T304-40 x GHB119

08-338-01p	Pioneer	Corn	Male Sterile, Fertility Restored, Visual Marker/ DP-32138-1
08-315-01p	Florigene	Rose	Altered Flower Color/ IFD-52401-4, IFD-52901-9
07-253-01p	Syngenta	Corn	Lepidopteran Resistant/ MIR 162
07-152-01p	Pioneer	Corn	Glyphosate & Imidazolinone Tolerant/ 98140
07-108-01p	Syngenta	Cotton	Lepidopteran Resistant/ COT67B
06-354-01p	Pioneer	Soybean	High Oleic Acid/ Event 305423
06-332-01p	Bayer CropScience	Cotton	Glyphosate Tolerant/ GHB614
06-298-01p	Monsanto	Corn	European Corn Borer Resistant/ MON 89034
06-271-01p	Pioneer	Soybean	Glyphosate & Acetolactate Synthase Tolerant/ DP-356Ø43-5
06-234-01p Extension of 98-329-01p	Bayer CropScience	Rice	Phosphinothricin Tolerant/ LLRICE601
06-178-01p	Monsanto	Soybean	Glyphosate Tolerant/ MON 89788
05-280-01p	Syngenta	Corn	Thermostable Alpha-amylase/ 3272
04-362-01p	Syngenta	Corn	Corn Rootworm Protected/ MIR604
04-337-01p	University of Florida	Papaya	Papaya Ringspot Virus Resistant/ X17-2
04-264-01p	ARS	Plum	Plum Pox Virus Resistant/ C5
04-229-01p	Monsanto	Corn	High Lysine/ LY038
04-125-01p	Monsanto	Corn	Corn Rootworm Resistant/

			MON 88017
04-110-01p_a1 04-110-01p	Monsanto & Forage Genetics	Alfalfa	Glyphosate Tolerant/ J101, J103
04-086-01p	Monsanto	Cotton	Glyphosate Tolerant/ MON 88913
03-353-01p	Dow	Corn	Corn Rootworm Resistant/ 59122
03-323-01p_a1 03-323-01p	Monsanto and KWS SAAT AG	Sugar Beet	Glyphosate Tolerant/ H7-1
03-181-01p Extension of 00-136-01p	Dow	Corn	Lepidopteran Resistant & Phosphinothricin Tolerant/ 6275
03-155-01p	Syngenta	Cotton	Lepidopteran Resistant/ COT102
03-036-02p	Mycogen/Dow	Cotton	Lepidopteran Resistant/ 3006-210-23
03-036-01p	Mycogen/Dow	Cotton	Lepidopteran Resistant/ 281-24-236
02-042-01p	Aventis	Cotton	Phosphinothricin Tolerant/ LLCotton25
01-324-01p Extension of 98-216-01p	Monsanto	Rapeseed	Glyphosate tolerant/ GT200
01-206-02p Extension of 97-205-01p	Aventis	Rapeseed	Phosphinothricin Tolerant & Pollination Control/ Topas 19/2
01-206-01p Extension of 98-278-01p	Aventis	Rapeseed	Phosphinothricin Tolerant/ MS1
01-137-01p	Monsanto	Corn	Corn Rootworm Resistant/ MON 863
01-121-01p	Vector	Tobacco	Reduced Nicotine/ Vector 21-41

00-342-01p	Monsanto	Cotton	Lepidopteran Resistant/ 15985
00-136-01p	Mycogen c/o Dow & Pioneer	Corn	Lepidopteran Resistant Phosphinothricin Tolerant/ 1507
00-011-01p Extension of 97-099-01p	Monsanto	Corn	Glyphosate Tolerant/ NK603
99-173-01p Extension of 97-204-01p	Monsanto	Potato	Potato Leafroll Virus & Colorado Potato Beetle Resistant/ RBMT22-82
98-349-01p Extension of 95-228-01p	AgrEvo	Corn	Phosphinothricin Tolerant and Male Sterile/ MS6
98-335-01p	U. of Saskatchewan	Flax	Tolerant to Soil Residues of Sulfonylurea Herbicide/ CDC Triffid
98-329-01p	AgrEvo	Rice	Phosphinothricin Tolerant/ LLRICE06, LLRICE62
98-278-01p	AgrEvo	Rapeseed	Phosphinothricin Tolerant and Pollination Control/ MS8, RF3
98-238-01p	AgrEvo	Soybean	Phosphinothricin Tolerant/ GU262
98-216-01p	Monsanto	Rapeseed	Glyphosate Tolerant/ RT73
98-173-01p	Novartis Seeds & Monsanto	Beet	Glyphosate Tolerant/ GTSB77
98-014-01p Extension of 96-068-01p	AgrEvo	Soybean	Phosphinothricin Tolerant/ A5547-127
97-342-01p	Pioneer	Corn	Male Sterile and Phosphinothricin Tolerant/ 676, 678, 680

97-339-01p	Monsanto	Potato	Colorado Potato Beetle and Potato Virus Y Resistant/ RBMT15-101, SEMT15-02, SEMT15-15
97-336-01p	AgrEvo	Beet	Phosphinothricin Tolerant/ T120-7
97-287-01p	Monsanto	Tomato	Lepidopteran Resistant/ 5345
97-265-01p	AgrEvo	Corn	Phosphinothricin Tolerant and Lepidopteran Resistant/ CBH-351
97-205-01p	AgrEvo	Rapeseed	Phosphinothricin Tolerant/ T45
97-204-01p	Monsanto	Potato	Potato Leafroll Virus & Colorado Potato Beetle Resistant/ RBMT21-129, RBMT21-152, RBMT21-350, RBMT22-82, RBMT22-186, RBMT22-238, RBMT22-262
97-148-01p	Bejo	Cichorium intybus	Male Sterile/ RM3-3, RM3-4, RM3-6
97-099-01p	Monsanto	Corn	Glyphosate Tolerant/ GA21
97-013-01p	Calgene	Cotton	Bromoxynil Tolerant and Lepidopteran Resistant/ 31807, 31808
97-008-01p	Du Pont	Soybean	High Oleic Acid Oil/ G94-1, G94-19, G-168
96-317-01p	Monsanto	Corn	Glyphosate Tolerant and European Corn Borer Resistant/ MON 802
96-291-01p	DeKalb	Corn	European Corn Borer Resistant/ DBT418
96-248-01p Extension of 92-196-01p	Calgene	Tomato	Fruit Ripening Altered/ 532A 4109a 5166
96-068-01p	AgrEvo	Soybean	Glufosinate Tolerant/

			W62, W98, A2704-12, A2704-21, A5547-35
96-051-01p	Cornell U	Papaya	Papaya Ringspot Virus Resistant/ 55-1, 63-1
96-017-01p Extension of 95-093-01p	Monsanto	Corn	European Corn Borer Resistant/ MON 809, MON 810
95-352-01p	Asgrow	Squash	Cucumber Mosaic Virus, Watermelon Mosaic Virus 2, and Zucchini Yellow Mosaic Virus Resistant/ CZW-3
95-338-01p	Monsanto	Potato	Colorado Potato Beetle Resistant/ SPBT02-5, SPBT02-7, ATBT04-6, ATBT04- 27, ATBT04-30, ATBT04-31, ATBT04-36
95-324-01p	Agritope	Tomato	Fruit Ripening Altered/ 35-1-N
95-256-01p	Du Pont	Cotton	Sulfonylurea Tolerant/ 19-51A
95-228-01p	Plant Genetic Systems	Corn	Male Sterile/MS3
95-195-01p	Northrup King	Corn	European Corn Borer Resistant/ Bt11
95-179-01p Extension of 92-196-01p	Calgene	Tomato	Fruit Ripening Altered/ 519a 4109a-4645, 540a 4109a-1823
95-145-01p	DeKalb	Corn	Glufosinate Tolerant/ B16
95-093-01p	Monsanto	Corn	Lepidopteran Resistant/ MON 80100
95-053-01p	Monsanto	Tomato	Fruit Ripening Altered/ 8338
95-045-01p	Monsanto	Cotton	Glyphosate Tolerant/

			1445, 1698
95-030-01p	Calgene	Tomato	Fruit Ripening Altered/ 105F 1436 2018, 105F 1436 2035, 105F 1436 2049, 35F 4109a 3023, 84F 4109a 148, 88F 4109a 2797, 121F 4109a 333, 121F 4109a 1071, 121F 4109a 1120, 137F 4109a 71, 138F 4109a 164, 519A 4109a 4527, 519A 4109a 4621, 519A 4109a 4676, 531A 4109a 2105, 531A 4109a 2270, 532A 4109a 5097, 540A 4109a 1739, 585A 4109a 3604, 585A 4109a 3530
Extension of 92-196-01p			
94-357-01p	AgrEvo	Corn	Glufosinate Tolerant/ T14, T25
94-319-01p	Ciba Seeds	Corn	Lepidopteran Resistant/ 176
94-308-01p	Monsanto	Cotton	Lepidopteran Resistant/ 531, 757, 1076
94-290-01p	Zeneca & Petoseed	Tomato	Fruit Polygalacturonase Level Decreased/ B, Da, F
94-257-01p	Monsanto	Potato	Coleopteran Resistant/ BT6, BT10, BT12, BT16, BT17, BT18, BT23
94-230-01p	Calgene	Tomato	Fruit Ripening Altered/ 114F 4109a 26, 114F 4109a 81
Extension of 92-196-01p			
94-228-01p	DNA Plant Tech	Tomato	Fruit Ripening Altered/ 1345-4
94-227-01p	Calgene	Tomato	Fruit Ripening Altered/ pCGN1436, pCGN4109
Extension of 92-196-01p			
94-090-01p	Calgene	Rapeseed	Oil Profile Altered/ pCGN3828-212/86-18,

			pCGN3828-212/86-23
93-258-01p	Monsanto	Soybean	Glyphosate Tolerant/ 4-30-2
93-196-01p	Calgene	Cotton	Bromoxynil Tolerant/ BXN
92-204-01p	Upjohn	Squash	Watermelon Mosaic Virus and Zucchini Yellow Mosaic Virus Resistant/ ZW-20
92-196-01p	Calgene	Tomato	Fruit Ripening Altered/ pCGN1547, pCGN1548, pCGN1557, pCGN1559, pCGN1578

[0065] Additional particularly useful plants containing single transformation events or combinations of transformation events are listed for example in the databases from various national or regional regulatory agencies (see for example http://gmoinfo.jrc.it/gmp_browse.aspx and [http://www.cera-](http://www.cera-gmc.org/?action=gm_crop_database)

5 [gmc.org/?action=gm_crop_database](http://www.cera-gmc.org/?action=gm_crop_database)).

[0066] Further particularly transgenic plants include plants containing a transgene in an agronomically neutral or beneficial position as described in any of the patent publications listed in Table C.

Table C

Trait	Reference	Remarks
Water use efficiency	WO 2000/073475	
	WO2009/150541	
	WO2009/150541	
	WO2012075429	
	WO2012077020	
	WO2012158594	
Nitrogen use efficiency	WO 1995/009911	
	WO 1997/030163	
	WO 2007/092704	
	WO 2007/076115	
	WO 2005/103270	
	WO 2002/002776	
	WO2008/051608	
	WO2008/112613	
	WO2009/015096	
	WO2009/061776	

	WO2009/105492	
	WO2009/105612	
	WO2009/117853	
	WO2010/006010	
	WO2009/117853	
	WO2009/061776	
	WO2009/015096	
	WO2009/105492	
	WO2009/105612	
	WO 2010/053621	
	WO 2010/053867	
	WO2010/077890	
	WO 2010/086220	
	WO 2010/111568	
	WO 2010/140388	
	WO2010/007496	
	WO2011/022597	
	WO2011/022608	
	WO2012087140	
Improved photosynthesis	WO 2008/056915	
	WO 2004/101751	
Nematode resistance	WO 1995/020669	
	WO 2001/051627	
	WO 2008/139334	
	WO 2008/095972	
	WO 2006/085966	
	WO 2003/033651	
	WO 1999/060141	
	WO 1998/012335	
	WO 1996/030517	
	WO 1993/018170	
	WO2008/095886	
	WO2008/095887	
	WO2008/095888	
	WO2008/095889	
	WO2008/095910	
	WO2008/095911	
	WO2008/095916	
	WO2008/095919	
	WO2008/095969	
	WO2008/095970	

	WO2008/095972	
	WO2008/110522	
	WO2008/139334	
	WO2008/152008	
	WO2010/077858	
	WO 2010/091230	
	WO 2010/102172	
	WO 2010/106163	
	WO2011/003783	
	WO2011/082217	
	WO2011/104153	
	WO2012007916	
	WO2012007919	
	WO2012009551	
	WO2012011034	
	WO2012012403	
	WO2012153274	
	WO2012156902	
Reduced pod dehiscence	WO 2006/009649	
	WO 2004/113542	
	WO 1999/015680	
	WO 1999/000502	
	WO 1997/013865	
	WO 1996/030529	
	WO 1994/023043	
Aphid resistance	WO 2006/125065	
	WO 1997/046080	
	WO 2008/067043	
	WO 2004/072109	
	WO2009/091860	
	WO2010036764	
Sclerotinia resistance	WO 2006/135717	
	WO 2006/055851	
	WO 2005/090578	
	WO 2005/000007	
	WO 2002/099385	
	WO 2002/061043	
Botrytis resistance	WO 2006/046861	
	WO 2002/085105	
Bremia resistance	US 20070022496	
	WO 2000/063432	

	WO 2004/049786	
	WO2009/111627	
	WO2009/111627	
Erwinia resistance	WO 2004/049786	
Closterovirus resistance	WO 2007/073167	
	WO 2007/053015	
	WO 2002/022836	
Stress tolerance (including drought tolerance)	WO 2010/019838	
	WO 2009/049110	
	WO2008/002480	
	WO2005/033318	
	WO2008/002480	
	WO2008/005210	
	WO2008/006033	
	WO2008/008779	
	WO2008/022486	
	WO2008/025097	
	WO2008/027534	
	WO2008/027540	
	WO2008/037902	
	WO2008/046069	
	WO2008/053487	
	WO2008/057642	
	WO2008/061240	
	WO2008/064222	
	WO2008/064341	
	WO2008/073617	
	WO2008/074025	
	WO2008/076844	
	WO2008/096138	
	WO2008/110848	
	WO2008/116829	
	WO2008/117537	
	WO2008/121320	
	WO2008/125245	
	WO2008/142034	
	WO2008/142036	
	WO2008/150165	
	WO2008/092935	
	WO2008/145675	

WO2009/010460	
WO2009/016240	
WO2009/031664	
WO2009/038581	
WO2009/049110	
WO2009/053511	
WO2009/054735	
WO2009/067580	
WO2009/073605	
WO2009/077611	
WO2009/079508	Also yield
WO2009/079529	
WO2009/083958	
WO2009/086229	Also yield
WO2009/092009	Also yield
WO2009/094401	
WO2009/094527	
WO2009/102965	Also biomass/starch/oil
WO2009/114733	
WO2009/117448	
WO2009/126359	
WO2009/126462	Also grain yield
WO2009/129162	
WO2009/132057	
WO2009/141824	
WO2009/148330	
WO 2010/055024	
WO 2010/058428	
WO 2010/064934	
WO2010/076756	
WO 2010/083178	
WO 2010/086221	
WO 2010/086277	
WO 2010/101818	
WO 2010/104848	
WO 2010/118338	
WO 2010/120017	
WO 2010/120054	
WO 2010/121316	
WO 2010/127579	
WO 2010/134654	

	WO 2010/139993	
	WO2010/039750	
	WO2011/034968	
	WO2011/001286	
	WO2011/017492	
	WO2011/018662	
	WO2011/024065	
	WO2011/038389	
	WO2011/46772	
	WO2011/053897	
	WO2011/052169	
	WO2011/063706	
	WO2011/067745	
	WO2011/079277	
	WO2011/080674	
	WO2011/083290	
	WO2011/083298	
	WO2011/091764	
	WO2011/052169	
	WO2011/053897	
	WO2011/056769	
	WO2011/063706	
	WO2011/067745	
	WO2011/083290	
	WO2011/083298	
	WO2011/091764	
	WO2011/096609	
	WO2011/122761	
	WO2012176167	
	WO2012139532	
	WO2012159196	
	WO2012162193	
	WO2012167023	
	WO2012172556	
	WO2012116396	
Tobamovirus resistance	WO 2006/038794	
	WO2009086850	
Yield	WO 2010/046221	NUE
	WO 2010/046471	
	WO 2010/049897	
	WO 2010/055837	

WO 2010/065867	ABST
WO2010/069847	
WO2010/075143	
WO2010/075243	
WO 2010/100595	
WO 2010/102220	NUE
WO 2010/104092	
WO 2010/108836	
WO 2010/120862	ABST
WO 2010/123667	
WO 2010/124953	
WO 2010/125036	
WO 2010/127969	
WO 2010/129501	
WO 2010/140388	
WO 2010/140672	
WO2011/011273	
WO2011/000466	
WO2011/003800	
WO2011/006717	
WO2011/008510	
WO2011/009801	
WO2011/011412	
WO2011/015985	
WO2011/020746	
WO2011/021190	
WO2011/025514	
WO2011/025515	
WO2011/025516	
WO2011/025840	
WO2011/031680	
WO2011/036160	
WO2011/036232	
WO2011/041796	
WO2011/044254	
WO2011/048009	
WO2011/053898	
WO2011/051120	
WO2011/058029	
WO2011/061656	
WO2011/085062	

	WO2011/088065	
	WO2011/053898	
	WO2011/058029	
	WO2011/061656	
	WO2011/085062	
	WO2011/088065	
	WO2011/095958	
	WO2011/097215	
	WO2011/099006	
	WO2011/104128	
	WO2011/104141	
	WO2011/104143	
	WO2011/104155	
	WO2011/106734	
	WO2011/106794	
	WO2011/109661	
	WO2011/114279	
	WO2011/114305	
	WO2011/114312	
	WO2011/114313	
	WO2011/117800	
	WO2011/135527	
	WO2011/136909	
	WO2011/139431	
	WO2011/140329	
	WO2011/146754	
	WO2011/147826	
	WO2011/157976	
	WO2011/161617	
	WO2011/161620	
	WO2011/109618	
	WO2011/159452	
	WO2012078949	
	WO2012083219	
	WO2012084742	
	WO2012084756	
	WO2012087903	
	WO2012087940	
	WO2012090500	
	WO2012091939	
	WO2012092106	

	WO2012092327	
	WO2012092573	
	WO2012092580	
	WO2012092596	
	WO2012093032	
	WO2012093833	
	WO2012097720	
	WO2012098517	
	WO2012102999	
	WO2012106321	
	WO2012158630	
	WO2012165678	
	WO2012112518	
	WO2012117324	
	WO2012117330	
	WO2012117368	
	WO2012119152	
	WO2012142106	
	WO2012142116	
	WO2012143830	
	WO2012143865	
	WO2012145269	
	WO2012148121	
	WO2012148122	
	WO2012148835	
	WO2012150598	
	WO2012153267	
	WO2012153277	
	WO2012156865	
	WO2012158926	
Oil content/composition	WO 2010/045324	
	WO 2010/053541	
	WO 2010/130725	
	WO 2010/140682	
	WO2011/006948	
	WO2011/049627	
	WO2011/060946	
	WO2011/062748	
	WO2011/064181	
	WO2011/064183	
	WO2011/075716	

	WO2011/079005	
	WO2011/049627	
	WO2011/062748	
	WO2011/064181	
	WO2011/064183	
	WO2011/079005	
	WO2011/146524	
	WO2011/161093	
	WO2011/163557	
	WO2011/163632	
	WO2011/163632	
	WO2012074385	
	WO2012074386	
	WO2012103452	
	WO2012117256	
Biopharmaceutical production	WO 2010/121818	
	WO2011/119115	
Improved recombination	WO2010/071418	
	WO 2010/133616	
plant appearance	WO 2010/069004	
	WO2011/060552	
Disease control (other)	WO 2010/059558	fungi
	WO2010/075352	Insects/non-Bt
	WO2010/075498	insects/Bt
	WO 2010/085289	insects/Bt
	WO 2010/085295	insects/Bt
	WO 2010/085373	insects/Bt
	WO2009/000736	fungi
	WO2009/065863	fungi
	WO2009/112505	fungi
	WO 2010/089374	bacteria
	WO 2010/120452	insects/Bt
	WO 2010/123904	virus
	WO 2010/135782	fungi
	WO2011/025860	fungi
	WO2011/041256	Insects
	WO2011/031006	Insects / Bt
	WO2011/031922	Insects / Bt
	WO2011/075584	Insects / Bt
	WO2011/075585	Insects / Bt
	WO2011/075586	Insects / Bt

WO2011/075587	Insects / Bt
WO2011/075588	Insects / Bt
WO2011/084622	Insects / Bt
WO2011/084626	Insects / Bt
WO2011/084627	Insects / Bt
WO2011/084629	Insects / Bt
WO2011/084630	Insects / Bt
WO2011/084631	Insects / Bt
WO2011/084314	Insects / Bt
WO2011/084324	Insects / Bt
WO2011/023571	Insects / Bt
WO2011/040880	
WO2011/082304	
WO2011/003783	
WO2011/020797	
WO2011/069953	fungi
WO2011/075584	Insects/Bt
WO2011/075585	Insects/Bt
WO2011/075586	Insects/Bt
WO2011/075587	Insects/Bt
WO2011/075588	Insects/Bt
WO2011/084314	Insects/Bt
WO2011/084324	Insects/Bt
WO2011/084622	Insects/Bt
WO2011/084626	Insects/Bt
WO2011/084627	Insects/Bt
WO2011/084629	Insects/Bt
WO2011/084630	Insects/Bt
WO2011/084631	Insects/Bt
WO2011/133892	Insects/Bt
WO2011/133895	Insects/Bt
WO2011/133896	Insects/Bt
WO2011/082304	
WO2011/100650	
WO2011/158242	
WO2012003207	Bacteria
WO2012004013	Fungi
WO2012004401	Fungi
WO2012006271	Fungi
WO2012006426	Fungi
WO2012006439	Fungi

	WO2012006443	Fungi
	WO2012006622	General
	WO2012015039	
	WO2012058266	Insects/Coleoptera
	WO2012058458	Insects/Coleoptera
	WO2012058528	Insects/Lepidoptera
	WO2012058730	Insects/Lepidoptera
	WO2012061513	Insects/Lepidoptera
	WO2012063200	Insects/Lepidoptera
	WO2012065166	Insects/Lepidoptera
	WO2012065219	Insects/Lepidoptera
	WO2012066008	Insects/non-Bt
	WO2012067127	Insects/non-Bt
	WO2012068966	Insects/non-Bt
	WO2012071039	Insects/non-Bt
	WO2012071040	Insects/non-Bt
	WO2012117406	Bacteria
	WO2012116938	Fungi
	WO2012147635	Fungi
	WO2012160528	Fungi
	WO2012172498	Fung
	WO2012178154	Fungi
	WO2012149316	Fungi
	WO2012175420	-
	WO2012109515A1	Insects/Coleoptera
	WO2012109430A2	Insects and nematodes
	WO2012122369A1	Insects/Lepidoptera
	WO2012131619A1	Insects/Lepidoptera
	WO2012139004A2	Insects/Lepidoptera
	WO2012143542A1	Insects/Non-Bt
	WO2012165961A1	Insects/Non-Bt
Herbicide tolerance	US 4761373	imidazolinone
	US 5304732	Imidazolinone
	US 5331107	Imidazolinone
	US 5718079	Imidazolinone
	US 6211438	Imidazolinone
	US 6211439	Imidazolinone
	US 6222100	Imidazolinone
	US 2003/0217381	Imidazolinone
	US 2003/0217381	Imidazolinone
	WO2004/106529	Imidazolinone

WO2000/27182	Imidazolinone
WO2005/20673	imidazolinone
WO 2001/85970	Imidazolinone
US 5545822	Imidazolinone
US 5736629	Imidazolinone
US 5773703,	Imidazolinone
US 5773704	Imidazolinone
US 5952553	Imidazolinone
US 6274796	Imidazolinone
WO 2004/106529	Imidazolinone
WO2004/16073	Imidazolinone
WO 2003/14357	Imidazolinone
WO 2003/13225	imidazolinone
WO 2003/14356	imidazolinone
US 5188642	glyphosate
US 4940835	glyphosate
US 5633435	glyphosate
US 5804425	glyphosate
US 5627061.	glyphosate
US 5646024	glufosinate
US 5561236	glufosinate
US 6333449	glufosinate
US 6933111	glufosinate
US 6468747.	glufosinate
US 6376754	glufosinate
US 7105724	dicamba
US 7105724	dicamba
WO 2008/051633	dicamba
US 7105724	dicamba
US 5670454	dicamba
US 7105724	dicamba
US 7105724	dicamba
US 7105724	dicamba
US 7105724	dicamba
US 5670454	dicamba
US 7105724	dicamba
US 7105724	dicamba
US 7105724	dicamba
US 5670454	dicamba
US 7105724	dicamba
US 7105724	dicamba

US 7105724	dicamba
US 7105724	dicamba
US 6153401	2,4-D
US 6100446	2,4-D
WO 2005/107437	2,4-D
US 5670454	2,4-D
US 5608147	2,4-D
US 5670454	2,4-D
WO 2004/055191	HPPD-inhibitor
WO 199638567	HPPD-inhibitor
US 6791014	HPPD-inhibitor
US 2002/0073443,	Protox-inhibitor
US 20080052798	Protox-inhibitor
WO2011/022470	
WO2011/034936	
WO2011/028832	
WO2011/028833	
WO2011/028836	
WO2011/068567	HPPD-inhibitor
WO2011/076345	HPPD-inhibitor
WO2011/085221	HPPD-inhibitor
WO2011/094199	
WO2011/094205	HPPD-inhibitor
WO2011/068567	HPPD-inhibitor
WO2011/085221	saflufenacil
WO2011/094199	HPPD-inhibitor
WO2011/094205	HPPD-inhibitor
WO2011/145015	HPPD-inhibitor
WO2012047595	2,4-D
WO2012048124	ACCCase-inhibitor
WO2012048136	Glyphosate
WO2012048807	Glyphosate
WO2012049663	Glyphosate
WO2012050962	Glyphosate
WO2012056401	HPPD-inhibitor
WO2012057466	PPX
WO2012057465	Protox-inhibitor
WO2012058223	ALS/SU
WO2012115968	,4-D
WO2012148818	2,4-D
WO2012148820	2,4-D

	WO2012106321	ACC-ase
	WO2012124808	Dicamba
	WO2012148275	Glyphosate
plant metabolism	WO2011/060920	
	WO2011/119115	
	WO2011/102394	
reproduction/pollination control	WO2011/113839	
	WO2012142311	
	WO2012163389	
Biofuels	WO2012073493	
Fruit ripening	WO2012073494	
Fiber quality	WO2012074386	
Carbohydrates	WO2012115697	
	WO2012132348	
	WO2012134906	
	WO2012174462	

[0067] Additional particularly useful plants containing single transformation events or combinations of transformation events are listed for example in the databases from various national or regional regulatory agencies (see for example http://gmoinfo.jrc.it/gmp_browse.aspx and http://www.cera-gmc.org/?action=gm_crop_database).

5 gmc.org/?action=gm_crop_database).

[0068] Particularly useful transgenic plants which may be treated according to the invention are plants containing transformation events, or a combination of transformation events, and that are listed for example in the databases for various national or regional regulatory agencies including Event 531/ PV-GHBK04 (cotton, insect control, described in WO 2002/040677), Event 1143-14A (cotton, insect control, not deposited, described in WO 06/128569); Event 1143-51B (cotton, insect control, not deposited, described in WO 06/128570); Event 1445 (cotton, herbicide tolerance, not deposited, described in US-A 2002-120964 or WO 02/034946); Event 17053 (rice, herbicide tolerance, deposited as PTA-9843, described in WO 10/117737); Event 17314 (rice, herbicide tolerance, deposited as PTA-9844, described in WO 10/117735); Event 281-24-236 (cotton, insect control - herbicide tolerance, deposited as PTA-6233, described in WO 05/103266 or US-A 2005-216969); Event 3006-210-23 (cotton, insect control - herbicide tolerance, deposited as PTA-6233, described in US-A 2007-143876 or WO 05/103266); Event 3272 (corn, quality trait, deposited as PTA-9972, described in WO 06/098952 or US-A 2006-230473); Event 33391 (wheat, herbicide tolerance, deposited as PTA-2347, described in WO 2002/027004), Event 40416 (corn, insect control - herbicide tolerance, deposited as ATCC PTA-11508, described in WO 11/075593); Event 43A47 (corn, insect control - herbicide tolerance, deposited as ATCC PTA-11509, described in WO 11/075595); Event 5307 (corn, insect control, deposited as ATCC PTA-9561, described in WO 10/077816); Event ASR-368 (bent grass, herbicide tolerance, deposited as ATCC PTA-4816,

described in US-A 2006-162007 or WO 04/053062); Event B16 (corn, herbicide tolerance, not deposited, described in US-A 2003-126634); Event BPS-CV127-9 (soybean, herbicide tolerance, deposited as NCIMB No. 41603, described in WO 10/080829); Event BLR1 (oilseed rape, restoration of male sterility, deposited as NCIMB 41193, described in WO 2005/074671), Event CE43-67B (cotton, insect control, deposited as DSM ACC2724, described in US-A 2009-217423 or WO 06/128573); Event CE44-69D (cotton, insect control, not deposited, described in US-A 2010-0024077); Event CE44-69D (cotton, insect control, not deposited, described in WO 06/128571); Event CE46-02A (cotton, insect control, not deposited, described in WO 06/128572); Event COT102 (cotton, insect control, not deposited, described in US-A 2006-130175 or WO 04/039986); Event COT202 (cotton, insect control, not deposited, described in US-A 2007-067868 or WO 05/054479); Event COT203 (cotton, insect control, not deposited, described in WO 05/054480);); Event DAS21606-3 / 1606 (soybean, herbicide tolerance, deposited as PTA-11028, described in WO 012/033794), Event DAS40278 (corn, herbicide tolerance, deposited as ATCC PTA-10244, described in WO 11/022469); Event DAS-44406-6 / pDAB8264.44.06.1 (soybean, herbicide tolerance, deposited as PTA-11336, described in WO 2012/075426), Event DAS-14536-7 / pDAB8291.45.36.2 (soybean, herbicide tolerance, deposited as PTA-11335, described in WO 2012/075429), Event DAS-59122-7 (corn, insect control - herbicide tolerance, deposited as ATCC PTA 11384 , described in US-A 2006-070139); Event DAS-59132 (corn, insect control - herbicide tolerance, not deposited, described in WO 09/100188); Event DAS68416 (soybean, herbicide tolerance, deposited as ATCC PTA-10442, described in WO 11/066384 or WO 11/066360); Event DP-098140-6 (corn, herbicide tolerance, deposited as ATCC PTA-8296, described in US-A 2009-137395 or WO 08/112019); Event DP-305423-1 (soybean, quality trait, not deposited, described in US-A 2008-312082 or WO 08/054747); Event DP-32138-1 (corn, hybridization system, deposited as ATCC PTA-9158, described in US-A 2009-0210970 or WO 09/103049); Event DP-356043-5 (soybean, herbicide tolerance, deposited as ATCC PTA-8287, described in US-A 2010-0184079 or WO 08/002872); Event EE-1 (brinjal, insect control, not deposited, described in WO 07/091277); Event FI117 (corn, herbicide tolerance, deposited as ATCC 209031, described in US-A 2006-059581 or WO 98/044140); Event FG72 (soybean, herbicide tolerance, deposited as PTA-11041, described in WO 2011/063413), Event GA21 (corn, herbicide tolerance, deposited as ATCC 209033, described in US-A 2005-086719 or WO 98/044140); Event GG25 (corn, herbicide tolerance, deposited as ATCC 209032, described in US-A 2005-188434 or WO 98/044140); Event GHB119 (cotton, insect control - herbicide tolerance, deposited as ATCC PTA-8398, described in WO 08/151780); Event GHB614 (cotton, herbicide tolerance, deposited as ATCC PTA-6878, described in US-A 2010-050282 or WO 07/017186); Event GJ11 (corn, herbicide tolerance, deposited as ATCC 209030, described in US-A 2005-188434 or WO 98/044140); Event GM RZ13 (sugar beet, virus resistance , deposited as NCIMB-41601, described in WO 10/076212); Event H7-1 (sugar beet, herbicide tolerance, deposited as NCIMB 41158 or NCIMB 41159, described in US-A 2004-172669 or WO 04/074492); Event JOPLIN1 (wheat, disease tolerance, not deposited, described in US-A 2008-064032); Event LL27 (soybean, herbicide tolerance, deposited as NCIMB41658, described in WO 06/108674 or

US-A 2008-320616); Event LL55 (soybean, herbicide tolerance, deposited as NCIMB 41660, described in WO 06/108675 or US-A 2008-196127); Event LLcotton25 (cotton, herbicide tolerance, deposited as ATCC PTA-3343, described in WO 03/013224 or US-A 2003-097687); Event LLRICE06 (rice, herbicide tolerance, deposited as ATCC 203353, described in US 6,468,747 or WO 00/026345); Event LLRice62 (rice, herbicide tolerance, deposited as ATCC 203352, described in WO 2000/026345), Event LLRICE601 (rice, herbicide tolerance, deposited as ATCC PTA-2600, described in US-A 2008-2289060 or WO 00/026356); Event LY038 (corn, quality trait, deposited as ATCC PTA-5623, described in US-A 2007-028322 or WO 05/061720); Event MIR162 (corn, insect control, deposited as PTA-8166, described in US-A 2009-300784 or WO 07/142840); Event MIR604 (corn, insect control, not deposited, described in US-A 2008-167456 or WO 05/103301); Event MON15985 (cotton, insect control, deposited as ATCC PTA-2516, described in US-A 2004-250317 or WO 02/100163); Event MON810 (corn, insect control, not deposited, described in US-A 2002-102582); Event MON863 (corn, insect control, deposited as ATCC PTA-2605, described in WO 04/011601 or US-A 2006-095986); Event MON87427 (corn, pollination control, deposited as ATCC PTA-7899, described in WO 11/062904); Event MON87460 (corn, stress tolerance, deposited as ATCC PTA-8910, described in WO 09/111263 or US-A 2011-0138504); Event MON87701 (soybean, insect control, deposited as ATCC PTA-8194, described in US-A 2009-130071 or WO 09/064652); Event MON87705 (soybean, quality trait - herbicide tolerance, deposited as ATCC PTA-9241, described in US-A 2010-0080887 or WO 10/037016); Event MON87708 (soybean, herbicide tolerance, deposited as ATCC PTA-9670, described in WO 11/034704); Event MON87712 (soybean, yield, deposited as PTA-10296, described in WO 2012/051199), Event MON87754 (soybean, quality trait, deposited as ATCC PTA-9385, described in WO 10/024976); Event MON87769 (soybean, quality trait, deposited as ATCC PTA-8911, described in US-A 2011-0067141 or WO 09/102873); Event MON88017 (corn, insect control - herbicide tolerance, deposited as ATCC PTA-5582, described in US-A 2008-028482 or WO 05/059103); Event MON88913 (cotton, herbicide tolerance, deposited as ATCC PTA-4854, described in WO 04/072235 or US-A 2006-059590); Event MON88302 (oilseed rape, herbicide tolerance, deposited as PTA-10955, described in WO 2011/153186), Event MON88701 (cotton, herbicide tolerance, deposited as PTA-11754, described in WO 2012/134808), Event MON89034 (corn, insect control, deposited as ATCC PTA-7455, described in WO 07/140256 or US-A 2008-260932); Event MON89788 (soybean, herbicide tolerance, deposited as ATCC PTA-6708, described in US-A 2006-282915 or WO 06/130436); Event MS11 (oilseed rape, pollination control - herbicide tolerance, deposited as ATCC PTA-850 or PTA-2485, described in WO 01/031042); Event MS8 (oilseed rape, pollination control - herbicide tolerance, deposited as ATCC PTA-730, described in WO 01/041558 or US-A 2003-188347); Event NK603 (corn, herbicide tolerance, deposited as ATCC PTA-2478, described in US-A 2007-292854); Event PE-7 (rice, insect control, not deposited, described in WO 08/114282); Event RF3 (oilseed rape, pollination control - herbicide tolerance, deposited as ATCC PTA-730, described in WO 01/041558 or US-A 2003-188347); Event RT73 (oilseed rape, herbicide tolerance, not deposited, described in WO 02/036831 or US-A 2008-070260); Event SYHT0H2 / SYN-

000H2-5 (soybean, herbicide tolerance, deposited as PTA-11226, described in WO 2012/082548), Event T227-1 (sugar beet, herbicide tolerance, not deposited, described in WO 02/44407 or US-A 2009-265817); Event T25 (corn, herbicide tolerance, not deposited, described in US-A 2001-029014 or WO 01/051654); Event T304-40 (cotton, insect control - herbicide tolerance, deposited as ATCC PTA-8171, 5 described in US-A 2010-077501 or WO 08/122406); Event T342-142 (cotton, insect control, not deposited, described in WO 06/128568); Event TC1507 (corn, insect control - herbicide tolerance, not deposited, described in US-A 2005-039226 or WO 04/099447); Event VIP1034 (corn, insect control - herbicide tolerance, deposited as ATCC PTA-3925., described in WO 03/052073), Event 32316 (corn, insect control-herbicide tolerance, deposited as PTA-11507, described in WO 11/084632), Event 4114 10 (corn, insect control-herbicide tolerance, deposited as PTA-11506, described in WO 11/084621), EE-GM3 / FG72 (soybean, herbicide tolerance, ATCC Accession N° PTA-11041, WO 2011/063413A2), event DAS-68416-4 (soybean, herbicide tolerance, ATCC Accession N° PTA-10442, WO 011/066360A1), event DAS-68416-4 (soybean, herbicide tolerance, ATCC Accession N° PTA-10442, WO 2011/066384A1), event DP-040416-8 (corn, insect control, ATCC Accession N° PTA-11508, WO 15 2011/075593A1), event DP-043A47-3 (corn, insect control, ATCC Accession N° PTA-11509, WO 2011/075595A1), event DP-004114-3 (corn, insect control, ATCC Accession N° PTA-11506, WO 2011/084621A1), event DP-032316-8 (corn, insect control, ATCC Accession N° PTA-11507, WO 2011/084632A1), event MON-88302-9 (oilseed rape, herbicide tolerance, ATCC Accession N° PTA-10955, WO 2011/153186A1), event DAS-21606-3 (soybean, herbicide tolerance, ATCC Accession No. 20 PTA-11028, WO 2012/033794A2), event MON-87712-4 (soybean, quality trait, ATCC Accession N°. PTA-10296, WO 2012/051199A2), event DAS-44406-6 (soybean, stacked herbicide tolerance, ATCC Accession N°. PTA-11336, WO 2012/075426A1), event DAS-14536-7 (soybean, stacked herbicide tolerance, ATCC Accession N°. PTA-11335, WO 2012/075429A1), event SYN-000H2-5 (soybean, herbicide tolerance, ATCC Accession N°. PTA-11226, WO 2012/082548A2), event DP-061061-7 25 (oilseed rape, herbicide tolerance, no deposit N° available, WO 2012071039A1), event DP-073496-4 (oilseed rape, herbicide tolerance, no deposit N° available, US2012131692), event 8264.44.06.1 (soybean, stacked herbicide tolerance, Accession N° PTA-11336, WO 2012075426A2), event 8291.45.36.2 (soybean, stacked herbicide tolerance, Accession N°. PTA-11335, WO 2012075429A2), event SYHT0H2 (soybean, ATCC Accession N°. PTA-11226, WO 2012/082548A2), event MON88701 30 (cotton, ATCC Accession N° PTA-11754, WO 2012/134808A1), event KK179-2 (alfalfa, ATCC Accession N° PTA-11833, WO2013003558A1), event pDAB8264.42.32.1 (soybean, stacked herbicide tolerance, ATCC Accession N° PTA-11993, WO 2013010094A1), event MZDT09Y (corn, ATCC Accession N° PTA-13025, WO 2013012775A1), event KK179-2 (alfalfa, ATCC Accession N° PTA-11833), WO2013003558A1, event pDAB8264.42.32.1 (soybean, stacked herbicide tolerance, ATCC 35 Accession N° PTA-1 1993), WO2013010094A1, event MZDT09Y (corn, ATCC Accession N° PTA-13025), WO2013012775A1, event VCO-01981-5 (corn, herbicide tolerance, NCIMB Accession N° 41842), WO2013014241A1, event DAS-81419-2 X DAS-68416-4 (soybean stacked insect resistance and

herbicide tolerance, ATCC Accession N° PTA- 10442), WO2013016516A1, event DAS-81419-2 (soybean stacked insect resistance and herbicide tolerance, ATCC Accession N° PTA-12006), WO2013016527A1, event HCEM485 (corn, herbicide tolerance, ATCC Accession N° PTA-12014), WO2013025400A1, event pDAB4468.18.07.1 (cotton, herbicide tolerance, ATCC Accession N° PTA-12456), WO2013112525A2, event pDAB4468.19.10.3 (cotton, herbicide tolerance, ATCC Accession N° PTA-12457), WO2013112527A1.

[0069] In an advantageous embodiment, the compounds of the formula (I) are used for treating transgenic plants comprising at least one gene or gene fragment coding for a Bt toxin or Vip-related toxin.

[0070] Preferably, the compounds of the formula (I) are used for treating transgenic plants comprising at least one gene or gene fragment coding for a Bt toxin. A Bt toxin is a protein originating from or derived from the soil bacterium *Bacillus thuringiensis* which either belongs to the group of the *crystal toxins* (Cry) or the *cytolytic toxins* (Cyt). In the bacterium, they are originally formed as protoxins and are only metabolized in alkaline medium - for example in the digestive tract of certain feed insects - to their active form. There, the active toxin then binds to certain hydrocarbon structures at cell surfaces causing pores to be formed which destroy the osmotic potential of the cell, which may effect cell lysis. The result is the death of the insects. Bt toxins are active in particular against certain harmful species from the orders of the Lepidoptera (butterflies), Homoptera, Diptera and Coleoptera (beetles) in all their development stages; i.e. from the egg larva via their juvenile forms to their adult forms.

[0071] It has been known for a long time that gene sequences coding for Bt toxins, parts thereof or else peptides or proteins derived from Bt toxins can be cloned with the aid of genetic engineering into agriculturally useful plants to generate transgenic plants having endogenous resistance to pests sensitive to Bt toxins. For the purpose of the invention, the transgenic plants coding for at least one Bt toxin or proteins derived therefrom are defined as “Bt plants”.

[0072] The “first generation” of such Bt plants generally only comprise the genes enabling the formation of a certain toxin, thus only providing resistance to one group of pathogens. An example of a commercially available maize variety comprising the gene for forming the Cry1Ab toxin is “YieldGard®” from Monsanto which is resistant to the European corn borer. In contrast, in the Bt cotton variety (Bollgard®), resistance to other pathogens from the family of the Lepidoptera is generated by introduction by cloning of the genes for forming the Cry1Ac toxin. Other transgenic crop plants, in turn, express genes for forming Bt toxins with activity against pathogens from the order of the Coleoptera. Examples that may be mentioned are the Bt potato variety “NewLeaf®” (Monsanto) capable of forming the Cry3A toxin, which is thus resistant to the Colorado potato beetle, and the transgenic maize variety “YieldGard®” (Monsanto) which is capable of forming the Cry 3Bb1 toxin and is thus protected against various species of the Western corn rootworm.

[0073] In a “second generation”, the multiply transgenic plants, already described above, expressing or comprising at least two foreign genes were generated.

[0074] Preference according to the invention is given to transgenic plants with Bt toxins from the group of the *Cry* family (see, for example, http://www.lifesci.susx.ac.uk/home/Neil_Crickmore/Bt/).

5 [0075] Preferred are transgenic plants with Bt toxins from the group of the

Name	Acc No.	NCBI Protein	NCBI Nuc	Authors	Year	Source Strain	Comment
Cry1Aa1	AAA22353	142765	142764	Schnepf et al	1985	Bt kurstaki HD1	
Cry1Aa2	AAA22552	551713	143100	Shibano et al	1985	Bt sotto	
Cry1Aa3	BAA00257	216284	216283	Shimizu et al	1988	Bt aizawai IPL7	
Cry1Aa4	CAA31886	40267	40266	Masson et al	1989	Bt entomocidus	
Cry1Aa5	BAA04468	535781	506190	Udayasuriyan et al	1994	Bt Fu-2-7	
Cry1Aa6	AAA86265	1171233	1171232	Masson et al	1994	Bt kurstaki NRD-12	
Cry1Aa7	AAD46139	5669035	5669034	Osman et al	1999	Bt C12	
Cry1Aa8	I26149			Liu	1996		DNA sequence only
Cry1Aa9	BAA77213	4666284	4666283	Nagamatsu et al	1999	Bt dendrolimus T84A1	
Cry1Aa10	AAD55382	5901703	5901702	Hou and Chen	1999	Bt kurstaki HD-1-02	

Cry1Aa11	CAA70856	6687073	6687072	Tounsi et al	1999	Bt kurstaki	
Cry1Aa12	AAP80146	32344731	32344730	Yao et al	2001	Bt Ly30	
Cry1Aa13	AAM44305	21239436	21239435	Zhong et al	2002	Bt sotto	
Cry1Aa14	AAP40639	37781497	37781496	Ren et al	2002	unpublished	
Cry1Aa15	AAY66993	67089177	67089176	Sauka et al	2005	Bt INTA Mol-12	
Cry1Aa16	HQ439776			Liu et al	2010	Bt Ps9-E2	No NCBI link June 13
Cry1Aa17	HQ439788			Liu et al	2010	Bt PS9-C12	No NCBI link June 13
Cry1Aa18	HQ439790			Liu et al	2010	Bt PS9-D12	No NCBI link June 13
Cry1Aa19	HQ685121	337732098	337732097	Li & Luo	2011	Bt LS-R-21	
Cry1Aa20	JF340156			Kumari & Kaur	2011	Bt SK-798	
Cry1Aa21	JN651496			Li Yuhong	2011	Bt LTS-209	No NCBI link June 13
Cry1Aa22	KC158223			El Khoury et al	2013	Bt Lip	
Cry1Ab1	AAA22330	142720	142719	Wabiko et al	1986	Bt berliner 1715	
Cry1Ab2	AAA22613	143227	143226	Thorne et al	1986	Bt kurstaki	
Cry1Ab3	AAA22561	143124	143123	Geiser et al	1986	Bt kurstaki HD1	
Cry1Ab4	BAA00071	216280	216279	Kondo et al	1987	Bt kurstaki HD1	

Cry1Ab5	CAA28405	40255	40254	Hofte et al	1986	Bt berliner 1715	
Cry1Ab6	AAA22420	142886	142885	Hefford et al	1987	Bt kurstaki NRD-12	
Cry1Ab7	CAA31620	40278	40277	Haider & Ellar	1988	Bt aizawai IC1	
Cry1Ab8	AAA22551	143099	143098	Oeda et al	1987	Bt aizawai IPL7	
Cry1Ab9	CAA38701	40273	40272	Chak & Jen	1993	Bt aizawai HD133	
Cry1Ab10	A29125			Fischhoff et al	1987	Bt kurstaki HD1	
Cry1Ab11	I12419			Ely & Tippet	1995	Bt A20	DNA sequence only
Cry1Ab12	AAC64003	3746545	3746544	Silva-Werneck et al	1998	Bt kurstaki S93	
Cry1Ab13	AAN76494	25990352	25990351	Tan et al	2002	Bt c005	
Cry1Ab14	AAG16877	10440886	10440885	Meza-Basso & Theoduloz	2000	Native Chilean Bt	
Cry1Ab15	AAO13302	27436100	27436098	Li et al	2001	Bt B-Hm-16	
Cry1Ab16	AAK55546	14190061	14190060	Yu et al	2002	Bt AC-11	
Cry1Ab17	AAT46415	48734426	48734425	Huang et al	2004	Bt WB9	
Cry1Ab18	AAQ88259	37048803	37048802	Stobdan et al	2004	Bt	
Cry1Ab19	AAW31761	56900936	56900935	Zhong et al	2005	Bt X-2	
Cry1Ab20	ABB72460	82395049	82395048	Liu et al	2006	BtC008	

Cry1Ab21	ABS18384	151655610	151655609	Swiecicka et al	2007	Bt IS5056	
Cry1Ab22	ABW87320	159024156	159024155	Wu and Feng	2008	BtS2491Ab	
Cry1Ab23	HQ439777			Liu et al	2010	Bt N32-2-2	No NCBI link June 13
Cry1Ab24	HQ439778			Liu et al	2010	Bt HD12	No NCBI link June 13
Cry1Ab25	HQ685122	337732100	337732099	Li & Luo	2011	Bt LS-R-30	
Cry1Ab26	HQ847729	320090245	320090244	Prathap Reddy et al	2011	DOR BT-1	
Cry1Ab27	JN135249			Ammounh et al	2011		
Cry1Ab28	JN135250			Ammounh et al	2011		
Cry1Ab29	JN135251			Ammounh et al	2011		
Cry1Ab30	JN135252			Ammounh et al	2011		
Cry1Ab31	JN135253			Ammounh et al	2011		
Cry1Ab32	JN135254			Ammounh et al	2011		
Cry1Ab33	AAS93798			Li et al	2012	Bt kenya K3	partial cds
Cry1Ab34	KC156668			Sampson et al	2012		No NCBI link June 13
Cry1Ab-like	AAK14336	13173238	13173237	Nagarathinam et al	2001	Bt kunthala RX24	uncertain sequence
Cry1Ab-like	AAK14337	13173240	13173239	Nagarathinam et al	2001	Bt kunthala RX28	uncertain sequence
Cry1Ab-like	AAK14338	13173242	13173241	Nagarathinam et al	2001	Bt kunthala RX27	uncertain sequence

Cry1Ab-like	ABG88858	110734449	110734448	Lin et al	2006	Bt ly4a3	insufficient sequence
Cry1Ac1	AAA22331			Adang et al	1985	Bt kurstaki HD73	
Cry1Ac2	AAA22338			Von Tersch et al	1991	Bt kenyae	
Cry1Ac3	CAA38098			Dardenne et al	1990	Bt BTS89A	
Cry1Ac4	AAA73077			Feitelson	1991	Bt kurstaki PS85A1	
Cry1Ac5	AAA22339			Feitelson	1992	Bt kurstaki PS81GG	
Cry1Ac6	AAA86266			Masson et al	1994	Bt kurstaki NRD-12	
Cry1Ac7	AAB46989			Herrera et al	1994	Bt kurstaki HD73	
Cry1Ac8	AAC44841			Omolo et al	1997	Bt kurstaki HD73	
Cry1Ac9	AAB49768			Gleave et al	1992	Bt DSIR732	
Cry1Ac10	CAA05505			Sun	1997	Bt kurstaki YBT-1520	
Cry1Ac11	CAA10270			Makhdoom & Riazuddin	1998		
Cry1Ac12	I12418			Ely & Tippet	1995	Bt A20	DNA sequence only
Cry1Ac13	AAD38701			Qiao et al	1999	Bt kurstaki HD1	
Cry1Ac14	AAQ06607			Yao et al	2002	Bt Ly30	

Cry1Ac15	AAN07788			Tzeng et al	2001	Bt from Taiwan	
Cry1Ac16	AAU87037			Zhao et al	2005	Bt H3	
Cry1Ac17	AAX18704			Hire et al	2005	Bt kenyaec HD549	
Cry1Ac18	AAV88347			Kaur & Allam	2005	Bt SK-729	
Cry1Ac19	ABD37053			Gao et al	2005	Bt C-33	
Cry1Ac20	ABB89046			Tan et al	2005		
Cry1Ac21	AAV66992			Sauka et al	2005	INTA Mol-12	
Cry1Ac22	ABZ01836			Zhang & Fang	2008	Bt W015-1	
Cry1Ac23	CAQ30431			Kashyap et al	2008	Bt	
Cry1Ac24	ABL01535			Arango et al	2008	Bt 146-158-01	
Cry1Ac25	FJ513324	237688242	237688241	Guan et al	2011	Bt Tm37-6	
Cry1Ac26	FJ617446	256003038	256003037	Guan et al	2011	Bt Tm41-4	
Cry1Ac27	FJ617447	256003040	256003039	Guan et al	2011	Bt Tm44-1B	
Cry1Ac28	ACM90319			Li et al	2009	Bt Q-12	
Cry1Ac29	DQ438941			Diego Sauka	2009	INTA TA24-6	
Cry1Ac30	GQ227507			Zhang et al	2010	Bt S1478-1	
Cry1Ac31	GU446674	319433505		Zhao et al	2010	Bt S3299-1	
Cry1Ac32	HM061081			Lu et al	2010	Bt ZQ-89	
Cry1Ac33	GQ866913	306977639	306977638	Kaur & Meena	2011	Bt SK-711	

Cry1Ac34	HQ230364	314906994		Kaur & Kumari	2010	Bt SK-783	
Cry1Ac35	JF340157			Kumari & Kaur	2011	Bt SK-784	
Cry1Ac36	JN387137			Kumari & Kaur	2011	Bt SK-958	
Cry1Ac37	JQ317685			Kumari & Kaur	2011	Bt SK-793	
Cry1Ac38	ACC86135			Lin et al	2008	Bt LSZ9408	
Cry1Ad1	AAA22340			Feitelson	1993	Bt aizawai PS81I	
Cry1Ad2	CAA01880			Anonymous	1995	Bt PS81RR1	
Cry1Ae1	AAA22410			Lee & Aronson	1991	Bt alesti	
Cry1Af1	AAB82749			Kang et al	1997	Bt NT0423	
Cry1Ag1	AAD46137			Mustafa	1999		
Cry1Ah1	AAQ14326			Tan et al	2000		
Cry1Ah2	ABB76664			Qi et al	2005	Bt alesti	
Cry1Ah3	HQ439779			Liu et al	2010	Bt S6	No NCBI link June 13
Cry1Ai1	AAO39719			Wang et al	2002		
Cry1Ai2	HQ439780			Liu et al	2010	Bt SC6H8	No NCBI link June 13
Cry1A-like	AAK14339			Nagarathinam et al	2001	Bt kunthala nags3	uncertain sequence
Cry1Ba1	CAA29898			Brizzard & Whiteley	1988	Bt thuringiensis HD2	

Cry1Ba2	CAA65003			Soetaert	1996	Bt entomocidus HD110	
Cry1Ba3	AAK63251			Zhang et al	2001		
Cry1Ba4	AAK51084			Nathan et al	2001	Bt entomocidus HD9	
Cry1Ba5	ABO20894			Song et al	2007	Bt sfw-12	
Cry1Ba6	ABL60921			Martins et al	2006	Bt S601	
Cry1Ba7	HQ439781			Liu et al	2010	Bt N17-37	No NCBI link June 13
Cry1Bb1	AAA22344			Donovan et al	1994	Bt EG5847	
Cry1Bb2	HQ439782			Liu et al	2010	Bt WBT-2	No NCBI link June 13
Cry1Bc1	CAA86568			Bishop et al	1994	Bt morrisoni	
Cry1Bd1	AAD10292			Kuo et al	2000	Bt wuhanensis HD525	
Cry1Bd2	AAM93496			Isakova et al	2002	Bt 834	
Cry1Be1	AAC32850			Payne et al	1998	Bt PS158C2	
Cry1Be2	AAQ52387			Baum et al	2003		
Cry1Be3	ACV96720	259156864		Sun et al	2010	Bt g9	
Cry1Be4	HM070026			Shu et al	2010		No NCBI link June 13
Cry1Bf1	CAC50778			Arnaut et al	2001		

Cry1Bf2	AAQ52380			Baum et al	2003		
Cry1Bg1	AAO39720			Wang et al	2002		
Cry1Bh1	HQ589331	315076091		Lira et al	2010	Bt PS46L	
Cry1Bi1	KC156700			Sampson et al	2012		No NCBI link June 13
Cry1Ca1	CAA30396			Honee et al	1988	Bt entomocidus 60.5	
Cry1Ca2	CAA31951			Sanchis et al	1989	Bt aizawai 7.29	
Cry1Ca3	AAA22343			Feitelson	1993	Bt aizawai PS81I	
Cry1Ca4	CAA01886			Van Mellaert et al	1990	Bt entomocidus HD110	
Cry1Ca5	CAA65457			Strizhov	1996	Bt aizawai 7.29	
Cry1Ca6 [1]	AAF37224			Yu et al	2000	Bt AF-2	
Cry1Ca7	AAG50438			Aixing et al	2000	Bt J8	
Cry1Ca8	AAM00264			Chen et al	2001	Bt c002	
Cry1Ca9	AAL79362			Kao et al	2003	Bt G10-01A	
Cry1Ca10	AAN16462			Lin et al	2003	Bt E05-20a	
Cry1Ca11	AAX53094			Cai et al	2005	Bt C-33	
Cry1Ca12	HM070027			Shu et al	2010		No NCBI link

							June 13
Cry1Ca13	HQ412621	312192962		Li & Luo	2010	Bt LB-R-78	
Cry1Ca14	JN651493			Li Yuhong	2011	Bt LTS-38	No NCBI link June 13
Cry1Cb1	M97880			Kalman et al	1993	Bt galleriae HD29	DNA sequence only
Cry1Cb2	AAG35409			Song et al	2000	Bt c001	
Cry1Cb3	ACD50894			Huang et al	2008	Bt 087	
Cry1Cb- like	AAX63901			Thammasittirong et al	2005	Bt TA476-1	insufficient sequence
Cry1Da1	CAA38099			Hofte et al	1990	Bt aizawai HD68	
Cry1Da2	I76415			Payne & Sick	1997		DNA sequence only
Cry1Da3	HQ439784			Liu et al	2010	Bt HD12	No NCBI link June 13
Cry1Db1	CAA80234			Lambert	1993	Bt BTS00349A	
Cry1Db2	AAK48937			Li et al	2001	Bt B-Pr-88	
Cry1Dc1	ABK35074			Lertwiriawong et al	2006	Bt JC291	
Cry1Ea1	CAA37933			Visser et al	1990	Bt kenya 4F1	
Cry1Ea2	CAA39609			Bosse et al	1990	Bt kenya	
Cry1Ea3	AAA22345			Feitelson	1991	Bt kenya	

						PS81F	
Cry1Ea4	AAD04732			Barboza-Corona et al	1998	Bt kenya LBIT-147	
Cry1Ea5	A15535			Botterman et al	1994		DNA sequence only
Cry1Ea6	AAL50330			Sun et al	1999	Bt YBT-032	
Cry1Ea7	AAW72936			Huehne et al	2005	Bt JC190	
Cry1Ea8	ABX11258			Huang et al	2007	Bt HZM2	
Cry1Ea9	HQ439785			Liu et al	2010	Bt S6	No NCBI link June 13
Cry1Ea10	ADR00398			Goncalves et al	2010	Bt BR64	
Cry1Ea11	JQ652456			Lin Qunxin et al	2012	Bt	
Cry1Ea12	KF601559			Baonan He	2013	Bt strain V4	No NCBI link Sep 13
Cry1Eb1	AAA22346			Feitelson	1993	Bt aizawai PS81A2	
Cry1Fa1	AAA22348			Chambers et al	1991	Bt aizawai EG6346	
Cry1Fa2	AAA22347			Feitelson	1993	Bt aizawai PS81I	
Cry1Fa3	HM070028			Shu et al	2010		No NCBI link June 13
Cry1Fa4	HM439638			Liu et al	2010	Bt mo3-D10	No NCBI link June 13
Cry1Fb1	CAA80235			Lambert	1993	Bt	

						BTS00349A	
Cry1Fb2	BAA25298			Masuda & Asano	1998	Bt morrisoni INA67	
Cry1Fb3	AAF21767			Song et al	1998	Bt morrisoni	
Cry1Fb4	AAC10641			Payne et al	1997		
Cry1Fb5	AAO13295			Li et al	2001	Bt B-Pr-88	
Cry1Fb6	ACD50892			Huang et al	2008	Bt 012	
Cry1Fb7	ACD50893			Huang et al	2008	Bt 087	
Cry1Ga1	CAA80233			Lambert	1993	Bt BTS0349A	
Cry1Ga2	CAA70506			Shevelev et al	1997	Bt wuhanensis	
Cry1Gb1	AAD10291			Kuo & Chak	1999	Bt wuhanensis HD525	
Cry1Gb2	AAO13756			Li et al	2000	Bt B-Pr-88	
Cry1Gc1	AAQ52381			Baum et al	2003		
Cry1Ha1	CAA80236			Lambert	1993	Bt BTS02069AA	
Cry1Hb1	AAA79694			Koo et al	1995	Bt morrisoni BF190	
Cry1Hb2	HQ439786			Liu et al	2010	Bt WBT-2	No NCBI link June 13
Cry1H- like	AAF01213			Srifah et al	1999	Bt JC291	insufficient sequence

CryIIa1	CAA44633			Tailor et al	1992	Bt kurstaki	
CryIIa2	AAA22354			Gleave et al	1993	Bt kurstaki	
CryIIa3	AAC36999			Shin et al	1995	Bt kurstaki HD1	
CryIIa4	AAB00958			Kostichka et al	1996	Bt AB88	
CryIIa5	CAA70124			Selvapandiyan	1996	Bt 61	
CryIIa6	AAC26910			Zhong et al	1998	Bt kurstaki S101	
CryIIa7	AAM73516			Porcar et al	2000	Bt	
CryIIa8	AAK66742			Song et al	2001		
CryIIa9	AAQ08616			Yao et al	2002	Bt Ly30	
CryIIa10	AAP86782			Espindola et al	2003	Bt thuringiensis	
CryIIa11	CAC85964			Tounsi et al	2003	Bt kurstaki BNS3	
CryIIa12	AAV53390			Grossi de Sa et al	2005	Bt	
CryIIa13	ABF83202			Martins et al	2006	Bt	
CryIIa14	ACG63871			Liu & Guo	2008	Bt11	
CryIIa15	FJ617445	256003036	256003035	Guan et al	2011	Bt E-1B	
CryIIa16	FJ617448	256003042	256003041	Guan et al	2011	Bt E-1A	
CryIIa17	GU989199			Li et al	2010	Bt MX2	
CryIIa18	ADK23801	300492624		Li et al	2010	Bt MX9	

Cry1Ia19	HQ439787			Liu et al	2010	Bt SC6H6	No NCBI link June 13
Cry1Ia20	JQ228426			Zhao Can	2011	Bt wu1H-3	No NCBI link June 13
Cry1Ia21	JQ228424			Zhao Can	2011	Bt you1D-9	No NCBI link June 13
Cry1Ia22	JQ228427			Zhao Can	2011	Bt wu1E-3	No NCBI link June 13
Cry1Ia23	JQ228428			Zhao Can	2011	Bt wu1E-4	No NCBI link June 13
Cry1Ia24	JQ228429			Zhao Can	2011	Bt wu2B-6	No NCBI link June 13
Cry1Ia25	JQ228430			Zhao Can	2011	Bt wu2G-11	No NCBI link June 13
Cry1Ia26	JQ228431			Zhao Can	2011	Bt wu2G-12	No NCBI link June 13
Cry1Ia27	JQ228432			Zhao Can	2011	Bt you2D-3	No NCBI link June 13
Cry1Ia28	JQ228433			Zhao Can	2011	Bt you2E-3	No NCBI link June 13
Cry1Ia29	JQ228434			Zhao Can	2011	Bt you2F-3	No NCBI link June 13
Cry1Ia30	JQ317686			Kumari & Kaur	2011	Bt 4J4	
Cry1Ia31	JX944038			Song et al	2012	Bt SC-7	
Cry1Ia32	JX944039			Song et al	2012	Bt SC-13	
Cry1Ia33	JX944040			Song et al	2012	Bt SC-51	

Cry1Ib1	AAA82114			Shin et al	1995	Bt entomocidus BP465	
Cry1Ib2	ABW88019			Guan et al	2007	Bt PP61	
Cry1Ib3	ACD75515			Liu & Guo	2008	Bt GS8	
Cry1Ib4	HM051227	301641366		Zhao et al	2010	Bt BF-4	
Cry1Ib5	HM070028			Shu et al	2010		No NCBI link June13
Cry1Ib6	ADK38579	300836937		Li et al	2010	Bt LB52	
Cry1Ib7	JN571740			Kumari & Kaur	2011	Bt SK-935	
Cry1Ib8	JN675714			Swamy et al	2011		
Cry1Ib9	JN675715			Swamy et al	2011		
Cry1Ib10	JN675716			Swamy et al	2011		
Cry1Ib11	JQ228423			Zhao Can	2011	Bt HD12	No NCBI link June 13
Cry1Ic1	AAC62933			Osman et al	1998	Bt C18	
Cry1Ic2	AAE71691			Osman et al	2001		
Cry1Id1	AAD44366			Choi	2000		
Cry1Id2	JQ228422			Zhao Can	2011	Bt HD12	No NCBI link June 13
Cry1Ie1	AAG43526			Song et al	2000	Bt BTC007	
Cry1Ie2	HM439636			Liu et al	2010	Bt T03B001	No NCBI link June 13

Cry1Ie3	KC156647			Sampson et al	2012		No NCBI link June 13
Cry1Ie4	KC156681			Sampson et al	2012		No NCBI link June 13
Cry1If1	AAQ52382			Baum et al	2003		
Cry1Ig1	KC156701			Sampson et al	2012		No NCBI link June 13
Cry1I-like	AAC31094			Payne et al	1998		insufficient sequence
Cry1I-like	ABG88859			Lin & Fang	2006	Bt ly4a3	insufficient sequence
Cry1Ja1	AAA22341			Donovan	1994	Bt EG5847	
Cry1Ja2	HM070030			Shu et al	2010		No NCBI link June 13
Cry1Ja3	JQ228425			Zhao Shiyuan	2011	Bt FH21	No NCBI link June 13
Cry1Jb1	AAA98959			Von Tersch & Gonzalez	1994	Bt EG5092	
Cry1Jc1	AAC31092			Payne et al	1998		
Cry1Jc2	AAQ52372			Baum et al	2003		
Cry1Jd1	CAC50779			Arnaut et al	2001	Bt	
Cry1Ka1	AAB00376			Koo et al	1995	Bt morrisoni BF190	
Cry1Ka2	HQ439783			Liu et al	2010	Bt WBT-2	No NCBI link June 13

Cry1La1	AAS60191			Je et al	2004	Bt kurstaki K1	
Cry1La2	HM070031			Shu et al	2010		No NCBI link June 13
Cry1Ma1	FJ884067			Noguera & Ibarra	2010	LBIT 1189	
Cry1Ma2	KC156659			Sampson et al	2012		No NCBI link June 13
Cry1Na1	KC156648			Sampson et al	2012		No NCBI link June 13
Cry1Nb1	KC156678			Sampson et al	2012		No NCBI link June 13

[0076] Particular preference is given to the genes or gene sections of the subfamilies cry1, cry2, cry3, cry5 and cry9; especially preferred are members of the subfamily cry1A such as cry1Aa, cry1Ac, cry2Ab.

[0077] Furthermore, it is preferred to use plants which, in addition to the genes for one or more Bt toxins, express or contain, if appropriate, also genes for expressing, for example, a protease or peptidase inhibitor (such as in WO-A 95/35031), of herbicide resistances (for example to glufosinate or glyphosate by expression of the pat gene or bar gene) or for becoming resistant to nematodes, fungi or viruses (for example by expressing a gluconase, chitinase). However, they may also be genetically modified in their metabolic properties, so that they show a qualitative and/or quantitative change of ingredients (for example by modification of the energy, carbohydrate, fatty acid or nitrogen metabolism or by metabolite currents influencing these (see above).

[0078] In one preferred embodiment, a Bt-plant, preferably a Bt-soybean, comprises event MON87701 which is described in, e.g., WO2009/064652. Thus, in one preferred embodiment, a Bt-soybean seeds comprising said event of which a representative sample was deposited at the ATCC under Accession No. PTA-8194 are treated with a ryanodine receptor modulator according to the present invention.

[0079] In another preferred embodiment, a Bt-soybean comprises event pDAB9582.814.19.1 and/or event pDAB4468.04.16.1 which are described in, e.g., WO 2013/016516. This breeding stacks comprise cry1F, cry1Ac and pat and aad-12 and pat, as described in WO 2012/075426. Thus, in one preferred

embodiment, a Bt-soybean seeds of which comprising said events were deposited at the ATCC under Accession No. PTA-10442 (pDAB4468.04.16.1) are treated with a ryanodine receptor modulator according to the present invention.

[0080] In one preferred embodiment, the method of the invention is characterized in that the Bt-plant, preferably a Bt-soybean plant, comprises at least one cry-gene or a cry-gene fragment coding for a Bt toxin.

[0081] In one preferred embodiment, said method is characterized in that the Bt-plant, preferably Bt-soybean plant, comprises at least one cry1A-gene or cry1A-gene fragment coding for a Bt toxin.

[0082] In one preferred embodiment, said method is characterized in that said Bt-plant, preferably Bt-soybean plant, further comprising a cryF gene or cryF-gene fragment coding for a Bt toxin.

[0083] In another preferred embodiment, said method is characterized in that said plant, preferably said soybean plant, comprises event MON87701.

[0084] In a more preferred embodiment, said soybean plant comprises event MON87701 and event MON89788, e.g. Intacta™ Roundup Ready™ 2 Pro.

[0085] In another preferred embodiment, said method is characterized in that said soybean plant comprising DNA that comprises a first sequence selected from the group consisting of bp 1385-1415 of SEQ ID NO: 1; bp 1350-1450 of SEQ ID NO: 1; bp 1300-1500 of SEQ ID NO: 1; bp 1200-1600 of SEQ ID NO: 1; bp 137- 168 of SEQ ID NO:2; bp 103-203 of SEQ ID NO:2; and bp 3-303 of SEQ ID NO:2; and a second sequence selected from the group consisting bp 2680-2780 of SEQ ID NO: 3; bp 2630-2830 of SEQ ID NO: 15; bp 2530-2930 of SEQ ID NO: 15; bp 9071-9171 of SEQ ID NO : 15 ; bp 9021 -9221 of SEQ ID NO : 15 ; and, bp 8921 -9321 of SEQ ID NO : 15 said first and second sequences being diagnostic for the presence of soybean event pDAB9582.814.19.1 :: pDAB4468.04.16.1. pDAB9582.814.19.1 :: pDAB4468.04.16.1 are disclosed in WO 2013/016516.

[0086] In one preferred embodiment, said method is characterized in that said soybean plant comprising a nucleotide sequence of SEQ ID NO: 4, SEQ ID NO:5, or complement thereof.

[0087] In one preferred embodiment, said method is characterized in that said soybean plant comprising a nucleotide sequence of SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:9 or complement thereof.

[0088] In one preferred embodiment, said method is characterized in that said soybean plant comprising a nucleotide sequence of SEQ ID NO:6 from positions 1 to 5757, the nucleotide sequence of SEQ ID NO:8 from positions 1 to 6426, and the nucleotide sequence of SEQ ID NO:7 from positions 379 to 2611, or complement thereof.

[0089] In one preferred embodiment, said method is characterized in that said soybean plant comprising a nucleotide sequence essentially of the nucleotide sequence of SEQ ID NO: 9 or complement thereof.

[0090] In another preferred embodiment, said method is characterized in that said pest is selected from the group consisting of *Pseudoplusia includens* (soybean looper), *Anticarsia gemmatilis* (velvet bean caterpillar) and *Spodoptera frugiperda* (fall armyworm).

[0091] In another preferred embodiment, said method is characterized in that the use form of the ryanodine receptor modulator is present in a mixture with at least one mixing partner.

[0092] A second aspect refers to a method for improving the utilization of the production potential of transgenic soybean plants in the absent of a pest. Preferred embodiments of this aspect are identical to the preferred embodiments disclosed for the first aspect of the present invention.

[0093] A third aspect refers to a synergistic composition comprising Bt toxins encoded by a nucleotide sequence that comprises

a first sequence selected from the group consisting of bp 1385-1415 of SEQ ID NO: 1; bp 1350-1450 of SEQ ID NO: 1; bp 1300-1500 of SEQ ID NO: 1; bp 1200-1600 of SEQ ID NO: 1; bp 137-168 of SEQ ID NO:2; bp 103-203 of SEQ ID NO:2; and bp 3-303 of SEQ ID NO:2; and a second sequence selected from the group consisting bp 2680-2780 of SEQ ID NO: 3; bp 2630-2830 of SEQ ID NO: 15; bp 2530-2930 of SEQ ID NO: 15; bp 9071-9171 of SEQ ID NO : 15 ; bp 9021 -9221 of SEQ ID NO : 15 ; and, bp 8921 -9321 of SEQ ID NO : 15 or

a nucleotide sequence of SEQ ID NO: 4, SEQ ID NO:5, or complement thereof

and a ryanodine receptor modulator as described herein.

[0094] A fourth aspect refers to a Bt-soybean plant, characterized in that at least 0.00001 g of a ryanodine receptor modulator as described herein is attached to it.

[0095] SEQ ID No: 1 (disclosed in WO 2013/016516) is the 5' DNA flanking border sequence for soybean event pDAB9582.814.19.1. Nucleotides 1-1400 are genomic sequence. Nucleotides 1401-1535 are a rearranged sequence from pDAB9582. Nucleotides 1536-1836 are insert sequence.

[0096] SEQ ID No: 2 (disclosed in WO 2013/016516) is the 3' DNA flanking border sequence for soybean event pDAB9582.814.19.1. Nucleotides 1-152 are insert sequence. Nucleotides 153-1550 are genomic sequence.

[0097] SEQ ID No: 3 (disclosed in WO 2013/016516) is the confirmed sequence of soybean event pDAB4468.04.16.1. Including the 5' genomic flanking sequence, pDAB4468 T-strand insert, and 3' genomic flanking sequence.

[0098] SEQ ID No: 4 (disclosed in WO 2009/064652) is a 20 nucleotide sequence representing the junction between the soybean genomic DNA and an integrated expression cassette. This sequence corresponds to positions 5748 to 5767 of SEQ ID NO: 9. In addition, SEQ ID NO: 1 is a nucleotide sequence corresponding to positions 5748 through 5757 of SEQ ID NO: 6 and the integrated right border of the TIC 107 expression cassette corresponding to positions 1 through 10 of SEQ ID NO: 8. SEQ ID NO: 1 also corresponds to positions 5748 to 5767 of the 5' flanking sequence, SEQ ID NO: 6.

[0099] SEQ ID No: 5 (disclosed in WO 2009/064652) is a 20 nucleotide sequence representing the junction between an integrated expression cassette and the soybean genomic DNA. This sequence corresponds to positions 12174 to 12193 of SEQ ID NO: 9. In addition, SEQ ID NO: 2 is a nucleotide sequence corresponding positions 6417 through 6426 of SEQ ID NO: 8 and the 3' flanking sequence corresponding to positions 379 through 388 of SEQ ID NO: 7.

[0100] SEQ ID No: 6 (disclosed in WO 2009/064652) is the 5' sequence flanking the inserted DNA of MON87701 up to and including a region of transformation DNA (T-DNA) insertion.

[0101] SEQ ID No: 7 (disclosed in WO 2009/064652) is the 3' sequence flanking the inserted DNA of MON87701 up to and including a region of T-DNA insertion.

[0102] SEQ ID No: 8 (disclosed in WO 2009/064652) is the sequence of the integrated TIC 107 expression cassette, including right and left border sequence after integration.

[0103] SEQ ID No: 9 (disclosed in WO 2009/064652) is a 14,416 bp nucleotide sequence representing the contig of the 5' sequence flanking the inserted DNA of MON87701 (SEQ ID NO: 6), the sequence of the integrated expression cassette (SEQ ID NO: 8) and the 3' sequence flanking the inserted DNA of MON87701 (SEQ ID NO: 7).

[0104] A nucleic acid molecule is said to be the "complement" of another nucleic acid molecule if they exhibit complete complementarity. As used herein, molecules are said to exhibit "complete complementarity" when every nucleotide of one of the molecules is complementary to a nucleotide of the other. Two molecules are said to be "minimally complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under at least conventional "low-stringency" conditions. Similarly, the molecules are said to be "complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under conventional "high-stringency" conditions. Conventional stringency conditions are described by Sambrook et al, 1989, and by Haymes et al, In: Nucleic Acid Hybridization, A Practical Approach, IRL Press, Washington, DC

(1985), Departures from complete complementarity are therefore permissible, as long as such departures do not completely preclude the capacity of the molecules to form a double-stranded structure. In order for a nucleic acid molecule to serve as a primer or probe it need only be sufficiently complementary in sequence to be able to form a stable double-stranded structure under the particular solvent and salt concentrations employed.

[0105] As used herein, a "substantially homologous sequence" is a nucleic acid sequence that will specifically hybridize to the complement of the nucleic acid sequence to which it is being compared under high stringency conditions. Appropriate stringency conditions which promote DNA hybridization, for example, 6.0 x sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 x SSC at 50°C, are known to those skilled in the art or can be found in Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0 x SSC at 50°C to a high stringency of about 0.2 x SSC at 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22°C, to high stringency conditions at about 65°C. Both temperature and salt may be varied, or either the temperature or the salt concentration may be held constant while the other variable is changed. In a preferred embodiment, a nucleic acid of the present invention will specifically hybridize to one or more of the nucleic acid molecules set forth in SEQ ID NO: 1 and 2 or complements thereof or fragments of either under moderately stringent conditions, for example at about 2.0 x SSC and about 65°C. In a particularly preferred embodiment, a nucleic acid of the present invention will specifically hybridize to one or more of the nucleic acid molecules set forth in SEQ ID NO: 1 and SEQ ID NO:2 or complements or fragments of either under high stringency conditions. In one aspect of the present invention, a preferred marker nucleic acid molecule of the present invention has the nucleic acid sequence set forth in SEQ ID NO:1 and SEQ ID NO:2 or complements thereof or fragments of either. In another aspect of the present invention, a preferred marker nucleic acid molecule of the present invention shares 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% and 100% sequence identity with the nucleic acid sequence set forth in SEQ ID NO:1 and SEQ ID NO:2 or complement thereof or fragments of either. In a further aspect of the present invention, a preferred marker nucleic acid molecule of the present invention shares 95% 96%, 97%, 98%, 99% and 100% sequence identity with the sequence set forth in SEQ ID NO:1 and SEQ ID NO: 2 or complement thereof or fragments of either. SEQ ID NO:1 and SEQ ID NO:2 may be used as markers in plant breeding methods to identify the progeny of genetic crosses similar to the methods described for simple sequence repeat DNA marker analysis, in "DNA markers: Protocols, applications, and overviews: (1997) 173-185, Cregan, et al., eds., Wiley-Liss NY"; all of which is herein incorporated by reference. The hybridization of the probe to the target DNA molecule can be detected by any number of methods known to those skilled in the art, these can include, but are not limited to, fluorescent tags, radioactive tags, antibody based tags, and chemiluminescent tags.

[0064] Regarding the amplification of a target nucleic acid sequence (e.g., by PCR) using a particular

amplification primer pair, "stringent conditions" are conditions that permit the primer pair to hybridize only to the target nucleic-acid sequence to which a primer having the corresponding wild-type sequence (or its complement) would bind and preferably to produce a unique amplification product, the amplicon, in a DNA thermal amplification reaction. [0065] The term "specific for (a target sequence)" indicates that a probe or primer hybridizes under stringent hybridization conditions only to the target sequence in a sample comprising the target sequence.

[0106] In a particularly preferred variant, the process according to the invention is used for treating transgenic vegetable, maize, soya bean, cotton, tobacco, rice, potato and sugar beet varieties. These are preferably Bt plants.

[0107] The vegetable plants or varieties are, for example, the following useful plants:

- potatoes: preferably starch potatoes, sweet potatoes and table potatoes;
- root vegetables: preferably carrots, turnips (swedes, stubble turnips (*Brassica rapa* var. *rapa*), spring turnips, autumn turnips (*Brassica campestris* ssp. *rapifera*), *Brassica rapa* L. ssp. *rapa* f. *teltowiensis*), scorzonera, Jerusalem artichoke, turnip-rooted parsley, parsnip, radish and horseradish;
- tuber vegetables: preferably kohlrabi, beetroot, celeriac, garden radish;
- bulb crops: preferably scallion, leek and onions (planting onions and seed onions);
- brassica vegetables: preferably headed cabbage (white cabbage, red cabbage, kale, savoy cabbage), cauliflowers, broccoli, curly kale, marrow-stem kale, seakale and Brussels sprouts;
- fruiting vegetables: preferably tomatoes (outdoor tomatoes, vine-ripened tomatoes, beef tomatoes, greenhouse tomatoes, cocktail tomatoes, industrial and fresh market tomatoes), melons, eggplants, aubergines, pepper (sweet pepper and hot pepper, Spanish pepper), chilli pepper, pumpkins, courgettes and cucumbers (outdoor cucumbers, greenhouse cucumbers snake gourds and gherkins);
- vegetable pulses: preferably bush beans (as sword beans, string beans, flageolet beans, wax beans, corn beans of green- and yellow-podded cultivars), pole beans (as sword beans, string beans, flageolet beans, wax beans of green-, blue- and yellow-podded cultivars), broadbeans (field beans, Windsor beans, cultivars having white- and black-spotted flowers), peas (chickling vetch, chickpeas, marrow peas, shelling peas, sugar-peas, smooth peas, cultivars having light- and dark-green fresh fruits) and lentils;

- green vegetables and stem vegetables: preferably Chinese cabbage, round-headed garden lettuce, curled lettuce, lamb's-lettuce, iceberg lettuce, romaine lettuce, oakleaf lettuce, endives, radicchio, lollo rossa, rucola lettuce, chicory, spinach, chard (leaf chard and stem chard) and parsley;
- 5 ○ other vegetables: preferably asparagus, rhubarb, chives, artichokes, mint varieties, sunflowers, Florence fennel, dill, garden cress, mustard, poppy seed, peanuts, sesame and salad chicory.

[0108] Bt vegetables including exemplary methods for preparing them are described in detail, for example, in Barton et al., 1987, Plant Physiol. 85 : 1103-1109; Vaeck et al., 1987, Nature 328 : 33-37 ;
10 Fischhoff et al., 1987, Bio/Technology 5 : 807-813. In addition, Bt vegetable plants are already known as commercial varieties, for example the potato cultivar NewLeaf® (Monsanto). The preparation of Bt vegetables is also described in US 6,072,105.

[0109] Likewise, Bt cotton is already known in principle, for example from US-A-5,322,938. In the context of the present invention, particular preference is given to Bt cotton with the trade names
15 NuCOTN33® and NuCOTN33B®.

[0110] The use and preparation of Bt maize has likewise already been known for a long time, for example from Ishida, Y., Saito, H., Ohta, S., Hiei, Y., Komari, T., and Kumashiro, T. (1996). High efficiency transformation of maize (*Zea mays* L.) mediated by *Agrobacterium tumefaciens*, Nature Biotechnology 4: 745-750. EP-B-0485506, too, describes the preparation of Bt maize plants.
20 Furthermore, different varieties of Bt maize are commercially available, for example under the following names (company/companies is/are in each case given in brackets): KnockOut® (Novartis Seeds), NaturGard® (Mycogen Seeds), Yieldgard® (Novartis Seeds, Monsanto, Cargill, Golden Harvest, Pioneer, DeKalb inter alia), Bt-Xtra® (DeKalb) and StarLink® (Aventis CropScience, Garst inter alia). For the purpose of the present invention, particular preference is given especially to the following maize
25 cultivars: KnockOut®, NaturGard®, Yieldgard®, Bt-Xtra® and StarLink®.

[0111] For soya beans, too, Roundup®Ready cultivar or cultivars resistant to the herbicide Liberty Link® are available and can be treated according to the invention. In the case of rice, a large number of “Golden Rice” lines are available which are likewise characterized in that, by virtue of a transgenic modification, they have an increased content of provitamin A. They, too, are examples of plants which
30 can be treated by the method according to the invention, with the advantages described.

[0112] The method according to the invention is suitable for controlling a large number of harmful organisms which occur in particular in vegetables, maize and cotton, in particular insects and arachnids, very particularly preferably insects. The pests mentioned include:

- From the order of the Anoplura (Phthiraptera),, for example, *Damalinia* spp., *Haematopinus* spp., *Linognathus* spp., *Pediculus* spp., *Trichodectes* spp..
- From the class of the Arachnida, for example, *Acarus siro*, *Aceria sheldoni*, *Aculops* spp., *Aculus* spp., *Amblyomma* spp., *Argas* spp., *Boophilus* spp., *Brevipalpus* spp., *Bryobia praetiosa*, *Chorioptes* spp., *Dermanyssus gallinae*, *Eotetranychus* spp., *Epitrimerus pyri*,
5 *Eutetranychus* spp., *Eriophyes* spp., *Hemitarsonemus* spp., *Hyalomma* spp., *Ixodes* spp., *Latrodectus mactans*, *Metatetranychus* spp., *Oligonychus* spp., *Ornithodoros* spp., *Panonychus* spp., *Phyllocoptruta oleivora*, *Polyphagotarsonemus latus*, *Psoroptes* spp., *Rhipicephalus* spp., *Rhizoglyphus* spp., *Sarcoptes* spp., *Scorpio maurus*, *Stenotarsonemus*
10 spp., *Tarsonemus* spp., *Tetranychus* spp., *Vasates lycopersici*.
- From the class of the Bivalva, for example, *Dreissena* spp..
- From the order of the Chilopoda, for example, *Geophilus* spp., *Scutigera* spp..
- From the order of the Coleoptera, for example, *Acanthoscelides obtectus*, *Adoretus* spp., *Agelastica alni*, *Agriotes* spp., *Amphimallon solstitialis*, *Anobium punctatum*,
15 *Anoplophora* spp., *Anthonomus* spp., *Anthrenus* spp., *Apogonia* spp., *Atomaria* spp., *Attagenus* spp., *Bruchidius obtectus*, *Bruchus* spp., *Ceuthorrhynchus* spp., *Cleonus mendicus*, *Conoderus* spp., *Cosmopolites* spp., *Costelytra zealandica*, *Curculio* spp., *Cryptorhynchus lapathi*, *Dermestes* spp., *Diabrotica* spp., *Epilachna* spp., *Faustinus cubae*, *Gibbium psylloides*, *Heteronychus arator*, *Hylamorpha elegans*, *Hylotrupes bajulus*,
20 *Hypera postica*, *Hypothenemus* spp., *Lachnosterna consanguinea*, *Leptinotarsa decemlineata*, *Lissorhoptrus oryzophilus*, *Lixus* spp., *Lyctus* spp., *Meligethes aeneus*, *Melolontha melolontha*, *Migdolus* spp., *Monochamus* spp., *Naupactus xanthographus*, *Niptus hololeucus*, *Oryctes rhinoceros*, *Oryzaephilus surinamensis*, *Otiorrhynchus sulcatus*, *Oxycetonia jucunda*, *Phaedon cochleariae*, *Phyllophaga* spp., *Popillia japonica*, *Premnotrypes* spp., *Psylliodes chrysocephala*, *Ptinus* spp., *Rhizobius ventralis*, *Rhizopertha dominica*, *Sitophilus* spp., *Sphenophorus* spp., *Sternechus* spp., *Symphyletes* spp.,
25 *Tenebrio molitor*, *Tribolium* spp., *Trogoderma* spp., *Tychius* spp., *Xylotrechus* spp., *Zabrus* spp..
- From the order of the Collembola, for example, *Onychiurus armatus*.
- From the order of the Dermaptera, for example, *Forficula auricularia*.
- From the order of the Diplopoda, for example, *Blaniulus guttulatus*.
- From the order of the Diptera, for example, *Aedes* spp., *Anopheles* spp., *Bibio hortulanus*,

- 5 *Calliphora erythrocephala*, *Ceratitis capitata*, *Chrysomyia* spp., *Cochliomyia* spp., *Cordylobia anthropophaga*, *Culex* spp., *Cuterebra* spp., *Dacus oleae*, *Dermatobia hominis*, *Drosophila* spp., *Fannia* spp., *Gastrophilus* spp., *Hylemyia* spp., *Hyppobosca* spp., *Hypoderma* spp., *Liriomyza* spp., *Lucilia* spp., *Musca* spp., *Nezara* spp., *Oestrus* spp., *Oscinella* frit, *Pegomyia hyoscyami*, *Phorbia* spp., *Stomoxys* spp., *Tabanus* spp., *Tannia* spp., *Tipula paludosa*, *Wohlfahrtia* spp..
- 10 ○ From the class of the Gastropoda, for example, *Arion* spp., *Biomphalaria* spp., *Bulinus* spp., *Deroceras* spp., *Galba* spp., *Lymnaea* spp., *Oncomelania* spp., *Succinea* spp..
- 15 ○ From the class of the helminths, for example, *Ancylostoma duodenale*, *Ancylostoma ceylanicum*, *Ancylostoma braziliensis*, *Ancylostoma* spp., *Ascaris lubricoides*, *Ascaris* spp., *Brugia malayi*, *Brugia timori*, *Bunostomum* spp., *Chabertia* spp., *Clonorchis* spp., *Cooperia* spp., *Dicrocoelium* spp., *Dictyocaulus filaria*, *Diphyllbothrium latum*, *Dracunculus medinensis*, *Echinococcus granulosus*, *Echinococcus multilocularis*, *Enterobius vermicularis*, *Faciola* spp., *Haemonchus* spp., *Heterakis* spp., *Hymenolepis nana*, *Hyostrongylus* spp., *Loa Loa*, *Nematodirus* spp., *Oesophagostomum* spp., *Opisthorchis* spp., *Onchocerca volvulus*, *Ostertagia* spp., *Paragonimus* spp., *Schistosomen* spp., *Strongyloides fuelleborni*, *Strongyloides stercoralis*, *Strongyloides* spp., *Taenia saginata*, *Taenia solium*, *Trichinella spiralis*, *Trichinella nativa*, *Trichinella britovi*, *Trichinella nelsoni*, *Trichinella pseudopsiralis*, *Trichostrongylus* spp., *Trichuris trichuria*, *Wuchereria bancrofti*.
- 20 ○ It is furthermore possible to control Protozoa, such as *Eimeria*.
- 25 ○ From the order of the Heteroptera, for example, *Anasa tristis*, *Antestiopsis* spp., *Blissus* spp., *Calocoris* spp., *Campylomma livida*, *Cavelerius* spp., *Cimex* spp., *Creontiades dilutus*, *Dasynus piperis*, *Dichelops furcatus*, *Diconocoris hewetti*, *Dysdercus* spp., *Euschistus* spp., *Eurygaster* spp., *Heliopeltis* spp., *Horcias nobilellus*, *Leptocoris* spp., *Leptoglossus phyllopus*, *Lygus* spp., *Macropes excavatus*, *Miridae*, *Nezara* spp., *Oebalus* spp., *Pentomidae*, *Piesma quadrata*, *Piezodorus* spp., *Psallus seriatus*, *Pseudacysta perseae*, *Rhodnius* spp., *Sahlbergella singularis*, *Scotinophora* spp., *Stephanitis nashi*, *Tibraca* spp., *Triatoma* spp..
- 30 ○ From the order of the Homoptera, for example, *Acyrtosipon* spp., *Aeneolamia* spp., *Agonosцена* spp., *Aleurodes* spp., *Aleurolobus barodensis*, *Aleurothrixus* spp., *Amrasca* spp., *Anuraphis cardui*, *Aonidiella* spp., *Aphanostigma piri*, *Aphis* spp., *Arboridia apicalis*, *Aspidiella* spp., *Aspidiotus* spp., *Atanus* spp., *Aulacorthum solani*, *Bemisia* spp., *Brachycaudus helichrysi*, *Brachycolus* spp., *Brevicoryne brassicae*, *Calligypona*

- marginata, Carnecephala fulgida, Ceratovacuna lanigera, Cercopidae, Ceroplastes spp., Chaetosiphon fragaefolii, Chionaspis tegalensis, Chlorita onukii, Chromaphis juglandicola, Chrysomphalus ficus, Cicadulina mbila, Cocomytilus halli, Coccus spp., Cryptomyzus ribis, Dalbulus spp., Dialeurodes spp., Diaphorina spp., Diaspis spp., Doralis spp., 5 Drosicha spp., Dysaphis spp., Dysmicoccus spp., Empoasca spp., Eriosoma spp., Erythroneura spp., Euscelis bilobatus, Geococcus coffeae, Homalodisca coagulata, Hyalopterus arundinis, Icerya spp., Idiocerus spp., Idioscopus spp., Laodelphax striatellus, Lecanium spp., Lepidosaphes spp., Lipaphis erysimi, Macrosiphum spp., Mahanarva fimbriolata, Melanaphis sacchari, Metcalfiella spp., Metopolophium dirhodum, Monellia 10 costalis, Monelliopsis pecanis, Myzus spp., Nasonovia ribisnigri, Nephotettix spp., Nilaparvata lugens, Oncometopia spp., Orthezia praelonga, Parabemisia myricae, Paratrioza spp., Parlatoria spp., Pemphigus spp., Peregrinus maidis, Phenacoccus spp., Phloeomyzus passerinii, Phorodon humuli, Phylloxera spp., Pinnaspis aspidistrae, Planococcus spp., Protopulvinaria pyriformis, Pseudaulacaspis pentagona, Pseudococcus 15 spp., Psylla spp., Pteromalus spp., Pyrilla spp., Quadraspidiotus spp., Quesada gigas, Rastrococcus spp., Rhopalosiphum spp., Saissetia spp., Scaphoides titanus, Schizaphis graminum, Selenaspidus articulatus, Sogata spp., Sogatella furcifera, Sogatodes spp., Stictocephala festina, Tenalaphara malayensis, Tinocallis caryaefoliae, Tomaspis spp., Toxoptera spp., Trialeurodes vaporariorum, Trioza spp., Typhlocyba spp., Unaspis spp., 20 Viteus vitifolii.
- From the order of the Hymenoptera, for example, Diprion spp., Hoplocampa spp., Lasius spp., Monomorium pharaonis, Vespa spp..
 - From the order of the Isopoda, for example, Armadillidium vulgare, Oniscus asellus, Porcellio scaber.
 - 25 ○ From the order of the Isoptera, for example, Reticulitermes spp., Odontotermes spp..
 - From the order of the Lepidoptera, for example, Acronicta major, Aedia leucomelas, Agrotis spp., Alabama argillacea, Anticarsia spp., Barathra brassicae, Bucculatrix thurberiella, Bupalus piniarius, Cacoecia podana, Capua reticulana, Carpocapsa pomonella, Cheimatoxia brumata, Chilo spp., Choristoneura fumiferana, Clysia ambiguella, Cnaphalocerus spp., 30 Earias insulana, Ephestia kuehniella, Euproctis chrysorrhoea, Euxoa spp., Feltia spp., Galleria mellonella, Helicoverpa spp., Heliothis spp., Hofmannophila pseudospretella, Homona magnanima, Hyponomeuta padella, Laphygma spp., Lithocolletis blancardella, Lithophane antennata, Loxagrotis albicosta, Lymantria spp., Malacosoma neustria, Mamestra brassicae, Mocis repanda, Mythimna separata, Oria spp., Oulema oryzae, Panolis 35 flammae, Pectinophora gossypiella, Phyllocnistis citrella, Pieris spp., Plutella xylostella,

Prodenia spp., *Pseudaletia* spp., *Pseudoplusia includens*, *Pyrausta nubilalis*, *Spodoptera* spp., *Thermesia gemmatalis*, *Tinea pellionella*, *Tineola bisselliella*, *Tortrix viridana*, *Trichoplusia* spp..

○ From the order of the Orthoptera, for example, *Acheta domesticus*, *Blatta orientalis*,
5 *Blattella germanica*, *Gryllotalpa* spp., *Leucophaea maderae*, *Locusta* spp., *Melanoplus* spp.,
Periplaneta americana, *Schistocerca gregaria*.

○ From the order of the Siphonaptera, for example, *Ceratophyllus* spp., *Xenopsylla cheopis*.

○ From the order of the Symphyla, for example, *Scutigerella immaculata*.

○ From the order of the Thysanoptera, for example, *Baliothrips biformis*, *Enneothrips*
10 *flavens*, *Frankliniella* spp., *Heliothrips* spp., *Hercinothrips femoralis*, *Kakothrips* spp.,
Rhipiphorothrips cruentatus, *Scirtothrips* spp., *Taeniothrips cardamoni*, *Thrips* spp..

○ From the order of the Thysanura, for example, *Lepisma saccharina*.

○ The phytoparasitic nematodes include, for example, *Anguina* spp., *Aphelenchoides* spp.,
15 *Belonoaimus* spp., *Bursaphelenchus* spp., *Ditylenchus dipsaci*, *Globodera* spp.,
Heliocotylenchus spp., *Heterodera* spp., *Longidorus* spp., *Meloidogyne* spp., *Pratylenchus*
spp., *Radopholus similis*, *Rotylenchus* spp., *Trichodorus* spp., *Tylenchorhynchus* spp.,
Tylenchulus spp., *Tylenchulus semipenetrans*, *Xiphinema* spp..

[0113] The method according to the invention for the treatment of Bt vegetables, Bt maize, Bt cotton, Bt
soya beans, Bt tobacco and also Bt rice, Bt sugar beets or Bt potatoes is particularly suitable for
20 controlling aphids (Aphidina), whiteflies (Trialeurodes), thrips (Thysanoptera), spider mites (Arachnida),
soft scale insects or mealy bugs (Coccoidae and Pseudococcoidae, respectively).

[0114] The active compounds which can be used according to the invention can be employed in
customary formulations, such as solutions, emulsions, wettable powders, water- and oil-based
suspensions, powders, dusts, pastes, soluble powders, soluble granules, granules for broadcasting,
25 suspoemulsion concentrates, natural compounds impregnated with active compound, synthetic substances
impregnated with active compound, fertilizers and also microencapsulations in polymeric substances.

[0115] These formulations are prepared in a known manner, for example by mixing the active
compounds with extenders, i.e. liquid solvents and/or solid carriers, if appropriate using surfactants, i.e.
emulsifiers and/or dispersants and/or foam-formers. The formulations are prepared either in suitable
30 plants or else before or during application.

[0116] Wettable powders are preparations which can be dispersed homogeneously in water and which, in addition to the active compound and beside a diluent or inert substance, also comprise wetting agents, for example polyethoxylated alkylphenols, polyethoxylated fatty alcohols, alkylsulphonates or alkylphenylsulphonates and dispersants, for example sodium lignosulphonate, sodium 2,2'-

5 dinaphthylmethane-6,6'-disulphonate.

[0117] Dusts are obtained by grinding the active compound with finely distributed solid substances, for example talc, natural clays, such as kaolin, bentonite, pyrophyllite or diatomaceous earth. Granules can be prepared either by spraying the active compound onto granular inert material capable of adsorption or by applying active compound concentrates to the surface of carrier substances, such as sand, kaolinites or granular inert material, by means of adhesives, for example polyvinyl alcohol, sodium polyacrylate or mineral oils. Suitable active compounds can also be granulated in the manner customary for the preparation of fertilizer granules - if desired as a mixture with fertilizers.

[0118] Suitable for use as auxiliaries are substances which are suitable for imparting to the composition itself and/or to preparations derived therefrom (for example spray liquors, seed dressings) particular properties such as certain technical properties and/or also particular biological properties. Typical suitable auxiliaries are: extenders, solvents and carriers.

[0119] Suitable extenders are, for example, water, polar and nonpolar organic chemical liquids, for example from the classes of the aromatic and non-aromatic hydrocarbons (such as paraffins, alkylbenzenes, alkylnaphthalenes, chlorobenzenes), the alcohols and polyols (which, if appropriate, may also be substituted, etherified and/or esterified), the ketones (such as acetone, cyclohexanone), esters (including fats and oils) and (poly)ethers, the unsubstituted and substituted amines, amides, lactams (such as N-alkylpyrrolidones) and lactones, the sulphones and sulfoxides (such as dimethyl sulfoxide).

[0120] If the extender used is water, it is also possible to employ, for example, organic solvents as auxiliary solvents. Essentially, suitable liquid solvents are: aromatics such as xylene, toluene or alkylnaphthalenes, chlorinated aromatics and chlorinated aliphatic hydrocarbons such as chlorobenzenes, chloroethylenes or methylene chloride, aliphatic hydrocarbons such as cyclohexane or paraffins, for example petroleum fractions, mineral and vegetable oils, alcohols such as butanol or glycol and also their ethers and esters, ketones such as acetone, methyl ethyl ketone, methyl isobutyl ketone or cyclohexanone, strongly polar solvents such as dimethyl sulfoxide, and also water.

[0121] Suitable solid carriers are for example, ammonium salts and ground natural minerals such as kaolins, clays, talc, chalk, quartz, attapulgite, montmorillonite or diatomaceous earth, and ground synthetic minerals, such as finely divided silica, alumina and silicates; suitable solid carriers for granules are: for example, crushed and fractionated natural rocks such as calcite, marble, pumice, sepiolite and dolomite, and also synthetic granules of inorganic and organic meals, and granules of organic material

such as paper, sawdust, coconut shells, maize cobs and tobacco stalks; suitable emulsifiers and/or foam-formers are: for example, nonionic and anionic emulsifiers, such as polyoxyethylene fatty acid esters, polyoxyethylene fatty alcohol ethers, for example alkylaryl polyglycol ethers, alkylsulphonates, alkyl sulphates, arylsulphonates and also protein hydrolysates; suitable dispersants are nonionic and/or ionic substances, for example from the classes of the alcohol-POE and/or -POP ethers, acid and/or POP POE esters, alkylaryl and/or POP POE ethers, fat and/or POP POE adducts, POE- and/or POP-polyol derivatives, POE- and/or POP-sorbitan or -sugar adducts, alkyl or aryl sulphates, alkyl- or arylsulphonates and alkyl or aryl phosphates or the corresponding PO-ether adducts. Furthermore, suitable oligo- or polymers, for example those derived from vinylic monomers, from acrylic acid, from EO and/or PO alone or in combination with, for example, (poly)alcohols or (poly)amines. It is also possible to employ lignin and its sulphonic acid derivatives, unmodified and modified celluloses, aromatic and/or aliphatic sulphonic acids and their adducts with formaldehyde.

[0122] Tackifiers such as carboxymethylcellulose and natural and synthetic polymers in the form of powders, granules or latices, such as gum arabic, polyvinyl alcohol and polyvinyl acetate, as well as natural phospholipids such as cephalins and lecithins, and synthetic phospholipids, can be used in the formulations.

[0123] It is possible to use colorants such as inorganic pigments, for example iron oxide, titanium oxide and Prussian Blue, and organic dyestuffs, such as alizarin dyestuffs, azo dyestuffs and metal phthalocyanine dyestuffs, and trace nutrients such as salts of iron, manganese, boron, copper, cobalt, molybdenum and zinc.

[0124] Other possible additives are perfumes, mineral or vegetable, optionally modified oils, waxes and nutrients (including trace nutrients), such as salts of iron, manganese, boron, copper, cobalt, molybdenum and zinc.

[0125] Stabilizers, such as low-temperature stabilizers, preservatives, antioxidants, light stabilizers or other agents which improve chemical and/or physical stability may also be present.

[0126] These individual types of formulation are known in principle and are described, for example, in: "Pesticides Formulations", 2nd Ed., Marcel Dekker N.Y.; Martens, 1979, "Spray Drying Handbook", 3rd Ed., G. Goodwin Ltd. London.

[0127] Based on his general expert knowledge, the person skilled in the art is able to choose suitable formulation auxiliaries (in this context, see, for example, Watkins, "Handbook of Insecticide Dust Diluents and Carriers", 2nd Ed., Darland Books, Caldwell N.J.).

[0128] In a preferred embodiment, the plants or plant parts are treated according to the invention with an oil-based suspension concentrate. An advantageous suspension concentrate is known from WO

2005/084435 (EP 1 725 104 A2). It consists of at least one room-temperature-solid active agrochemical substance, at least one “closed” penetrant, at least one vegetable oil or mineral oil, at least one nonionic surfactant and/or at least one anionic surfactant, and optionally one or more additives from the groups of the emulsifiers, foam inhibitors, preservatives, antioxidants, colorants and/or inert filler materials.

- 5 Preferred embodiments of the suspension concentrate are described in the above-mentioned WO 2005/084435. For the purpose of the disclosure, both documents are incorporated herein in their entirety by way of reference.

[0129] In a further preferred embodiment, the plants or plant parts are treated according to the invention with compositions comprising ammonium or phosphonium salts and, if appropriate, penetrants.

- 10 Advantageous compositions are known from WO2007/068355 and from the not prior-published EP 07109732.3. They consist of at least one compound of the formula (I) and at least one ammonium or phosphonium salt and, if appropriate, penetrants. Preferred embodiments are described in WO2007/068355 and the not prior-published EP 07109732.3. For the purpose of the disclosure, these documents are incorporated herein in their entirety by way of reference.

- 15 [0130] In general, the formulations comprise from 0.01 to 98% by weight of active compound, preferably from 0.5 to 90%. In wettable powders, the active compound concentration is, for example, from about 10 to 90% by weight, the remainder to 100% by weight consisting of customary formulation components. In the case of emulsifiable concentrates, the active compound concentration can be from about 5 to 80% by weight. In most cases, formulations in the form of dusts comprise from 5 to 20% by
20 weight of active compound, sprayable solutions comprise about 2 to 20% by weight. In the case of granules, the active compound content depends partially on whether the active compound is present in liquid or solid form and on which granulation auxiliaries, fillers, etc., are used.

- [0131] The required application rate may also vary with external conditions such as, inter alia, temperature and humidity. It may vary within wide limits, for example between 0.1 g/h and 5.0 kg/ha or
25 more of active substance. However, they are preferably between 0.1 g/ha and 1.0 kg/ha. Owing to the synergistic effects between Bt vegetables and the insecticide, particular preference is given to application rates of from 0.1 to 500 g/ha.

[0132] For compounds of the formula (I), preference is given to application rates of from 10 to 500 g/ha; particularly preferred are from 10 to 200 g/ha.

- 30 [0133] In a particular embodiment of the method according to the invention, the compound of the formula (I) is employed in an application rate of from 0.1 g/ha to 5.0 kg/ha, preferably from 0.1 to 500 g/ha and particularly preferably from 50 to 500 g/ha and especially preferably from 50 to 200 g/ha.

[0134] In their commercial formulations and in the use forms prepared from these formulations, the active compounds according to the invention may be present as mixtures with other active compounds,

such as insecticides, attractants, sterilants, acaricides, nematocides, fungicides, growth-regulating substances or herbicides.

[0135] A mixture with other known compounds, such as herbicides, fertilizers, growth regulators, safeners, semiochemicals, or else with agents for improving plant properties is also possible.

- 5 [0136] The active compound content of the use forms prepared from the commercial formulations can be from 0.00000001 to 95% by weight, preferably between 0.00001 and 1% by weight, of active compound.

Example**Compound (I-5) on transgenic Bt-plant****Spodoptera frugiperda – spray application on transgenic soy bean, field trial**

[0137] For preparing the stock solution, 20 mg of active compound is solved in 200µl of

- 5 dimethylformamide and filled-up with 9.78 ml SC blank formulation of Belt. The final test concentrations are prepared by dilution with water.

[0138] The test is conducted with conventional soybean plants (*Glycine max*; non-transgenic) and transgenic soybean plants containing a Cry1Ac gene (Intacta from Monsanto). When the plants are in stage V2 (3 nodes with 2 unfolded trifoliolates), they are treated by spray application with the active compound preparation. After application, clip-cages with 5-6 L2 larvae of the fall army worm (*Spodoptera frugiperda*) are placed on the leaves.

- 10 [0139] After the specified period of time, feeding damage (white holes on leaves) of *Spodoptera frugiperda* on conventional soybean, Fig. 1a, in comparison to Intacta soybean, Fig. 1b, is visualized on 3 randomly picked soybean leaves out of 5 replicate plots (R₁-R₅).

- 15 [0140] According to the present application in this test the following combinations of transgenic plant and compound shows a superior effect compared to the treated, non-transgenic plant respectively the non-treated, transgenic plant:

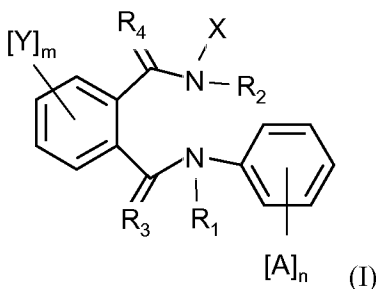
[0141] Table A

3 days after application (3 DAA)			
Infection 1 + 3 days (Inf 1+3)			
5 replicates per variety			
	Compound	Conc. [g ai/ha]	Soy variety
1	Untreated control		Conventional
2	Untreated control		Intacta
9	Compound (I-5)	12	Conventional
10	Compound (I-5)	24	Conventional
11	Compound (I-5)	36	Conventional
12	Compound (I-5)	12	Intacta
13	Compound (I-5)	24	Intacta
14	Compound (I-5)	36	Intacta
15	SC blank formulation	0	Conventional
16	SC blank formulation	0	Intacta
17	Water	0	Conventional
18	Water	0	Intacta

- 20 Results of the experiments 1, 2 and 9 to 18 of Table A are shown in Fig 1a and 1b

Patent claims:

1. Method for improving the utilization of the production potential of a transgenic plant and/or for controlling/combating/treating insect or nematode pests, characterized in that the plant is treated with an effective amount of at least one compound of the formula (I)



wherein

A represents individually halogen, cyano, nitro, hydroxyl, amino, C₁-C₈ alkyl group, substituted C₁-C₈ alkyl group having at least one substituent elected from the group consisting of halogen, hydroxy, cyano, nitro, amino, halo C₁-C₃ alkyl group, C₁-C₃ alkoxy group, halo C₁-C₃ alkoxy group, C₁-C₃ alkylthio group, halo C₁-C₃ alkylthio group, C₁-C₃ alkylsulfinyl group, halo C₁-C₃ alkylsulfinyl group, C₁-C₃ alkylsulfonyl group, halo C₁-C₃ alkylsulfonyl group and C₁-C₃ alkylthio, C₁-C₃ alkyl group; further, an arbitrary saturated carbon atom in said optionally substituted C₁-C₈ alkyl group;

n represents 0, 1, 2, 3 or 4, preferably 0, 1 or 2;

R₁ represents hydrogen, halogen, cyano C₁-C₈ alkyl or C₁-C₈ haloalkyl;

R₂ represents hydrogen, halogen, cyano C₁-C₈ alkyl or C₁-C₈ haloalkyl;

R₃ represents O or S;

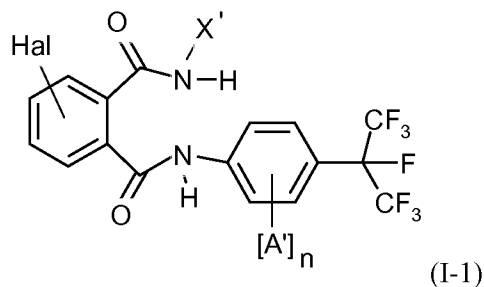
R₄ represents O or S;

Y represents individually hydrogen, halogen, cyano, nitro, C₁-C₆ alkyl group, halo C₁-C₆ alkyl group, C₂-C₆ alkenyl group, halo C₂-C₆ alkenyl group, C₂-C₆ alkynyl group, halo C₂-C₆ alkynyl group, C₃-C₆ cycloalkyl group, halo C₃-C₆ cycloalkyl group, C₁-C₆ alkoxy group, halo C₁-C₆ alkoxy group, C₁-C₆ alkylthio group, halo C₁-C₆ alkylthio group, C₁-C₆ alkylsulfinyl group, halo C₁-C₆ alkylsulfinyl group, C₁-C₆ alkylsulfonyl group, or halo C₁-C₆ alkylsulfonyl group;

m represents 0, 1, 2, 3, or 4;

X represents a C₁-C₈ alkyl group or a substituted C₁-C₈ alkyl group having at least one substituent selected from the group consisting of halogen, hydroxy, cyano, nitro, amino, halo C₁-C₃ alkyl group, C₁-C₃ alkoxy group, halo C₁-C₃ alkoxy group

2. Method according to Claim 1, characterized in that the compound of the formula (I) is formula (I-1):



wherein

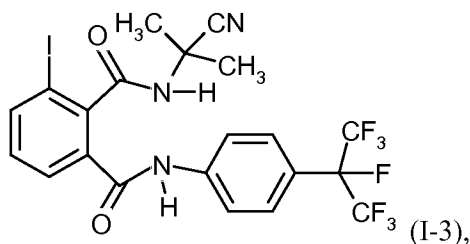
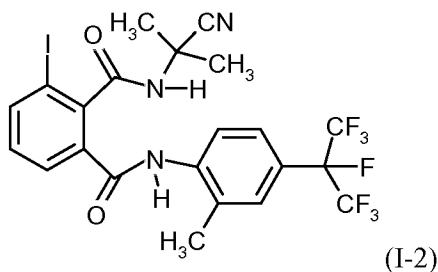
5 Hal represents F, Cl, I or Br; and

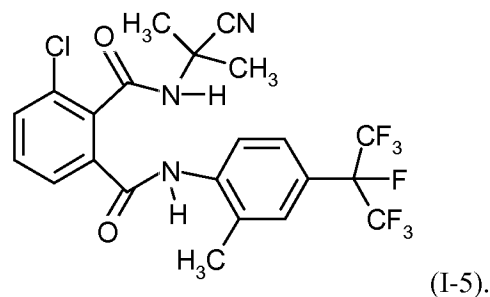
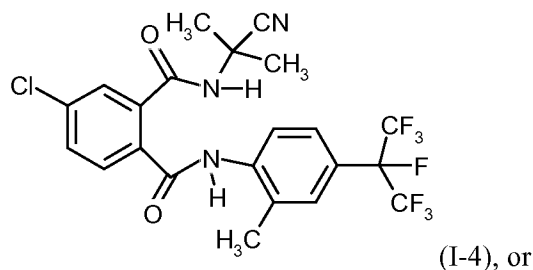
X' represents C₁-C₆ alkyl or substituted C₁-C₆ alkyl having at least one substituent selected from the group consisting of halogen, hydroxy, cyano, nitro, amino, halo C₁-C₃ alkyl group, preferably a C₁-C₆ cyanoalkyl;

10 A' represents C₁-C₃ alkyl, C₁-C₃ haloalkyl, halogen, preferably methyl, halomethyl, ethyl or haloethyl, more preferably methyl or ethyl;

n represents 0, 1, 2, 3 or 4, preferably 0, 1 or 2, more preferably 1.

3. Method according to Claim 1 or Claim 2, characterized in that the compound of the formula (I) is selected from the group consisting of compound (I-2), (I-3), (I-4) or (I-5):

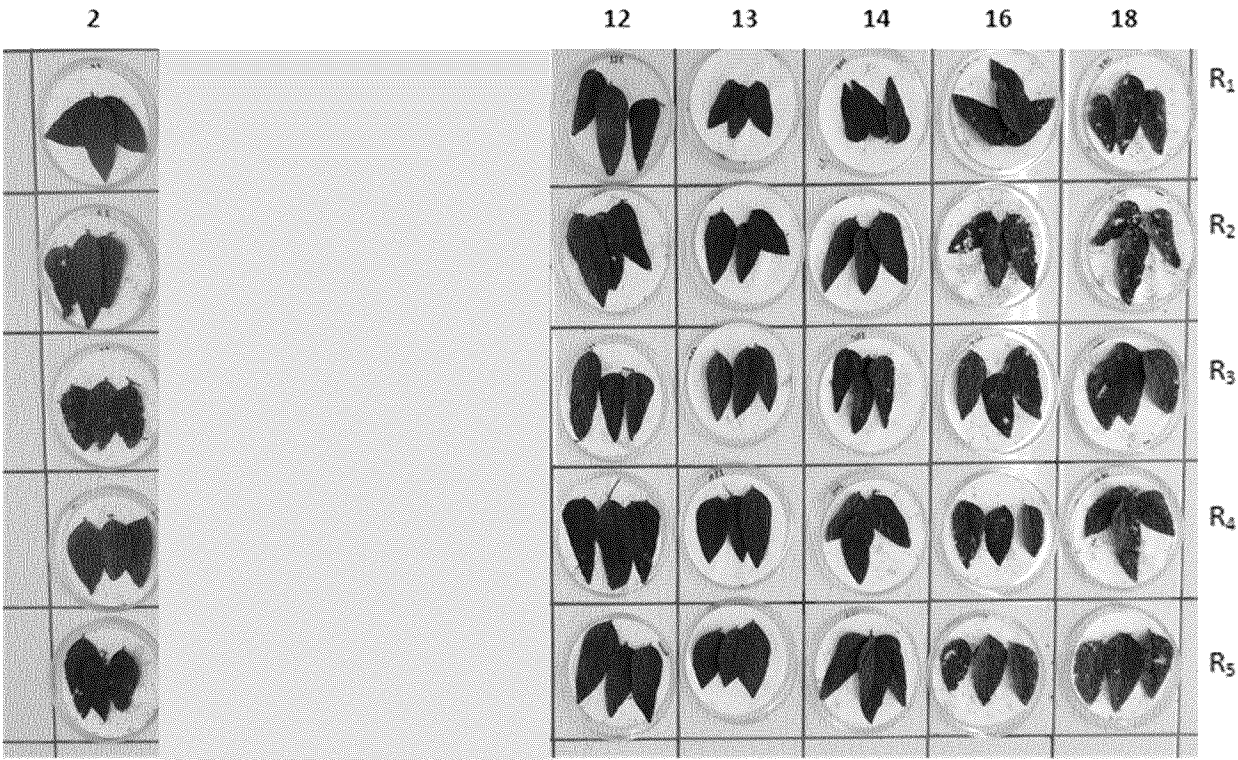




4. Method according to Claim 3, characterized in that the compound of the formula (I) is compound (I-5).
5. Method according to any of Claims 1 to 4, characterized in that the transgenic plant contains at least one cry-gene or a cry-gene fragment coding for a Bt toxin.
6. Method according to Claim 5, characterized in that the Bt toxin is encoded by a cry gene or a cry-gene fragment selected from the subgroup cry1A.
7. Method according to claim 6, characterized in that the Bt toxin is encoded by a cry gene or a cry-gene fragment selected from the subgroups cry1Aa, cry1Ab and cry1Ac or a hybrid thereof.
8. Method according to any one of claims 1 to 8, characterized in that the Bt toxin is encoded by a bt-gene or fragment thereof comprising event MON87701.
9. Method according to any one of claims 1 to 8, characterized in that the transgenic plant is a vegetable plant, maize plant, soya bean plant, cotton plant, tobacco plant, rice plant, sugar beet plant, oilseed rape plant or potato plant.
10. Method according to any of Claims 1 to 9, characterized in that the use form of the compound of the formula (I) is present in a mixture with at least one mixing partner.
11. Synergistic composition comprising a Bt toxin, preferably a Bt toxin encoded by a bt-gene or fragment thereof comprising event MON87701, and a compound of formula (I) as described in any one of claims 1 to 4.

12. Synergistic composition according to claim 11, characterized in that the Bt toxin is encoded by a cry gene or a cry-gene fragment selected from the group consisting of cry1, cry2, cry3, cry5 and cry9, preferably cry1.
- 5 13. Synergistic composition according to claim 12, characterized in that the Bt toxin is encoded by a cry gene or a cry-gene fragment selected from the subgroup cry1A, especially preferred cry1Aa, cry1Ab and cry1Ac.
14. Synergistic composition according to claim 13, characterized in that the Bt toxin is encoded by a bt-gene or fragment thereof comprising event MON87701.
- 10 15. A Bt plant, characterized in that at least 0.00001 g of a compound of formula (I), preferably compound (I-5), is attached to it.

Fig. 1a: 3 DAA – INF1+3 – Soybean INTACTA



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Fig. 1b: 3 DAA – INF1+3 – Soybean conventional

