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(54) Title: PLANTS HAVING INCREASED TOLERANCE TO HERBICIDES

(57) Abstract: The present invention refers to a method for controlling undesired vegetation at a plant cultivation site, the method comprising the steps of providing, at said site, a plant that comprises at least one nucleic acid comprising a nucleotide sequence encoding a wild-type or a mutated protoporphyrinogen oxidase (PPO) which is resistant or tolerant to a PPO-inhibiting herbicide by applying to said site an effective amount of said herbicide. The invention further refers to plants comprising wild-type or mutated PPO enzymes, and methods of obtaining such plants.

PLANTS HAVING INCREASED TOLERANCE TO HERBICIDES

This application claims priority to US provisional applications number US 61/864671 and US 61/864672 the contents of which are incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

The present invention relates in general to methods for conferring on plants agricultural level tolerance to a herbicide. Particularly, the invention refers to plants having an increased tolerance to PPO-inhibiting herbicides. More specifically, the present invention relates to methods and plants obtained by mutagenesis and cross-breeding and transformation that have an increased tolerance to PPO-inhibiting herbicides.

BACKGROUND OF THE INVENTION

Herbicides that inhibit protoporphyrinogen oxidase (hereinafter referred to as Protox or PPO; EC: 1.3.3.4), a key enzyme in the biosynthesis of protoporphyrin IX, have been used for selective weed control since the 1960s. PPO catalyzes the last common step in chlorophyll and heme biosynthesis which is the oxidation of protoporphyrinogen IX to protoporphyrin IX. (Matringe et al. 1989. Biochem. 1. 260: 231). PPO-inhibiting herbicides include many different structural classes of molecules (Duke et al. 1991 . Weed Sci. 39: 465; Nandihalli et al. 1992. Pesticide Biochem. Physiol. 43: 193; Matringe et al. 1989. FEBS Lett. 245: 35; Yanase and Andoh. 1989. Pesticide Biochem. Physiol. 35: 70). These herbicidal compounds include the diphenylethers {e.g. lactofen, (+-)-2-ethoxy-1-methyl-2-oxoethyl 5-{2-chloro-4-(trifluoromethyl)phenoxy}-2-nitrobenzoate; acifluorfen, 5-{2-chloro-4-(trifluoromethyl)phenoxy}-2-nitrobenzoic acid; its methyl ester; or oxyfluorfen, 2-chloro-1-(3-ethoxy-4-nitrophenoxy)-4-(trifluorobenzene)}, oxidiazoles, (e.g. oxidiazon, 3-{2,4-dichloro-5-(1-methylethoxy)phenyl}-5-(1,1-dimethylethyl)-1 ,3,4-oxadiazol-2-(3H)-one), cyclic imides (e.g. S-23142, N-(4-chloro-2-fluoro-5-propargyloxyphenyl)-3,4,5,6-tetrahydrophthalimide; chlorophthalim, N-(4-chlorophenyl)-3,4,5,6-tetrahydrophthalimide), phenyl pyrazoles (e.g. TNPP-ethyl, ethyl 2-{1 -(2,3,4-trichlorophenyl)-4-nitropyrazolyl-5-oxy}propionate; M&B 39279), pyridine derivatives (e.g. LS 82-556), and phenopylate and its O-phenylpyrrolidino- and piperidinocarbamate analogs. Many of these compounds competitively inhibit the normal reaction catalyzed by the enzyme, apparently acting as substrate analogs.

Application of PPO-inhibiting herbicides results in the accumulation of protoporphyrinogen IX in the chloroplast and mitochondria, which is believed to leak into the cytosol where it is oxidized by a peroxidase. When exposed to light, protoporphyrin IX causes formation of singlet oxygen in the cytosol and the formation of other reactive oxygen species, which can cause lipid peroxidation and membrane disruption leading to rapid cell death (Lee et al. 1993. Plant Physiol. 102: 881).

Not all PPO enzymes are sensitive to herbicides which inhibit plant PPO enzymes. Both the Escherichia coli and Bacillus subtilis PPO enzymes (Sasarmen et al. 1993. Can. J. Microbiol.

39: 1155; Dailey et al. 1994. J. Biol. Chem. 269: 813) are resistant to these herbicidal inhibitors. Mutants of the unicellular alga Chlamydomonas reinhardtii resistant to the phenylimide herbicide S-23142 have been reported (Kataoka et al. 1990. J. Pesticide Sci. 15: 449; Shibata et al. 1992. In Research in Photosynthesis, Vol. III, N. Murata, ed. Kluwer: Netherlands. pp. 567-70). At least one of these mutants appears to have an altered PPO activity that is resistant not only to the herbicidal inhibitor on which the mutant was selected, but also to other classes of protox inhibitors (Oshio et al. 1993. Z. Naturforsch. 48c: 339; Sato et al. 1994. In ACS Symposium on Porphyric Pesticides, S. Duke, ed. ACS Press: Washington, D.C.). A mutant tobacco cell line has also been reported that is resistant to the inhibitor S-21432 (Che et al. 1993. Z. Naturforsch. 48c: 350). Auxotrophic E. coli mutants have been used to confirm the herbicide resistance of cloned plant PPO-inhibting herbicides.

Three main strategies are available for making plants tolerant to herbicides, i.e. (1) detoxifying the herbicide with an enzyme which transforms the herbicide, or its active metabolite, into non-toxic products, such as, for example, the enzymes for tolerance to bromoxynil or to basta (EP242236, EP337899); (2) mutating the target enzyme into a functional enzyme which is less sensitive to the herbicide, or to its active metabolite, such as, for example, the enzymes for tolerance to glyphosate (EP293356, Padgette S. R. et al., J.Biol. Chem., 266, 33, 1991); or (3) overexpressing the sensitive enzyme so as to produce quantities of the target enzyme in the plant which are sufficient in relation to the herbicide, in view of the kinetic constants of this enzyme, so as to have enough of the functional enzyme available despite the presence of its inhibitor. The third strategy was described for successfully obtaining plants which were tolerant to PPO inhibitors (see e.g. US5,767,373 or US5,939,602, and patent family members thereof.). In addition, US 2010/0100988 and WO 2007/024739 discloses nucleotide sequences encoding amino acid sequences having enzymatic activity such that the amino acid sequences are resistant to PPO inhibitor herbicidal chemicals, in particular 3-phenyluracil inhibitor specific PPO mutants.

WO 2012/080975 discloses plants the tolerance of which to a PPO-inhibiting herbicide named "benzoxazinone-derivative" herbicide (1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione) had been increased by transforming said plants with nucleic acids encoding mutated PPO enzymes. In particular, WO 2012/080975 discloses that the introduction of nucleic acids which code for a mutated PPO of an Amaranthus type II PPO in which the Arginine at position 128 had been replaced by a leucine, alanine, or valine, and the phenylalanine at position 420 had been replaced by a methionine, cysteine, isoleucine, leucine, or threonine, confers increased tolerance/resistance to a benzoxazinone-derivative herbicide.

The inventors of the present invention have now surprisingly found that those types of double-mutants and, furthermore, novel substitutions for R128 and F420 which are not disclosed in WO 2012/080975 confer increased tolerance/resistance to a wide variety of PPO inhibitors including, but not limited to a "benzoxazinone-derivative" (1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione) herbicide described in WO 2012/080975. Thus, to date, the prior art has not described

PPO-inhibiting herbicide tolerant plants containing a mutated PPO nucleic acid according to the present invention, which are tolerant/resistant to a broad spectrum of PPO inhibitors. Therefore, what is needed in the art are crop plants and crop plants having increased tolerance to herbicides such as PPO-inhibiting herbicide and containing at least one wildtype and/or mutated PPO nucleic acid according to the present invention. Also needed are methods for controlling weed growth in the vicinity of such crop plants or crop plants. These compositions and methods would allow for the use of spray over techniques when applying herbicides to areas containing crop plants or crop plants.

SUMMARY OF THE INVENTION

The problem is solved by the present invention which refers to a method for controlling undesired vegetation at a plant cultivation site, the method comprising the steps of:

a) providing, at said site, a plant that comprises at least one nucleic acid comprising a nucleotide sequence encoding a wild type protoporphyrinogen oxidase (PPO) or a mutated protoporphyrinogen oxidase (PPO) which is resistant or tolerant to a PPO-inhibiting herbicide,
b) applying to said site an effective amount of said herbicide.

In addition, the present invention refers to a method for identifying a PPO-inhibiting herbicide by using a wild-type or mutated PPO of the present invention encoded by a nucleic acid which comprises the nucleotide sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, or 47, or a variant thereof.

Said method comprises the steps of:

a) generating a transgenic cell or plant comprising a nucleic acid encoding a mutated PPO of the present invention, wherein the mutated PPO of the present invention is expressed;
b) applying a PPO-inhibiting herbicide to the transgenic cell or plant of a) and to a control cell or plant of the same variety;
c) determining the growth or the viability of the transgenic cell or plant and the control cell or plant after application of said test compound, and
d) selecting test compounds which confer reduced growth to the control cell or plant as compared to the growth of the transgenic cell or plant.

Another object refers to a method of identifying a nucleotide sequence encoding a mutated PPO which is resistant or tolerant to a PPO-inhibiting herbicide, the method comprising:

a) generating a library of mutated PPO-encoding nucleic acids,
b) screening a population of the resulting mutated PPO-encoding nucleic acids by expressing each of said nucleic acids in a cell or plant and treating said cell or plant with a PPO-inhibiting herbicide,
c) comparing the PPO-inhibiting herbicide-tolerance levels provided by said population of mutated PPO encoding nucleic acids with the PPO-inhibiting herbicide-tolerance level provided by a control PPO-encoding nucleic acid,
d) selecting at least one mutated PPO-encoding nucleic acid that provides a significantly

increased level of tolerance to a PPO-inhibiting herbicide as compared to that provided by the control PPO-encoding nucleic acid.

In a preferred embodiment, the mutated PPO-encoding nucleic acid selected in step d) provides at least 2-fold as much tolerance to a PPO-inhibiting herbicide as compared to that provided by the control PPO-encoding nucleic acid.

The resistance or tolerance can be determined by generating a transgenic plant comprising a nucleic acid sequence of the library of step a) and comparing said transgenic plant with a control plant.

Another object refers to a method of identifying a plant or algae containing a nucleic acid encoding a mutated PPO which is resistant or tolerant to a PPO-inhibiting herbicide, the method comprising:

a) identifying an effective amount of a PPO-inhibiting herbicide in a culture of plant cells or green algae.
b) treating said plant cells or green algae with a mutagenizing agent,
c) contacting said mutagenized cells population with an effective amount of PPO-inhibiting herbicide, identified in a),
d) selecting at least one cell surviving these test conditions,
e) PCR-amplification and sequencing of PPO genes from cells selected in d) and comparing such sequences to wild-type PPO gene sequences, respectively.

In a preferred embodiment, the mutagenizing agent is ethylmethanesulfonate.

Another object refers to an isolated and/or recombinantly produced and/or chemically synthesized (synthetic) nucleic acid encoding a mutated PPO, the nucleic acid comprising the sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, or 47, or a variant thereof, as defined hereinafter.

Another object refers to an isolated mutated PPO polypeptide, the polypeptide comprising the sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, or 48, a variant, derivative, orthologue, paralogue or homologue thereof, as defined hereinafter.

In a preferred embodiment, the nucleic acid being identifiable by a method as defined above.

In another embodiment, the invention refers to a plant cell transformed by and expressing a wild-type or a mutated PPO nucleic acid according to the present invention or a plant which has been mutated to obtain a plant expressing, preferably over-expressing a wild-type or a mutated PPO nucleic acid according to the present invention, wherein expression of said nucleic acid in the plant cell results in increased resistance or tolerance to a PPO-inhibiting herbicide as compared to a wild type variety of the plant cell.

In another embodiment, the invention refers to a plant comprising a plant cell according to the

present invention, wherein expression of the nucleic acid in the plant results in the plant's increased resistance to PPO-inhibiting herbicide as compared to a wild type variety of the plant.

In another embodiment, the invention refers to a plant that expresses a mutagenized or recombinant mutated PPO polypeptide, and wherein said mutated PPO confers upon the plant increased herbicide tolerance as compared to the corresponding wild-type variety of the plant when expressed therein

The plants of the present invention can be transgenic or non-transgenic.

Preferably, the expression of the nucleic acid of the invention in the plant results in the plant's increased resistance to PPO-inhibiting herbicides as compared to a wild type variety of the plant.

In another embodiment, the invention refers to a method for growing the plant according to the present invention while controlling weeds in the vicinity of said plant, said method comprising the steps of:

a) growing said plant ; and
b) applying a herbicide composition comprising a PPO-inhibiting herbicide to the plant and weeds, wherein the herbicide normally inhibits protoporphyrinogen oxidase, at a level of the herbicide that would inhibit the growth of a corresponding wild-type plant.

In another embodiment, the invention refers to a seed produced by a transgenic plant comprising a plant cell of the present invention, or to a seed produced by the non-transgenic plant that expresses a mutagenized PPO polypeptide, wherein the seed is true breeding for an increased resistance to a PPO-inhibiting herbicide as compared to a wild type variety of the seed.

In another embodiment, the invention refers to a method of producing a transgenic plant cell with an increased resistance to a PPO-inhibiting herbicide as compared to a wild type variety of the plant cell comprising, transforming the plant cell with an expression cassette comprising a wild-type or a mutated PPO nucleic acid.

In another embodiment, the invention refers to a method of producing a transgenic plant comprising, (a) transforming a plant cell with an expression cassette comprising a wild-type or a mutated PPO nucleic acid, and (b) generating a plant with an increased resistance to PPO-inhibiting herbicide from the plant cell.

Preferably, the expression cassette further comprises a transcription initiation regulatory region and a translation initiation regulatory region that are functional in the plant.

In another embodiment, the invention relates to using the mutated PPO of the invention as selectable marker. The invention provides a method of identifying or selecting a transformed plant cell, plant tissue, plant or part thereof comprising a) providing a transformed plant cell,

plant tissue, plant or part thereof, wherein said transformed plant cell, plant tissue, plant or part thereof comprises an isolated nucleic acid encoding a mutated PPO polypeptide of the invention as described hereinafter, wherein the polypeptide is used as a selection marker, and wherein said transformed plant cell, plant tissue, plant or part thereof may optionally comprise a further isolated nucleic acid of interest; b) contacting the transformed plant cell, plant tissue, plant or part thereof with at least one PPO-inhibiting inhibiting compound; c) determining whether the plant cell, plant tissue, plant or part thereof is affected by the inhibitor or inhibiting compound; and d) identifying or selecting the transformed plant cell, plant tissue, plant or part thereof.

The invention is also embodied in purified mutated PPO proteins that contain the mutations described herein, which are useful in molecular modeling studies to design further improvements to herbicide tolerance. Methods of protein purification are well known, and can be readily accomplished using commercially available products or specially designed methods, as set forth for example, in Protein Biotechnology, Walsh and Headon (Wiley, 1994).

In another embodiment, the invention relates to a combination useful for weed control, comprising (a) a polynucleotide encoding a mutated PPO polypeptide according to the present invention, which polynucleotide is capable of being expressed in a plant to thereby provide to that plant tolerance to a PPO inhibiting herbicide; and (b) a PPO inhibiting herbicide.

In another embodiment, the invention relates to a process for preparing a combination useful for weed control comprising (a) providing a polynucleotide encoding a mutated PPO polypeptide according to the present invention, which polynucleotide is capable of being expressed in a plant to thereby provide to that plant tolerance to a PPO inhibiting herbicide; and (b) providing a PPO inhibiting herbicide.

In a preferred embodiment, said step of providing a polynucleotide comprises providing a plant containing the polynucleotide.

In another preferred embodiment, said step of providing a polynucleotide comprises providing a seed containing the polynucleotide.

In another preferred embodiment, said process further comprises a step of applying the PPO inhibiting herbicide to the seed.

In another embodiment, the invention relates to the use of a combination useful for weed control, comprising (a) a polynucleotide encoding a mutated PPO polypeptide according to the present invention, which polynucleotide is capable of being expressed in a plant to thereby provide to that plant tolerance to a PPO inhibiting herbicide; and (b) a PPO inhibiting herbicide, to control weeds at a plant cultivation site.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows an amino acid sequence alignment of Amaranthus tuberculatus (A.tuberculatus), Amaranthus tuberculatus resistant (A.tuberculatus_R), Arabidopsis thaliana long (A.thaliana_2), Spinacia oleracea short (S.oleracea_2), Nicotiana tabacum short (N.tabacum_2), Glycine max (Glycinejmax), Arabidopsis thaliana short (A.thaliana_1), Nicotiana tabacum long (N.tabacurrM), Chlamydomonas reinhardtii long (C.reinhardtiM), Zea mays (Z.mays), Oryza sativa (0.sativa_1), Solanum tuberosum (S.tuberosum), Cucumis sativus (C.sativus), Cichorium intybus (C.intybus_1), Spinacia oleracea long (S.oleracea_1), Polytomella sp. Pringsheim 198.80 (Polytomella) PPO sequences. Conserved regions are indicated in light grey, grey and black.

Figure 2 shows wildtype and transgenic Arabidopsis plants comprising a nucleic encoding a mutated PPO polypeptide (based on SEQ ID NO:2; AMATU_PPO2_R128A_420V); 1 = Kixor [saflufenacil]; **2** = BAS 850H [1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione]; **3** = Spotlight [fluroxypyr]; 4 = Kixor + Spotlight; A = non-transgenic (for any PPOi treatment); **B =** AMATU_PPO2_R128A_420V transgenic plants)

Figure 3 shows T1 Transformed corn 7 days after treatment with 100 g saflufenacil + 50 g ai/ha BAS 850H + 1% (v/v) MSO. Plants were sprayed at the V2-V3 stage. **1** = untransformed control; **2** = Tp-Fdx_AmtuPPX2L_R1 28A_F420V (Transit peptide of Silene pratensis Ferredoxin fused to mutated PPO); **3** = AmtuPPX2L_R128A_F420L

Figure 4 shows TO Transformed corn 3 days after treatment. Plants were sprayed with 0 or 50 g ai/ha BAS 850H + 1% MSO at the V2-V3 stage. **1** = wildtype, **2 =** AmatuPPX2L_R128L_F420M; **3** = AmatuPPX2L_R128A_F420l; 4 = AmatuPPX2L_R128A_F420V; **5** = AmatuPPX2L_R128A_F420L; **6** = AmatuPPX2L-R128M_F420I; **7** = AmatuPPX2L_ R128M_F420L; **8** = AmatuPPX2L_ R128M_F420V

Figure 5 shows T1 transformed soybean 7 days after treatment with the indicated herbicide + 1% (v/v) MSO. Plants were sprayed at the V2-V3 stage; A = unsprayed; **B** = saflufenacil 150 g ai/ha; **C** = BAS 850H 100 g ai/ha; **1** = wildtype control plant; **2** = AmtuPPX2L_R128A_F420M; **3** = AmtuPPX2L_R128A_F420l; 4 = AmtuPPX2L_R128A_F420V;

Figure 6 shows TO Transformed soybean clones 7 days after indicated treatment. Plants were sprayed at the V2-V3 stage; **1** = wildtype control; **2** = AmtuPPX2L_R128L_F420V; A = saflufenacil g ai/ha + 1% MSO; B = BAS 850H g ai/ha + 1% MSO

Figure 7 shows T2 Transformed soybean 4 days after the indicated treatment. Plants were sprayed at the V2-V3 stage. Treatments contained 1% (v/v) MSO (methylated soy oil - based spray adjuvant; also known as Destiny HC); **1** = wildtype; **2** = AmtuPPX2L_R128A_F420V; **3 =** AmtuPPX2L_R128A_F420L; 4 = AmtuPPX2L_R128A_F420M; **5** = AmtuPPX2L_R128A_F420l; A = unsprayed; **B** = 100 g ai/ha saflufenacil+50 g ai/ha BAS 850H; **C** = 200 g ai/ha saflufenacil+100 g ai/ha BAS 850H; D = 100 g ai/ha saflufenacil+140 g ai/ha flumioxazin; **E =** 100 g ai/ha saflufenacil+560 g ai/ha sulfentrazone;

KEY TO SEQUENCE LISTING

Table 1

SEQ. ID NO:	Description	Organism	Gene	Accession No:
1	PPO nucleic acid	Amaranthus tuberculatus	PPX2L_WC	DQ3861 14
2	PPO amino acid	Amaranthus tuberculatus	ABD52326	
3	PPO nucleic acid	Amaranthus tuberculatus	PPX2L_AC	DQ3861 17
4	PPO amino acid	Amaranthus tuberculatus	ABD52329	
5	PPO nucleic acid	Amaranthus tuberculatus	PPX2L_CC_R	DQ3861 18
6	PPO amino acid	Amaranthus tuberculatus	ABD52330	
7	PPO nucleic acid	Amaranthus tuberculatus	PPX2L_AC_R	DQ3861 16
8	PPO amino acid	Amaranthus tuberculatus	ABD52328	
9	PPO nucleic acid	Arabidopsis thaliana	PPX	AB007650
10	PPO amino acid	Arabidopsis thaliana	BAB08301	
11	PPO nucleic acid	Nicotiana tabacum	ppxl	AF0441 28
12	PPO amino acid	Nicotiana tabacum	AAD02290	
13	PPO nucleic acid	Cichorium intybus	PPX1	AF160961
14	PPO amino acid	Cichorium intybus	AF1 60961_1	
15	PPO nucleic acid	Spinacia oleracea	SO-POX1	AB029492
16	PPO amino acid	Spinacia oleracea	BAA96808	
17	PPO nucleic acid	Spinacia oleracea	SO-POX2	AB046993
18	PPO amino acid	Spinacia oleracea	BAB6071 0	
19	PPO nucleic acid	Solanum tuberosum	PPOX	AJ225 107

20	PPO amino acid	Solanum tuberosum	CAA12400	
21	PPO nucleic acid	Zea mays	ZM_BFc0091B03	BT063659
22	PPO amino acid	Zea mays	ACN28356	
23	PPO nucleic acid	Zea mays	prpo2	NM_001 111534
24	PPO amino acid	Zea mays	NP_00 1105004	
25	PPO nucleic acid	Chlamydomonas	Ppx1	AF068635
26	PPO amino acid	Chlamydomonas	AAC79685	
27	PPO nucleic acid	Polytomella	PPO	AF332964
28	PPO amino acid	Polytomella	AF332964_1	
29	PPO nucleic acid	Sorghum bicolor	Hyp. Protein	XM_002446665
30	PPO amino acid	Sorghum bicolor	XP_002446710	
31	PPO nucleic acid	Oryza sativa	PPOX1	AB057771
32	PPO amino acid	Oryza sativa	BAB39760	
33	PPO nucleic acid	Amaranthus tuberculatus	PPX2	DQ3861 13
34	PPO amino acid	Amaranthus tuberculatus	ABD52325	
35	PPO nucleic acid	Arabidopsis thaliana	PPOX	NM_1 78952
36	PPO amino acid	Arabidopsis thaliana	NP_849283	
37	PPO nucleic acid	Nicotiana tabacum	ppxll	AF044129
38	PPO amino acid	Nicotiana tabacum	AAD02291	
39	PPO nucleic acid	Glycine max	hemG	AB025102
40	PPO amino acid	Glycine max	BAA76348	

41	PPO nucleic acid	Cucumis sativus	CsPPO	AB5 12426
42	PPO amino acid	Cucumis sativus	BAH84864.1	
43	PPO nucleic acid	Oryza sativa	Hyp. Protein	AL606613
44	PPO amino acid	Oryza sativa	CAE01661	
45	PPO nucleic acid	Oryza sativa	amine oxidase	
46	PPO amino acid	Oryza sativa	Os04g41 260.1	
47	PPO nucleic acid	Amaranthus tuberculatus	PPX1	
48	PPO amino acid	Amaranthus tuberculatus	PP01	

DETAILED DESCRIPTION

The articles "a" and "an" are used herein to refer to one or more than one (i.e., to at least one) of the grammatical object of the article. By way of example, "an element" means one or more elements.

As used herein, the word "comprising," or variations such as "comprises" or "comprising," will be understood to imply the inclusion of a stated element, integer or step, or group of elements, integers or steps, but not the exclusion of any other element, integer or step, or group of elements, integers or steps.

The inventors of the present invention have found, that the tolerance or resistance of a plant to a PPO-inhibiting herbicide could be remarkably increased by overexpressing a nucleic acid encoding a mutated PPO polypeptide comprising the sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, or 48, a variant, derivative, orthologue, paralogue or homologue thereof.

The present invention refers to a method for controlling undesired vegetation at a plant cultivation site, the method comprising the steps of:

a) providing, at said site, a plant that comprises at least one nucleic acid comprising a nucleotide sequence encoding a wild-type protoporphyrinogen oxidase or a mutated protoporphyrinogen oxidase (mutated PPO) which is resistant or tolerant to a PPO-inhibiting herbicide,
b) applying to said site an effective amount of said herbicide.

The term "control of undesired vegetation" is to be understood as meaning the killing of weeds and/or otherwise retarding or inhibiting the normal growth of the weeds. Weeds, in the broadest

sense, are understood as meaning all those plants which grow in locations where they are undesired, e.g. (crop) plant cultivation sites. The weeds of the present invention include, for example, dicotyledonous and monocotyledonous weeds. Dicotyledonous weeds include, but are not limited to, weeds of the genera: Sinapis, Lepidium, Galium, Stellaria, Matricaria, Anthemis, Galinsoga, Chenopodium, Urtica, Senecio, Amaranthus, Portulaca, Xanthium, Convolvulus, Ipomoea, Polygonum, Sesbania, Ambrosia, Cirsium, Carduus, Sonchus, Solanum, Rorippa, Rotala, Lindernia, Lamium, Veronica, Abutilon, Emex, Datura, Viola, Galeopsis, Papaver, Centaurea, Trifolium, Ranunculus, and Taraxacum. Monocotyledonous weeds include, but are not limited to, weeds of of the genera: Echinochloa, Setaria, Panicum, Digitaria, Phleum, Poa, Festuca, Eleusine, Brachiaria, Lolium, Bromus, Avena, Cyperus, Sorghum, Agropyron, Cynodon, Monochoria, Fimbristyslis, Sagittaria, Eleocharis, Scirpus, Paspalum, Ischaemum, Sphenoclea, Dactyloctenium, Agrostis, Alopecurus, and Apera. In addition, the weeds of the present invention can include, for example, crop plants that are growing in an undesired location. For example, a volunteer maize plant that is in a field that predominantly comprises soybean plants can be considered a weed, if the maize plant is undesired in the field of soybean plants.

The term "plant" is used in its broadest sense as it pertains to organic material and is intended to encompass eukaryotic organisms that are members of the Kingdom Plantae, examples of which include but are not limited to vascular plants, vegetables, grains, flowers, trees, herbs, bushes, grasses, vines, ferns, mosses, fungi and algae, etc, as well as clones, offsets, and parts of plants used for asexual propagation (e.g. cuttings, pipings, shoots, rhizomes, underground stems, clumps, crowns, bulbs, corms, tubers, rhizomes, plants/tissues produced in tissue culture, etc.). The term "plant" further encompasses whole plants, ancestors and progeny of the plants and plant parts, including seeds, shoots, stems, leaves, roots (including tubers), flowers, florets, fruits, pedicles, peduncles, stamen, anther, stigma, style, ovary, petal, sepal, carpel, root tip, root cap, root hair, leaf hair, seed hair, pollen grain, microspore, cotyledon, hypocotyl, epicotyl, xylem, phloem, parenchyma, endosperm, a companion cell, a guard cell, and any other known organs, tissues, and cells of a plant, and tissues and organs, wherein each of the aforementioned comprise the gene/nucleic acid of interest. The term "plant" also encompasses plant cells, suspension cultures, callus tissue, embryos, meristematic regions, gametophytes, sporophytes, pollen and microspores, again wherein each of the aforementioned comprises the gene/nucleic acid of interest.

Plants that are particularly useful in the methods of the invention include all plants which belong to the superfamily Viridiplantae, in particular monocotyledonous and dicotyledonous plants including fodder or forage legumes, ornamental plants, food crops, trees or shrubs selected from the list comprising Acer spp., Actinidia spp., Abelmoschus spp., Agave sisalana, Agropyron spp., Agrostis stolonifera, Allium spp., Amaranthus spp., Ammophila arenaria, Ananas comosus, Annona spp., Apium graveolens, Arachis spp, Artocarpus spp., Asparagus officinalis, Avena spp. (e.g. Avena sativa, Avena fatua, Avena byzantina, Avena fatua var. sativa, Avena hybrida), Averrhoa carambola, Bambusa sp., Benincasa hispida, Bertholletia excelsea, Beta vulgaris, Brassica spp. (e.g. Brassica napus, Brassica rapa ssp. [canola, oilseed rape, turnip rape]), Cadaba farinosa, Camellia sinensis, Canna indica, Cannabis sativa,

Capsicum spp., Carex elata, Carica papaya, Carissa macrocarpa, Carya spp., Carthamus tinctorius, Castanea spp., Ceiba pentandra, Cichorium endivia, Cinnamomum spp., Citrullus lanatus, Citrus spp., Cocos spp., Coffea spp., Colocasia esculenta, Cola spp., Corchorus sp., Coriandrum sativum, Corylus spp., Crataegus spp., Crocus sativus, Cucurbita spp., Cucumis spp., Cynara spp., Daucus carota, Desmodium spp., Dimocarpus longan, Dioscorea spp., Diospyros spp., Echinochloa spp., Elaeis (e.g. Elaeis guineensis, Elaeis oleifera), Eleusine coracana, Eragrostis tef, Erianthus sp., Eriobotrya japonica, Eucalyptus sp., Eugenia uniflora, Fagopyrum spp., Fagus spp., Festuca arundinacea, Ficus carica, Fortunella spp., Fragaria spp., Ginkgo biloba, Glycine spp. (e.g. Glycine max, Soja hispida or Soja max), Gossypium hirsutum, Helianthus spp. (e.g. Helianthus annuus), Hemerocallis fulva, Hibiscus spp., Hordeum spp. (e.g. Hordeum vulgare), Ipomoea batatas, Juglans spp., Lactuca sativa, Lathyrus spp., Lens culinaris, Linum usitatissimum, Litchi chinensis, Lotus spp., Luffa acutangula, Lupinus spp., Luzula sylvatica, Lycopersicon spp. (e.g. Lycopersicon esculentum, Lycopersicon lycopersicum, Lycopersicon pyriforme), Macrotyloma spp., Malus spp., Malpighia emarginata, Mammea americana, Mangifera indica, Manihot spp., Manilkara zapota, Medicago sativa, Melilotus spp., Mentha spp., Miscanthus sinensis, Momordica spp., Morus nigra, Musa spp., Nicotiana spp., Olea spp., Opuntia spp., Ornithopus spp., Oryza spp. (e.g. Oryza sativa, Oryza latifolia), Panicum miliaceum, Panicum virgatum, Passiflora edulis, Pastinaca sativa, Pennisetum sp., Persea spp., Petroselinum crispum, Phalaris arundinacea, Phaseolus spp., Phleum pratense, Phoenix spp., Phragmites australis, Physalis spp., Pinus spp., Pistacia vera, Pisum spp., Poa spp., Populus spp., Prosopis spp., Prunus spp., Psidium spp., Punica granatum, Pyrus communis, Quercus spp., Raphanus sativus, Rheum rhabarbarum, Ribes spp., Ricinus communis, Rubus spp., Saccharum spp., Salix sp., Sambucus spp., Secale cereale, Sesamum spp., Sinapis sp., Solanum spp. (e.g. Solanum tuberosum, Solanum integrifolium or Solanum lycopersicum), Sorghum bicolor, Spinacia spp., Syzygium spp., Tagetes spp., Tamarindus indica, Theobroma cacao, Trifolium spp., Tripsacum dactyloides, Triticosecale rimpaui, Triticum spp. (e.g. Triticum aestivum, Triticum durum, Triticum turgidum, Triticum hybernum, Triticum macha, Triticum sativum, Triticum monococcum or Triticum vulgare), Tropaeolum minus, Tropaeolum majus, Vaccinium spp., Vicia spp., Vigna spp., Viola odorata, Vitis spp., Zea mays, Zizania palustris, Ziziphus spp., amaranth, artichoke, asparagus, broccoli, Brussels sprouts, cabbage, canola, carrot, cauliflower, celery, collard greens, flax, kale, lentil, oilseed rape, okra, onion, potato, rice, soybean, strawberry, sugar beet, sugar cane, sunflower, tomato, squash, tea and algae, amongst others. According to a preferred embodiment of the present invention, the plant is a crop plant. Examples of crop plants include inter alia soybean, sunflower, canola, alfalfa, rapeseed, cotton, tomato, potato or tobacco. Further preferebly, the plant is a monocotyledonous plant, such as sugarcane. Further preferably, the plant is a cereal, such as rice, maize, wheat, barley, millet, rye, sorghum or oats.

In a preferred embodiment, the plant has been previously produced by a process comprising recombinantly preparing a plant by introducing and over-expressing a wild-type or mutated PPO transgene according to the present invention, as described in greater detail hereinfter.

In another preferred embodiment, the plant has been previously produced by a process comprising in situ mutagenizing plant cells, to obtain plant cells which express a mutated PPO.

As disclosed herein, the nucleic acids of the invention find use in enhancing the herbicide tolerance of plants that comprise in their genomes a gene encoding a herbicide-tolerant wild-type or mutated PPO protein. Such a gene may be an endogenous gene or a transgene, as described hereinafter.

Therefore, in another embodiment the present invention refers to a method of increasing or enhancing the PPO-inhibitor herbicide tolerance or resistance of a plant, the method comprising overexpressing a nucleic acid encoding a mutated PPO polypeptide comprising the sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, or 48, a variant, derivative, orthologue, paralogue or homologue thereof.

Additionally, in certain embodiments, the nucleic acids of the present invention can be stacked with any combination of polynucleotide sequences of interest in order to create plants with a desired phenotype. For example, the nucleic acids of the present invention may be stacked with any other polynucleotides encoding polypeptides having pesticidal and/or insecticidal activity, such as, for example, the Bacillus thuringiensis toxin proteins (described in U.S. Patent Nos. 5,366,892; 5,747,450; 5,737,514; 5,723,756; 5,593,881 ; and Geiser et al (1986) Gene 48: 109).

By way of example, polynucleotides that may be stacked with the nucleic acids of the present invention include nucleic acids encoding polypeptides conferring resistance to pests/pathogens such as viruses, nematodes, insects or fungi, and the like. Exemplary polynucleotides that may be stacked with nucleic acids of the invention include polynucleotides encoding: polypeptides having pesticidal and/or insecticidal activity, such as other Bacillus thuringiensis toxic proteins (described in U.S. Pat. Nos. 5,366,892; 5,747,450; 5,737,514; 5,723,756; 5,593,881 ; and Geiser et al., (1986) Gene 48:109), lectins (Van Damme et al. (1994) Plant Mol. Biol. 24:825, pentin (described in U.S. Pat. No. 5,981 ,722), and the like; traits desirable for disease or herbicide resistance (e.g., fumonisin detoxification genes (U.S. Pat. No. 5,792,931); avirulence and disease resistance genes (Jones et al. (1994) Science 266:789; Martin et al., (1993) Science 262:1432; Mindrinos et al. (1994) Cell 78:1089); acetolactate synthase (ALS) mutants that lead to herbicide resistance such as the S4 and/or Hra mutations; glyphosate resistance (e.g., 5-enol-pyrovyl-shikimate-3-phosphate-synthase (EPSPS) gene, described in U.S. Pat. Nos. 4,940,935 and 5,188,642; or the glyphosate N-acetyltransferase (GAT) gene, described in Castle et al. (2004) Science, 304:1 151-1 154; and in U.S. Patent App. Pub. Nos. 20070004912, 20050246798, and 20050060767)); glufosinate resistance (e.g, phosphinothricin acetyl transferase genes PAT and BAR, described in U.S. Pat. Nos. 5,561 ,236 and 5,276,268); resistance to herbicides including sulfonyl urea, DHT (2,4D), and PPO herbicides (e.g., glyphosate acetyl transferase, aryloxy alkanoate dioxygenase, acetolactate synthase, and protoporphyrinogen oxidase); a cytochrome P450 or variant thereof that confers herbicide resistance or tolerance to, inter alia, HPPD herbicides (U.S. patent application Ser. No. 12/156,247; U.S. Pat. Nos. 6,380,465; 6,121 ,512; 5,349,127; 6,649,814; and 6,300,544; and PCT Patent App. Pub. No. WO2007000077); and traits desirable for processing or process products such as high oil (e.g., U.S. Pat. No. 6,232,529); modified oils (e.g., fatty acid desaturase genes (U.S. Pat. No. 5,952,544; WO 94/1 1516)); modified starches (e.g., ADPG pyrophosphorylases (AGPase), starch synthases (SS), starch branching enzymes (SBE), and

starch debranching enzymes (SDBE)); and polymers or bioplastics (e.g., U.S. Pat. No. 5,602,321; beta-ketothiolase, polyhydroxybutyrate synthase, and acetoacetyl-CoA reductase (Schubert et al. (1988) J. Bacteriol. 170:5837-5847) facilitate expression of polyhydroxyalkanoates (PHAs)); the disclosures of which are herein incorporated by reference.

In a particularly preferred embodiment, the plant comprises at least one additional heterologous nucleic acid comprising a nucleotide sequence encoding a herbicide tolerance enzyme selected, for example, from the group consisting of 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS), Glyphosate acetyl transferase (GAT), Cytochrome P450, phosphinothricin acetyltransferase (PAT), Acetohydroxyacid synthase (AHAS; EC 4.1 .3.18, also known as acetolactate synthase or ALS), Protoporphyrinogen oxidase (PPGO), Phytoene desaturase (PD) and dicamba degrading enzymes as disclosed in WO 02/068607. The combinations generated can also include multiple copies of any one of the polynucleotides of interest.

Generally, the term "herbicide" is used herein to mean an active ingredient that kills, controls or otherwise adversely modifies the growth of plants. The preferred amount or concentration of the herbicide is an "effective amount" or "effective concentration." By "effective amount" and "effective concentration" is intended an amount and concentration, respectively, that is sufficient to kill or inhibit the growth of a similar, wild-type, plant, plant tissue, plant cell, or host cell, but that said amount does not kill or inhibit as severely the growth of the herbicide-resistant plants, plant tissues, plant cells, and host cells of the present invention. Typically, the effective amount of a herbicide is an amount that is routinely used in agricultural production systems to kill weeds of interest. Such an amount is known to those of ordinary skill in the art. Herbicidal activity is exhibited by herbicides useful for the the present invention when they are applied directly to the plant or to the locus of the plant at any stage of growth or before planting or emergence. The effect observed depends upon the plant species to be controlled, the stage of growth of the plant, the application parameters of dilution and spray drop size, the particle size of solid components, the environmental conditions at the time of use, the specific compound employed, the specific adjuvants and carriers employed, the soil type, and the like, as well as the amount of chemical applied. These and other factors can be adjusted as is known in the art to promote non-selective or selective herbicidal action. Generally, it is preferred to apply the herbicide postemergence to relatively immature undesirable vegetation to achieve the maximum control of weeds.

By a "herbicide-tolerant" or "herbicide-resistant" plant, it is intended that a plant that is tolerant or resistant to at least one herbicide at a level that would normally kill, or inhibit the growth of, a normal or wild-type plant. By "herbicide-tolerant wildtype or mutated PPO protein" or "herbicide - resistant wildtype or mutated PPO protein", it is intended that such a PPO protein displays higher PPO activity, relative to the PPO activity of a wild-type PPO protein, when in the presence of at least one herbicide that is known to interfere with PPO activity and at a concentration or level of the herbicide that is known to inhibit the PPO activity of the wild-type mutated PPO protein. Furthermore, the PPO activity of such a herbicide-tolerant or herbicide-resistant mutated PPO protein may be referred to herein as "herbicide-tolerant" or "herbicide-resistant" PPO activity.

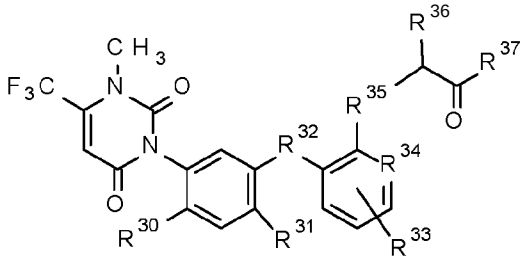
Generally, if the PPO-inhibiting herbicides (also referred to as compounds A) and/or the herbicidal compounds B as described herein, which can be employed in the context of the present invention, are capable of forming geometrical isomers, for example E/Z isomers, it is possible to use both, the pure isomers and mixtures thereof, in the compositions useful for the present the invention. If the PPO-inhibting herbicides A and/or the herbicidal compounds B as described herein have one or more centers of chirality and, as a consequence, are present as enantiomers or diastereomers, it is possible to use both, the pure enantiomers and diastereomers and their mixtures, in the compositions according to the invention. If the PPO-inhibting herbicides A and/or the herbicidal compounds B as described herein have ionizable functional groups, they can also be employed in the form of their agriculturally acceptable salts. Suitable are, in general, the salts of those cations and the acid addition salts of those acids whose cations and anions, respectively, have no adverse effect on the activity of the active compounds. Preferred cations are the ions of the alkali metals, preferably of lithium, sodium and potassium, of the alkaline earth metals, preferably of calcium and magnesium, and of the transition metals, preferably of manganese, copper, zinc and iron, further ammonium and substituted ammonium in which one to four hydrogen atoms are replaced by C_{1-C4}-alkyl, hydroxy-C_{i-C4}-alkyl, C_{i-C4}-alkoxy-C_{i-C4}-alkyl, hydroxy-C_{i-C4}-alkoxy-C_{i-C4}-alkyl, phenyl or benzyl, preferably ammonium, methylammonium, isopropylammonium, dimethylammonium, diisopropylammonium, trimethylammonium, heptylammonium, dodecylammonium, tetradecylammonium, tetramethylammonium, tetraethylammonium, tetrabutylammonium, 2-hydroxyethylammonium (olamine salt), 2-(2-hydroxyeth-1-oxy)eth-1-ylammonium (diglycolamine salt), di(2-hydroxyeth-1-yl)ammonium (diolamine salt), tris(2-hydroxyethyl)ammonium (trolamine salt), tris(2-hydroxypropyl)ammonium, benzyltrimethylammonium, benzyltriethylammonium, N,N,N-trimethylethanolammonium (choline salt), furthermore phosphonium ions, sulfonium ions, preferably tri(C_1-C_4-alkyl)sulfonium, such as trimethylsulfonium, and sulfoxonium ions, preferably tri(C_{i}-C_4-alkyl)sulfoxonium, and finally the salts of polybasic amines such as N,N-bis-(3-aminopropyl)methylamine and diethylenetriamine. Anions of useful acid addition salts are primarily chloride, bromide, fluoride, iodide, hydrogensulfate, methylsulfate, sulfate, dihydrogenphosphate, hydrogenphosphate, nitrate, bicarbonate, carbonate, hexafluorosilicate, hexafluorophosphate, benzoate and also the anions of C_{i}-C_4-alkanoic acids, preferably formate, acetate, propionate and butyrate.

The PPO-inhibting herbicides A and/or the herbicidal compounds B as described herein having a carboxyl group can be employed in the form of the acid, in the form of an agriculturally suitable salt as mentioned above or else in the form of an agriculturally acceptable derivative, for example as amides, such as mono- and di-C_{1-C6}-alkylamides or arylamides, as esters, for example as allyl esters, propargyl esters, C_1-C_{10}-alkyl esters, alkoxyalkyl esters, tefuryl ((tetrahydrofuran-2-yl)methyl) esters and also as thioesters, for example as C_{i}-C_{io}-alkylthio esters. Preferred mono- and di-C_{i-C6}-alkylamides are the methyl and the dimethylamides. Preferred arylamides are, for example, the anilides and the 2-chloroanilides. Preferred alkyl esters are, for example, the methyl, ethyl, propyl, isopropyl, butyl, isobutyl, pentyl, mexyl (1-methylhexyl), meptyl (1-methylheptyl), heptyl, octyl or isooctyl (2-ethylhexyl) esters. Preferred C_{i}-C_4-alkoxy-C_{i}-C_4-alkyl esters are the straight-chain or branched C_{i}-C_4-alkoxy ethyl esters, for example the 2-methoxyethyl, 2-ethoxyethyl, 2-butoxyethyl (butotyl), 2-butoxypropyl or 3-

butoxypropyl ester. An example of a straight-chain or branched C_1-C_{10}-alkylthio ester is the ethylthio ester.

Examples of PPO inhibiting herbicides which can be used according to the present invention are acifluorfen, acifluorfen-sodium , aclonifen, azafenidin, bencarbazone, benzfendizone, bifenox, butafenacil, carfentrazone, carfentrazone-ethyl, chlomethoxyfen, cinidon-ethyl, fluazolate, flufenpyr, flufenpyr-ethyl , flumiclorac, flumiclorac-pentyl , flumioxazin, fluoroglycofen, fluoroglycofen-ethyl, fluthiacet, fluthiacet-methyl, fomesafen, halosafen, lactofen, oxadiargyl, oxadiazon, oxyfluorfen, pentoxazone, profluazol, pyraclonil, pyraflufen, pyraflufen-ethyl, saflufenacil, sulfentrazone, thidiazimin, tiafenacil , chlornitrofen, flumipropyn, fluoronitrofen, flupropacil, furyloxyfen, nitrofluorfen, ethyl [3-[2-chloro-4-fluoro-5-(1 -methyl-6-trifluoromethyl-2,4-dioxo-1 ,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31 -6; S-3 100), N-ethyl-3-2,6-dichloro-4-trifluoromethylphenoxy)-5-methyl-1 /-/-pyrazole-1 -carboxamide (CAS 452098-92-9), N-tetrahydrofurfuryl-3-(2,6-dichloro-4-trifluoromethylphenoxy)-5-methyl-1 *H*-pyrazole-1 -carboxamide (CAS 9 15396-43-9), N-ethyl-3-(2-chloro-6-fluoro-4-trifluoromethyl-phenoxy)-5-methyl-1 /-/-pyrazole-1 -carboxamide (CAS 452099-05-7), N-tetrahydrofurfuryl-3-(2-chloro-6-fluoro-4-trifluoromethylphenoxy)-5-methyl-1 /-/-pyrazole-1 -carboxamide (CAS 4521 00-03-7), 3-[7-fluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl]-1 ,5-dimethyl-6-thioxo-[1 ,3,5]triazinan-2,4-dione (CAS 451484-50-7), 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), 2-(2,2,7-Trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl)-4,5,6,7-tetrahydro-isoindole-1 ,3-dione (CAS 13001 18-96-0), 1-Methyl-6-trifluoromethyl-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl)-1 H-pyrimidine-2,4-dione, methyl (E)-4-[2-chloro-5-[4-chloro-5-(difluoromethoxy)-1 /-/-methyl-pyrazol-3-yl]-4-fluoro-phenoxy]-3-methoxy-but-2-enoate [CAS 948893-00-37, 3-[7-Chloro-5-fluoro-2-(trifluoromethyl)-1H-benzimidazol-4-yl]-1 -methyl-6-(trifluoromethyl)-1 H-pyrimidine-2,4-dione (CAS 2 12754-02-4), and

uracils of formula III



III,

wherein

R^{30} and R^{31} independently of one another are F, Cl or CN;

R^{32} is O or S;

R^{33} is H, F, Cl, CH_3 or OCH_3;

R^{34} is CH or N;

R^{35} is O or S;

R^{36} is H, CN, CH_3, CF_3, OCH_3, OC_2H_5, SCH_3, SC_2H_5, $(CO)OC_2H_5$ or CH_2R^{38},

wherein R^{38} is F, Cl, OCH_3, SCH_3, SC_2H_5, CH_2F, CH_2Br or CH_2OH;

and

R^{37} is (Ci-C_6-alkyl)amino, (C_1-C_6-dialkyl)amino, (NH)OR^{39}, OH, OR^{40} or SR^{40}

wherein R^{39} is CH_3, C_2H_5 or phenyl; and

R^{40} is independently of one another Ci-C6 -alkyl, C_2-C6 -alkenyl, C3-C6-alkynyl, Ci-C6 -haloalkyl, Ci-C6 -alkoxy-Ci-Cs-alkyl, Ci-C6 -alkoxy-Ci-C_6-alkoxy-Ci-C6 -alkyl, C_2-C6 -cyanoalkyl, Ci-C_4-alkoxy-carbonyl-Ci-C_4-alkyl, Ci-C4 -alkyl-carbonyl-amino, Ci-C6 -alkylsulfinyl-Ci-C6-alkyl, Ci-C_6-alkyl-sulfonyl-Ci-C6-alkyl, Ci-C6 -dialkoxy-Ci-C6-alkyl, Ci-C6 -alkyl-carbonyloxy-Ci-C6-alkyl, phenyl-carbonyl-Ci-C6-alkyl, tri(C_1-C3 -alkyl)-silyl-Ci-Ce-alkyl, tri(C_1-C3 -alkyl)-silyl-Ci-C_6-alkenyl, tri(Ci-C_3-alkyl)-silyl-C_1-Ce -alkynyl, tri(Ci-C3-alkyl)-silyl-Ci-C6-alkoxy-Ci-C6-alkyl, dimethylamino, tetrahydropyranyl, tetrahydrofuranyl-Ci-C_3-alkyl, phenyl-Ci-C6 -alkoxy-Ci-C6-alkyl, phenyl-Ci-C3-alkyl, pyridyl-Ci-C3-alkyl, pyridyl, phenyl,

which pyridyls and phenyls independently of one another are substituted by one to five substituents selected from the group consisting of halogen, Ci-C_3-alkyl or Ci-C_2-haloalkyl;

C3-C6 -cycloalkyl or C_3-C6 -cycloalkyl-Ci-C_4-alkyl,

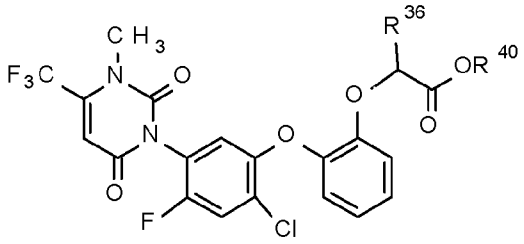
which cycloalkyls indenpently of one another are unsubstituted or substituted by one to five substituents selected from the group consisting of halogen, Ci-C_3-alkyl and Ci-C_2-haloalkyl;

including their agriculturally acceptable alkali metal salts or ammonium salts.

Preferred PPO-inhibiting herbicides that can be used according to the present invention are: Acifluorfen, acifluorfen-sodium, azafenidin, bencarbazone, benzfendizone, butafenacil, carfentrazone-ethyl, cinidon-ethyl, flufenpyr-ethyl, flumiclorac-pentyl, flumioxazin, fluoroglycofen-ethyl, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxadiazon, oxyfluorfen, pentoxazone, pyraflufen-ethyl, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]-acetate (CAS 353292-31-6; S-3100), N-ethyl-3-(2,6-dichloro-4-trifluoromethylphenoxy)-5-methyl-1 H-pyrazole-1 -carboxamide (CAS 452098-92-9), N-tetrahydrofurfuryl-3-(2,6-dichloro-4-trifluoromethylphenoxy)-5-methyl-1 /-/-pyrazole-1-carboxamide (CAS 915396-43-9), N-ethyl-3-(2-chloro-6-fluoro-4-trifluoromethylphenoxy)-5-methyl-1 H-pyrazole-1 -carboxamide (CAS 452099-05-7), N-tetrahydrofurfuryl-3-(2-chloro-6-fluoro-4-trifluoromethylphenoxy)-5-methyl-1 /-/-pyrazole-1-carboxamide (CAS 452100-03-7), 3-[7-fluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl]-1 ,5-dimethyl-6-thioxo-[1 ,3,5]triazinan-2,4-dione (CAS 451484-50-7), 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), 2-(2,2,7-Trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl)-4,5,6,7-tetrahydro-isoindole-1 ,3-dione (CAS 13001 18-96-0);1-Methyl-6-trifluoromethyl-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl)-1 H-pyrimidine-2,4-dione (CAS 13041 13-05-0), 3-[7-Chloro-5-fluoro-2-(trifluoromethyl)-l H-benzimidazol-4-yl]-1-methyl-6-(trifluoromethyl)-1 H-pyrimidine-2,4-dione

(CAS 212754-02-4)

uracils of formula 111.1 (corresponding to uracils of formula III, wherein R^{30} is F, R^{31} is Cl, R^{32} is O; R^{33} is H; R^{34} is CH; R^{35} is O and R^{37} is OR^{40})



III.1,

wherein

R^{36} is OCH_3, OC2H5, SCH_3 or SC2H5;

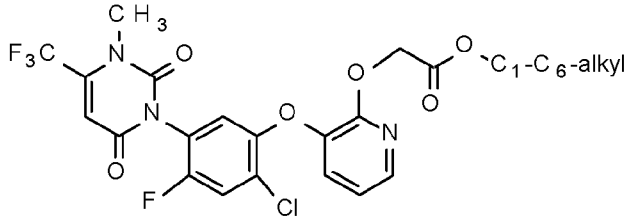
and

R^{40} is Ci-C_6-alkyl, C_2-C_6-alkenyl, C_3-C_3-alkynyl, Ci-C_6-haloalkyl, Ci-C_6-alkoxy-Ci-C_6-alkyl, Ci-C6-alkoxy-CrC6-alkoxy-Ci-C6-alkyl, Ci-C3-cyanoalkyl, phenyl-Ci-C3-alkyl, pyridyl-Ci-C_3-alkyl, C_{3-C6}-cycloalkyl or C_{3-C6}-cycloalkyl-Ci-C4-alkyl,

which cycloalkyls are unsubstituted or substituted by one to five substituents selected from the group consisting of halogen, Ci-C3-alkyl and Ci-C2-haloalkyl;

and

uracils of formula III.2 (corresponding to uracils of formula III, wherein R^{30} is F; R^{31} is Cl; R^{32} is O; R^{33} is H; R^{34} is N; R^{35} is O and R^{37} is OR^{40} with R^{40} is Ci-C_6-alkyl)

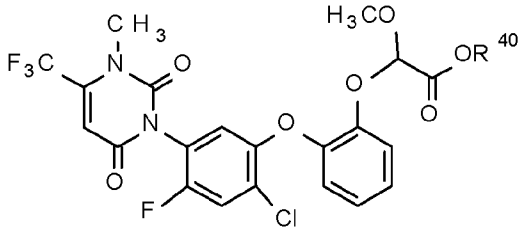


III.2,

Particularly preferred PPO-inhibiting herbicides that can be used according to the present invention are:

acifluorfen, acifluorfen-sodium, butafenacil, carfentrazone-ethyl, cinidon-ethyl, flumioxazin, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)-phenoxy]-2-pyridyloxy]acetate (CAS 353292-31-6; S-3100), 3-[7-fluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[1,4]oxazin-6-yl]-1,5-dimethyl-6-thioxo-[1,3,5]triazinan-2,4-dione (CAS 451484-50-7), 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione (CAS 1258836-72-4), and 2-(2,2,7-Trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1,4]oxazin-6-yl)-4,5,6,7-tetrahydro-isoindole-1,3-dione (CAS 13001 18-96-0), 1-Methyl-6-trifluoromethyl-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1,4]oxazin-6-yl)-1 H-pyrimidine-2,4-dione (CAS 13041 13-05-0),

uracils of formula III.1.1 (corresponding to uracils of formula III, wherein R^{30} is F, R^{31} is Cl, R^{32} is O; R^{33} is H; R^{34} is CH; R^{35} is O, R^{36} is OCH_3 and R^{37} is OR^{40})



III.1.1,

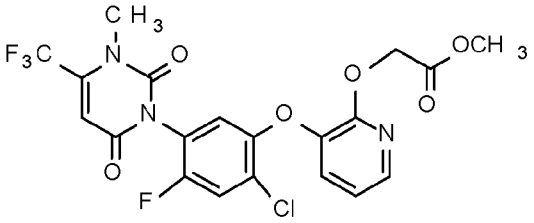
wherein

R^{40} is Ci-C_6-alkyl, C_2-C_6-alkenyl, C_3-C_6-alkynyl, Ci-C_6-haloalkyl, Ci-C_6-alkoxy-Ci-C_6-alkyl, Ci-C6-alkoxy-Ci-C6-alkoxy-Ci-C6-alkyl, Ci-C3-cyanoalkyl, phenyl-Ci-C3-alkyl, pyridyl-Ci-C3-alkyl, C_{3-C6}-cycloalkyl or C_{3-C6}-cycloalkyl-Ci-C_4-alkyl,

which cycloalkyls are unsubstituted or substituted by one to five substituents selected from the group consisting of halogen, Ci-C3-alkyl andCi-C2-haloalkyl;

is preferably CH_3, CH2CH2OC2H5, CH_2CHF_2, cyclohexyl, (1-methylcyclopropyl)methyl or CH2 (pyridine-4-yl);

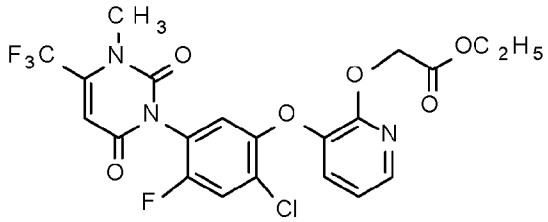
uracils of formula III.2.1 (corresponding to uracils of formula III, wherein R^{30} is F; R^{31} is Cl; R^{32} is O; R^{33} is H; R^{34} is N; R^{35} is O and R^{37} is OR^{40} with R^{40} is CH_3)



III.2.1,

and

uracils of formula III.2.2 (corresponding to uracils of formula III, wherein R^{30} is F; R^{31} is Cl; R^{32} is O; R^{33} is H; R^{34} is N; R^{35} is O and R^{37} is OR^{40} with R^{40} is C2H5)



III.2.2,

Especially preferred PPO-inhibiting herbicides are the PPO-inhibiting herbicides. 1 to A.14 listed below in table A:

Table A

A.1	acifluorfen
A.2	butafenacil
A.3	carfentrazone-ethyl
A.4	cinidon-ethyl
A.5	flumioxazin
A.6	fluthiacet-methyl

A.7	fomesafen
A.8	lactofen
A.9	oxadiargyl
A.10	oxyfluorfen
A.1 1	saflufenacil
A.12	sulfentrazone
A.13	ethyl [3-[2-chloro-4-fluoro-5-(1 -methyl-6-trifluoromethyl-2,4-dioxo-1 ,2,3,4-tetra-hydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31 -6)
A.14	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4)

The PPO-inhibiting herbicides described above that are useful to carry out the present invention are often best applied in conjunction with one or more other herbicides to obtain control of a wider variety of undesirable vegetation. For example, PPO-inhibiting herbicides may further be used in conjunction with additional herbicides to which the crop plant is naturally tolerant, or to which it is resistant via expression of one or more additional transgenes as mentioned supra, or to which it is resistant via mutagenesis and breeding methods as described hereinafter.
When used in conjunction with other targeting herbicides, the PPO-inhibiting herbicides, to which the plant of the present invention had been made resistant or tolerant, can be formulated with the other herbicide or herbicides, tank mixed with the other herbicide or herbicides, or applied sequentially with the other herbicide or herbicides.

Suitable components for mixtures are, for example, selected from the herbicides of class b1) to b15)

B) herbicides of class b1) to b15):

- b1) lipid biosynthesis inhibitors;
- b2) acetolactate synthase inhibitors (ALS inhibitors);
- b3) photosynthesis inhibitors;
- b4) protoporphyrinogen-IX oxidase inhibitors,
- b5) bleacher herbicides;
- b6) enolpyruvyl shikimate 3-phosphate synthase inhibitors (EPSP inhibitors);
- b7) glutamine synthetase inhibitors;
- b8) 7,8-dihydropteroate synthase inhibitors (DHP inhibitors);
- b9) mitosis inhibitors;
- b1O) inhibitors of the synthesis of very long chain fatty acids (VLCFA inhibitors);
- b11) cellulose biosynthesis inhibitors;
- b12) decoupler herbicides;
- b13) auxinic herbicides;
- b14) auxin transport inhibitors; and
- b15) other herbicides selected from the group consisting of bromobutide, chlorflurenol, chlorflurenol-methyl, cinmethylin, cumyluron, dalapon, dazomet, difenzoquat, difenzoquat-metilsulfate, dimethipin, DSMA, dymron, endothal and its salts, etobenzanid, flamprop, flamprop-isopropyl, flamprop-methyl, flamprop-M-

isopropyl, flamprop-M-methyl, flurenol, flurenol-butyl, flurprimidol, fosamine, fosamine-ammonium, indanofan, indaziflam, maleic hydrazide, mefluidide, metam, methiozolin (CAS 403640-27-7), methyl azide, methyl bromide, methyl-dymron, methyl iodide, MSMA, oleic acid, oxaziclomefone, pelargonic acid, pyributicarb, quinoclamine, triaziflam, tridiphane and 6-chloro-3-(2-cyclopropyl-6-methylphenoxy)-4-pyridazinol (CAS 499223-49-3) and its salts and esters;

including their agriculturally acceptable salts or derivatives.

Examples of herbicides B which can be used in combination with the PPO-inhibiting herbicides according to the present invention are:

b1) from the group of the lipid biosynthesis inhibitors:
ACC-herbicides such as alloxydim, alloxydim-sodium, butroxydim, clethodim, clodinafop, clodinafop-propargyl, cycloxydim, cyhalofop, cyhalofop-butyl, diclofop, diclofop-methyl, fenoxaprop, fenoxaprop-ethyl, fenoxaprop-P, fenoxaprop-P-ethyl, fluazifop, fluazifop-butyl, fluazifop-P, fluazifop-P-butyl, haloxyfop, haloxyfop-methyl, haloxyfop-P, haloxyfop-P-methyl, metamifop, pinoxaden, profoxydim, propaquizafop, quizalofop, quizalofop-ethyl, quizalofop-tefuryl, quizalofop-P, quizalofop-P-ethyl, quizalofop-P-tefuryl, sethoxydim, tepraloxydim, tralkoxydim,
4-(4'-Chloro-4-cyclopropyl-2'-fluoro[1,1'-biphenyl]-3-yl)-5-hydroxy-2,2,6,6-tetramethyl-2H-pyran-3(6H)-one (CAS 1312337-72-6); 4-(2',4'-Dichloro-4-cyclopropyl[1,1'-biphenyl]-3-yl)-5-hydroxy-2,2,6,6-tetramethyl-2H-pyran-3(6H)-one (CAS 1312337-45-3); 4-(4'-Chloro-4-ethyl-2'-fluoro[1,1'-biphenyl]-3-yl)-5-hydroxy-2,2,6,6-tetramethyl-2H-pyran-3(6H)-one (CAS 1033757-93-5); 4-(2',4'-Dichloro-4-ethyl[1,1'-biphenyl]-3-yl)-2,2,6,6-tetramethyl-2H-pyran-3,5(4H,6H)-dione (CAS 1312340-84-3); 5-(Acetyloxy)-4-(4'-chloro-4-cyclopropyl-2'-fluoro[1,1'-biphenyl]-3-yl)-3,6-dihydro-2,2,6,6-tetramethyl-2H-pyran-3-one (CAS 1312337-48-6); 5-(Acetyloxy)-4-(2',4'-dichloro-4-cyclopropyl-[1,1'-biphenyl]-3-yl)-3,6-dihydro-2,2,6,6-tetramethyl-2H-pyran-3-one; 5-(Acetyloxy)-4-(4'-chloro-4-ethyl-2'-fluoro[1,1'-biphenyl]-3-yl)-3,6-dihydro-2,2,6,6-tetramethyl-2H-pyran-3-one (CAS 1312340-82-1); 5-(Acetyloxy)-4-(2',4'-dichloro-4-ethyl[1,1'-biphenyl]-3-yl)-3,6-dihydro-2,2,6,6-tetramethyl-2H-pyran-3-one (CAS 1033760-55-2); 4-(4'-Chloro-4-cyclopropyl-2'-fluoro[1,1'-biphenyl]-3-yl)-5,6-dihydro-2,2,6,6-tetramethyl-5-oxo-2H-pyran-3-yl carbonic acid methyl ester (CAS 1312337-51-1); 4-(2',4'-Dichloro-4-cyclopropyl-[1,1'-biphenyl]-3-yl)-5,6-dihydro-2,2,6,6-tetramethyl-5-oxo-2H-pyran-3-yl carbonic acid methyl ester; 4-(4'-Chloro-4-ethyl-2'-fluoro[1,1'-biphenyl]-3-yl)-5,6-dihydro-2,2,6,6-tetramethyl-5-oxo-2H-pyran-3-yl carbonic acid methyl ester (CAS 1312340-83-2); 4-(2',4'-Dichloro-4-ethyl[1,1'-biphenyl]-3-yl)-5,6-dihydro-2,2,6,6-tetramethyl-5-oxo-2H-pyran-3-yl carbonic acid methyl ester (CAS 1033760-58-5); and
non ACC herbicides such as benfuresate, butylate, cycloate, dalapon, dimepiperate, EPTC, esprocarb, ethofumesate, flupropanate, molinate, orbencarb, pebulate, prosulfocarb, TCA, thiobencarb, tiocarbazil, triallate and vernolate;

b2) from the group of the ALS inhibitors:
sulfonylureas such as amidosulfuron, azimsulfuron, bensulfuron, bensulfuron-methyl, chlorimuron, chlorimuron-ethyl, chlorsulfuron, cinosulfuron, cyclosulfamuron, ethametsulfuron,

ethametsulfuron-methyl, ethoxysulfuron, flazasulfuron, flucetosulfuron, flupyrsulfuron, flupyrsulfuron-methyl-sodium, foramsulfuron, halosulfuron, halosulfuron-methyl, imazosulfuron, iodosulfuron, iodosulfuron-methyl-sodium, iofensulfuron, iofensulfuron-sodium, mesosulfuron, metazosulfuron, metsulfuron, metsulfuron-methyl, nicosulfuron, orthosulfamuron, oxasulfuron, primisulfuron, primisulfuron-methyl, propyrisulfuron, prosulfuron, pyrazosulfuron, pyrazosulfuron-ethyl, rimsulfuron, sulfometuron, sulfometuron-methyl, sulfosulfuron, thifensulfuron, thifensulfuron-methyl, triasulfuron, tribenuron, tribenuron-methyl, trifloxysulfuron, triflusulfuron, triflusulfuron-methyl and tritosulfuron,
imidazolinones such as imazamethabenz, imazamethabenz-methyl, imazamox, imazapic, imazapyr, imazaquin and imazethapyr, triazolopyrimidine herbicides and sulfonamides such as cloransulam, cloransulam-methyl, diclosulam, flumetsulam, florasulam, metosulam, penoxsulam, pyrimisulfan and pyroxsulam,
pyrimidinylbenzoates such as bispyribac, bispyribac-sodium, pyribenzoxim, pyriftalid, pyriminobac, pyriminobac-methyl, pyrithiobac, pyrithiobac-sodium, 4-[[[2-[(4,6-dimethoxy-2-pyrimidinyl)oxy]phenyl]methyl]amino]-benzoic acid-1-methylethyl ester (CAS 4201 38-41-6), 4-[[[2-[(4,6-dimethoxy-2-pyrimidinyl)oxy]phenyl]methyl]amino]-benzoic acid propyl ester (CAS 420138-40-5), N-(4-bromophenyl)-2-[(4,6-dimethoxy-2-pyrimidinyl)oxy]benzenemethanamine (CAS 420138-01-8),
sulfonylaminocarbonyl-triazolinone herbicides such as flucarbazone, flucarbazone-sodium, propoxycarbazone, propoxycarbazone-sodium, thiencarbazone and thiencarbazone-methyl; and triafamone;
among these, a preferred embodiment of the invention relates to those compositions comprising at least one imidazolinone herbicide;

b3) from the group of the photosynthesis inhibitors:
amicarbazone, inhibitors of the photosystem II, e.g. triazine herbicides, including of chlorotriazine, triazinones, triazindiones, methylthiotriazines and pyridazinones such as ametryn, atrazine, chloridazone, cyanazine, desmetryn, dimethametryn.hexazinone, metribuzin, prometon, prometryn, propazine, simazine, simetryn, terbumeton, terbuthylazin, terbutryn and trietazin, aryl urea such as chlorobromuron, chlorotoluron, chloroxuron, dimefuron, diuron, fluometuron, isoproturon, isouron, linuron, metamitron, methabenzthiazuron, metobenzuron, metoxuron, monolinuron, neburon, siduron, tebuthiuron and thiadiazuron, phenyl carbamates such as desmedipham, karbutilat, phenmedipham, phenmedipham-ethyl, nitrile herbicides such as bromofenoxim, bromoxynil and its salts and esters, ioxynil and its salts and esters, uraciles such as bromacil, lenacil and terbacil, and bentazon and bentazon-sodium, pyridate, pyridafol, pentanochlor and propanil and inhibitors of the photosystem I such as diquat, diquat-dibromide, paraquat, paraquat-dichloride and paraquat-dimetilsulfate. Among these, a preferred embodiment of the invention relates to those compositions comprising at least one aryl urea herbicide. Among these, likewise a preferred embodiment of the invention relates to those compositions comprising at least one triazine herbicide. Among these, likewise a preferred embodiment of the invention relates to those compositions comprising at least one nitrile herbicide;

b4) from the group of the protoporphyrinogen-IX oxidase inhibitors:

acifluorfen, acifluorfen-sodium, azafenidin, bencarbazone, benzfendizone, bifenox, butafenacil, carfentrazone, carfentrazone-ethyl, chlomethoxyfen, cinidon-ethyl, fluazolate, flufenpyr, flufenpyr-ethyl, flumiclorac, flumiclorac-pentyl, flumioxazin, fluoroglycofen, fluoroglycofen-ethyl, fluthiacet, fluthiacet-methyl, fomesafen, halosafen, lactofen, oxadiargyl, oxadiazon, oxyfluorfen, pentoxazone, profluazol, pyraclonil, pyraflufen, pyraflufen-ethyl, saflufenacil, sulfentrazone, thidiazimin, tiafenacil, ethyl [3-[2-chloro^4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1 ,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31-6; S-3100, N-ethyl-3-(2,6-dichloro-4-trifluoromethylphenoxy)-5-methyl-1 H-pyrazole-1 -carboxamide (CAS 452098-92-9), N-tetrahydrofurfuryl-3-(2,6-dichloro-4-trifluoromethylphenoxy)-5-methyl-1 /-/-pyrazole-1 -carboxamide (CAS 915396-43-9), N-ethyl-3-(2-chloro-6-fluoro-4-trifluoromethylphenoxy)-5-methyl-1 /-/-pyrazole-1 -carboxamide (CAS 452099-05-7), N-tetrahydrofurfuryl-3-(2-chloro-6-fluoro-4-trifluoromethylphenoxy)-5-methyl-1 /-/-pyrazole-1 -carboxamide (CAS 452100-03-7), 3-[7-fluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl]-1 ,5-dimethyl-6-thioxo-[1 ,3,5]triazinan-2,4-dione, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), 2-(2,2,7-Trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl)-4,5,6,7-tetrahydro-isoindole-1,3-dione, 1-Methyl-6-trifluoromethyl-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl)-1 H-pyrimidine-2,4-dione (CAS 13041 13-05-0), methyl (£)-4-[2-chloro-5-[4-chloro-5-(difluoromethoxy)-1 /-/-methyl-pyrazol-3-yl]-4-fluoro-phenoxy]-3-methoxy-but-2-enoate [CAS 948893-00-37, and 3-[7-Chloro-5-fluoro-2-(trifluoromethyl)-1 H-benzimidazol-4-yl]-1-methyl-6-(trifluoromethyl)-1 H-pyrimidine-2,4-dione (CAS 212754-02-4);

b5) from the group of the bleacher herbicides:
PDS inhibitors: beflubutamid, diflufenican, fluridone, flurochloridone, flurtamone, norflurazon, picolinafen, and 4-(3-trifluoromethylphenoxy)-2-(4-trifluoromethylphenyl)pyrimidine (CAS 180608-33-7), HPPD inhibitors: benzobicyclon, benzofenap, clomazone, isoxaflutole, mesotrione, pyrasulfotole, pyrazolynate, pyrazoxyfen, sulcotrione, tefuryltrione, tembotrione, topramezone and bicyclopyrone, bleacher, unknown target: aclonifen, amitrole and flumeturon;

b6) from the group of the EPSP synthase inhibitors:
glyphosate, glyphosate-isopropylammonium, glyposate-potassium and glyphosate-trimesium (sulfosate);

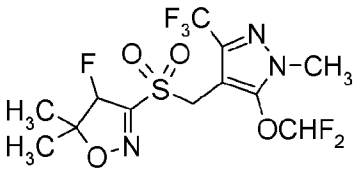
b7) from the group of the glutamine synthase inhibitors:
bilanaphos (bialaphos), bilanaphos-sodium, glufosinate, glufosinate-P and glufosinate-ammonium;

b8) from the group of the DHP synthase inhibitors:
asulam;

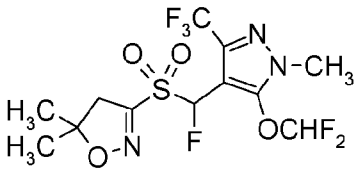
b9) from the group of the mitosis inhibitors:
compounds of group K1: dinitroanilines such as benfluralin, butralin, dinitramine, ethalfluralin, fluchloralin, oryzalin, pendimethalin, prodiamine and trifluralin, phosphoramidates such as amiprophos, amiprophos-methyl, and butamiphos, benzoic acid herbicides such as chlorthal,

chlorthal-dimethyl, pyridines such as dithiopyr and thiazopyr, benzamides such as propyzamide and tebutam; compounds of group K2: chlorpropham, propham and carbetamide, among these, compounds of group K1, in particular dinitroanilines are preferred;

b10) from the group of the VLCFA inhibitors:
chloroacetamides such as acetochlor, alachlor, butachlor, dimethachlor, dimethenamid, dimethenamid-P, metazachlor, metolachlor, metolachlor-S, pethoxamid, pretilachlor, propachlor, propisochlor and thenylchlor, oxyacetanilides such as flufenacet and mefenacet, acetanilides such as diphenamid, naproanilide and napropamide, tetrazolinones such fentrazamide, and other herbicides such as anilofos, cafenstrole, fenoxasulfone, ipfencarbazone, piperophos, pyroxasulfone and isoxazoline compounds of the formulae II.1, II.2, II.3, II.4, II.5, II.6, II.7, II.8 and II.9



II.1



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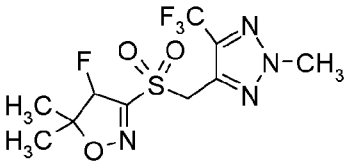

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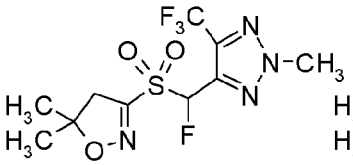
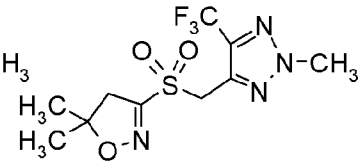
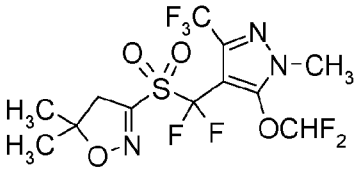


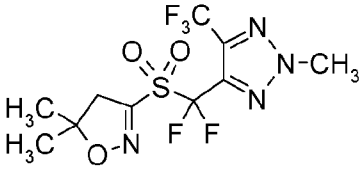
II.4



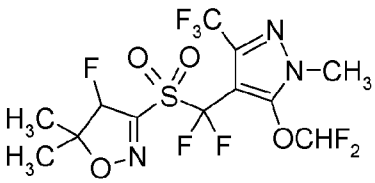
II.5



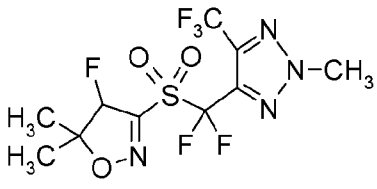
II.6



II.7



II.8



II.9

the isoxazoline compounds of the formula (I)I are known in the art, e.g. from WO 2006/024820, WO 2006/037945, WO 2007/071900 and WO 2007/096576;

among the VLCFA inhibitors, preference is given to chloroacetamides and oxyacetamides;

b11) from the group of the cellulose biosynthesis inhibitors:

chlorthiamid, dichlobenil, flupoxam, indaziflam, triaziflam, isoxaben and 1-Cyclohexyl-5-pentafluorphenyloxy-1 4-[1 ,2,4,6]thiatriazin-3-ylamine;

b12) from the group of the decoupler herbicides:
dinoseb, dinoterb and DNOC and its salts;

b13) from the group of the auxinic herbicides:
2,4-D and its salts and esters such as clacyfos, 2,4-DB and its salts and esters, aminocyclopyrachlor and its salts and esters, aminopyralid and its salts such as aminopyralid-tris(2-hydroxypropyl)ammonium and its esters, benazolin, benazolin-ethyl, chloramben and its salts and esters, clomeprop, clopyralid and its salts and esters, dicamba and its salts and esters, dichlorprop and its salts and esters, dichlorprop-P and its salts and esters, fluroxypyr, fluroxypyr-butometyl, fluroxypyr-meptyl, halauxifen and its salts and esters (CAS 943832-60-8); MCPA and its salts and esters, MCPA-thioethyl, MCPB and its salts and esters, mecoprop and its salts and esters, mecoprop-P and its salts and esters, picloram and its salts and esters, quinclorac, quinmerac, TBA (2,3,6) and its salts and esters and triclopyr and its salts and esters;

b14) from the group of the auxin transport inhibitors: diflufenzopyr, diflufenzopyr-sodium, naptalam and naptalam-sodium;

b15) from the group of the other herbicides: bromobutide, chlorflurenol, chlorflurenol-methyl, cinmethylin, cumyluron, cyclopyrimorate (CAS 499223-49-3) and its salts and esters, dalapon, dazomet, difenzoquat, difenzoquat-metilsulfate, dimethipin, DSMA, dymron, endothal and its salts, etobenzanid, flamprop, flamprop-isopropyl, flamprop-methyl, flamprop-M-isopropyl, flamprop-M-methyl, flurenol, flurenol-butyl, flurprimidol, fosamine, fosamine-ammonium, indanofan, indaziflam, maleic hydrazide, mefluidide, metam, methiozolin (CAS 403640-27-7), methyl azide, methyl bromide, methyl-dymron, methyl iodide, MSMA, oleic acid, oxaziclomefone, pelargonic acid, pyributicarb, quinoclamine, triaziflam and tridiphane..

Preferred herbicides B that can be used in combination with the PPO-inhibiting herbicides according to the present invention are:

b1) from the group of the lipid biosynthesis inhibitors:
clethodim, clodinafop-propargyl, cycloxydim, cyhalofop-butyl, diclofop-methyl, fenoxaprop-P-ethyl, fluazifop-P-butyl, haloxyfop-P-methyl, metamifop, pinoxaden, profoxydim, propaquizafop, quizalofop-P-ethyl, quizalofop-P-tefuryl, sethoxydim, tepraloxydim, tralkoxydim, 4-(4'-Chloro-4-cyclopropyl-2'-fluoro[1,1'-biphenyl]-3-yl)-5-hydroxy-2,2,6,6-tetramethyl-2H-pyran-3(6H)-one (CAS 1312337-72-6); 4-(2',4'-Dichloro-4-cyclopropyl[1,1'-biphenyl]-3-yl)-5-hydroxy-2,2,6,6-tetramethyl-2H-pyran-3(6H)-one (CAS 1312337-45-3); 4-(4'-Chloro-4-ethyl-2'-fluoro[1 ,1'-biphenyl]-3-yl)-5-hydroxy-2,2,6,6-tetramethyl-2H-pyran-3(6H)-one (CAS 1033757-93-5); 4-(2',4'-Dichloro-4-ethyl[1 ,1'-biphenyl]-3-yl)-2,2,6,6-tetramethyl-2H-pyran-3,5(4H,6H)-dione (CAS 1312340-84-3); 5-(Acetyloxy)-4-(4'-chloro-4-cyclopropyl-2'-fluoro[1 ,1'-biphenyl]-3-yl)-3,6-dihydro-2,2,6,6-tetramethyl-2H-pyran-3-one (CAS 1312337-48-6); 5-(Acetyloxy)-4-(2 ',4'-dichloro-4-cyclopropyl- [1 ,1'-biphenyl]-3-yl)-3,6-dihydro-2,2,6,6-tetramethyl-2H-pyran-3-one; 5-

(Acetyloxy)-4-(4'-chloro-4-ethyl-2'-flu oro[1,1'-biphenyl]-3-yl)-3,6-dihydro-2,2,6,6-tetramethyl-2H-pyran-3-one (CAS 1312340-82-1); 5-(Acetyloxy)-4-(2',4'-dichloro-4-ethyl[1 ,1'-biphenyl]-3-yl)-3,6-dihydro-2,2,6,6-tetramethyl-2H-pyran-3-one (CAS 1033760-55-2); 4-(4'-Chloro-4-cyclopropyl-2'-fluoro[1 ,1'-biphenyl]-3-yl)-5,6-dihydro-2,2,6,6-tetramethyl-5-oxo-2H-pyran-3-yl carbonic acid methyl ester (CAS 1312337-51-1); 4-(2',4'-Dichloro -4-cyclopropyl- [1,1'-biphenyl]-3-yl)-5,6-dihydro-2,2,6,6-tetramethyl-5-oxo-2H-pyran-3-yl carbonic acid methyl ester; 4-(4'-Chloro-4-ethyl-2'-fluoro[1 ,1'-biphenyl]-3-yl)-5,6-dihydro-2,2,6,6-tetramethyl-5-oxo-2H-pyran-3-yl carbonic acid methyl ester (CAS 1312340-83-2); 4-(2',4'-Dichloro-4-ethyl[1 ,1'-biphenyl]-3-yl)-5,6-dihydro-2,2,6,6-tetramethyl-5-oxo-2H-pyran-3-yl carbonic acid methyl ester (CAS 1033760-58-5); benfuresate, dimepiperate, EPTC, esprocarb, ethofumesate, molinate, orbencarb, prosulfocarb, thiobencarb and triallate;

b2) from the group of the ALS inhibitors:
amidosulfuron, azimsulfuron, bensulfuron-methyl, bispyribac-sodium, chlorimuron-ethyl, chlorsulfuron, cloransulam-methyl, cyclosulfamuron, diclosulam, ethametsulfuron-methyl, ethoxysulfuron, flazasulfuron, florasulam, flucarbazone-sodium, flucetosulfuron, flumetsulam, flupyrsulfuron-methyl-sodium, foramsulfuron, halosulfuron-methyl, imazamethabenz-methyl, imazamox, imazapic, imazapyr, imazaquin, imazethapyr, imazosulfuron, iodosulfuron, iodosulfuron-methyl-sodium, iofensulfuron, iofensulfuron-sodium, mesosulfuron, metazosulfuron, metosulam, metsulfuron-methyl, nicosulfuron, orthosulfamuron, oxasulfuron, penoxsulam, primisulfuron-methyl, propoxycarbazon-sodium, propyrisulfuron, prosulfuron, pyrazosulfuron-ethyl, pyribenzoxim, pyrimisulfan, pyriftalid, pyriminobac-methyl, pyrithiobac-sodium, pyroxsulam, rimsulfuron, sulfometuron-methyl, sulfosulfuron, thiencarbazone-methyl, thifensulfuron-methyl, triasulfuron, tribenuron-methyl, trifloxysulfuron, triflusulfuron-methyl, tritosulfuron and triafamone;

b3) from the group of the photosynthesis inhibitors:
ametryn, amicarbazone, atrazine, bentazone, bentazone-sodium, bromoxynil and its salts and esters, chloridazone, chlorotoluron, cyanazine, desmedipham, diquat-dibromide, diuron, fluometuron, hexazinone, ioxynil and its salts and esters, isoproturon, lenacil, linuron, metamitron, methabenzthiazuron, metribuzin, paraquat, paraquat-dichloride, phenmedipham, propanil, pyridate, simazine, terbutryn, terbuthylazine and thidiazuron;

b4) from the group of the protoporphyrinogen-IX oxidase inhibitors:
acifluorfen, acifluorfen-sodium, azafenidin, bencarbazone, benzfendizone, butafenacil, carfentrazone-ethyl, cinidon-ethyl, flufenpyr-ethyl, flumiclorac-pentyl, flumioxazin, fluoroglycofen-ethyl, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxadiazon, oxyfluorfen, pentoxazone, pyraflufen-ethyl, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]-acetate (CAS 353292-31-6; S-3100), N-ethyl-3-(2,6-dichloro-4-trifluoromethylphenoxy)-5-methyl-1 /-/-pyrazole-1-carboxamide (CAS 452098-92-9), N-tetrahydrofurfuryl-3-(2,6-dichloro-4-trifluoromethylphenoxy)-5-methyl-1 /-/-pyrazole-1-carboxamide (CAS 915396-43-9), N-ethyl-3-(2-chloro-6-fluoro-4-trifluoromethylphenoxy)-5-methyl-1 /-/-pyrazole-1-carboxamide (CAS 452099-05-7), N-tetrahydrofurfuryl-3-(2-chloro-6-fluoro-4-trifluoromethylphenoxy)-5-methyl-1 /-/-pyrazole-

1-carboxamide (CAS 452100-03-7), 3-[7-fluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl]-1 ,5-dimethyl-6-thioxo-[1 ,3,5]triazinan-2,4-dione, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), 2-(2,2,7-Trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl)-4,5,6,7-tetrahydro-isoindole-1 ,3-dione ;1-Methyl-6-trifluoromethyl-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl)-1 H-pyrimidine-2,4-dione, and 3-[7-Chloro-5-fluoro-2-(trifluoromethyl)-1 H-benzimidazol-4-yl]-1-methyl-6-(trifluoromethyl)-1 H-pyrimidine-2,4-dione (CAS 212754-02-4);

b5) from the group of the bleacher herbicides:
aclonifen, beflubutamid, benzobicyclon, clomazone, diflufenican, flurochloridone, flurtamone, isoxaflutole, mesotrione, norflurazon, picolinafen, pyrasulfotole, pyrazolynate, sulcotrione, tefuryltrione, tembotrione, topramezone, bicyclopyrone, 4-(3-trifluoromethylphenoxy)-2-(4-trifluoromethylphenyl)pyrimidine (CAS 180608-33-7), amitrole and flumeturon;

b6) from the group of the EPSP synthase inhibitors:
glyphosate, glyphosate-isopropylammonium, glyphosate-potassium and glyphosate-trimesium (sulfosate);

b7) from the group of the glutamine synthase inhibitors:
glufosinate, glufosinate-P, glufosinate-ammonium;

b8) from the group of the DHP synthase inhibitors: asulam;

b9) from the group of the mitosis inhibitors:
benfluralin, dithiopyr, ethalfluralin, oryzalin, pendimethalin, thiazopyr and trifluralin;

b10) from the group of the VLCFA inhibitors:
acetochlor, alachlor, anilofos, butachlor, cafenstrole, dimethenamid, dimethenamid-P, fentrazamide, flufenacet, mefenacet, metazachlor, metolachlor, S-metolachlor, naproanilide, napropamide, pretilachlor, fenoxasulfone, ipfencarbazone, pyroxasulfone thenylchlor and isoxazoline-compounds of the formulae II.1.1, II.2, II.3, II.4, II.5, II.6, II.7, II.8 and II.9 as mentioned above;

b11) from the group of the cellulose biosynthesis inhibitors: dichlobenil, flupoxam, isoxaben and 1-Cyclohexyl-5-pentafluorphenyloxy-1 4-[1 ,2,4,6]thiatriazin-3-ylamine;

b13) from the group of the auxinic herbicides:
2,4-D and its salts and esters, aminocyclopyrachlor and its salts and esters, aminopyralid and its salts such as aminopyralid-tris(2-hydroxypropyl)ammonium and its esters, clopyralid and its salts and esters, dicamba and its salts and esters, dichlorprop-P and its salts and esters, fluroxypyr-meptyl, halauxifen and its salts and esters (CAS 943832-60-8), MCPA and its salts and esters, MCPB and its salts and esters, mecoprop-P and its salts and esters, picloram and its salts and esters, quinclorac, quinmerac and triclopyr and its salts and esters;

b14) from the group of the auxin transport inhibitors: diflufenzopyr and diflufenzopyr-sodium;

b15) from the group of the other herbicides: bromobutide, cinmethylin, cumyluron, cyclopyrimorate (CAS 499223^19-3) and its salts and esters, dalapon, difenzoquat, difenzoquat-metilsulfate, DSMA, dymron (= daimuron), flamprop, flamprop-isopropyl, flamprop-methyl, flamprop-M-isopropyl, flamprop-M-methyl, indanofan, indaziflam, metam, methylbromide, MSMA, oxaziclomefone, pyributicarb, triaziflam and tridiphane.

Particularly preferred herbicides B that can be used in combination with the PPO-inhibiting herbicides according to the present invention are:

b1) from the group of the lipid biosynthesis inhibitors: clodinafop-propargyl, cycloxydim, cyhalofop-butyl, fenoxaprop-P-ethyl, pinoxaden, profoxydim, tepraloxydim, tralkoxydim, 4-(4'-Chloro-4-cyclopropyl-2'-fluoro[1 ,1'-biphenyl]-3-yl)-5-hydroxy-2,2,6,6-tetramethyl-2H-pyran-3(6H)-one (CAS 1312337-72-6); 4-(2',4'-Dichloro-4-cyclopropyl[1 ,1'-biphenyl]-3-yl)-5-hydroxy-2,2,6,6-tetramethyl-2H-pyran-3(6H)-one (CAS 1312337-45-3); 4-(4'-Chloro-4-ethyl-2'-fluoro[1 ,1'-biphenyl]-3-yl)-5-hydroxy-2,2,6,6-tetramethyl-2H-pyran-3(6H)-one (CAS 1033757-93-5); 4-(2',4'-Dichloro-4-ethyl[1 ,1'-biphenyl]-3-yl)-2,2,6,6-tetramethyl-2H-pyran-3,5(4H,6H)-dione (CAS 1312340-84-3); 5-(Acetyloxy)-4-(4'-chloro-4-cyclopropyl-2'-fluoro[1,1'-biphenyl]-3-yl)-3,6-dihydro-2,2,6,6-tetramethyl-2H-pyran-3-one (CAS 1312337-48-6); 5-(Acetyloxy)-4-(2',4'-dichloro-4-cyclopropyl- [1,1'-biphenyl]-3-yl)-3,6-dihydro-2,2,6,6-tetramethyl-2H-pyran-3-one; 5-(AcetyloxyH^'-chloro^-ethyl^'-fluorofl J'-bipheny^-S-yO-S^-dihydro^^^^-tetramethyl^H-pyran-3-one (CAS 1312340-82-1); 5-(Acetyloxy)-4-(2',4'-dichloro-4-ethyl[1 ,1'-biphenyl]-3-yl)-3,6-dihydro-2,2,6,6-tetramethyl-2H-pyran-3-one (CAS 1033760-55-2); 4-(4'-Chloro-4-cyclopropyl-2'-fluoro[1 ,1'-biphenyl]-3-yl)-5,6-dihydro-2,2,6,6-tetramethyl-5-oxo-2H-pyran-3-yl carbonic acid methyl ester (CAS 1312337-51-1); 4-(2',4'-Dichloro -4-cyclopropyl- [1,1'-biphenyl]-3-yl)-5,6-dihydro-2,2,6,6-tetramethyl-5-oxo-2H-pyran-3-yl carbonic acid methyl ester; 4-(4'-Chloro-4-ethyl-2'-fluoro[1 ,1'-biphenyl]-3-yl)-5,6-dihydro-2,2,6,6-tetramethyl-5-oxo-2H-pyran-3-yl carbonic acid methyl ester (CAS 1312340-83-2); 4-(2',4'-Dichloro-4-ethyl[1 ,1'-biphenyl]-3-yl)-5,6-dihydro-2,2,6,6-tetramethyl-5-oxo-2H-pyran-3-yl carbonic acid methyl ester (CAS 1033760-58-5); esprocarb, prosulfocarb, thiobencarb and triallate;

b2) from the group of the ALS inhibitors: bensulfuron-methyl, bispyribac-sodium, cyclosulfamuron, diclosulam, flumetsulam, flupyrsulfuron-methyl-sodium, foramsulfuron, imazamox, imazapic, imazapyr, imazaquin, imazethapyr, imazosulfuron, iodosulfuron, iodosulfuron-methyl-sodium, iofensulfuron, iofensulfuron-sodium, mesosulfuron, metazosulfuron, nicosulfuron, penoxsulam, propoxycarbazon-sodium, propyrisulfuron, pyrazosulfuron-ethyl, pyroxsulam, rimsulfuron, sulfosulfuron, thiencarbazon-methyl, tritosulfuron and triafamone;

b3) from the group of the photosynthesis inhibitors: ametryn, atrazine, diuron, fluometuron, hexazinone, isoproturon, linuron, metribuzin, paraquat, paraquat-dichloride, propanil, terbutryn and terbuthylazine;

b4) from the group of the protoporphyrinogen-IX oxidase inhibitors: acifluorfen, acifluorfen-

sodium, butafenacil, cinidon-ethyl, carfentrazone-ethyl, flumioxazin, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl , oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1 -methyl-6-trifluoromethyl-2,4-dioxo-1 ,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31 -6; S-31 00), 3-[7-fluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl]-1 ,5-dimethyl-6-thioxo-[1 ,3,5]triazinan-2,4-dione, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72^1), and 2-(2,2,7-Trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl)-4,5,6,7-tetrahydro-isoindole-1 ,3-dione, and 1-Methyl-6-trifluoromethyl-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl)-1 H-pyrimidine-2,4-dione;

b5) from the group of the bleacher herbicides: clomazone, diflufenican, flurochloridone, isoxaflutole, mesotrione, picolinafen, sulcotrione, tefuryltrione, tembotrione, topramezone, bicyclopyrone, amitrole and flumeturon;

b6) from the group of the EPSP synthase inhibitors: glyphosate, glyphosate-isopropylammonium and glyphosate-trimesium (sulfosate);

b7) from the group of the glutamine synthase inhibitors: glufosinate, glufosinate-P and glufosinate-ammonium;

b9) from the group of the mitosis inhibitors: pendimethalin and trifluralin;

b10) from the group of the VLCFA inhibitors: acetochlor, cafenstrole, dimethenamid-P, fentrazamide, flufenacet, mefenacet, metazachlor, metolachlor, S-metolachlor, fenoxasulfone, ipfencarbazone and pyroxasulfone; likewise, preference is given to isoxazoline compounds of the formulae 111, II.2, 113, II.4, II.5, II.6, *W.7,* II.8 and II.9 as mentioned above;

b11) from the group of the cellulose biosynthesis inhibitors: isoxaben;

b13) from the group of the auxinic herbicides: 2,4-D and its salts and esters such as clacyfos, and aminocyclopyrachlor and its salts and esters, aminopyralid and its salts and its esters, clopyralid and its salts and esters, dicamba and its salts and esters, fluroxypyr-meptyl, quinclorac and quinmerac;

b14) from the group of the auxin transport inhibitors: diflufenzopyr and diflufenzopyr-sodium,

b15) from the group of the other herbicides: dymron (= daimuron), indanofan, indaziflam, oxaziclomefone and triaziflam.

Moreover, it may be useful to apply the PPO-inhibiting herbicides, when used in combination with a compound B described SUPRA, in combination with safeners. Safeners are chemical compounds which prevent or reduce damage on useful plants without having a major impact on the herbicidal action of herbicides towards unwanted plants. They can be applied either before

sowings (e.g. on seed treatments, shoots or seedlings) or in the pre-emergence application or post-emergence application of the useful plant.

Furthermore, the safeners C, the PPO-inhibiting herbicides and/or the herbicides B can be applied simultaneously or in succession.

Suitable safeners are e.g. (quinolin-8-oxy)acetic acids, 1-phenyl-5-haloalkyl-1 H-1 ,2,4-triazol-3-carboxylic acids, 1-phenyl-4,5-dihydro-5-alkyl-1 H-pyrazol-3,5-dicarboxylic acids, 4,5-dihydro-5,5-diaryl-3-isoxazol carboxylic acids, dichloroacetamides, alpha-oximinophenylacetonitriles, acetophenonoximes, 4,6-dihalo-2-phenylpyrimidines, N-[[4-(aminocarbonyl)phenyl]sulfonyl]-2-benzoic amides, 1,8-naphthalic anhydride, 2-halo-4-(haloalkyl)-5-thiazol carboxylic acids, phosphorthiolates and N-alkyl-O-phenylcarbamates and their agriculturally acceptable salts and their agriculturally acceptable derivatives such amides, esters, and thioesters, provided they have an acid group.

Examples of preferred safeners C are benoxacor, cloquintocet, cyometrinil, cyprosulfamide, dichlormid, dicyclonon, dietholate, fenchlorazole, fenclorim, flurazole, fluxofenim, furilazole, isoxadifen, mefenpyr, mephenate, naphthalic anhydride, oxabetrinil, 4-(dichloroacetyl)-1-oxa-4-azaspiro[4.5]decane (MON4660, CAS 71526-07-3) and 2,2,5-trimethyl-3-(dichloroacetyl)-1,3-oxazolidine (R-29148, CAS 52836-31-4).

Especially preferred safeners C are benoxacor, cloquintocet, cyprosulfamide, dichlormid, fenchlorazole, fenclorim, flurazole, fluxofenim, furilazole, isoxadifen, mefenpyr, naphthalic anhydride, oxabetrinil, 4-(dichloroacetyl)-1-oxa-4-azaspiro[4.5]decane (MON4660, CAS 71526-07-3) and 2,2,5-trimethyl-3-(dichloroacetyl)-1 ,3-oxazolidine (R-29148, CAS 52836-31-4).

Particularly preferred safeners C are benoxacor, cloquintocet, cyprosulfamide, dichlormid, fenchlorazole, fenclorim, furilazole, isoxadifen, mefenpyr, naphtalic anhydride, 4-(dichloroacetyl)-1-oxa-4-azaspiro[4.5]decane (MON4660, CAS 71526-07-3), and 2,2,5-trimethyl-3-(dichloroacetyl)-1 ,3-oxazolidine (R-291 48, CAS 52836-31 -4).

Also preferred safeners C are benoxacor, cloquintocet, cyprosulfamide, dichlormid, fenchlorazole, fenclorim, furilazole, isoxadifen, mefenpyr, 4-(dichloroacetyl)-1-oxa-4-azaspiro-[4.5]decane (MON4660, CAS 71526-07-3) and 2,2,5-trimethyl-3-(dichloroacetyl)-1 ,3-oxazolidine (R-291 48, CAS 52836-31 -4)..

Particularly preferred safeners C, which, as component C, are constituent of the composition according to the invention are the safeners C as defined above; in particular the safeners C.1 - C.12 listed below in table C:

Table C

	Safener C
	C.1 benoxacor
	C.2 cloquintocet

	C.3 cyprosulfamide
	C.4 dichlormid
	C.5 fenchlorazole
	C.6 fenclorim
	C.7 furilazole
	C.8 isoxadifen
	C.9 mefenpyr
	C.10 naphtalic acid anhydride
	C.1 1 4-(dichloroacetyl)-1-oxa-4-azaspiro[4.5]decane (MON4660, CAS 71526-07-3)
	C.12 2,2,5-trimethyl-3-(dichloro-acetyl)-1 ,3-oxazolidine (R-29148, CAS 52836-31-4)

The PPO-inhibiting herbicides (compounds A) and the active compounds B of groups b1) to b15) and the active compounds C are known herbicides and safeners, see, for example, The Compendium of Pesticide Common Names (http://www.alanwood.net/pesticides/); Farm Chemicals Handbook 2000 volume 86, Meister Publishing Company, 2000; B. Hock, C. Fedtke, R. R. Schmidt, Herbizide [Herbicides], Georg Thieme Verlag, Stuttgart 1995; W. H. Ahrens, Herbicide Handbook, 7th edition, Weed Science Society of America, 1994; and K. K. Hatzios, Herbicide Handbook, Supplement for the 7th edition, Weed Science Society of America, 1998. 2,2,5-Trimethyl-3-(dichloroacetyl)-1 ,3-oxazolidine [CAS No. 52836-31-4] is also referred to as R-29148. 4-(Dichloroacetyl)-1-oxa-4-azaspiro[4.5]decane [CAS No. 71526-07-3] is also referred to as AD-67 and MON 4660.

The assignment of the active compounds to the respective mechanisms of action is based on current knowledge. If several mechanisms of action apply to one active compound, this substance was only assigned to one mechanism of action.

Active compounds B and C having a carboxyl group can be employed in the form of the acid, in the form of an agriculturally suitable salt as mentioned above or else in the form of an agriculturally acceptable derivative in the compositions according to the invention.

In the case of dicamba, suitable salts include those, where the counterion is an agriculturally acceptable cation. For example, suitable salts of dicamba are dicamba-sodium, dicamba-potassium, dicamba-methylammonium, dicamba-dimethylammonium, dicamba-isopropylammonium, dicamba-diglycolamine, dicamba-olamine, dicamba-diolamine, dicamba-trolamine, dicamba-N,N-bis-(3-aminopropyl)methylamine and dicamba-diethylenetriamine. Examples of a suitable ester are dicamba-methyl and dicamba-butotyl.
Suitable salts of 2,4-D are 2,4-D-ammonium, 2,4-D-dimethylammonium, 2,4-D-diethylammonium, 2,4-D-diethanolammonium (2,4-D-diolamine), 2,4-D-triethanolammonium, 2,4-D-isopropylammonium, 2,4-D-triisopropanolammonium, 2,4-D-heptylammonium, 2,4-D-dodecylammonium, 2,4-D-tetradecylammonium, 2,4-D-triethylammonium, 2,4-D-tris(2-hydroxypropyl)ammonium, 2,4-D-tris(isopropyl)ammonium, 2,4-D-trolamine, 2,4-D-lithium, 2,4-

D-sodium. Examples of suitable esters of 2,4-D are 2,4-D-butotyl, 2,4-D-2-butoxypropyl, 2,4-D-3-butoxypropyl, 2,4-D-butyl, 2,4-D-ethyl, 2,4-D-ethylhexyl, 2,4-D-isobutyl, 2,4-D-isooctyl, 2,4-D-isopropyl, 2,4-D-meptyl, 2,4-D-methyl, 2,4-D-octyl, 2,4-D-pentyl, 2,4-D-propyl, 2,4-D-tefuryl and clacyfos.

Suitable salts of 2,4-DB are for example 2,4-DB-sodium, 2,4-DB-potassium and 2,4-DB-dimethylammonium. Suitable esters of 2,4-DB are for example 2,4-DB-butyl and 2,4-DB-isoctyl.

Suitable salts of dichlorprop are for example dichlorprop-sodium, dichlorprop-potassium and dichlorprop-dimethylammonium. Examples of suitable esters of dichlorprop are dichlorprop-butotyl and dichlorprop-isoctyl.

Suitable salts and esters of MCPA include MCPA-butotyl, MCPA-butyl, MCPA-dimethyl-ammonium, MCPA-diolamine, MCPA-ethyl, MCPA-thioethyl, MCPA-2-ethylhexyl, MCPA-isobutyl, MCPA-isoctyl, MCPA-isopropyl, MCPA-isopropylammonium, MCPA-methyl, MCPA-olamine, MCPA-potassium, MCPA-sodium and MCPA-trolamine.

A suitable salt of MCPB is MCPB sodium. A suitable ester of MCPB is MCPB-ethyl.

Suitable salts of clopyralid are clopyralid-potassium, clopyralid-olamine and clopyralid-tris-(2-hydroxypropyl)ammonium. Example of suitable esters of clopyralid is clopyralid-methyl.

Examples of a suitable ester of fluroxypyr are fluroxypyr-meptyl and fluroxypyr-2-butoxy-1-methylethyl, wherein fluroxypyr-meptyl is preferred.

Suitable salts of picloram are picloram-dimethylammonium, picloram-potassium, picloram-triisopropanolammonium, picloram-triisopropylammonium and picloram-trolamine. A suitable ester of picloram is picloram-isoctyl.

A suitable salt of triclopyr is triclopyr-triethylammonium. Suitable esters of triclopyr are for example triclopyr-ethyl and triclopyr-butotyl.

Suitable salts and esters of chloramben include chloramben-ammonium, chloramben-diolamine, chloramben-methyl, chloramben-methylammonium and chloramben-sodium. Suitable salts and esters of 2,3,6-TBA include 2,3,6-TBA-dimethylammonium, 2,3,6-TBA-lithium, 2,3,6-TBA-potassium and 2,3,6-TBA-sodium.

Suitable salts and esters of aminopyralid include aminopyralid-potassium and aminopyralid-tris(2-hydroxypropyl)ammonium.

Suitable salts of glyphosate are for example glyphosate-ammonium, glyphosate-diammonium, glyphoste-dimethylammonium, glyphosate-isopropylammonium, glyphosate-potassium, glyphosate-sodium, glyphosate-trimesium as well as the ethanolamine and diethanolamine salts, preferably glyphosate-diammonium, glyphosate-isopropylammonium and glyphosate-trimesium (sulfosate).

A suitable salt of glufosinate is for example glufosinate-ammonium.

A suitable salt of glufosinate-P is for example glufosinate-P-ammonium.

Suitable salts and esters of bromoxynil are for example bromoxynil-butyrate, bromoxynil-heptanoate, bromoxynil-octanoate, bromoxynil-potassium and bromoxynil-sodium.

Suitable salts and esters of ioxonil are for example ioxonil-octanoate, ioxonil-potassium and ioxonil-sodium.

Suitable salts and esters of mecoprop include mecoprop-butotyl, mecoprop-dimethylammonium, mecoprop-diolamine, mecoprop-ethadyl, mecoprop-2-ethylhexyl, mecoprop-isoctyl, mecoprop-methyl, mecoprop-potassium, mecoprop-sodium and mecoprop-trolamine.

Suitable salts of mecoprop-P are for example mecoprop-P-butotyl, mecoprop-P-

dimethylammonium, mecoprop-P-2-ethylhexyl, mecoprop-P-isobutyl, mecoprop-P-potassium and mecoprop-P-sodium.
A suitable salt of diflufenzopyr is for example diflufenzopyr-sodium.
A suitable salt of naptalam is for example naptalam-sodium.
Suitable salts and esters of aminocyclopyrachlor are for example aminocyclopyrachlor-dimethylammonium, aminocyclopyrachlor-methyl, aminocyclopyrachlor-triisopropanolammonium, aminocyclopyrachlor-sodium and aminocyclopyrachlor-potassium.
A suitable salt of quinclorac is for example quinclorac-dimethylammonium.
A suitable salt of quinmerac is for example quinclorac-dimethylammonium.
A suitable salt of imazamox is for example imazamox-ammonium.
Suitable salts of imazapic are for example imazapic-ammonium and imazapic-isopropylammonium.
Suitable salts of imazapyr are for example imazapyr-ammonium and imazapyr-isopropylammonium.
A suitable salt of imazaquin is for example imazaquin-ammonium.
Suitable salts of imazethapyr are for example imazethapyr-ammonium and imazethapyr-isopropylammonium.
A suitable salt of topramezone is for example topramezone-sodium.

The preferred embodiments of the invention mentioned herein below have to be understood as being preferred either independently from each other or in combination with one another.

According to a preferred embodiment of the invention, the composition comprises as component B at least one, preferably exactly one herbicide B.

According to another preferred embodiment of the invention, the composition comprises at least two, preferably exactly two, herbicides B different from each other.

According to another preferred embodiment of the invention, the composition comprises at least three, preferably exactly three, herbicides B different from each other.

According to another preferred embodiment of the invention, the composition comprises as component A at least one, preferably exactly one PPO-inhibiting herbicide, preferably acifluorfen, acifluorfen-sodium, butafenacil, cinidon-ethyl, carfentrazone-ethyl, flumioxazin, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1 ,2,3,4-tetrahydropyrimidin-3-yl)-phenoxy]-2-pyridyloxy]acetate (CAS 353292-31-6; S-3100;, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), especially preferred saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), and as component B at least one, preferably exactly one, herbicide B.

According to another preferred embodiment of the invention, the composition comprises as

component A at least one, preferably exactly preferably exactly one PPO-inhibiting herbicide, preferably acifluorfen, acifluorfen-sodium, butafenacil, cinidon-ethyl, carfentrazone-ethyl, flumioxazin, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1 ,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31 -6; S-31 00), 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), especially preferred saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), and at least two, preferably exactly two, herbicides B different from each other.

According to another preferred embodiment of the invention, the composition comprises as component A at least one, preferably exactly preferably exactly one PPO-inhibiting herbicide, preferably acifluorfen, acifluorfen-sodium, butafenacil, cinidon-ethyl, carfentrazone-ethyl, flumioxazin, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1 ,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31-6; S-31 00), 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), especially preferred saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4) and at least three, preferably exactly three, herbicides B different from each other.

According to another preferred embodiment of the invention, the composition comprises, in addition to a PPO-inhibiting herbicide, preferably acifluorfen, acifluorfen-sodium, butafenacil, cinidon-ethyl, carfentrazone-ethyl, flumioxazin, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31 -6; S-31 00), 1,5-dimethyl-6-thioxo-3-(2,2 ***J***-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), especially preferred saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), at least one and especially exactly one herbicidally active compound from group b1), in particular selected from the group consisting of clethodim, clodinafop-propargyl, cycloxydim, cyhalofop-butyl, fenoxaprop-P-ethyl, fluazifop, pinoxaden, profoxydim, quizalofop, sethoxydim, tepraloxydim, tralkoxydim, esprocarb, prosulfocarb, thiobencarb and triallate.

According to another preferred embodiment of the invention, the composition comprises, in addition to a PPO-inhibiting herbicide, preferably acifluorfen, acifluorfen-sodium, butafenacil, cinidon-ethyl, carfentrazone-ethyl, flumioxazin, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31 -6; S-31 00, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4) especially

preferred saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), at least one and especially exactly one herbicidally active compound from group b2), in particular selected from the group consisting of bensulfuron-methyl, bispyribac-sodium, cloransulam-methyl, cyclosulfamuron, diclosulam, flumetsulam, flupyrsulfuron-methyl-sodium, foramsulfuron, halosulfuron-methyl, imazamox, imazapic, imazapyr, imazaquin, imazethapyr, imazosulfuron, iodosulfuron, iodosulfuron-methyl-sodium, mesosulfuron-methyl, metazosulfuron, nicosulfuron, penoxsulam, propoxycarbazon-sodium, pyrazosulfuron-ethyl, pyrithiobac-sodium, pyroxsulam, rimsulfuron, sulfosulfuron, thiencarbazon-methyl, thifensulfuron-methyl, trifloxysulfuron and tritosulfuron.

According to another preferred embodiment of the invention, the composition comprises, in addition to a a PPO-inhibiting herbicide, preferably acifluorfen, acifluorfen-sodium, butafenacil, cinidon-ethyl, carfentrazone-ethyl, flumioxazin, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31 -6; S-31 00), 1,5-dimethyl-6-thioxo-3-(2,2 ***J***-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), especially preferred saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2 ***J***-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), at least one and especially exactly one herbicidally active compound from group b3), in particular selected from the group consisting of ametryn, atrazine, bentazon, bromoxynil, diuron, fluometuron, hexazinone, isoproturon, linuron, metribuzin, paraquat, paraquat-dichloride, prometryne, propanil, terbutryn and terbuthylazine.

According to another preferred embodiment of the invention, the composition comprises, in addition to a a PPO-inhibiting herbicide, preferably acifluorfen, acifluorfen-sodium, butafenacil, cinidon-ethyl, carfentrazone-ethyl, flumioxazin, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31 -6; S-31 00), 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), especially preferred saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), at least one and especially exactly one herbicidally active compound from group b4), in particular selected from the group consisting of acifluorfen, acifluorfen-sodium, azafenidin, bencarbazone, benzfendizone, bifenox, butafenacil, carfentrazone, carfentrazone-ethyl, chlomethoxyfen, cinidon-ethyl, fluazolate, flufenpyr, flufenpyr-ethyl, flumiclorac, flumiclorac-pentyl, flumioxazin, fluoroglycofen, fluoroglycofen-ethyl, fluthiacet, fluthiacet-methyl, fomesafen, halosafen, lactofen, oxadiargyl, oxadiazon, oxyfluorfen, pentoxazone, profluazol, pyraclonil, pyraflufen, pyraflufen-ethyl, saflufenacil, sulfentrazone, thidiazimin, tiafenacil, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1 ,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31-6; S-31 00), N-ethyl-3-(2,6-dichloro^-trifluoromethylphenoxy)-5-methyl-1 H-pyrazole-1-carboxamide (CAS 452098-92-9), N-tetrahydrofurfuryl-3-(2,6-dichloro-4-

trifluoromethylphenoxy)-5-methyl-1 /-/-pyrazole-1-carboxannicle (CAS 915396-43-9), N-ethyl-3-(2-chloro-6-fluoro-4-trifluoromethylphenoxy)-5-methyl-1 /-/-pyrazole-1-carboxamide (CAS 452099-05-7), N-tetrahydrofurfuryl-3-(2-chloro-6-fluoro-4-trifluoromethylphenoxy)-5-methyl-1 /-/-pyrazole-1-carboxamide (CAS 452100-03-7), 3-[7-fluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl]-1 ,5-dimethyl-6-thioxo-[1 ,3,5]triazinan-2,4-dione, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), 2-(2,2,7-Trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl)-4,5,6,7-tetrahydro-isoindole-1 ,3-dione, 1-Methyl-6-trifluoromethyl-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl)-1 H-pyrimidine-2,4-dione, methyl (E)-4-[2-chloro-5-[4-chloro-5-(difluoromethoxy)-1 /-/-methyl-pyrazol-3-yl]-4-fluoro-phenoxy]-3-methoxy-but-2-enoate [CAS 948893-00-37, 3-[7-Chloro-5-fluoro-2-(trifluoromethyl)-1H-benzimidazol-4-yl]-1-methyl-6-(trifluoromethyl)-1 H-pyrimidine-2,4-dione (CAS 212754-02-4).

According to another preferred embodiment of the invention, the composition comprises, in addition to a a PPO-inhibiting herbicide, preferably acifluorfen, acifluorfen-sodium, butafenacil, cinidon-ethyl, carfentrazone-ethyl, flumioxazin, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31 -6; S-31 00), 1,5-dimethyl-6-thioxo-3-(2,2 ***J***-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), especially preferred saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), at least one and especially exactly one herbicidally active compound from group b5), in particular selected from the group consisting of clomazone, diflufenican, flurochloridone, isoxaflutole, mesotrione, picolinafen, sulcotrione, tefuryltrione, tembotrione, topramezone, bicyclopyrone, amitrole and flumeturon.

According to another preferred embodiment of the invention, the composition comprises, in addition to a a PPO-inhibiting herbicide, preferably acifluorfen, acifluorfen-sodium, butafenacil, cinidon-ethyl, carfentrazone-ethyl, flumioxazin, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31 -6; S-31 00), 1,5-dimethyl-6-thioxo-3-(2,2 ***J***-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), especially preferred saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), at least one and especially exactly one herbicidally active compound from group b6), in particular selected from the group consisting of glyphosate, glyphosate-isopropylammonium and glyphosate-trimesium (sulfosate).

According to another preferred embodiment of the invention, the composition comprises, in addition to a a PPO-inhibiting herbicide, preferably acifluorfen, acifluorfen-sodium, butafenacil, cinidon-ethyl, carfentrazone-ethyl, flumioxazin, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-

trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)p^ enoxy]-2-pyridyloxy]acetate (CAS 353292-31 -6; S-31 00), 1,5-dimethyl-6-thioxo-3-(2,2 J-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), especially preferred saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2 J-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), at least one and especially exactly one herbicidally active compound from group b7), in particular selected from the group consisting of glufosinate, glufosinate-P and glufosinate-ammonium.

According to another preferred embodiment of the invention, the composition comprises, in addition to a a PPO-inhibiting herbicide, preferably acifluorfen, acifluorfen-sodium, butafenacil, cinidon-ethyl, carfentrazone-ethyl, flumioxazin, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31 -6; S-31 00, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4) especially preferred saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2 J-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), at least one and especially exactly one herbicidally active compound from group b9), in particular selected from the group consisting of pendimethalin and trifluralin.

According to another preferred embodiment of the invention, the composition comprises, in addition to a PPO-inhibiting herbicide, preferably acifluorfen, acifluorfen-sodium, butafenacil, cinidon-ethyl, carfentrazone-ethyl, flumioxazin, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31 -6; S-31 00, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4);, especially preferred saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), at least one and especially exactly one herbicidally active compound from group b10), in particular selected from the group consisting of acetochlor, cafenstrole, dimethenamid-P, fentrazamide, flufenacet, mefenacet, metazachlor, metolachlor, S-metolachlor, fenoxasulfone and pyroxasulfone.
Likewise, preference is given to compositions comprising in addition to a a PPO-inhibiting herbicide, preferably acifluorfen, acifluorfen-sodium, butafenacil, cinidon-ethyl, carfentrazone-ethyl, flumioxazin, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1 ,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31-6; S-31 00), 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), especially preferred saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), at least one and especially exactly one herbicidally active compound from group b10), in particular selected from the group consisting of isoxazoline compounds of the formulae 11.1 , II.2, 113, II.4, II.5, II.6, II.7, II.8 and II.9, as defined above.

According to another preferred embodiment of the invention, the composition comprises, in addition to a PPO-inhibiting herbicide, preferably acifluorfen, acifluorfen-sodium, butafenacil, cinidon-ethyl, carfentrazone-ethyl, flumioxazin, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31-6; S-31 00, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione (CAS 1258836-72-4), especially preferred saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione (CAS 1258836-72-4), at least one and especially exactly one herbicidally active compound from group b13), in particular selected from the group consisting of 2,4-D and its salts and esters, aminocyclopyrachlor and its salts and esters, aminopyralid and its salts such as aminopyralid-tris(2-hydroxypropyl)ammonium and its esters, clopyralid and its salts and esters, dicamba and its salts and esters, fluroxypyr-meptyl, quinclorac and quinmerac.

According to another preferred embodiment of the invention, the composition comprises, in addition to a PPO-inhibiting herbicide, preferably acifluorfen, acifluorfen-sodium, butafenacil, cinidon-ethyl, carfentrazone-ethyl, flumioxazin, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31-6; S-31 00), 1,5-dimethyl-6-thioxo-3-(2,2*J*-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione (CAS 1258836-72-4), especially preferred saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione (CAS 1258836-72-4), at least one and especially exactly one herbicidally active compound from group b14), in particular selected from the group consisting of diflufenzopyr and diflufenzopyr-sodium.

According to another preferred embodiment of the invention, the composition comprises, in addition to a PPO-inhibiting herbicide, preferably acifluorfen, acifluorfen-sodium, butafenacil, cinidon-ethyl, carfentrazone-ethyl, flumioxazin, fluthiacet-methyl, fomesafen, lactofen, oxadiargyl, oxyfluorfen, saflufenacil, sulfentrazone, ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31-6; S-31 00), 1,5-dimethyl-6-thioxo-3-(2,2*J*-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione (CAS 1258836-72-4), especially preferred saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione (CAS 1258836-72-4), at least one and especially exactly one herbicidally active compound from group b15), in particular selected from the group consisting of dymron (= daimuron), indanofan, indaziflam, oxaziclomefone and triaziflam.

Here and below, the term "binary compositions" includes compositions comprising one or more, for example 1, 2 or 3, active compounds of the PPO-inhibiting herbicide and either one or more, for example 1, 2 or 3, herbicides B.

In binary compositions comprising at least one PPO-inhibiting herbicide as component A and at least one herbicide B, the weight ratio of the active compounds A:B is generally in the range of from 1:1000 to 1000:1, preferably in the range of from 1:500 to 500:1, in particular in the range of from 1:250 to 250:1 and particularly preferably in the range of from 1:75 to 75:1.

Particularly preferred herbicides B are the herbicides B as defined above; in particular the herbicides B.1 - B.229 listed below in table B:

Table B:

	Herbicide B
B.1	clethodim
B.2	clodinafop-propargyl
B.3	cycloxydim
B.4	cyhalofop-butyl
B.5	fenoxaprop-ethyl
B.6	fenoxaprop-P-ethyl
B.7	fluazifop
B.8	metamifop
B.9	pinoxaden
B.10	profoxydim
B.11	quizalofop
B.12	sethoxydim
B.13	tepraloxydim
B.14	tralkoxydim
B.15	esprocarb
B.16	ethofumesate
B.17	molinate
B.18	prosulfocarb
B.19	thiobencarb
B.20	triallate
B.21	bensulfuron-methyl
B.22	bispyribac-sodium
B.23	cloransulam-methyl
B.24	chlorsulfuron
B.25	clorimuron
B.26	cyclosulfamuron
B.27	diclosulam
B.28	florasulam
B.29	flumetsulam
B.30	flupyrsulfuron-methyl-sodium
B.31	foramsulfuron
B.32	halosulfuron-methyl
B.33	imazamox

	Herbicide B
B.34	imazamox-ammonium
B.35	imazapic
B.36	imazapic-ammonium
B.37	imazapic-isopropylammonium
B.38	imazapyr
B.39	imazapyr-ammonium
B.40	imazapyr-isopropylammonium
B.41	imazaquin
B.42	imazaquin-ammonium
B.43	imazethapyr
B.44	imazethapyr-ammonium
B.45	imazethapyr-isopropylammonium
B.46	imazosulfuron
B.47	iodosulfuron-methyl-sodium
B.48	iofensulfuron
B.49	iofensulfuron-sodium
B.50	mesosulfuron-methyl
B.51	metazosulfuron
B.52	metsulfuron-methyl
B.53	metosulam
B.54	nicosulfuron
B.55	penoxsulam
B.56	propoxycarbazon-sodium
B.57	pyrazosulfuron-ethyl
B.58	pyribenzoxim
B.59	pyriftalid
B.60	pyrithiobac-sodium
B.61	pyroxsulam
B.62	propyrisulfuron
B.63	rimsulfuron
B.64	sulfosulfuron
B.65	thiencarbazone-methyl

	Herbicide B
B.66	thifensulfuron-methyl
B.67	tribenuron-methyl
B.68	trifloxysulfuron
B.69	tritosulfuron
B.70	triafamone
B.71	ametryne
B.72	atrazine
B.73	bentazon
B.74	bromoxynil
B.75	bromoxynil-octanoate
B.76	bromoxynil-heptanoate
B.77	bromoxynil-potassium
B.78	diuron
B.79	fluometuron
B.80	hexazinone
B.81	isoproturon
B.82	linuron
B.83	metamitron
B.84	metribuzin
B.85	prometryne
B.86	propanil
B.87	simazin
B.88	terbuthylazine
B.89	terbutryn
B.90	paraquat-dichloride
B.91	acifluorfen
B.92	acifluorfen-sodium
B.93	azafenidin
B.94	bencarbazone
B.95	benzfendizone
B.96	bifenox
B.97	butafenacil
B.98	carfentrazone
B.99	carfentrazone-ethyl
B.100	chlomethoxyfen
B.101	cinidon-ethyl
B.102	fluazolate
B.103	flufenpyr
B.104	flufenpyr-ethyl
B.105	flumiclorac
B.106	flumiclorac-pentyl

	Herbicide B
B.107	flumioxazin
B.108	fluoroglycofen
B.109	fluoroglycofen-ethyl
B.1 10	fluthiacet
B.1 11	fluthiacet-methyl
B.1 12	fomesafen
B.1 13	halosafen
B.1 14	lactofen
B.1 15	oxadiargyl
B.1 16	oxadiazon
B.1 17	oxyfluorfen
B.1 18	pentoxazone
B.1 19	profluazol
B.120	pyraclonil
B.121	pyraflufen
B.122	pyraflufen-ethyl
B.123	saflufenacil
B.124	sulfentrazone
B.125	thidiazimin
B.126	tiafenacil
B.127	ethyl [3-[2-chloro-4-fluoro-5-(1 -methyl-6-trifluoromethyl-2,4-di-oxo-1 ,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyl-oxy]acetate (CAS 353292-31-6)
B.128	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]-oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4)
B.129	N-ethyl-3-(2,6-dichloro-4-trifluoromethylphenoxy)-5-methyl-1 H-pyrazole-1-carboxamide (CAS 452098-92-9)
B.130	N-tetrahydrofurfuryl-3-(2,6-dichloro-4-trifluoromethylphenoxy)-5-methyl-1 H-pyrazole-1-carboxamide (CAS 915396-43-9)

	Herbicide B
B.131	N-ethyl-3-(2-chloro-6-fluoro-4-trifluoromethylphenoxy)-5-methyl-1 H-pyrazole-1 -carboxamide (CAS 452099-05-7)
B.132	N-tetrahydrofurfuryl-3-(2-chloro-6-fluoro-4-trifluoro-methylphenoxy)-5-methyl-1 *H*-pyrazole-1 -carboxamide (CAS 4521 00-03-7)
B.133	3-[7-fluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl]-1 ,5-dimethyl-6-thioxo-[1 ,3,5]triazinan-2,4-dione
B.134	2-(2,2,7-Trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl)-4, 5,6,7-tetrahydro-isoindole-1 ,3-dione
B.135	1-Methyl-6-trifluoromethyl-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl)-1 H-pyrimidine-2,4-dione
B.136	methyl (E)-4-[2-chloro-5-[4-chloro-5-(difluoromethoxy)-1 *H*-methyl-pyrazol-3-yl]-4-fluoro-phenoxy]-3-methoxy-but-2-enoate [CAS 948893-00-3]
B.137	3-[7-Chloro-5-fluoro-2-(trifluorom ethyl)-1 H-benzimidazol-4-yl]-1 -methyl-6-(trifluorom ethyl)- 1H-pyrimidine-2,4-dione (CAS 212754-02-4)
B.138	benzobicyclon
B.139	clomazone
B.140	diflufenican
B.141	flurochloridone
B.142	isoxaflutole
B.143	mesotrione
B.144	norflurazone
B.145	picolinafen

	Herbicide B
B.146	sulcotrione
B.147	tefuryltrione
B.148	tembotrione
B.149	topramezone
B.150	topramezone-sodium
B.151	bicyclopyrone
B.152	amitrole
B.153	fluometuron
B.154	glyphosate
B.155	glyphosate-ammonium
B.156	glyphosate-dimethylammonium
B.157	glyphosate-isopropylammonium
B.158	glyphosate-trimesium (sulfosate)
B.159	glyphosate-potassium
B.160	glufosinate
B.161	glufosinate-ammonium
B.162	glufosinate-P
B.163	glufosinate-P-ammonium
B.164	pendimethalin
B.165	trifluralin
B.166	acetochlor
B.167	butachlor
B.168	cafenstrole
B.169	dimethenamid-P
B.170	fentrazamide
B.171	flufenacet
B.172	mefenacet
B.173	metazachlor
B.174	metolachlor
B.175	S-metolachlor
B.176	pretilachlor
B.177	fenoxasulfone
B.178	isoxaben
B.179	ipfencarbazone
B.180	pyroxasulfone
B.181	2,4-D
B.182	2,4-D-isobutyl
B.183	2,4-D-dimethylammonium
B.184	2,4-D-N .N.N-trimethylethanolammonium

	Herbicide B
B.185	aminopyralid
B.186	aminopyralid-methyl
B.187	aminopyralid-tris(2-hydroxypropyl)ammonium
B.188	clopyralid
B.189	clopyralid-methyl
B.190	clopyralid-olamine
B.191	dicamba
B.192	dicamba-butotyl
B.193	dicamba-diglycolamine
B.194	dicamba-dimethylammonium
B.195	dicamba-diolamine
B.196	dicamba-isopropylammonium
B.197	dicamba-potassium
B.198	dicamba-sodium
B.199	dicamba-trolamine
B.200	dicamba-N,N-bis-(3-aminopropyl)methylamine
B.201	dicamba-diethylenetriamine
B.202	fluroxypyr
B.203	fluroxypyr-meptyl
B.204	MCPA
B.205	MCPA-2-ethylhexyl
B.206	MCPA-dimethylammonium

	Herbicide B
B.207	quinclorac
B.208	quinclorac-dimethylammonium
B.209	quinmerac
B.210	quinmerac-dimethylammonium
B.211	aminocyclopyrachlor
B.212	aminocyclopyrachlor-potassium
B.213	aminocyclopyrachlor-methyl
B.214	diflufenzopyr
B.215	diflufenzopyr-sodium
B.216	dymron
B.217	indanofan
B.218	indaziflam
B.219	oxaziclomefone
B.220	triaziflam
B.221	II.1
B.222	II.2
B.223	II.3
B.224	II.4
B.225	II.5
B.226	II.6
B.227	II.7
B.228	II.8
B.229	II.9

Particularly preferred are compositions 1.1 to 1.229, comprising acifluorfen and the substance(s) as defined in the respective row of table B-1 :

Table B-1 (compositions 1.1 to 1.229):

comp. no.	herbi-cide B
1.1	B.1
1.2	B.2
1.3	B.3
1.4	B.4
1.5	B.5
1.6	B.6
1.7	B.7
1.8	B.8
1.9	B.9
1.10	B.10

1.11	B.11
1.12	B.12
1.13	B.13
1.14	B.14
1.15	B.15
1.16	B.16
1.17	B.17
1.18	B.18
1.19	B.19
1.20	B.20

1.21	B.21
1.22	B.22
1.23	B.23
1.24	B.24
1.25	B.25
1.26	B.26
1.27	B.27
1.28	B.28
1.29	B.29
1.30	B.30

1.31	B.31
1.32	B.32
1.33	B.33
1.34	B.34
1.35	B.35
1.36	B.36
1.37	B.37
1.38	B.38
1.39	B.39
1.40	B.40
1.41	B.41
1.42	B.42
1.43	B.43
1.44	B.44
1.45	B.45
1.46	B.46
1.47	B.47
1.48	B.48
1.49	B.49
1.50	B.50
1.51	B.51
1.52	B.52
1.53	B.53
1.54	B.54
1.55	B.55
1.56	B.56
1.57	B.57
1.58	B.58.
1.59	B.59
1.60	B.60
1.61	B.61
1.62	B.62
1.63	B.63
1.64	B.64
1.65	B.65
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1.67	B.67
1.68	B.68
1.69	B.69
1.70	B.70
1.71	B.71
1.72	B.72
1.73	B.73

1.74	B.74
1.75	B.75
1.76	B.76
1.77	B.77
1.78	B.78
1.79	B.79
1.80	B.80
1.81	B.81
1.82	B.82
1.83	B.83
1.84	B.84
1.85	B.85
1.86	B.86
1.87	B.87
1.88	B.88
1.89	B.89
1.90	B.90
1.91	B.91
1.92	B.92
1.93	B.93
1.94	B.94
1.95	B.95
1.96	B.96
1.97	B.97
1.98	B.98
1.99	B.99
1.100	B.100
1.101	B.101
1.102	B.102
1.103	B.103
1.104	B.104
1.105	B.105
1.106	B.106
1.107	B.107
1.108	B.108
1.109	B.109
1.1 10	B.1 10
1.1 11	B.1 11
1.1 12	B.1 12
1.1 13	B.1 13
1.1 14	B.1 14
1.1 15	B.1 15
1.1 16	B.1 16

1.1 17	B.1 17
1.1 18	B.1 18
1.1 19	B.1 19
1.120	B.120
1.121	B.121
1.122	B.122
1.123	B.123
1.124	B.124
1.125	B.125
1.126	B.126
1.127	B.127
1.128	B.128
1.129	B.129
1.130	B.130
1.131	B.131
1.132	B.132
1.133	B.133
1.134	B.134
1.135	B.135
1.136	B.136
1.137	B.137
1.138	B.138
1.139	B.139
1.140	B.140
1.141	B.141
1.142	B.142
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1.144	B.144
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1.147	B.147
1.148	B.148
1.149	B.149
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1.151	B.151
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1.160	B.160
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1.162	B.162
1.163	B.163
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1.165	B.165
1.166	B.166
1.167	B.167
1.168	B.168
1.169	B.169
1.170	B.170
1.171	B.171
1.172	B.172
1.173	B.173
1.174	B.174
1.175	B.175
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1.177	B.177
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1.191	B.191
1.192	B.192
1.193	B.193
1.194	B.194
1.195	B.195
1.196	B.196
1.197	B.197
1.198	B.198
1.199	B.199
1.200	B.200
1.201	B.201
1.202	B.202
1.203	B.203
1.204	B.204
1.205	B.205
1.206	B.206
1.207	B.207
1.208	B.208
1.209	B.209
1.210	B.210
1.21 1	B.21 1
1.212	B.212
1.213	B.213
1.214	B.214
1.215	B.215
1.216	B.216
1.217	B.217
1.218	B.218
1.219	B.219
1.220	B.220
1.221	B.221
1.222	B.222
1.223	B.223
1.224	B.224
1.225	B.225
1.226	B.226
1.227	B.227
1.228	B.228
1.229	B.229

Also especially preferred are compositions 2.1 . to 2.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A acifluorfen-sodium.

Also especially preferred are compositions 3.1 . to 3.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A azafenidin.

Also especially preferred are compositions 4.1 . to 4.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A bencarbazone.

Also especially preferred are compositions 5.1. to 5.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A benzfendizone.

Also especially preferred are compositions 6.1 . to 6.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A bifenox.

Also especially preferred are compositions 7.1 . to 7.229 which differ from the corresponding compositions 1.1 to 1.227 only in that they comprise as component A butafenacil.

Also especially preferred are compositions 8.1 . to 8.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A carfentrazone.

Also especially preferred are compositions 9.1 . to 9.229which differ from the corresponding compositions 1.1 to 1. 229 only in that they comprise as component A carfentrazone-ethyl.

Also especially preferred are compositions 10.1. to 10.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A chlomethoxyfen.

Also especially preferred are compositions 11.1 . to 11.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A cinidon-ethyl.

Also especially preferred are compositions 12.1 . to 12.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A fluazolate.

Also especially preferred are compositions 13.1 . to 13.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A flufenpyr.

Also especially preferred are compositions 14.1. to 14.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A flufenpyr-ethyl.

Also especially preferred are compositions 15.1 . to 15.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A flumiclorac.

Also especially preferred are compositions 16.1 . to 16.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A flumiclorac-pentyl.

Also especially preferred are compositions 17.1. to 17.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A flumioxazin.

Also especially preferred are compositions 18.1. to 18.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A fluoroglycofen.

Also especially preferred are compositions 19.1. to 19.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A fluoroglycofen-ethyl.

Also especially preferred are compositions 20.1. to 20.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A fluthiacet.

Also especially preferred are compositions 21.1. to 21.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A fluthiacet-methyl.

Also especially preferred are compositions 22.1. to 22.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A fomesafen.

Also especially preferred are compositions 23.1. to 23.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A halosafen.

Also especially preferred are compositions 24.1. to 24.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A lactofen.

Also especially preferred are compositions 25.1. to 25.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A oxadiargyl.

Also especially preferred are compositions 26.1. to 26.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A oxadiazon.

Also especially preferred are compositions 27.1. to 27.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A oxyfluorfen.

Also especially preferred are compositions 28.1. to 28.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A pentoxazone.

Also especially preferred are compositions 29.1. to 29.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A profluazol.

Also especially preferred are compositions 30.1. to 30.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A pyraclonil.

Also especially preferred are compositions 31.1. to 31.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A pyraflufen.

Also especially preferred are compositions 32.1. to 32.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A pyraflufen-ethyl.

Also especially preferred are compositions 33.1. to 33.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A saflufenacil.

Also especially preferred are compositions 34.1. to 34.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A sulfentrazone.

Also especially preferred are compositions 35.1. to 35.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A thidiazimin.

Also especially preferred are compositions 36.1. to 36.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A tiafenacil.

Also especially preferred are compositions 37.1. to 37.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A ethyl [3-[2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1 ,2,3,4-tetrahydropyrimidin-3-yl)phenoxy]-2-pyridyloxy]acetate (CAS 353292-31-6; S-3100).

Also especially preferred are compositions 38.1. to 38.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A 1,5-dimethyl-6-thioxo-3-(2,27-trifluoro-3-oxo-4-(prop-2-ynyl)-3^-dihydro-2H-benzo[b][1 ^]oxazin-6-yl)-1 ,3,5-triazinane-2^-dione (CAS 1258836-72-4)

Also especially preferred are compositions 39.1. to 39.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A N-ethyl-3-(2,6-dichloro-4-trifluoromethylphenoxy)-5-methyl-1 /-/-pyrazole-1-carboxamide (CAS 452098-92-9).

Also especially preferred are compositions 40.1. to 40.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A N-tetrahydrofurfuryl-3-(2,6-dichloro-4-trifluoromethylphenoxy)-5-methyl-1 /-/-pyrazole-1-carboxamide (CAS 915396-43-9).

Also especially preferred are compositions 41.1. to 41.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A N-ethyl-3-(2-chloro-6-fluoro-4-trifluoromethylphenoxy)-5-methyl-1 H-pyrazole-1-carboxamide (CAS 452099-05-7).

Also especially preferred are compositions 42.1. to 42.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A N-tetrahydrofurfuryl-3-(2-chloro-6-fluoro-4-trifluoromethylphenoxy)-5-methyl-1 /-/-pyrazole-1-carboxamide (CAS 452100-03-7).

Also especially preferred are compositions 43.1 . to 43.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A 3-[7-fluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[1,4]oxazin-6-yl]-1 ,5-dimethyl-6-thioxo-[1,3,5]triazinan-2,4-dione.

Also especially preferred are compositions 44.1. to 44.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A methyl (£)-4-[2-chloro-5-[4-chloro-5-(difluoromethoxy)-1 H-methyl-pyrazol-3-yl]-4-fluoro-phenoxy]-3-methoxy-but-2-enoate (CAS 948893-00-3).

Also especially preferred are compositions 45.1. to 45.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A 3-[7-Chloro-5-fluoro-2-(trifluoromethyl)-1 H-benzimidazol-4-yl]-1-methyl-6-(trifluoromethyl)-1 H-pyrimidine-2,4-dione (CAS 212754-02-4).

Also especially preferred are compositions 46.1 . to 46.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A 2-(2,2,7-Trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl)-4,5,6,7-tetrahydro-isoindole-1,3-dione.

Also especially preferred are compositions 47.1 . to 47.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they comprise as component A 1-Methyl-6-trifluoromethyl-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-3,4-dihydro-2H-benzo[1 ,4]oxazin-6-yl)-1 H-pyrimidine-2,4-dione

Also especially preferred are compositions 48.1 . to 48.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they additionally comprise benoxacor as safener C.

Also especially preferred are compositions 49.1 . to 49.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they additionally comprise cloquintocet as safener C.

Also especially preferred are compositions 50.1. to 50.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they additionally comprise cyprosulfamide as safener C.

Also especially preferred are compositions 51.1. to 51.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they additionally comprise dichlormid as safener C.

Also especially preferred are compositions 52.1 . to 52.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they additionally comprise fenchlorazole as safener C.

Also especially preferred are compositions 53.1 . to 53.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they additionally comprise fenclorim as safener C.

Also especially preferred are compositions 54.1 . to 54.229 which differ from the corresponding

compositions 1.1 to 1.229 only in that they additionally comprise furilazole as safener C.

Also especially preferred are compositions 55.1. to 55.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they additionally comprise isoxadifen as safener C.

Also especially preferred are compositions 56.1. to 56.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they additionally comprise mefenpyr as safener C.

Also especially preferred are compositions 57.1. to 57.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they additionally comprise 4-(dichloroacetyl)-1 -oxa-4-azaspiro[4.5]decane (MON4660, CAS 71526-07-3) as safener C.

Also especially preferred are compositions 58.1. to 58.229 which differ from the corresponding compositions 1.1 to 1.229 only in that they additionally comprise 2,2,5-trimethyl-3-(dichloroacetyl)-1,3-oxazolidine (R-29148, CAS 52836-31 -4) as safener C.

It is generally preferred to use the compounds of the invention in combination with herbicides that are selective for the crop being treated and which complement the spectrum of weeds controlled by these compounds at the application rate employed. It is further generally preferred to apply the compounds of the invention and other complementary herbicides at the same time, either as a combination formulation or as a tank mix.

It is recognized that the polynucleotide molecules and polypeptides of the invention encompass polynucleotide molecules and polypeptides comprising a nucleotide or an amino acid sequence that is sufficiently identical to nucleotide sequences set forth in SEQ ID Nos: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, or 47, or to the amino acid sequences set forth in SEQ ID Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, or 48. The term "sufficiently identical" is used herein to refer to a first amino acid or nucleotide sequence that contains a sufficient or minimum number of identical or equivalent (e.g., with a similar side chain) amino acid residues or nucleotides to a second amino acid or nucleotide sequence such that the first and second amino acid or nucleotide sequences have a common structural domain and/or common functional activity.

Generally, "sequence identity" refers to the extent to which two optimally aligned DNA or amino acid sequences are invariant throughout a window of alignment of components, e.g., nucleotides or amino acids. An "identity fraction" for aligned segments of a test sequence and a reference sequence is the number of identical components that are shared by the two aligned sequences divided by the total number of components in reference sequence segment, i.e., the entire reference sequence or a smaller defined part of the reference sequence. "Percent identity" is the identity fraction times 100. Optimal alignment of sequences for aligning a comparison window are well known to those skilled in the art and may be conducted by tools such as the local homology algorithm of Smith and Waterman, the homology alignment algorithm of Needleman and Wunsch, the search for similarity method of Pearson and Lipman, and preferably by computerized implementations of these algorithms such as GAP, BESTFIT, FASTA, and TFASTA available as

part of the GCG. Wisconsin Package. (Accelrys Inc. Burlington, Mass.)

Polynucleotides and Oligonucleotides

By an "isolated polynucleotide", including DNA, RNA, or a combination of these, single or double stranded, in the sense or antisense orientation or a combination of both, dsRNA or otherwise, we mean a polynucleotide which is at least partially separated from the polynucleotide sequences with which it is associated or linked in its native state. That means other nucleic acid molecules are present in an amount less than 5% based on weight of the amount of the desired nucleic acid, preferably less than 2% by weight, more preferably less than 1% by weight, most preferably less than 0.5% by weight. Preferably, an "isolated" nucleic acid is free of some of the sequences that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated herbicide resistance and/or tolerance related protein encoding nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be free from some of the other cellular material with which it is naturally associated, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. Preferably, the isolated polynucleotide is at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other components with which they are naturally associated. As the skilled addressee would be aware, an isolated polynucleotide can be an exogenous polynucleotide present in, for example, a transgenic organism which does not naturally comprise the polynucleotide.

Furthermore, the terms "polynucleotide(s)", "nucleic acid sequence(s)", "nucleotide sequence(s)", "nucleic acid(s)", "nucleic acid molecule" are used interchangeably herein and refer to nucleotides, either ribonucleotides or deoxyribonucleotides or a combination of both, in a polymeric unbranched form of any length.

The term "mutated PPO nucleic acid" refers to a PPO nucleic acid having a sequence that is mutated from a wild-type PPO nucleic acid and that confers increased PPO-inhibiting herbicide tolerance to a plant in which it is expressed. Furthermore, the term "mutated protoporphyrinogen oxidase (mutated PPO)" refers to the replacement of an amino acid of the wild-type primary sequences SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, or 48, or a variant, a derivative, a homologue, an orthologue, or paralogue thereof, with another amino acid. The expression "mutated amino acid" will be used below to designate the amino acid which is replaced by another amino acid, thereby designating the site of the mutation in the primary sequence of the protein.

In a preferred embodiment, the PPO nucleotide sequence encoding a mutated PPO comprises the sequence of SEQ ID NO: 1, 3, 23, 29, 37, 45, or 47, or a variant or derivative thereof.

Furthermore, it will be understood by the person skilled in the art that the PPO nucleotide

sequences encompasse homologues, paralogues and and orthologues of SEQ ID NO: 1, 3, 23, 29, 37, 45, or 47, as defined hereinafter.

The term "variant" with respect to a sequence (e.g., a polypeptide or nucleic acid sequence such as - for example - a transcription regulating nucleotide sequence of the invention) is intended to mean substantially similar sequences. For nucleotide sequences comprising an open reading frame, variants include those sequences that, because of the degeneracy of the genetic code, encode the identical amino acid sequence of the native protein. Naturally occurring allelic variants such as these can be identified with the use of well-known molecular biology techniques, as, for example, with polymerase chain reaction (PCR) and hybridization techniques. Variant nucleotide sequences also include synthetically derived nucleotide sequences, such as those generated, for example, by using site-directed mutagenesis and for open reading frames, encode the native protein, as well as those that encode a polypeptide having amino acid substitutions relative to the native protein, e.g. the mutated PPO according to the present invention as disclosed herein. Generally, nucleotide sequence variants of the invention will have at least 30, 40, 50, 60, to 70%, e.g., preferably 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, to 79%, generally at least 80%, e.g., 81%-84%, at least 85%, e.g., 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, to 98% and 99% nucleotide "sequence identity" to the nucleotide sequence of SEQ ID NO: SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, or 47. The % identity of a polynucleotide is determined by GAP (Needleman and Wunsch, 1970) analysis (GCG program) with a gap creation penalty=5, and a gap extension penalty=0.3. Unless stated otherwise, the query sequence is at least 45 nucleotides in length, and the GAP analysis aligns the two sequences over a region of at least 45 nucleotides. Preferably, the query sequence is at least 150 nucleotides in length, and the GAP analysis aligns the two sequences over a region of at least 150 nucleotides. More preferably, the query sequence is at least 300 nucleotides in length and the GAP analysis aligns the two sequences over a region of at least 300 nucleotides. Even more preferably, the GAP analysis aligns the two sequences over their entire length.

Polypeptides

By "substantially purified polypeptide" or "purified" a polypeptide is meant that has been separated from one or more lipids, nucleic acids, other polypeptides, or other contaminating molecules with which it is associated in its native state. It is preferred that the substantially purified polypeptide is at least 60% free, more preferably at least 75% free, and more preferably at least 90% free from other components with which it is naturally associated. As the skilled addressee will appreciate, the purified polypeptide can be a recombinantly produced polypeptide. The terms "polypeptide" and "protein" are generally used interchangeably and refer to a single polypeptide chain which may or may not be modified by addition of non-amino acid groups. It would be understood that such polypeptide chains may associate with other polypeptides or proteins or other molecules such as co-factors. The terms "proteins" and "polypeptides" as used herein also include variants, mutants, modifications, analogous and/or derivatives of the polypeptides of the invention as described herein.

The % identity of a polypeptide is determined by GAP (Needleman and Wunsch, 1970) analysis

(GCG program) with a gap creation penalty=5, and a gap extension penalty=0.3. The query sequence is at least 25 amino acids in length, and the GAP analysis aligns the two sequences over a region of at least 25 amino acids. More preferably, the query sequence is at least 50 amino acids in length, and the GAP analysis aligns the two sequences over a region of at least 50 amino acids. More preferably, the query sequence is at least 100 amino acids in length and the GAP analysis aligns the two sequences over a region of at least 100 amino acids. Even more preferably, the query sequence is at least 250 amino acids in length and the GAP analysis aligns the two sequences over a region of at least 250 amino acids. Even more preferably, the GAP analysis aligns the two sequences over their entire length.

With regard to a defined polypeptide, it will be appreciated that % identity figures higher than those provided above will encompass preferred embodiments. Thus, where applicable, in light of the minimum % identity figures, it is preferred that the PPO polypeptide of the invention comprises an amino acid sequence which is at least 40%, more preferably at least 45%, more preferably at least 50%, more preferably at least 55%, more preferably at least 60%, more preferably at least 65%, more preferably at least 70%, more preferably at least 75%, more preferably at least 80%, more preferably at least 85%, more preferably at least 90%, more preferably at least 91%, more preferably at least 92%, more preferably at least 93%, more preferably at least 94%, more preferably at least 95%, more preferably at least 96%, more preferably at least 97%, more preferably at least 98%, more preferably at least 99%, more preferably at least 99.1%, more preferably at least 99.2%, more preferably at least 99.3%, more preferably at least 99.4%, more preferably at least 99.5%, more preferably at least 99.6%, more preferably at least 99.7%, more preferably at least 99.8%, and even more preferably at least 99.9% identical to SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, or 48.

By "variant" polypeptide is intended a polypeptide derived from the protein of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, or 48 by deletion (so-called truncation) or addition of one or more amino acids to the N-terminal and/or C-terminal end of the native protein; deletion or addition of one or more amino acids at one or more sites in the native protein; or substitution of one or more amino acids at one or more sites in the native protein. Such variants may result from, for example, genetic polymorphism or from human manipulation. Methods for such manipulations are generally known in the art.

"Derivatives" of a protein encompass peptides, oligopeptides, polypeptides, proteins and enzymes having amino acid substitutions, deletions and/or insertions relative to the unmodified protein in question and having similar biological and functional activity as the unmodified protein from which they are derived.

"Homologues" of a protein encompass peptides, oligopeptides, polypeptides, proteins and enzymes having amino acid substitutions, deletions and/or insertions relative to the unmodified protein in question and having similar biological and functional activity as the unmodified protein from which they are derived.

A deletion refers to removal of one or more amino acids from a protein.

An insertion refers to one or more amino acid residues being introduced into a predetermined site in a protein. Insertions may comprise N-terminal and/or C-terminal fusions as well as intra-sequence insertions of single or multiple amino acids. Generally, insertions within the amino acid sequence will be smaller than N- or C-terminal fusions, of the order of about 1 to 10 residues. Examples of N- or C-terminal fusion proteins or peptides include the binding domain or activation domain of a transcriptional activator as used in the yeast two-hybrid system, phage coat proteins, (histidine)-6-tag, glutathione S-transferase-tag, protein A, maltose-binding protein, dihydrofolate reductase, Tag•100 epitope, c-myc epitope, FLAG®-epitope, lacZ, CMP (calmodulin-binding peptide), HA epitope, protein C epitope and VSV epitope.

A substitution refers to replacement of amino acids of the protein with other amino acids having similar properties (such as similar hydrophobicity, hydrophilicity, antigenicity, propensity to form or break a-helical structures or β-sheet structures). Amino acid substitutions are typically of single residues, but may be clustered depending upon functional constraints placed upon the polypeptide and may range from 1 to 10 amino acids; insertions will usually be of the order of about 1 to 10 amino acid residues. The amino acid substitutions are preferably conservative amino acid substitutions. Conservative substitution tables are well known in the art (see for example Creighton (1984) Proteins. W.H. Freeman and Company (Eds).

Table 2: Examples of conserved amino acid substitutions

Residue	Conservative Substitutions	Residue	Conservative Substitutions
Ala	Ser	Leu	Ile; Val
Arg	Lys	Lys	Arg; Gln
Asn	Gln; His	Met	Leu; Ile
Asp	Glu	Phe	Met; Leu; Tyr
Gln	Asn	Ser	Thr; Gly
Cys	Ser	Thr	Ser; Val
Glu	Asp	Trp	Tyr
Gly	Pro	Tyr	Trp; Phe
His	Asn; Gln	Val	Ile; Leu
Ile	Leu, Val		

Amino acid substitutions, deletions and/or insertions may readily be made using peptide synthetic techniques well known in the art, such as solid phase peptide synthesis and the like, or by recombinant DNA manipulation. Methods for the manipulation of DNA sequences to produce substitution, insertion or deletion variants of a protein are well known in the art. For example, techniques for making substitution mutations at predetermined sites in DNA are well known to those skilled in the art and include M13 mutagenesis, T7-Gen in vitro mutagenesis (USB, Cleveland, OH), QuickChange Site Directed mutagenesis (Stratagene, San Diego, CA), PCR-mediated site-directed mutagenesis or other site-directed mutagenesis protocols.

"Derivatives" further include peptides, oligopeptides, polypeptides which may, compared to the amino acid sequence of the naturally-occurring form of the protein, such as the protein of interest, comprise substitutions of amino acids with non-naturally occurring amino acid residues, or

additions of non-naturally occurring amino acid residues. "Derivatives" of a protein also encompass peptides, oligopeptides, polypeptides which comprise naturally occurring altered (glycosylated, acylated, prenylated, phosphorylated, myristoylated, sulphated etc.) or non-naturally altered amino acid residues compared to the amino acid sequence of a naturally-occurring form of the polypeptide. A derivative may also comprise one or more non-amino acid substituents or additions compared to the amino acid sequence from which it is derived, for example a reporter molecule or other ligand, covalently or non-covalently bound to the amino acid sequence, such as a reporter molecule which is bound to facilitate its detection, and non-naturally occurring amino acid residues relative to the amino acid sequence of a naturally-occurring protein. Furthermore, "derivatives" also include fusions of the naturally-occurring form of the protein with tagging peptides such as FLAG, HIS6 or thioredoxin (for a review of tagging peptides, see Terpe, Appl. Microbiol. Biotechnol. 60, 523-533, 2003).

"Orthologues" and "paralogues" encompass evolutionary concepts used to describe the ancestral relationships of genes. Paralogues are genes within the same species that have originated through duplication of an ancestral gene; orthologues are genes from different organisms that have originated through speciation, and are also derived from a common ancestral gene. A non-limiting list of examples of such orthologues are shown in Table 1.

It is well-known in the art that paralogues and orthologues may share distinct domains harboring suitable amino acid residues at given sites, such as binding pockets for particular substrates, compounds such as e.g. herbicides, or binding motifs for interaction with other proteins.

The term "domain" refers to a set of amino acids conserved at specific positions along an alignment of sequences of evolutionarily related proteins. While amino acids at other positions can vary between homologues, amino acids that are highly conserved at specific positions indicate amino acids that are likely essential in the structure, stability or function of a protein. Identified by their high degree of conservation in aligned sequences of a family of protein homologues, they can be used as identifiers to determine if any polypeptide in question belongs to a previously identified polypeptide family.

The term "motif or "consensus sequence" refers to a short conserved region in the sequence of evolutionarily related proteins. Motifs are frequently highly conserved parts of domains, but may also include only part of the domain, or be located outside of conserved domain (if all of the amino acids of the motif fall outside of a defined domain).

Specialist databases exist for the identification of domains, for example, SMART (Schultz et al. (1998) Proc. Natl. Acad. Sci. USA 95, 5857-5864; Letunic et al. (2002) Nucleic Acids Res 30, 242-244), InterPro (Mulder et al., (2003) Nucl. Acids. Res. 31, 315-318), Prosite (Bucher and Bairoch (1994), A generalized profile syntax for biomolecular sequences motifs and its function in automatic sequence interpretation. (In) ISMB-94; Proceedings 2nd International Conference on Intelligent Systems for Molecular Biology. Altman R., Brutlag D., Karp P., Lathrop R., Searls D., Eds., pp53-61 , AAAI Press, Menlo Park; Hulo et al., Nucl. Acids. Res. 32:D134-D137, (2004)), or Pfam (Bateman et al., Nucleic Acids Research 30(1): 276-280 (2002)). A set of tools for in silico

analysis of protein sequences is available on the ExPASy proteomics server (Swiss Institute of Bioinformatics (Gasteiger et al., ExPASy: the proteomics server for in-depth protein knowledge and analysis, Nucleic Acids Res. 31:3784-3788(2003)). Domains or motifs may also be identified using routine techniques, such as by sequence alignment.

Methods for the alignment of sequences for comparison are well known in the art, such methods include GAP, BESTFIT, BLAST, FASTA and TFASTA. GAP uses the algorithm of Needleman and Wunsch ((1970) J Mol Biol 48: 443-453) to find the global (i.e. spanning the complete sequences) alignment of two sequences that maximizes the number of matches and minimizes the number of gaps. The BLAST algorithm (Altschul et al. (1990) J Mol Biol 215: 403-10) calculates percent sequence identity and performs a statistical analysis of the similarity between the two sequences. The software for performing BLAST analysis is publicly available through the National Centre for Biotechnology Information (NCBI). Homologues may readily be identified using, for example, the ClustalW multiple sequence alignment algorithm (version 1.83), with the default pairwise alignment parameters, and a scoring method in percentage. Global percentages of similarity and identity may also be determined using one of the methods available in the MatGAT software package (Campanella et al., BMC Bioinformatics. 2003 Jul 10;4:29. MatGAT: an application that generates similarity/identity matrices using protein or DNA sequences.). Minor manual editing may be performed to optimise alignment between conserved motifs, as would be apparent to a person skilled in the art. Furthermore, instead of using full-length sequences for the identification of homologues, specific domains may also be used. The sequence identity values may be determined over the entire nucleic acid or amino acid sequence or over selected domains or conserved motif(s), using the programs mentioned above using the default parameters. For local alignments, the Smith-Waterman algorithm is particularly useful (Smith TF, Waterman MS (1981) J. Mol. Biol 147(1);195-7).

The inventors of the present invention have found that by substituting one or more of the key amino acid residues, employing e.g. one of the above described methods to mutate the encoding nucleic acids, the herbicide tolerance or resistance could be remarkably increased as compared to the activity of the wild type PPO enzymes with SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, or 48. Preferred substitutions of mutated PPO are those that increase the herbicide tolerance of the plant, but leave the biological activitiy of the oxidase activity substantially unaffected.

Accordingly, in another object of the present invention the key amino acid residues of a PPO enzyme comprising SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, or 48, a variant, derivative, orthologue, paralogue or homologue thereof, is substituted by any other amino acid.

In one embodiment, the key amino acid residues of a PPO enzyme, a variant, derivative, orthologue, paralogue or homologue thereof, is substituted by a conserved amino acid as depicted in Table 2.

It will be understood by the person skilled in the art that amino acids located in a close proximity to

the positions of amino acids mentioned below may also be substituted. Thus, in another embodiment the variant of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, or 48, a variant, derivative, orthologue, paralogue or homologue thereof comprises a mutated PPO, wherein an amino acid ±3, ±2 or ± 1 amino acid positions from a key amino acid is substituted by any other amino acid.

Based on techniques well-known in the art, a highly characteristic sequence pattern can be developed, by means of which further of mutated PPO candidates with the desired activity may be searched.

Searching for further mutated PPO candidates by applying a suitable sequence pattern would also be encompassed by the present invention. It will be understood by a skilled reader that the present sequence pattern is not limited by the exact distances between two adjacent amino acid residues of said pattern. Each of the distances between two neighbours in the above patterns may, for example, vary independently of each other by up to ±10, ± 5, ±3, ±2 or ± 1 amino acid positions without substantially affecting the desired activity.

Furthermore, by applying the method of site directed mutagenesis, in particular saturation mutagenes (see e.g. Schenk et ***al,*** Biospektrum 03/2006, pages 277-279), the inventors of the present invention have identified and generated specific amino acid subsitutions and combinations thereof, which - when introduced into a plant by transforming and expressing the respective mutated PPO encoding nucleic acid - confer increased herbicide resistance or tolerance to a PPO inhibiting herbicide to said plant.

Thus, in a particularly preferred embodiment, the variant or derivative of the mutated PPO refers to a polypeptide comprising SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 24, SEQ ID NO: 30, SEQ ID NO: 38, SEQ ID NO: 46, or SEQ ID NO: 48, comprising a single amino acid substitution of the following Table 3a. .

Table 3a: Single amino acid substitutions within SEQ ID NO: 2, SEQ ID NO:4, SEQ ID NO: 24, SEQ ID NO: 30, SEQ ID NO: 38, SEQ ID NO: 46, SEQ ID NO: 48,

Mutation Number	SEQ ID NO:	Key amino acid position combination	Preferred Substitution
1	2	Arg128	Ala
2	2	Arg128	Leu
3	2	Arg128	Val
4	2	Arg128	lie
5	2	Arg128	Met
6	2	Arg128	His
7	2	Arg128	Lys
8	2	Arg128	Asp
9	2	Arg128	Glu
10	2	Arg128	Ser

11	2	Arg128	Thr
12	2	Arg128	Asn
13	2	Arg128	Gin
14	2	Arg128	Cys
15	2	Arg128	Gly
16	2	Arg128	Pro
17	2	Arg128	Phe
18	2	Arg128	Tyr
19	2	Arg128	Trp
20	2	Phe420	Ala
21	2	Phe420	Leu
22	2	Phe420	Val
23	2	Phe420	lie
24	2	Phe420	Met
25	2	Phe420	His
26	2	Phe420	Lys
27	2	Phe420	Asp
28	2	Phe420	Glu
29	2	Phe420	Ser
30	2	Phe420	Thr
31	2	Phe420	Asn
32	2	Phe420	Gin
33	2	Phe420	Cys
34	2	Phe420	Gly
35	2	Phe420	Pro
36	2	Phe420	Phe
37	2	Phe420	Tyr
38	2	Phe420	Trp
39	4	Arg128	Ala
40	4	Arg128	Leu
41	4	Arg128	Val
42	4	Arg128	lie
43	4	Arg128	Met
44	4	Arg128	His
45	4	Arg128	Lys
46	4	Arg128	Asp
47	4	Arg128	Glu
48	4	Arg128	Ser
49	4	Arg128	Thr
50	4	Arg128	Asn
51	4	Arg128	Gin
52	4	Arg128	Cys
53	4	Arg128	Gly

54	4	Arg128	Pro
55	4	Arg128	Phe
56	4	Arg128	Tyr
57	4	Arg128	Trp
58	4	Phe420	Ala
59	4	Phe420	Leu
60	4	Phe420	Val
61	4	Phe420	lie
62	4	Phe420	Met
63	4	Phe420	His
64	4	Phe420	Lys
65	4	Phe420	Asp
66	4	Phe420	Glu
67	4	Phe420	Ser
68	4	Phe420	Thr
69	4	Phe420	Asn
70	4	Phe420	Gin
71	4	Phe420	Cys
72	4	Phe420	Gly
73	4	Phe420	Pro
74	4	Phe420	Phe
75	4	Phe420	Tyr
76	4	Phe420	Trp
77	24	Arg130	Ala
78	24	Arg130	Leu
79	24	Arg130	Val
80	24	Arg130	lie
81	24	Arg130	Met
82	24	Arg130	His
83	24	Arg130	Lys
84	24	Arg130	Asp
85	24	Arg130	Glu
86	24	Arg130	Ser
87	24	Arg130	Thr
88	24	Arg130	Asn
89	24	Arg130	Gin
90	24	Arg130	Cys
91	24	Arg130	Gly
92	24	Arg130	Pro
93	24	Arg130	Phe
94	24	Arg130	Tyr
95	24	Arg130	Trp
96	24	Phe433	Ala

97	24	Phe433	Leu
98	24	Phe433	Val
99	24	Phe433	lie
100	24	Phe433	Met
101	24	Phe433	His
102	24	Phe433	Lys
103	24	Phe433	Asp
104	24	Phe433	Glu
105	24	Phe433	Ser
106	24	Phe433	Thr
107	24	Phe433	Asn
108	24	Phe433	Gin
109	24	Phe433	Cys
110	24	Phe433	Gly
111	24	Phe433	Pro
112	24	Phe433	Phe
113	24	Phe433	Tyr
114	24	Phe433	Trp
115	30	Arg130	Ala
116	30	Arg130	Leu
117	30	Arg130	Val
118	30	Arg130	lie
119	30	Arg130	Met
120	30	Arg130	His
121	30	Arg130	Lys
122	30	Arg130	Asp
123	30	Arg130	Glu
124	30	Arg130	Ser
125	30	Arg130	Thr
126	30	Arg130	Asn
127	30	Arg130	Gin
128	30	Arg130	Cys
129	30	Arg130	Gly
130	30	Arg130	Pro
131	30	Arg130	Phe
132	30	Arg130	Tyr
133	30	Arg130	Trp
134	30	Phe433	Ala
135	30	Phe433	Leu
136	30	Phe433	Val
137	30	Phe433	lie
138	30	Phe433	Met
139	30	Phe433	His

140	30	Phe433	Lys
141	30	Phe433	Asp
142	30	Phe433	Glu
143	30	Phe433	Ser
144	30	Phe433	Thr
145	30	Phe433	Asn
146	30	Phe433	Gin
147	30	Phe433	Cys
148	30	Phe433	Gly
149	30	Phe433	Pro
150	30	Phe433	Phe
151	30	Phe433	Tyr
152	30	Phe433	Trp
153	38	Arg98	Ala
154	38	Arg98	Leu
155	38	Arg98	Val
156	38	Arg98	lie
157	38	Arg98	Met
158	38	Arg98	His
159	38	Arg98	Lys
160	38	Arg98	Asp
161	38	Arg98	Glu
162	38	Arg98	Ser
163	38	Arg98	Thr
164	38	Arg98	Asn
165	38	Arg98	Gin
166	38	Arg98	Cys
167	38	Arg98	Gly
168	38	Arg98	Pro
169	38	Arg98	Phe
170	38	Arg98	Tyr
171	38	Arg98	Trp
172	38	Phe392	Ala
173	38	Phe392	Leu
174	38	Phe392	Val
175	38	Phe392	lie
176	38	Phe392	Met
177	38	Phe392	His
178	38	Phe392	Lys
179	38	Phe392	Asp
180	38	Phe392	Glu
181	38	Phe392	Ser
182	38	Phe392	Thr

183	38	Phe392	Asn
184	38	Phe392	Gin
185	38	Phe392	Cys
186	38	Phe392	Gly
187	38	Phe392	Pro
188	38	Phe392	Phe
189	38	Phe392	Tyr
190	38	Phe392	Trp
191	46	Arg139	Ala
192	46	Arg139	Leu
193	46	Arg139	Val
194	46	Arg139	lie
195	46	Arg139	Met
196	46	Arg139	His
197	46	Arg139	Lys
198	46	Arg139	Asp
199	46	Arg139	Glu
200	46	Arg139	Ser
201	46	Arg139	Thr
202	46	Arg139	Asn
203	46	Arg139	Gin
204	46	Arg139	Cys
205	46	Arg139	Gly
206	46	Arg139	Pro
207	46	Arg139	Phe
208	46	Arg139	Tyr
209	46	Arg139	Trp
210	46	Phe465	Ala
211	46	Phe465	Leu
212	46	Phe465	Val
213	46	Phe465	lie
214	46	Phe465	Met
215	46	Phe465	His
216	46	Phe465	Lys
217	46	Phe465	Asp
218	46	Phe465	Glu
219	46	Phe465	Ser
220	46	Phe465	Thr
221	46	Phe465	Asn
222	46	Phe465	Gin
223	46	Phe465	Cys
224	46	Phe465	Gly
225	46	Phe465	Pro

226	46	Phe465	Phe
227	46	Phe465	Tyr
228	46	Phe465	Trp
229	48	Arg157	Ala
230	48	Arg157	Leu
231	48	Arg157	Val
232	48	Arg157	lie
233	48	Arg157	Met
234	48	Arg157	His
235	48	Arg157	Lys
236	48	Arg157	Asp
237	48	Arg157	Glu
238	48	Arg157	Ser
239	48	Arg157	Thr
240	48	Arg157	Asn
241	48	Arg157	Gin
242	48	Arg157	Cys
243	48	Arg157	Gly
244	48	Arg157	Pro
245	48	Arg157	Phe
246	48	Arg157	Tyr
247	48	Arg157	Trp
248	48	Tyr439	Ala
249	48	Tyr439	Leu
250	48	Tyr439	Val
251	48	Tyr439	lie
252	48	Tyr439	Met
253	48	Tyr439	His
254	48	Tyr439	Lys
255	48	Tyr439	Asp
256	48	Tyr439	Glu
257	48	Tyr439	Ser
258	48	Tyr439	Thr
259	48	Tyr439	Asn
260	48	Tyr439	Gin
261	48	Tyr439	Cys
262	48	Tyr439	Gly
263	48	Tyr439	Pro
264	48	Tyr439	Phe
265	48	Tyr439	Tyr
266	48	Tyr439	Trp

In a further particularly preferred embodiment, the variant or derivative of the mutated PPO refers

to a polypeptide comprising SEQ ID NO: 2, SEQ ID NO:4, SEQ ID NO: 24, SEQ ID NO: 30, SEQ ID NO: 38, SEQ ID NO: 46, SEQ ID NO: 48, comprising a combination of amino acid substitutions selected from the following Table 3b.

Table **3b:** SEQ ID NO: 2, SEQ ID NO:4, SEQ ID NO: 24, SEQ ID NO: 30, SEQ ID NO: 38, SEQ ID NO: 46, SEQ ID NO: 48, (combined amino acid substitutions)

Combination Number	SEQ ID NO:	Key amino acid position combination	Preferred Substitution
267	2 & 4	Arg128	Leu
		Phe420	Ala
268	2 & 4	Arg128	Leu
		Phe420	Leu
269	2 & 4	Arg128	Leu
		Phe420	Val
270	2 & 4	Arg128	Leu
		Phe420	lie
271	2 & 4	Arg128	Leu
		Phe420	Met
272	2 & 4	Arg128	Ala
		Phe420	Ala
273	2 & 4	Arg128	Ala
		Phe420	Leu
274	2 & 4	Arg128	Ala
		Phe420	Val
275	2 & 4	Arg128	Ala
		Phe420	lie
276	2 & 4	Arg128	Ala
		Phe420	Met
277	2 & 4	Arg128	Val
		Phe420	Ala
278	2 & 4	Arg128	Val
		Phe420	Leu
279	2 & 4	Arg128	Val
		Phe420	Val
280	2 & 4	Arg128	Val
		Phe420	lie
281	2 & 4	Arg128	Val
		Phe420	Met
282	2 & 4	Arg128	lie
		Phe420	Ala
283	2 & 4	Arg128	lie
		Phe420	Leu

284	2 & 4	Arg128	lie
		Phe420	Val
285	2 & 4	Arg128	lie
		Phe420	lie
286	2 & 4	Arg128	lie
		Phe420	Met
287	2 & 4	Arg128	Met
		Phe420	Ala
288	2 & 4	Arg128	Met
		Phe420	Leu
289	2 & 4	Arg128	Met
		Phe420	Val
290	2 & 4	Arg128	Met
		Phe420	lie
291	2 & 4	Arg128	Met
		Phe420	Met
292	2 & 4	Arg128	Tyr
		Phe420	Ala
293	2 & 4	Arg128	Tyr
		Phe420	Leu
294	2 & 4	Arg128	Tyr
		Phe420	Val
295	2 & 4	Arg128	Tyr
		Phe420	lie
296	2 & 4	Arg128	Tyr
		Phe420	Met
297	2 & 4	Arg128	Gly
		Phe420	Ala
298	2 & 4	Arg128	Gly
		Phe420	Leu
299	2 & 4	Arg128	Gly
		Phe420	Val
300	2 & 4	Arg128	Gly
		Phe420	lie
301	2 & 4	Arg128	Gly
		Phe420	Met
302	2 & 4	Arg128	Asn
		Phe420	Ala
303	2 & 4	Arg128	Asn
		Phe420	Leu
304	2 & 4	Arg128	Asn
		Phe420	Val
305	2 & 4	Arg128	Asn

		Phe420	lie
306	2 & 4	Arg128	Asn
		Phe420	Met
307	2 & 4	Arg128	Cys
		Phe420	Ala
308	2 & 4	Arg128	Cys
		Phe420	Leu
309	2 & 4	Arg128	Cys
		Phe420	Val
310	2 & 4	Arg128	Cys
		Phe420	lie
311	2 & 4	Arg128	Cys
		Phe420	Met
312	2 & 4	Arg128	Phe
		Phe420	Ala
313	2 & 4	Arg128	Phe
		Phe420	Leu
314	2 & 4	Arg128	Phe
		Phe420	Val
315	2 & 4	Arg128	Phe
		Phe420	lie
316	2 & 4	Arg128	Phe
		Phe420	Met
317	2 & 4	Arg128	Ser
		Phe420	Ala
318	2 & 4	Arg128	Ser
		Phe420	Leu
319	2 & 4	Arg128	Ser
		Phe420	Val
320	2 & 4	Arg128	Ser
		Phe420	lie
321	2 & 4	Arg128	Ser
		Phe420	Met
322	2 & 4	Arg128	Thr
		Phe420	Ala
323	2 & 4	Arg128	Thr
		Phe420	Leu
324	2 & 4	Arg128	Thr
		Phe420	Val
325	2 & 4	Arg128	Thr
		Phe420	lie
326	2 & 4	Arg128	Thr
		Phe420	Met

327	2 & 4	Arg128	Gin
		Phe420	Ala
328	2 & 4	Arg128	Gin
		Phe420	Leu
329	2 & 4	Arg128	Gin
		Phe420	Val
330	2 & 4	Arg128	Gin
		Phe420	lie
331	2 & 4	Arg128	Gin
		Phe420	Met
332	2 & 4	Arg128	His
		Phe420	Ala
333	2 & 4	Arg128	His
		Phe420	Leu
334	2 & 4	Arg128	His
		Phe420	Val
335	2 & 4	Arg128	His
		Phe420	lie
336	2 & 4	Arg128	His
		Phe420	Met
337	24	Arg130	Leu
		Phe433	Ala
338	24	Arg130	Leu
		Phe433	Leu
339	24	Arg130	Leu
		Phe433	Val
340	24	Arg130	Leu
		Phe433	lie
341	24	Arg130	Leu
		Phe433	Met
342	24	Arg130	Ala
		Phe433	Ala
343	24	Arg130	Ala
		Phe433	Leu
344	24	Arg130	Ala
		Phe433	Val
345	24	Arg130	Ala
		Phe433	lie
346	24	Arg130	Ala
		Phe433	Met
347	24	Arg130	Val
		Phe433	Ala
348	24	Arg130	Val

		Phe433	Leu
349	24	Arg130	Val
		Phe433	Val
350	24	Arg130	Val
		Phe433	lie
351	24	Arg130	Val
		Phe433	Met
352	24	Arg130	lie
		Phe433	Ala
353	24	Arg130	lie
		Phe433	Leu
354	24	Arg130	lie
		Phe433	Val
355	24	Arg130	lie
		Phe433	lie
356	24	Arg130	lie
		Phe433	Met
357	24	Arg130	Met
		Phe433	Ala
358	24	Arg130	Met
		Phe433	Leu
359	24	Arg130	Met
		Phe433	Val
360	24	Arg130	Met
		Phe433	lie
361	24	Arg130	Met
		Phe433	Met
362	24	Arg130	Tyr
		Phe433	Ala
363	24	Arg130	Tyr
		Phe433	Leu
364	24	Arg130	Tyr
		Phe433	Val
365	24	Arg130	Tyr
		Phe433	lie
366	24	Arg130	Tyr
		Phe433	Met
367	24	Arg130	Gly
		Phe433	Ala
368	24	Arg130	Gly
		Phe433	Leu
369	24	Arg130	Gly
		Phe433	Val

370	24	Arg130	Gly
		Phe433	lie
371	24	Arg130	Gly
		Phe433	Met
372	24	Arg130	Asn
		Phe433	Ala
373	24	Arg130	Asn
		Phe433	Leu
374	24	Arg130	Asn
		Phe433	Val
375	24	Arg130	Asn
		Phe433	lie
376	24	Arg130	Asn
		Phe433	Met
377	24	Arg130	Cys
		Phe433	Ala
378	24	Arg130	Cys
		Phe433	Leu
379	24	Arg130	Cys
		Phe433	Val
380	24	Arg130	Cys
		Phe433	lie
381	24	Arg130	Cys
		Phe433	Met
382	24	Arg130	Phe
		Phe433	Ala
383	24	Arg130	Phe
		Phe433	Leu
384	24	Arg130	Phe
		Phe433	Val
385	24	Arg130	Phe
		Phe433	lie
386	24	Arg130	Phe
		Phe433	Met
387	24	Arg130	Ser
		Phe433	Ala
388	24	Arg130	Ser
		Phe433	Leu
389	24	Arg130	Ser
		Phe433	Val
390	24	Arg130	Ser
		Phe433	lie
391	24	Arg130	Ser

		Phe433	Met
392	24	Arg130	Thr
		Phe433	Ala
393	24	Arg130	Thr
		Phe433	Leu
394	24	Arg130	Thr
		Phe433	Val
395	24	Arg130	Thr
		Phe433	lie
396	24	Arg130	Thr
		Phe433	Met
397	24	Arg130	Gin
		Phe433	Ala
398	24	Arg130	Gin
		Phe433	Leu
399	24	Arg130	Gin
		Phe433	Val
400	24	Arg130	Gin
		Phe433	lie
401	24	Arg130	Gin
		Phe433	Met
402	24	Arg130	His
		Phe433	Ala
403	24	Arg130	His
		Phe433	Leu
404	24	Arg130	His
		Phe433	Val
405	24	Arg130	His
		Phe433	lie
406	24	Arg130	His
		Phe433	Met
407	30	Arg130	Leu
		Phe433	Ala
408	30	Arg130	Leu
		Phe433	Leu
409	30	Arg130	Leu
		Phe433	Val
410	30	Arg130	Leu
		Phe433	lie
411	30	Arg130	Leu
		Phe433	Met
412	30	Arg130	Ala
		Phe433	Ala

413	30	Arg130	Ala
		Phe433	Leu
414	30	Arg130	Ala
		Phe433	Val
415	30	Arg130	Ala
		Phe433	lie
416	30	Arg130	Ala
		Phe433	Met
417	30	Arg130	Val
		Phe433	Ala
418	30	Arg130	Val
		Phe433	Leu
419	30	Arg130	Val
		Phe433	Val
420	30	Arg130	Val
		Phe433	lie
421	30	Arg130	Val
		Phe433	Met
422	30	Arg130	lie
		Phe433	Ala
423	30	Arg130	lie
		Phe433	Leu
424	30	Arg130	lie
		Phe433	Val
425	30	Arg130	lie
		Phe433	lie
426	30	Arg130	lie
		Phe433	Met
427	30	Arg130	Met
		Phe433	Ala
428	30	Arg130	Met
		Phe433	Leu
429	30	Arg130	Met
		Phe433	Val
430	30	Arg130	Met
		Phe433	lie
431	30	Arg130	Met
		Phe433	Met
432	30	Arg130	Tyr
		Phe433	Ala
433	30	Arg130	Tyr
		Phe433	Leu
434	30	Arg130	Tyr

		Phe433	Val
435	30	Arg130	Tyr
		Phe433	lie
436	30	Arg130	Tyr
		Phe433	Met
437	30	Arg130	Gly
		Phe433	Ala
438	30	Arg130	Gly
		Phe433	Leu
439	30	Arg130	Gly
		Phe433	Val
440	30	Arg130	Gly
		Phe433	lie
441	30	Arg130	Gly
		Phe433	Met
442	30	Arg130	Asn
		Phe433	Ala
443	30	Arg130	Asn
		Phe433	Leu
444	30	Arg130	Asn
		Phe433	Val
445	30	Arg130	Asn
		Phe433	lie
446	30	Arg130	Asn
		Phe433	Met
447	30	Arg130	Cys
		Phe433	Ala
448	30	Arg130	Cys
		Phe433	Leu
449	30	Arg130	Cys
		Phe433	Val
450	30	Arg130	Cys
		Phe433	lie
451	30	Arg130	Cys
		Phe433	Met
452	30	Arg130	Phe
		Phe433	Ala
453	30	Arg130	Phe
		Phe433	Leu
454	30	Arg130	Phe
		Phe433	Val
455	30	Arg130	Phe
		Phe433	lie

456	30	Arg130	Phe
		Phe433	Met
457	30	Arg130	Ser
		Phe433	Ala
458	30	Arg130	Ser
		Phe433	Leu
459	30	Arg130	Ser
		Phe433	Val
460	30	Arg130	Ser
		Phe433	lie
461	30	Arg130	Ser
		Phe433	Met
462	30	Arg130	Thr
		Phe433	Ala
463	30	Arg130	Thr
		Phe433	Leu
464	30	Arg130	Thr
		Phe433	Val
465	30	Arg130	Thr
		Phe433	lie
466	30	Arg130	Thr
		Phe433	Met
467	30	Arg130	Gin
		Phe433	Ala
468	30	Arg130	Gin
		Phe433	Leu
469	30	Arg130	Gin
		Phe433	Val
470	30	Arg130	Gin
		Phe433	lie
471	30	Arg130	Gin
		Phe433	Met
472	30	Arg130	His
		Phe433	Ala
473	30	Arg130	His
		Phe433	Leu
474	30	Arg130	His
		Phe433	Val
475	30	Arg130	His
		Phe433	lie
476	30	Arg130	His
		Phe433	Met
477	38	Arg98	Leu

		Phe392	Ala
478	38	Arg98	Leu
		Phe392	Leu
479	38	Arg98	Leu
		Phe392	Val
480	38	Arg98	Leu
		Phe392	lie
481	38	Arg98	Leu
		Phe392	Met
482	38	Arg98	Ala
		Phe392	Ala
483	38	Arg98	Ala
		Phe392	Leu
484	38	Arg98	Ala
		Phe392	Val
485	38	Arg98	Ala
		Phe392	lie
486	38	Arg98	Ala
		Phe392	Met
487	38	Arg98	Val
		Phe392	Ala
488	38	Arg98	Val
		Phe392	Leu
489	38	Arg98	Val
		Phe392	Val
490	38	Arg98	Val
		Phe392	lie
491	38	Arg98	Val
		Phe392	Met
492	38	Arg98	lie
		Phe392	Ala
493	38	Arg98	lie
		Phe392	Leu
494	38	Arg98	lie
		Phe392	Val
495	38	Arg98	lie
		Phe392	lie
496	38	Arg98	lie
		Phe392	Met
497	38	Arg98	Met
		Phe392	Ala
498	38	Arg98	Met
		Phe392	Leu

499	38	Arg98	Met
		Phe392	Val
500	38	Arg98	Met
		Phe392	lie
501	38	Arg98	Met
		Phe392	Met
502	38	Arg98	Tyr
		Phe392	Ala
503	38	Arg98	Tyr
		Phe392	Leu
504	38	Arg98	Tyr
		Phe392	Val
505	38	Arg98	Tyr
		Phe392	lie
506	38	Arg98	Tyr
		Phe392	Met
507	38	Arg98	Gly
		Phe392	Ala
508	38	Arg98	Gly
		Phe392	Leu
509	38	Arg98	Gly
		Phe392	Val
510	38	Arg98	Gly
		Phe392	lie
511	38	Arg98	Gly
		Phe392	Met
512	38	Arg98	Asn
		Phe392	Ala
513	38	Arg98	Asn
		Phe392	Leu
514	38	Arg98	Asn
		Phe392	Val
515	38	Arg98	Asn
		Phe392	lie
516	38	Arg98	Asn
		Phe392	Met
517	38	Arg98	Cys
		Phe392	Ala
518	38	Arg98	Cys
		Phe392	Leu
519	38	Arg98	Cys
		Phe392	Val
520	38	Arg98	Cys

		Phe392	lie
521	38	Arg98	Cys
		Phe392	Met
522	38	Arg98	Phe
		Phe392	Ala
523	38	Arg98	Phe
		Phe392	Leu
524	38	Arg98	Phe
		Phe392	Val
525	38	Arg98	Phe
		Phe392	lie
526	38	Arg98	Phe
		Phe392	Met
527	38	Arg98	Ser
		Phe392	Ala
528	38	Arg98	Ser
		Phe392	Leu
529	38	Arg98	Ser
		Phe392	Val
530	38	Arg98	Ser
		Phe392	lie
531	38	Arg98	Ser
		Phe392	Met
532	38	Arg98	Thr
		Phe392	Ala
533	38	Arg98	Thr
		Phe392	Leu
534	38	Arg98	Thr
		Phe392	Val
535	38	Arg98	Thr
		Phe392	lie
536	38	Arg98	Thr
		Phe392	Met
537	38	Arg98	Gin
		Phe392	Ala
538	38	Arg98	Gin
		Phe392	Leu
539	38	Arg98	Gin
		Phe392	Val
540	38	Arg98	Gin
		Phe392	lie
541	38	Arg98	Gin
		Phe392	Met

542	38	Arg98	His
		Phe392	Ala
543	38	Arg98	His
		Phe392	Leu
544	38	Arg98	His
		Phe392	Val
545	38	Arg98	His
		Phe392	lie
546	38	Arg98	His
		Phe392	Met
547	46	Arg139	Leu
		Phe465	Ala
548	46	Arg139	Leu
		Phe465	Leu
549	46	Arg139	Leu
		Phe465	Val
550	46	Arg139	Leu
		Phe465	lie
551	46	Arg139	Leu
		Phe465	Met
552	46	Arg139	Ala
		Phe465	Ala
553	46	Arg139	Ala
		Phe465	Leu
554	46	Arg139	Ala
		Phe465	Val
555	46	Arg139	Ala
		Phe465	lie
556	46	Arg139	Ala
		Phe465	Met
557	46	Arg139	Val
		Phe465	Ala
558	46	Arg139	Val
		Phe465	Leu
559	46	Arg139	Val
		Phe465	Val
560	46	Arg139	Val
		Phe465	lie
561	46	Arg139	Val
		Phe465	Met
562	46	Arg139	lie
		Phe465	Ala
563	46	Arg139	lie

		Phe465	Leu
564	46	Arg139	lie
		Phe465	Val
565	46	Arg139	lie
		Phe465	lie
566	46	Arg139	lie
		Phe465	Met
567	46	Arg139	Met
		Phe465	Ala
568	46	Arg139	Met
		Phe465	Leu
569	46	Arg139	Met
		Phe465	Val
570	46	Arg139	Met
		Phe465	lie
571	46	Arg139	Met
		Phe465	Met
572	46	Arg139	Tyr
		Phe465	Ala
573	46	Arg139	Tyr
		Phe465	Leu
574	46	Arg139	Tyr
		Phe465	Val
575	46	Arg139	Tyr
		Phe465	lie
576	46	Arg139	Tyr
		Phe465	Met
577	46	Arg139	Gly
		Phe465	Ala
578	46	Arg139	Gly
		Phe465	Leu
579	46	Arg139	Gly
		Phe465	Val
580	46	Arg139	Gly
		Phe465	lie
581	46	Arg139	Gly
		Phe465	Met
582	46	Arg139	Asn
		Phe465	Ala
583	46	Arg139	Asn
		Phe465	Leu
584	46	Arg139	Asn
		Phe465	Val

585	46	Arg139	Asn
		Phe465	lie
586	46	Arg139	Asn
		Phe465	Met
587	46	Arg139	Cys
		Phe465	Ala
588	46	Arg139	Cys
		Phe465	Leu
589	46	Arg139	Cys
		Phe465	Val
590	46	Arg139	Cys
		Phe465	lie
591	46	Arg139	Cys
		Phe465	Met
592	46	Arg139	Phe
		Phe465	Ala
593	46	Arg139	Phe
		Phe465	Leu
594	46	Arg139	Phe
		Phe465	Val
595	46	Arg139	Phe
		Phe465	lie
596	46	Arg139	Phe
		Phe465	Met
597	46	Arg139	Ser
		Phe465	Ala
598	46	Arg139	Ser
		Phe465	Leu
599	46	Arg139	Ser
		Phe465	Val
600	46	Arg139	Ser
		Phe465	lie
601	46	Arg139	Ser
		Phe465	Met
602	46	Arg139	Thr
		Phe465	Ala
603	46	Arg139	Thr
		Phe465	Leu
604	46	Arg139	Thr
		Phe465	Val
605	46	Arg139	Thr
		Phe465	lie
606	46	Arg139	Thr

		Phe465	Met
607	46	Arg139	Gin
		Phe465	Ala
608	46	Arg139	Gin
		Phe465	Leu
609	46	Arg139	Gin
		Phe465	Val
610	46	Arg139	Gin
		Phe465	lie
611	46	Arg139	Gin
		Phe465	Met
612	46	Arg139	His
		Phe465	Ala
613	46	Arg139	His
		Phe465	Leu
614	46	Arg139	His
		Phe465	Val
615	46	Arg139	His
		Phe465	lie
616	46	Arg139	His
		Phe465	Met
617	48	Arg157	Leu
		Tyr439	Ala
618	48	Arg157	Leu
		Tyr439	Leu
619	48	Arg157	Leu
		Tyr439	Val
620	48	Arg157	Leu
		Tyr439	lie
621	48	Arg157	Leu
		Tyr439	Met
622	48	Arg157	Ala
		Tyr439	Ala
623	48	Arg157	Ala
		Tyr439	Leu
624	48	Arg157	Ala
		Tyr439	Val
625	48	Arg157	Ala
		Tyr439	lie
626	48	Arg157	Ala
		Tyr439	Met
627	48	Arg157	Val
		Tyr439	Ala

628	48	Arg157	Val
		Tyr439	Leu
629	48	Arg157	Val
		Tyr439	Val
630	48	Arg157	Val
		Tyr439	lie
631	48	Arg157	Val
		Tyr439	Met
632	48	Arg157	lie
		Tyr439	Ala
633	48	Arg157	lie
		Tyr439	Leu
634	48	Arg157	lie
		Tyr439	Val
635	48	Arg157	lie
		Tyr439	lie
636	48	Arg157	lie
		Tyr439	Met
637	48	Arg157	Met
		Tyr439	Ala
638	48	Arg157	Met
		Tyr439	Leu
639	48	Arg157	Met
		Tyr439	Val
640	48	Arg157	Met
		Tyr439	lie
641	48	Arg157	Met
		Tyr439	Met
642	48	Arg157	Tyr
		Tyr439	Ala
643	48	Arg157	Tyr
		Tyr439	Leu
644	48	Arg157	Tyr
		Tyr439	Val
645	48	Arg157	Tyr
		Tyr439	lie
646	48	Arg157	Tyr
		Tyr439	Met
647	48	Arg157	Gly
		Tyr439	Ala
648	48	Arg157	Gly
		Tyr439	Leu
649	48	Arg157	Gly

		Tyr439	Val
650	48	Arg157	Gly
		Tyr439	lie
651	48	Arg157	Gly
		Tyr439	Met
652	48	Arg157	Asn
		Tyr439	Ala
653	48	Arg157	Asn
		Tyr439	Leu
654	48	Arg157	Asn
		Tyr439	Val
655	48	Arg157	Asn
		Tyr439	lie
656	48	Arg157	Asn
		Tyr439	Met
657	48	Arg157	Cys
		Tyr439	Ala
658	48	Arg157	Cys
		Tyr439	Leu
659	48	Arg157	Cys
		Tyr439	Val
660	48	Arg157	Cys
		Tyr439	lie
661	48	Arg157	Cys
		Tyr439	Met
662	48	Arg157	Phe
		Tyr439	Ala
663	48	Arg157	Phe
		Tyr439	Leu
664	48	Arg157	Phe
		Tyr439	Val
665	48	Arg157	Phe
		Tyr439	lie
666	48	Arg157	Phe
		Tyr439	Met
667	48	Arg157	Ser
		Tyr439	Ala
668	48	Arg157	Ser
		Tyr439	Leu
669	48	Arg157	Ser
		Tyr439	Val
670	48	Arg157	Ser
		Tyr439	lie

671	48	Arg157	Ser
		Tyr439	Met
672	48	Arg157	Thr
		Tyr439	Ala
673	48	Arg157	Thr
		Tyr439	Leu
674	48	Arg157	Thr
		Tyr439	Val
675	48	Arg157	Thr
		Tyr439	lie
676	48	Arg157	Thr
		Tyr439	Met
677	48	Arg157	Gin
		Tyr439	Ala
678	48	Arg157	Gin
		Tyr439	Leu
679	48	Arg157	Gin
		Tyr439	Val
680	48	Arg157	Gin
		Tyr439	lie
681	48	Arg157	Gin
		Tyr439	Met
682	48	Arg157	His
		Tyr439	Ala
683	48	Arg157	His
		Tyr439	Leu
684	48	Arg157	His
		Tyr439	Val
685	48	Arg157	His
		Tyr439	lie
686	48	Arg157	His
		Tyr439	Met

It is to be understood that any amino acid besides the ones mentioned in the above tables 3 could be used as a substitutent. Assays to test for the functionality of such mutants are readily available in the art, and respectively, described in the Example section of the present invention.

In a preferred embodiment, the mutated PPO refers to a polypeptide of SEQ ID NO: 2 or SEQ ID NO: 4 in which the amino acid sequence differs from an amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 4 at position 128, and/or position 420.

Examples of differences at these amino acid positions include, but are not limited to, one or more of the following:

the amino acid at or corresponding to position 128 of SEQ ID NO:2 is other than Arginine;
the amino acid at or corresponding to position 420 of SEQ ID NO:2 is other than Phenylalanine,

In some embodiments, the mutated PPO enzyme of SEQ ID NO: 2 or SEQ ID NO: 4 comprises one or more of the following:

the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Leu, Ala, Val, or lie;
the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val, Met, Ala, lie, or Leu;

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Leu, Ala, Val, lie, Met, Tyr, Gly, Asn, Cys, Phe, Ser, Thr, Gin, or His, and/or the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala, Leu, Val, lie, or Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Leu, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Leu, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Leu, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Leu, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Leu, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ala, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ala, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ala, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ala, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ala, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Val, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Val, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Val, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Val, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Val, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is lie, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is lie, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is lie, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is lie, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is lie, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Met, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Met, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Met, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Met, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Met, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Tyr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Tyr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Tyr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Tyr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Tyr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gly, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gly, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gly, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gly, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gly, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Asn, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Asn, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Asn, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Asn, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Asn, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Cys, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Cys, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Cys, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Cys, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Cys, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Phe, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Phe, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Phe, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Phe, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Phe, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ser, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ser, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ser, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ser, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ser, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Thr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Thr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Thr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Thr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Thr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gin, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gin, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gin, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gin, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gin, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is His, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is His, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is His, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is His, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is His, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Leu, Ala, Val, lie, Met, Tyr, Gly, Asn, Cys, Phe, Ser, Thr, Gin, His, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala, Leu, Val, lie, Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Leu, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Leu, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Leu, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Leu, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Leu, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ala, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ala, and the amino acid at or

corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ala, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ala, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ala, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Val, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Val, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Val, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Val, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Val, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:

the amino acid at or corresponding to position 128 of SEQ ID NO:2 is lie, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is lie, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is lie, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is lie, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is lie, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Met, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Met, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Met, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Met, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a

variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Met, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Tyr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Tyr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Tyr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Tyr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Tyr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gly, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gly, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gly, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gly, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gly, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Asn, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Asn, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Asn, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Asn, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Asn, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Cys, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Cys, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Cys, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Cys, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Cys, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Phe, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Phe, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Phe, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Phe, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Phe, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ser, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ser, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ser, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ser, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ser, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Thr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Thr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Thr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Thr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Thr, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gin, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gin, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gin, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gin, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Gin, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is His, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is His, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is His, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is His, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is His, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In a particularly preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, or SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ala, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Met.

In another particularly preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, or SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ala, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is lie.

In another particularly preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, or SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ala, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Leu.

In an especially preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 2, or SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Ala, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another especially preferred embodiment, the the mutated PPO comprises a sequence of SEQ ID NO: 2, or SEQ ID NO: 4, a variant, derivative, orthologue, paralogue or homologue thereof, in which the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Leu, Ala, Val, lie, Met, Tyr, Gly, Asn, Cys, Phe, Ser, Thr, Gin, or His, and the amino acid at or corresponding to position 433 is Ala, Leu, Val, lie, or Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Leu, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:

the amino acid at or corresponding to position 130 is Leu, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Leu, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Leu, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Leu, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ala, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ala, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ala, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ala, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ala, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a

variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Val, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Val, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Val, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Val, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Val, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is lie, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is lie, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is lie, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is lie, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is lie, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Met, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Met, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Met, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Met, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Met, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Tyr, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Tyr, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Tyr, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Tyr, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Tyr, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gly, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gly, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gly, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gly, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gly, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Asn, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Asn, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Asn, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Asn, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Asn, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Cys, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Cys, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Cys, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Cys, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Cys, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Phe, and the amino acid at or corresponding

to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Phe, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Phe, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Phe, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Phe, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ser, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ser, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ser, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ser, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:

the amino acid at or corresponding to position 130 is Ser, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Thr, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Thr, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Thr, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Thr, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Thr, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gin, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gin, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gin, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a

variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gin, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gin, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is His, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is His, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is His, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is His, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 24, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is His, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Leu, Ala, Val, lie, Met, Tyr, Gly, Asn, Cys, Phe, Ser, Thr, Gin, His, and the amino acid at or corresponding to position 433 is Ala, Leu, Val, lie, Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Leu, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Leu, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Leu, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Leu, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Leu, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ala, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ala, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ala, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ala, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ala, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Val, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Val, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Val, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Val, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Val, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is lie, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is lie, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is lie, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is lie, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is lie, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Met, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Met, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Met, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Met, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Met, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Tyr, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Tyr, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Tyr, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Tyr, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Tyr, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gly, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gly, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gly, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gly, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gly, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Asn, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Asn, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Asn, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Asn, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Asn, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Cys, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Cys, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Cys, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Cys, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Cys, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Phe, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Phe, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Phe, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Phe, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Phe, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ser, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ser, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ser, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ser, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Ser, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Thr, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Thr, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Thr, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Thr, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Thr, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gin, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gin, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gin, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gin, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is Gin, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is His, and the amino acid at or corresponding to position 433 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is His, and the amino acid at or corresponding to position 433 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is His, and the amino acid at or corresponding to position 433 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is His, and the amino acid at or corresponding to position 433 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 30, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 130 is His, and the amino acid at or corresponding to position 433 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Leu, Ala, Val, lie, Met, Tyr, Gly, Asn, Cys, Phe, Ser, Thr, Gin, His, and the amino acid at or corresponding to position 392 is Ala, Leu, Val, lie, Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Leu, and the amino acid at or corresponding to position 392 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Leu, and the amino acid at or corresponding to position 392 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Leu, and the amino acid at or corresponding to position 392 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Leu, and the amino acid at or corresponding to position 392 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Leu, and the amino acid at or corresponding to position 392 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Ala, and the amino acid at or corresponding to position 392 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Ala, and the amino acid at or corresponding to position 392 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Ala, and the amino acid at or corresponding to position 392 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Ala, and the amino acid at or corresponding to position 392 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Ala, and the amino acid at or corresponding to position 392 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Val, and the amino acid at or corresponding to position 392 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Val, and the amino acid at or corresponding to position 392 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Val, and the amino acid at or corresponding to position 392 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Val, and the amino acid at or corresponding to position 392 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Val, and the amino acid at or corresponding to position 392 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is lie, and the amino acid at or corresponding to position 392 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is lie, and the amino acid at or corresponding to position 392 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is lie, and the amino acid at or corresponding to position 392 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is lie, and the amino acid at or corresponding to position 392 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is lie, and the amino acid at or corresponding to position 392 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Met, and the amino acid at or corresponding to position 392 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Met, and the amino acid at or corresponding to position 392 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Met, and the amino acid at or corresponding to position 392 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Met, and the amino acid at or corresponding to position 392 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Met, and the amino acid at or corresponding to position 392 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Tyr, and the amino acid at or corresponding to position 392 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Tyr, and the amino acid at or corresponding to position 392 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Tyr, and the amino acid at or corresponding to position 392 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Tyr, and the amino acid at or corresponding to position 392 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Tyr, and the amino acid at or corresponding to position 392 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Gly, and the amino acid at or corresponding to position 392 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Gly, and the amino acid at or corresponding to position 392 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Gly, and the amino acid at or corresponding to position 392 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Gly, and the amino acid at or corresponding to position 392 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Gly, and the amino acid at or corresponding to position 392 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Asn, and the amino acid at or corresponding to position 392 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Asn, and the amino acid at or corresponding to position 392 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Asn, and the amino acid at or corresponding to position 392 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Asn, and the amino acid at or corresponding to position 392 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Asn, and the amino acid at or corresponding to position 392 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Cys, and the amino acid at or corresponding to position 392 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Cys, and the amino acid at or corresponding to position 392 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Cys, and the amino acid at or corresponding to position 392 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Cys, and the amino acid at or corresponding to position 392 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Cys, and the amino acid at or corresponding to position 392 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Phe, and the amino acid at or corresponding to position 392 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Phe, and the amino acid at or corresponding to position 392 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Phe, and the amino acid at or corresponding to position 392 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Phe, and the amino acid at or corresponding to position 392 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Phe, and the amino acid at or corresponding to position 392 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Ser, and the amino acid at or corresponding to position 392 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Ser, and the amino acid at or corresponding to position 392 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Ser, and the amino acid at or corresponding to position 392 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Ser, and the amino acid at or corresponding to position 392 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Ser, and the amino acid at or corresponding to position 392 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Thr, and the amino acid at or corresponding to position 392 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Thr, and the amino acid at or corresponding to position 392 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Thr, and the amino acid at or corresponding to position 392 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Thr, and the amino acid at or corresponding to position 392 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Thr, and the amino acid at or corresponding to position 392 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Gin, and the amino acid at or corresponding to position 392 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Gin, and the amino acid at or corresponding to position 392 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Gin, and the amino acid at or corresponding to position 392 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Gin, and the amino acid at or corresponding to position 392 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is Gin, and the amino acid at or corresponding to position 392 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is His, and the amino acid at or corresponding to position 392 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is His, and the amino acid at or corresponding to position 392 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is His, and the amino acid at or corresponding to position 392 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is His, and the amino acid at or corresponding to position 392 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 38, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 98 is His, and the amino acid at or corresponding to position 392 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Leu, Ala, Val, lie, Met, Tyr, Gly, Asn, Cys, Phe, Ser, Thr, Gin, His, and the amino acid at or corresponding to position 465 is Ala, Leu, Val, lie, Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Leu, and the amino acid at or corresponding to position 465 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Leu, and the amino acid at or corresponding to position 465 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Leu, and the amino acid at or corresponding

to position 465 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Leu, and the amino acid at or corresponding to position 465 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Leu, and the amino acid at or corresponding to position 465 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Ala, and the amino acid at or corresponding to position 465 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Ala, and the amino acid at or corresponding to position 465 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Ala, and the amino acid at or corresponding to position 465 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Ala, and the amino acid at or corresponding to position 465 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Ala, and the amino acid at or corresponding to position 465 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Val, and the amino acid at or corresponding to position 465 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:

the amino acid at or corresponding to position 139 is Val, and the amino acid at or corresponding to position 465 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Val, and the amino acid at or corresponding to position 465 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Val, and the amino acid at or corresponding to position 465 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Val, and the amino acid at or corresponding to position 465 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Ile, and the amino acid at or corresponding to position 465 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Ile, and the amino acid at or corresponding to position 465 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Ile, and the amino acid at or corresponding to position 465 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Ile, and the amino acid at or corresponding to position 465 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Ile, and the amino acid at or corresponding to position 465 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a

variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Met, and the amino acid at or corresponding to position 465 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Met, and the amino acid at or corresponding to position 465 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Met, and the amino acid at or corresponding to position 465 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Met, and the amino acid at or corresponding to position 465 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Met, and the amino acid at or corresponding to position 465 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Tyr, and the amino acid at or corresponding to position 465 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Tyr, and the amino acid at or corresponding to position 465 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Tyr, and the amino acid at or corresponding to position 465 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Tyr, and the amino acid at or corresponding to position 465 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Tyr, and the amino acid at or corresponding to position 465 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Gly, and the amino acid at or corresponding to position 465 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Gly, and the amino acid at or corresponding to position 465 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Gly, and the amino acid at or corresponding to position 465 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Gly, and the amino acid at or corresponding to position 465 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Gly, and the amino acid at or corresponding to position 465 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Asn, and the amino acid at or corresponding to position 465 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Asn, and the amino acid at or corresponding to position 465 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Asn, and the amino acid at or corresponding to position 465 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Asn, and the amino acid at or corresponding to position 465 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Asn, and the amino acid at or corresponding to position 465 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Cys, and the amino acid at or corresponding to position 465 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Cys, and the amino acid at or corresponding to position 465 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Cys, and the amino acid at or corresponding to position 465 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Cys, and the amino acid at or corresponding to position 465 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Cys, and the amino acid at or corresponding to position 465 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Phe, and the amino acid at or corresponding to position 465 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Phe, and the amino acid at or corresponding to position 465 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Phe, and the amino acid at or corresponding to position 465 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Phe, and the amino acid at or corresponding to position 465 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Phe, and the amino acid at or corresponding to position 465 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Ser, and the amino acid at or corresponding to position 465 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Ser, and the amino acid at or corresponding to position 465 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Ser, and the amino acid at or corresponding to position 465 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Ser, and the amino acid at or corresponding to position 465 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Ser, and the amino acid at or corresponding to position 465 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Thr, and the amino acid at or corresponding to position 465 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Thr, and the amino acid at or corresponding to position 465 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Thr, and the amino acid at or corresponding to position 465 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Thr, and the amino acid at or corresponding to position 465 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Thr, and the amino acid at or corresponding to position 465 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Gin, and the amino acid at or corresponding to position 465 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Gin, and the amino acid at or corresponding to position 465 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Gin, and the amino acid at or corresponding to position 465 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Gin, and the amino acid at or corresponding to position 465 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is Gin, and the amino acid at or corresponding to position 465 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is His, and the amino acid at or corresponding to position 465 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is His, and the amino acid at or corresponding to position 465 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is His, and the amino acid at or corresponding to position 465 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is His, and the amino acid at or corresponding to position 465 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 46, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 139 is His, and the amino acid at or corresponding to position 465 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Leu, Ala, Val, lie, Met, Tyr, Gly, Asn, Cys, Phe, Ser, Thr, Gin, His, and the amino acid at or corresponding to position 439 is Ala, Leu, Val, lie, Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Leu, and the amino acid at or corresponding to position 439 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Leu, and the amino acid at or corresponding to position 439 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:

the amino acid at or corresponding to position 157 is Leu, and the amino acid at or corresponding to position 439 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Leu, and the amino acid at or corresponding to position 439 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Leu, and the amino acid at or corresponding to position 439 is Met.
In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Ala, and the amino acid at or corresponding to position 439 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Ala, and the amino acid at or corresponding to position 439 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Ala, and the amino acid at or corresponding to position 439 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Ala, and the amino acid at or corresponding to position 439 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Ala, and the amino acid at or corresponding to position 439 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Val, and the amino acid at or corresponding to position 439 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:

the amino acid at or corresponding to position 157 is Val, and the amino acid at or corresponding to position 439 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Val, and the amino acid at or corresponding to position 439 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Val, and the amino acid at or corresponding to position 439 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Val, and the amino acid at or corresponding to position 439 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Ile, and the amino acid at or corresponding to position 439 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Ile, and the amino acid at or corresponding to position 439 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Ile, and the amino acid at or corresponding to position 439 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Ile, and the amino acid at or corresponding to position 439 is Ile.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Ile, and the amino acid at or corresponding to position 439 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a

variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Met, and the amino acid at or corresponding to position 439 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Met, and the amino acid at or corresponding to position 439 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Met, and the amino acid at or corresponding to position 439 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Met, and the amino acid at or corresponding to position 439 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Met, and the amino acid at or corresponding to position 439 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Tyr, and the amino acid at or corresponding to position 439 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Tyr, and the amino acid at or corresponding to position 439 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Tyr, and the amino acid at or corresponding to position 439 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Tyr, and the amino acid at or corresponding to position 439 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Tyr, and the amino acid at or corresponding to position 439 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Gly, and the amino acid at or corresponding to position 439 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Gly, and the amino acid at or corresponding to position 439 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Gly, and the amino acid at or corresponding to position 439 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Gly, and the amino acid at or corresponding to position 439 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Gly, and the amino acid at or corresponding to position 439 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Asn, and the amino acid at or corresponding to position 439 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Asn, and the amino acid at or corresponding to position 439 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Asn, and the amino acid at or corresponding to position 439 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Asn, and the amino acid at or corresponding to position 439 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Asn, and the amino acid at or corresponding to position 439 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Cys, and the amino acid at or corresponding to position 439 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Cys, and the amino acid at or corresponding to position 439 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Cys, and the amino acid at or corresponding to position 439 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Cys, and the amino acid at or corresponding to position 439 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Cys, and the amino acid at or corresponding to position 439 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Phe, and the amino acid at or corresponding to position 439 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Phe, and the amino acid at or corresponding to position 439 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Phe, and the amino acid at or corresponding to position 439 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Phe, and the amino acid at or corresponding to position 439 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Phe, and the amino acid at or corresponding to position 439 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Ser, and the amino acid at or corresponding to position 439 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Ser, and the amino acid at or corresponding to position 439 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Ser, and the amino acid at or corresponding to position 439 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Ser, and the amino acid at or corresponding to position 439 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Ser, and the amino acid at or corresponding to position 439 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Thr, and the amino acid at or corresponding to position 439 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Thr, and the amino acid at or corresponding to position 439 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Thr, and the amino acid at or corresponding to position 439 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Thr, and the amino acid at or corresponding to position 439 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Thr, and the amino acid at or corresponding to position 439 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Gin, and the amino acid at or corresponding to position 439 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Gin, and the amino acid at or corresponding to position 439 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Gin, and the amino acid at or corresponding to position 439 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Gin, and the amino acid at or corresponding to position 439 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is Gin, and the amino acid at or corresponding to position 439 is Met.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is His, and the amino acid at or corresponding to position 439 is Ala.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is His, and the amino acid at or corresponding to position 439 is Leu.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is His, and the amino acid at or corresponding to position 439 is Val.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is His, and the amino acid at or corresponding to position 439 is lie.

In another preferred embodiment, the mutated PPO comprises a sequence of SEQ ID NO: 48, a variant, derivative, orthologue, paralogue or homologue thereof, in which:
the amino acid at or corresponding to position 157 is His, and the amino acid at or corresponding to position 439 is Met.

It will be within the knowledge of the skilled artisan to identify conserved regions and motifs shared between the homologues, orthologues and paralogues encoded by SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, or 47, such as those depicted in Table 1. Having identified such conserved regions that may represent suitable binding motifs, amino acids corresponding to the amino acids listed in Table 3a and 3b, can be chosen to be subsituted by any other amino acid, for example by conserved amino acids as shown in table 2, preferably by the amino acids of tables 3a and 3b.
Table **3c** shows an overview of preferred mutation sites that are shared between homologues, orthologues and paralogues listed in Table 1.

Table 3c

SEQ ID NO	Pos 1	Pos 2	**Pos 3**	Pos 4	Pos 5	Pos 6	Pos 7	Pos 8	Pos 9	Pos 10	Pos 11	Pos 12	Pos 13	Pos 14	Pos 15
2	N126	K127	**R128**	Y129	I130	A131	S149	I151	A154	P164	K169	E182	S183	E189	F196
4	N126	K127	**R128**	Y129	I130	A131	S149	I151	A154	P164	K169	E182	S183	E189	F196
6	N126	K127	**R128**	Y129	I130	A131	S149	I151	A154	P164	K169	E182	S183	E189	F196
8	N126	K127	**R128**	Y129	I130	A131	S149	I151	A154	P164	K169	E182	S183	E189	F196
10	K145	K146	**R147**	Y148	I149	V150	S168	V170	T173	P183	K188	E200	S201	Q207	V214
12	A153	P154	**R155**	F156	V157	L158	F176	L178	I181	F189	-	E203	S204	R210	V217
14	A160	P161	**R162**	F163	V164	L165	F183	L185	F188	F196	-	E210	S211	R217	V224
16	S167	P168	**R169**	F170	V171	L172	F190	L192	F195	L203	-	E217	S218	R224	V231
18	N125	K126	**R127**	Y128	I129	A130	S148	I150	A153	P163	K168	E181	S182	E188	F195
20	A162	P163	**R164**	F165	V166	L167	F185	L187	I190	F198	-	E212	S213	R219	V226
22	A140	P141	**R142**	F143	V144	L145	F163	L165	I168	L176	-	E190	S191	R197	V204
24	H128	K129	**R130**	Y131	I132	V133	S151	V153	T156	P166	T174	E187	S188	E194	V201
26	A165	P166	**R167**	F168	V169	W170	F187	L189	I192	L200	-	E215	S216	R222	V229
28	L128	P129	**R130**	W131	I132	L133	-	L152	T155	V165	-	E180	S181	R187	I194
30	H128	K129	**R130**	Y131	I132	V133	S151	V153	T156	P166	T174	E187	S188	E194	V201
32	A141	P142	**R143**	F144	V145	L146	F164	L166	I169	L177	-	E191	S192	R198	V205
34	N96	K97	**R98**	Y99	I100	A101	S119	I121	A124	P134	K139	E152	S153	E159	F166
36	A142	P143	**R144**	F145	V146	L147	F165	L167	I170	F178	-	E192	S193	R199	V206
38	N96	K97	**R98**	Y99	I100	A101	S119	F121	T124	P134	N139	E150	S151	Q157	V164
40	H96	K97	**R98**	Y99	I100	V101	S119	L121	A124	P134	R139	E152	S153	E159	V166
42	A28	P29	**R30**	F31	V32	L33	F51	L53	I56	F64	-	E78	S79	R85	V92
44	H93	K94	**R95**	Y96	I97	V98	S116	V118	T121	P131	R139	E152	S153	C158	V165
46	H137	K138	**R139**	Y140	I141	V142	S160	V162	T165	P175	R183	E196	S197	E203	V210
48	A155	P156	**R157**	F158	V159	L160	F178	L180	F183	L191	-	E205	S206	R212	V219

Table 3c continued

SEQ ID NO	Pos 16	Pos 17	Pos 18	Pos 19	Pos 20	Pos 21	Pos 22	Pos 23	Pos 24	Pos 25	Pos 26	Pos 27	Pos 28	Pos 29	Pos 30
2	D202	C209	G210	G211	L216	M218	H219	H220	N227	S234	S246	K259	P260	R261	L295
4	D202	C209	G210	G211	L216	M218	H219	H220	N227	S234	S246	K259	P260	R261	L295
6	D202	C209	G210	-	L215	M217	Y218	H219	N226	S233	S245	K258	P259	R260	L294
8	D202	C209	G210	-	L215	M217	H218	H219	N226	S233	S245	K258	P259	R260	L294
10	D220	S227	A228	A229	L234	M236	K237	H238	N245	S249	A261	K276	K277	G278	L312
12	E223	Y230	A231	G232	L237	M239	K240	A241	K248	G254	E266	K281	P282	K283	S316
14	E230	Y237	A238	G239	L244	M246	K247	A248	N255	G261	D273	K288	P289	K290	T323
16	E237	Y244	A245	G246	L251	M253	K254	A255	V262	G268	E280	K295	P296	K297	S330
18	D201	S208	G209	G210	L215	M217	R218	H219	N226	S233	S245	K259	P260	R261	L295
20	E232	Y239	A240	G241	L246	M248	K249	A250	K257	G263	E275	T290	P291	K292	S325
22	E210	Y217	A218	G219	L224	M226	K227	A228	R235	G241	E253	K268	P269	K270	T303
24	D207	S214	A215	G216	L221	I223	R224	H225	N232	S239	A251	R266	R267	N268	L302
26	E235	Y242	A243	G244	L249	M251	K252	A253	I260	G266	E278	K294	P295	K296	V329
28	E200	Y207	A208	G209	L214	M216	R217	A218	E225	G232	N244	S271	S272	S273	V306
30	D207	S214	A215	G216	L221	I223	C224	H225	N232	S239	A251	R266	R267	N268	L302
32	E211	Y218	A219	G220	L225	M227	K228	A229	R236	G242	E254	T269	P270	K271	T304
34	D172	C179	G180	G181	L186	M188	H189	H190	N197	S204	S216	K230	P231	R232	L266
36	E212	Y219	A220	G221	L226	M228	K229	A230	K237	G243	E255	K270	P271	Q272	S305
38	D170	C177	G178	G179	L184	M186	H187	H188	N195	S202	P214	K229	K230	R231	L265
40	D172	S179	A180	A181	L186	M188	R189	H190	N197	S204	A216	N231	K232	H233	L267
42	E98	Y105	A106	G107	L112	M114	K115	A116	R123	G129	E141	K156	P157	K158	S191
44	D171	S178	G179	G180	L185	I187	R188	H189	N196	S203	T215	G230	R231	N232	L266
46	D216	S223	G224	G225	L230	I232	R233	H234	N241	S248	T260	G275	R276	N277	L311
48	E225	Y232	A233	G234	L239	M241	K242	A243	T250	G256	E268	K283	P284	K285	S318

Table 3c continued

SEQ ID NO	Pos 31	Pos 32	Pos 33	Pos 34	Pos 35	Pos 36	Pos 37	Pos 38	Pos 39	Pos 40	**Pos 41**	Pos 42	Pos 43	Pos 44	**Pos 45**
2	Q301	G308	S324	R335	G346	F349	L351	D352	T358	L384	**L397**	F417	T418	T419	**F420**
4	Q301	G308	S324	R335	G346	F349	L351	D352	T358	L384	**L397**	F417	T418	T419	**F420**
6	Q300	G307	S323	R334	G345	F348	L350	D351	T357	L383	**L396**	F416	T417	T418	**F419**
8	Q300	G307	S323	R334	G345	F348	L350	D351	T357	L383	**L396**	F416	T417	T418	**F419**
10	S318	E323	R337	C348	G359	F362	L364	N365	N371	L397	**L410**	Y430	T431	T432	**F433**
12	E322	-	Q340	Y351	A365	L368	N370	F371	G377	L404	**L414**	L434	L435	N436	**Y437**
14	E329	-	Q347	Y358	A372	L375	K377	F378	A384	L411	**L421**	L441	L442	N443	**Y444**
16	S336	-	R354	Y365	A379	L382	K384	F385	A391	L418	**L428**	I448	L449	N450	**Y451**
18	H301	E308	P324	N335	E346	F349	L351	D352	S358	L384	**L397**	Y417	T418	T419	**F420**
20	E331	-	R349	Y360	A374	L377	S379	F380	A386	L413	**L423**	L443	L444	N445	**Y446**
22	D309	-	Q327	Y338	A352	L355	R357	F358	A364	L391	**L401**	L421	L422	N423	**Y424**
24	F308	G315	T336	S347	G358	V361	L363	D364	D370	L396	**L410**	Y430	T431	T432	**F433**
26	A335	-	F353	Y364	A378	L381	S383	F384	G390	L418	**L428**	L448	L449	N450	**Y451**
28	Q312	A319	V362	F373	A388	L391	E393	V394	A400	L430	**L440**	L460	L461	N462	**F463**
30	L308	G315	T336	S347	G358	F361	L363	D364	D370	L396	**L410**	Y430	T431	T432	**F433**
32	D310	-	Q328	Y339	A353	L356	I358	F359	A365	L392	**L402**	L422	L423	N424	**Y425**
34	Q272	G279	S295	R306	G317	F320	L322	D323	S329	L355	**L368**	F388	T389	T390	**F391**
36	E311	-	Q329	H340	A354	L357	K359	L360	A366	L393	**L403**	L423	L424	N425	**Y426**
38	C271	D278	S296	C307	G318	F321	L323	N324	D330	L356	**L369**	Y389	T390	T391	**F392**
40	H273	Q280	D294	Y305	G316	F319	L321	N322	S328	L354	**L367**	Y387	T388	T389	**F390**
42	D197	-	L215	Y226	A240	L243	K245	F246	A252	L279	**L289**	L309	L310	N311	**Y312**
44	C272	G279	S300	S311	G322	F325	L327	D328	D334	L360	**L374**	Y394	T395	S396	**F397**

46	C317	G324	S345	S356	G367	F370	L372	D373	D379	L405	**L419**	Y462	T463	S464	**F465**
48	L324	-	R342	Y353	A367	L370	K372	F373	A379	L406	**L416**	I436	L437	S438	**Y439**

Table 3c continued

SEQ ID NO	Pos 46	Pos 47	Pos 48	Pos 49	Pos 50	Pos 51	Pos 52	Pos 53	Pos 54	Pos 55	Pos 56	Pos 57	Pos 58	Pos 59
2	A432	T434	K438	L449	T451	F462	Y470	S476	V477	D482	Y493	K498	E515	K528
4	A432	T434	K438	L449	T451	F462	Y470	S476	V477	D482	Y493	K498	E515	K528
6	A431	T433	K437	L448	T450	F461	Y469	S475	V476	D481	Y492	K497	E514	K527
8	A431	T433	K437	L448	T450	F461	Y469	C475	V476	D481	Y492	K497	E514	K527
10	A445	T447	K451	L462	V464	Y475	Y483	S489	V490	D495	Y506	R511	D528	K541
12	K449	E451	V455	K468	K470	V481	F489	D495	T496	K501	L514	V519	S536	-
14	K456	E458	V462	R475	D477	V488	F496	D502	I503	K508	L521	V526	A543	-
16	K463	K465	A469	N482	N484	V495	F503	D509	L510	K515	L528	V533	A550	-
18	A432	T434	K438	L449	T451	Y462	Y470	S476	V477	E482	Y493	K498	E515	K525
20	K458	E460	V464	K477	K479	V490	F498	D504	T505	K510	L523	V528	S545	-
22	K436	E438	V442	N455	T457	V468	F476	D482	L483	K488	L501	V506	S523	-
24	A445	T447	K451	L462	V464	Y475	Y483	S489	V490	E495	Y506	K511	D528	N541
26	Q463	T465	V469	K482	D484	V495	F503	E509	Q510	R515	L528	V533	A550	A563
28	A475	P477	A481	R495	G497	V508	F516	D522	R523	K528	L545	V550	E567	-
30	A445	T447	K451	L462	V464	Y475	Y483	S489	V490	E495	Y506	K511	D528	N541
32	K437	E439	V443	N456	K458	V469	F477	D483	H484	K489	L502	V507	S524	-
34	A403	T405	K409	L420	T422	F433	Y441	S447	V448	D453	Y464	K469	E486	K499
36	K438	E440	V444	-	-	-	F447	D453	I454	K459	L472	V477	I494	-
38	A404	R406	K410	L421	A423	Y434	Y442	S448	V449	D454	Y465	R470	D487	-
40	A402	T404	R408	L419	A421	Y432	Y440	S446	V447	D452	F463	K468	D485	T498
42	Q324	E326	I330	N343	N345	V356	F364	D370	V371	K376	L389	V394	-	-
44	A409	T411	K415	L426	V428	H439	Y447	L453	V454	A459	Y470	K475	D492	D505

4[illegible]	Λ4[illegible]7	[illegible] 4[illegible]9	K4[illegible]	_494	V49[illegible]	X[illegible]	[illegible] 1[illegible]	_[illegible]21	V[illegible]	Λ[illegible]27	[illegible] 5[illegible]	K[illegible]4[illegible]	Q[illegible]	Q[illegible]
4[illegible]	K[illegible]1	[illegible] 4[illegible]	Λ4[illegible]	N4[illegible]	N4[illegible]	V4[illegible]	F491	D4[illegible]	V49[illegible]	K[illegible]	_[illegible] 1[illegible]	V[illegible]21	8[illegible]	-

In addition, the present invention refers to a method for identifying a PPO-inhibiting herbicide by using a mutated PPO encoded by a nucleic acid which comprises the nucleotide sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, or 47, or a variant or derivative thereof.

Said method comprises the steps of:

a) generating a transgenic cell or plant comprising a nucleic acid encoding a mutated PPO, wherein the mutated PPO is expressed;
b) applying a PPO-inhibiting herbicide to the transgenic cell or plant of a) and to a control cell or plant of the same variety;
c) determining the growth or the viability of the transgenic cell or plant and the control cell or plant after application of said PPO-inhibiting herbicide, and
d) selecting "PPO-inhibiting herbicides" which confer reduced growth to the control cell or plant as compared to the growth of the transgenic cell or plant.

By "control cell" or "similar, wild-type, plant, plant tissue, plant cell or host cell" is intended a plant, plant tissue, plant cell, or host cell, respectively, that lacks the herbicide-resistance characteristics and/or particular polynucleotide of the invention that are disclosed herein. The use of the term "wild-type" is not, therefore, intended to imply that a plant, plant tissue, plant cell, or other host cell lacks recombinant DNA in its genome, and/or does not possess herbicide-resistant characteristics that are different from those disclosed herein.

Another object refers to a method of identifying a nucleotide sequence encoding a mutated PPO which is resistant or tolerant to a PPO-inhibiting herbicide, the method comprising:

a) generating a library of mutated PPO-encoding nucleic acids,
b) screening a population of the resulting mutated PPO-encoding nucleic acids by expressing each of said nucleic acids in a cell or plant and treating said cell or plant with a PPO-inhibiting herbicide,
c) comparing the PPO-inhibiting herbicide-tolerance levels provided by said population of mutated PPO encoding nucleic acids with the PPO-inhibiting herbicide-tolerance level provided by a control PPO-encoding nucleic acid,
d) selecting at least one mutated PPO-encoding nucleic acid that provides a significantly increased level of tolerance to a PPO-inhibiting herbicide as compared to that provided by the control PPO-encoding nucleic acid.

In a preferred embodiment, the mutated PPO-encoding nucleic acid selected in step d) provides at least 2-fold as much resistance or tolerance of a cell or plant to a PPO-inhibiting herbicide as compared to that provided by the control PPO-encoding nucleic acid.

In a further preferred embodiment, the mutated PPO-encoding nucleic acid selected in step d) provides at least 2-fold, at least 5-fold, at least 10-fold, at least 20-fold, at least 50-fold, at least 100-fold, at least 500-fold, as much resistance or tolerance of a cell or plant to a PPO-inhibiting herbicide as compared to that provided by the control PPO-encoding nucleic acid.

The resistance or tolerance can be determined by generating a transgenic plant or host cell, preferably a plant cell, comprising a nucleic acid sequence of the library of step a) and comparing said transgenic plant with a control plant or host cell, preferably a plant cell.

Another object refers to a method of identifying a plant or algae containing a nucleic acid comprising a nucleotide sequence encoding a wild-type or mutated PPO which is resistant or tolerant to a PPO-inhibiting herbicide, the method comprising:

a) identifying an effective amount of a PPO-inhibiting herbicide in a culture of plant cells or green algae that leads to death of said cells.
b) treating said plant cells or green algae with a mutagenizing agent,
c) contacting said mutagenized cells population with an effective amount of PPO-inhibiting herbicide, identified in a),
d) selecting at least one cell surviving these test conditions,
e) PCR-amplification and sequencing of PPO genes from cells selected in d) and comparing such sequences to wild-type PPO gene sequences, respectively.

In a preferred embodiment, said mutagenizing agent is ethylmethanesulfonate (EMS).

Many methods well known to the skilled artisan are available for obtaining suitable candidate nucleic acids for identifying a nucleotide sequence encoding a mutated PPO from a variety of different potential source organisms including microbes, plants, fungi, algae, mixed cultures etc. as well as environmental sources of DNA such as soil. These methods include inter alia the preparation of cDNA or genomic DNA libraries, the use of suitably degenerate oligonucleotide primers, the use of probes based upon known sequences or complementation assays (for example, for growth upon tyrosine) as well as the use of mutagenesis and shuffling in order to provide recombined or shuffled mutated PPO-encoding sequences.

Nucleic acids comprising candidate and control PPO encoding sequences can be expressed in yeast, in a bacterial host strain, in an alga or in a higher plant such as tobacco or Arabidopsis and the relative levels of inherent tolerance of the PPO encoding sequences screened according to a visible indicator phenotype of the transformed strain or plant in the presence of different concentrations of the selected PPO-inhibiting herbicide. Dose responses and relative shifts in dose responses associated with these indicator phenotypes (formation of brown color, growth inhibition, herbicidal effect etc) are conveniently expressed in terms, for example, of GR50 (concentration for 50% reduction of growth) or MIC (minimum inhibitory concentration) values where increases in values correspond to increases in inherent tolerance of the expressed PPO. For example, in a relatively rapid assay system based upon transformation of a bacterium such as E. coli, each mutated PPO encoding sequence may be expressed, for example, as a DNA sequence under expression control of a controllable promoter such as the lacZ promoter and taking suitable account, for example by the use of synthetic DNA, of such issues as codon usage in order to obtain as comparable a level of expression as possible of different PPO sequences. Such strains expressing nucleic acids comprising alternative candidate PPO sequences may be plated out on different concentrations of the selected PPO-inhibiting herbicide in, optionally, a tyrosine supplemented medium and the relative levels of inherent tolerance of the expressed PPO enzymes

estimated on the basis of the extent and MIC for inhibition of the formation of the brown, ochronotic pigment.

In another embodiment, candidate nucleic acids are transformed into plant material to generate a transgenic plant, regenerated into morphologically normal fertile plants which are then measured for differential tolerance to selected PPO-inhibiting herbicides as described in the Example section hereinafter. Many suitable methods for transformation using suitable selection markers such as kanamycin, binary vectors such as from Agrobacterium and plant regeneration as, for example, from tobacco leaf discs are well known in the art. Optionally, a control population of plants is likewise transformed with a nucleic acid expressing the control PPO. Alternatively, an untransformed dicot plant such as Arabidopsis or Tobacco can be used as a control since this, in any case, expresses its own endogenous PPO. The average, and distribution, of herbicide tolerance levels of a range of primary plant transformation events or their progeny to PPO-inhibiting herbicides described supra are evaluated in the normal manner based upon plant damage, meristematic bleaching symptoms etc. at a range of different concentrations of herbicides. These data can be expressed in terms of, for example, GR50 values derived from dose/response curves having "dose" plotted on the x-axis and "percentage kill", "herbicidal effect", "numbers of emerging green plants" etc. plotted on the y-axis where increased GR50 values correspond to increased levels of inherent tolerance of the expressed PPO. Herbicides can suitably be applied pre-emergence or post-emergence.

Another object of the present invention refers to an isolated nucleic acid encoding a mutated PPO as disclosed SUPRA, wherein the nucleic acid comprises the nucleotide sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45 or 47, or a variant or derivative thereof.

In one embodiment, the nucleic acid is identifiable by a method as defined above.

In a preferred embodiment, the encoded mutated PPO is a variant of SEQ ID NO: 2 or SEQ ID NO. 4, or an orthologue thereof, which includes one or more of the following: the amino acid at or corresponding to position 128 of SEQ ID NO:2 is other than Arginine; and/or the amino acid at or corresponding to position 420 of SEQ ID NO:2 is other than Phenylalanine.

In another embodiment, the invention refers to a plant cell transformed by a nucleic acid encoding a mutated PPO polypeptide according to the present invention or to a plant cell which has been mutated to obtain a plant expressing a nucleic acid encoding a mutated PPO polypeptide according to the present invention, wherein expression of the nucleic acid in the plant cell results in increased resistance or tolerance to a PPO-inhibiting herbicide as compared to a wild type variety of the plant cell. Preferably, the mutated PPO polypeptide encoding nucleic acid comprises a polynucleotide sequence selected from the group consisting of: a) a polynucleotide as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45 or 47, or a variant or derivative thereof; b) a polynucleotide encoding a polypeptide as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, or 48, or a variant or derivative thereof; c) a polynucleotide comprising at least 60 consecutive nucleotides of

any of a) or b); and d) a polynucleotide complementary to the polynucleotide of any of a) through c).

The term "expression/expressing" or "gene expression" means the transcription of a specific gene or specific genes or specific genetic construct. The term "expression" or "gene expression" in particular means the transcription of a gene or genes or genetic construct into structural RNA (rRNA, tRNA) or mRNA with or without subsequent translation of the latter into a protein. The process includes transcription of DNA and processing of the resulting mRNA product.

To obtain the desired effect, i.e. plants that are tolerant or resistant to the PPO-inhibiting herbicide derivative herbicide of the present invention, it will be understood that the at least one nucleic acid is "over-expressed" by methods and means known to the person skilled in the art.

The term "increased expression" or "overexpression" as used herein means any form of expression that is additional to the original wild-type expression level. Methods for increasing expression of genes or gene products are well documented in the art and include, for example, overexpression driven by appropriate promoters, the use of transcription enhancers or translation enhancers. Isolated nucleic acids which serve as promoter or enhancer elements may be introduced in an appropriate position (typically upstream) of a non-heterologous form of a polynucleotide so as to upregulate expression of a nucleic acid encoding the polypeptide of interest. For example, endogenous promoters may be altered in vivo by mutation, deletion, and/or substitution (see, Kmiec, US 5,565,350; Zarling et al., W09322443), or isolated promoters may be introduced into a plant cell in the proper orientation and distance from a gene of the present invention so as to control the expression of the gene.

If polypeptide expression is desired, it is generally desirable to include a polyadenylation region at the 3'-end of a polynucleotide coding region. The polyadenylation region can be derived from the natural gene, from a variety of other plant genes, or from T-DNA. The 3' end sequence to be added may be derived from, for example, the nopaline synthase or octopine synthase genes, or alternatively from another plant gene, or less preferably from any other eukaryotic gene.

An intron sequence may also be added to the 5' untranslated region (UTR) or the coding sequence of the partial coding sequence to increase the amount of the mature message that accumulates in the cytosol. Inclusion of a spliceable intron in the transcription unit in both plant and animal expression constructs has been shown to increase gene expression at both the mRNA and protein levels up to 1000-fold (Buchman and Berg (1988) Mol. Cell biol. 8: 4395-4405; Callis et al. (1987) Genes Dev 1:1 183-1200). Such intron enhancement of gene expression is typically greatest when placed near the 5' end of the transcription unit. Use of the maize introns Adh1-S intron 1, 2, and 6, the Bronze-1 intron are known in the art. For general information see: The Maize Handbook, Chapter 116, Freeling and Walbot, Eds., Springer, N.Y. (1994)

The term "introduction" or "transformation" as referred to herein encompasses the transfer of an exogenous polynucleotide into a host cell, irrespective of the method used for transfer. Plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be

transformed with a genetic construct of the present invention and a whole plant regenerated there from. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen, embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristem, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and hypocotyl meristem). The polynucleotide may be transiently or stably introduced into a host cell and may be maintained non-integrated, for example, as a plasmid. Alternatively, it may be integrated into the host genome. The resulting transformed plant cell may then be used to regenerate a transformed plant in a manner known to persons skilled in the art.

The transfer of foreign genes into the genome of a plant is called transformation. Transformation of plant species is now a fairly routine technique. Advantageously, any of several transformation methods may be used to introduce the gene of interest into a suitable ancestor cell. The methods described for the transformation and regeneration of plants from plant tissues or plant cells may be utilized for transient or for stable transformation. Transformation methods include the use of liposomes, electroporation, chemicals that increase free DNA uptake, injection of the DNA directly into the plant, particle gun bombardment, transforrmation using viruses or pollen and microprojection. Methods may be selected from the calcium/polyethylene glycol method for protoplasts (Krens, F.A. et al., (1982) Nature 296, 72-74; Negrutiu I et al. (1987) Plant Mol Biol 8: 363-373); electroporation of protoplasts (Shillito R.D. et al. (1985) Bio/Technol 3, 1099-1 102); microinjection into plant material (Crossway A et al., (1986) Mol. Gen Genet 202: 179-185); DNA or RNA-coated particle bombardment (Klein TM et al., (1987) Nature 327: 70) infection with (non-integrative) viruses and the like. Transgenic plants, including transgenic crop plants, are preferably produced via Agrobacterium-mediated transformation. An advantageous transformation method is the transformation in planta. To this end, it is possible, for example, to allow the agrobacteria to act on plant seeds or to inoculate the plant meristem with agrobacteria. It has proved particularly expedient in accordance with the invention to allow a suspension of transformed agrobacteria to act on the intact plant or at least on the flower primordia. The plant is subsequently grown on until the seeds of the treated plant are obtained (Clough and Bent, Plant J. (1998) 16, 735-743). Methods for Agrobacterium-mediated transformation of rice include well known methods for rice transformation, such as those described in any of the following: European patent application EP 1198985 A1, Aldemita and Hodges (Planta 199: 612-617, 1996); Chan et al. (Plant Mol Biol 22 (3): 491-506, 1993), Hiei et al. (Plant J 6 (2): 271-282, 1994), which disclosures are incorporated by reference herein as if fully set forth. In the case of corn transformation, the preferred method is as described in either Ishida et al. (Nat. Biotechnol 14(6): 745-50, 1996) or Frame et al. (Plant Physiol 129(1): 13-22, 2002), which disclosures are incorporated by reference herein as if fully set forth. Said methods are further described by way of example in B. Jenes et al., Techniques for Gene Transfer, in: Transgenic Plants, Vol. 1, Engineering and Utilization, eds. S.D. Kung and R. Wu, Academic Press (1993) 128-143 and in Potrykus Annu. Rev. Plant Physiol. Plant Molec. Biol. 42 (1991) 205-225). The nucleic acids or the construct to be expressed is preferably cloned into a vector, which is suitable for transforming Agrobacterium tumefaciens, for example pBin19 (Bevan et al., Nucl. Acids Res. 12 (1984) 871 1). Agrobacteria transformed by such a vector can then be used in known manner for the transformation of plants, such as plants used as a model, like

Arabidopsis (Arabidopsis thaliana is within the scope of the present invention not considered as a crop plant), or crop plants such as, by way of example, tobacco plants, for example by immersing bruised leaves or chopped leaves in an agrobacterial solution and then culturing them in suitable media. The transformation of plants by means of Agrobacterium tumefaciens is described, for example, by Hofgen and Willmitzer in Nucl. Acid Res. (1988) 16, 9877 or is known inter alia from F.F. White, Vectors for Gene Transfer in Higher Plants; in Transgenic Plants, Vol. 1, Engineering and Utilization, eds. S.D. Kung and R. Wu, Academic Press, 1993, pp. 15-38.

In addition to the transformation of somatic cells, which then have to be regenerated into intact plants, it is also possible to transform the cells of plant meristems and in particular those cells which develop into gametes. In this case, the transformed gametes follow the natural plant development, giving rise to transgenic plants. Thus, for example, seeds of Arabidopsis are treated with agrobacteria and seeds are obtained from the developing plants of which a certain proportion is transformed and thus transgenic [Feldman, KA and Marks MD (1987). Mol Gen Genet 208:274-289; Feldmann K (1992). In: C Koncz, N-H Chua and J Shell, eds, Methods in Arabidopsis Research. Word Scientific, Singapore, pp. 274-289]. Alternative methods are based on the repeated removal of the inflorescences and incubation of the excision site in the center of the rosette with transformed agrobacteria, whereby transformed seeds can likewise be obtained at a later point in time (Chang (1994). Plant J. 5: 551-558; Katavic (1994). Mol Gen Genet, 245: 363-370). However, an especially effective method is the vacuum infiltration method with its modifications such as the 'floral dip" method. In the case of vacuum infiltration of Arabidopsis, intact plants under reduced pressure are treated with an agrobacterial suspension [Bechthold, N (1993). C R Acad Sci Paris Life Sci, 316: 1194-1 199], while in the case of the "floral dip" method the developing floral tissue is incubated briefly with a surfactant-treated agrobacterial suspension [Clough, SJ and Bent AF (1998) The Plant J. 16, 735-743]. A certain proportion of transgenic seeds are harvested in both cases, and these seeds can be distinguished from non-transgenic seeds by growing under the above-described selective conditions. In addition the stable transformation of plastids is of advantages because plastids are inherited maternally is most crops reducing or eliminating the risk of transgene flow through pollen. The transformation of the chloroplast genome is generally achieved by a process which has been schematically displayed in Klaus et al., 2004 [Nature Biotechnology 22 (2), 225-229]. Briefly the sequences to be transformed are cloned together with a selectable marker gene between flanking sequences homologous to the chloroplast genome. These homologous flanking sequences direct site specific integration into the plastome. Plastidal transformation has been described for many different plant species and an overview is given in Bock (2001) Transgenic plastids in basic research and plant biotechnology. J Mol Biol. 2001 Sep 21; 312 (3):425-38 or Maliga, P (2003) Progress towards commercialization of plastid transformation technology. Trends Biotechnol. 21, 20-28. Further biotechnological progress has recently been reported in form of marker free plastid transform ants, which can be produced by a transient co-integrated maker gene (Klaus et al., 2004, Nature Biotechnology 22(2), 225-229). The genetically modified plant cells can be regenerated via all methods with which the skilled worker is familiar. Suitable methods can be found in the abovementioned publications by S.D. Kung and R. Wu, Potrykus or Hofgen and Willmitzer.

Generally after transformation, plant cells or cell groupings are selected for the presence of one or

more markers which are encoded by plant-expressible genes co-transferred with the gene of interest, following which the transformed material is regenerated into a whole plant. To select transformed plants, the plant material obtained in the transformation is, as a rule, subjected to selective conditions so that transformed plants can be distinguished from untransformed plants. For example, the seeds obtained in the above-described manner can be planted and, after an initial growing period, subjected to a suitable selection by spraying. A further possibility consists in growing the seeds, if appropriate after sterilization, on agar plates using a suitable selection agent so that only the transformed seeds can grow into plants. Alternatively, the transformed plants are screened for the presence of a selectable marker such as the ones described above.

Following DNA transfer and regeneration, putatively transformed plants may also be evaluated, for instance using Southern analysis, for the presence of the gene of interest, copy number and/or genomic organisation. Alternatively or additionally, expression levels of the newly introduced DNA may be monitored using Northern and/or Western analysis, both techniques being well known to persons having ordinary skill in the art.

The generated transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, a first generation (or T1) transformed plant may be selfed and homozygous second-generation (or T2) transformants selected, and the T2 plants may then further be propagated through classical breeding techniques. The generated transformed organisms may take a variety of forms. For example, they may be chimeras of transformed cells and non-transformed cells; clonal transformants (e.g., all cells transformed to contain the expression cassette); grafts of transformed and untransformed tissues (e.g., in plants, a transformed rootstock grafted to an untransformed scion).

Preferably, the wild-type or mutated PPO nucleic acid comprises a polynucleotide sequence selected from the group consisting of : a) a polynucleotide as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, or 47, or a variant or derivative thereof; b) a polynucleotide encoding a polypeptide as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, or 48, or a variant or derivative thereof; c) a polynucleotide comprising at least 60 consecutive nucleotides of any of a) or b); and d) a polynucleotide complementary to the polynucleotide of any of a) through c).

Preferably, the expression of the nucleic acid in the plant results in the plant's increased resistance to PPO-inhibiting herbicide as compared to a wild type variety of the plant.

In another embodiment, the invention refers to a plant, preferably a transgenic plant, comprising a plant cell according to the present invention, wherein expression of the nucleic acid in the plant results in the plant's increased resistance to PPO-inhibiting herbicide as compared to a wild type variety of the plant.

The plants described herein can be either transgenic crop plants or non-transgenic plants.

For the purposes of the invention, "transgenic", "transgene" or "recombinant" means with regard to,

for example, a nucleic acid sequence, an expression cassette, gene construct or a vector comprising the nucleic acid sequence or an organism transformed with the nucleic acid sequences, expression cassettes or vectors according to the invention, all those constructions brought about by recombinant methods in which either

(a) the nucleic acid sequences encoding proteins useful in the methods of the invention, or

(b) genetic control sequence(s) which is operably linked with the nucleic acid sequence according to the invention, for example a promoter, or

(c) a) and b)

are not located in their natural genetic environment or have been modified by recombinant methods, it being possible for the modification to take the form of, for example, a substitution, addition, deletion, inversion or insertion of one or more nucleotide residues in order to allow for the expression of the mutated PPO of the present invention. The natural genetic environment is understood as meaning the natural genomic or chromosomal locus in the original plant or the presence in a genomic library. In the case of a genomic library, the natural genetic environment of the nucleic acid sequence is preferably retained, at least in part. The environment flanks the nucleic acid sequence at least on one side and has a sequence length of at least 50 bp, preferably at least 500 bp, especially preferably at least 1000 bp, most preferably at least 5000 bp. A naturally occurring expression cassette - for example the naturally occurring combination of the natural promoter of the nucleic acid sequences with the corresponding nucleic acid sequence encoding a polypeptide useful in the methods of the present invention, as defined above - becomes a transgenic expression cassette when this expression cassette is modified by non-natural, synthetic ("artificial") methods such as, for example, mutagenic treatment. Suitable methods are described, for example, in US 5,565,350 or WO 00/1 581 5.

A transgenic plant for the purposes of the invention is thus understood as meaning, as above, that the nucleic acids of the invention are not at their natural locus in the genome of said plant, it being possible for the nucleic acids to be expressed homologously or heterologously. However, as mentioned, transgenic also means that, while the nucleic acids according to the invention or used in the inventive method are at their natural position in the genome of a plant, the sequence has been modified with regard to the natural sequence, and/or that the regulatory sequences of the natural sequences have been modified. Transgenic is preferably understood as meaning the expression of the nucleic acids according to the invention at an unnatural locus in the genome, i.e. homologous or, preferably, heterologous expression of the nucleic acids takes place. Preferred transgenic plants are mentioned herein. Furthermore, the term "transgenic" refers to any plant, plant cell, callus, plant tissue, or plant part, that contains all or part of at least one recombinant polynucleotide. In many cases, all or part of the recombinant polynucleotide is stably integrated into a chromosome or stable extra-chromosomal element, so that it is passed on to successive generations. For the purposes of the invention, the term "recombinant polynucleotide" refers to a polynucleotide that has been altered, rearranged, or modified by genetic engineering. Examples include any cloned polynucleotide, or polynucleotides, that are linked or joined to heterologous sequences. The term "recombinant" does not refer to alterations of polynucleotides that result from naturally occurring events, such as spontaneous mutations, or from non-spontaneous mutagenesis followed by selective breeding.

Plants containing mutations arising due to non-spontaneous mutagenesis and selective breeding are referred to herein as non-transgenic plants and are included in the present invention. In embodiments wherein the plant is transgenic and comprises multiple mutated PPO nucleic acids, the nucleic acids can be derived from different genomes or from the same genome. Alternatively, in embodiments wherein the plant is non-transgenic and comprises multiple mutated PPO nucleic acids, the nucleic acids are located on different genomes or on the same genome. As used herein, "mutagenized" refers to an organism or DNA thereof having alteration(s) in the biomolecular sequence of its native genetic material as compared to the sequence of the genetic material of a corresponding wild-type organism or DNA, wherein the alteration(s) in genetic material were induce and/or selected by human action. Methods of inducing mutations can induce mutations in random positions in the genetic material or can induce mutations in specific locations in the genetic material (i.e., can be directed mutagenesis techniques), such as by use of a genoplasty technique.

In certain embodiments, the present invention involves herbidicide-resistant plants that are produced by mutation breeding. Such plants comprise a polynucleotide encoding a mutated PPO and are tolerant to one or more PPO-inhibiting herbicides. Such methods can involve, for example, exposing the plants or seeds to a mutagen, particularly a chemical mutagen such as, for example, ethyl methanesulfonate (EMS) and selecting for plants that have enhanced tolerance to at least one or more PPO-inhibiting herbicide.

However, the present invention is not limited to herbicide-tolerant plants that are produced by a mutagenesis method involving the chemical mutagen EMS. Any mutagenesis method known in the art may be used to produce the herbicide-resistant plants of the present invention. Such mutagenesis methods can involve, for example, the use of any one or more of the following mutagens: radiation, such as X-rays, Gamma rays (e.g., cobalt 60 or cesium 137), neutrons, (e.g., product of nuclear fission by uranium 235 in an atomic reactor), Beta radiation (e.g., emitted from radioisotopes such as phosphorus 32 or carbon 14), and ultraviolet radiation (preferably from 2500 to 2900 nm), and chemical mutagens such as base analogues (e.g., 5-bromo-uracil), related compounds (e.g., 8-ethoxy caffeine), antibiotics (e.g., streptonigrin), alkylating agents (e.g., sulfur mustards, nitrogen mustards, epoxides, ethylenamines, sulfates, sulfonates, sulfones, lactones), azide, hydroxylamine, nitrous acid, or acridines. Herbicide-resistant plants can also be produced by using tissue culture methods to select for plant cells comprising herbicide-resistance mutations and then regenerating herbicide-resistant plants therefrom. See, for example, U.S. Patent Nos. 5,773,702 and 5,859,348, both of which are herein incorporated in their entirety by reference. Further details of mutation breeding can be found in "Principals of Cultivar Development" Fehr, 1993 Macmillan Publishing Company the disclosure of which is incorporated herein by reference

In addition to the definition above, the term "plant" is intended to encompass crop plants at any stage of maturity or development, as well as any tissues or organs (plant parts) taken or derived from any such plant unless otherwise clearly indicated by context. Plant parts include, but are not limited to, stems, roots, flowers, ovules, stamens, leaves, embryos, meristematic regions, callus tissue, anther cultures, gametophytes, sporophytes, pollen, microspores, protoplasts, and the like.

The plant of the present invention comprises at least one mutated PPO nucleic acid or over-

expressed wild-type PPO nucleic acid, and has increased tolerance to a PPO-inhibiting herbicide as compared to a wild-type variety of the plant. It is possible for the plants of the present invention to have multiple wild-type or mutated PPO nucleic acids from different genomes since these plants can contain more than one genome. For example, a plant contains two genomes, usually referred to as the A and B genomes. Because PPO is a required metabolic enzyme, it is assumed that each genome has at least one gene coding for the PPO enzyme (i.e. at least one PPO gene). As used herein, the term "PPO gene locus" refers to the position of an PPO gene on a genome, and the terms "PPO gene" and "PPO nucleic acid" refer to a nucleic acid encoding the PPO enzyme. The PPO nucleic acid on each genome differs in its nucleotide sequence from an PPO nucleic acid on another genome. One of skill in the art can determine the genome of origin of each PPO nucleic acid through genetic crossing and/or either sequencing methods or exonuclease digestion methods known to those of skill in the art.

The present invention includes plants comprising one, two, three, or more mutated PPO alleles, wherein the plant has increased tolerance to a PPO-inhibiting herbicide as compared to a wild-type variety of the plant. The mutated PPO alleles can comprise a nucleotide sequence selected from the group consisting of a polynucleotide as defined in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, or 47, or a variant or derivative thereof, a polynucleotide encoding a polypeptide as defined in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, or 48, or a variant or derivative, homologue, orthologue, paralogue thereof, a polynucleotide comprising at least 60 consecutive nucleotides of any of the aforementioned polynucleotides; and a polynucleotide complementary to any of the aforementioned polynucleotides.

"Alleles" or "allelic variants" are alternative forms of a given gene, located at the same chromosomal position. Allelic variants encompass Single Nucleotide Polymorphisms (SNPs), as well as Small Insertion/Deletion Polymorphisms (INDELs). The size of INDELs is usually less than 100 bp. SNPs and INDELs form the largest set of sequence variants in naturally occurring polymorphic strains of most organisms

The term "variety" refers to a group of plants within a species defined by the sharing of a common set of characteristics or traits accepted by those skilled in the art as sufficient to distinguish one cultivar or variety from another cultivar or variety. There is no implication in either term that all plants of any given cultivar or variety will be genetically identical at either the whole gene or molecular level or that any given plant will be homozygous at all loci. A cultivar or variety is considered "true breeding" for a particular trait if, when the true-breeding cultivar or variety is self-pollinated, all of the progeny contain the trait. The terms "breeding line" or "line" refer to a group of plants within a cultivar defined by the sharing of a common set of characteristics or traits accepted by those skilled in the art as sufficient to distinguish one breeding line or line from another breeding line or line. There is no implication in either term that all plants of any given breeding line or line will be genetically identical at either the whole gene or molecular level or that any given plant will be homozygous at all loci. A breeding line or line is considered "true breeding" for a particular trait if, when the true-breeding line or breeding line is self-pollinated, all of the progeny contain the trait. In the present invention, the trait arises from a mutation in a PPO gene of the plant or seed.

In some embodiments, traditional plant breeding is employed whereby the PPO-inhibiting herbicides-tolerant trait is introduced in the progeny plant resulting therefrom. In one embodiment, the present invention provides a method for producing a PPO-inhibiting herbicides-tolerant progeny plant, the method comprising: crossing a parent plant with a PPO-inhibiting herbicides-tolerant plant to introduce the PPO-inhibiting herbicides-tolerance characteristics of the PPO-inhibiting herbicides-tolerant plant into the germplasm of the progeny plant, wherein the progeny plant has increased tolerance to the PPO-inhibiting herbicides relative to the parent plant. In other embodiments, the method further comprises the step of introgressing the PPO-inhibiting herbicides-tolerance characteristics through traditional plant breeding techniques to obtain a descendent plant having the PPO-inhibiting herbicides-tolerance characteristics

The herbicide-resistant plants of the invention that comprise polynucleotides encoding mutated PPO polypeptides also find use in methods for increasing the herbicide-resistance of a plant through conventional plant breeding involving sexual reproduction. The methods comprise crossing a first plant that is a herbicide-resistant plant of the invention to a second plant that may or may not be resistant to the same herbicide or herbicides as the first plant or may be resistant to different herbicide or herbicides than the first plant. The second plant can be any plant that is capable of producing viable progeny plants (i.e., seeds) when crossed with the first plant. Typically, but not necessarily, the first and second plants are of the same species. The methods can optionally involve selecting for progeny plants that comprise the mutated PPO polypeptides of the first plant and the herbicide resistance characteristics of the second plant. The progeny plants produced by this method of the present invention have increased resistance to a herbicide when compared to either the first or second plant or both. When the first and second plants are resistant to different herbicides, the progeny plants will have the combined herbicide tolerance characteristics of the first and second plants. The methods of the invention can further involve one or more generations of backcrossing the progeny plants of the first cross to a plant of the same line or genotype as either the first or second plant. Alternatively, the progeny of the first cross or any subsequent cross can be crossed to a third plant that is of a different line or genotype than either the first or second plant. The present invention also provides plants, plant organs, plant tissues, plant cells, seeds, and non-human host cells that are transformed with the at least one polynucleotide molecule, expression cassette, or transformation vector of the invention. Such transformed plants, plant organs, plant tissues, plant cells, seeds, and non-human host cells have enhanced tolerance or resistance to at least one herbicide, at levels of the herbicide that kill or inhibit the growth of an untransformed plant, plant tissue, plant cell, or non-human host cell, respectively. Preferably, the transformed plants, plant tissues, plant cells, and seeds of the invention are Arabidopsis thaliana and crop plants.

In other aspects, plants of the invention include those plants which, in addition to being tolerant to PPO-inhibiting herbicides, have been subjected to further genetic modifications by breeding, mutagenesis or genetic engineering, e.g. have been rendered tolerant to applications of specific other classes of herbicides, such as AHAS inhibitors; auxinic herbicides; bleaching herbicides such as hydroxyphenylpyruvate dioxygenase (HPPD) inhibitors or phytoene desaturase (PDS) inhibitors; EPSPS inhibitors such as glyphosate; glutamine synthetase (GS) inhibitors such as glufosinate; lipid biosynthesis inhibitors such as acetyl CoA carboxylase (ACCase) inhibitors; or

oxynil {i.e. bromoxynil or ioxynil) herbicides as a result of conventional methods of breeding or genetic engineering, Thus, PPO-inhibiting herbicides-tolerant plants of the invention can be made resistant to multiple classes of herbicides through multiple genetic modifications, such as resistance to both glyphosate and glufosinate or to both glyphosate and a herbicide from another class such as HPPD inhibitors, AHAS inhibitors, or ACCase inhibitors. These herbicide resistance technologies are, for example, described in Pest Management Science (at volume, year, page): 61, 2005, 246; 61, 2005, 258; 61, 2005, 277; 61, 2005, 269; 61, 2005, 286; 64, 2008, 326; 64, 2008, 332; Weed Science 57, 2009, 108; Australian Journal of Agricultural Research 58, 2007, 708; Science 316, 2007, 1185; and references quoted therein. For example, PPO-inhibiting herbicides-tolerant plants of the invention, in some embodiments, may be tolerant to ACCase inhibitors, such as "dims" {e.g., cycloxydim, sethoxydim, clethodim, or tepraloxydim), "fops" {e.g. , clodinafop, diclofop, fluazifop, haloxyfop, or quizalofop), and "dens" (such as pinoxaden); to auxinic herbicides, such as dicamba; to EPSPS inhibitors, such as glyphosate; to other PPO inhibitors; and to GS inhibitors, such as glufosinate.

In addition to these classes of inhibitors, PPO-inhibiting herbicides-tolerant plants of the invention may also be tolerant to herbicides having other modes of action, for example, chlorophyll/carotenoid pigment inhibitors, cell membrane disrupters, photosynthesis inhibitors, cell division inhibitors, root inhibitors, shoot inhibitors, and combinations thereof.

Such tolerance traits may be expressed, e.g. : as mutant or wildtype PPO proteins, as mutant AHASL proteins, mutant ACCase proteins, mutant EPSPS proteins, or mutant glutamine synthetase proteins; or as mutant native, inbred, or transgenic aryloxyalkanoate dioxygenase (AAD or DHT), haloarylnitrilase (BXN), 2,2-dichloropropionic acid dehalogenase (DEH), glyphosate-N-acetyltransferase (GAT), glyphosate decarboxylase (GDC), glyphosate oxidoreductase (GOX), glutathione-S-transferase (GST), phosphinothricin acetyltransferase (PAT or bar), or CYP450s proteins having an herbicide-degrading activity.

PPO-inhibiting herbicides- tolerant plants hereof can also be stacked with other traits including, but not limited to, pesticidal traits such as Bt Cry and other proteins having pesticidal activity toward coleopteran, lepidopteran, nematode, or other pests; nutrition or nutraceutical traits such as modified oil content or oil profile traits, high protein or high amino acid concentration traits, and other trait types known in the art.

Furthermore, in other embodiments, PPO-inhibiting herbicides-tolerant plants are also covered which are, by the use of recombinant DNA techniques and/or by breeding and/or otherwise selected for such characteristics, rendered able to synthesize one or more insecticidal proteins, especially those known from the bacterial genus Bacillus, particularly from Bacillus thuringiensis, such as [delta]-endotoxins, e.g. CrylA(b), CrylA(c), CrylF, CrylF(a2), CryllA(b), CryllIA, CryllIB(bl) or Cry9c; vegetative insecticidal proteins (VIP), e.g. VIP1 , VIP2, VIP3 or VIP3A; insecticidal proteins of bacteria colonizing nematodes, e.g. Photorhabdus spp. or Xenorhabdus spp.; toxins produced by animals, such as scorpion toxins, arachnid toxins, wasp toxins, or other insect-specific neurotoxins; toxins produced by fungi, such streptomycete toxins; plant lectins, such as pea or barley lectins; agglutinins; proteinase inhibitors, such as trypsin inhibitors, serine protease

inhibitors, patatin, cystatin or papain inhibitors; ribosome-inactivating proteins (RIP), such as ricin, maize-RIP, abrin, luffin, saporin or bryodin; steroid metabolism enzymes, such as 3-hydroxy-steroid oxidase, ecdysteroid-IDP-glycosyl-transferase, cholesterol oxidases, ecdysone inhibitors or HMG- CoA-reductase; ion channel blockers, such as blockers of sodium or calcium channels; juvenile hormone esterase; diuretic hormone receptors (helicokinin receptors); stilben synthase, bibenzyl synthase, chitinases or glucanases. In the context of the present invention these insecticidal proteins or toxins are to be understood expressly also as pre-toxins, hybrid proteins, truncated or otherwise modified proteins. Hybrid proteins are characterized by a new combination of protein domains, (see, e.g. WO 02/015701). Further examples of such toxins or genetically modified plants capable of synthesizing such toxins are disclosed, e.g., in EP-A 374 753, WO 93/007278, WO 95/34656, EP-A 427 529, EP-A 451 878, WO 03/18810 und WO 03/52073. The methods for producing such genetically modified plants are generally known to the person skilled in the art and are described, e.g. in the publications mentioned above. These insecticidal proteins contained in the genetically modified plants impart to the plants producing these proteins tolerance to harmful pests from all taxonomic groups of arthropods, especially to beetles (Coeloptera), two-winged insects (Diptera), and moths (Lepidoptera) and to nematodes (Nematoda).

In some embodiments, expression of one or more protein toxins (e.g., insecticidal proteins) in the PPO-inhibiting herbicides-tolerant plants is effective for controlling organisms that include, for example, members of the classes and orders: Coleoptera such as the American bean weevil Acanthoscelides obtectus; the leaf beetle Agelastica alni; click beetles (Agriotes lineatus, Agriotes obscurus, Agriotes bicolor); the grain beetle Ahasverus advena; the summer schafer Amphimallon solstitialis; the furniture beetle Anobium punctatum; Anthonomus spp. (weevils); the Pygmy mangold beetle Atomaria linearis; carpet beetles (Anthrenus spp., Attagenus spp.); the cowpea weevil Callosobruchus maculates; the fried fruit beetle Carpophilus hemipterus; the cabbage seedpod weevil Ceutorhynchus assimilis; the rape winter stem weevil Ceutorhynchus picitarsis; the wireworms Conoderus vespertinus and Conoderus falli; the banana weevil Cosmopolites sordidus; the New Zealand grass grub Costelytra zealandica; the June beetle Cotinis nitida; the sunflower stem weevil Cylindrocopturus adspersus; the larder beetle Dermestes lardarius; the corn rootworms Diabrotica virgifera, Diabrotica virgifera virgifera, and Diabrotica barberi; the Mexican bean beetle Epilachna varivestis; the old house borer Hylotropes bajulus; the lucerne weevil Hypera postica; the shiny spider beetle Gibbium psylloides; the cigarette beetle Lasioderma serricorne; the Colorado potato beetle Leptinotarsa decemlineata; Lyctus beetles {Lyctus spp. , the pollen beetle Meligethes aeneus; the common cockshafer Melolontha melolontha; the American spider beetle Mezium americanum; the golden spider beetle Niptus hololeuc s; the grain beetles Oryzaephilus surinamensis and Oryzaephilus Mercator; the black vine weevil Otiorhynchus sulcatus; the mustard beetle Phaedon cochleariae, the crucifer flea beetle Phyllotreta cruciferae; the striped flea beetle Phyllotreta striolata; the cabbage steam flea beetle Psylliodes chrysocephala; Ptinus spp. (spider beetles); the lesser grain borer Rhizopertha dominica; the pea and been weevil Sitona lineatus; the rice and granary beetles Sitophilus oryzae and Sitophilus granaries; the red sunflower seed weevil Smicronyx fulvus; the drugstore beetle Stegobium paniceum; the yellow mealworm beetle Tenebrio molitor, the flour beetles Tribolium castaneum and Tribolium confusum; warehouse and cabinet beetles {Trogoderma spp.); the sunflower beetle Zygogramma exclamationis; Dermaptera (earwigs) such as the European earwig Forficula

auricularia and the striped earwig Labidura riparia; Dictyoptera such as the oriental cockroach Blatta orientalis; the greenhouse millipede Oxidus gracilis; the beet fly Pegomyia betae; the frit fly Oscinella frit; fruitflies (Dacus spp., Drosophila spp.); Isoptera (termites) including species from the familes Hodotermitidae, Kalotermitidae, Mastotermitidae, Rhinotermitidae, Serritermitidae, Termitidae, Termopsidae; the tarnished plant bug Lygus lineolaris; the black bean aphid Aphis fabae; the cotton or melon aphid Aphis gossypii; the green apple aphid Aphis pomi; the citrus spiny whitefly Aleurocanthus spiniferus; the sweet potato whitefly Bemesia tabaci; the cabbage aphid Brevicoryne brassicae; the pear psylla Cacopsylla pyricola; the currant aphid Cryptomyzus ribis; the grape phylloxera Daktulosphaira vitifoliae; the citrus psylla Diaphorina citri; the potato leafhopper Empoasca fabae; the bean leafhopper Empoasca Solana; the vine leafhopper Empoasca vitis; the woolly aphid Eriosoma lanigerum; the European fruit scale Eulecanium corni; the mealy plum aphid Hyalopterus arundinis; the small brown planthopper Laodelphax striatellus; the potato aphid Macrosiphum euphorbiae; the green peach aphid Myzus persicae; the green rice leafhopper Nephotettix cinticeps; the brown planthopper Nilaparvata lugens; the hop aphid Phorodon humuli; the bird-cherry aphid Rhopalosiphum padi; the grain aphid Sitobion avenae; Lepidoptera such as Adoxophyes orana (summer fruit tortrix moth); Archips podana (fruit tree tortrix moth); Bucculatrix pyrivorella (pear leafminer); Bucculatrix thurberiella (cotton leaf perforator); Bupalus piniarius (pine looper); Carpocapsa pomonella (codling moth); Chilo suppressalis (striped rice borer); Choristoneura fumiferana (eastern spruce budworm); Cochylis hospes (banded sunflower moth); Diatraea grandiosella (southwestern corn borer); Eupoecilia ambiguella (European grape berry moth); Helicoverpa armigera (cotton bollworm); Helicoverpa zea (cotton bollworm); Heliothis vires cens (tobacco budworm), Homeosoma electellum (sunflower moth); Homona magnanima (oriental tea tree tortrix moth); Lithocolletis blancardella (spotted tentiform leafminer); Lymantria dispar (gypsy moth); Malacosoma neustria (tent caterpillar); Mamestra brassicae (cabbage armyworm); Mamestra configurata (Bertha armyworm); Operophtera brumata (winter moth); Ostrinia nubilalis (European corn borer), Panolis flammea (pine beauty moth), Phyllocnistis citrella (citrus leafminer); Pieris brassicae (cabbage white butterfly); Rachiplusia ni (soybean looper); Spodoptera exigua (beet armywonn); Spodoptera littoralis (cotton leafworm); Sylepta derogata (cotton leaf roller); Trichoplusia ni (cabbage looper); Orthoptera such as the common cricket Acheta domesticus, tree locusts (Anacridium spp.), the migratory locust Locusta migratoria, the twostriped grasshopper Melanoplus bivittatus, the differential grasshopper Melanoplus differ entialis, the redlegged grasshopper Melanoplus femurrubrum, the migratory grasshopper Melanoplus sanguinipes, the northern mole cricket Neocurtilla hexadectyla, the red locust Nomadacris septemfasciata, the shortwinged mole cricket Scapteriscus abbreviatus, the southern mole cricket Scapteriscus borellii, the tawny mole cricket Scapteriscus vicinus, and the desert locust Schistocerca gregaria; Symphyla such as the garden symphylan Scutigerella immaculata; Thysanoptera such as the tobacco thrips Frankliniella fusca, the flower thrips Frankliniella intonsa, the western flower thrips Frankliniella occidentalism the cotton bud thrips Frankliniella schultzei, the banded greenhouse thrips Hercinothrips femoralis, the soybean thrips Neohydatothrips variabilis, Kelly's citrus thrips Pezothrips kellyanus, the avocado thrips Scirtothrips perseae, the melon thrips Thrips palmi, and the onion thrips Thrips tabaci; and the like, and combinations comprising one or more of the foregoing organisms.

In some embodiments, expression of one or more protein toxins (e.g., insecticidal proteins) in the

PPO-inhibiting herbicides-tolerant plants is effective for controlling flea beetles, i.e. members of the flea beetle tribe of family Chrysomelidae, preferably against Phyllotreta spp., such as Phyllotreta cruciferae and/or Phyllotreta triolata. In other embodiments, expression of one or more protein toxins {e.g., insecticidal proteins) in the PPO-inhibiting herbicides- tolerant plants is effective for controlling cabbage seedpod weevil, the Bertha armyworm, Lygus bugs, or the diamondback moth. Furthermore, in one embodiment, PPO-inhibiting herbicides-tolerant plants are also covered which are, e.g. by the use of recombinant DNA techniques and/or by breeding and/or otherwise selected for such traits, rendered able to synthesize one or more proteins to increase the resistance or tolerance of those plants to bacterial, viral or fungal pathogens. The methods for producing such genetically modified plants are generally known to the person skilled in the art.

Furthermore, in another embodiment, PPO-inhibiting herbicides-tolerant plants are also covered which are, e.g. by the use of recombinant DNA techniques and/or by breeding and/or otherwise selected for such traits, rendered able to synthesize one or more proteins to increase the productivity (e.g. oil content), tolerance to drought, salinity or other growth-limiting environmental factors or tolerance to pests and fungal, bacterial or viral pathogens of those plants.

Furthermore, in other embodiments, PPO-inhibiting herbicides-tolerant plants are also covered which are, e.g. by the use of recombinant DNA techniques and/or by breeding and/or otherwise selected for such traits, altered to contain a modified amount of one or more substances or new substances, for example, to improve human or animal nutrition, e.g. oil crops that produce health-promoting long-chain omega-3 fatty acids or unsaturated omega-9 fatty acids (e.g. Nexera(R) rape, Dow Agra Sciences, Canada).

Furthermore, in some embodiments, PPO-inhibiting herbicides-tolerant plants are also covered which are, e.g. by the use of recombinant DNA techniques and/or by breeding and/or otherwise selected for such traits, altered to contain increased amounts of vitamins and/or minerals, and/or improved profiles of nutraceutical compounds.

In one embodiment, PPO-inhibiting herbicides-tolerant plants of the present invention, relative to a wild-type plant, comprise an increased amount of, or an improved profile of, a compound selected from the group consisting of: glucosinolates (e.g., glucoraphanin (4-methylsulfinylbutyl-glucosinolate), sulforaphane, 3-indolylmethyl-glucosinolate(glucobrassicin), I -methoxy-3-indolylmethyl-glucosinolate (neoglucobrassicin)); phenolics (e.g., flavonoids (e.g., quercetin, kaempferol), hydroxycinnamoyl derivatives (e.g., 1 ,2,2'- trisinapoylgentiobiose, 1 ,2-diferuloylgentiobiose, 1,2'-disinapoyl-2-feruloylgentiobiose, 3-0- caffeoyl-quinic (neochlorogenic acid)); and vitamins and minerals (e.g., vitamin C, vitamin E, carotene, folic acid, niacin, riboflavin, thiamine, calcium, iron, magnesium, potassium, selenium, and zinc).

In another embodiment, PPO-inhibiting herbicides-tolerant plants of the present invention, relative to a wild-type plant, comprise an increased amount of, or an improved profile of, a

compound selected from the group consisting of: progoitrin; isothiocyanates; indoles (products of glucosinolate hydrolysis); glutathione; carotenoids such as beta-carotene, lycopene, and the xanthophyll carotenoids such as lutein and zeaxanthin; phenolics comprising the flavonoids such as the flavonols (e.g. quercetin, rutin), the flavans/tannins (such as the procyanidins comprising coumarin, proanthocyanidins, catechins, and anthocyanins); flavones; phytoestrogens such as coumestans, lignans, resveratrol, isoflavones e.g. genistein, daidzein, and glycitein; resorcyclic acid lactones; organosulphur compounds; phytosterols; terpenoids such as carnosol, rosmarinic acid, glycyrrhizin and saponins; chlorophyll; chlorphyllin, sugars, anthocyanins, and vanilla. In other embodiments, PPO-inhibiting herbicides-tolerant plants of the present invention, relative to a wild-type plant, comprise an increased amount of, or an improved profile of, a compound selected from the group consisting of: vincristine, vinblastine, taxanes (e.g., taxol (paclitaxel), baccatin III, 10-desacetylbaccatin III, 10-desacetyl taxol, xylosyl taxol, 7- epitaxol, 7-epibaccatin III, 10-desacetylcephalomannine, 7-epicephalomannine, taxotere, cephalomannine, xylosyl cephalomannine, taxagifine, 8-benxoyloxy taxagifine, 9-acetyloxy taxusin, 9-hydroxy taxusin, taiwanxam, taxane la, taxane lb, taxane lc, taxane Id, GMP paclitaxel, 9-dihydro 13-acetylbaccatin III, 10-desacetyl-7-epitaxol, tetrahydrocannabinol (THC), cannabidiol (CBD), genistein, diadzein, codeine, morphine, quinine, shikonin, ajmalacine, serpentine, and the like.

It is to be understood that the plant of the present invention can comprise a wild type PPO nucleic acid in addition to a mutated PPO nucleic acid. It is contemplated that the PPO-inhibiting herbicide tolerant lines may contain a mutation in only one of multiple PPO isoenzymes. Therefore, the present invention includes a plant comprising one or more mutated PPO nucleic acids in addition to one or more wild type PPO nucleic acids.

In another embodiment, the invention refers to a seed produced by a transgenic plant comprising a plant cell of the present invention, wherein the seed is true breeding for an increased resistance to a PPO-inhibiting herbicide as compared to a wild type variety of the seed.

In another embodiment, the invention refers to a method of producing a transgenic plant cell with an increased resistance to a PPO-inhibiting herbicide as compared to a wild type variety of the plant cell comprising, transforming the plant cell with an expression cassette comprising a mutated PPO nucleic acid.

In another embodiment, the invention refers to a method of producing a transgenic plant comprising, (a) transforming a plant cell with an expression cassette comprising a mutated PPO nucleic acid, and (b) generating a plant with an increased resistance to PPO-inhibiting herbicide from the plant cell.

Consequently, mutated PPO nucleic acids of the invention are provided in expression cassettes for expression in the plant of interest. The cassette will include regulatory sequences operably linked to a mutated PPO nucleic acid sequence of the invention. The term "regulatory element" as used herein refers to a polynucleotide that is capable of regulating the transcription of an operably linked polynucleotide. It includes, but not limited to, promoters, enhancers, introns, 5' UTRs, and 3' UTRs.

By "operably linked" is intended a functional linkage between a promoter and a second sequence, wherein the promoter sequence initiates and mediates transcription of the DNA sequence corresponding to the second sequence. Generally, operably linked means that the nucleic acid sequences being linked are contiguous and, where necessary to join two protein coding regions, contiguous and in the same reading frame. The cassette may additionally contain at least one additional gene to be cotransformed into the organism. Alternatively, the additional gene(s) can be provided on multiple expression cassettes.

Such an expression cassette is provided with a plurality of restriction sites for insertion of the mutated PPO nucleic acid sequence to be under the transcriptional regulation of the regulatory regions. The expression cassette may additionally contain selectable marker genes.

The expression cassette of the present invention will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region (i.e., a promoter), a mutated PPO encoding nucleic acid sequence of the invention, and a transcriptional and translational termination region (i.e., termination region) functional in plants. The promoter may be native or analogous, or foreign or heterologous, to the plant host and/or to the mutated PPO nucleic acid sequence of the invention. Additionally, the promoter may be the natural sequence or alternatively a synthetic sequence. Where the promoter is "foreign" or "heterologous" to the plant host, it is intended that the promoter is not found in the native plant into which the promoter is introduced. Where the promoter is "foreign" or "heterologous" to the mutated PPO nucleic acid sequence of the invention, it is intended that the promoter is not the native or naturally occurring promoter for the operably linked mutated PPO nucleic acid sequence of the invention. As used herein, a chimeric gene comprises a coding sequence operably linked to a transcription initiation region that is heterologous to the coding sequence.

While it may be preferable to express the mutated PPO nucleic acids of the invention using heterologous promoters, the native promoter sequences may be used. Such constructs would change expression levels of the mutated PPO protein in the plant or plant cell. Thus, the phenotype of the plant or plant cell is altered.

The termination region may be native with the transcriptional initiation region, may be native with the operably linked mutated PPO sequence of interest, may be native with the plant host, or may be derived from another source (i.e., foreign or heterologous to the promoter, the mutated PPO nucleic acid sequence of interest, the plant host, or any combination thereof). Convenient termination regions are available from the Ti-plasmid of A. tumefaciens , such as the octopine synthase and nopaline synthase termination regions. See also Guerineau et al. (1991) Mol. Gen. Genet. 262: 141-144; Proudfoot (1991) Cell 64:671-674; Sanfacon et al. (1991) Genes Dev. 5: 141-149; Mogen et al. (1990) Plant Cell 2: 1261-1272; Munroe et al. (1990) Gene 91: 151-158; Ballas t al. (1989) Nucleic Acids Res. 17:7891-7903; and Joshi et al. (1987) Nucleic Acid Res. 15:9627-9639. Where appropriate, the gene(s) may be optimized for increased expression in the transformed plant. That is, the genes can be synthesized using plant-preferred codons for improved expression. See, for example, Campbell and Gowri (1990) Plant Physiol. 92: 1-1 1 for a discussion of host-preferred codon usage. Methods are available in the art for synthesizing plant-

preferred genes. See, for example, U.S. Patent Nos. 5,380,831 , and 5,436,391 , and Murray et al. (1989) Nucleic Acids Res. 17:477-498, herein incorporated by reference.

Additional sequence modifications are known to enhance gene expression in a cellular host. These include elimination of sequences encoding spurious polyadenylation signals, exon-intron splice site signals, transposon-like repeats, and other such well-characterized sequences that may be deleterious to gene expression. The G-C content of the sequence may be adjusted to levels average for a given cellular host, as calculated by reference to known genes expressed in the host cell. When possible, the sequence is modified to avoid predicted hairpin secondary mRNA structures. Nucleotide sequences for enhancing gene expression can also be used in the plant expression vectors. These include the introns of the maize Adhl, intronl gene (Callis et al. Genes and Development 1: 1183-1 200, 1987), and leader sequences, (W- sequence) from the Tobacco Mosaic virus (TMV), Maize Chlorotic Mottle Virus and Alfalfa Mosaic Virus (Gallie et al. Nucleic Acid Res. 15:8693-871 1, 1987 and Skuzeski et al. Plant Mol. Biol. 15:65-79, 1990). The first intron from the shrunken- 1 locus of maize, has been shown to increase expression of genes in chimeric gene constructs. U.S. Pat. Nos. 5,424,412 and 5,593,874 disclose the use of specific introns in gene expression constructs, and Gallie et al. (Plant Physiol. 106:929-939, 1994) also have shown that introns are useful for regulating gene expression on a tissue specific basis. To further enhance or to optimize mutated PPO gene expression, the plant expression vectors of the invention may also contain DNA sequences containing matrix attachment regions (MARs). Plant cells transformed with such modified expression systems, then, may exhibit overexpression or constitutive expression of a nucleotide sequence of the invention.

The expression cassettes of the present invention may additionally contain 5' leader sequences in the expression cassette construct. Such leader sequences can act to enhance translation. Translation leaders are known in the art and include: picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5' noncoding region) (Elroy-Stein et al. (1989) Proc. Natl. Acad. ScL USA 86:6126-6130); potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Gallie et al. (1995) Gene 165(2):233-238), MDMV leader (Maize Dwarf Mosaic Virus) (Virology 154:9-20), and human immunoglobulin heavy-chain binding protein (BiP) (Macejak et al. (1991) Nature 353:90-94); untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4) (Jobling et al. (1987) Nature 325:622-625); tobacco mosaic virus leader (TMV) (Gallie et al. (1989) in Molecular Biology of RNA, ed. Cech (Liss, New York), pp. 237-256); and maize chlorotic mottle virus leader (MCMV) (Lommel et al. (1991) Virology 81:382-385). See also, Della-Cioppa et al. (1987) Plant Physiol. 84:965-968. Other methods known to enhance translation can also be utilized, for example, introns, and the like.

In preparing the expression cassette, the various DNA fragments may be manipulated, so as to provide for the DNA sequences in the proper orientation and, as appropriate, in the proper reading frame. Toward this end, adapters or linkers may be employed to join the DNA fragments or other manipulations may be involved to provide for convenient restriction sites, removal of superfluous DNA, removal of restriction sites, or the like. For this purpose, in vitro mutagenesis, primer repair, restriction, annealing, resubstitutions, e.g., transitions and trans versions, may be involved.

A number of promoters can be used in the practice of the invention. The promoters can be selected based on the desired outcome. The nucleic acids can be combined with constitutive, tissue -preferred, or other promoters for expression in plants. Such constitutive promoters include, for example, the core promoter of the Rsyn7 promoter and other constitutive promoters disclosed in WO 99/43838 and U.S. Patent No. 6,072,050; the core CaMV 35S promoter (Odell et al. (1985) Nature 313:810-812); rice actin (McElroy et al. (1990) Plant Cell 2: 163-171); ubiquitin (Christensen et al. (1989) Plant Mol. Biol. 12:619-632 and Christensen et al. (1992) Plant Mol. Biol. 18:675-689); pEMU (Last et al. (1991) Theor. Appl. Genet. 81:581- 588); MAS (Velten et al. (1984) EMBO J. 3:2723-2730); ALS promoter (U.S. Patent No. 5,659,026), and the like. Other constitutive promoters include, for example, U.S. Patent Nos. 5,608,149; 5,608,144; 5,604,121 ; 5,569,597; 5,466,785; 5,399,680; 5,268,463; 5,608,142; and 6,177,61 1.

Tissue-preferred promoters can be utilized to target enhanced mutated PPO expression within a particular plant tissue. Such tissue-preferred promoters include, but are not limited to, leaf - preferred promoters, root-preferred promoters, seed- preferred promoters, and stem-preferred promoters. Tissue-preferred promoters include Yamamoto et al. (1997) Plant J. 12(2):255-265; Kawamata et al. (1997) Plant Cell Physiol. 38(7):792-803; Hansen et al. (1997) Mol. Gen Genet. 254(3):337-343; Russell et al. (1997) Transgenic Res. 6(2): 157-168; Rinehart et al. (1996) Plant Physiol. 112(3): 1331-1341 ; Van Camp et al. (1996) Plant Physiol. 112(2): 525-535; Canevascini et al. (1996) Plant Physiol. 112(2):51 3-524; Yamamoto et al. (1994) Plant Cell Physiol. 35(5):773-778; Lam (1994) Results Probl. Cell Differ. 20: 181- 196; Orozco et al. (1993) Plant Mol Biol. 23(6): 1129-1 138; Matsuoka e/ [alpha]/. (1993) Proc Natl. Acad. Sci. USA 90(20):9586-9590; and Guevara-Garcia et al. (1993) Plant J. 4(3):495-505. Such promoters can be modified, if necessary, for weak expression. In one embodiment, the nucleic acids of interest are targeted to the chloroplast for expression.

In this manner, where the nucleic acid of interest is not directly inserted into the chloroplast, the expression cassette will additionally contain a chloroplast-targeting sequence comprising a nucleotide sequence that encodes a chloroplast transit peptide to direct the gene product of interest to the chloroplasts. Such transit peptides are known in the art. With respect to chloroplast-targeting sequences, "operably linked" means that the nucleic acid sequence encoding a transit peptide (i.e., the chloroplast-targeting sequence) is linked to the mutated PPO nucleic acid of the invention such that the two sequences are contiguous and in the same reading frame. See, for example, Von Heijne et al. (1991) Plant Mol. Biol. Rep. 9: 104-126; Clark et al. (1989) J. Biol. Chem. 264:17544-17550; Della-Cioppa et al. (1987) Plant Physiol. 84:965-968; Romer et al. (1993) Biochem. Biophys. Res. Commun. 196:1414-1421; and Shah et al. (1986) Science 233:478-481 . While the mutated PPO proteins of the invention include a native chloroplast transit peptide, any chloroplast transit peptide known in the art can be fused to the amino acid sequence of a mature mutated PPO protein of the invention by operably linking a choloroplast-targeting sequence to the 5'-end of a nucleotide sequence encoding a mature mutated PPO protein of the invention. Chloroplast targeting sequences are known in the art and include the chloroplast small subunit of ribulose-l,5-bisphosphate carboxylase (Rubisco) (de Castro Silva Filho et al. (1996) Plant Mol. Biol. 30:769-780; Schnell et al. (1991) J. Biol. Chem. 266(5):3335-3342); 5 -(enolpyruvyl)shikimate-3 -phosphate synthase (EPSPS) (Archer et al. (1990) J. Bioenerg.

Biomemb. 22(6):789-810); tryptophan synthase (Zhao et al. (1995) J. Biol. Chem. 270(1 1):6081-6087); plastocyanin(Lawrence et al. (1997) J. Biol. Chem. 272(33):20357-20363); chorismate synthase (Schmidt et al. (1993) J. Biol. Chem. 268(36):27447-27457); and the light harvesting chlorophyll a/b binding protein (LHBP) (Lamppa et al. (1988) J. Biol. Chem. 263: 14996-14999). See also Von Heijne et al. (1991) Plant Mol. Biol. Rep. 9: 104- 126; Clark et al. (1989) J. Biol. Chem. 264:17544-17550; Della-Cioppa et al. (1987) Plant Physiol. 84:965-968; Romer et al. (1993) Biochem. Biophys. Res. Commun. 196: 1414-1421 ; and Shah et al. (1986) Science 233:478-481 .

In a preferred embodiment, the targeting sequence comprises a nucleotide sequence that encodes a transit peptide comprising the amino acid sequence of SEQ ID NO: 49, 50, 51, 52, or 53 (Ferredoxin transit peptide Fdxtp). Preferably, the transit peptide encoding nucleic acid is operably linked such that the transit peptide is fused to the valine at position 46 in SEQ ID NO: 2 or 4.

In another preferred embodiment, the transit peptide encoding nucleic acid is operably linked such that the transit peptide is fused to the aspartic acid at position 71 in SEQ ID NO: 48.

In a particularly preferred embodiment, the nucleic acid sequence encoding a transit peptide comprises the sequence of SEQ ID NO: 54 (for expression in corn codon-optimized nucleic acid encoding the Ferredoxin transit peptide of Silene pratensis) or SEQ ID NO: 55 (for expression in soy codon-optimized nucleic acid encoding the Ferredoxin transit peptide of Silene pratensis).

Methods for transformation of chloroplasts are known in the art. See, for example, Svab et al. (1990) Proc. Natl. Acad. ScL USA 87:8526-8530; Svab and Maliga (1993) Proc. Natl. Acad. Sci. USA 90:91 3-91 7; Svab and Maliga (1993) EMBO J. 12:601-606. The method relies on particle gun delivery of DNA containing a selectable marker and targeting of the DNA to the plastid genome through homologous recombination. Additionally, plastid transformation can be accomplished by transactivation of a silent plastid-borne transgene by tissue-preferred expression of a nuclear-encoded and plastid-directed RNA polymerase. Such a system has been reported in McBride et al. (1994) Proc. Natl. Acad. Sci. USA 91:7301-7305. The nucleic acids of interest to be targeted to the chloroplast may be optimized for expression in the chloroplast to account for differences in codon usage between the plant nucleus and this organelle. In this manner, the nucleic acids of interest may be synthesized using chloroplast-preferred codons. See, for example, U.S. Patent No. 5,380,831 , herein incorporated by reference.

In a preferred embodiment, the mutated PPO nucleic acid comprises a polynucleotide sequence selected from the group consisting of: a) a polynucleotide as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, or 47, or a variant or derivative thereof; b) a polynucleotide encoding a polypeptide as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, or 48, or a variant or derivative thereof; c) a polynucleotide comprising at least 60 consecutive nucleotides of any of a) or c); and d) a polynucleotide complementary to the polynucleotide of any of a) through c)

Preferably, the expression cassette of the present invention further comprises a transcription

initiation regulatory region and a translation initiation regulatory region that are functional in the plant.

While the polynucleotides of the invention find use as selectable marker genes for plant transformation, the expression cassettes of the invention can include another selectable marker gene for the selection of transformed cells. Selectable marker genes, including those of the present invention, are utilized for the selection of transformed cells or tissues. Marker genes include, but are not limited to, genes encoding antibiotic resistance, such as those encoding neomycin phosphotransferase II (NEO) and hygromycin phosphotransferase (HPT), as well as genes conferring resistance to herbicidal compounds, such as glufosinate ammonium, bromoxynil, imidazolinones, and 2,4-dichlorophenoxyacetate (2,4-D). See generally, Yarranton (1992) Curr. Opin. Biotech. 3 :506-51 1 ; Christophers on et al (1992) Proc. Natl. Acad. ScL USA 89:6314-6318; Yao et al. (1992) Cell 7 1:63-72; Reznikoff (1992) Mol Microbiol 6:2419-2422; Barkley et al (1980) in The Operon, pp. 177-220; Hu et al (1987) Cell 48:555-566; Brown et al (1987) Cell 49:603-612; Figge et al (1988) Cell 52:713-722; Deuschle et al (1989) Proc. Natl Acad. AcL USA 86:5400-5404; Fuerst et al (1989) Proc. Natl Acad. ScL USA 86:2549-2553; Deuschle et al (1990) Science 248:480-483; Gossen (1993) Ph.D. Thesis, University of Heidelberg; Reines et al (1993) Proc. Natl Acad. ScL USA 90: 1917-1921 ; Labow et al (1990) Mol Cell Biol 10:3343-3356; Zambretti et al (1992) Proc. Natl Acad. ScL USA 89:3952-3956; Bairn et al (1991) Proc. Natl Acad. ScL USA 88:5072-5076; Wyborski et al (1991) Nucleic Acids Res. 19:4647-4653; Hillenand-Wissman (1989) Topics Mol Struc. Biol 10: 143- 162; Degenkolb et al (1991) Antimicrob. Agents Chemother. 35: 1591-1595; Kleinschnidt et al (1988) Biochemistry 27: 1094-1 104; Bonin (1993) Ph.D. Thesis, University of Heidelberg; Gossen et al (1992) Proc. Natl Acad. ScL USA 89:5547- 5551; Oliva et al (1992) Antimicrob. Agents Chemother. 36:913-919; Hlavka et al (1985) Handbook of Experimental Pharmacology, Vol. 78 (Springer-Verlag, Berlin); Gill et al (1988) Nature 334:721-724. Such disclosures are herein incorporated by reference. The above list of selectable marker genes is not meant to be limiting. Any selectable marker gene can be used in the present invention.

The invention further provides an isolated recombinant expression vector comprising the expression cassette containing a mutated PPO nucleic acid as described above, wherein expression of the vector in a host cell results in increased tolerance to a PPO-inhibiting herbicide as compared to a wild type variety of the host cell. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid," which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors." In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However,

the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses, and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cells and those that direct expression of the nucleotide sequence only in certain host cells or under certain conditions. It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of polypeptide desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce polypeptides or peptides, including fusion polypeptides or peptides, encoded by nucleic acids as described herein (e.g., mutated PPO polypeptides, fusion polypeptides, etc.).

In a preferred embodiment of the present invention, the mutated PPO polypeptides are expressed in plants and plants cells such as unicellular plant cells (such as algae) (See Falciatore et al., 1999, Marine Biotechnology 1(3):239-251 and references therein) and plant cells from higher plants (e.g., the spermatophytes, such as crop plants). A mutated PPO polynucleotide may be "introduced" into a plant cell by any means, including transfection, transformation or transduction, electroporation, particle bombardment, agroinfection, biolistics, and the like.

Suitable methods for transforming or transfecting host cells including plant cells can be found in Sambrook et al. (Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989) and other laboratory manuals such as Methods in Molecular Biology, 1995, Vol. 44, Agrobacterium protocols, ed: Gartland and Davey, Humana Press, Totowa, New Jersey. As increased tolerance to PPO-inhibiting herbicides is a general trait wished to be inherited into a wide variety of plants like maize, wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed and canola, manihot, pepper, sunflower and tagetes, solanaceous plants like potato, tobacco, eggplant, and tomato, Vicia species, pea, alfalfa, bushy plants (coffee, cacao, tea), Salix species, trees (oil palm, coconut), perennial grasses, and forage crops, these crop plants are also preferred target plants for a genetic engineering as one further embodiment of the present invention. In a preferred embodiment, the plant is a crop plant. Forage crops include, but are not limited to, Wheatgrass, Canarygrass, Bromegrass, Wildrye Grass, Bluegrass, Orchardgrass, Alfalfa, Salfoin, Birdsfoot Trefoil, Alsike Clover, Red Clover, and Sweet Clover.

In one embodiment of the present invention, transfection of a mutated PPO polynucleotide into a plant is achieved by Agrobacterium mediated gene transfer. One transformation method known to those of skill in the art is the dipping of a flowering plant into an Agrobacteria solution, wherein the Agrobacteria contains the mutated PPO nucleic acid, followed by breeding of the transformed gametes. Agrobacterium mediated plant transformation can be performed using for example the

GV3101(pMP90) (Koncz and Schell, 1986, Mol. Gen. Genet. 204:383-396) or LBA4404 (Clontech) Agrobacterium tumefaciens strain. Transformation can be performed by standard transformation and regeneration techniques (Deblaere et al., 1994, Nucl. Acids. Res. 13:4777-4788; Gelvin, Stanton B. and Schilperoort, Robert A, Plant Molecular Biology Manual, 2nd Ed. - Dordrecht : Kluwer Academic Publ., 1995. - in Sect., Ringbuc Zentrale Signatur: BT1 1-P ISBN 0-7923-2731-4; Glick, Bernard R. and Thompson, John E., Methods in Plant Molecular Biology and Biotechnology, Boca Raton : CRC Press, 1993 360 S., ISBN 0-8493-5164-2). For example, rapeseed can be transformed via cotyledon or hypocotyl transformation (Moloney et al., 1989, Plant Cell Report 8:238-242; De Block et al., 1989, Plant Physiol. 91:694-701). Use of antibiotics for Agrobacterium and plant selection depends on the binary vector and the Agrobacterium strain used for transformation. Rapeseed selection is normally performed using kanamycin as selectable plant marker. Agrobacterium mediated gene transfer to flax can be performed using, for example, a technique described by Mlynarova et al., 1994, Plant Cell Report 13:282-285. Additionally, transformation of soybean can be performed using for example a technique described in European Patent No. 0424 047, U.S. Patent No. 5,322,783, European Patent No. 0397 687, U.S. Patent No. 5,376,543, or U.S. Patent No. 5,169,770. Transformation of maize can be achieved by particle bombardment, polyethylene glycol mediated DNA uptake, or via the silicon carbide fiber technique. (See, for example, Freeling and Walbot "The maize handbook" Springer Verlag: New York (1993) ISBN 3-540-97826-7). A specific example of maize transformation is found in U.S. Patent No. 5,990,387, and a specific example of wheat transformation can be found in PCT Application No. WO 93/07256.

According to the present invention, the introduced mutated PPO polynucleotide may be maintained in the plant cell stably if it is incorporated into a non-chromosomal autonomous replicon or integrated into the plant chromosomes. Alternatively, the introduced mutated PPO polynucleotide may be present on an extra-chromosomal non-replicating vector and be transiently expressed or transiently active. In one embodiment, a homologous recombinant microorganism can be created wherein the mutated PPO polynucleotide is integrated into a chromosome, a vector is prepared which contains at least a portion of an PPO gene into which a deletion, addition, or substitution has been introduced to thereby alter, e.g., functionally disrupt, the endogenous PPO gene and to create a mutated PPO gene. To create a point mutation via homologous recombination, DNA-RNA hybrids can be used in a technique known as chimeraplasty (Cole-Strauss et al., 1999, Nucleic Acids Research 27(5): 1323-1 330 and Kmiec, 1999, Gene therapy American Scientist 87(3):240-247). Other homologous recombination procedures in Triticum species are also well known in the art and are contemplated for use herein.

In the homologous recombination vector, the mutated PPO gene can be flanked at its 5' and 3' ends by an additional nucleic acid molecule of the PPO gene to allow for homologous recombination to occur between the exogenous mutated PPO gene carried by the vector and an endogenous PPO gene, in a microorganism or plant. The additional flanking PPO nucleic acid molecule is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several hundreds of base pairs up to kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see e.g., Thomas, K. R., and Capecchi, M. R., 1987, Cell 51:503 for a description of homologous recombination vectors or Strepp et al., 1998, PNAS,

95(8):4368-4373 for cDNA based recombination in Physcomitrella patens). However, since the mutated PPO gene normally differs from the PPO gene at very few amino acids, a flanking sequence is not always necessary. The homologous recombination vector is introduced into a microorganism or plant cell (e.g., via polyethylene glycol mediated DNA), and cells in which the introduced mutated PPO gene has homologously recombined with the endogenous PPO gene are selected using art-known techniques.

In another embodiment, recombinant microorganisms can be produced that contain selected systems that allow for regulated expression of the introduced gene. For example, inclusion of a mutated PPO gene on a vector placing it under control of the lac operon permits expression of the mutated PPO gene only in the presence of IPTG. Such regulatory systems are well known in the art.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but they also apply to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein. A host cell can be any prokaryotic or eukaryotic cell. For example, a mutated PPO polynucleotide can be expressed in bacterial cells such as C. glutamicum, insect cells, fungal cells, or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells), algae, ciliates, plant cells, fungi or other microorganisms like C. glutamicum. Other suitable host cells are known to those skilled in the art.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (i.e., express) a mutated PPO polynucleotide. Accordingly, the invention further provides methods for producing mutated PPO polypeptides using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a mutated PPO polypeptide has been introduced, or into which genome has been introduced a gene encoding a wild-type or mutated PPO polypeptide) in a suitable medium until mutated PPO polypeptide is produced. In another embodiment, the method further comprises isolating mutated PPO polypeptides from the medium or the host cell. Another aspect of the invention pertains to isolated mutated PPO polypeptides, and biologically active portions thereof. An "isolated" or "purified" polypeptide or biologically active portion thereof is free of some of the cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of mutated PPO polypeptide in which the polypeptide is separated from some of the cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of a mutated PPO polypeptide having less than about 30% (by dry weight) of non-mutated PPO material (also referred to herein as a "contaminating polypeptide"), more preferably less than about 20% of non-mutated PPO material, still more preferably less than about 10% of non-mutated PPO material, and most preferably less than about 5% non-mutated PPO

material.

When the mutated PPO polypeptide, or biologically active portion thereof, is recombinantly produced, it is also preferably substantially free of culture medium, i.e., culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the polypeptide preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of mutated PPO polypeptide in which the polypeptide is separated from chemical precursors or other chemicals that are involved in the synthesis of the polypeptide. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of a mutated PPO polypeptide having less than about 30% (by dry weight) of chemical precursors or non-mutated PPO chemicals, more preferably less than about 20% chemical precursors or non-mutated PPO chemicals, still more preferably less than about 10% chemical precursors or non-mutated PPO chemicals, and most preferably less than about 5% chemical precursors or non-mutated PPO chemicals. In preferred embodiments, isolated polypeptides, or biologically active portions thereof, lack contaminating polypeptides from the same organism from which the mutated PPO polypeptide is derived. Typically, such polypeptides are produced by recombinant expression of, for example, a mutated PPO polypeptide in plants other than, or in microorganisms such as C. glutamicum, ciliates, algae, or fungi.

In other aspects, a method for treating a plant of the present invention is provided.

In some embodiments, the method comprises contacting the plant with an agronomically acceptable composition.

In another aspect, the present invention provides a method for preparing a descendent seed. The method comprises planting a seed of or capable of producing a plant of the present invention. In one embodiment, the method further comprises growing a descendent plant from the seed; and harvesting a descendant seed from the descendent plant. In other embodiments, the method further comprises applying a PPO-inhibiting herbicides herbicidal composition to the descendent plant.

In another embodiment, the invention refers to harvestable parts of the transgenic plant according to the present invention. Preferably, the harvestable parts comprise the PPO nucleic acid or PPO protein of the present invention. The harvestable parts may be seeds, roots, leaves and/or flowers comprising the PPO nucleic acid or PPO protein or parts thereof. Preferred parts of soy plants are soy beans comprising the PPO nucleic acid or PPO protein.

In another embodiment, the invention refers to products derived from a plant according to the present invention, parts thereof or harvestable parts thereof. A preferred plant product is fodder, seed meal, oil, or seed-treatment-coated seeds. Preferably, the meal and/or oil comprises the mutated PPO nucleic acids or PPO proteins of the present invention.

In another embodiment, the invention refers to a method for the production of a product, which method comprises

a) growing the plants of the invention or obtainable by the methods of invention and
b) producing said product from or by the plants of the invention and/or parts, e.g. seeds, of these plants.

In a further embodiment the method comprises the steps

a) growing the plants of the invention,
b) removing the harvestable parts as defined above from the plants and
c) producing said product from or by the harvestable parts of the invention.

The product may be produced at the site where the plant has been grown, the plants and/or parts thereof may be removed from the site where the plants have been grown to produce the product. Typically, the plant is grown, the desired harvestable parts are removed from the plant, if feasible in repeated cycles, and the product made from the harvestable parts of the plant. The step of growing the plant may be performed only once each time the methods of the invention is performed, while allowing repeated times the steps of product production e.g. by repeated removal of harvestable parts of the plants of the invention and if necessary further processing of these parts to arrive at the product. It is also possible that the step of growing the plants of the invention is repeated and plants or harvestable parts are stored until the production of the product is then performed once for the accumulated plants or plant parts. Also, the steps of growing the plants and producing the product may be performed with an overlap in time, even simultaneously to a large extend or sequentially. Generally the plants are grown for some time before the product is produced.

In one embodiment the products produced by said methods of the invention are plant products such as, but not limited to, a foodstuff, feedstuff, a food supplement, feed supplement, fiber, cosmetic and/or pharmaceutical. Foodstuffs are regarded as compositions used for nutrition and/or for supplementing nutrition. Animal feedstuffs and animal feed supplements, in particular, are regarded as foodstuffs.

In another embodiment the inventive methods for the production are used to make agricultural products such as, but not limited to, plant extracts, proteins, amino acids, carbohydrates, fats, oils, polymers, vitamins, and the like.

It is possible that a plant product consists of one or more agricultural products to a large extent.

As described above, the present invention teaches compositions and methods for increasing the PPO-inhibiting tolerance of a crop plant or seed as compared to a wild-type variety of the plant or seed. In a preferred embodiment, the PPO-inhibiting tolerance of a crop plant or seed is increased such that the plant or seed can withstand a PPO-inhibiting herbicide application of preferably approximately 1-1000 g ai ha^{-1}, more preferably 1-200 g ai ha^{-1}, even more preferably 5-150 g ai

ha^{-1}, and most preferably 10-100 g ai ha^{-1}. As used herein, to "withstand" a PPO-inhibiting herbicide application means that the plant is either not killed or only moderately injured by such application. It will be understood by the person skilled in the art that the application rates may vary, depending on the environmental conditions such as temperature or humidity, and depending on the chosen kind of herbicide (active ingredient ai).

Furthermore, the present invention provides methods that involve the use of at least one PPO-inhibiting herbicide, optionally in combination with one or more herbicidal compounds B, and, optionally, a safener C, as described in detail supra.

In these methods, the PPO-inhibiting herbicide can be applied by any method known in the art including, but not limited to, seed treatment, soil treatment, and foliar treatment. Prior to application, the PPO-inhibiting herbicide can be converted into the customary formulations, for example solutions, emulsions, suspensions, dusts, powders, pastes and granules. The use form depends on the particular intended purpose; in each case, it should ensure a fine and even distribution of the compound according to the invention.

By providing plants having increased tolerance to PPO-inhibiting herbicide, a wide variety of formulations can be employed for protecting plants from weeds, so as to enhance plant growth and reduce competition for nutrients. A PPO-inhibiting herbicide can be used by itself for pre-emergence, post-emergence, pre-planting, and at-planting control of weeds in areas surrounding the crop plants described herein, or a PPO-inhibiting herbicide formulation can be used that contains other additives. The PPO-inhibiting herbicide can also be used as a seed treatment. Additives found in a PPO-inhibiting herbicide formulation include other herbicides, detergents, adjuvants, spreading agents, sticking agents, stabilizing agents, or the like. The PPO-inhibiting herbicide formulation can be a wet or dry preparation and can include, but is not limited to, flowable powders, emulsifiable concentrates, and liquid concentrates. The PPO-inhibiting herbicide and herbicide formulations can be applied in accordance with conventional methods, for example, by spraying, irrigation, dusting, or the like.

Suitable formulations are described in detail in PCT/EP2009/063387 and PCT/EP2009/063386, which are incorporated herein by reference.

It should also be understood that the foregoing relates to preferred embodiments of the present invention and that numerous changes may be made therein without departing from the scope of the invention. The invention is further illustrated by the following examples, which are not to be construed in any way as imposing limitations upon the scope thereof. On the contrary, it is to be clearly understood that resort may be had to various other embodiments, modifications, and equivalents thereof, which, after reading the description herein, may suggest themselves to those skilled in the art without departing from the spirit of the present invention and/or the scope of the appended claims.

EXAMPLES

EXAMPLE 1: Site-directed mutagenesis of Amaranthus PPO

All nucleic acid coding sequence and all single and double mutants based on SEQ ID NO: 1, 3, 5, 7, 9, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, were synthesized and cloned by Geneart (Geneart AG, Regensburg, Germany). Rational design mutants were synthesized by Geneart. Random PPO gene libraries were synthesized by Geneart. Plasmids were isolated from *E. coli* TOP10 by performing a plasmid minpreparation and confirmed by DNA sequencing.

EXAMPLE 2: Expression and purification of recombinant wildtype and mutant PPO

(Taken from: Franck E. Dayan, Pankaj R. Daga, Stephen O. Duke, Ryan M. Lee, Patrick J. Tranel, Robert J. Doerksen. Biochemical and structural consequences of a glycine deletion in the a-8 helix of protoporphyrinogen oxidase. Biochimica et Biophysica Acta 1804 (2010), 1548-56) Clones in pRSET vector were transformed into BL21 (DE3)-pLysS strain of *E. coli.* Cells were grown in 250 mL of LB with 100 µgmL-1 of carbenicillin, shaking overnight at 37 °C. Cultures were diluted in 1 L of LB with antibiotic and grown at 37 °C shaking for 2 h, induced with 1 imM IPTG and grown at 25 °C shaking for 5 more hours. The cells were harvested by centrifugation at 1600xg, washed with 0.09% NaCI, and stored at -80 °C. Cells were lysed using a French press at 140 MPa in 50 mM sodium phosphate pH 7.5, 1 M NaCI, 5 mM imidazole, 5% glycerol, and 1 µg mL- 1 leupeptin. Following lysis, 0.5 U of benzonase (Novagen, EMD Chemicals, Inc., Gibbstown, NJ) and PMSF (final concentration of 1 mM) were added. Cell debris was removed by centrifugation at 3000xg. His-tagged PPO proteins were purified on a nickel activated Hitrap Chelating HP column (GE Healthcare Bio-Sciences Corp., Piscataway, NJ) equilibrated with 20 mM sodium phosphate pH 8.0, 50 mM NaCI, 5 mM imidazole, 5 mM MgCI2, 0.1mM EDTA, and 17% glycerol. PPO is eluted with 250 mM imidazole. The active protein was desalted on a PD-10 column (GE Healthcare Bio-Sciences Corp., Piscataway, NJ) equilibrated with a 20 mM sodium phosphate buffer, pH 7.5, 5 mM MgCI2, 1 mM EDTA and 17% glycerol. Each litre of culture provided approximately 10 mg of pure PPO, which was stored at -20 °C until being used in assays.

EXAMPLE 3: PPO Enzyme Assay (non-recombinant)

PPO protein (EC 1.3.3.4) was extracted from coleoptiles or shoots (150 g fresh weight) of dark-grown corn, black nightshade, morning glory, and velvetleaf seedlings as described previously (Grossmann et al. 2010). Before harvesting, the seedlings were allowed to green for 2 hours in the light in order to achieve the highest specific enzyme activities in the thylakoid fractions at low chlorophyll concentrations. At high chlorophyll concentrations significant quenching of fluorescence occurs, which limits the amount of green thylakoids that can be used in the test. Plant materials were homogenized in the cold with a Braun blender using a fresh-weight-to-volume ratio of 1:4. Homogenization buffer consisted of tris(hydroxymethyl)aminomethane (Tris)-HCI (50 mM; pH 7.3), sucrose (0.5 M), magnesium chloride (1 mM), ethylenediaminetetraacetic acid (EDTA) (1 mM) and bovine serum albumin (2 g L^{-1}). After filtration through four layers of Miracloth, crude plastid preparations were obtained after centrifugation at 10 000 x g for 5 min and resuspension in homogenization buffer before centrifugation at 150 x g for 2 min to remove crude cell debris. The supernatant was centrifuged at 4000 x g for 15 min and the pellet fraction was resuspended in 1 ml of a buffer containing Tris-HCI (50 mM; pH 7.3), EDTA (2 mM), leupeptin (2 µM), pepstatin (2 µM) and glycerol (200 ml L^{-1}) and stored at -80°C until use. Protein was determined in the enzyme extract with bovine serum albumin as a standard. PPO activity was assayed fluorometrically by

monitoring the rate of Proto formation from chemically reduced protoporphyrinogen IX under initial velocity conditions. The assay mixture consisted of Tris-HCl (100 mM; pH 7.3), EDTA (1 mM), dithiothreitol (5 mM), Tween 80 (0.085%), protoporphyrinogen IX (2 μM), and 40 μg extracted protein in a total volume of 200 μl. The reaction was initiated by addition of substrate protoporphyrinogen IX at 22°C. saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione (CAS 1258836-72-4), flumioxazin, butafenacil, acifluorfen, lactofen, bifenox, sulfentrazone, and photosynthesis inhibitor diuron as negative control were prepared in dimethyl sulfoxide (DMSO) solution (0.1 mM concentration of DMSO in the assay) and added to the assay mixture in concentrations of 0.005 pM to 5 μM before incubation. Fluorescence was monitored directly from the assay mixture using a POLARstar Optima / Galaxy (BMG) with excitation at 405 nm and emission monitored at 630 nm. Non-enzymatic activity in the presence of heat-inactivated extract was negligible. Inhibition of enzyme activity induced by the herbicide was expressed as percentage inhibition relative to untreated controls. Molar concentrations of compound required for 50% enzyme inhibition (IC_{50} values) were calculated by fitting the values to the dose-response equation using non-linear regression analysis.

EXAMPLE 4: PPO Enzyme Assay (recombinant)

Proto was purchased from Sigma-Aldrich (Milwaukee, WI). Protogen was prepared according to Jacobs and Jacobs (N.J. Jacobs, J.M. Jacobs, Assay for enzymatic protoporphyrinogen oxidation, a late step in heme synthesis, Enzyme 28 (1982) 206-219). Assays were conducted in 100 mM sodium phosphate pH 7.4 with 0.1 mM EDTA, 0.1% Tween 20, 5 μM FAD, and 500mM imidazole. Dose-response curves with the PPO inhibitors saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione (CAS 1258836-72-4), flumioxazin, butafenacil, acifluorfen, lactofen, bifenox, sulfentrazone, and photosynthesis inhibitor diuron as negative control, and MC-15608 were obtained in the presence of 150 μM Protogen. Dose response was measured between the inhibitor concentration range of 1,00E-05 M to 1,00E-12 M. The excitation and emission bandwidths were set at 1.5 and 30 nm, respectively. All assays were made in duplicates or triplicates and measured using a POLARstar Optima / Galaxy (BMG) with excitation at 405 nm and emission monitored at 630 nm. Molar concentrations of compound required for 50% enzyme inhibition (IC50 values) were calculated by fitting the values to the dose-response equation using non-linear regression analysis. The results are shown in Table 4.

Table 4a: IC50 values for various mutated PPO (mutated PPO)

Amino Acid Substitution	**SEQ. ID NO.**	**Relative Ezyme Activity (FU/min)**	**Saflufenacil**	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione
			IC50 **(M)**	
PPO herbicide sensitive PP02 WC	2	1000	1,86E-09	5.17E-10
PPO herbicide sensitive PP02 AC	4	800	1.78E-10	5.96E-11

dG210	6 & 8	80	1,60E-06	2,12E-09
R128L	2	700	2,22E-07	7J3E-10
R128L	2	700	2,22E-07	7,73E-10
R128A	2	730	1,29E-07	1,40E-10
R128C	4	515	5,57E-07	1,16E-10
R128D	4	ND	ND	ND
R128E	4	ND	ND	ND
R128F	4	280	5,25E-07	2,21 E-10
R128G	4	440	9,91 E-07	4,71 E-1 1
R128H	4	640	1,02E-08	6,15E-1 1
R128I	4	250	3,65E-07	9,80E-1 1
R128K	4	180	9,65E-1 1	ND
R128L	4	280	3,88E-07	1,01 E-10
R128M	4	200	6,97E-07	3,56E-1 1
R128N	4	420	5,79E-07	4,33E-1 1
R128P	4	ND	ND	ND
R128Q	4	480	1,94E-07	1,09E-1 1
R128S	4	490	2,46E-07	1.12E-1 1
R128T	4	510	2,1 1E-07	3.79E-1 1
R128V	4	600	2,49E-07	6.70E-1 1
R128W	4	ND	ND	ND
R128Y	4	230	2,19E-06	5.77E-1 1
F420A	4	ND	ND	ND
F420V	2	200	1,59E-06	1,61 E-09
F420V	2	330		1,61 E-09
F420M	2	350	6,77E-07	2,75E-10
F420M	2	700		2.18E-10
F420L	2	200	7,20E-06	9,93E-10
F420I	2	200	9,19E-07	4,95E-10
R128A, F420V	2	510	>0,00001	2,50E-08
R128A+F420M	2	400	>0,00001	6,24 E-09
R128A+F420L	2	300	>0,00001	1,62E-08
R128A+F420I	2	330	>0,00001	2,46E-08
R128A_F420A	4	ND	ND	ND
R128L_F420A	4	ND	ND	ND
R128L_F420L	4	300	>0,00001	1,71 E-06
R128L_F420I	4	450	>0,00001	1,23E-06
R128L_F420V	4	300	>0,00001	1,51 E-06
R128L_F420M	4	400	>0,00001	2,46E-07
R128LF420A	4	ND	ND	ND
R128LF420L	4	200	>0,00001	4,66E-07
R128LF420I	4	100	>0,00001	4,33E-07
R128LF420V	4	470	>0,00001	4,24 E-07

R128LF420M	4	500	>0,00001	5,82E-08
R128V_F420A	4	ND	ND	ND
R128V_F420L	4	370	>0,00001	4,41 E-07
R128V_F420I	4	300	>0,00001	2,23E-07
R128V_F420V	4	300	>0,00001	4,46E-07
R128V_F420M	4	460	>0,00001	4,27E-08
R128M_F420A	4	ND	ND	ND
R128M_F420L	4	300	>0,00001	6,95E-07
R128M_F420I	4	350	>0,00001	4,45E-07
R128M_F420V	4	270	>0,00001	7,04E-07
R128M_F420M	4	480	>0,00001	7,05E-08

Table 4b: IC50 values for various mutated PPO (mutated PPO)

Construct	SEQ. ID NO.	rate (FU/min)	Saflufenacil	1,5-dimethyl-6-thioxo-3-(2,2J-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione
			IC50 (M)	
PPO herbicide sensitive PP02 WC	2	1000	1,86E-09	5.17E-10
PPO herbicide sensitive PP02 AC	4	800	1.78E-10	5.96E-11
dG210	6 & 8	80	1,60E-06	2,12E-09
R128L	2	700	2,22E-07	7,73E-10
R128K	4	180	9.65E-11	not determined
R128Q	4	481	1,94E-07	1.09E-11
R128S	4	491	2,46E-07	1.13E-11
R128M	4	200	6,97E-07	3.56E-11
R128T	4	721	2,11E-07	3.79E-11
R128N	4	421	5.79E-07	4.33E-11
R128G	4	436	9,91 E-07	4,71 E-11
R128Y	4	230	2.19E-06	5.77E-11
R128H	4	636	1,02E-08	6.15E-11
R128V	4	923	2,49E-07	7.00E-11
R128I	4	250	3.65E-07	9.80E-11
R128C	4	933	5,57E-07	1.16E-10
R128A	4	731	1,29E-07	1.40E-10
R128F	4	278	5,25E-07	2,21 E-10
R128L	4	700	2,22E-07	7,73E-10
R128A, L397D	2	98	≥1,00E-5	5,90E-09
R128A, F420M	2	378	≥1,00E-5	6,24E-09
R128Q, F420M	4	473	≥1,00E-5	1.54E-08

R128A, F420L	2	281	≥1,00E-5	1,62E-08
R128S, F420M	4	310	≥1,00E-5	1,77E-08
R128C, F420M	4	329	≥1,00E-5	2,30E-08
R128A, F420I	2	330	≥1,00E-5	2,46E-08
R128A, F420V	2	512	≥1,00E-5	2,50E-08
R128H, F420M	4	252	≥1,00E-5	2,92E-08
R128G, F420M	4	100	≥1,00E-5	3,02E-08
R128V, F420M	4	666	≥1,00E-5	4,27E-08
R128S, F420I	4	150	≥1,00E-5	4,64E-08
R128Q, F420I	4	202	≥1,00E-5	5,43E-08
R128T, F420M	4	303	≥1,00E-5	5,54E-08
R128I, F420M	4	497	≥1,00E-5	5,82E-08
R128S, F420L	4	110	≥1,00E-5	6,24E-08
R128Q, F420L	4	150	≥1,00E-5	6,90E-08
R128M, F420M	4	479	≥1,00E-5	7,05E-08
R128F, F420M	4	120	≥1,00E-5	7,84E-08
R128M, F420M	4	306	≥1,00E-5	8,26E-08
R128N, F420M	4	208	≥1,00E-5	1,01 E-07
R128C, F420I	4	204	≥1,00E-5	1,20E-07
R128M, F420I	4	250	≥1,00E-5	1,44 E-07
R128H, F420I	4	195	≥1,00E-5	1,47E-07
R128T, F420V	4	120	≥1,00E-5	1,50 E-07
R128Y, F420M	4	200	≥1,00E-5	1,61 E-07
R128H, F420L	4	185	≥1,00E-5	1,69 E-07
R128N, F420I	4	100	≥1,00E-5	1,75 E-07
R128H, F420V	4	74	≥1,00E-5	1,82 E-07
R128C, F420L	4	217	≥1,00E-5	1,89 E-07
R128Q, F420V	4	113	≥1,00E-5	2,02 E-07
R128N, F420L	4	100	≥1,00E-5	2,10E-07
R128C, F420V	4	223	≥1,00E-5	2,16E-07
R128V, F420I	4	300	≥1,00E-5	2,23E-07
R128T, F420I	4	238	≥1,00E-5	2,29E-07
R128L, F420M	4	518	≥1,00E-5	2,46E-07
R128M, F420L	4	211	≥1,00E-5	2,49E-07
R128T, F420L	4	157	≥1,00E-5	3,97 E-07
R128M, F420V	4	127	≥1,00E-5	4,00 E-07
R128I, F420V	4	464	≥1,00E-5	4,24 E-07
R128I, F420I	4	128	≥1,00E-5	4,33 E-07
R128V, F420L	4	365	≥1,00E-5	4,41 E-07
R128M, F420I	4	343	≥1,00E-5	4,45E-07
R128V, F420V	4	300	≥1,00E-5	4,47E-07
R128I, F420L	4	281	≥1,00E-5	4,66 E-07
R128Y, F420I	4	90	≥1,00E-5	6,1 1E-07
R128A, AG210	4	170	≥1,00E-5	6,57 E-07
R128M, F420L	4	300	≥1,00E-5	6,95 E-07
R128M, F420V	4	261	≥1,00E-5	7,04 E-07

R128F, F420L	4	101	≥1,00E-5	8,68E-07
R128L, F420I	4	453	≥1,00E-5	1,23E-06
R128L, F420V	4	289	≥1,00E-5	1,51 E-06
R128L, F420L	4	300	≥1,00E-5	1,71 E-06
R128D	4	Low or no enzyme activity measured		
R128E	4	Low or no enzyme activity measured		
R128P	4	Low or no enzyme activity measured		
R128W	4	Low or no enzyme activity measured		
R128A, F420A	2	Low or no enzyme activity measured		
R128L, F420A	4	Low or no enzyme activity measured		
R128I, F420A	4	Low or no enzyme activity measured		
R128V, F420A	4	Low or no enzyme activity measured		
R128M, F420A	4	Low or no enzyme activity measured		
R128M, F420A	4	Low or no enzyme activity measured		
R128N, F420A	4	Low or no enzyme activity		

		measured		
R128Y, F420A	4	Low or no enzyme activity measured		
R128Y, F420L	4	Low or no enzyme activity measured		
R128Y, F420V	4	Low or no enzyme activity measured		
R128G, F420A	4	Low or no enzyme activity measured		
R128G, F420L	4	Low or no enzyme activity measured		
R128G, F420I	4	Low or no enzyme activity measured		
R128G, F420V	4	Low or no enzyme activity measured		
R128H, F420A	4	Low or no enzyme activity measured		
R128N, F420V	4	Low or no enzyme activity measured		
R128C, F420A	4	Low or no enzyme activity measured		
R128F, F420A	4	Low or no enzyme activity measured		
R128F, F420I	4	Low or no enzyme		

		activity measured		
R128F, F420V	4	Low or no enzyme activity measured		
R128S, F420A	4	Low or no enzyme activity measured		
R128S, F420V	4	Low or no enzyme activity measured		
R128T, F420A	4	Low or no enzyme activity measured		
R128Q, F420A	4	Low or no enzyme activity measured		

IC50 (M): Concentration of inhibitor required for 50% inhibition of enzyme activity; ≥1,00E-5: indicates a very high IC50 over the measurement bounderies, which reflects very high in vitro tolerance.

Table 4c

Common Name	IUPAC Name	SEQ ID	Mutation	rate (FU/min)	IC50 (M)	inhibition (%) at 1x10-5 M
FOMESAFEN		2 or 4	WT	650	1,32E-09	
FOMESAFEN		4	R128A, F420M	362	6,60E-06	
FOMESAFEN		4	R128A, F420L	316	9,91E-06	
FOMESAFEN		4	R128A, F420V	478	1,61E-06	
FOMESAFEN		4	R128I, F420L	202	≥ 1,00E-05	38
FOMESAFEN		4	R128I, F420V	292	2,79E-06	
FOMESAFEN		4	R128V, F420M	413	≥ 1,00E-05	47
FOMESAFEN		4	R128M, F420M	289	≥ 1,00E-05	48
FOMESAFEN		4	R128Y, F420I	99	2,15E-05	
FOMESAFEN		4	R128Y, F420M	174	≥ 1,00E-05	28
FOMESAFEN		4	R128N, F420M	153	1,07E-05	
FOMESAFEN		4	R128C, F420L	192	≥ 1,00E-05	42
FOMESAFEN		4	R128C, F420V	160	2,36E-06	
FOMESAFEN		4	R128C, F420M	277	1,10E-05	
FOMESAFEN		4	R128H, F420M	184	2,91E-06	
LACTOFEN	(2-ethoxy-1-methyl-2-oxo-ethyl) 5-[2-chloro-4-(trifluoromethyl)phenoxy]-2-nitro-benzoate	2 or 4	WT	650	2,93E-10	

LACTOFEN	(2-ethoxy-1-methyl-2-oxo-ethyl) 5-[2-chloro-4-(trifluoromethyl)phenoxy]-2-nitro-benzoate	4	R128A, F420M	362	4,57E-08	
LACTOFEN	(2-ethoxy-1-methyl-2-oxo-ethyl) 5-[2-chloro-4-(trifluoromethyl)phenoxy]-2-nitro-benzoate	4	R128A, F420L	316	6,88E-08	
LACTOFEN	(2-ethoxy-1-methyl-2-oxo-ethyl) 5-[2-chloro-4-(trifluoromethyl)phenoxy]-2-nitro-benzoate	4	R128A, F420V	478	8,45E-09	
LACTOFEN	(2-ethoxy-1-methyl-2-oxo-ethyl) 5-[2-chloro-4-(trifluoromethyl)phenoxy]-2-nitro-benzoate	4	R128I, F420L	202	1,30E-07	
LACTOFEN	(2-ethoxy-1-methyl-2-oxo-ethyl) 5-[2-chloro-4-(trifluoromethyl)phenoxy]-2-nitro-benzoate	4	R128I, F420V	292	1,40E-08	
LACTOFEN	(2-ethoxy-1-methyl-2-oxo-ethyl) 5-[2-chloro-4-(trifluoromethyl)phenoxy]-2-nitro-benzoate	4	R128V, F420M	413	9,41E-08	
LACTOFEN	(2-ethoxy-1-methyl-2-oxo-ethyl) 5-[2-chloro-4-(trifluoromethyl)phenoxy]-2-nitro-benzoate	4	R128M, F420M	289	1,31E-07	
LACTOFEN	(2-ethoxy-1-methyl-2-oxo-ethyl) 5-[2-chloro-4-(trifluoromethyl)phenoxy]-2-nitro-benzoate	4	R128Y, F420I	99	4,80E-08	

LACTOFEN	(2-ethoxy-1-methyl-2-oxo-ethyl) 5-[2-chloro-4-(trifluoromethyl)phenoxy]-2-nitro-benzoate	4	R128Y, F420M	174	1,43E-07	
LACTOFEN	(2-ethoxy-1-methyl-2-oxo-ethyl) 5-[2-chloro-4-(trifluoromethyl)phenoxy]-2-nitro-benzoate	4	R128N, F420M	153	1,67E-07	
LACTOFEN	(2-ethoxy-1-methyl-2-oxo-ethyl) 5-[2-chloro-4-(trifluoromethyl)phenoxy]-2-nitro-benzoate	4	R128C, F420L	192	1,42E-07	
LACTOFEN	(2-ethoxy-1-methyl-2-oxo-ethyl) 5-[2-chloro-4-(trifluoromethyl)phenoxy]-2-nitro-benzoate	4	R128C, F420V	160	1,50E-08	
LACTOFEN	(2-ethoxy-1-methyl-2-oxo-ethyl) 5-[2-chloro-4-(trifluoromethyl)phenoxy]-2-nitro-benzoate	4	R128C, F420M	277	6,39E-08	
LACTOFEN	(2-ethoxy-1-methyl-2-oxo-ethyl) 5-[2-chloro-4-(trifluoromethyl)phenoxy]-2-nitro-benzoate	4	R128H, F420M	184	6,13E-08	
BUTAFENACIL		2 or 4	WT	650	1,38E-10	
BUTAFENACIL		4	R128A, F420M	362	1,40E-08	
BUTAFENACIL		4	R128A, F420L	316	9,17E-08	
BUTAFENACIL		4	R128A, F420V	478	2,51E-08	
BUTAFENACIL		4	R128I, F420L	202	8,02E-08	
BUTAFENACIL		4	R128I, F420V	292	2,56E-08	

BUTAFENACIL		4	R128V, F420M	413	1,05E-08	
BUTAFENACIL		4	R128M, F420M	289	4,38E-08	
BUTAFENACIL		4	R128Y, F420I	99	5,47E-08	
BUTAFENACIL		4	R128Y, F420M	174	5,04E-08	
BUTAFENACIL		4	R128N, F420M	153	2,84E-08	
BUTAFENACIL		4	R128C, F420L	192	1,10E-07	
BUTAFENACIL		4	R128C, F420V	160	6,69E-08	
BUTAFENACIL		4	R128C, F420M	277	2,31E-08	
BUTAFENACIL		4	R128H, F420M	184	1,28E-08	
CARFENTRAZONE-ETHYL		2 or 4	WT	650	1,03E-09	
CARFENTRAZONE-ETHYL		4	R128A, F420M	362	6,72E-08	
CARFENTRAZONE-ETHYL		4	R128A, F420L	316	4,29E-07	
CARFENTRAZONE-ETHYL		4	R128A, F420V	478	7,97E-07	
CARFENTRAZONE-ETHYL		4	R128I, F420L	202	1,61E-07	
CARFENTRAZONE-ETHYL		4	R128I, F420V	292	2,07E-07	
CARFENTRAZONE-ETHYL		4	R128V, F420M	413	2,29E-08	
CARFENTRAZONE-ETHYL		4	R128M, F420M	289	7,86E-08	

CARFENTRAZONE-ETHYL		4	R128Y, F420I	99	2,82E-07	
CARFENTRAZONE-ETHYL		4	R128Y, F420M	174	8,52E-08	
CARFENTRAZONE-ETHYL		4	R128N, F420M	153	1,88E-07	
CARFENTRAZONE-ETHYL		4	R128C, F420L	192	3,08E-07	
CARFENTRAZONE-ETHYL		4	R128C, F420V	160	3,96E-07	
CARFENTRAZONE-ETHYL		4	R128C, F420M	277	2,99E-08	
CARFENTRAZONE-ETHYL		4	R128H, F420M	184	1,21E-07	
ACIFLUORFEN	5-(2-CHLORO-4-TRIFLUOROMETHYL-PHENOXY)-2-NITRO-BENZOIC ACID	2 or 4	WT	650	3,36E-08	
ACIFLUORFEN	5-(2-CHLORO-4-TRIFLUOROMETHYL-PHENOXY)-2-NITRO-BENZOIC ACID	4	R128A, F420M	362	≥ 1,00E-05	27
ACIFLUORFEN	5-(2-CHLORO-4-TRIFLUOROMETHYL-PHENOXY)-2-NITRO-BENZOIC ACID	4	R128A, F420L	316	≥ 1,00E-05	20
ACIFLUORFEN	5-(2-CHLORO-4-TRIFLUOROMETHYL-PHENOXY)-2-NITRO-BENZOIC ACID	4	R128A, F420V	478	6,67E-06	
ACIFLUORFEN	5-(2-CHLORO-4-TRIFLUOROMETHYL-PHENOXY)-2-NITRO-BENZOIC ACID	4	R128I, F420L	202	≥ 1,00E-05	16
ACIFLUORFEN	5-(2-CHLORO-4-TRIFLUOROMETHYL-PHENOXY)-2-NITRO-BENZOIC ACID	4	R128I, F420V	292	1,21E-05	

ACIFLUORFEN	5-(2-CHLORO-4-TRIFLUOROMETHYL-PHENOXY)-2-NITRO-BENZOIC ACID	4	R128V, F420M	413	≥ 1,00E-05	17
ACIFLUORFEN	5-(2-CHLORO-4-TRIFLUOROMETHYL-PHENOXY)-2-NITRO-BENZOIC ACID	4	R128M, F420M	289	≥ 1,00E-05	21
ACIFLUORFEN	5-(2-CHLORO-4-TRIFLUOROMETHYL-PHENOXY)-2-NITRO-BENZOIC ACID	4	R128Y, F420I	99	≥ 1,00E-05	21
ACIFLUORFEN	5-(2-CHLORO-4-TRIFLUOROMETHYL-PHENOXY)-2-NITRO-BENZOIC ACID	4	R128Y, F420M	174	≥ 1,00E-05	15
ACIFLUORFEN	5-(2-CHLORO-4-TRIFLUOROMETHYL-PHENOXY)-2-NITRO-BENZOIC ACID	4	R128N, F420M	153	≥ 1,00E-05	39
ACIFLUORFEN	5-(2-CHLORO-4-TRIFLUOROMETHYL-PHENOXY)-2-NITRO-BENZOIC ACID	4	R128C, F420L	192	≥ 1,00E-05	17
ACIFLUORFEN	5-(2-CHLORO-4-TRIFLUOROMETHYL-PHENOXY)-2-NITRO-BENZOIC ACID	4	R128C, F420V	160	6,72E-06	
ACIFLUORFEN	5-(2-CHLORO-4-TRIFLUOROMETHYL-PHENOXY)-2-NITRO-BENZOIC ACID	4	R128C, F420M	277	≥ 1,00E-05	33
ACIFLUORFEN	5-(2-CHLORO-4-TRIFLUOROMETHYL-PHENOXY)-2-NITRO-BENZOIC ACID	4	R128H, F420M	184	≥ 1,00E-05	48
FLUMIOXAZIN	2-(7-fluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	2 or 4	WT	650	9,58E-11	
FLUMIOXAZIN	2-(7-fluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128A, F420M	362	8,43E-06	

FLUMIOXAZIN	2-(7-fluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128A, F420L	316	≥ 1,00E-05	-8
FLUMIOXAZIN	2-(7-fluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128A, F420V	478	6,34E-06	
FLUMIOXAZIN	2-(7-fluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128I, F420L	202	≥ 1,00E-05	9
FLUMIOXAZIN	2-(7-fluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128I, F420V	292	≥ 1,00E-05	41
FLUMIOXAZIN	2-(7-fluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128V, F420M	413	≥ 1,00E-05	34
FLUMIOXAZIN	2-(7-fluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128M, F420M	289	≥ 1,00E-05	21
FLUMIOXAZIN	2-(7-fluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128Y, F420I	99	≥ 1,00E-05	19
FLUMIOXAZIN	2-(7-fluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128Y, F420M	174	≥ 1,00E-05	-2

FLUMIOXAZIN	2-(7-fluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128N, F420M	153	6,15E-06	
FLUMIOXAZIN	2-(7-fluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128C, F420L	192	≥ 1,00E-05	-11
FLUMIOXAZIN	2-(7-fluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128C, F420V	160	7,28E-06	
FLUMIOXAZIN	2-(7-fluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128C, F420M	277	≥ 1,00E-05	48
FLUMIOXAZIN	2-(7-fluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128H, F420M	184	≥ 1,00E-05	30
CINIDON-ETHYL	ethyl (Z)-2-chloro-3-[2-chloro-5-(1,3-dioxo-4,5,6,7-tetrahydroisoindol-2-yl)phenyl]prop-2-enoate	2 or 4	WT	650	6,69E-10	
CINIDON-ETHYL	ethyl (Z)-2-chloro-3-[2-chloro-5-(1,3-dioxo-4,5,6,7-tetrahydroisoindol-2-yl)phenyl]prop-2-enoate	4	R128A, F420M	362	1,60E-06	
CINIDON-ETHYL	ethyl (Z)-2-chloro-3-[2-chloro-5-(1,3-dioxo-4,5,6,7-tetrahydroisoindol-2-yl)phenyl]prop-2-enoate	4	R128A, F420L	316	≥ 1,00E-05	48

CINIDON-ETHYL	ethyl (Z)-2-chloro-3-[2-chloro-5-(1,3-dioxo-4,5,6,7-tetrahydroisoindol-2-yl)phenyl]prop-2-enoate	4	R128A, F420V	478	5,43E-06	
CINIDON-ETHYL	ethyl (Z)-2-chloro-3-[2-chloro-5-(1,3-dioxo-4,5,6,7-tetrahydroisoindol-2-yl)phenyl]prop-2-enoate	4	R128I, F420L	202	9,51E-06	
CINIDON-ETHYL	ethyl (Z)-2-chloro-3-[2-chloro-5-(1,3-dioxo-4,5,6,7-tetrahydroisoindol-2-yl)phenyl]prop-2-enoate	4	R128I, F420V	292	4,72E-06	
CINIDON-ETHYL	ethyl (Z)-2-chloro-3-[2-chloro-5-(1,3-dioxo-4,5,6,7-tetrahydroisoindol-2-yl)phenyl]prop-2-enoate	4	R128V, F420M	413	1,78E-06	
CINIDON-ETHYL	ethyl (Z)-2-chloro-3-[2-chloro-5-(1,3-dioxo-4,5,6,7-tetrahydroisoindol-2-yl)phenyl]prop-2-enoate	4	R128M, F420M	289	3,84E-06	
CINIDON-ETHYL	ethyl (Z)-2-chloro-3-[2-chloro-5-(1,3-dioxo-4,5,6,7-tetrahydroisoindol-2-yl)phenyl]prop-2-enoate	4	R128Y, F420I	99	≥ 1,00E-05	38
CINIDON-ETHYL	ethyl (Z)-2-chloro-3-[2-chloro-5-(1,3-dioxo-4,5,6,7-tetrahydroisoindol-2-yl)phenyl]prop-2-enoate	4	R128Y, F420M	174	1,08E-05	
CINIDON-ETHYL	ethyl (Z)-2-chloro-3-[2-chloro-5-(1,3-dioxo-4,5,6,7-tetrahydroisoindol-2-yl)phenyl]prop-2-enoate	4	R128N, F420M	153	≥ 1,00E-05	48

CINIDON-ETHYL	ethyl (Z)-2-chloro-3-[2-chloro-5-(1,3-dioxo-4,5,6,7-tetrahydroisoindol-2-yl)phenyl]prop-2-enoate	4	R128C, F420L	192	≥ 1,00E-05	42
CINIDON-ETHYL	ethyl (Z)-2-chloro-3-[2-chloro-5-(1,3-dioxo-4,5,6,7-tetrahydroisoindol-2-yl)phenyl]prop-2-enoate	4	R128C, F420V	160	9,43E-06	
CINIDON-ETHYL	ethyl (Z)-2-chloro-3-[2-chloro-5-(1,3-dioxo-4,5,6,7-tetrahydroisoindol-2-yl)phenyl]prop-2-enoate	4	R128C, F420M	277	2,45E-06	
CINIDON-ETHYL	ethyl (Z)-2-chloro-3-[2-chloro-5-(1,3-dioxo-4,5,6,7-tetrahydroisoindol-2-yl)phenyl]prop-2-enoate	4	R128H, F420M	184	≥ 1,00E-05	41
OXIFLUORFEN	2-CHLORO-1-(3-ETHOXY-4-NITROPHENOXY)-4-(TRIFLUOROMETHYL)BENZENE	2 or 4	WT	650	1,04E-09	
OXIFLUORFEN	2-CHLORO-1-(3-ETHOXY-4-NITROPHENOXY)-4-(TRIFLUOROMETHYL)BENZENE	4	R128A, F420M	365	2,17E-07	
OXIFLUORFEN	2-CHLORO-1-(3-ETHOXY-4-NITROPHENOXY)-4-(TRIFLUOROMETHYL)BENZENE	4	R128A, F420L	343	5,58E-07	
OXIFLUORFEN	2-CHLORO-1-(3-ETHOXY-4-NITROPHENOXY)-4-(TRIFLUOROMETHYL)BENZENE	4	R128A, F420V	550	2,35E-08	

OXIFLUORFEN	2-CHLORO-1-(3-ETHOXY-4-NITROPHENOXY)-4-(TRIFLUOROMETHYL)BENZENE	4	R128I, F420L	196	4,21E-06	
OXIFLUORFEN	2-CHLORO-1-(3-ETHOXY-4-NITROPHENOXY)-4-(TRIFLUOROMETHYL)BENZENE	4	R128I, F420V	326	1,98E-07	
OXIFLUORFEN	2-CHLORO-1-(3-ETHOXY-4-NITROPHENOXY)-4-(TRIFLUOROMETHYL)BENZENE	4	R128V, F420M	482	1,05E-06	
OXIFLUORFEN	2-CHLORO-1-(3-ETHOXY-4-NITROPHENOXY)-4-(TRIFLUOROMETHYL)BENZENE	4	R128M, F420M	323	7,36E-07	
OXIFLUORFEN	2-CHLORO-1-(3-ETHOXY-4-NITROPHENOXY)-4-(TRIFLUOROMETHYL)BENZENE	4	R128Y, F420I	75	1,17E-06	
OXIFLUORFEN	2-CHLORO-1-(3-ETHOXY-4-NITROPHENOXY)-4-(TRIFLUOROMETHYL)BENZENE	4	R128Y, F420M	175	1,13E-06	
OXIFLUORFEN	2-CHLORO-1-(3-ETHOXY-4-NITROPHENOXY)-4-(TRIFLUOROMETHYL)BENZENE	4	R128N, F420M	174	3,91E-07	
OXIFLUORFEN	2-CHLORO-1-(3-ETHOXY-4-NITROPHENOXY)-4-(TRIFLUOROMETHYL)BENZENE	4	R128C, F420L	188	1,49E-06	

OXIFLUORFEN	2-CHLORO-1-(3-ETHOXY-4-NITROPHENOXY)-4-(TRIFLUOROMETHYL)BENZENE	4	R128C, F420V	225	6,52E-08	
OXIFLUORFEN	2-CHLORO-1-(3-ETHOXY-4-NITROPHENOXY)-4-(TRIFLUOROMETHYL)BENZENE	4	R128C, F420M	271	4,16E-07	
OXIFLUORFEN	2-CHLORO-1-(3-ETHOXY-4-NITROPHENOXY)-4-(TRIFLUOROMETHYL)BENZENE	4	R128H, F420M	196	3,68E-07	
OXADIARGYL		2 or 4	WT	650	3,64E-10	
OXADIARGYL		4	R128A, F420M	365	1,97E-08	
OXADIARGYL		4	R128A, F420L	343	1,37E-06	
OXADIARGYL		4	R128A, F420V	550	4,38E-08	
OXADIARGYL		4	R128I, F420L	196	8,64E-07	
OXADIARGYL		4	R128I, F420V	326	2,76E-08	
OXADIARGYL		4	R128V, F420M	482	3,40E-08	
OXADIARGYL		4	R128M, F420M	323	3,33E-08	
OXADIARGYL		4	R128Y, F420I	75	1,73E-07	
OXADIARGYL		4	R128Y, F420M	175	3,60E-08	
OXADIARGYL		4	R128N, F420M	174	1,28E-07	
OXADIARGYL		4	R128C, F420L	188	3,01E-06	
OXADIARGYL		4	R128C, F420V	225	1,46E-07	
OXADIARGYL		4	R128C, F420M	271	6,24E-08	
OXADIARGYL		4	R128H, F420M	196	1,32E-08	

S-3100	ethyl 2-[[3-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]-2-pyridyl]oxy]acetate	2 or 4	WT	650	1,35E-10	
S-3100	ethyl 2-[[3-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]-2-pyridyl]oxy]acetate	4	R128A, F420M	365	3,71E-08	
S-3100	ethyl 2-[[3-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]-2-pyridyl]oxy]acetate	4	R128A, F420L	343	2,77E-07	
S-3100	ethyl 2-[[3-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]-2-pyridyl]oxy]acetate	4	R128A, F420V	550	4,75E-08	
S-3100	ethyl 2-[[3-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]-2-pyridyl]oxy]acetate	4	R128I, F420L	196	2,01E-07	
S-3100	ethyl 2-[[3-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]-2-pyridyl]oxy]acetate	4	R128I, F420V	326	4,38E-08	
S-3100	ethyl 2-[[3-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]-2-pyridyl]oxy]acetate	4	R128V, F420M	482	3,58E-08	
S-3100	ethyl 2-[[3-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]-2-pyridyl]oxy]acetate	4	R128M, F420M	323	4,83E-08	

S-3100	ethyl 2-[[3-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]-2-pyridyl]oxy]acetate	4	R128Y, F420I	75	4,64E-07	
S-3100	ethyl 2-[[3-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]-2-pyridyl]oxy]acetate	4	R128Y, F420M	175	8,92E-08	
S-3100	ethyl 2-[[3-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]-2-pyridyl]oxy]acetate	4	R128N, F420M	174	1,92E-07	
S-3100	ethyl 2-[[3-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]-2-pyridyl]oxy]acetate	4	R128C, F420L	188	6,81E-07	
S-3100	ethyl 2-[[3-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]-2-pyridyl]oxy]acetate	4	R128C, F420V	225	1,24E-07	
S-3100	ethyl 2-[[3-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]-2-pyridyl]oxy]acetate	4	R128C, F420M	271	6,95E-08	
S-3100	ethyl 2-[[3-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]-2-pyridyl]oxy]acetate	4	R128H, F420M	196	4,18E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-	2 or 4	WT	650	5,17E-10	

	triazinane-2,4-dione					
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128A, F420M	321	7,02E-09	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128A, F420M	362	7,95E-09	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128A, F420M	365	6,10E-09	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128A, F420L	316	2,96E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128A, F420L	343	1,56E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-	4	R128A, F420V	478	4,14E-08	

	benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione					
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128A, F420V	550	2,13E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128A, F420V	555	3,99E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128I, F420L	202	4,05E-07	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128I, F420L	196	2,45E-07	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128I, F420I	95	1,38E-07	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-	4	R128I, F420V	292	2,14E-07	

	benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione					
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128I, F420V	326	3,15E-07	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128I, F420M	328	6,10E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128V, F420M	413	6,50E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128V, F420M	482	4,86E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128M, F420M	235	7,69E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-	4	R128M, F420M	289	7,07E-08	

	benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione					
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128M, F420M	323	4,84E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128Y, F420I	99	4,82E-07	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128Y, F420I	75	2,63E-06	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128Y, F420M	174	2,85E-07	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128Y, F420M	175	1,02E-07	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-	4	R128G, F420M	153	1,26E-08	

	benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione					
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128Q, F420M	432	1,07E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128H, F420L	193	7,98E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128H, F420I	191	8,22E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128N, F420M	153	7,12E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128N, F420M	174	4,97E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-	4	R128C, F420L	192	1,00E-07	

	benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione					
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128C, F420L	188	1,83E-07	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128C, F420V	160	1,66E-07	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128C, F420V	225	2,66E-07	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128C, F420M	277	2,53E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128C, F420M	271	2,33E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-	4	R128F, F420L	129	1,01E-06	

	benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione					
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128F, F420M	136	1,21E-07	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128S, F420M	328	2,40E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128T, F420M	275	4,33E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128H, F420V	95	7,63E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	4	R128H, F420M	184	2,64E-08	
BAS 850H	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-	4	R128H, F420M	196	2,13E-08	

	benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione					
850 analogon	2-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	2 or 4	WT	650	1,46E-10	
850 analogon	2-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128A, F420M	365	6,41E-07	
850 analogon	2-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128A, F420L	343	1,14E-05	
850 analogon	2-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128A, F420V	550	2,74E-07	
850 analogon	2-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128I, F420L	196	≥ 1,00E-05	6
850 analogon	2-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128I, F420V	326	4,32E-06	
850 analogon	2-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128V, F420M	482	3,11E-06	

850 analogon	2-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128M, F420M	323	≥ 1,00E-05	48
850 analogon	2-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128Y, F420I	75	≥ 1,00E-05	32
850 analogon	2-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128Y, F420M	175	≥ 1,00E-05	41
850 analogon	2-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128N, F420M	174	≥ 1,00E-05	43
850 analogon	2-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128C, F420L	188	≥ 1,00E-05	11
850 analogon	2-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128C, F420V	225	3,70E-06	
850 analogon	2-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128C, F420M	271	3,57E-06	
850 analogon	2-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)-4,5,6,7-tetrahydroisoindole-1,3-dione	4	R128H, F420M	196	3,07E-06	

850 analogon	1-methyl-6-(trifluoromethyl)-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)pyrimidine-2,4-dione	2 or 4	WT	650	3,15E-10	
850 analogon	1-methyl-6-(trifluoromethyl)-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)pyrimidine-2,4-dione	4	R128A, F420M	365	2,56E-09	
850 analogon	1-methyl-6-(trifluoromethyl)-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)pyrimidine-2,4-dione	4	R128A, F420L	343	1,62E-08	
850 analogon	1-methyl-6-(trifluoromethyl)-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)pyrimidine-2,4-dione	4	R128A, F420V	550	6,33E-09	
850 analogon	1-methyl-6-(trifluoromethyl)-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)pyrimidine-2,4-dione	4	R128I, F420L	196	2,69E-07	
850 analogon	1-methyl-6-(trifluoromethyl)-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)pyrimidine-2,4-dione	4	R128I, F420V	326	9,01E-08	
850 analogon	1-methyl-6-(trifluoromethyl)-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)pyrimidine-2,4-dione	4	R128V, F420M	482	4,65E-08	
850 analogon	1-methyl-6-(trifluoromethyl)-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)pyrimidine-2,4-dione	4	R128M, F420M	323	4,94E-08	

850 analogon	1-methyl-6-(trifluoromethyl)-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)pyrimidine-2,4-dione	4	R128Y, F420I	75	4,46E-07	
850 analogon	1-methyl-6-(trifluoromethyl)-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)pyrimidine-2,4-dione	4	R128Y, F420M	175	1,13E-07	
850 analogon	1-methyl-6-(trifluoromethyl)-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)pyrimidine-2,4-dione	4	R128N, F420M	174	5,94E-08	
850 analogon	1-methyl-6-(trifluoromethyl)-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)pyrimidine-2,4-dione	4	R128C, F420L	188	6,72E-08	
850 analogon	1-methyl-6-(trifluoromethyl)-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)pyrimidine-2,4-dione	4	R128C, F420V	225	2,60E-08	
850 analogon	1-methyl-6-(trifluoromethyl)-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)pyrimidine-2,4-dione	4	R128C, F420M	271	1,11E-08	
850 analogon	1-methyl-6-(trifluoromethyl)-3-(2,2,7-trifluoro-3-oxo-4-prop-2-ynyl-1,4-benzoxazin-6-yl)pyrimidine-2,4-dione	4	R128H, F420M	196	1,05E-08	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-	2 or 4	WT	650	4,11E-10	

	yl]phenoxy]phenoxy]-2-methoxy-acetate					
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128A, F420M	321	8,19E-09	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128A, F420L	343	4,70E-08	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128A, F420V	555	2,32E-08	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128I, F420L	196	7,13E-08	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128I, F420I	95	2,27E-08	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-	4	R128I, F420V	326	1,71E-08	

	(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate					
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128I, F420M	328	1,15E-08	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128V, F420M	482	1,49E-08	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128M, F420M	235	1,62E-08	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128Y, F420I	75	2,86E-08	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128G, F420M	153	4,76E-08	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-	4	R128Q, F420M	432	7,14E-08	

	(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate					
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128H, F420L	193	4,47E-08	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128H, F420I	191	7,54E-08	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128N, F420M	174	1,20E-07	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128C, F420V	225	1,16E-08	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128C, F420M	271	1,16E-08	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-	4	R128F, F420L	129	4,84E-08	

	(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate					
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128F, F420M	136	2,81E-09	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128S, F420M	328	3,62E-08	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-l]pheno]pheno] 2 metho acetate	4	R128T, F420M	275	2 79E 08	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-l]pheno]pheno] 2 metho acetate	4	R128H, F420V	25	6 93E 09	
	methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-l]pheno]pheno] 2 metho acetate	4	R128H, F420M	1?6	1 76E 08	
	2-ethoxyethyl 2-[2-[2-chloro-4-fluoro-5-[3-th l 2 6 di 4	2	WT	650	3 80E 10	

	(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate					
	2-ethoxyethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128A, F420M	321	1,51E-08	
	2-ethoxyethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128A, F420V	555	2,92E-08	
	2-ethoxyethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128I, F420M	328	1,39E-08	
	2-ethoxyethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128M, F420M	235	2,24E-08	
	2-ethoxyethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128S, F420M	328	4,68E-08	
	2-ethoxyethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-	4	R128T, F420M	275	2,93E-08	

	(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate					
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	2 or 4	WT	650	5,23E-10	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128A, F420M	321	2,27E-08	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128A, F420L	343	9,37E-08	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128A, F420V	555	4,16E-08	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128I, F420L	196	1,07E-07	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-	4	R128I, F420I	95	1,82E-06	

	(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate					
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128I, F420V	326	3,78E-08	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128I, F420M	328	1,06E-08	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128V, F420M	482	1,49E-08	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128M, F420M	235	3,22E-08	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128Y, F420I	75	6,82E-07	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-	4	R128G, F420M	153	5,14E-08	

	(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate					
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128Q, F420M	432	1,72E-07	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128H, F420L	193	6,93E-07	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128H, F420I	191	1,31E-06	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128N, F420M	174	1,48E-07	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128C, F420V	225	1,01E-07	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-	4	R128C, F420M	271	2,98E-08	

	(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate					
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128F, F420L	129	1,18E-06	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128F, F420M	136	6,26E-08	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128S, F420M	328	5,24E-08	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128T, F420M	275	1,17E-07	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128H, F420V	95	9,06E-08	
	cyclohexyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-	4	R128H, F420M	196	2,97E-07	

	(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate					
	4-pyridylmethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	2 or 4	WT	650	4,27E-10	
	4-pyridylmethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128A, F420M	321	1,22E-08	
	4-pyridylmethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128A, F420V	555	2,61E-08	
	4-pyridylmethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128I, F420M	328	1,56E-08	
	4-pyridylmethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128M, F420M	235	3,34E-08	
	4-pyridylmethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-	4	R128S, F420M	328	5,65E-08	

	(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate					
	4-pyridylmethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128T, F420M	275	5,88E-08	
	(1-methylcyclopropyl)methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	2 or 4	WT	650	4,16E-10	
	(1-methylcyclopropyl)methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128A, F420M	321	1,19E-08	
	(1-methylcyclopropyl)methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128A, F420V	555	4,25E-08	
	(1-methylcyclopropyl)methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128I, F420M	328	1,37E-08	
	(1-methylcyclopropyl)methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-	4	R128M, F420M	235	2,47E-08	

	(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate					
	(1-methylcyclopropyl)methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128S, F420M	328	6,94E-08	
	(1-methylcyclopropyl)methyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128T, F420M	275	5,77E-08	
	2,2-difluoroethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	2 or 4	WT	650	4,43E-10	
	2,2-difluoroethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128A, F420M	321	4,93E-08	
	2,2-difluoroethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128A, F420V	555	6,42E-08	
	2,2-difluoroethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-	4	R128I, F420M	328	4,61E-08	

	(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate					
	2,2-difluoroethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128M, F420M	235	1,06E-07	
	2,2-difluoroethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128S, F420M	328	9,94E-08	
	2,2-difluoroethyl 2-[2-[2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)pyrimidin-1-yl]phenoxy]phenoxy]-2-methoxy-acetate	4	R128T, F420M	275	1,50E-07	

IC50 (M): Concentration of inhibitor required for 50% inhibition of enzyme activity; >1,00E-5: indicates a very high IC50 over the measurement bounderies, which reflects very high in vitro tolerance.

EXAMPLE 5: Engineering PPO-derivative herbicide tolerant plants having wildtype or mutated PPO sequences.

PPO-derivative herbicide tolerant soybean *(Glyceine max),* corn (Zea *mays),* and Canola *(Brassica napus* or *Brassica Rapa var.* or *Brassica campestris L.)* plants are produced by a method as described by Olhoft ef *al.* (US patent 2009/0049567). For transformation of soybean or *Arabidopsis thaliana,* Wildtype or Mutated PPO sequences based on one of the following sequences SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, are cloned with standard cloning techniques as described in Sambrook ef *al.* (Molecular cloning (2001) Cold Spring Harbor Laboratory Press) in a binary vector containing resistance marker gene cassette (AHAS) and mutated PPO sequence (marked as GOI) in between ubiquitin promoter (PcUbi) and nopaline synthase terminator (NOS) sequence. For corn transformation, Wildtype or Mutated PPO sequences are cloned with standard cloning techniques as described in Sambrook ef *al.* (Molecular cloning (2001) Cold Spring Harbor Laboratory Press) in a binary vector containing resistance marker gene cassette (AHAS) and mutated PPO sequence (marked as GOI) in between corn ubiquitin promoter (ZmUbi) and nopaline synthase terminator (NOS) sequence. Binary plasmids are introduced to *Agrobacterium tumefaciens* for plant transformation. Plasmid constructs are introduced into soybean's axillary meristem cells at the primary node of seedling explants via A*grob*acfer/um-mediated transformation. After inoculation and co-cultivation with *Agrobacteria,* the explants are transferred to shoot introduction media without selection for one week. The explants were subsequently transferred to a shoot induction medium with 1-3 μM imazapyr (Arsenal) for 3 weeks to select for transformed cells. Explants with healthy callus/shoot pads at the primary node are then transferred to shoot elongation medium containing 1-3 μM imazapyr until a shoot elongated or the explant died. Transgenic plantlets are rooted, subjected to TaqMan analysis for the presence of the transgene, transferred to soil and grown to maturity in greenhouse. Transformation of corn plants are done by a method described by McElver and Singh (WO 2008/124495). Plant transformation vector constructs containing mutated PPO sequences are introduced into maize immature embryos via *Agrobacterium-mediated* transformation.

Transformed cells were selected in selection media supplemented with 0.5-1 .5 μM imazethapyr for 3-4 weeks. Transgenic plantlets were regenerated on plant regeneration media and rooted afterwards. Transgenic plantlets are subjected to TaqMan analysis for the presence of the transgene before being transplanted to potting mixture and grown to maturity in greenhouse. *Arabidopsis thaliana* are transformed with wildtype or mutated PPO sequences by floral dip method as decribed by McElver and Singh (WO 2008/124495). Transgenic Arabidopsis plants were subjected to TaqMan analysis for analysis of the number of integration loci. Transformation of *Oryza sativa* (rice) are done by protoplast transformation as decribed by Peng ef *al.* (US 6653529) TO or T1 transgenic plant of soybean, corn, and rice containing mutated PPO sequences are tested for improved tolerance to PPO-derived herbicides in greenhouse studies and mini-plot studies with the following PPO-inhibiting herbicides: saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), flumioxazin, butafenacil, acifluorfen, lactofen, bifenox, sulfentrazone, and photosynthesis inhibitor diuron as negative control.

Transgenic *Arabidopsis thaliana* plants were assayed for improved tolerance to saflufenacil, 1,5-

dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3^ dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione (CAS 1258836-72-4), flumioxazin, butafenacil, acifluorfen, lactofen, bifenox, sulfentrazone, and photosynthesis inhibitor diuron as negative control in 48-well plates. Therefore, T2 seeds are surface sterilized by stirring for 5 min in ethanol + water (70+30 by volume), rinsing one time with ethanol + water (70+30 by volume) and two times with sterile, deionized water. The seeds are resuspended in 0.1% agar dissolved in water (w/v) Four to five seeds per well are plated on solid nutrient medium consisting of half-strength murashige skoog nutrient solution, pH 5.8 (Murashige and Skoog (1962) *Physiologia Plantarum* 15: 473-497). Compounds are dissolved in dimethylsulfoxid (DMSO) and added to the medium prior solidification (final DMSO concentration 0.1 %). Multi well plates are incubated in a growth chamber at 22°C, 75% relative humidity and 110 µmol Phot * m^{-2} * s^{-1} with 14 : 10 h light : dark photoperiod. Growth inhibition is evaluated seven to ten days after seeding in comparison to wild type plants.

Additionally, transgenic T 1 *Arabidopsis* plants were tested for improved tolerance to PPO-inhibiting herbicides in greenhouse studies with the following PPO-inhibiting herbicides: saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione (CAS 1258836-72-4), flumioxazin, butafenacil, acifluorfen, lactofen, bifenox, sulfentrazone, and photosynthesis inhibitor diuron as negative control.

Results are shown in Table 5:

Table 5a: Germination Assay

Tolerance trails with: 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione			
Test Event	SEQ ID NO	Mutation	Tolerance Factor (non-transgenic Arabidopsis = 1)
1	4	R128A, F420V	300
2	4	R128A, F420V	300
3	4	R128A, F420V	3
4	4	R128A, F420V	300
5	4	R128A, F420V	300
6	4	R128A, F420V	200
7	4	R128A, F420V	3
8	4	R128A, F420V	300
9	4	R128A, F420V	300
10	4	R128A, F420V	300
11	4	R128A, F420V	40
12	4	R128A, F420V	3
13	4	R128A, F420V	300
14	4	R128A, F420V	3
15	4	R128A, F420V	200
16	4	R128A, F420V	200
17	4	R128A, F420V	300

18	4	R128A, F420V	3
19	4	R128A, F420V	75
20	4	R128A, F420V	200
21	4	R128A, F420V	300
22	4	R128A, F420V	3
23	4	R128A, F420V	8
24	4	R128A, F420V	75
25	4	R128A, F420V	200
26	4	R128A, F420V	300
1	4	F420V	75
2	4	F420V	75
3	4	F420V	35
4	4	F420V	75
5	4	F420V	300
6	4	F420V	300
7	4	F420V	300
8	4	F420V	300
9	4	F420V	300
10	4	F420V	300
11	4	F420V	3
12	4	F420V	8
13	4	F420V	300
14	4	F420V	20
15	4	F420V	300
16	4	F420V	300
17	4	F420V	300
18	4	F420V	35
19	4	F420V	3
20	4	F420V	300
21	4	F420V	300
22	4	F420V	300
23	4	F420V	300
24	4	F420V	300

Table 5b: Relative tolerance rates of transgenic Arabidopsis plants as compared to a non-transgenic Arabidopsis plant **(non-transgenic = 1.0),** treated with various PPO inhibitors. Growth inhibition is evaluated seven to ten days after seeding in comparison to wild type plants.

Mut PPO	**Saflufenacil**	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-	**Flumioxazin**	**Fomesafen**	**Lactofen**	**Sulfentrazon**

		6-yl)-1 ,3,5-triazinane-2,4-dione				
AMATLL PP02_wt	10	13	17	19	8	
AMATU_ PPO2_dG21 0	100	33	107	29	19	203
AMATU_PP02_ R 128L	160	23	126	27	22	186
AMATU_PP02_ dG21 0_R1 28L	1200	153	271	29	29	244
AMATU_PP02_ F420I	80	367	286	18	17	193
AMATU_PP02_ F420M	168	102	271	29	29	16 1
AMATU_PP02_ F420L	192	253	286	23	19	111
AMATU_PP02_ R 128A_F420I	1200	333	286	29	27	621
AMATU_PP02_ R 128A_F420L	1200	333	286	29	29	7 17
AMATU_PP02_ R 128A_F420M	1160	204	286	29	29	

Table 5 c: Phytotox values of transgenic Arabidopsis plants as compared to a non-transgenic Arabidopsis plant **(non-transgenic = 100% damage),** treated with 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2 **-ynyl**)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6 **-yl**)-1 ,3,5-triazinane-2,4-dione.

				Injury Rating 0 - 100%		
				(0 = no injury, 100 = total control)		
				300	150	75
Line	Assesment DAT (DAT = Days After Treatment)	SEQJ D	Substitution	1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione g/H a + 1%MSO		
1	7	2 & 4	R 128A_F420V	40	95	95
1	7	2 & 4	R 128A_F420V	100	25	0
1	7	2 & 4	R 128A_F420V	25	35	35
1	19	2 & 4	R 128A_F420V	28	90	90
1	19	2 & 4	R 128A_F420V	100	60	25
1	19	2 & 4	R 128A_F420V	25	30	30
2	7	2 & 4	F420V	98	95	95
2	7	2 & 4	F420V	25	90	15
2	7	2 & 4	F420V	25	15	15

2	19	2 & 4	F420V	95	90	98
2	19	2 & 4	F420V	55	85	40
2	19	2 & 4	F420V	45	45	30

Table 5 d: Relative tolerance rates of transgenic Arabidopsis plants as compared to a non-transgenic Arabidopsis plant **on a scale from 0 - 100, were 100 is 100% damage,** treated with single and mixtures of PPO inhibitors (e.g. Saflufenacil plus 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione). Plant growth injury is evaluated seven to ten days after application in comparison to wild type plants.

			non-transgenic Arabidopsis	non-transgenic Arabidopsis	non-transgenic Arabidopsis	Ø non-transgenic Arabidopsis	Ø R128A, F420V 1	Ø R128A, F420V 2	Ø R128A, F420V 3	Ø F420V 1	Ø F420V 2	Ø F420V 3	Ø R128A, F420V 1 to 3	Ø F420V 1 to 3
			POST	POST	POST	POST	POST	POST	POST	POST	POST	POST		
PPO Herbicide (+ 1% MSO)	g ai/ha	DAT	7	7	7	7	7	7	7	7	7	7		
Saflufenacil + 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione	50 + 25		98	98	98	98	23	23	21	33	33	27	22	31
	25 + 50		98	98	98	98	16	19	16	27	22	16	17	22
	100 + 50		98	98	98	98	15	26	23	55	47	43	21	48
	50 + 100		98	98	98	98	10	20	28	35	33	31	19	33
	200 + 100		98	98	98	98	25	23	28	63	60	66	25	63
	100 + 200		98	98	98	98	30	29	26	58	45	56	28	53
Saflufenacil	75		98	98	98	98	16	22	18	39	36	51	18	42
	150		98	98	98	98	18	24	18	60	55	66	20	60
	300		98	98	98	98	22	22	19	77	72	78	21	76
1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-	75		98	98	98	98	18	24	11	17	9	8	18	11
	150		98	98	98	98	23	20	30	28	11	12	24	17
	300		98	98	98	98	26	33	36	36	22	22	32	26

dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione														

Table 5 e shows phytotox values on a scale from 0 - **100**, were **100** is 100% damage.

		ARBTH WT	AMATU_PPO2_R128A_F420V	AMATU_PPO2_R128A_F420V	AMATU_PPO2_R128A_F420V	AMATU_PPO2_L397D_F420V	AMATU_PPO2_L397D_F420V
	event	1	A	B	D	O	P
compound	g ai/ha						
KIXOR + VALOR (Flumioxazin) + DESTINY HC	75 + 400 + 3750	100	8	0	20	0	7
	50 + 200 + 3750	100	0	0	12	0	7
	25 + 100 + 3750	100	0	17	12	0	3
KIXOR + SPOTLIGHT (Carfentrazone) + DESTINY HC	75 + 120 + 3750	100	5	3	13	15	22
	50 + 60 + 3750	100	0	3	3	5	7
	25 + 30 + 3750	100	0	7	3	3	3
KIXOR + BAS 850 00 H + DESTINY HC	75 + 200 + 3750	100	3	8	22	13	15
	50 + 100 + 3750	100	0	7	13	10	10
	25 + 50 + 3750	100	0	15	15	7	7
BAS 850 00 H + VALOR (Flumioxazin) + DESTINY HC	200 + 400 + 3750	100	10	12	20	17	17
	100 + 200 + 3750	100	2	7	13	10	10
	50 + 100 + 3750	100	0	0	3	3	0
BAS 850 00 H +	200 + 120 + 3750	100	8	20	23	17	20

SPOTLIGHT (Carfentrazone) + DESTI NY HC	100 + 60 + 3750	100	3	12	7	8	7
	50 + 30 + 3750	100	0	7	7	0	3

Table 5f shows phytotox values on a scale from 0 – 100, were 100 is 100% damage

		ARBTH WT	AMATU_PPO2 F420V				AMATU_PPO2 R128A_F420V				AMATU_PPO2 L397D				AMATU_PPO2 L397D_F420V			
	repetition	1	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
compound	g ai/ha																	
Kixor	200	100	85	90	95	80	10	10	40	10	95	95	85	90	30	0	10	10
	100	100	65	70	70	65	10	0	10	10	85	85	80	80	10	0	20	10
	50	100	50	30	50	50	0	0	10	10	65	65	50	70	10	20	10	40
BAS 850H	300	100	70	50	40	50	20	30	20	30	90	100	70	85	10	20	50	10
	150	100	60	40	40	65	10	10	40	50	75	70	70	70	20	10	30	0
	75	100	30	40	30	40	0	0	10	20	70	80	60	65	10	10	40	10
Carfentrazone	200	100	40	10	50	20	30	40	10	10	65	60	50	65	20	20	20	10
	100	100	10	10	40	20	10	10	10	10	60	50	30	30	20	20	50	10
	50	100	10	10	40	10	10	10	30	0	30	60	20	30	30	10	50	20
Kixor + Carfentrazone	75 +120	100	40	70	75	65	10	10	10	10	90	80	55	65	40	30	10	10
	37,5 + 60	100	30	65	70	50	10	30	0	0	70	80	55	50	10	10	10	10
	18,75 + 30	100	30	30	30	30	10	30	30	0	60	70	10	20	10	10	75	20

Table 5g shows phytotox values on a scale from 0 – 100, were 100 is 100% damage

compound	repetition g ai/ha	wild type	AMATU_PPO2_F420M		AMATU_PPO2_R128A_F420M		AMATU_PPO2_R128A_F420V		AMATU_PPO2_L397D_F420V		AMATU_PPO2_L397D	
	Event		A	B	A	B	A	D	O	A	E	O
Oxyfluorfen Kixor MSO 1%	800 + 75 + 3750	100	70	73	15	5	75	55	7,5	75	78	73
	800 + 50 + 3750	100	65	63	18	10	50	53	23	83	78	68
	800 + 25 + 3750	100	65	58	13	13	63	43	5	83	68	53
Oxyfluorfen Flumioxazin MSO 1%	800 + 400 + 3750	100	60	60	13	20	63	60	20	83	63	43
	800 + 200 + 3750	100	65	55	25	23	73	43	35	80	60	38
	800 + 100 + 3750	100	63	53	40	35	70	40	5	85	50	38
Oxyfluorfen BAS 850H MSO 1%	800 + 200 + 3750	100	75	70	60	58	70	60	20	90	95	83
	800 + 100 + 3750	100	73	65	63	50	75	55	13	93	100	78
	800 + 50 + 3750	100	73	50	43	50	73	60	25	88	88	70
Fomesafen BAS 850H MSO 1%	300 + 200 + 3750	100	85	85	63	55	80	78	60	97	90	73
	300 + 100 + 3750	100	85	85	58	55	85	78	70	95	93	83
	300 + 50 + 3750	100	93	83	48	55	85	80	63	94	90	75
Oxyfluorfen	800 + 600 +	100	85	95	60	50	90	83	58	93	68	40

Fomesafen MSO 1%	3750											
	800 + 450 + 3750	100	88	85	58	48	80	80	50	94	58	35
	800 + 300 + 3750	100	80	80	60	43	80	80	65	97	58	45
Flumioxazin Carfentrazone MSO 1%	100 + 120 + 3750	100	68	70	58	55	45	28	0	78	80	60
	100 + 60 + 3750	100	60	60	50	43	40	45	0	83	73	60
	100 + 30 + 3750	100	65	60	45	43	53	43	5	97	70	60
Oxyfluorfen Carfentrazone MSO 1%	800 + 120 + 3750	100	45	43	43	35	65	68	25	88	68	53
	800 + 60 + 3750	100	38	25	10	33	58	60	35	88	58	53
	800 + 30 + 3750	100	38	18	10	25	65	58	30	95	55	30

EXAMPLE 6: Tissue Culture Conditions.

An *in vitro* tissue culture mutagenesis assay has been developed to isolate and characterize plant tissue (e.g., maize, rice tissue) that is tolerant to protoporphyrinogen oxidase inhibiting herbicides, (saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,27-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione (CAS 1258836-72-4), flumioxazin, butafenacil, acifluorfen, lactofen, bifenox, sulfentrazone, and photosynthesis inhibitor diuron as negative control). The assay utilizes the somaclonal variation that is found in *in vitro* tissue culture. Spontaneous mutations derived from somaclonal variation can be enhanced by chemical mutagenesis and subsequent selection in a stepwise manner, on increasing concentrations of herbicide.

The present invention provides tissue culture conditions for encouraging growth of friable, embryogenic maize or rice callus that is regenerable. Calli were initiated from 4 different maize or rice cultivars encompassing *Zea mays* and Japonica (Taipei 309, Nipponbare, Koshihikari) and Indica (Indica 1) varieties, respectively. Seeds were surface sterilized in 70% ethanol for approximately 1 min followed by 20% commercial Clorox bleach for 20 minutes. Seeds were rinsed with sterile water and plated on callus induction media. Various callus induction media were tested. The ingredient lists for the media tested are presented in Table 6.

Table 6

Ingredient	Supplier	R001M	R025M	R026M	R327M	R008M	MS711R
B5 Vitamins	Sigma					1.0 X	
MS salts	Sigma			1.0 X	1.0 X	1.0 X	1.0 X
MS Vitamins	Sigma			1.0 X	1.0 X		
N6 salts	Phytotech	4.0 g/L	4.0g/L				
N6 vitamins	Phytotech	1.0 X	1.0 X				
L-Proline	Sigma	2.9 g/L	0.5 g/L				1.2 g/L
Casamino Acids	BD	0.3 g/L	0.3 g/L	2 g/L			
Casein Hydrolysate	Sigma						1.0 g/L
L-Asp Monohydrate	Phytotech						150 mg/L
Nicotinic Acid	Sigma						0.5 mg/L
Pyridoxine HCl	Sigma						0.5 mg/L
Thiamine HCl	Sigma						1.0 mg/L
Myo-inositol	Sigma						100 mg/L
MES	Sigma	500 mg/L	500 mg/L	500 mg/L	500 mg/L	500 mg/L	500 mg/L
Maltose	VWR	30 g/L	30 g/L	30 g/L	30 g/L		
Sorbitol	Duchefa			30 g/L			
Sucrose	VWR					10 g/L	30 g/L
NAA	Duchefa					50 µg/L	
2,4-D	Sigma	2.0 mg/L					1.0 mg/L
$MgCl_2 \cdot 6H_2O$	VWR					750 mg/L	
→pH		5.8	5.8	5.8	5.8	5.8	5.7
Gelrite	Duchefa	4.0 g/L				2.5 g/L	
Agarose Type1	Sigma		7.0 g/L	10 g/L	10 g/L		
→Autoclave		15 min	15 min	15 min	15 min	15 min	20 min
Kinetin	Sigma		2.0 mg/L	2.0 mg/L			
NAA	Duchefa		1.0 mg/L	1.0 mg/L			
ABA	Sigma		5.0 mg/L				
Cefotaxime	Duchefa		0.1 g/L	0.1 g/L	0.1 g/L		
Vancomycin	Duchefa		0.1 g/L	0.1 g/L	0.1 g/L		
G418 Disulfate	Sigma		20 mg/L	20 mg/L	20 mg/L		

R001 M callus induction media was selected after testing numerous variations. Cultures were kept in the dark at 30°C. Embryogenic callus was subcultured to fresh media after 10-14 days.

EXAMPLE 7: Selection of Herbicide-tolerant Calli.

Once tissue culture conditions were determined, further establishment of selection conditions were established through the analysis of tissue survival in kill curves with saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione (CAS 1258836-72-4), flumioxazin, butafenacil, acifluorfen, lactofen, bifenox, sulfentrazone, and photosynthesis inhibitor diuron as negative control. Careful consideration of

accumulation of the herbicide in the tissue, as well as its persistence and stability in the cells and the culture media was performed. Through these experiments, a sub-lethal dose has been established for the initial selection of mutated material. After the establishment of the starting dose of saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), flumioxazin, butafenacil, acifluorfen, lactofen, bifenox, sulfentrazone, and photosynthesis inhibitor diuron as negative control in selection media, the tissues were selected in a step-wise fashion by increasing the concentration of the PPO inhibitor with each transfer until cells are recovered that grew vigorously in the presence of toxic doses. The resulting calli were further subcultured every 3-4 weeks to R001 M with selective agent. Over 26,000 calli were subjected to selection for 4-5 subcultures until the selective pressure was above toxic levels as determined by kill curves and observations of continued culture. Alternatively, liquid cultures initiated from calli in MS71 1R with slow shaking and weekly subcultures. Once liquid cultures were established, selection agent was added directly to the flask at each subculture. Following 2-4 rounds of liquid selection, cultures were transferred to filters on solid R001 M media for further growth.

EXAMPLE 8: Regeneration of Plants.

Tolerant tissue was regenerated and characterized molecularly for PPO gene sequence mutations and/or biochemically for altered PPO activity in the presence of the selective agent. In addition, genes involved directly and/or indirectly in tetrapyrrole biosynthesis and/or metabolism pathways were also sequenced to characterize mutations. Finally, enzymes that change the fate (e.g. metabolism, translocation, transportaion) were also sequence to characterized mutations. Following herbicide selection, calli were regenerated using a media regime of R025M for 10 - 14 days, R026M for ca. 2 weeks, R327M until well formed shoots were developed, and R008S until shoots were well rooted for transfer to the greenhouse. Regeneration was carried out in the light. No selection agent was included during regeneration. Once strong roots were established, M0 regenerants were transplant to the greenhouse in square or round pots. Transplants were maintained under a clear plastic cup until they were adapted to greenhouse conditions. The greenhouse was set to a day/night cycle of 27°C/21°C (80°F/70°F) with 600W high pressure sodium lights supplementing light to maintain a 14 hour day length. Plants were watered according to need, depending in the weather and fertilized daily.

EXAMPLE 9: Sequence Analysis.

Leaf tissue was collected from clonal plants separated for transplanting and analyzed as individuals. Genomic DNA was extracted using a Wizard® 96 Magnetic DNA Plant System kit (Promega, US Patent Nos. 6,027,945 & 6,368,800) as directed by the manufacturer. Isolated DNA was PCR amplified using the appropriate forward and reverse primer.

PCR amplification was performed using Hotstar Taq DNA Polymerase (Qiagen) using touchdown thermocycling program as follows: 96°C for 15 min, followed by 35 cycles (96°C, 30 sec; 58°C - 0.2 °C per cycle, 30 sec; 72°C, 3 min and 30 sec), 10 min at 72°C. PCR products were verified for concentration and fragment size via agarose gel electrophoresis. Dephosphorylated PCR products were analyzed by direct sequence using the PCR primers (DNA Landmarks, or Entelechon). Chromatogram trace files (.scf) were analyzed for mutation relative to the wild-type gene using

Vector NTI Advance 10™ (Invitrogen). Based on sequence information, mutations were identified in several individuals. Sequence analysis was performed on the representative chromatograms and corresponding AlignX alignment with default settings and edited to call secondary peaks.

EXAMPLE 10: Demonstration of Herbicide-tolerance.

T0 or T1 transgenic plant of soybean, corn, Canola varieties and rice containing PP01 and or PP02 sequences are tested for improved tolerance to herbicides in greenhouse studies and mini-plot studies with the following herbicides: saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2 *J* -trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), flumioxazin, butafenacil, acifluorfen, lactofen, bifenox, sulfentrazone, and photosynthesis inhibitor diuron as negative control. For the pre-emergence treatment, the herbicides are applied directly after sowing by means of finely distributing nozzles. The containers are irrigated gently to promote germination and growth and subsequently covered with transparent plastic hoods until the plants have rooted. This cover causes uniform germination of the test plants, unless this has been impaired by the herbicides. For post emergence treatment, the test plants are first grown to a height of 3 to 15 cm, depending on the plant habit, and only then treated with the herbicides. For this purpose, the test plants are either sown directly, and grown in the same containers or they are first grown separately and transplanted into the test containers a few days prior to treatment.

For testing of T0 plants, cuttings can be used. In the case of soybean plants, an optimal shoot for cutting is about 7.5 to 10 cm tall, with at least two nodes present. Each cutting is taken from the original transformant (mother plant) and dipped into rooting hormone powder (indole-3-butyric acid, IBA). The cutting is then placed in oasis wedges inside a bio-dome. Wild type cuttings are also taken simultaneously to serve as controls. The cuttings are kept in the bio-dome for 5-7 days and then transplanted to pots and then acclimated in the growth chamber for two more days. Subsequently, the cuttings are transferred to the greenhouse, acclimated for approximately 4 days, and then subjected to spray tests as indicated. Depending on the species, the plants are kept at 10-25°C or 20-35°C. The test period extends over 3 weeks. During this time, the plants are tended and their response to the individual treatments is evaluated. Herbicide injury evaluations are taken at 2 and 3 weeks after treatment. Plant injury is rated on a scale of 0% to 100%, 0% being no injury and 100% being complete death.

Transgenic *Arabidopsis thaliana* plants were assayed for improved tolerance to saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione (CAS 1258836-72-4), flumioxazin, butafenacil, acifluorfen, lactofen, bifenox, sulfentrazone, and photosynthesis inhibitor diuron as negative control, in 48-well plates. Therefore, T2 seeds are surface sterilized by stirring for 5 min in ethanol + water (70+30 by volume), rinsing one time with ethanol + water (70+30 by volume) and two times with sterile, deionized water. The seeds are resuspended in 0.1% agar dissolved in water (w/v) Four to five seeds per well are plated on solid nutrient medium consisting of half-strength murashige skoog nutrient solution, pH 5.8 (Murashige and Skoog (1962) *Physiologia Plantarum* 15: 473-497). Compounds are dissolved in dimethylsulfoxid (DMSO) and added to the medium prior solidification (final DMSO concentration 0.1%). Multi well plates are incubated in a growth chamber at 22°C,

75% relative humidity and 110 μτιοΙ Phot * m^{-2} * s^{-1} with 14 : 10 h light : dark photoperiod. Growth inhibition is evaluated seven to ten days after seeding in comparison to wild type plants. Additionally, transgenic T1 *Arabidopsis* plants were tested for improved tolerance to herbicides in greenhouse studies with the following herbicides: saflufenacil , 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), flumioxazin, butafenacil, acifluorfen, lactofen, bifenox, sulfentrazone, and photosynthesis inhibitor diuron as negative control. Results are shown in **Table 5** and **Figure 2.**

EXAMPLE 11: Herbicide Selection Using Tissue Culture.

Media was selected for use and kill curves developed as specified above. For selection, different techniques were utilized. Either a step wise selection was applied, or an immediate lethal level of herbicide was applied. In either case, all of the calli were transferred for each new round of selection. Selection was 4-5 cycles of culture with 3-5 weeks for each cycle. Cali were placed onto nylon membranes to facilitate transfer (200 micron pore sheets, Biodesign, Saco, Maine). Membranes were cut to fit 100x20 mm Petri dishes and were autoclaved prior to use 25-35 calli (average weight/calli being 22mg) were utilized in every plate. In addition, one set of calli were subjected to selection in liquid culture media with weekly subcultures followed by further selection on semi-solid media. Mutant lines were selected using saflufenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4), flumioxazin, butafenacil, acifluorfen, lactofen, bifenox, sulfentrazone, and photosynthesis inhibitor diuron as negative control. Efficiencies of obtaining mutants was high either based on a percentage of calli that gave rise to a regenerable, mutant line or the number of lines as determined by the gram of tissue utilized.

EXAMPLE 12: Maize whole plant transformation and PPO inhibitor tolerance testing.

Immature embryos were transformed according to the procedure outlined in Peng et al. (WO2006/136596). Plants were tested for the presence of the T-DNA by Taqman analysis with the target being the nos terminator which is present in all constructs. Healthy looking plants were sent to the greenhouse for hardening and subsequent spray testing. The plants were individually transplanted into MetroMix 360 soil in 4" pots. Once in the greenhouse (day/night cycle of 27oC /21 oC with 14 hour day length supported by 600W high pressure sodium lights), they were allowed to grow for 14 days. They were then sprayed with a treatment of 25 to 200 g ai/ha saflufenacil + 1.0% v/v methylated seed oil (MSO) and / or 25 - 200 g ai/ha 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (CAS 1258836-72-4) plus 1% MSO. Other PPO inhibiting herbicides were also tested in a similar fashion for confirming cross resistance: flumioxazin, butafenacil, acifluorfen, lactofen, bifenox, sulfentrazone, and photosynthesis inhibitor diuron as negative control. Herbicide injury evaluations were taken at 7, 14 and 21 days after treatment. Herbicide injury evaluations were taken 2, 7, 14 and 21 days post-spray to look for injury to new growth points and overall plant health. The top survivors were transplanted into gallon pots filled with MetroMix 360 for seed production. **Results are shown in Table 7 and Figures 3, and 4.**

Table 7a Transgenic T0 corn events were sprayed in the greenhouse with the indicated amount of compound + 1% (v/v) MSO at V2 stage. Herbicide injury was evaluated 7 days after treatment with

a 0 to 9 rating scale where 0 is no injury relative to an unsprayed wild type check and 9 is completely dead.

Table 7a

SEQ ID	Event	0	BAS800H (g ai/ha)		BAS850H (g ai/ha)		
			50	75	50	75	100
AmtuPPX2L_R128A_F420V	1	0					
	2	0					
	3	0					
	4	0					
	5	0					
	6	0					
	7	0					
	8	0					
	9				4		
	10				4		
	11				4		
	12				4		
	13				3		
	14				4		
	15				4		
	16				3		
	17						4
	18						4
AmtuPPX2L_R128A_F420I	1	1					
	2	1					
	3	1					
	4	0					
	5	0					
	6	2					
	7	0					
	8	1					
	9	1					
	10	1					
	11		8				
	12		1				
	13		4				
	14		1				
	15		0				
	16				6		
	17				0		
	18				2		
	19				2		

	20				1		
	21					5	
	22					1	
	23	0					
	24	0					
	25	0					
	26	0					
	27	0					
	28		0				
	29		0				
	30				0		
	31				1		
	32				0		
	33				0		
	34				3		
	35					1	
	36	0					
	37	0					
	38	0					
	39					4	
	40				0		
	41				2		
	42				1		
	43						4
AmtuPPX2L_R128A_F420L	1	0					
	2				3		
	3						2
	4	0					
	5				2		
	6						2
	7	0					
	8				2		
	9	0					
	10				2		
	11	0					
	12				3		
	13	0					
	14				3		
	15	0					
	16				2		
	17	0					
	18						2
	19	0					
	20						2
	21	0					

	22	0					
	23	0					
	24	0					
	25	2					
AmtuPPX2L_R128A_F420V	1	0					
	2				1		
	3						1
	4	0					
	5				4		
	6						5
	7	0					
	8				3		
	9						1
	10	0					
	11				6		
	12	0					
	13				3		
	14	0					
	15				1		
	16	0					
	17				3		
	18	0					
	19						1
	20	0					
	21						5
	22	0					
	23						1
	24	0					
	25	3					
	26	1					
	27	1					
Tp-Fdx::c-AmtuPPX2L_R128A_F420V	1	0					
	2	0					
	3	0					
	4				0		
	5				1		
	6				0		
	7	0					
	8				0		
	9						0
	10	0					
	11				0		
	12	0					

	13				0		
	14						1
	15			2			
AmtuPPX2L_R128L_F420M	1	0			1		
	2				1		
	3				0		
	4				5		
	5				1		
	6				5		
	7				3		
	8				2		
	9				8		
	10				2		
	11				2		
	12				0		
	13	0			0		
	14	0			2		
	15				0		
	16				0		
	17				3		
	18				3		
	19				6		
	20				1		
	21				4		
	22				3		
	23				2		
	24				2		
	25				0		
	26				0		
	27				0		
	28				2		
	29				2		
	30				1		
	31				0		
	32				2		
	33				2		
	34				1		
	35				4		
	36				1		
	37				2		
AmtuPPX2L_R128M_F420I	1	0			7		
	2	0			0		
	3	0		0	1		0
	4				1		

	5				1		
	6				0		
	7				2		
	8	0			1	0	
	9	0			0	1	
	10	0			0		
	11	0			1		
	12	0			1		
	13	0			4		
	14	0			0		
	15	0			1		
	16	0			1		
	17				2		
	18				4		
	19				2		
	20				0		
	21				0		
	22				0		
	23				0		
	24				1		
	25				4		
	26				0		
	27				0		
	28				0		
	29				2		
	30				3		
	31	0			3		
	32	0			1	2	
	33				4		
	34	0			3		
	35	0			1		2
	36				4		
	37				1		
AmtuPPX2L_R128M_F420L	1	1			1		
	2				0		
	3				4		
	4				0		
	5	0			1	2	
	6	0			0		
	7				0		
	8				1		
	9				6		
	10				0		
	11				0		
	12				0		

	13	0			1		
	14	0			3		
	15				2		
	16	0			1		
	17	0			3		
	18				0		
AmtuPPX2L_R128M_F420V	1	0			0		
	2	0			3		
	3	0			0		
	4	0			0		
	5	0		1	0		0
	6	0			5		
	7				6		
	8				1		
	9				5		
	10				1		
	11				0		
	12				0		
	13				0		
	14	2			0		
	15	0			0		
	16	1			1		
	17	0			0		1
	18				1		
	19				0		
	20				1		
	21				0		
	22				1		
	23				0		
	24				0		
	25				0		
	26	2			0		
	27	0			0		
	28	1			1		
	29	0			0		1
	30				1		
	31				0		
	32				1		
	33				0		
	34				1		
	35				0		
	36				0		
	37				0		
	38				2		
	39				0		

	40				1		

Table 7 b Transgenic T1 corn events were sprayed in the field with 100 g ai BAS800H and 50 g ai BAS850H + 1% (v/v) MSO at V2-V3 developmental stage. Herbicide injury was evaluated at 3, 7, 14, and 21 days after treatment (DAT) with a 0 to 100 rating scale where 0 is no injury relative to an unsprayed wild type check and 100 is completely dead

Construct	SEQ ID	Event	3 DAT	7 DAT	14 DAT	21 DAT
RTP1 1136-1	AmtuPPX2L_R128A_ _F420V	1	20	30	0	0
RTP1 1141-1	AmtuPPX2L_R128A_ _F420I	2	70	80	70	80
RTP1 1141-1		3	20	10	10	10
RTP1 1141-1		4	10	0	30	20
RTP1 1141-1		5	10	0	20	10
RTP1 1141-1		6	10	0	10	0
RTP1 1141-1		7	10	0	30	20
RTP1 1141-1		8	80	80	70	70
RTP1 1141-1		9	10	0	10	0
RTP1 1141-1		10	10	10	40	30
RTP1 1141-1		11	10	10	30	20
RTP1 1142-2	AmtuPPX2L_R128A_ _F420L	12	10	30	10	10
RTP1 1142-2		13	10	10	30	20
RTP1 1142-2		14	10	10	20	20
RTP1 1142-2		15	10	10	30	20
RTP1 1142-2		16	20	30	40	20
RTP1 1142-2		17	10	0	20	0
RTP1 1142-2		18	10	10	10	0
RTP1 1142-2		19	20	10	10	0
RTP1 1142-2		20	10	10	10	0
RTP1 1142-2		21	10	10	10	0
RTP1 1142-2		22	10	0	10	0
RTP1 1142-2		23	20	40	50	50
RTP1 1142-2		24	50	80		
RTP1 1142-2		25	10	10	0	0
RTP1 1142-2		26	0	10	10	0
RTP1 1142-2		27	10	20	20	0
RTP1 1142-2		28	10	20	20	10
RTP1 1142-2		29	10	20	30	10
RTP1 1142-2		30	10	40	40	20
RTP1 1142-2		31	0	30	40	20
RTP1 1143-2	AmtuPPX2L_R128A_ _F420V	32	10	40	40	20
RTP1 1143-2		33	10	30	30	10
RTP1 1143-2		34	10	20	20	10
RTP1 1143-2		35	10	40	40	20
RTP1 1143-2		36	10	20	10	0

RTP1 1144-2	Tp-Fdx: :c-AmtuPPX2L_R1 28A_F420V	37	20	10	10	0
RTP1 1144-2		38	20	10	10	0
RTP1 1144-2		39	0	0	10	0
RTP1 1144-2		40	30	20	20	0
RTP1 1144-2		41	40	10	10	0
RTP1 1144-2		42	20	10	0	0
RTP1 1144-2		43	0	10	0	0
RTP1 1144-2		44	30	10	10	0
RTP1 1144-2		45	20	20	0	0

EXAMPLE 13: Soybean transformation and PPO Inhibitor tolerance testing.

Soybean cv Jake was transformed as previously described by Siminszky et al., Phytochem Rev. 5:445-458 (2006). After regeneration, transformants were transplanted to soil in small pots, placed in growth chambers (16 hr day/ 8 hr night; 25°C day/ 23°C night; 65% relative humidity; 130-150 microE m-2 s-1) and subsequently tested for the presence of the T-DNA via Taqman analysis. After a few weeks, healthy, transgenic positive, single copy events were transplanted to larger pots and allowed to grow in the growth chamber. An optimal shoot for cutting was about 3-4 inches tall, with at least two nodes present. Each cutting was taken from the original transformant (mother plant) and dipped into rooting hormone powder (indole-3-butyric acid, IBA). The cutting was then placed in oasis wedges inside a bio-dome. The mother plant was taken to maturity in the greenhouse and harvested for seed. Wild type cuttings were also taken simultaneously to serve as negative controls. The cuttings were kept in the bio-dome for 5-7 days and then transplanted to 3 inch pots and then acclimated in the growth chamber for two more days. Subsequently, the cuttings were transferred to the greenhouse, acclimated for approximately 4 days, and then sprayed with a treatment of 0 - 200 g ai/ha saflufenacil plus 1% MSO and / or 25 - 200 g ai/ha 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione (CAS 1258836-72-4) plus 1% MSO. Other PPO inhibiting herbicides were also tested in a similar fashion for confirming cross resistance: flumioxazin, butafenacil, acifluorfen, lactofen, bifenox, sulfentrazone, and photosynthesis inhibitor diuron as negative control. Herbicide injury evaluations were taken at 2, 7, 14 and 21 days after treatment. Results are shown in **Table 8, and Figures 5, 6, and 7.**

Table 8 a: Injury score from 0-9 taken 1 week after treatment of wildtype soybeans and soybeans expressing mutated PPO with either Kixor or 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione + 1% MSO

Data of T0 cuttings											
Injury score from 0-9 taken 1 week after treatment with either Kixor or 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione + 1% MSO											
		Kixor						1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione			
GOI	# events	0	12,5	25	50	100	200	12,5	25	50	75
wild type Jake variety		0	9	9	9	9	9	7	8	9	9
NitabPPX2	13	0	3	6	9	*	*	6	6	*	*
NitabPPX2_R98A_F392V	9	1	*	*	0	2	2	*	0	0	*
AmtuPPX2L	10	0	2	4	7	*	*	3	5	*	*
AmtuPPX2L_dG210	13	0	*	1	2	1	*	*	1	3	*
AmtuPPX2L_dG210_R128L	12	0	*	0	1	1	*	*	2	3	*
AmtuPPX2L_F420L	7	0	1	0	0	*	*	2	1	*	*
AmtuPPX2L_F420M	8	0	*	0	3	3	*	*	1	2	*
AmtuPPX2L_R128A_F420L	6	0	*	0	1	1	*	*	0	*	*
AmtuPPX2L_R128A_F420M	7	*	*	*	*	2	2	*	3	3	4
AmtuPPX2L_R128A_F420I	9	0	*	*	*	*	1	*	2	2	3
AmtuPPX2L_R128A_F420V	14	*	*	*	*	2	2	*	2	2	3

Table 8 b: Greenhouse data - segregating T1 individuals. Rated for injury (0-9 point scale) 1 week after treatment

GOI	wild type	AmtuPPX2L R128A_F420L	AmtuPPX2L R128A_F420L	AmtuPPX2L R128A_F420V	AmtuPPX2L L397D_F420V	AmtuPPX2L R128A_F420M	AmtuPPX2L R128A_F420M	AmtuPPX2L R128A_F420I	AmtuPPX2L R128A_F420I
Event		SDS-10642	SDS-10787	SDS-11034	SDS-10652	SDS-10990	SDS-10985	SDS10791	SDS-10648
unsprayed	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	1	1	1
	1	0	*	*	0	0	0	0	0
Saflufenacil 150 g ai/ha	9	0	6	0	3	9	1	1	5
	9	0	5	0	5	3	0	0	5
	9	0	4	5	3	0	*	9	4
	9	0	0	1	4	1	3	9	4
	9	0	4	0	6	3	2	9	6
	9	1	4	0	4	3	0	9	5
	9	1	4	0	3	3	0	1	3
	9	0	9	2	5	4	1	2	4
1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione 100 g ai/ha	9	6	4	4	9	9	9	3	4
	9	5	5	4	4	7	9	2	9
	9	5	9	4	4	6	6	4	4

	9	5	9	3	4	6	9	9	5
	9	5	5	2	4	9	6	3	5
	8	9	5	3	9	7	9	5	5
	9	5	6	3	4	6	9	4	4
	9	4	6	2	4	9	6	4	5
Fomesafen	5	0	1	2	1	1	3	6	5
600 g ai/ha	5	1	1	0	2	3	0	3	3
	4	0	0	0	0	0	0	3	3
	4	1	0	2	0	4	1	1	3
	4	0	2	0	1	5	3	4	3
	5	1	5	1	0	5	3	2	3
	4	1	2	1	2	0	1	1	3
	5	0	3	1	4	1	5	1	4
Flumioxazin	9	3	9	5	9	6	9	3	9
150 g ai/ha	9	3	5	4	6	5	6	3	9
	9	2	4	6	6	6	4	3	5
	9	1	5	5	5	5	5	1	9
	9	3	5	9	5	6	9	1	5
	9	9	9	3	4	6	6	3	9
	9	1	4	6	4	9	4	1	5
	9	2	5	5	6	6	9	3	9
Sulfentrazone	9	1	5	1	9	3	3	9	3
350 g ai/ha	9	0	5	3	*	3	3	9	4
	7	3	4	3	6	4	8	9	3
	7	1	6	9	3	9	3	2	4
	8	2	9	0	5	4	*	1	5
	9	0	9	1	3	3	4	2	5
	9	0	5	1	5	9	3	9	3
	9	3	5	1	6	3	1	9	8

Sulfentrazone	9	3	3	3	2	3	1	3	3
700 g ai/ha	9	1	4	3	3	4	9	3	2
	9	3	6	3	7	9	2	3	9
	9	2	4	2	7	4	3	4	3
	9	2	5	1	4	4	4	9	4
	9	2	6	3	4	4	3	2	4
	9	0	5	4	6	9	2	9	4
	9	2	6	2	4	9	9	9	4
Oxyfluorfen	8	2	6	4	4	4	1	4	5
600 g ai/ha	7	4	*	9	4	8	3	8	7
	8	3	5	5	5	4	4	4	6
	9	2	8	4	6	3	3	5	8
	7	8	5	4	6	4	4	5	6
	8	3	6	5	9	9	3	5	8
	9	2	6	5	4	4	4	4	9
	7	3	5	6	4	5	9	3	3
Oxyfluorfen	9	3	6	5	5	9	5	9	5
1200 g ai/ha	9	4	6	6	5	5	4	4	9
	9	3	5	6	4	4	4	5	9
	9	3	8	6	4	5	8	5	4
	8	2	5	5	3	5	8	5	5
	9	4	5	6	4	5	5	9	9
	9	3	9	6	4	4	4	5	9
	8	3	5	5	5	5	5	4	5

Table 8 c: Field data - T1 generation. Rated for injury (1-5 point scale) 3 days after treatment.

GOI	wild type	AmtuPPX2L R128A_F420M	AmtuPPX2L R128A_F420I	AmtuPPX2L R128A_F420I	AmtuPPX2L R128A_F420I	AmtuPPX2L R128A_F420V	AmtuPPX2L L397D_F420V
Event		SDS-11052	SDS-10648	SDS-10791	SDS-11014	SDS-11035	SDS-11034
unsprayed	1	1	1	1	1	1	1
1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione (=„benzoxazin“; BAS 850H) 100 g ai/ha	5	3	3	2	2	2	3
benzoxazin 50 g ai/ha	5	3	3	2	2	2	2
Saflufenacil 150 g ai/ha	5	2	2	2	2	2	2
Saflufenacil 75 g ai/ha	5	2	2	2	2	2	2

Rating	Phenotype (phytotoxicity) of surviving plants
1	no obvious damage (no phytotoxicity)
2	minor amount of leaf damage, plant will survive
3	moderate amount of leaf damage, plant will survive
4	severe amount of leaf damage, plant will survive
5	no surviving plants - all plants dead/dying

Table 8d: Field data - T1 generation soybeans rated for injury with 1-5 point scale.								
Injury rating taken 3 days after treatment								
Genotype		Event	benzoxazin +Saflufenacil (100gai/ha + 100gai/ha)	benzoxazin + Saflufenacil (50gai/ha + 50 gai/ha)	benzoxazin (100 gai/ha)	benzoxazin (50 gai/ha)	Saflufenacil (150 gai/ha)	Saflufenacil (75 gai/ha)
	GOI		Rating					
Wildtype		Jake	5	5	5	5	5	5
LTM377-1	AmtuPPX2L_dG210	SDS-10656	4	4	4	4	3,5	3,5
LTM377-1	AmtuPPX2L_dG210	SDS-10562	*	*	3	3	4	4
LTM377-1	AmtuPPX2L_dG210	SDS-10566	*	*	3	3	4	4
LTM387-1	AmtuPPX2L_R128A_F420V	SDS-11034	*	*	2	2	2	3
LTM387-1	AmtuPPX2L_R128A_F420V	SDS-11035	*	*	2	2	2	2
LTM387-1	AmtuPPX2L_R128A_F420V	SDS-10998	2,5	2,5	2,5	2,5	2	2
LTM387-1	AmtuPPX2L_R128A_F420V	SDS-11105	3,5	3	3	3	2,5	2,5
LTM387-1	AmtuPPX2L_R128A_F420V	SDS-11110	3,5	3	3	3	2,5	2,5

Table 8e: Field data - T1 generation soybeans rated for injury with 1-5 point scale.				
Injury rating taken 3 days after treatment				
Genotype	GOI	Event	Saflufenacil (150 gai/ha)	Saflufenacil (75 gai/ha)
			Rating	
Wildtype		Jake	5	5
LTM382-2	AmtuPPX2L_F420L	SDS-10533	2,5	2,5
LTM382-2	AmtuPPX2L_F420L	SDS-10544	2,5	2,5
LTM382-2	AmtuPPX2L_F420L	SDS-10558	2	2,5
LTM383-1	AmtuPPX2L_F420M	SDS-10645	3	4
LTM383-1	AmtuPPX2L_F420M	SDS-10761	3	3
LTM383-1	AmtuPPX2L_F420M	SDS-10633	3	3
LTM383-1	AmtuPPX2L_F420M	SDS-10635	3,5	3,5
LTM383-1	AmtuPPX2L_F420M	SDS-10646	2,5	2,5
LTM384-1	AmtuPPX2L_R1 28A_F420L	SDS-10642	2	2
LTM384-1	AmtuPPX2L_R1 28A_F420L	SDS-10787	2,5	3
LTM385-1	AmtuPPX2L_R1 28A_F420M	SDS-11052	3	3
LTM385-1	AmtuPPX2L_R1 28A_F420M	SDS-10985	2	2
LTM385-1	AmtuPPX2L_R1 28A_F420M	SDS-10990	2,5	2,5
LTM385-1	AmtuPPX2L_R1 28A_F420M	SDS-11011	2	2
LTM386-1	AmtuPPX2L_R1 28A_F420l	SDS-10648	3	3
LTM386-1	AmtuPPX2L_R1 28A_F420l	SDS-10791	2	2
LTM386-1	AmtuPPX2L_R1 28A_F420l	SDS-11014	2	2
LTM386-1	AmtuPPX2L_R1 28A_F420l	SDS-10658	3,5	3,5
LTM386-1	AmtuPPX2L_R1 28A_F420l	SDS-10776	2,5	2
LTM386-1	AmtuPPX2L_R1 28A_F420l	SDS-11036	2,5	2,5
LTM386-1	AmtuPPX2L_R1 28A_F420l	SDS-11111	2,5	2,5
LTM386-1	AmtuPPX2L_R1 28A_F420l	SDS-11118	2	2

Table 8f Soy TO plants greenhouse data

SEQ ID	event number	Herbicide treatment g ai/ha & injury scores 1 WAT					
		Saflufenacil			1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H -benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione		
		0	100	200	25	50	75
AmtuPPX2L_R1 28L_F420V	1	0	4	6	3	4	5
	2	0	1	2	0	1	3

Table 8g Field data - T1 generation. Rated for injury (1-5 point scale) 7 or 14 days after treatment (DAT) 1. Herbicide treatment 1 occurred at the V3-V4 stage and herbicide treatment 2 occurred 10 days later at ~V6 stage.

		saflufenacil + BAS 850H	saflufenacil + BAS 850H	BAS 850H	BAS 850H	saflufenacil	saflufenacil
	Herbicide treatment 1	150 g ai/ha + 100 g ai/ha	300 g ai/ha + 300 g ai/ha	100 g ai/ha	300 g ai/ha	150 g ai/ha	300 g ai/ha
	Herbicide treatment 2	0	300 g ai/ha + 300 g ai/ha	0	300 g ai/ha	0	300 g ai/ha
	Timing of injury rating	7 DAT	14 DAT	7DAT	14 DAT	7DAT	14 DAT
SEQ ID 2 or 4	Event #	Injury rating					
	wild type	5	5	5	5	5	5
AmtuPPX2L_R128A_F420L	1	2,5	3	2,5	3	1	1
AmtuPPX2L_R128A_F420L	2	3	3,5	3,5	3,5	3	2
AmtuPPX2L_R128A_F420M	3	2	3	3	3,5	1,5	1,5
AmtuPPX2L_R128A_F420M	4	2	3	3	3,5	1,5	1
AmtuPPX2L_R128A_F420I	5	2,5	3	3	3,5	1,5	1
AmtuPPX2L_R128A_F420I	6	3	3,5	3	3,5	3	3
AmtuPPX2L_R128A_F420I	7	2	3	3	3,5	1,5	1,5
AmtuPPX2L_R128A_F420I	8	1	2	2,5	2,5	1	2
AmtuPPX2L_R128A_F420I	9	1	1	2,5	1,5	1	1
AmtuPPX2L_R128A_F420V	10	3	3	3,5	3	3	3

Table 8h Greenhouse data - T2 generation; Data are the average injury score (0-9 scale) of up to 4 individuals per homozygous T2 event. Injury was evaluated 1 week after treatment in the greenhouse. BAS800H refers to Saflufenacil/Kixor; BAS 850H refers to 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione (or "Benzoxazin"), BAS850-Analog refers to 1-methyl-6-(trifluoromethyl)-3-(2,274rifluoro-3-oxo-4-prop-2-ynyl-1 ,4-benzoxazin-6-yl)pyrimidine-2,4-dione (described in detail in WO2011/57935)

Herbicide	g ai/ha	WT	AmtuPPX2L_R128A_F420L	AmtuPPX2L_R128A_F420M	AmtuPPX2L_R128A_F420I	AmtuPPX2L_R128A_F420V
unsprayed check	0	0,5	1,3	1,0	1,0	1,3
saflufenacil	100	9,0	4,3	4,0	2,0	2,7
BAS 850H	50					
1% (v/v) MSO						
saflufenacil	200	9,0	4,5	5,0	1,8	2,8
BAS 850H	100					
1% (v/v) MSO						
saflufenacil	100	9,0	4,8	5,0	0,5	2,0
flumioxazin	140					
1% (v/v) MSO						
saflufenacil	100	9,0	0,7	1,0	0,3	1,0
sulfentrazone	560					
1% (v/v) MSO						
saflufenacil	100	9,0	5,0	6,0	5,0	4,7
BAS 850-Analog	50					
1% (v/v) MSO						

Table 8i Greenhouse data - T2 generation; Various mixture ratios of saflufenacil and 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1,3,5-triazinane-2,4-dione. Data are the average injury score (0-9 scale) of up to 4 individuals per homozygous T2 event. Injury was evaluated 1 week after treatment in the greenhouse. BAS800H refers to Saflufenacil/Kixor; BAS 850H refers to 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3-oxo-4-(prop-2-ynyl)-3,4-dihydro-2H-benzo[b][1 ,4]oxazin-6-yl)-1 ,3,5-triazinane-2,4-dione ("Benzoxazin"), all mutants based on AmtuPPX2L (SEQ ID NO:2 or 4

Herbicide	g ai/ha	wild type	R128A_F420L (event a)	R128A_F420L (event b)	R128A_F420V (event a)	R128A_F420V (event b)	R128A_F420V (event c)
saflufenacil + BAS 850H	unsprayed	0,3	0,3	1,3	2,0	0,8	1,0
	6.25 + 3.125	8,3	4,0	6,0	0,5	0,3	0,0
	12.5 + 6.25	9,0	0,7	6,0	1,0	0,3	1,0
	25 + 12.5	9,0	1,5	7,5	1,7	1,0	3,5
	50 + 25	9,0	2,8	7,5	1,0	2,5	2,0
	100 + 50	9,0	5,0	6,0	2,3	2,3	4,0
	200 + 100	9,0	5,0	6,7	3,5	3,5	4,5
	400 + 200	9,0	4,7	8,5	3,3	2,8	4,3
	800 + 400	9,0	5,3	8,5	3,0	3,8	4,3

Rating	Phenotype (phototoxicity) of surviving plants
1	no obvious damage (no phytotoxicity)
2	minor amount of leaf damage, plant will survive
3	moderate amount of leaf damage, plant will survive
4	severe amount of leaf damage, plant will survive
5	no surviving plants - all plants dead/dying

The following gives a definition of the injury scores measured above:

Score Description of injury

0 No Injury

1 Minimal injury, only a few patches of leaf injury or chlorosis.

2 Minimal injury with slightly stronger chlorosis. Overall growth points remain undamaged.

3 Slightly stronger injury on secondary leaf tissue, but primary leaf and growth points are still undamaged.

4 Overall plant morphology is slightly different, some chlorosis and necrosis in secondary growth points and leaf tissue. Stems are intact. Regrowth is highly probable within 1 week.

5 Overall plant morphology is clearly different, some chlorosis and necrosis on a few leaves and growth points, but primary growth point is intact. Stem tissue is still green. Regrowth is highly probably within 1 week.

6 Strong injury can be seen on the new leaflet growth. Plant has a high probability to survive only through regrowth at different growth points. Most of the leaves are chlorotic/ necrotic but stem tissue is still green. May have regrowth but with noticeable injured appearance.

7 Most of the active growth points are necrotic. There may be a single growth point that could survive and may be partially chlorotic or green and partially necrotic. Two leaves may still be chlorotic with some green; the rest of the plant including stem is necrotic.

8 Plant will likely die, and all growth points are necrotic. One leaf may still be chlorotic with some green. The remainder of the plant is necrotic.

9 Plant is dead.

* Not tested

Claims:

1. A method for controlling undesired vegetation at a plant cultivation site, the method comprising the steps of:
   a) providing, at said site, a plant that comprises at least one nucleic acid comprising a nucleotide sequence encoding a mutated protoporphyrinogen oxidase (PPO) which is resistant or tolerant to a "PPO inhibiting herbicide" and/or
   b) applying to said site an effective amount of said herbicide,
   wherein the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Leu, Ala, Val, lie, Met, Tyr, Gly, Asn, Cys, Phe, Ser, Thr, Gin, or His, and/or the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala, Leu, Val, lie, or Met.

2. The method according to claim 1, wherein the nucleotide sequence of a) comprises the sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45 or 47, or a variant or derivative thereof.

3. The method according to claims any of claims 1 to 2, wherein the plant comprises at least one additional heterologous nucleic acid comprising a nucleotide sequence encoding a herbicide tolerance enzyme.

4. The method according to any of claims 1 to 3 wherein the PPO inhibiting herbicide is applied in conjunction with one or more additional herbicides.

5. An isolated and/or recombinant and/or synthetic nucleic acid encoding a mutated PPO polypeptide, wherein the nucleic acid comprises the nucleotide sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45 or 47, or a variant or derivative thereof, wherein the mutated PPO comprises a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which the amino acid at or corresponding to position 128 of SEQ ID NO:2 is other than Arginine; and/or the amino acid at or corresponding to position 420 of SEQ ID NO: 2 is other than Phenylalanine.

6. The nucleic acid of claim 6, wherein the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Leu, Ala, Val, lie, Met, Tyr, Gly, Asn, Cys, Phe, Ser, Thr, Gin, or His, and/or the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala, Leu, Val, lie, or Met.

7. A mutated PPO polypeptide comprising a sequence of SEQ ID NO: 2, a variant, derivative, orthologue, paralogue or homologue thereof, in which the amino acid at or corresponding to position 128 of SEQ ID NO:2 is Leu, Ala, Val, lie, Met, Tyr, Gly, Asn, Cys, Phe, Ser, Thr, Gin, or His, and the amino acid at or corresponding to position 420 of SEQ ID NO:2 is Ala, Leu, Val, lie, or Met, wherein said mutated PPO polypeptide confers in-

creased resistance or tolerance to a PPO inhibiting herbicide in a plant as compared to a wild type plant.

8. A transgenic plant cell transformed by and expressing a nucleic acid encoding a mutated PPO polypeptide as defined in claim 7, wherein expression of the nucleic acid in the plant cell results in increased resistance or tolerance to a PPO inhibiting herbicide as compared to a wild type variety of the plant cell.

9. The transgenic plant cell of claim 8, wherein the mutated PPO polypeptide encoding nucleic acid comprises a polynucleotide sequence selected from the group consisting of: a) a polynucleotide as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45 or 47, or a variant or derivative thereof; b) a polynucleotide encoding a polypeptide as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, or 48, or a variant or derivative thereof; c) a polynucleotide comprising at least 60 consecutive nucleotides of any of a) or b); and d) a polynucleotide complementary to the polynucleotide of any of a) through c).

10. A transgenic plant comprising a plant cell as defined in claim 8 or 9, wherein expression of the mutated PPO polypeptide encoding nucleic acid in the plant results in the plant's increased resistance to PPO inhibiting herbicide as compared to a wild type plant.

11. A plant cell mutagenized to obtain a plant cell which expresses a nucleic acid encoding a mutated PPO polypeptide as defined in claim 7.

12. A plant that expresses a mutagenized or recombinant mutated PPO polypeptide as defined in claim 7, and wherein said mutated PPO confers upon the plant increased herbicide tolerance as compared to the corresponding wild-type variety of the plant when expressed therein.

13. A method for growing a plant as defined in claim 10 or 12 while controlling weeds in the vicinity of said plant, said method comprising the steps of:

a) growing said plant ; and

b) applying a herbicide composition comprising a PPO-inhibiting herbicide to the plant and weeds, wherein the herbicide normally inhibits protoporphyrinogen oxidase, at a level of the herbicide that would inhibit the growth of a corresponding wild-type plant.

14. A seed produced by a plant comprising a plant cell as defined in claim 8, 9, or 11, or by a plant as defined in claim 10 or 12, wherein the seed is true breeding for an increased resistance to a PPO inhibiting herbicide as compared to a wild type variety of the seed.

15. A method of producing a transgenic plant cell with an increased resistance to a PPO inhibiting herbicide as compared to a wild type variety of the plant cell comprising, trans-

forming the plant cell with an expression cassette comprising a nucleic acid encoding a mutated PPO polypeptide as defined in claim 7.

16. A method of producing a transgenic plant comprising, (a) transforming a plant cell with an expression cassette comprising a nucleic acid encoding a mutated PPO polypeptide as defined in claim 7, and (b) generating a plant with an increased resistance to PPO inhibiting herbicide from the plant cell.

17. The method of claim 15 or 16, wherein the nucleic acid encoding the mutated PPO polypeptide comprises a polynucleotide sequence selected from the group consisting of : a) a polynucleotide as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45 or 47, or a variant or derivative thereof; b) a polynucleotide encoding a polypeptide as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, or 48, or a variant or derivative thereof; c) a polynucleotide comprising at least 60 consecutive nucleotides of any of a) or b); and d) a polynucleotide complementary to the polynucleotide of any of a) through c).

18. The method of any of claims 15 to 17, wherein the expression cassette further comprises a transcription initiation regulatory region and a translation initiation regulatory region that are functional in the plant.

19. An expression cassette comprising a nucleic acid encoding a mutated PPO polypeptide as defined in claim 7, a transcription initiation regulatory region and a translation initiation regulatory region that are functional in the plant, and a chloroplast-targeting sequence comprising a nucleotide sequence that encodes a chloroplast transit peptide.

20. The expression cassette of claim 19, wherein the targeting sequence comprises a nucleotide sequence that encodes a transit peptide comprising the amino acid sequence of SEQ ID NO: 49, 50, 51, 52, or 53.

21. A method of identifying or selecting a transformed plant cell, plant tissue, plant or part thereof comprising: i) providing a transformed plant cell, plant tissue, plant or part thereof, wherein said transformed plant cell, plant tissue, plant or part thereof comprises a polynucleotide as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45 or 47, or a variant or derivative thereof, wherein the polynucleotide encodes a mutated PPO polypeptide as defined in claim 7 that is used as a selection marker, and wherein said transformed plant cell, plant tissue, plant or part thereof may comprise a further isolated polynucleotide; ii) contacting the transformed plant cell, plant tissue, plant or part thereof with at least one PPO inhibiting compound; iii) determining whether the plant cell, plant tissue, plant or part thereof is affected by the PPO inhibiting compound; and iv) identifying or selecting the transformed plant cell, plant tissue, plant or part thereof.

22. A combination useful for weed control, comprising (a) a polynucleotide encoding a mutated PPO polypeptide as defined in claim 7, which polynucleotide is capable of being expressed in a plant to thereby provide to that plant tolerance to a PPO inhibiting herbicide; and (b) a PPO inhibiting herbicide.

23. A process for preparing a combination useful for weed control comprising (a) providing a polynucleotide encoding a mutated PPO polypeptide as defined in claim 7, which polynucleotide is capable of being expressed in a plant to thereby provide to that plant tolerance to a PPO inhibiting herbicide; and (b) providing a PPO inhibiting herbicide.

24. The process according to claim 23, wherein said step of providing a polynucleotide comprises providing a plant containing the polynucleotide.

25. The process according to claim 23, wherein said step of providing a polynucleotide comprises providing a seed containing the polynucleotide.

26. The process according to claim 25, further comprising a step of applying the PPO inhibiting herbicide to the seed.

27. Use of a combination as defined in claim 22 to control weeds at a plant cultivation site.

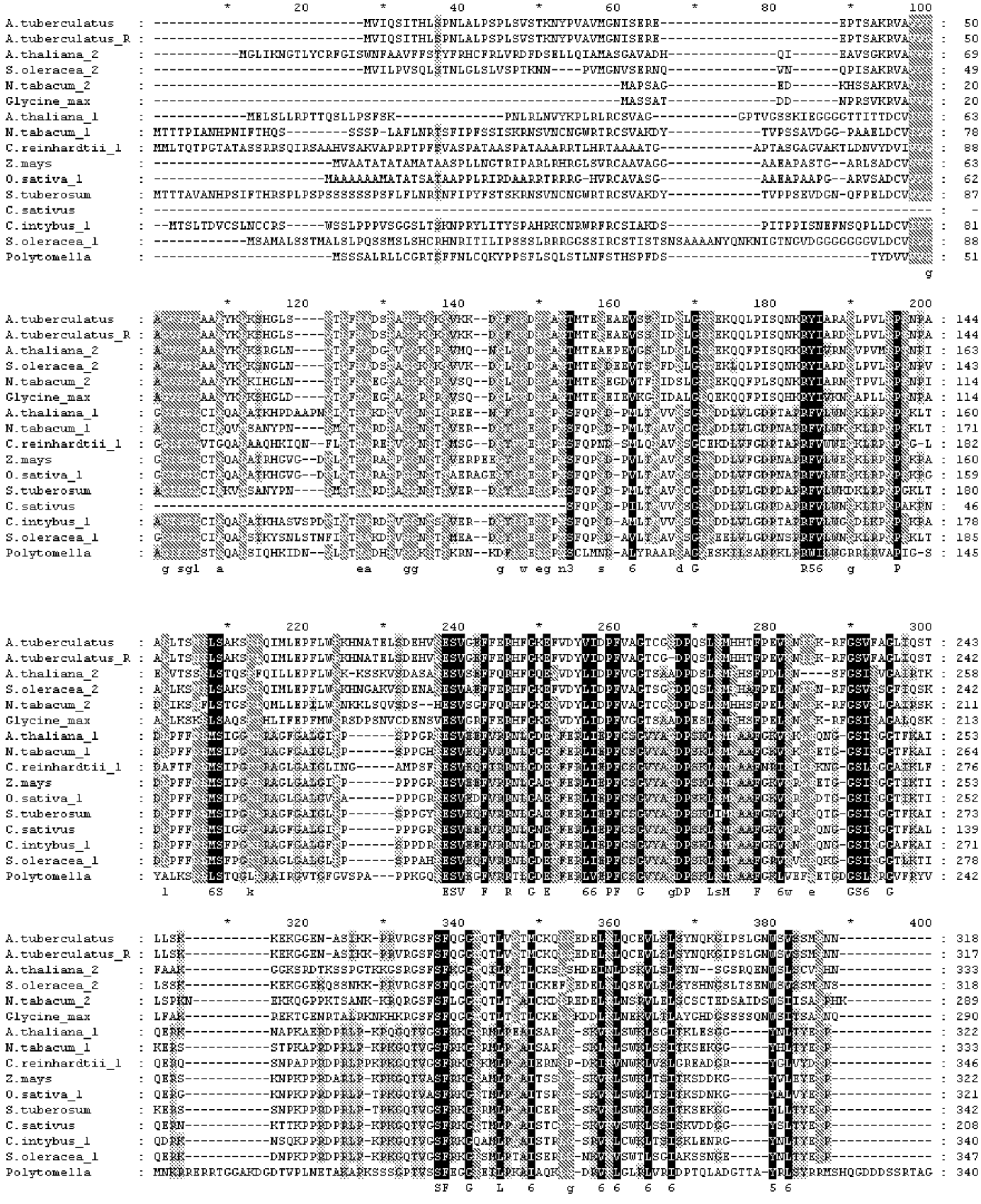


Figure 1

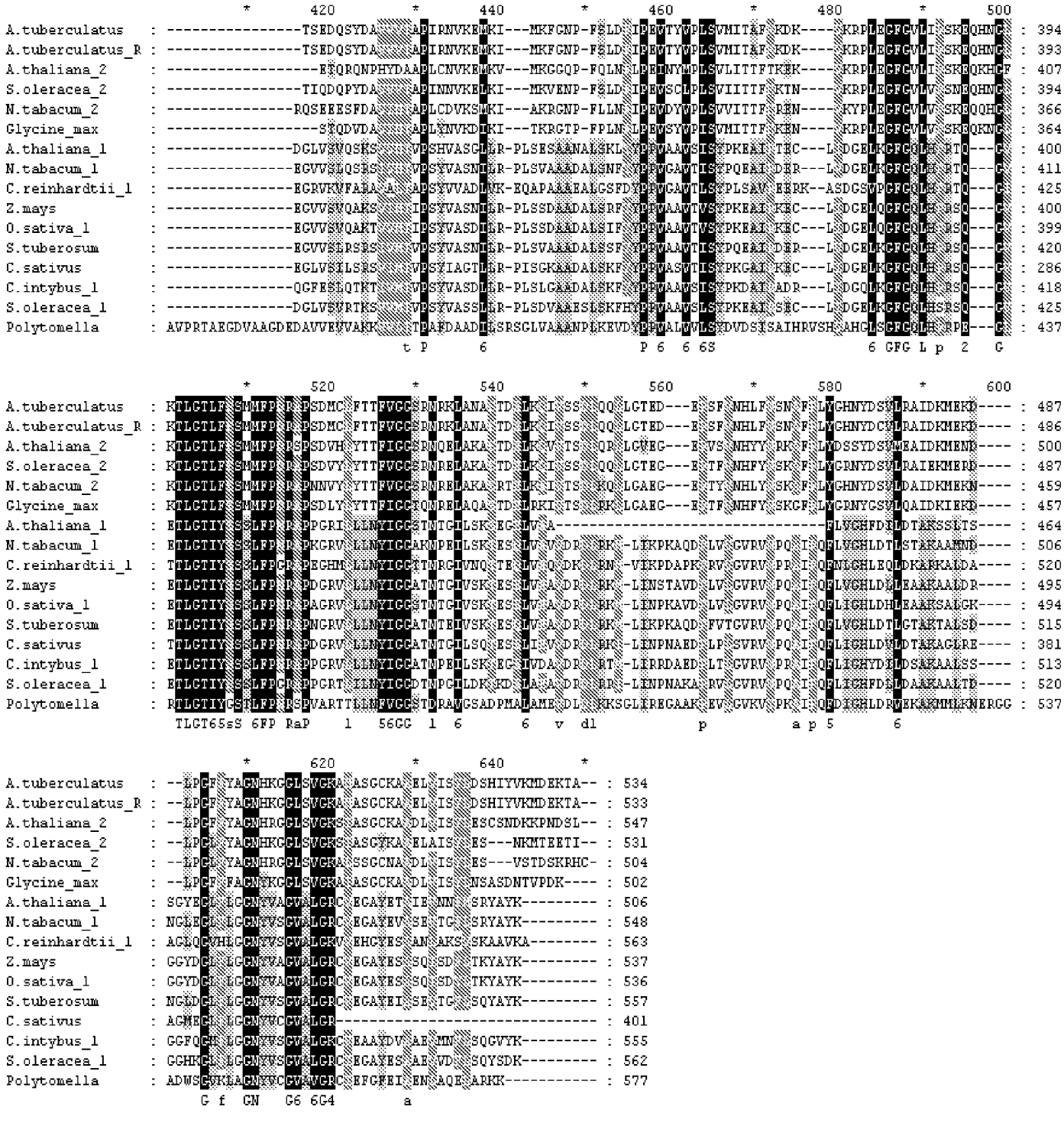


Figure 1 - continued

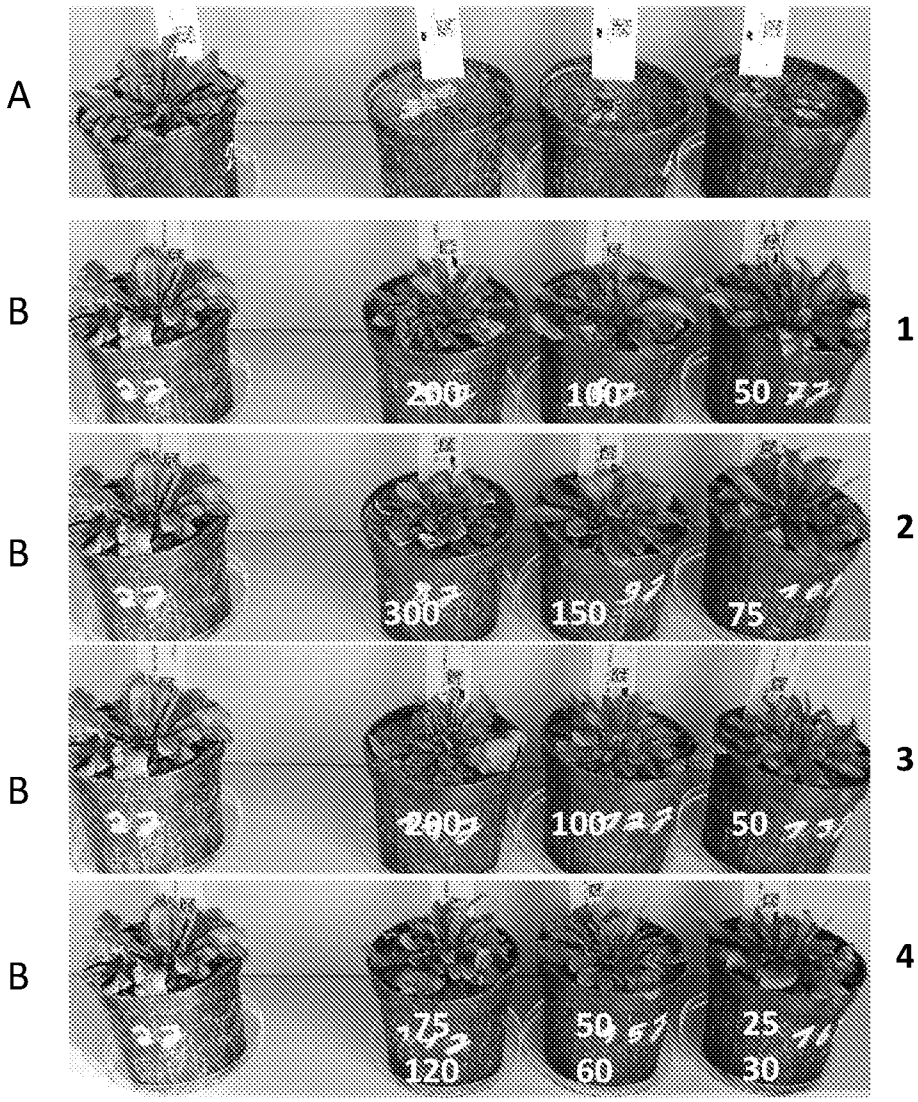
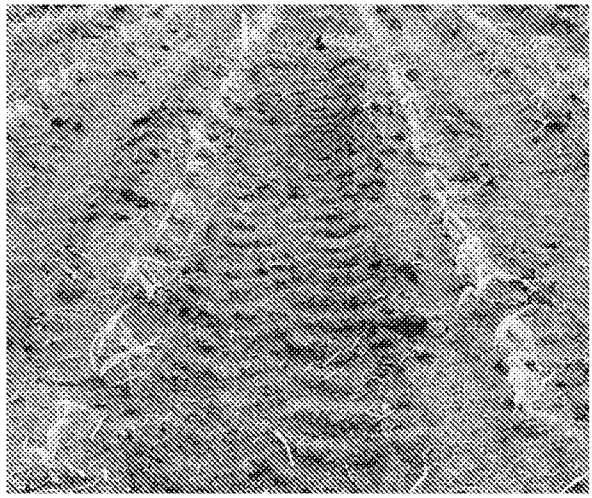


Figure 2



1

2

3

Figure 3

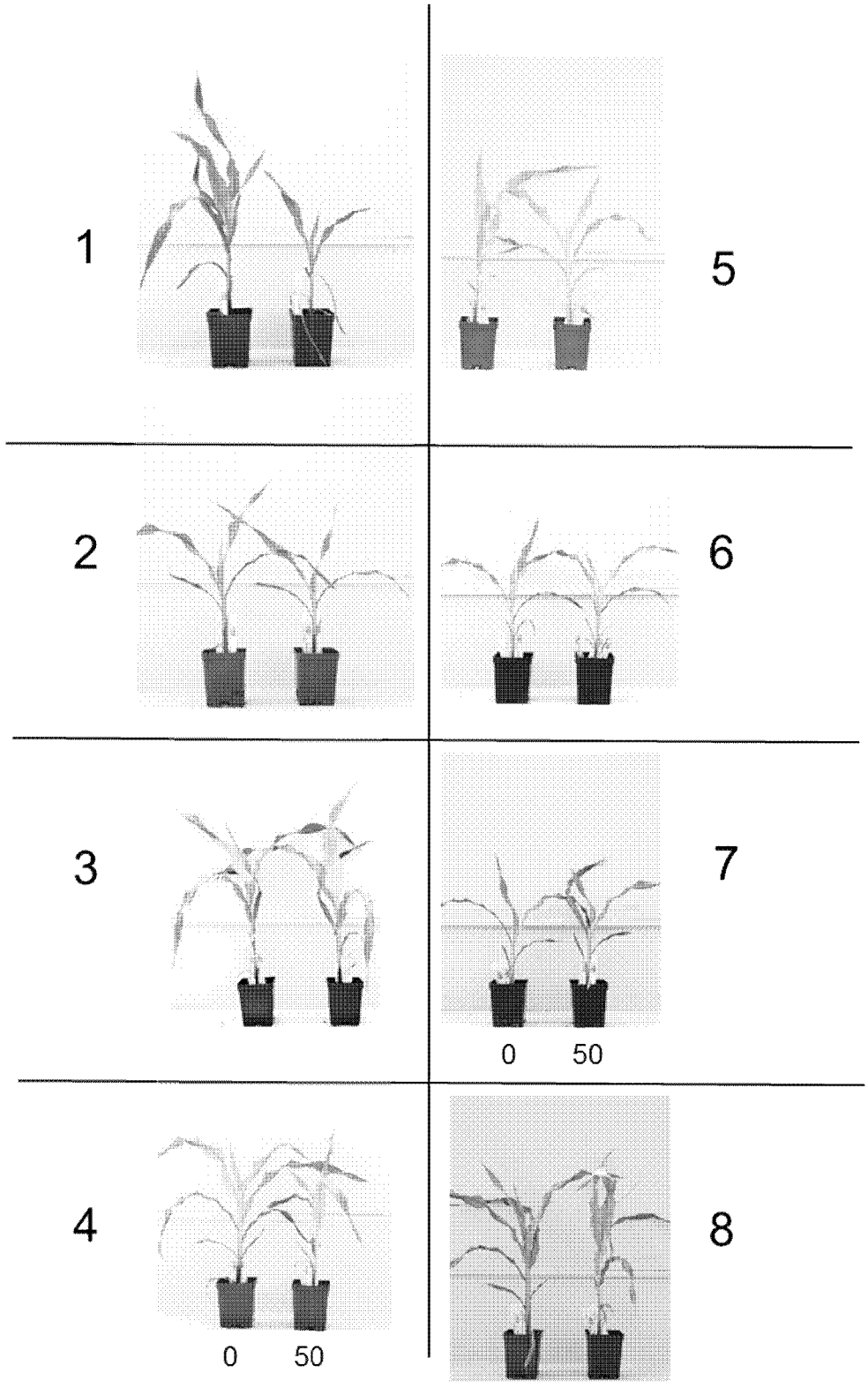


Figure 4

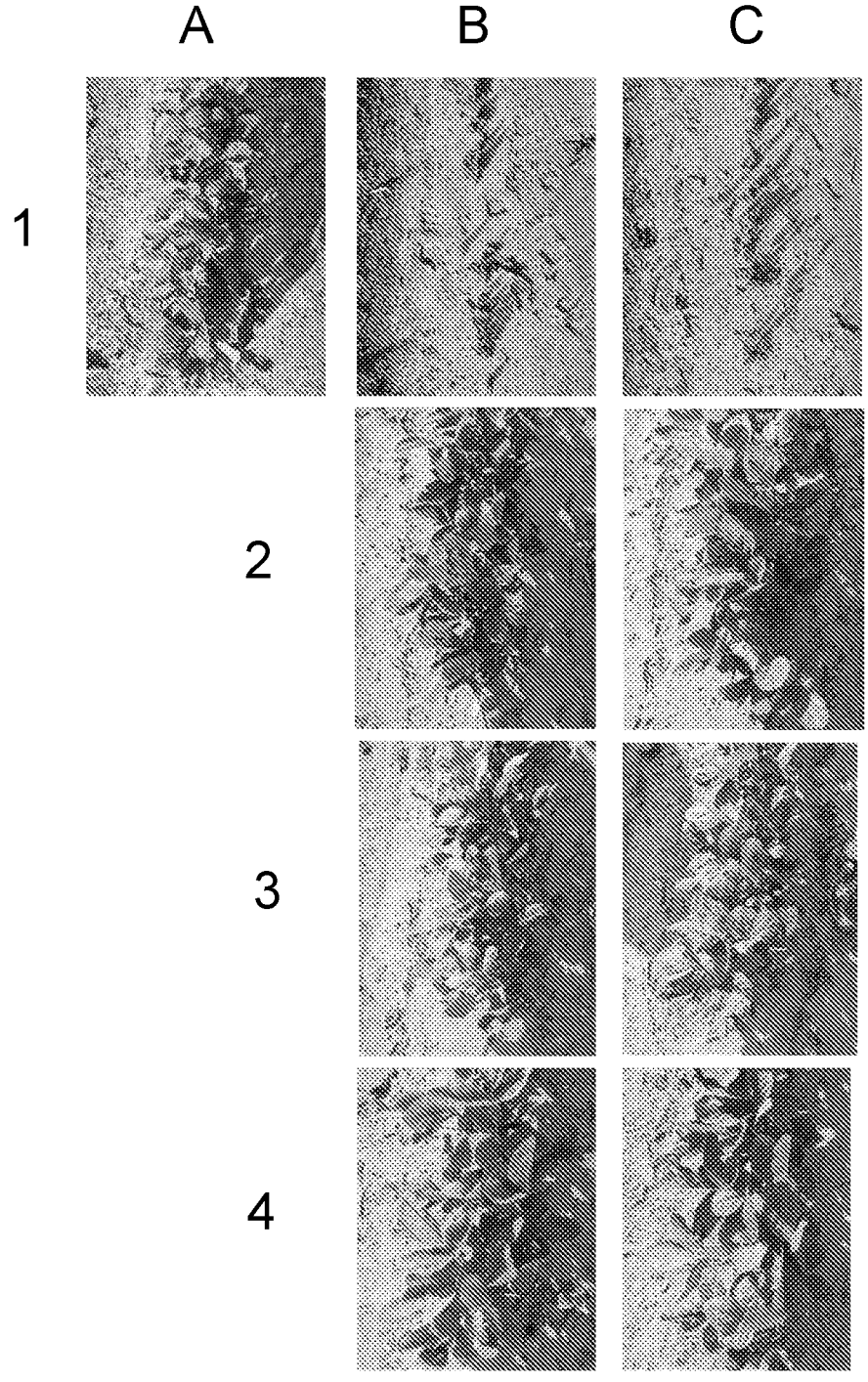


Figure 5

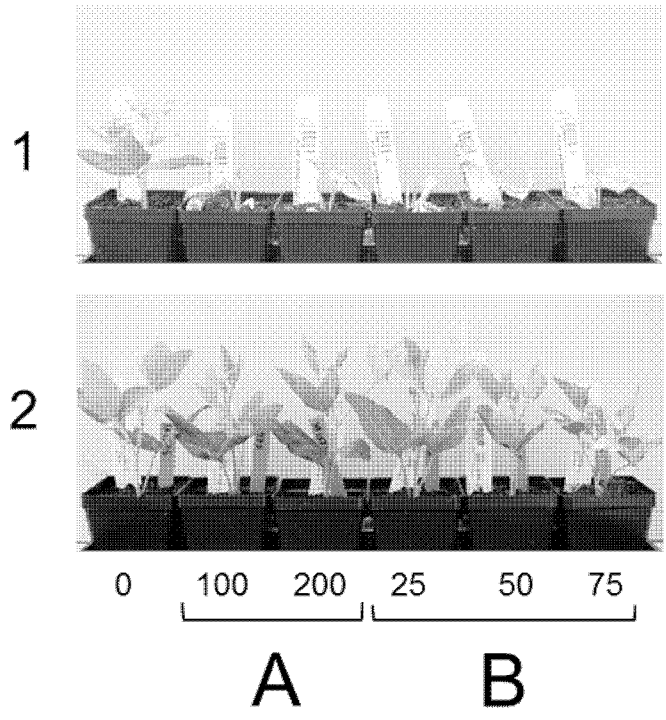


Figure 6

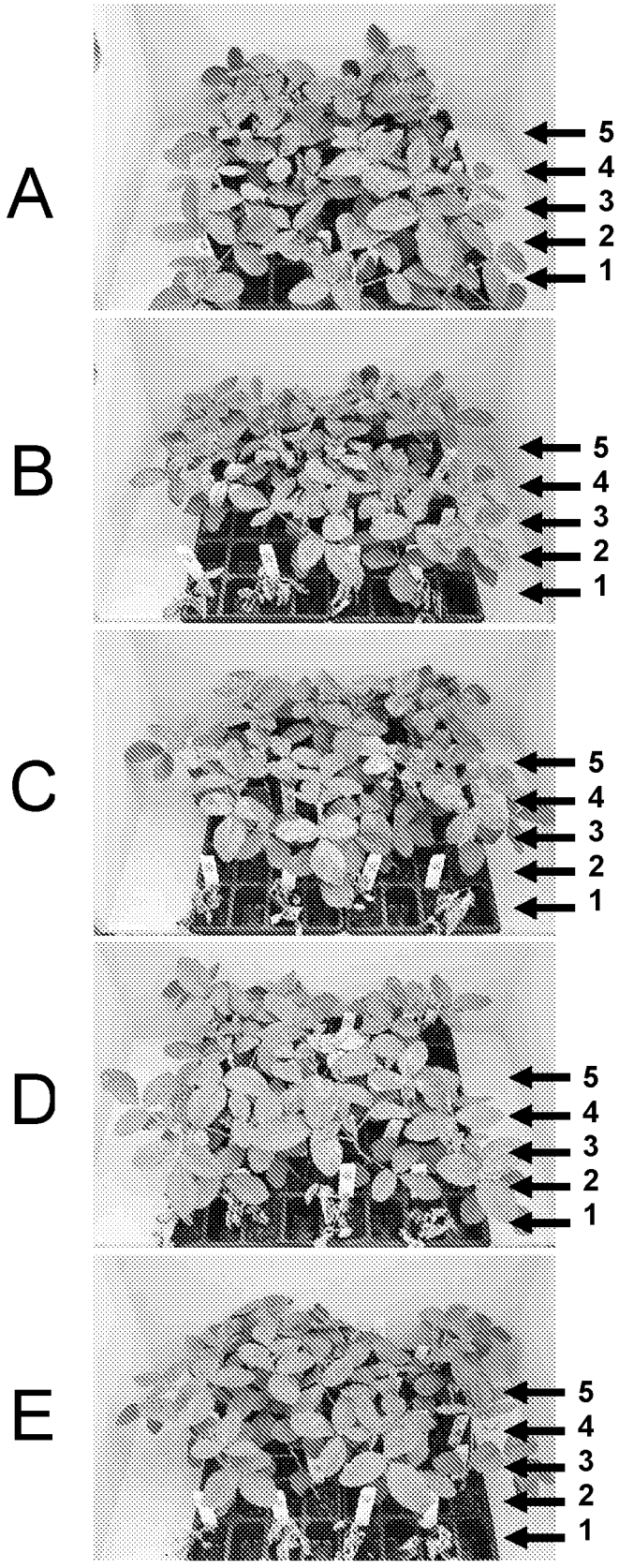


Figure 7