Office de la Propriété Intellectuelle du Canada
Un organisme d'Industrie Canada

Canadian Intellectual Property Office
An agency of Industry Canada

CA 2931549 A1 2015/06/04

(21) 2 931 549

(12) DEMANDE DE BREVET CANADIEN
CANADIAN PATENT APPLICATION

(13) A1

(86) **Date de dépôt PCT/PCT Filing Date:** 2014/11/25
(87) **Date publication PCT/PCT Publication Date:** 2015/06/04
(85) **Entrée phase nationale/National Entry:** 2016/05/25
(86) **N° demande PCT/PCT Application No.:** EP 2014/075454
(87) **N° publication PCT/PCT Publication No.:** 2015/078828
(30) **Priorité/Priority:** 2013/11/28 (EP13194780.6)

(51) **Cl.Int./Int.Cl.** ***A01N 43/713*** (2006.01), ***A01N 25/00*** (2006.01), ***A01N 43/70*** (2006.01), ***A01N 43/707*** (2006.01), ***A01N 57/20*** (2006.01), ***A01P 13/00*** (2006.01)

(71) **Demandeur/Applicant:**
BAYER CROPSCIENCE AKTIENGESELLSCHAFT, DE

(72) **Inventeurs/Inventors:**
POREE, FABIEN, DE;
WALDRAFF, CHRISTIAN, DE;
LABER, BERND, DE;
KOHN, ARNIM, DE;
GATZWEILER, ELMAR, DE;
TRABOLD, KLAUS, DE

(74) **Agent:** FETHERSTONHAUGH & CO.

(54) **Titre : UTILISATION DE 2-CHLORO-3-(METHYLSULFANYL)-N-(1-METHYL-1H-TETRAZOL-5-YL)-4-(TRIFLUOROMETHYL)BENZAMIDE OU DE SES SELS POUR LUTTER CONTRE LES PLANTES INDESIRABLES DANS DES ZONES DE CULTURE DE PLANTES TRANSGENIQUES TOLERANTES AUX HERBICIDES A BASE D'INHIBITEURS DE L'HPPD**

(54) **Title: USE OF 2-CHLORO-3-(METHYLSULFANYL)-N-(1-METHYL-1H-TETRAZOL-5-YL)-4-(TRIFLUOROMETHYL)BENZAMIDE OR ITS SALTS FOR CONTROLLING UNWANTED PLANTS IN AREAS OF TRANSGENIC CROP PLANTS BEINGTOLERANT TO HPPD INHIBITOR HERBICIDES**

(57) **Abrégé/Abstract:**
The use of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4- (thfluoromethyl)benzannide or its salts for controlling unwanted plants in areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides by containing one or more chimeric gene(s) comprising (I) a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, (b) Pseudomonas, (c) Synechococcoideae, (d) Blepharismidae, (e) Rhodococcus, (f) Picrophilaceae, (g) Kordia, or (II) one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably from Pseudomonas, or (III) one or more DNA sequences encoding mutated maize (Zea mays) or soybean (Glycine max) HPPD each being mutated as described in WO 2012/021785.

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
4 June 2015 (04.06.2015)

WIPO | PCT

(10) International Publication Number
WO 2015/078828 A3

(51) **International Patent Classification**:
A01N 43/713 (2006.01) *A01N 57/20* (2006.01)
A01N 25/00 (2006.01) *A01N 43/707* (2006.01)
A01N 43/70 (2006.01) *A01P 13/00* (2006.01)

(21) **International Application Number**:
PCT/EP2014/075454

(22) **International Filing Date**:
25 November 2014 (25.11.2014)

(25) **Filing Language**: English

(26) **Publication Language**: English

(30) **Priority Data**:
13194780.6 28 November 2013 (28.11.2013) EP

(71) **Applicant**: **BAYER CROPSCIENCE AG** [DE/DE]; Alfred-Nobel-Str. 50, 40789 Monheim am Rhein (DE).

(72) **Inventors**: **POREE, Fabien**; Dunantring 89, 65936 Frankfurt (DE). **WALDRAFF, Christian**; Franz-Lehar-Weg 7, 61118 Bad Vilbel (DE). **LABER, Bernd**; Graf-von-Stauffenberg-Str. 12, 65510 Idstein (DE). **KÖHN, Arnim**; Ringstr. 12, 55270 Klein-Winternheim (DE). **GATZ-WEILER, Elmar**; Am Nauheimer Bach 22, 61231 Bad Nauheim (DE).

(74) **Agents**: **BIP PATENTS** et al.; Bayer Intellectual Property GmbH, Alfred-Nobel-Str. 10, 40789 Monheim am Rhein (DE).

(81) **Designated States** *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) **Designated States** *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

— *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*

Published:

— *with international search report (Art. 21(3))*

— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*

— *with sequence listing part of description (Rule 5.2(a))*

(88) **Date of publication of the international search report**:
1 October 2015

WO 2015/078828 A3

(54) **Title**: USE OF 2-CHLORO-3-(METHYLSULFANYL)-N-(1-METHYL-1H-TETRAZOL-5-YL)-4-(TRIFLUOROMETHYL)BENZAMIDE OR ITS SALTS FOR CONTROLLING UNWANTED PLANTS IN AREAS OF TRANSGENIC CROP PLANTS BEING TOLERANT TO HPPD INHIBITOR HERBICIDES

(57) **Abstract**: The use of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4- (thfluoromethyl)benzannide or its salts for controlling unwanted plants in areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides by containing one or more chimeric gene(s) comprising (I) a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, (b) Pseudomonas, (c) Synechococcoideae, (d) Blepharismidae, (e) Rhodococcus, (f) Picrophilaceae, (g) Kordia, or (II) one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably from Pseudomonas, or (III) one or more DNA sequences encoding mutated maize (Zea mays) or soybean (Glycine max) HPPD each being mutated as described in WO 2012/021785.

Use of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts for controlling unwanted plants in areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides

Description

The invention relates to the use of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts or controlling unwanted plants in areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides.

WO 2012/028579 (PCT/EP2011/064820) discloses several new N-(tetrazol-5-yl)- or N-(triazol-3-yl)arylcarboxamides and their use as HPPD inhibitor herbicides for weed control and WO 2012/130685 (PCT/EP2012/054981) generically discloses the use of N-(tetrazol-5-yl)- or N-(triazol-3-yl)arylcarboxamides on transgenic plants and also named individual N-(tetrazol-5-yl)- or N-(triazol-3-yl)arylcarboxamides to be applied on certain transgenic plants.

HPPD inhibitor herbicides can be used against grass and/or broad leaf weeds in crop plants that display metabolic tolerance, such as maize (Zea mays) in which they are rapidly degraded (Schulz et al., (1993). FEBS letters, 318, 162-166; Mitchell et al., (2001) Pest Management Science, Vol 57, 120-128; Garcia et al., (2000) Biochem., 39, 7501-7507; Pallett et al., (2001) Pest Management Science, Vol 57, 133-142). In order to extend the scope of these HPPD inhibitor herbicides, several efforts have been developed in order to confer to plants, particularly plants without or with an underperforming metabolic tolerance, a tolerance level acceptable under agronomic field conditions.

Meanwhile transgenic plants have been engineered by by-passing HPPD-mediated production of homogentisate (US 6,812,010), overexpressing the sensitive enzyme so as to produce quantities of the target enzyme in the plant which are sufficient in relation to the herbicide has been performed (WO96/38567).

Alternatively, transgenic plants have been generated expressing HPPD proteins that have been mutated at various positions in order to obtain a target enzyme which, while retaining its properties of catalysing the transformation of HPP into homogentisate, is less sensitive to HPPD inhibitor herbicides than is the native HPPD before mutation (for example see at EP496630, WO 99/24585).

More recently, the introduction of a *Pseudomonas* HPPD gene into the plastid genome of tobacco and soybean has shown to be more effective than nuclear transformation, conferring even tolerance to post-emergence application of at least one HPPD inhibitor (Dufourmantel et al., 2007, Plant Biotechnol J.5(1):118-33).

In WO 2009/144079, a nucleic acid sequence encoding a mutated hydroxyphenylpyruvate dioxygenase (HPPD) at position 336 of the *Pseudomonas fluorescens* HPPD protein and its use for obtaining plants which are tolerant to HPPD inhibitor herbicides is disclosed.
Further mutants of the *Pseudomonas fluorescens* HPPD protein comprising mutations at various sites and their ability to confer restistance to certain HPPD inhibitor heribicides are described in the PCT application filed (on September 13, 2013) under the PCT application number PCT/US2013/59598 (WO2014/043435) and claiming priorities of US61/701,037 (filed on September 14, 2012), US 61/766,057 (filed on February 18, 2013), and US 61/790,404 (filed in March 15, 2013).
Some of these mutants, i.e. mutants of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435)), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435)), or (iii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435)) are hereby incorporated by reference concerning the production of the respective transgenic plants conferring tolerance to HPPD inhibitor herbicides under its abbreviations PfHPPDEvo33, PfHPPDEvo40, and PfHPPDEvo41, respectively.

In the before, the amino acid named first characterizes the amino acid being present in the wild-type *Pseudomonas fluorescens* HPPD protein and the character given in the brackets identifies the respective amino acid in the 3 letter code, whereas the character given in front of the brackets identifies the respective amino acid in the 1 letter code.

In WO 04/024928, the inventors have sought to increase the prenylquinone biosynthesis (e.g., synthesis of plastoquinones, tocopherols) in the cells of plants by increasing the flux of the HPP precursor into the cells of these plants. This has been done by connecting the synthesis of said precursor to the "shikimate" pathway by overexpression of the prephenate-dehydrogenase (PDH). They have also noted that the transformation of plants with a gene encoding a PDH enzyme makes it possible to increase the tolerance of said plants to HPPD inhibitors.

In WO 2002/046387, an gene obtained from Avena sativa encoding an HPPD was described to generate plants overexpressing such gene and thereby causing tolerance to various HPPD-inhobitor herbicides

In WO 2008/150473, the combination of two distinct tolerance mechanisms – a modified *Avena sativa* gene coding for a mutant HPPD enzyme and a CYP450 Maize monooxygenase (nsf1 gene) – was exemplified in order to obtain an improved tolerance to HPPD inhibitor herbicides, but no data have been disclosed demonstrating the synergistic effects based on the combination of both proteins.

In WO 2010/085705, several mutants of the Avena sativa HPPD were described as well as plants comprising genes encoding such mutated HPPD and thereby causing an increased tolerance to various HPPD-inhibitor herbicides compared to non-mutated HPPD.

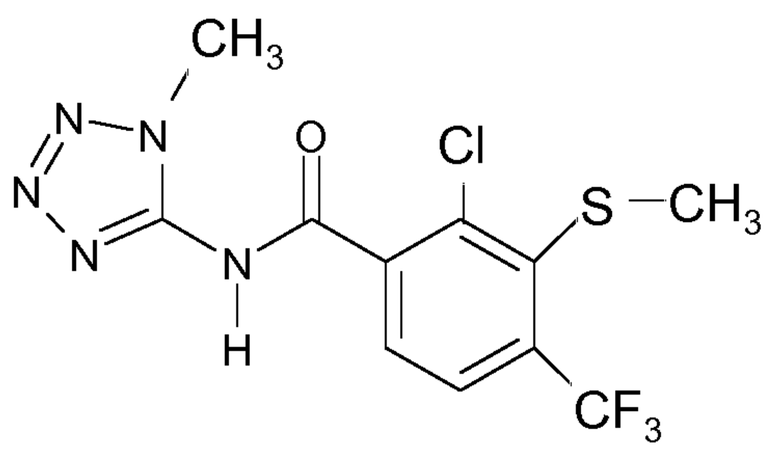
In WO 2012/021785, several mutants along HPPD proteins of various organisms, preferably HPPD obtained from maize were described. Data were obtained from such mutated HPPD enzymes *in vitro* as well as from plants comprising genes encoding such mutated HPPD and thereby causing an increased tolerance to various HPPD-inhibitor herbicides compared to non-mutated HPPD.

Recently, several new genes encoding HPPD enzymes from various organisms have been identified and employed for obtaining crop plants that show an agronomically useful level of tolerance concerning the application of various HPPD inhibitor herbicides, like such (i) obtained form bacteria belonging to the subfamily Synechococcoideae and certain mutants thereof as disclosed in WO2011/076877(PCT/EP2010/070561), (ii) obtained from protists belonging to the family Blepharismidae as disclosed in WO2011/076882 (PCT/EP2010/070567); (iii) obtained from bacteria belonging to the genus Rhodococcus and certain mutants thereof as disclosed in WO2011/076892 (PCT/EP2010/070578); (iv) obtained from Euryarchaeota belonging to the family Picrophilaceae and certain mutants thereof as disclosed in WO2011/076885 (PCT/EP2010/070570); or (v)obtained from bacteria belonging to the genus Kordia and certain mutants thereof disclosed as in WO2011/076889 (PCT/EP2010/070575) and which are hereby incorporated by reference concerning the production of the respective transgenic plants conferring tolerance to HPPD inhibitor herbicides.

It has now been found that a specific N-(tetrazol-5-yl)arylcarboxamide, i.e. the 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or salts thereof can be employed on transgenic crop plants being tolerant to HPPD inhibitor herbicides by containing one or more genes conferring tolerance to HPPD inhibitor herbicides.

Subject matter of the present invention is the use of the 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide,

as also described by below formula (I)



(I)

or its salts

for controlling unwanted plants in areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides by containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), especially preferable HPPD encoding genes from maize (Zea mays) or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the *Pseudomonas fluorescens* HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598(WO2014/043435) and being disclosed in present application under SEQ ID No. 25), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under

SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 27), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 29), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the *Pseudomonas (=Comamonas) testosteroni* HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the *Pseudomonas aeruginosa* strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in

PCT/US2013/59598(WO2014/043435) , and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)-benzamide to be used according to the invention can be prepared as described in detail in WO 2012/028579 which is hereby incorporated by reference.

As it relates to the salts of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide, preferably a sodium, potassium, magnesium, calcium, ammonium, $(C_1$-$C_4)$-alkylammonium, di-$(C_1$-C_4-alkyl)ammonium, tri-$(C_1$-C_4-alkyl)ammonium, tetra-$(C_1$-C_4-alkyl)ammonium, tri-$(C_1$-C_4-alkyl)sulphonium, $(C_5$- or $C_6)$-cycloalkylammonium, or di-$(C_1$-C_2-alkyl)benzylammonium salt, more preferably a sodium, potassium, magnesium, calcium, ammonium salt, even more preferably a sodium, potassium, magnesium, calcium, ammonium salt, and very particularly a sodium, potassium, or ammonium salt is meant.

As already disclosed in WO 2012/028579, N-(tetrazol-5-yl) arylcarboxamides on transgenic plants and also named individual N-(tetrazol-5-yl) arylcarboxamides generically covering 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide to be used according to the invention and its salts, have excellent herbicidal efficacy against a broad spectrum of economically important monocotyledonous and dicotyledonous annual harmful plants. The active compounds act efficiently even on perennial weeds which produce shoots from rhizomes, rootstocks and other perennial organs and which are difficult to control.

The present invention therefore relates to a method for controlling unwanted plants, in areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides by containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably

comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435) , more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and

being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (Comamonas) testeroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and

being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37) comprising the application of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts as defined above to the plants (for example harmful plants such as monocotyledonous or dicotyledonous weeds or undesired crop plants), to the seed (for example grains, seeds or vegetative propagules such as tubers or shoot parts with buds) or to the area on which the plants grow (for example the area under cultivation). Specific examples may be mentioned of some representatives of the monocotyledonous and dicotyledonous weed flora which can be controlled by the compounds according to the invention, without the enumeration being restricted to certain species.

Monocotyledonous harmful plants of the genera: Aegilops, Agropyron, Agrostis, Alopecurus, Apera, Avena, Brachiaria, Bromus, Cenchrus, Commelina, Cynodon, Cyperus, Dactyloctenium, Digitaria, Echinochloa, Eleocharis, Eleusine, Eragrostis, Eriochloa, Festuca, Fimbristylis, Heteranthera, Imperata, Ischaemum, Leptochloa, Lolium, Monochoria, Panicum, Paspalum, Phalaris, Phleum, Poa, Rottboellia, Sagittaria, Scirpus, Setaria, Sorghum.

Dicotyledonous weeds of the genera: Abutilon, Amaranthus, Ambrosia, Anoda, Anthemis, Aphanes, Artemisia, Atriplex, Bellis, Bidens, Capsella, Carduus, Cassia, Centaurea, Chenopodium, Cirsium, Convolvulus, Datura, Desmodium, Emex, Erysimum, Euphorbia, Galeopsis, Galinsoga, Galium, Hibiscus, Ipomoea, Kochia, Lamium, Lepidium, Lindernia, Matricaria, Mentha, Mercurialis, Mullugo, Myosotis, Papaver, Pharbitis, Plantago, Polygonum, Portulaca, Ranunculus, Raphanus, Rorippa, Rotala, Rumex, Salsola, Senecio, Sesbania, Sida, Sinapis, Solanum, Sonchus, Sphenoclea, Stellaria, Taraxacum, Thlaspi, Trifolium, Urtica, Veronica, Viola, Xanthium.

Trangenic crop plants of economically important crops to which the 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts might be applied are, for example dicotyledonous crops of the genera Arachis, Beta, Brassica, Cucumis, Cucurbita, Helianthus, Daucus, Glycine, Gossypium, Ipomoea, Lactuca, Linum, Lycopersicon, Nicotiana, Phaseolus, Pisum, Solanum, Vicia, or monocotyledonous crops of the genera Allium, Ananas, Asparagus, Avena, Hordeum,

Oryza, Panicum, Saccharum, Secale, Sorghum, Triticale, Triticum, Zea, in particular Zea and Triticum.

This is why the present invention preferably relates to the method for controlling unwanted plants, in areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides by containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E

(Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu)

-> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37) comprising the application of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts to the plants (for example harmful plants such as monocotyledonous or dicotyledonous weeds or undesired crop plants), to the seed (for example grains, seeds or vegetative propagules such as tubers or shoot parts with buds) or to the area on which the plants grow (for example the area under cultivation) in dicotyledonous crops of the genera Arachis, Beta, Brassica, Cucumis, Cucurbita, Helianthus, Daucus, Glycine, Gossypium, Ipomoea, Lactuca, Linum, Lycopersicon, Nicotiana, Phaseolus, Pisum, Solanum, Vicia, or monocotyledonous crops of the genera Allium, Ananas, Asparagus, Avena, Hordeum, Oryza, Panicum, Saccharum, Secale, Sorghum, Triticale, Triticum, Zea, in particular Zea and Triticum.

It is preferred to use the 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts in economically important transgenic crops of useful plants and ornamentals, for example of cereals such as wheat, barley, rye, oats, sorghum/millet, rice, cassava and maize or else crops of sugar beet, sugar cane, cotton, soybean, oilseed rape, potato, tomato, peas and other vegetables, which crops contain one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma

japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at

position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

The invention also relates to the use, in a method for transforming plants, of a nucleic acid which encodes an HPPD as a marker gene or as a coding sequence which makes

it possible to confer to the plant tolerance to herbicides which are HPPD inhibitors, and the use of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts on plants containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named

PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40

and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

In the commercial production of crops, it is desirable to eliminate under reliable pesticidial management unwanted plants (i.e.,"weeds") from a field of crop plants. An ideal treatment would be one which could be applied to an entire field but which would eliminate only the unwanted plants while leaving the crop plants unaffected. One such treatment system would involve the use of crop plants which are tolerant to an herbicide so that when the herbicide is sprayed on a field of herbicide-tolerant crop plants, the crop plants would continue to thrive while non-herbicide-tolerant weeds are killed or severely damaged. Ideally, such treatment systems would take advantage of varying herbicide properties so that weed control could provide the best possible combination of flexibility and economy. For example, individual herbicides have different longevities in the field, and some herbicides persist and are effective for a relatively long time after they are applied to a field while other herbicides are quickly broken down into other and/or non-active compounds. An ideal treatment system would allow the use of different herbicides so that growers could tailor the choice of herbicides for a particular situation.

While a number of herbicide-tolerant crop plants are presently commercially available, one issue that has arisen for many commercial herbicides and herbicide/crop combinations is that individual herbicides typically have incomplete spectrum of activity against common weed species. For most individual herbicides which have been in use for some time, populations of herbicide resistant weed species and biotypes have become more prevalent (see, e.g., Tranel and Wright (2002) *Weed Science* 50: 700-712; Owen and Zelaya *(2005) Pest Manag. Sci.* 61: 301-311). Transgenic plants which are resistant to more than one herbicide have been described (see, e.g., W02005/012515). However, improvements in every aspect of crop production, weed

control options, extension of residual weed control, and improvement in crop yield are continuously in demand.

The above defined chimeric gene(s) encoding one or more HPPD protein(s) or mutants thereof being functional in transgenic plants in order to perform tolerance to the HPPD inhibitor 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts is/are advantageously combined in plants with other genes which encode proteins or RNAs that confer useful agronomic properties to such plants. Among the genes which encode proteins or RNAs that confer useful agronomic properties on the transformed plants, mention can be made of the DNA sequences encoding proteins which confer tolerance to one or more herbicides that, according to their chemical structure, differ from HPPD inhibitor herbicides, and others which confer tolerance to certain insects, those which confer tolerance to certain diseases and or biotic and abiotic stresses, DNAs that encodes RNAs that provide nematode or insect control, etc..
Such genes are in particular described in published PCT Patent Applications WO 91/02071 and WO95/06128.

Among the DNA sequences encoding proteins which confer tolerance to certain herbicides on the transformed plant cells and plants, mention can be made of a bar or PAT gene or the *Streptomyces coelicolor* gene described in WO2009/152359 which confers tolerance to glufosinate herbicides, a gene encoding a suitable EPSPS which confers tolerance to herbicides having EPSPS as a target, such as glyphosate and its salts (US 4,535,060, US 4,769,061, US 5,094,945, US 4,940,835, US 5,188,642, US 4,971,908, US 5,145,783, US 5,310,667, US 5,312,910, US 5,627,061, US 5,633,435), or a gene encoding glyphosate oxydoreductase (US 5,463,175).

Among the DNA sequences encoding a suitable EPSPS which confer tolerance to the herbicides which have EPSPS as a target, mention will more particularly be made of the gene which encodes a plant EPSPS, in particular maize EPSPS, particularly a maize EPSPS which comprises two mutations, particularly a mutation at amino acid position 102 and a mutation at amino acid position 106 (WO 2004/074443), and which is described in Patent Application US 6566587, hereinafter named double mutant maize EPSPS or 2mEPSPS, or the gene which encodes an EPSPS isolated from

Agrobacterium and which is described by SEQ ID No. 2 and SEQ ID No. 3 of US Patent 5,633,435, also named CP4.

Among the DNA sequences encoding a suitable EPSPS which confer tolerance to the herbicides which have EPSPS as a target, mention will more particularly be made of the gene which encodes an EPSPS GRG23 from Arthrobacter globiformis, but also the mutants GRG23 ACE1, GRG23 ACE2, or GRG23 ACE3, particularly the mutants or variants of GRG23 as described in WO2008/100353, such as GRG23(ace3)R173K of SEQ ID No. 29 in WO2008/100353.

In the case of the DNA sequences encoding EPSPS, and more particularly encoding the above genes, the sequence encoding these enzymes is advantageously preceded by a sequence encoding a transit peptide, in particular the “optimized transit peptide” described in US Patent 5,510,471 or 5,633,448.

In WO 2007/024782, plants being tolerant to glyphosate and at least one ALS (acetolactate synthase) inhibitor are disclosed. More specifically plants containing genes encoding a GAT (Glyphosate-N-Acetyltransferase) polypeptide and a polypeptide conferring resistance to ALS inhibitors are disclosed.

In US 6855533, transgenic tobacco plants containing mutated Arabidopsis ALS/AHAS genes were disclosed.

In US 6,153,401, plants containing genes encoding 2,4-D-monooxygenases conferring tolerance to 2,4-D (2,4-dichlorophenoxyacetic acid) by metabolisation are disclosed.

In US7838733, WO2005/107437, WO2007/053482, WO2008/141154, and US2010/0251432 plants containing genes encoding 2,4-D-dioxygenases conferring tolerance to 2,4-D (2,4-dichlorophenoxyacetic acid), other phenoxy auxin herbicides and aryloxyphenoxypropionate herbicides by metabolisation are disclosed.

In US 2008/0119361 and US 2008/0120739, plants containing genes encoding Dicamba monooxygenases conferring tolerance to dicamba (3,6-dichloro-2-methoxybenzoic acid) by metabolisation are disclosed.

In WO2011/028833 and WO2011/028832 plants containing genes encoding mutagenized or recombinant Acetyl-coenzyme-A carboylase (ACCase) conferring

tolerance to at least one herbicide is selected from the group consisting of alloxydim, butroxydim, clethodim, cloproxydim, cycloxydim, sethoxydim, tepraloxydim, tralkoxydim, chlorazifop, clodinafop, clofop, diclofop, fenoxaprop, fenoxaprop-P, fenthiaprop, fluazifop, fluazifop-P, haloxyfop, haloxyfop-P, isoxapyrifop, propaquizafop, quizalofop, quizalofop-P, trifop, and pinoxaden or agronomically acceptable salts or esters of any ofthese herbicides are disclosed.

All the above mentioned herbicide tolerance traits can be combined with those performing HPPD tolerance in plants concerning 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts by containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or

(III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435) , and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K

(Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

Among the DNA sequences encoding proteins concerning properties of tolerance to insects, mention will more particularly be made of the Bt proteins widely described in the literature and well known to those skilled in the art. Mention will also be made of proteins extracted from bacteria such as *Photorhabdus* (WO 97/17432 & WO 98/08932).

Among such DNA sequences encoding proteins of interest which confer novel properties of tolerance to insects, mention will more particularly be made of the Bt Cry or VIP proteins widely described in the literature and well known to those skilled in the art. These include the Cry1F protein or hybrids derived from a Cry1F protein (e.g., the hybrid Cry1A-Cry1F proteins described in US 6,326,169; US 6,281,016; US 6,218,188, or toxic fragments thereof), the Cry1A-type proteins or toxic fragments thereof, preferably the Cry1Ac protein or hybrids derived from the Cry1Ac protein (e.g., the hybrid Cry1Ab-Cry1Ac protein described in US 5,880,275) or the Cry1Ab or Bt2 protein or insecticidal fragments thereof as described in EP451878, the Cry2Ae, Cry2Af or Cry2Ag proteins as described in WO02/057664 or toxic fragments thereof, the Cry1A.105 protein described in WO 2007/140256 (SEQ ID No. 7) or a toxic fragment thereof, the VIP3Aa19 protein of NCBI accession ABG20428, the VIP3Aa20 protein of NCBI accession ABG20429 (SEQ ID No. 2 in WO 2007/142840), the VIP3A proteins

produced in the COT202 or COT203 cotton events (WO 2005/054479 and WO 2005/054480, respectively), the Cry proteins as described in WO01/47952, the VIP3Aa protein or a toxic fragment thereof as described in Estruch et al. (1996), Proc Natl Acad Sci U S A. 28;93(11):5389-94 and US 6,291,156, the insecticidal proteins from *Xenorhabdus* (as described in WO98/50427), *Serratia* (particularly from *S. entomophila*) or *Photorhabdus* species strains, such as Tc-proteins from Photorhabdus as described in WO98/08932 (e.g., Waterfield et al., 2001, Appl Environ Microbiol. 67(11):5017-24; Ffrench-Constant and Bowen, 2000, Cell Mol Life Sci.; 57(5):828-33). Also any variants or mutants of any one of these proteins differing in some (1-10, preferably 1-5) amino acids from any of the above sequences, particularly the sequence of their toxic fragment, or which are fused to a transit peptide, such as a plastid transit peptide, or another protein or peptide, is included herein.

The present invention also relates to the use of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts in transgenic plants comprising a chimeric gene (or expression cassette) which comprises a coding sequence as well as heterologous regulatory elements, at the 5' and/or 3' position, at least at the 5' position, which are able to function in a host organism, in particular plant cells or plants, with the coding sequence containing at least one nucleic acid sequence which encodes an HPPD derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably

comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598

(WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

In another particular embodiment, the present invention relates to the use of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts in transgenic plant comprising a chimeric gene as previously described, wherein the chimeric gene contains in the 5' position of the nucleic acid sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) (I) derived from a member of a group of organisms, consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding

HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G

(Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37) a nucleic acid sequence which encodes a plant transit peptide, with this sequence being arranged between the promoter region and the nucleic acid sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) (I) derived from a member of a

group of organisms, consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339

and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339

and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37) so as to permit expression of a transit peptide/HPPD fusion protein.

In a further particular embodiment, the present invention relates to the use of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts on plants, plant parts, or plant seeds containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position

335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as

the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37) or to the use of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)-benzamide or its salts on soil where such plants, plant parts or seeds are to be grown or sown, either alone or in combination with one or more other known herbicides acting in a different matter to HPPD inhibitors.

In a further particular embodiment, 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts can applied in combination either in mixture, simultaneously or successively with HPPD inhibitor herbicides selected from the group consisting of triketones (named triketone HPPD inhibitor), such as tembotrione, sulcotrione, mesotrione, bicyclopyrone, tefuryltrione, particularly tembotrione, of the class diketone such as diketonitrile of the class of isoxazoles such as isoxaflutole or of the class of pyrazolinates (named pyrazolinate HPPD inhibitor), such as pyrasulfotole, pyrazolate, topramezone, benzofenap, even more specifically present invention relates to the application of tembotrione, mesotrione, diketonitrile, bicyclopyrone, tefuryltrione, benzofenap, pyrasulfotole, pyrazolate and sulcotrione to such HPPD inhibitor tolerant plants, plant parts or plant seeds containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more

preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a

mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and

being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

As a regulatory sequence which functions as a promoter in plant cells and plants, use may be made of any promoter sequence of a gene which is naturally expressed in plants, in particular a promoter which is expressed especially in the leaves of plants, such as for example “constitutive” promoters of bacterial, viral or plant origin, or “light-dependent” promoters, such as that of a plant ribulose-biscarboxylase/oxygenase (RuBisCO) small subunit gene, or any suitable known promoter-expressible which may be used. Among the promoters of plant origin, mention will be made of the histone promoters as described in EP 0 507 698 A1, the rice actin promoter (US 5,641,876), or a plant ubiquitin promoter (US 5,510,474). Among the promoters of a plant virus gene, mention will be made of that of the cauliflower mosaic virus (CaMV 19S or 35S, Sanders et al. (1987), Nucleic Acids Res. 15(4):1543-58.), the circovirus (AU 689 311) or the Cassava vein mosaic virus (CsVMV, US 7,053,205).

In a further particular embodiment, present invention relates to the use of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts on plants, plant parts, or plant seeds comprising a promoter sequence specific for particular regions or tissues of plants can be used to express one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably

comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as

the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), such as promoters specific for seeds (Datla, R. et al., 1997, Biotechnology Ann. Rev. 3, 269-296), especially the napin promoter (EP 255 378 A1), the phaseolin promoter, the glutenin promoter, the helianthinin promoter (WO 92/17580), the albumin promoter (WO 98/45460), the oleosin promoter (WO 98/45461), the SAT1 promoter or the SAT3 promoter (PCT/US98/06978).

Use may also be made of an inducible promoter advantageously chosen from the phenylalanine ammonia lyase (PAL), HMG-CoA reductase (HMG), chitinase, glucanase, proteinase inhibitor (PI), PR1 family gene, nopaline synthase (nos) and vspB promoters (US 5 670 349, Table 3), the HMG2 promoter (US 5 670 349), the

apple beta-galactosidase (ABG1) promoter and the apple aminocyclopropane carboxylate synthase (ACC synthase) promoter (WO 98/45445).

The genes encoding hydroxyphenylpyruvate dioxygenase (HPPD) (I) derived from a member of a group of organisms, consisting of one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E

(Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu)

-> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37) may also be used in combination with the promoter, of other regulatory sequences, which are located between the promoter and the coding sequence, such as transcription activators ("enhancers"), for instance the translation activator of the tobacco mosaic virus (TMV) described in Application WO 87/07644, or of the tobacco etch virus (TEV) described by Carrington & Freed 1990, J. Virol. 64: 1590-1597, for example, or introns such as the adh1 intron of maize or intron 1 of rice actin in order to perform a sufficient tolerance to 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)-benzamide or its salts.

In a further particular embodiment, the present invention relates to the use of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts on plants, plant parts, or plant seeds containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f)

Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in

PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), and also containing a CYP450 Maize monooxygenase (nsf1 gene) gene being under the control of an identical or different plant expressible promoter in order to confer tolerance to 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts.

As a regulatory terminator or polyadenylation sequence, use may be made of any corresponding sequence of bacterial origin, such as for example the nos terminator of *Agrobacterium tumefaciens*, of viral origin, such as for example the CaMV 35S terminator, or of plant origin, such as for example a histone terminator as described in published Patent Application EP 0 633 317 A1.

It is to be understood that in order to obtain an optimized expression by a host adapted codon usage of the respective chimeric gene(s), one could adopt non-planta genes to the codon usage of the respective plant organism in which such chimeric genes will be inserted. Accordingly, in all of the described chimeric genes expressing HPPD of non-planta origin, the respective HPPD encocing DNA sequence can be replaced by an amended DNA sequence encoding the identical amino acid sequence, i.e. SEQ ID No. 3 can be replaced by SEQ ID No. 5, SEQ ID No. 6 can be replaced by SEQ ID No. 18, SEQ ID No. 8 can be replaced by SEQ ID No. 19, SEQ ID No. 10 can be replaced by SEQ ID No. 20, SEQ ID No. 12 can be replaced by SEQ ID No. 21, SEQ ID No. 14 can be replaced by SEQ ID No. 22, SEQ ID No, 16 can be replaced by SEQ ID No.23.

The term "gene", as used herein refers to a DNA coding region flanked by 5' and/or 3' regulatory sequences allowing a RNA to be transcribed which can be translated to a protein, typically comprising at least a promoter region. A "chimeric gene", when referring to an HPPD encoding DNA, refers to an HPPD encoding DNA sequence having 5' and/or 3' regulatory sequences different from the naturally occurring bacterial 5' and/or 3' regulatory sequences which drive the expression of the HPPD protein in its native host cell (also referred to as “heterologous promoter” or “heterologous regulatory sequences”).

The terms “DNA/protein comprising the sequence X” and "DNA/protein with the sequence comprising sequence X", as used herein, refer to a DNA or protein including or containing at least the sequence X in their nucleotide or amino acid sequence, so that other nucleotide or amino acid sequences can be included at the 5’ (or N-terminal) and/or 3’ (or C-terminal) end, e.g., a N-terminal transit or signal peptide. The term "comprising", as used herein, is open-ended language in the meaning of "including", meaning that other elements then those specifically recited can also be present. The term "consisting of", as used herein, is closed-ended language, i.e., only those elements specifically recited are present. The term “DNA encoding a protein comprising sequence X”, as used herein, refers to a DNA comprising a coding sequence which after transcription and translation results in a protein containing at least amino acid sequence X. A DNA encoding a protein need not be a naturally occurring DNA, and can be a semi-synthetic, fully synthetic or artificial DNA and can include introns and 5’ and/or 3’ flanking regions. The term “nucleotide sequence”, as

used herein, refers to the sequence of a DNA or RNA molecule, which can be in single- or double-stranded form.

HPPD proteins according to the invention may be equipped with a signal peptide according to procedures known in the art, see, e.g., published PCT patent application WO 96/10083, or they can be replaced by another peptide such as a chloroplast transit peptide (e.g., Van Den Broeck et al., 1985, Nature 313, 358, or a modified chloroplast transit peptide of US patent 5, 510,471) causing transport of the protein to the chloroplasts, by a secretory signal peptide or a peptide targeting the protein to other plastids, mitochondria, the ER, or another organelle, or it can be replaced by a methionine amino acid or by a methionine-alanine dipeptide. Signal sequences for targeting to intracellular organelles or for secretion outside the plant cell or to the cell wall are found in naturally targeted or secreted proteins, preferably those described by Klösgen et al. (1989, Mol. Gen. Genet. 217, 155-161), Klösgen and Weil (1991, Mol. Gen. Genet. 225, 297-304), Neuhaus & Rogers (1998, Plant Mol. Biol. 38, 127-144), Bih et al. (1999, J. Biol. Chem. 274, 22884-22894), Morris et al. (1999, Biochem. Biophys. Res. Commun. 255, 328-333), Hesse et al. (1989, EMBO J. 8 2453-2461), Tavladoraki et al. (1998, FEBS Lett. 426, 62-66), Terashima et al. (1999, Appl. Microbiol. Biotechnol. 52, 516-523), Park et al. (1997, J. Biol. Chem. 272, 6876-6881), Shcherban et al. (1995, Proc. Natl. Acad. Sci USA 92, 9245-9249), all of which are incorporated herein by reference, particularly the signal peptide sequences from targeted or secreted proteins of corn, cotton, soybean, or rice. A DNA sequence encoding such a plant signal peptide can be inserted in the chimeric gene encoding the HPPD protein for expression in plants.

The invention also encompasses variant HPPD enzymes which are amino acid sequences similar to the HPPD amino acid sequence of SEQ ID No. 2, SEQ ID No. ID No. 4, SEQ ID No. 7, SEQ ID No. 9, SEQ ID No. 11, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17, SEQ ID No. 25; SEQ ID No. 27, SEQ ID No.29, SEQ ID No 31, SEQ ID No 32, SEQ ID No 33, SEQ ID No 35, SEQ ID No 36, SEQ ID No 37, SEQ ID No 39, SEQ ID No 40, and SEQ ID No 41, SEQ ID No 43, SEQ ID No 46 and wherein in each of the before one or more amino acids have been inserted, deleted or substituted. In the present context, variants of an amino acid sequence refer to those polypeptides, enzymes or proteins which have a similar catalytic activity as the amino acid sequences described herein, notwithstanding any amino acid

substitutions, additions or deletions thereto. Preferably the variant amino acid sequence has a sequence identity of at least about 80%, or 85 or 90%, 95%, 97%, 98% or 99% with the amino acid sequence ofSEQ ID No. 2, SEQ ID No. ID No. 4, SEQ ID No. 7, SEQ ID No. 9, SEQ ID No. 11, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17, SEQ ID No. 25, SEQ ID No. 27, SEQ ID No 29, SEQ ID No 31, SEQ ID No 32, SEQ ID No 33, SEQ ID No 35, SEQ ID No 36, SEQ ID No 37, SEQ ID No 39, SEQ ID No 40, and SEQ ID No 41, SEQ ID No 43, and SEQ ID No 46, respectively . Also preferably, a polypeptide comprising the variant amino acid sequence has HPPD enzymatic activity. Methods to determine HPPD enzymatic activity are well known in the art and include assays as extensively described in WO 2009/144079 or in WO 2002/046387, or in PCT/EP2010/070561.

Substitutions encompass amino acid alterations in which an amino acid is replaced with a different naturally-occurring or a non-conventional amino acid residue. Such substitutions may be classified as "conservative', in which an amino acid residue contained in an HPPD protein of this invention is replaced with another naturally-occurring amino acid of similar character, for example Gly↔Ala, Val↔Ile↔Leu, Asp↔Glu, Lys↔Arg, Asn↔Gln or Phe↔Trp↔Tyr. Substitutions encompassed by the present invention may also be "non-conservative", in which an amino acid residue which is present in an HPPD protein of the invention is substituted with an amino acid with different properties, such as a naturally-occurring amino acid from a different group (e.g. substituting a charged or hydrophobic amino acid with alanine. Amino acid substitutions are typically of single residues, but may be of multiple residues, either clustered or dispersed. Amino acid deletions will usually be of the order of about 1-10 amino acid residues, while insertions may be of any length. Deletions and insertions may be made to the N-terminus, the C-terminus or be internal deletions or insertions. Generally, insertions within the amino acid sequence will be smaller than amino- or carboxy-terminal fusions and of the order of 1 to 4 amino acid residues. “Similar amino acids”, as used herein, refers to amino acids that have similar amino acid side chains, i.e. amino acids that have polar, non-polar or practically neutral side chains. “Non-similar amino acids”, as used herein, refers to amino acids that have different amino acid side chains, for example an amino acid with a polar side chain is non-similar to an amino acid with a non-polar side chain. Polar side chains usually tend to be present on the surface of a protein where they can interact with the aqueous environment found in cells (“hydrophilic” amino acids). On the other hand, “non-polar” amino acids tend to

reside within the center of the protein where they can interact with similar non-polar neighbours ("hydrophobic" amino acids"). Examples of amino acids that have polar side chains are arginine, asparagine, aspartate, cysteine, glutamine, glutamate, histidine, lysine, serine, and threonine (all hydrophilic, except for cysteine which is hydrophobic). Examples of amino acids that have non-polar side chains are alanine, glycine, isoleucine, leucine, methionine, phenylalanine, proline, and tryptophan (all hydrophobic, except for glycine which is neutral).

Unless otherwise stated in the examples, all procedures for making and manipulating recombinant DNA are carried out by the standard procedures described in Sambrook et al., Molecular Cloning - A Laboratory Manual, Second Ed., Cold Spring Harbor Laboratory Press, NY (1989), and in Volumes 1 and 2 of Ausubel et al. (1994) Current Protocols in Molecular Biology, Current Protocols, USA. Standard materials and methods for plant molecular biology work are described in Plant Molecular Biology Labfax (1993) by R.R.D. Croy, jointly published by BIOS Scientific Publications Ltd (UK) and Blackwell Scientific Publications (UK). Procedures for PCR technology can be found in "PCR protocols: a guide to methods and applications", Edited by M.A. Innis, D.H. Gelfand, J.J. Sninsky and T.J. White (Academic Press, Inc., 1990).

The terms "tolerance", "tolerant" or "less sensitive" are interchangeable used and mean the relative levels of inherent tolerance of the HPPD screened according to a visible indicator phenotype of the strain or plant transformed with a nucleic acid comprising the gene coding for the respective HPPD protein in the presence of different concentrations of the various HPPD inhibitor herbicides. Dose responses and relative shifts in dose responses associated with these indicator phenotypes (formation of brown colour, growth inhibition, bleaching, 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 HPPD, 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 HPPD. Herbicides can suitably be applied pre-emergence or post emergence.

Likewise, tolerance level is screened via transgenesis, regeneration, breeding and spray testing of a test plant such as tobacco, or a crop plant such as soybean or cotton and according to these results, such plants are at least 2-4x more tolerant to 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4 (trifluoromethyl)-benzamide than plants that do not contain any exogenous gene encoding an HPPD protein,

"Host organism" or “host” is understood as being any unicellular or multicellular heterologous organism into which the nucleic acid or chimeric gene according to the invention can be introduced for the purpose of producing HPPD. These organisms are, in particular, bacteria, for example *E. coli*, yeast, in particular of the genera *Saccharomyces* or *Kluyveromyces*, Pichia, fungi, in particular *Aspergillus*, a baculovirus or, preferably, plant cells and plants.

"Plant cell" is understood, according to the invention, as being any cell which is derived from or found in a plant and which is able to form or is part of undifferentiated tissues, such as calli, differentiated tissues such as embryos, parts of plants, plants or seeds. This includes protoplasts and pollen, cultivated plants cells or protoplasts grown in vitro, and plant cells that can regenerate into a complete plant.

"Plant" is understood, according to the invention, as being any differentiated multicellular organism which is capable of photosynthesis, in particular a monocotyledonous or dicotyledonous organism, more especially cultivated plants which are or are not intended for animal or human nutrition, such as maize or corn, wheat, *Brassica spp.* plants such as *Brassica napus* or *Brassica juncea*, soya spp, rice, sugarcane, beetroot, tobacco, cotton, vegetable plants such as cucumber, leek, carrot, tomato, lettuce, peppers, melon, watermelon, etc. Transgenic plants, as used herein, refer to plants comprising one or more foreign or heterologous gene(s) stably inserted in their genome.

In order perform tolerance to 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts, any promoter sequence of a gene which is expressed naturally in plants, or any hybrid or combination of promoter elements of genes expressed naturally in plants, including *Agrobacterium* or plant virus promoters, or any promoter which is suitable for controlling the transcription of a herbicide

tolerance gene in plants, can be used as the promoter sequence in the plants of the invention (named “plant-expressible promoter” herein). Examples of such suitable plant-expressible promoters are described above. In one embodiment of this invention, such plant-expressible promoters are operably-linked to a (I) DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) that is derived from a member of a group of organisms consisting of(a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at

position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position

336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

According to the invention, it is also possible to use, in combination with the promoter regulatory sequence, other regulatory sequences which are located between the promoter and the coding sequence, such as intron sequences, or transcription activators (enhancers) in order to perform tolerace to 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts. Examples of such suitable regulatory sequences are described above.

Any corresponding sequence of bacterial or viral origin, such as the nos terminator from *Agrobacterium tumefaciens*, or of plant origin, such as a histone terminator as described in application EP 0 633 317 A1, may be used as transcription termination (and polyadenylation) regulatory sequence.

In a further particular embodiment, the present invention relates to the use of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts on plants, plant parts, or plant seeds containing a nucleic acid sequence which encodes a transit peptide is employed 5' (upstream) of the nucleic acid sequence encoding the exogenous chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of(a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a

DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and

being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), and also containing with this transit peptide sequence being arranged between the promoter region and the sequence encoding the exogenous HPPD so as to permit expression of a transit peptide-HPPD fusion protein. The transit peptide makes it possible to direct the HPPD into the plastids, more especially the chloroplasts, with the fusion protein being cleaved

between the transit peptide and the HPPD protein when the latter enters the plastid. The transit peptide may be a single peptide, such as an EPSPS transit peptide (described in US patent 5,188,642) or a transit peptide of the plant ribulose bisphosphate carboxylase/ oxygenase small subunit (RuBisCO ssu), where appropriate, including a few amino acids of the N-terminal part of the mature RuBisCO ssu (EP 189 707 A1), or else may be a fusion of several transit peptides such as a transit peptide which comprises a first plant transit peptide which is fused to a part of the N-terminal sequence of a mature protein having a plastid location, with this part in turn being fused to a second plant transit peptide as described in patent EP 508 909 A1, and, more especially, the optimized transit peptide which comprises a transit peptide of the sunflower RuBisCO ssu fused to 22 amino acids of the N-terminal end of the maize RuBisCO ssu, in turn fused to the transit peptide of the maize RuBisCO ssu, as described, with its coding sequence, in patent EP508909 A1.

The present invention also relates to the transit peptide HPPD fusion protein and a nucleic acid or plant-expressible chimeric gene encoding such fusion protein, wherein the two elements of this fusion protein are as defined above.

In a further particular embodiment, the present invention relates to the use of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts on plants, plant parts, or plant seeds obtained by cloning, transformation with a expression vector, which expression vector contains at least one chimeric gene encoding the hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA

sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at

position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named A3xmi09H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37). In addition to the above chimeric gene, this vector can contain an origin of replication. This vector can be a plasmid or plasmid portion, a cosmid, or a bacteriophage or a virus which has been transformed by introducing the chimeric gene according to the invention. Transformation vectors are well known to the skilled person and widely described in the literature. The transformation vector which can be used, in particular, for transforming plant cells or plants may be a virus, which can be employed for transforming plant cells or plants and which additionally contains its own replication and expression elements. The vector for transforming plant cells or plants is preferably a plasmid, such as a disarmed *Agrobacterium* Ti plasmid.

In a further particular embodiment, the present invention relates to the use of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts on plants, plant parts, or plant seeds containing a chimeric gene which comprises a sequence encoding the hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of(a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at

position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position

336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37) , and the use of the plants or seeds in a field to grow a crop and harvest a plant product, e.g., soya spp, rice, wheat, barley or corn grains or cotton bolls, where in one embodiment said use involves the application of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts to such plants to control weeds.

In another particular embodiment, the present invention relates to the use of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts on plants, plant parts, or plant seeds characterized in that it contains one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of(a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by

SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas

aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), and in addition further contains a chimeric gene comprising a plant-expressible promoter as described above, operably-linked to a nucleic acid sequence encoding a PDH (prephenate dehydrogenase) enzyme (US 2005/0257283) in order to confer tolerance to 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts. A plant comprising such two transgenes can be obtained by transforming a plant with one transgene, and then re-transforming this transgenic plant with the second transgene, or by transforming a plant with the two transgenes simultaneously (in the same or in 2 different transforming DNAs or vectors), or by crossing a plant comprising the first transgene with a plant comprising the second transgene, as is well known in the art.

One transformation method in order to obtain plants, plant parts or seeds being tolerant to 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts by containing one or more chimeric gene(s) (I)

comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W

(Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -

> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), comprises bombarding cells, protoplasts or tissues with solid or liquid particles to which DNA is attached, or containing DNA. Another transformation method comprises using, as mean for transfer into the plant, a chimeric gene which is inserted into an *Agrobacterium tumefaciens* Ti plasmid or an *Agrobacterium rhizogenes* Ri plasmid. Other methods may be used, such as microinjection or electroporation or otherwise direct gene transfer using PEG. The skilled person can select any appropriate method for transforming the host organism of choice, in particular the plant cell or the plant. As examples, the technology for soybean transformation has been extensively described in the examples 1 to 3 disclosed in EP 1186666 A1, incorporated herein by reference. For rice, Agrobacterium-mediated transformation (Hiei et al., 1994 Plant J 6:271-282, and Hiei et al., 1997 Plant Mol Biol. 35:205-21, incorporated herein by reference), electroporation (US 5,641,664 and US 5,679,558, incorporated herein by reference), or bombardment (Christou et al., 1991, Biotechnology 9:957 incorporated herein by reference) could be performed. A suitable technology for transformation of monocotyledonous plants, and particularly rice, is described in WO 92/09696, incorporated herein by reference. For cotton, Agrobacterium-mediated transformation (Gould J.H. and Magallanes-Cedeno M., 1998 Plant Molecular Biology reporter, 16:1-10 and Zapata C., 1999, Theoretical Applied Genetics, 98(2):1432-2242 incorporated herein by reference), polybrene and/or treatment-mediated transformation (Sawahel W.A., 2001, - Plant Molecular Biology reporter, 19:377a-377f, incorporated herein by reference) have been described.

Alternatively, 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts may be used on plants, plant parts, or plant seeds containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp.,

more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni

HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), which HPPD is expressed directly in the plastids, such as the chloroplasts, using transformation of the plastid, such as the chloroplast genome. A suitable method

comprises the bombardment of plant cells or tissue by solid particles coated with the DNA or liquid particles comprising the DNA, and integration of the introduced gene by homologous recombination. Suitable vectors and selection systems are known to the person skilled in the art. An example of means and methods which can be used for such integration into the chloroplast genome of tobacco plants is given in WO 06/108830, the content of which is hereby incorporated by reference

The present invention also relates to a method for obtaining a plant tolerant to 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts, characterized in that the plant is transformed with one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598

(WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at

position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

Therefore, the present invention also relates to a method for obtaining a plant tolerant to 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts by containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g)

Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA

sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), characterized in that the plant contains one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA

sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro)

replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), which comprises a coding sequence as well as a heterologous regulatory element in the 5' and optionally in the 3' positions, which are able to function in a host organism, characterized in that the coding sequence comprises at least a nucleic acid sequence defining a gene encoding an HPPD of the invention as previously described in order to perform a sufficiently high level of tolerance to 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts.

In one embodiment of this invention, the HPPD inhibitor in the above method is the 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts either alone or in combination with one or more HPPD inhibitor herbicides selected from the group consisting of triketone or pyrazolinate herbicide, preferably tembotrione, mesotrione, bicyclopyrone, tefuryltrione, pyrasulfotole, pyrazolate, diketonitrile, benzofenap, or sulcotrione, particularly tembotrione.

The invention also relates to a method for selectively removing weeds or preventing the germination of weeds in a field to be planted with plants or to be sown with seeds, or in a plant crop, by application of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts to such field or plant crop, which method is characterized in that the 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts is applied to plants which have been transformed in accordance with one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882,

WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in

PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), either before sowing the crop (hereinafter named pre-planting application), before emergence of the crop (hereinafter named pre-emergence application), or after emergence of the crop (hereinafter named post-emergence application).

The invention also relates to a method for controlling in an area or a field which contains transformed seeds as previously described in the present invention, which method comprises applying, to the said area of the field, a dose of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts which is toxic for the said weeds, without significantly affecting the seeds or plants containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding

HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G

(Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

The present invention also relates to a method for cultivating the plants which have been transformed with one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598

(WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435),

and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), which method comprises planting seeds comprising a chimeric gene of before, in an area of a field which is appropriate for cultivating the said plants, and in applying, if weeds are present, a dose, which is toxic for the weeds, of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts to the said area of the said field, without significantly affecting the said transformed seeds or the said transformed plants, and in then harvesting the cultivated plants or plant parts when they reach the desired stage of maturity and, where appropriate, in separating the seeds from the harvested plants.

In the above methods, 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts can be applied in accordance with the invention, either before sowing the crop, before the crop emerges or after the crop emerges.

Within the meaning of the present invention, "herbicide" is understood as being a herbicidally active substance on its own or such a substance which is combined with an additive which alters its efficacy, such as, for example, an agent which increases its activity (a synergistic agent) or which limits its activity (a safener). It is of course to be understood that, for their application in practice, the above herbicides are combined, in a manner which is known per se, with the formulation adjuvants which are customarily employed in agricultural chemistry.

Thus, transgenic plants can be obtained which - in addition to the one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical

to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G

(Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37) - have modified properties as the result of overexpression, suppression or inhibition of homologous (= natural) genes or gene sequences or expression of heterologous (= foreign) genes or gene sequences.

On the plants, plant cells or seeds containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of(a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598

(WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435),

and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), it is preferred to employ 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts in combination with one or more further HPPD inhibitor herbicides belonging to the class of triketones, such as tembotrione, sulcotrione and mesotrione, or of the class of pyrazolinates, such as pyrasulfotole and topramezone, particularly selected from tembotrione, sulcotrione, topramezone, bicyclopyrone, tefuryltrione and mesotrione, more particularly tembotrione in transgenic crops which are also resistant to growth regulators such as, for example, 2,4-D or dicamba, or against herbicides which inhibit essential plant enzymes, for example acetolactate synthases (ALS), EPSP synthases, glutamine synthases (GS), Acetyl-coenzyme A carboxylase (ACCase), or against herbicides from the group of the ALS inhibitors, glyphosate, glufosinate, ACCase inhibitors and analogous active substances.

The invention therefore also relates to the use of herbicides applied to HPPD tolerant plants containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f)

Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598(WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in

PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), for controlling harmful plants (i.e. weeds) which also extends to transgenic crop plants comprising a second or more herbicide resistance(s) beside the resistance against 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts.

2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)-benzamide or its salts can be formulated in various ways, depending on the prevailing biological and/or physico-chemical parameters. Examples of possible formulations are: wettable powders (WP), water-soluble powders (SP), water-soluble concentrates, emulsifiable concentrates (EC), emulsions (EW), such as oil-in-water and water-in-oil emulsions,

sprayable solutions, suspension concentrates (SC), oil- or water-based dispersions, oil-miscible solutions, capsule suspensions (CS), dusts (DP), seed-dressing products, granules for application by broadcasting and on the soil, granules (GR) in the form of microgranules, spray granules, coated granules and adsorption granules, water-dispersible granules (WG), water-soluble granules (SG), ULV formulations, microcapsules and waxes.

These individual types of formulation are known in principle and are described, for example, in: Winnacker-Küchler, "Chemische Technologie" [Chemical technology], volume 7, C. Hanser Verlag Munich, 4th Ed. 1986; Wade van Valkenburg, "Pesticide Formulations", Marcel Dekker, N.Y., 1973; K. Martens, "Spray Drying" Handbook, 3rd Ed. 1979, G. Goodwin Ltd. London.

The formulation auxiliaries required, such as inert materials, surfactants, solvents and further additives, are also known and are described, for example, in: Watkins, "Handbook of Insecticide Dust Diluents and Carriers", 2nd Ed., Darland Books, Caldwell N.J., H.v. Olphen, "Introduction to Clay Colloid Chemistry"; 2nd Ed., J. Wiley & Sons, N.Y.; C. Marsden, "Solvents Guide"; 2nd Ed., Interscience, N.Y. 1963; McCutcheon's "Detergents and Emulsifiers Annual", MC Publ. Corp., Ridgewood N.J.; Sisley and Wood, "Encyclopedia of Surface Active Agents", Chem. Publ. Co. Inc., N.Y. 1964; Schönfeldt, "Grenzflächenaktive Äthylenoxidaddukte" [Interface-active ethylene oxide adducts], Wiss. Verlagsgesell., Stuttgart 1976; Winnacker-Küchler, "Chemische Technologie" [Chemical technology], volume 7, C. Hanser Verlag Munich, 4th Ed. 1986.

Based on these formulations, it is also possible to prepare combinations with other pesticidally active substances such as, for example, insecticides, acaricides, herbicides, fungicides, and with safeners, fertilizers and/or growth regulators, for example in the form of a ready mix or a tank mix.

Wettable powders are preparations which are uniformly dispersible in water and which, besides the active substance, also comprise ionic and/or nonionic surfactants (wetters, dispersers), for example polyoxyethylated alkylphenols, polyoxyethylated fatty alcohols, polyoxyethylated fatty amines, fatty alcohol polyglycol ether sulfates, alkanesulfonates, alkylbenzenesulfonates, sodium lignosulfonate, sodium

2,2'-dinaphthylmethane-6,6'-disulfonate, sodium dibutylnaphthalenesulfonate or else sodium oleoylmethyltaurinate, besides a diluent or inert substance. To prepare the wettable powders, the herbicidally active substances are ground finely, for example in customary apparatuses such as hammer mills, blower mills and air-jet mills, and mixed with the formulation auxiliaries, either simultaneously or subsequently.

Emulsifiable concentrates are prepared by dissolving the active substance in an organic solvent, for example butanol, cyclohexanone, dimethylformamide, xylene or else higher-boiling aromatics or hydrocarbons or mixtures of the organic solvents with addition of one or more ionic and/or nonionic surfactants (emulsifiers). Examples of emulsifiers which may be used are: calcium alkylarylsulfonates such as calcium dodecylbenzenesulfonate, or nonionic emulsifiers such as fatty acid polyglycol esters, alkylarylpolyglycol ethers, fatty alcohol polyglycol ethers, propylene oxide/ethylene oxide condensates, alkyl polyethers, sorbitan esters such as, for example, sorbitan fatty acid esters or polyoxyethylene sorbitan esters such as, for example, polyoxyethylene sorbitan fatty acid esters.

Dusts are obtained by grinding the active substance with finely divided solid materials such as, for example, talcum, natural clays such as kaolin, bentonite and pyrophyllite, or diatomaceous earth.

Suspension concentrates can be water- or oil-based. They can be prepared for example by wet-grinding by means of commercially available bead mills, if appropriate with addition of surfactants as already listed above for example in the case of the other formulation types.

Emulsions, for example oil-in-water emulsions (EW), can be prepared for example by means of stirrers, colloid mills and/or static mixers using aqueous organic solvents and, if appropriate, surfactants, as have already been mentioned for example above for the other formulation types.

Granules can be prepared either by spraying the active substance onto adsorptive, granulated inert material, or by applying active substance concentrates to the surface of carriers such as sand, kaolinites or granulated inert material with the aid of stickers, for example polyvinyl alcohol, sodium polyacrylate or else mineral oils. Suitable active

substances can also be granulated in the manner which is customary for the production of fertilizer granules, if desired as a mixture with fertilizers.

Water-dispersible granules are generally prepared by customary methods such as spray drying, fluidized-bed granulation, disk granulation, mixing with high-speed stirrers, and extrusion without solid inert material.

To prepare disk granules, fluidized-bed granules, extruder granules and spray granules, see, for example, methods in "Spray-Drying Handbook" 3rd ed. 1979, G. Goodwin Ltd., London; J.E. Browning, "Agglomeration", Chemical and Engineering 1967, pages 147 et seq.; "Perry's Chemical Engineer's Handbook", 5th Ed., McGraw-Hill, New York 1973, p. 8-57.

For further details of the formulation of crop protection products see, for example, G.C. Klingman, "Weed Control as a Science", John Wiley and Sons, Inc., New York, 1961, pages 81-96 and J.D. Freyer, S.A. Evans, "Weed Control Handbook", 5th Ed., Blackwell Scientific Publications, Oxford, 1968, pages 101-103.

As a rule, the agrochemical preparations comprise from 0.1 to 99% by weight, in particular from 0.1 to 95% by weight, of compounds according to the invention.
In wettable powders, the active substance concentration is, for example, approximately 10 to 90% by weight, the remainder to 100% by weight being composed of customary formulation constituents. In the case of emulsifiable concentrates, the active substance concentration can amount to approximately 1 to 90, preferably 5 to 80% by weight. Formulations in the form of dusts comprise from 1 to 30% by weight of active substance, preferably in most cases from 5 to 20% by weight of active substance, and sprayable solutions comprise approximately from 0.05 to 80, preferably from 2 to 50% by weight of active substance. In the case of water-dispersible granules, the active substance content depends partly on whether the active compound is in liquid or solid form, and on the granulation auxiliaries, fillers and the like which are being used. In the case of the water-dispersible granules, for example, the active substance content is between 1 and 95% by weight, preferably between 10 and 80% by weight.

In addition, the active substance formulations mentioned comprise, if appropriate, the auxiliaries which are conventional in each case, such as stickers, wetters, dispersants,

emulsifiers, penetrations, preservatives, antifreeze agents, solvents, fillers, carriers, colorants, antifoams, evaporation inhibitors, and pH and viscosity regulators.

Based on these formulations, it is also possible to prepare combinations of an HPPD inhibitor herbicide of the class of triketones, such as tembotrione, sulcotrione and mesotrione, or of the class of pyrazolinates, such as pyrasulfotole and topramezone, particularly selected from tembotrione, sulcotrione, topramezone, bicyclopyrone, tefuryltrione and mesotrione, more particularly tembotrione with other pesticidally active substances such as, for example, insecticides, acaricides, herbicides, fungicides, and with safeners, fertilizers and/or growth regulators, for example in the form of a ready mix or a tank mix to be applied to HPPD tolerant plants according to the invention.

Formulation examples

a) A dust is obtained by mixing 10 parts by weight of a compound of the formula (I) and/or a salt thereof and 90 parts by weight of talc as inert substance and comminuting the mixture in a hammer mill.

b) A wettable powder which is readily dispersible in water is obtained by mixing 25 parts by weight of a compound of the formula (I) and/or a salt thereof, 64 parts by weight of kaolin-containing quartz as inert substance, 10 parts by weight of potassium lignosulfonate and 1 part by weight of sodium oleoylmethyltaurinate as wetting agent and dispersant, and grinding the mixture in a pinned-disk mill.

c) A readily water-dispersible dispersion concentrate is obtained by mixing 20 parts by weight of a compound of the formula (I) and/or a salt thereof with 6 parts by weight of alkylphenol polyglycol ether (®Triton X 207), 3 parts by weight of isotridecanol polyglycol ether (8 EO) and 71 parts by weight of paraffinic mineral oil (boiling range for example about 255 to above 277°C) and grinding the mixture in a ball mill to a fineness of below 5 microns.

d) An emulsifiable concentrate is obtained from 15 parts by weight of a compound of the formula (I) and/or a salt thereof, 75 parts by weight of cyclohexanone as solvent and 10 parts by weight of oxethylated nonylphenol as emulsifier.

e) Water-dispersible granules are obtained by mixing
75 parts by weight of a compound of the formula (I) and/or a salt thereof,
10 parts by weight of calcium lignosulfonate,
5 parts by weight of sodium lauryl sulfate,
3 parts by weight of polyvinyl alcohol and
7 parts by weight of kaolin,
grinding the mixture in a pinned-disk mill, and granulating the powder in a fluidized bed by spraying on water as granulating liquid.

f) Water-dispersible granules are also obtained by homogenizing and precomminuting, in a colloid mill,
25 parts by weight of a compound of the formula (I) and/or a salt thereof,
5 parts by weight of sodium 2,2'-dinaphthylmethane-6,6'-disulfonate,
2 parts by weight of sodium oleoylmethyltaurinate,
1 part by weight of polyvinyl alcohol,
17 parts by weight of calcium carbonate and
50 parts by weight of water,
subsequently grinding the mixture in a bead mill and atomizing and drying the resulting suspension in a spray tower by means of a single-substance nozzle.

A further apect of present invention is the use of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts to HPPD tolerant plants containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence

identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro)

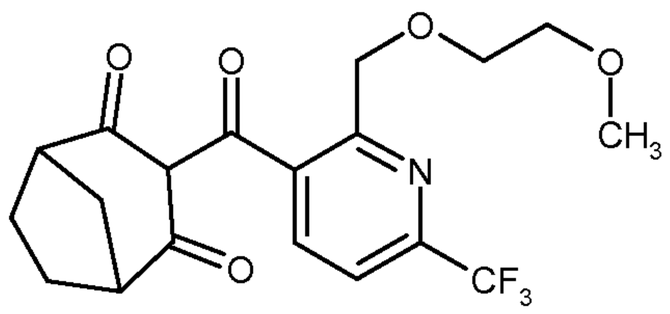
replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), in combination with further HPPD inhibitor herbicide belonging to the class of triketones, such as tembotrione, sulcotrione and mesotrione, or belonging to the class of pyrazolinates, such as pyrasulfotole and topramezone, particularly selected from tembotrione, sulcotrione, topramezone, bicyclopyrone, tefuryltrione and mesotrione, more particularly tembotrione in mixed formulations or in the tank mix, and/or with further known active substances which are based on the inhibition of, for example, acetolactate synthase, acetyl-CoA carboxylase, cellulose synthase,

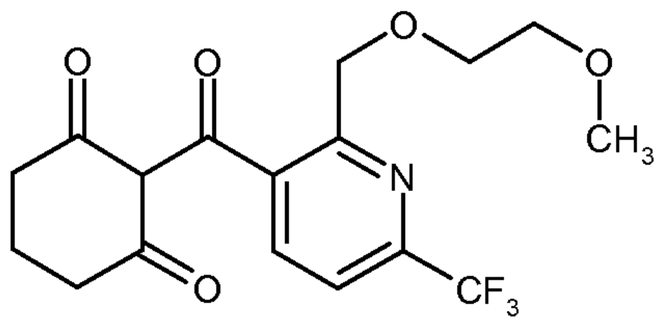
enolpyruvylshikimate-3-phosphate synthase, glutamine synthetase, p-hydroxyphenylpyruvate dioxygenase, phytoene desaturase, photosystem I, photosystem II, protoporphyrinogen oxidase, as are described in, for example, Weed Research 26 (1986) 441-445 or "The Pesticide Manual", 14th edition, The British Crop Protection Council and the Royal Soc. of Chemistry, 2003 and the literature cited therein. Known herbicides or plant growth regulators which can be combined with the compounds according to the invention are, for example, the following active substances (the compounds are either designated by the common name according to the International Organization for Standardization (ISO) or by a chemical name, if appropriate together with the code number) and always comprise all use forms such as acids, salts, esters and isomers such as stereoisomers and optical isomers. In this context, one and in some cases also several use forms are mentioned by way of example:

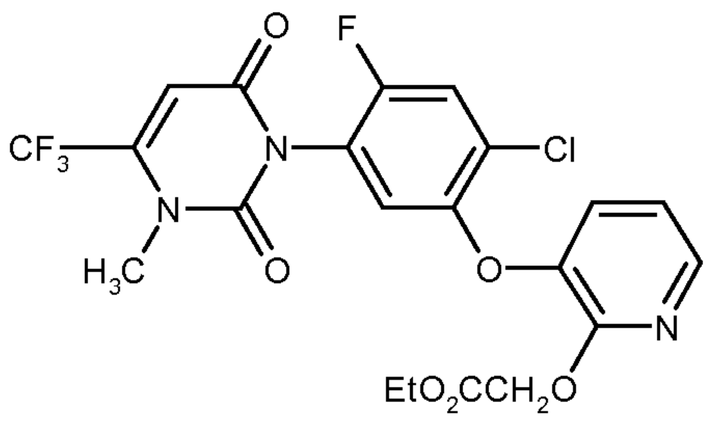
acetochlor, acibenzolar, acibenzolar-S-methyl, acifluorfen, acifluorfen-sodium, aclonifen, alachlor, allidochlor, alloxydim, alloxydim-sodium, ametryne, amicarbazone, amidochlor, amidosulfuron, aminocyclopyrachlor, aminopyralid, amitrole, ammonium sulfamate, ancymidol, anilofos, asulam, atrazine, azafenidin, azimsulfuron, aziprotryne, BAH-043, BAS-140H, BAS-693H, BAS-714H, BAS-762H, BAS-776H, BAS-800H, beflubutamid, benazolin, benazolin-ethyl, bencarbazone, benfluralin, benfuresate, bensulide, bensulfuron-methyl, bentazone, benzfendizone, benzobicyclon, benzofenap, benzofluor, benzoylprop, bifenox, bilanafos, bilanafos-sodium, bispyribac, bispyribac-sodium, bromacil, bromobutide, bromofenoxim, bromoxynil, bromuron, buminafos, busoxinone, butachlor, butafenacil, butamifos, butenachlor, butralin, butroxydim, butylate, cafenstrole, carbetamide, carfentrazone, carfentrazone-ethyl, chlomethoxyfen, chloramben, chlorazifop, chlorazifop-butyl, chlorbromuron, chlorbufam, chlorfenac, chlorfenac-sodium, chlorfenprop, chlorflurenol, chlorflurenol-methyl, chloridazon, chlorimuron, chlorimuron-ethyl, chlormequat-chloride, chlornitrofen, chlorophthalim, chlorthal-dimethyl, chlorotoluron, chlorsulfuron, cinidon, cinidon-ethyl, cinmethylin, cinosulfuron, clethodim, clodinafop clodinafop-propargyl, clofencet, clomazone, clomeprop, cloprop, clopyralid, cloransulam, cloransulam-methyl, cumyluron, cyanamide, cyanazine, cyclanilide, cycloate, cyclosulfamuron, cycloxydim, cycluron, cyhalofop, cyhalofop-butyl, cyperquat, cyprazine, cyprazole, 2,4-D, 2,4-DB, daimuron/dymron, dalapon, daminozide, dazomet, n-decanol, desmedipham, desmetryn, detosyl-pyrazolate (DTP), di-allate, dicamba, dichlobenil,

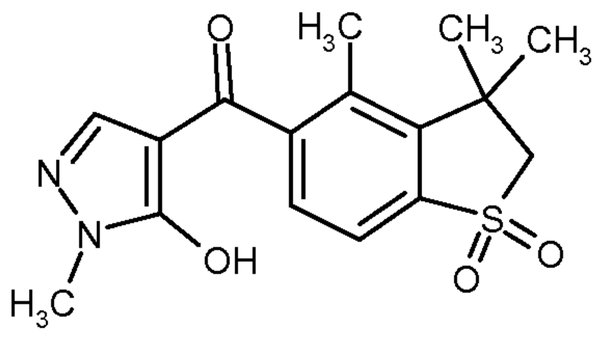
dichlorprop, dichlorprop-P, diclofop, diclofop-methyl, diclofop-P-methyl, diclosulam, diethatyl, diethatyl-ethyl, difenoxuron, difenzoquat, diflufenican, diflufenzopyr, diflufenzopyr-sodium, dimefuron, dikegulac-sodium, dimefuron, dimepiperate, dimethachlor, dimethametryn, dimethenamid, dimethenamid-P, dimethipin, dimetrasulfuron, dinitramine, dinoseb, dinoterb, diphenamid, dipropetryn, diquat, diquat-dibromide, dithiopyr, diuron, DNOC, eglinazine-ethyl, endothal, EPTC, esprocarb, ethalfluralin, ethametsulfuron-methyl, ethephon, ethidimuron, ethiozin, ethofumesate, ethoxyfen, ethoxyfen-ethyl, ethoxysulfuron, etobenzanid, F-5331, i.e. N-[2-chloro-4-fluoro-5-[4-(3-fluoro-propyl)-4,5-dihydro-5-oxo-1H-tetrazol-1-yl]-phenyl]ethanesulfonamide, fenoprop, fenoxaprop, fenoxaprop-P, fenoxaprop-ethyl, fenoxaprop-P-ethyl, fentrazamide, fenuron, flamprop, flamprop-M-isopropyl, flamprop-M-methyl, flazasulfuron, florasulam, fluazifop, fluazifop-P, fluazifop-butyl, fluazifop-P-butyl, fluazolate, flucarbazone, flucarbazone-sodium, flucetosulfuron, fluchloralin, flufenacet (thiafluamide), flufenpyr, flufenpyr-ethyl, flumetralin, flumetsulam, flumiclorac, flumiclorac-pentyl, flumioxazin, flumipropyn, fluometuron, fluorodifen, fluoroglycofen, fluoroglycofen-ethyl, flupoxam, flupropacil, flupropanate, flupyrsulfuron, flupyrsulfuron-methyl-sodium, flurenol, flurenol-butyl, fluridone, flurochloridone, fluroxypyr, fluroxypyr-meptyl, flurprimidol, flurtamone, fluthiacet, fluthiacet-methyl, fluthiamide, fomesafen, foramsulfuron, forchlorfenuron, fosamine, furyloxyfen, gibberellic acid, glufosinate, L-glufosinate, L-glufosinate-ammonium, glufosinate-ammonium, glyphosate, glyphosate-isopropylammonium, H-9201, halosafen, halosulfuron, halosulfuron-methyl, haloxyfop, haloxyfop-P, haloxyfop-ethoxyethyl, haloxyfop-P-ethoxyethyl, haloxyfop-methyl, haloxyfop-P-methyl, hexazinone, HNPC-9908, HOK-201, HW-02, imazamethabenz, imazamethabenz-methyl, imazamox, imazapic, imazapyr, imazaquin, imazethapyr, imazosulfuron, inabenfide, indanofan, indoleacetic acid (IAA), 4-indol-3-ylbutyric acid (IBA), iodosulfuron, iodosulfuron-methyl-sodium, ioxynil, isocarbamid, isopropalin, isoproturon, isouron, isoxaben, isoxachlortole, isoxaflutole, isoxapyrifop, KUH-043, KUH-071, karbutilate, ketospiradox, lactofen, lenacil, linuron, maleic hydrazide, MCPA, MCPB, MCPB-methyl, -ethyl and -sodium, mecoprop, mecoprop-sodium, mecoprop-butotyl, mecoprop-P-butotyl, mecoprop-P-dimethylammonium, mecoprop-P-2-ethylhexyl, mecoprop-P-potassium, mefenacet, mefluidide, mepiquat-chloride, mesosulfuron, mesosulfuron-methyl, methabenzthiazuron, metam, metamifop, metamitron, metazachlor, methazole, methoxyphenone, methyldymron, 1-methylcyclopropene, methyl isothiocyanate, metobenzuron, metobenzuron, metobromuron, metolachlor, S-

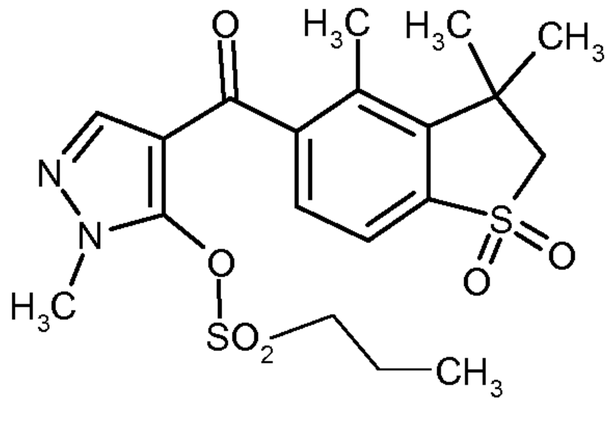
metolachlor, metosulam, metoxuron, metribuzin, metsulfuron, metsulfuron-methyl, molinate, monalide, monocarbamide, monocarbamide dihydrogen sulfate, monolinuron, monosulfuron, monuron, MT 128, MT-5950, i.e. N-[3-chloro-4-(1-methylethyl)-phenyl]-2-methylpentanamide, NGGC-011, naproanilide, napropamide, naptalam, NC-310, i.e. 4-(2,4-dichlorobenzoyl)-1-methyl-5-benzyloxypyrazole, neburon, nicosulfuron, nipyraclofen, nitralin, nitrofen, nitrophenolat-sodium (isomer mixture), nitrofluorfen, nonanoic acid, norflurazon, orbencarb, orthosulfamuron, oryzalin, oxadiargyl, oxadiazon, oxasulfuron, oxaziclomefone, oxyfluorfen, paclobutrazole, paraquat, paraquat dichloride, pelargonic acid (nonanoic acid), pendimethalin, pendralin, penoxsulam, pentanochlor, pentoxazone, perfluidone, pethoxamid, phenisopham, phenmedipham, phenmedipham-ethyl, picloram, picolinafen, pinoxaden, piperophos, pirifenop, pirifenop-butyl, pretilachlor, primisulfuron, primisulfuron-methyl, probenazole, profluazol, procyazine, prodiamine, prifluraline, profoxydim, prohexadione, prohexadione-calcium, prohydrojasmone, prometon, prometryn, propachlor, propanil, propaquizafop, propazine, propham, propisochlor, propoxycarbazone, propoxycarbazone-sodium, propyzamide, prosulfalin, prosulfocarb, prosulfuron, prynachlor, pyraclonil, pyraflufen, pyraflufen-ethyl, pyrazolynate (pyrazolate), pyrazosulfuron-ethyl, pyrazoxyfen, pyribambenz, pyribambenz-isopropyl, pyribenzoxim, pyributicarb, pyridafol, pyridate, pyriftalid, pyriminobac, pyriminobac-methyl, pyrimisulfan, pyrithiobac, pyrithiobac-sodium, pyroxasulfone, pyroxsulam, quinclorac, quinmerac, quinoclamine, quizalofop, quizalofop-ethyl, quizalofop-P, quizalofop-P-ethyl, quizalofop-P-tefuryl, rimsulfuron, saflufenacil, secbumeton, sethoxydim, siduron, simazine, simetryn, SN-106279, sulf-allate (CDEC), sulfentrazone, sulfometuron, sulfometuron-methyl, sulfosate (glyphosate-trimesium), sulfosulfuron, SYN-523, SYP-249, SYP-298, SYP-300, tebutam, tebuthiuron, tecnazene, tepraloxydim, terbacil, terbucarb, terbuchlor, terbumeton, terbuthylazine, terbutryne, TH-547, thenylchlor, thiafluamide, thiazafluron, thiazopyr, thidiazimin, thidiazuron, thiencarbazone, thiencarbazone-methyl, thifensulfuron, thifensulfuron-methyl, thiobencarb, tiocarbazil, tralkoxydim, tri-allate, triasulfuron, triaziflam, triazofenamide, tribenuron, tribenuron-methyl, trichloroacetic acid (TCA), triclopyr, tridiphane, trietazine, trifloxysulfuron, trifloxysulfuron-sodium, trifluralin, triflusulfuron, triflusulfuron-methyl, trimeturon, trinexapac, trinexapac-ethyl, tritosulfuron, tsitodef, uniconazole, uniconazole-P, vernolate, ZJ-0166, ZJ-0270, ZJ-0543, ZJ-0862 and the following compounds











Compositions of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts and one or more of the above listed compounds are not yet known in the art.

Therefore, a further subject of present invention are compositions comprising 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts (component (A)) and one or more, preferably one, component(s) (B) selected from the sub-groups B1 to B11, with:

B1 consisting of 1,3-diketo compounds, comprising
prohexadione, prohexadione-calcium, trinexapac-ethy,
alloxydim, alloxydim-sodium, butroxydim, clethodim, cycloxydim, ketospiradox,
profoxydim, sethoxydim, tepraloxydim, tralkoxydim,
mesotrione, sulcotrione, tefuryltrione, tembotrione, bicyclopyrone,
fenquinotrione, SL-261,
pinoxaden,

B2 consisting of (sulfon)amides, comprising

beflubutamide, bromobutide, dimethenamide, dimethenamide-P, diphenamide, napropamide, pethoxamid, N-[3-chloro-4-(1-methylethyl)-phenyl]-2-methylpentanamide,
naptalam, propyzamide,
diflufenican, etobenzanid, flufenacet, mefenacet, mefluidide, pentanochlor, picolinafen, propanil, N-phenylphthalamic acid,
acetochlor, alachlor, amidochlor, butachlor, butenachlor, dimethachlor, metazachlor, metolachlor, S-metolachlor, pretilachlor, propachlor, propisochlor, (2-chloro-6'-ethyl-N-isopropoxymethylaceto-o-toluidide), thenylchlor,
asulam, carbaryl, carbetamide, chlorpropham, desmedipham, phenmedipham, propham,
butylate, cycloate, dimepiperate, EPTC, esprocarb, methasulfocarb, molinate, orbencarb, pebulate, prosulfocarb, pyributicarb, thiobencarb, tri-allate, vernolate,
amidosulfuron, azimsulfuron, bensulfuron, bensulfuron-methyl, clorimuron, chlorimuron-ethyl, chlorsulfuron, cinosulfuron, cyclosulfamuron, ethametsulfuron, ethametsulfuron-methyl, ethoxysulfuron, flazasulfuron, flucetosulfuron, flupyrsulfuron-methyl-sodium, foramsulfuron, halosulfuron-methyl, imazosulfuron, iodosulfuron, iodosulfuron-methyl-sodium, mesosulfuron, mesosulfuron-methyl, metazosulfuron, methiopyrsulfuron, metsulfuron, metsulfuron-methyl, monosulfuron, monosulfuron-ester, nicosulfuron, orthosulfamuron, oxasulfuron, primisulfuron-methyl, propyrisulfuron, prosulfuron, pyrasulfuron, pyrazosulfuron-ethyl, rimsulfuron, sulfometuron, sulfometuron-methyl, sulfosulfuron, thifensulfuron, thifensulfuron-methyl, triasulfuron, tribenuron, tribenuron-methyl, trifloxysulfuron, trifloxysulfuron (sodium), triflusulfuron, triflusulfuron-methyl, tritosulfuron, (benzoic acid, 2-[[[[[4-methoxy-6-(methylthio)-2-pyrimidinyl]amino]carbonyl]amino]sulfonyl]methyl ester), flucarbazone, flucarbazone-sodium, ipfencarbazone, propoxycarbazone, propoxycarbazone-sodium, thiencarbazone, thiencarbazone-methyl, cloransulam, cloransulam-methyl, diclosulam, florasulam, flumetsulam, metosulam, penoxsulam, pyroxsulam,
3-chloro-N-[(4,6-dimethoxypyrimidin-2-yl)carbamoyl]-1-methyl-4-(5-methyl-5,6-dihydro-1,4,2-dioxazin-3-yl)-1H-pyrazole-5-sulfonamide,

B3 consisting of arylnitriles, comprising

bromoxynil, bromoxynil-butyrate, bromoxynil-potassium, bromoxynil-heptanoate, bromoxynil-octanoate, detosyl-pyrazolate (DTP), dichlobenil, ioxynil, ioxynil-octanoate, ioxynil-potassium, ioxynil-sodium, pyraclonil,

B4 consisting of azoles, comprising
benzofenap, pyrazolynate (pyrazolate), pyrazoxyfen, pyroxasulfone, topramezone, pyrasulfotole, tolpyralate, 3-(3-chloro-5-{[1-methyl-3-(trifluoromethyl)-1H-pyrazol-5-yl]oxy}phenoxy)-1-methyl-5-(trifluoromethyl)-1H-pyrazole, 3-(3-iodo-5-{[1-methyl-3-(trifluoromethyl)-1H-pyrazol-5-yl]oxy}phenoxy)-1-methyl-5-(trifluoromethyl)-1H-pyrazole, 1-ethyl-3-(3-fluoro-5-{[1-methyl-3-(trifluoromethyl)-1H-pyrazol-5-yl]oxy}phenoxy)-5-(trifluoromethyl)-1H-pyrazole,
pyraflufen, pyraflufen-ethyl, fenoxasulfone, fluazolate,
isouron, isoxaben, isoxaflutole,
imazamethabenz, imazamethabenz-methyl, imazapic, imazapic-ammonium, imazapyr, imazapyr-isopropyl-ammonium, imazaquin, imazaquin-ammonium, imazethapyr, imazethapyr-ammonium
azafenidin, methazole, oxadiargyl, oxadiazon,
amicarbazone, bencarbazone, carfentrazone, carfentrazone-ethyl, sulfentrazone, ,
amitrole, paclobutrazol, uniconazole, uniconazole-P, cafenstrole,
fentrazamide,

B5 consisting other herbicides, comprising
allidochlor, aminocyclopyrachlor, aminocyclopyrachlor-potassium, aminocyclopyrachlor-methyl, N-acetylthiazolidine-4-carboxylic acid, acrolein, aminopyralid, ammonium pelargonate, ammonium sulfamate, aviglycine, benazolin, benazolin-ethyl, benfluralin, benfuresate, bentazone, benzobicyclon, 6-benzylaminopurine, borax, brassinolide, bromofenoxim, butralin, carvone, catechin, chlorfenac, chlorfenac-sodium, chlorfenprop, chlorflurenol, chlorflurenol-methyl, chloridazon, chlormequat chloride, chloroacetic acid, chlorphthalim, chlorthal-dimethyl, cinidon, cinidon-ethyl, cinmethylin, clofencet, clomazone, cloxyfonac, cyanamide, cyclanilide, cyclopyrimorate, 6-isopentylamino-purin, kinetin, zeatin, dalapon, daminozide, dazomet, n-decanol, difenzoquat metilsulfate, 2,6-diisopropylnaphthalene, dikegulac, dikegulac-

sodium, dimethipin, dimethylarsenic acid, dinitramine, dinoterb, diquat, diquat dibromide, dithiopyr, DNOC, endothal, endothal-dipotassium, endothal-disodium, endothal-mono(N,N-dimetylalkylammonium), ethafluralin, ethofumesate, ethylchlozate, ferrous sulfate, flamprop, flamprop-M-isopropyl, flamprop-M-methyl, fluchloralin, flufenpyr, flufenpyr-ethyl, flumetralin, flumiclorac, flumiclorac-pentyl, flumioxazin, flupropanate, flurenol, flurenol-butyl, flurenol-dimetylammonium-metyl, fluridone, flurochloridone, flurtamone, fluthiacet, fluthiacet-metyl, gibberillic acid, halauxifen, halauxifen-methyl, halauxifen salts, indanofan, isopropalin, isoprothiolane, maleic hydrazide, mepiquat chloride, metam, methiozolin, methylarsonic acid, 1-methylcyclopropene, methyl isothiocyanate, nitrophenolate mixture, nonanoic acid, norflurazon, oleic acid, oryzalin, oxaziclomefone, paraquat, paraquat dichloride, pendimethalin, pentachlorophenol, pentoxazone, petroleum oils, prodiamine, n-propyl dihydrojasmonate, pyridafol, pyridate, quinoclamine, sintofen, sodium chlorate, sulfuric acid, tar oils, TCA, TCA sodium, tecnazene, thiazopyr, triacontanol, triafamone, trifluralin and urea sulfate,

B6 consisting of (het)arylcarboxylic acids, comprising
chloramben, dicamba, dicamba salts, 2,3,6-TBA,
clopyralid, fluroxypyr, fluroxypyr-methyl, inabenfide, picloram, triclopyr,
quinclorac, quinmerac,
indol-3-ylacetic acid, 4-indol-3-ylbutyric acid,
2-(1-naphthyl)acetamide, 1-naphthylacetic acid, 2-naphthyloxyacetic acid,

B7 consisting of organic phosphorus compounds, comprising
anilofos, bensulide, bilanafos, bilanafos-sodium, butimafos, clacyfos, fosamine, glufosinate, glufosinate salts, glufosinate-ammonium, glufosinate-sodium, glufosinate-P, L-glufosinate-ammonium, L-glufosinate-sodium, glyphosate, glyphosate salts, glyphosate-isopropyl-ammonium, glyphosate-ammonium, glyphosate-dimethylammonium, glyphosate-trimesium (=sulfosate), glyphosate-diammonium, glyphosate-potassium, glyphosate-sodium, piperophos, ethephon and tribufos,

B8 consisting of phenyl ether, comprising
acifluorfen, acifluorfen-sodium, aclonifen, fluoroglycofen, fluoroglycofen-ethyl, fomesafen, fomesafen-sodium, halosafen, lactofen, oxyfluorfen,
bifenox, ethoxyfen-ethyl,
clomeprop,
cloprop, dichlorprop, dichlorprop-P, mecoprop, mecoprop-sodium, mecoprop-butotyl, mecoprop-P, mecoprop-P-butotyl, mecoprop-P-dimethylammonium, mecoprop-P-2-ethylhexyl, mecoprop-P-potassium,
4-CPA, 2,4-D, 2,4-D-butotyl, 2,4-D-butyl, 2,4-D-choline, 2,4-D-dimethylammonium, 2,4-D-diolamin, 2,4-D-ethyl, 2,4-D-2-ethylhexyl, 2,4-D-isobutyl, 2,4-D-isooctyl, 2,4-D- iso-propyl-ammonium, 2,4-D-potassium, 2,4-D-triisopropanolammonium, 2,4-D-trolamine, MCPA, MCPA-butotyl, MCPA-dimethylammonium, MCPA-2-ethylhexyl. MCPA-isopropylammonium, MCPA-potassium, MCPA-sodium, MCPA-thioethyl,
2,4-DB, MCPB, MCPB-methyl, MCPB-ethyl-sodium,
clodinafop-ethyl, clodinafop-propargyl, cyhalofop, cyhalofop-butyl, diclofop, diclofop-methyl, diclofop-P, diclofop-P-methyl, fenoxaprop, fenoxaprop-P, fenoxaprop-P-ethyl, fluazifop, fluazifop-butyl, fluazifop-P, fluazifop-P-butyl, haloxyfop, haloxyfop-P, metamifop, propaquizafop, quizalafop, quizalafop-ethyl, quizalafop-P, quizalafop-P-ethyl, quizalafop-P-tefuryl,

B9 consisting of pyrimidines, comprising
ancymidol, flurprimidol, pyrimisulfan,
bispyribac, bispyribac-sodium, pyribenzoxim, pyriminobac, pyriminobac-methyl, pyribambenz, pyribambenz-isopropyl, pyribambenz-propyl,
pyriftalid, pyrithiobac, pyrithiobac-sodium,
benzfendizone, bromacil, butafenacil, lenacil, saflufenacil, terbacil, tiafenacil,
2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]-N-[methyl(1-methylethyl)-sulfamoyl]benzamide,
ethyl[(3-{2-chloro-5-[2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]-4-fluorophenoxy}pyridin-2-yl)oxy]acetate

B10 consisting of (thio)ureas, comprising
cumyluron,

chlorbromuron, chlorotoluron, chloroxuron, daimuron, diflufenzopyr, diflufenzopyr-sodium, dimefuron, diuron, fluometuron, forchlorfenuron, isoproturon, karbutilate, linuron, methyldymron, metobromuron, metoxuron, monolinuron, neburon, siduron, terbucarb, thidiazuron,
methiuron,
tebuthiuron,
methabenzthiazuron,

B11 consisting of triazines, comprising
triaziflam, indaziflam,
atrazine, cyanazine, cyprazine, propazine, simazine, terbumeton, terbuthylazine, trietazine,
prometon,
ametryn, dimethametryn, prometryn, simetryn, terbutryn,
ethozin, hexazinon, metamitron, metribuzin,
trifludimoxazin.

In a further embodiment, these herbicidal compositions comprise one or more safeners (component (C)) selected from the group consisting of benoxacor (C1), cloquintocet-mexyl (C2), cyprosulfamide (C3), dichlormid (C4), fenclorim (C5), fenchlorazole (C6), furilazole (C7), isoxadifen-ethyl (C8), mefenpyr-diethyl (C9), 4-(dichloroacetyl)-1-oxa-4-azaspiro[4.5]decane of CAS 71526-07-3 (C10), 2,2,5-trimethyl-3-(dechloroacetyl)-1,3-oxazolidine of CAS 52836-31-4 (C11). 2-methoxy-N-({4-[(methylcarbamoyl)amino]phenyl}sulfonyl)benzamid der CAS 129531-12-0 (C12).

Components (B) and (C) are also known, for example, from "The Pesticide Manual", 15th edition, The British Crop Protection Council and the Royal Soc. of Chemistry, and from the website http://www.alanwood.net/pesticides/.

Any of these inventive compositions may comprise or be used together with additional further components, for example other kinds of active crop protection ingredients and/or additives and/or formulation auxiliaries customary in crop protection.

Component (A), component(s)(B) and optionally the safener(s) (component (C)) can be applied in a known manner, for example together (for example as a co-formulation or as a tank-mix) or else at different times in short succession (splitting), for example to the plants, plant parts, plant seeds or the area on which the plants grow. It is possible, for example, to apply the individual active compounds or the herbicide-safener combination in several portions (sequential application), for example pre-emergence applications followed by post-emergence applications, or early post-emergence applications followed by post-emergence applications at an intermediate or late stage. Preference is given to the joint or immediately successive application of the active compounds in the respective combination. It is also possible to use the individual active compounds or the herbicide-safener combination for seed treatment.

Preference is given to those compositions according to the invention comprising (2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide as component (A)

Preferred components (B) selected from sub-group B1 are clethodim, mesotrione, sulcotrione, tefuryltrione, tembotrione and bicyclopyrone.

Particularly preferred components (B) selected from sub-group B1 are clethodim, mesotrione, bicyclopyrone and tembotrione

Exceptionally preferred components (B) selected from of sub-group B1 are bicyclopyrone and tembotrione.

Preferred components (B) selected from sub-group B2 are acetochlor, diclosulam, diflufenican, flumetsulam, foramsulfuron, nicosulfuron, S-metolachlor, thiencarbazone-methyl, dimethenamide-P, rimsulfuron, alachlor, chlorimuron-ethyl, florasulam, flucarbazone-sodium, flufenacet, iodosulfuron-methyl-sodium, ethoxysulfuron, ipfencarbazone, metsulfuron-methyl, propoxycarbazone-sodium and tribenuron-methyl.

Particularly preferred components (B) selected from sub-group B2 are acetochlor, diclosulam, diflufenican, foramsulfuron, nicosulfuron, S-metolachlor, thiencarbazone-

methyl, dimethenamide-P, rimsulfuron, alachlor, chlorimuron-ethyl, florasulam, flucarbazone-sodium, flufenacet and iodosulfuron-methyl-sodium.
Most preferred components (B) selected from sub-group B2 are acetochlor, diclosulam, diflufenican, foramsulfuron, nicosulfuron, S-metolachlor and thiencarbazone-methyl.

Preferred components (B) selected from sub-group B3 are bromoxynil and ioxynil.

Particularly preferred herbicide of group B3 is bromoxynil.

Preferred components (B) selected from sub-group B4 are amicarbazone, carfentrazone-ethyl, imazapyr, imazethapyr, isoxaflutole, oxadiargyl, oxadiazon, pyrasulfotole, pyroxasulfone and topramezone.

Particularly preferred herbicide of group B4 are carfentrazone-ethyl, imazapyr, imazethapyr, isoxaflutole, oxadiargyl, oxadiazon and pyroxasulfone.

Exceptionally preferred herbicide of group B4 are imazapyr, isoxaflutole and pyroxasulfone.

Preferred components (B) selected from sub-group B5 are paraquat dichloride, pendimethalin, aminopyralid, flumioxazin, flurtamone, halauxifen, halauxifen-methyl, halauxifen salts, pyridate, bentazone, cinidon-ethyl, clomazone and trifluralin.

Particularly preferred herbicides of group B5 are paraquat dichloride, pendimethalin, aminopyralid, flumioxazin, flurtamone, halauxifen, halauxifen-methyl, halauxifen salts and pyridate.

Exceptionally preferred components (B) selected from sub-group B5 are paraquat dichloride and pendimethalin.

Preferred components (B) selected from sub-group B6 are dicamba, dicamba salts and fluroxypyr.

Particularly preferred components (B) selected from sub-group B6 are dicamba and dicamba salts.

Exceptionally preferred component (B) selected from sub-group B6 is dicamba.

Preferred components (B) selected from sub-group B7 are glufosinate, glufosinate-ammonium, L-glufosinate-ammonium, glyphosate, glyphosate-isopropyl-ammonium

Particularly preferred components (B) selected from sub-group B7 are glufosinate-ammonium and glyphosate.

Exceptionally preferred components (B) selected from sub-group B7 are glufosinate-ammonium and glyphosate.

Preferred components (B) selected from sub-group B8 are 2,4-D, 2,4-D-butotyl, 2,4-D-butyl, 2,4-D-choline, 2,4-D-dimethylammonium, 2,4-D-diolamin, 2,4-D-ethyl, 2,4-D-2-ethylhexyl, 2,4-D-isobutyl, 2,4-D-isooctyl, 2,4-D- iso-propyl-ammonium, 2,4-D-potassium, 2,4-D-triisopropanolammonium, 2,4-D-trolamine, fenoxaprop-P-ethyl, lactofen, fluazifop-P-butyl, aclonifen and haloxyfop-P.

Particularly preferred components (B) selected from sub-group B8 are 2,4-D, 2,4-D-butotyl, 2,4-D-butyl, 2,4-D-choline, 2,4-D-dimethylammonium, 2,4-D-diolamin, 2,4-D-ethyl, 2,4-D-2-ethylhexyl, 2,4-D-isobutyl, 2,4-D-isooctyl, 2,4-D- iso-propyl-ammonium, 2,4-D-potassium, 2,4-D-triisopropanolammonium, 2,4-D-trolamine, fenoxaprop-P-ethyl, lactofen and fluazifop-P-butyl.

Exceptionally preferred components (B) selected from sub-group B8 are 2,4-D, 2,4-D-butotyl, 2,4-D-butyl, 2,4-D-choline, 2,4-D-dimethylammonium, 2,4-D-diolamin, 2,4-D-ethyl, 2,4-D-2-ethylhexyl, 2,4-D-isobutyl, 2,4-D-isooctyl, 2,4-D- iso-propyl-ammonium, 2,4-D-potassium, 2,4-D-triisopropanolammonium, 2,4-D-trolamine, fenoxaprop-P-ethyl and lactofen.

Preferred component (B) selected from sub-group B9 is saflufenacil.

Preferred components (B) selected from sub-group B10 are diuron, diflufenzopyr and fluometuron.

Particularly preferred components (B) selected from sub-group B10 are diuron and diflufenzopyr.

Exceptionally preferred components (B) selected from sub-group B10 is diuron.

Preferred components (B) selected from sub-group B11 are atrazine, indaziflam, terbuthylazine and metribuzin.

In the herbicidal compositions according to the invention, the application rate of the herbicides of (2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide component (A) or salts thereof is usually from 1 to 500 g of active ingredient (a.i.) per hectare, preferably from 2 to 300 g of a.i./ha, particularly preferably from 3 to 200 g of a.i./ha. The application rate of component (B) is usually from 1 to 5000 g of active ingredient per hectare, preferably from 2 to 3000 g of a.i./ha, particularly preferably from 3 to 2000 g of a.i./ha. The application rate of the safeners (component (C)) is usually from 1 to 500 g of active ingredient per hectare, preferably from 2 to 400 g of a.i./ha, particularly preferably from 3 to 300 g of a.i./ha.
The application rate required of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts to be applied to areas where HPPD tolerant plants containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f)

Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in

PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37) are growing varies as a function of the external conditions such as temperature, humidity, the nature of the herbicide used and the like. It can vary within wide limits, for example between 0.001 and 1.0 kg/ha and more of active substance, but it is preferably between 0.005 and 750 g/ha.

In case of combined applications of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts and herbicides that differ from 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)-benzamide or its salts to the HPPD tolerant plants containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD)

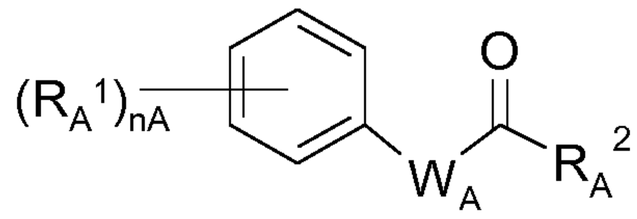
derived from a member of a group of organisms, consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339

and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339

and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), these mixtures may cause crop injury, based on the presence herbicides different to 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts. In order to reduce/eliminate such crop injuries, appropriate safeners may be added. These safeners, which are employed in antidotically active amounts, reduce the phytotoxic side effects of herbicides/pesticides used, for example in economically important crops, such as cereals (wheat, barley, rye, corn, rice, millet), alfalfa, sugar beet, sugarcane, oilseed rape, cotton and soya spp., preferably corn, cotton, sugarbeet, or soya spp.

The safeners are preferably selected from the group consisting of:

A) compounds of the formula (S-I)



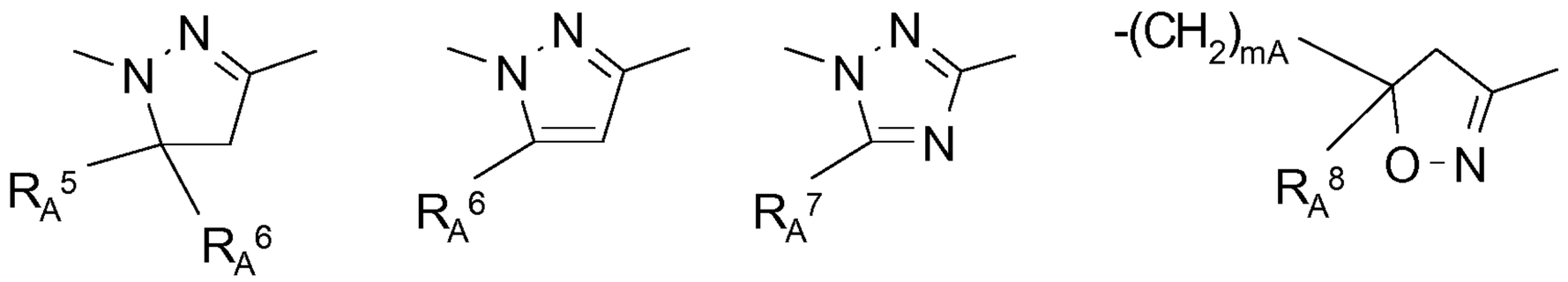
(S-I)

where the symbols and indices have the following meanings:

n_A is a natural number from 0 to 5, preferably from 0 to 3;

R_A^1 is halogen, (C_1-C_4)-alkyl, (C_1-C_4)-alkoxy, nitro or (C_1-C_4)-haloalkyl;

W_A is an unsubstituted or substituted divalent heterocyclic radical from the group consisting of partially unsaturated or aromatic five-membered heterocycles having 1 to 3 hetero ring atoms of the type N or O, where at least one nitrogen atom and at most one oxygen atom is present in the ring, preferably a radical from the group consisting of (W_A^1) to (W_A^4),



(W_A^1) (W_A^2) (W_A^3) (W_A^4)

m_A is 0 or 1;

R_A^2 is OR_A^3, SR_A^3 or $NR_A^3R_A^4$ or a saturated or unsaturated 3- to 7-membered heterocycle having at least one nitrogen atom and up to 3 heteroatoms, preferably from the group consisting of O and S, which is attached via the nitrogen atom to the carbonyl group in (S-I) and which is unsubstituted or substituted by radicals from the group consisting of (C_1-C_4)-alkyl, (C_1-C_4)-alkoxy and optionally substituted phenyl, preferably a radical of the formula OR_A^3, NHR_A^4 or $N(CH_3)_2$, in particular of the formula OR_A^3;

R_A^3 is hydrogen or an unsubstituted or substituted aliphatic hydrocarbon radical having preferably a total of 1 to 18 carbon atoms;

R_A^4 is hydrogen, (C_1-C_6)-alkyl, (C_1-C_6)-alkoxy or substituted or unsubstituted phenyl;

R_A^5 is H, (C_1-C_8)-alkyl, (C_1-C_8)-haloalkyl), (C_1-C_4)-alkoxy-(C_1-C_8)-alkyl, cyano or $COOR_A^9$ where R_A^9 is hydrogen, (C_1-C_8)-alkyl, (C_1-C_8)-haloalkyl, (C_1-C_4)-alkoxy-(C_1-C_4)-alkyl, (C_1-C_6)-hydroxyalkyl, (C_3-C_{12})-cycloalkyl or tri-(C_1-C_4)-alkylsilyl;

R_A^6, R_A^7, R_A^8 are identical or different and are hydrogen, (C_1-C_8)-alkyl, (C_1-C_8)-haloalkyl, (C_3-C_{12})-cycloalkyl or substituted or unsubstituted phenyl;

preferably:

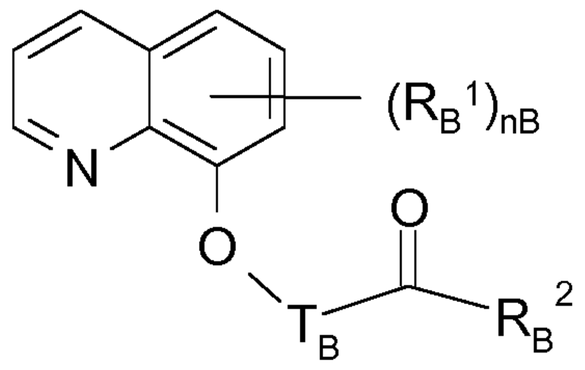
a) compounds of the type of the dichlorophenylpyrazoline-3-carboxylic acid, preferably compounds such as ethyl 1-(2,4-dichlorophenyl)-5-(ethoxycarbonyl)-5-methyl-2-pyrazoline-3-carboxylate (S1-1) ("mefenpyr-diethyl", see Pestic. Man.), and related compounds, as described in WO 91/07874;

b) derivatives of dichlorophenylpyrazolecarboxylic acid, preferably compounds such as ethyl 1-(2,4-dichlorophenyl)-5-methylpyrazole-3-carboxylate (S1-2), ethyl 1-(2,4-dichlorophenyl)-5-isopropylpyrazole-3-carboxylate (S1-3), ethyl 1-(2,4-dichlorophenyl)-5-(1,1-dimethylethyl)pyrazole-3-carboxylate (S1-4), ethyl 1-(2,4-dichlorophenyl)-5-phenylpyrazole-3-carboxylate (S1-5) and related compounds, as described in EP-A-333 131 and EP-A-269 806;

c) compounds of the type of the triazolecarboxylic acids, preferably compounds such as fenchlorazole(-ethyl ester), i.e. ethyl 1-(2,4-dichlorophenyl)-5-trichloromethyl-(1H)-1,2,4-triazole-3-carboxylate (S1-6), and related compounds, as described in EP-A-174 562 and EP-A-346 620;

d) compounds of the type of the 5-benzyl- or 5-phenyl-2-isoxazoline-3-carboxylic acid or the 5,5-diphenyl-2-isoxazoline-3-carboxylic acid, preferably compounds such as ethyl 5-(2,4-dichlorobenzyl)-2-isoxazoline-3-carboxylate (S1-7) or ethyl 5-phenyl-2-isoxazoline-3-carboxylate (S1-8) and related compounds, as described in WO 91/08202, or ethyl 5,5-diphenyl-2-isoxazolinecarboxylate (S1-9) ("isoxadifen-ethyl") or n-propyl 5,5-diphenyl-2-isoxazolinecarboxylate (S1-10) or ethyl 5-(4-fluorophenyl)-5-phenyl-2-isoxazoline-3-carboxylate (S1-11), as described in the patent application WO-A-95/07897.

B) Quinoline derivatives of the formula (S-II)



(S-II)

where the symbols and indices have the following meanings:

R_B^1 is halogen, $(C_1\text{-}C_4)$-alkyl, $(C_1\text{-}C_4)$-alkoxy, nitro or $(C_1\text{-}C_4)$-haloalkyl;

n_B is a natural number from 0 to 5, preferably from 0 to 3;

R_B^2 OR_B^3, SR_B^3 or $NR_B^3R_B^4$ or a saturated or unsaturated 3- to 7-membered heterocycle having at least one nitrogen atom and up to 3 heteroatoms, preferably from the group consisting of O and S, which is attached via the nitrogen atom to the carbonyl group in (S-II) and is unsubstituted or substituted by radicals from the group consisting of (C_1-C_4)-alkyl, (C_1-C_4)-alkoxy or optionally substituted phenyl, preferably a radical of the formula OR_B^3, NHR_B^4 or $N(CH_3)_2$, in particular of the formula OR_B^3;

R_B^3 is hydrogen or an unsubstituted or substituted aliphatic hydrocarbon radical having preferably a total of 1 to 18 carbon atoms;

R_B^4 is hydrogen, (C_1-C_6)-alkyl, (C_1-C_6)-alkoxy or substituted or unsubstituted phenyl;

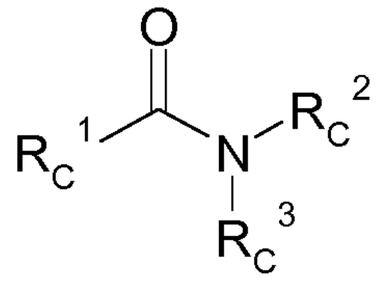
T_B is a (C_1- or C_2)-alkanediyl chain which is unsubstituted or substituted by one or two (C_1-C_4)-alkyl radicals or by [(C_1-C_3)-alkoxy]carbonyl;

preferably:

a) compounds of the type of the 8-quinolinoxyacetic acid (S2), preferably 1-methylhexyl (5-chloro-8-quinolinoxy)acetate (common name "cloquintocet-mexyl" (S2-1) (see Pestic. Man.),
1,3-dimethylbut-1-yl (5-chloro-8-quinolinoxy)acetate (S2-2),
4-allyloxybutyl (5-chloro-8-quinolinoxy)acetate (S2-3),
1-allyloxyprop-2-yl (5-chloro-8-quinolinoxy)acetate- (S2-4),
ethyl (5-chloro-8-quinolinoxy)acetate (S2-5),
methyl (5-chloro-8-quinolinoxy)acetate (S2-6),
allyl (5-chloro-8-quinolinoxy)acetate (S2-7),
2-(2-propylideneiminoxy)-1-ethyl (5-chloro-8-quinolinoxy)acetate (S2-8), 2-oxoprop-1-yl (5-chloro-8-quinolinoxy)acetate (S2-9) and related compounds, as described in EP-A-86 750, EP-A-94 349 and EP-A-191 736 or EP-A-0 492 366, and also their hydrates and salts, as described in WO-A-2002/034048.

b) Compounds of the type of the (5-chloro-8-quinolinoxy)malonic acid, preferably compounds such as diethyl (5-chloro-8-quinolinoxy)malonate, diallyl (5-chloro-8-quinolinoxy)malonate, methyl ethyl (5-chloro-8-quinolinoxy)malonate and related compounds, as described in EP-A-0 582 198.

C) Compounds of the formula (S-III)



(S-III)

where the symbols and indices have the following meanings:

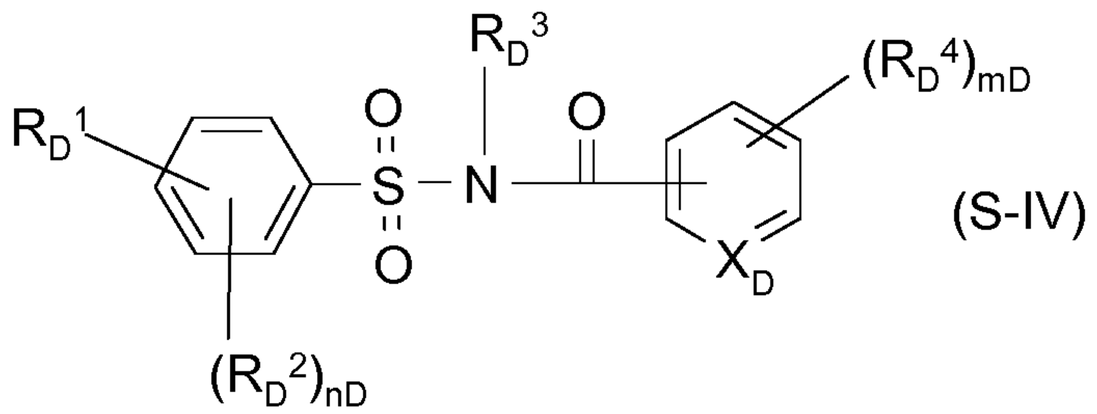
R_C^1 is (C_1-C_4)-alkyl, (C_1-C_4)-haloalkyl, (C_2-C_4)-alkenyl, (C_2-C_4)-haloalkenyl, (C_3-C_7)-cycloalkyl, preferably dichloromethyl;

R_C^2, R_C^3 are identical or different and are hydrogen, (C_1-C_4)-alkyl, (C_2-C_4)-alkenyl, (C_2-C_4)-alkynyl, (C_1-C_4)-haloalkyl, (C_2-C_4)-haloalkenyl, (C_1-C_4)-alkylcarbamoyl-(C_1-C_4)-alkyl, (C_2-C_4)-alkenylcarbamoyl-(C_1-C_4)-alkyl, (C_1-C_4)-alkoxy-(C_1-C_4)-alkyl, dioxolanyl-(C_1-C_4)-alkyl, thiazolyl, furyl, furylalkyl, thienyl, piperidyl, substituted or unsubstituted phenyl, or R_C^2 and R_C^3 together form a substituted or unsubstituted heterocyclic ring, preferably an oxazolidine, thiazolidine, piperidine, morpholine, hexahydropyrimidine or benzoxazine ring;

preferably:

Active compounds of the type of the dichloroacetamides which are frequently used as pre-emergence safener (soil-acting safeners), such as, for example,
"dichlormid" (see Pestic.Man.) (= N,N-diallyl-2,2-dichloroacetamide),
"R-29148" (= 3-dichloroacetyl-2,2,5-trimethyl-1,3-oxazolidine from Stauffer),
"R-28725" (= 3-dichloroacetyl-2,2,-dimethyl-1,3-oxazolidine from Stauffer),
"benoxacor" (see Pestic. Man.) (= 4-dichloroacetyl-3,4-dihydro-3-methyl-2H-1,4-benzoxazine),
"PPG-1292" (= N-allyl-N-[(1,3-dioxolan-2-yl)methyl]dichloroacetamide from PPG Industries),
"DKA-24" (= N-allyl-N-[(allylaminocarbonyl)methyl]dichloroacetamide from Sagro-Chem),
"AD-67" or "MON 4660" (= 3-dichloroacetyl-1-oxa-3-aza-spiro[4,5]decane from Nitrokemia or Monsanto),
"TI-35" (= 1-dichloroacetylazepane from TRI-Chemical RT)
"diclonon" (dicyclonone) or "BAS145138" or "LAB145138" (= 3-dichloroacetyl-2,5,5-trimethyl-1,3-diazabicyclo[4.3.0]nonane from BASF) and
"furilazole" or "MON 13900" (see Pestic. Man.) (= (RS)-3-dichloroacetyl-5-(2-furyl)-2,2-dimethyloxazolidine).

D) N-Acylsulfonamides of the formula (S-IV) and their salts



(S-IV)

in which

X_D is CH or N;

R_D^1 is $CO\text{-}NR_D^5R_D^6$ or $NHCO\text{-}R_D^7$;

R_D^2 is halogen, $(C_1\text{-}C_4)$-haloalkyl, $(C_1\text{-}C_4)$-haloalkoxy, nitro, $(C_1\text{-}C_4)$-alkyl, $(C_1\text{-}C_4)$-alkoxy, $(C_1\text{-}C_4)$-alkylsulfonyl, $(C_1\text{-}C_4)$-alkoxycarbonyl or $(C_1\text{-}C_4)$-alkylcarbonyl;

R_D^3 is hydrogen, $(C_1\text{-}C_4)$-alkyl, $(C_2\text{-}C_4)$-alkenyl or $(C_2\text{-}C_4)$-alkynyl;

R_D^4 is halogen, nitro, $(C_1\text{-}C_4)$-alkyl, $(C_1\text{-}C_4)$-haloalkyl, $(C_1\text{-}C_4)$-haloalkoxy, $(C_3\text{-}C_6)$-cycloalkyl, phenyl, $(C_1\text{-}C_4)$-alkoxy, cyano, $(C_1\text{-}C_4)$-alkylthio, $(C_1\text{-}C_4)$-alkylsulfinyl, $(C_1\text{-}C_4)$-alkylsulfonyl, $(C_1\text{-}C_4)$-alkoxycarbonyl or $(C_1\text{-}C_4)$-alkylcarbonyl;

R_D^5 is hydrogen, $(C_1\text{-}C_6)$-alkyl, $(C_3\text{-}C_6)$-cycloalkyl, $(C_2\text{-}C_6)$-alkenyl, $(C_2\text{-}C_6)$-alkynyl, $(C_5\text{-}C_6)$-cycloalkenyl, phenyl or 3- to 6-membered heterocyclyl containing v_D heteroatoms from the group consisting of nitrogen, oxygen and sulfur, where the seven last-mentioned radicals are substituted by v_D substituents from the group consisting of halogen, $(C_1\text{-}C_6)$-alkoxy, $(C_1\text{-}C_6)$-haloalkoxy, $(C_1\text{-}C_2)$-alkylsulfinyl, $(C_1\text{-}C_2)$-alkylsulfonyl, $(C_3\text{-}C_6)$-cycloalkyl, $(C_1\text{-}C_4)$-alkoxycarbonyl, $(C_1\text{-}C_4)$-alkylcarbonyl and phenyl and, in the case of cyclic radicals, also $(C_1\text{-}C_4)$-alkyl and $(C_1\text{-}C_4)$-haloalkyl;

R_D^6 is hydrogen, $(C_1\text{-}C_6)$-alkyl, $(C_2\text{-}C_6)$-alkenyl or $(C_2\text{-}C_6)$-alkynyl, where the three last-mentioned radicals are substituted by v_D radicals from the group consisting of halogen, hydroxy, $(C_1\text{-}C_4)$-alkyl, $(C_1\text{-}C_4)$-alkoxy and $(C_1\text{-}C_4)$-alkylthio, or

R_D^5 and R_D^6 together with the nitrogen atom carrying them form a pyrrolidinyl or piperidinyl radical;

R_D^7 is hydrogen, $(C_1\text{-}C_4)$-alkylamino, di-$(C_1\text{-}C_4)$-alkylamino, $(C_1\text{-}C_6)$-alkyl, $(C_3\text{-}C_6)$-cycloalkyl, where the 2 last-mentioned radicals are substituted by v_D substituents from

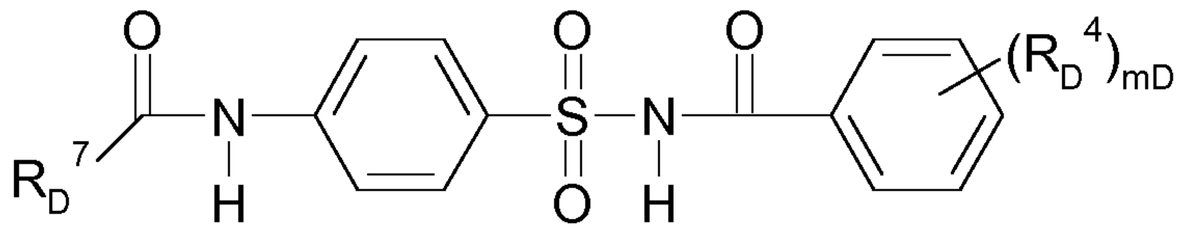
the group consisting of halogen, (C_1-C_4)-alkoxy, halogen-(C_1-C_6)-alkoxy and (C_1-C_4)-alkylthio and, in the case of cyclic radicals, also (C_1-C_4)-alkyl and (C_1-C_4)-haloalkyl;

n_D is 0, 1 or 2;

m_D is 1 or 2;

v_D is 0, 1, 2 or 3;

from among these, preference is given to compounds of the type of the N-acylsulfonamides, for example of the formula (S-V) below, which are known, for example, from WO 97/45016



(S-V)

in which

R_D^7 is (C_1-C_6)-alkyl, (C_3-C_6)-cycloalkyl, where the 2 last-mentioned radicals are substituted by v_D substituents from the group consisting of halogen, (C_1-C_4)-alkoxy, halogen-(C_1-C_6)-alkoxy and (C_1-C_4)-alkylthio and, in the case of cyclic radicals, also (C_1-C_4)-alkyl and (C_1-C_4)-haloalkyl;

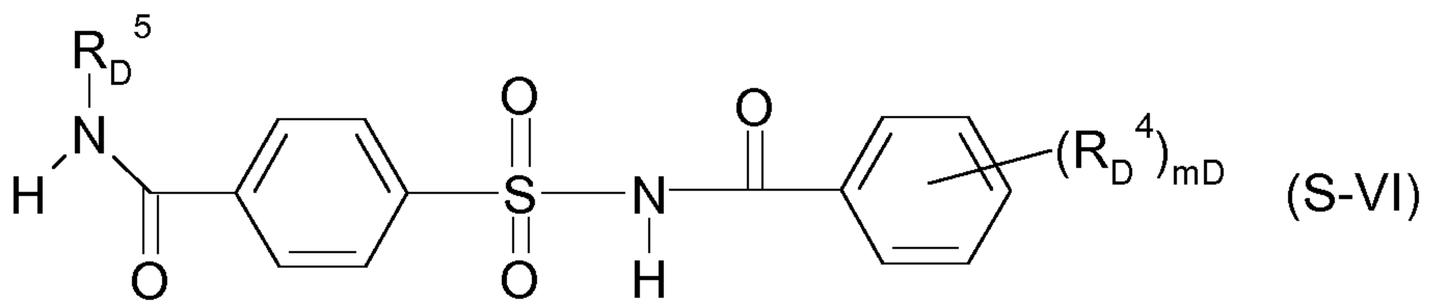
R_D^4 is halogen, (C_1-C_4)-alkyl, (C_1-C_4)-alkoxy, CF_3;

m_D is 1 or 2;

v_D is 0, 1, 2 or 3;

and also

acylsulfamoylbenzamides, for example of the formula (S-VI) below, which are known, for example, from WO 99/16744,



(S-VI)

for example those in which

R_D^5 = cyclopropyl and (R_D^4) = 2-OMe ("cyprosulfamide", S3-1),

R_D^5 = cyclopropyl and (R_D^4) = 5-Cl-2-OMe (S3-2),

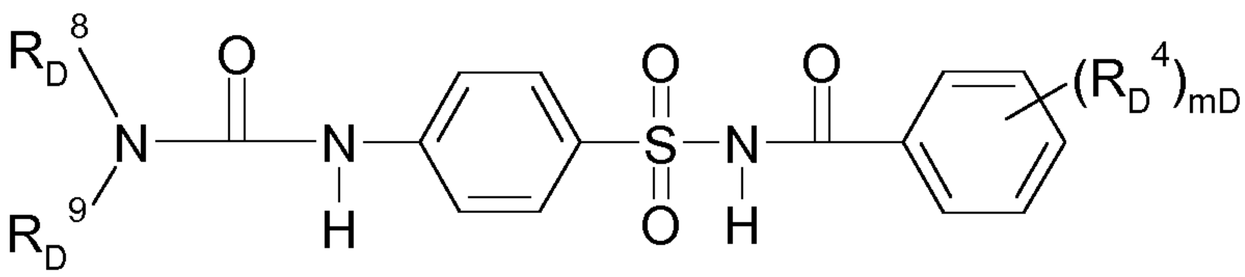
R_D^5 = ethyl and (R_D^4) = 2-OMe (S3-3),

R_D^5 = isopropyl and (R_D^4) = 5-Cl-2-OMe (S3-4) and

R_D^5 = isopropyl and (R_D^4) = 2-OMe (S3-5);

and also

compounds of the type of the N-acylsulfamoylphenylureas of the formula (S-VII), which are known, for example, from EP-A-365484



(S-VII)

in which

R_D^8 and R_D^9 independently of one another are hydrogen, (C_1-C_8)-alkyl, (C_3-C_8)-cycloalkyl, (C_3-C_6)-alkenyl, (C_3-C_6)-alkynyl,

R_D^4 is halogen, (C_1-C_4)-alkyl, (C_1-C_4)-alkoxy, CF_3

m_D is 1 or 2;

from among these in particular

1-[4-(N-2-methoxybenzoylsulfamoyl)phenyl]-3-methylurea,

1-[4-(N-2-methoxybenzoylsulfamoyl)phenyl]-3,3-dimethylurea,

1-[4-(N-4,5-dimethylbenzoylsulfamoyl)phenyl]-3-methylurea,

1-[4-(N-naphthoylsulfamoyl)phenyl]-3,3-dimethylurea,

G) active compounds from the class of the hydroxyaromatics and aromatic-aliphatic carboxylic acid derivatives, for example

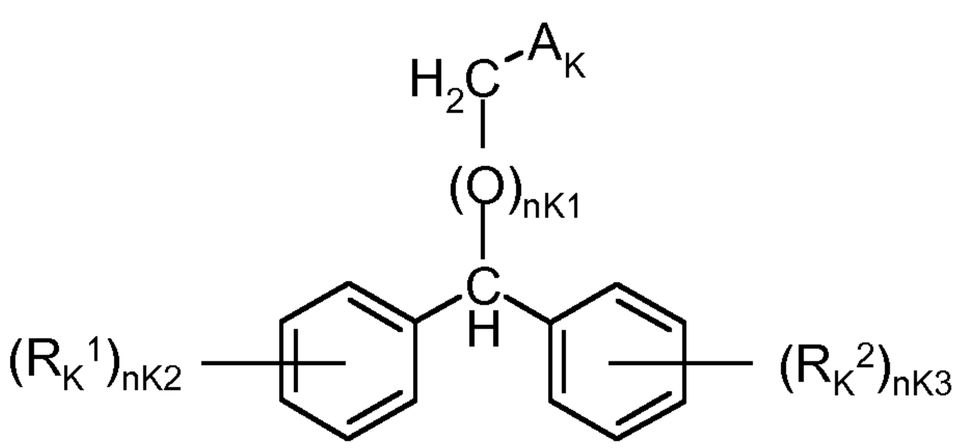
ethyl 3,4,5-triacetoxybenzoate, 3,5-dimethoxy-4-hydroxybenzoic acid, 3,5-dihydroxybenzoic acid, 4-hydroxysalicylic acid, 4-fluorosalicyclic acid, 1,2-dihydro-2-oxo-6-trifluoromethylpyridine-3-carboxamide, 2-hydroxycinnamic acid, 2,4-dichlorocinnamic acid, as described in WO 2004084631, WO 2005015994, WO 2006007981, WO 2005016001;

H) active compounds from the class of the 1,2-dihydroquinoxalin-2-ones, for example

1-methyl-3-(2-thienyl)-1,2-dihydroquinoxalin-2-one, 1-methyl-3-(2-thienyl)-1,2-dihydroquinoxaline-2-thione, 1-(2-aminoethyl)-3-(2-thienyl)-1,2-dihydroquinoxalin-2-one hydrochloride, 1-(2-methylsulfonylaminoethyl)-3-(2-thienyl)-1,2-dihydro-quinoxalin-2-one, as described in WO 2005112630,

l) active compounds which, in addition to a herbicidal action against harmful plants, also have safener action on crop plants such as rice, such as, for example, "dimepiperate" or "MY-93" (see Pestic. Man.) (=S-1-methyl-1-phenylethyl piperidine-1-thiocarboxylate), which is known as safener for rice against damage by the herbicide molinate,
"daimuron" or "SK 23" (see Pestic. Man.) (= 1-(1-methyl-1-phenylethyl)-3-p-tolylurea), which is known as safener for rice against damage by the herbicide imazosulfuron,
"cumyluron" = "JC-940" (= 3-(2-chlorophenylmethyl)-1-(1-methyl-1-phenyl-ethyl)urea, see JP-A-60087254), which is known as safener for rice against damage by a number of herbicides,
"methoxyphenone" or "NK 049" (= 3,3'-dimethyl-4-methoxybenzophenone), which is known as safener for rice against damage by a number of herbicides,
"CSB" (= 1-bromo-4-(chloromethylsulfonyl)benzene) (CAS Reg. No. 54091-06-4 from Kumiai), which is known as safener against damage by a number of herbicides in rice,

K) compounds of the formula (S-IX),
as described in WO-A-1998/38856



(S-IX)

in which the symbols and indices have the following meanings:

R_K^1, R_K^2 independently of one another are halogen, $(C_1$-$C_4)$-alkyl, $(C_1$-$C_4)$-alkoxy, $(C_1$-$C_4)$-haloalkyl, $(C_1$-$C_4)$-alkylamino, di-$(C_1$-$C_4)$-alkylamino, nitro;

A_K is $COOR_K^3$ or $COOR_K^4$

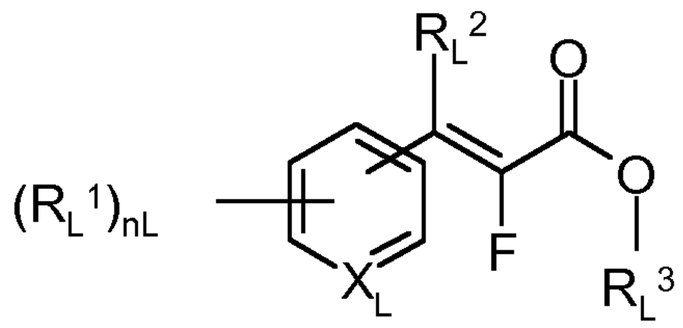
R_K^3, R_K^4 independently of one another are hydrogen, $(C_1$-$C_4)$-alkyl, $(C_2$-$C_6)$-alkenyl, $(C_2$-$C_4)$-alkynyl, cyanoalkyl, $(C_1$-$C_4)$-haloalkyl, phenyl, nitrophenyl, benzyl, halobenzyl, pyridinylalkyl or alkylammonium,

n_K^1 is 0 or 1,

n_K^2, n_K^3 independently of one another are 0, 1 or 2

preferably: methyl (diphenylmethoxy)acetate (CAS Reg. No.: 41858-19-9),

L) compounds of the formula (S-X),
as described in WO A-98/27049



(S-X)

in which the symbols and indices have the following meanings:

X_L is CH or N,

n_L is, in the case that X=N, an integer from 0 to 4 and,
in the case that X=CH, an integer from 0 to 5,

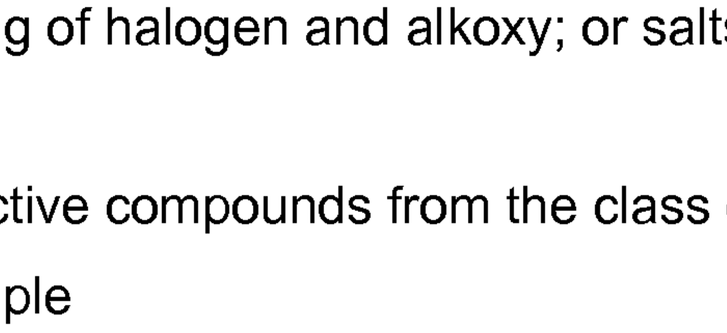
R_L^1 is halogen, (C_1-C_4)-alkyl, (C_1-C_4)-haloalkyl, (C_1-C_4)-alkoxy, (C_1-C_4)-haloalkoxy, nitro, (C_1-C_4)-alkylthio, (C_1-C_4)-alkylsulfonyl, (C_1-C_4)-alkoxycarbonyl, optionally substituted phenyl, optionally substituted phenoxy,

R_L^2 is hydrogen or (C_1-C_4)-alkyl,

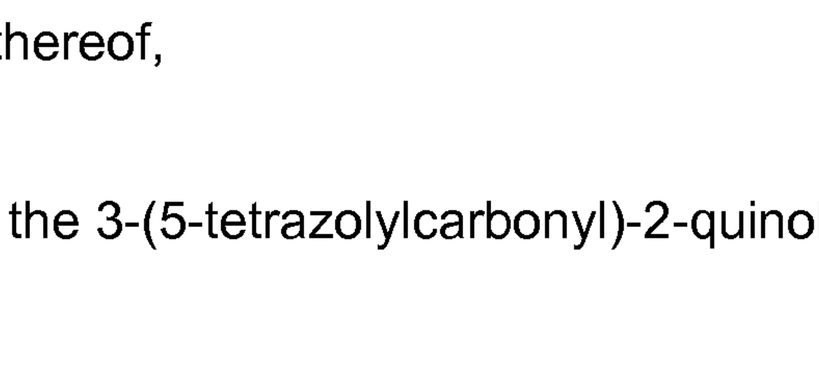
R_L^3 is hydrogen, (C_1-C_8)-alkyl, (C_2-C_4)-alkenyl, (C_2-C_4)-alkynyl or aryl, where each of the carbon-containing radicals mentioned above is unsubstituted or substituted by one or more, preferably by up to three, identical or different radicals from the group consisting of halogen and alkoxy; or salts thereof,

M) active compounds from the class of the 3-(5-tetrazolylcarbonyl)-2-quinolones, for example
1,2-dihydro-4-hydroxy-1-ethyl-3-(5-tetrazolylcarbonyl)-2-quinolone (CAS Reg. No.: 219479-18-2), 1,2-dihydro-4-hydroxy-1-methyl-3-(5-tetrazolylcarbonyl)-2-quinolone (CAS Reg. No.: 95855-00-8), as described in WO-A-1999000020,

N) compounds of the formula (S-XI) or (S-XII),
as described in WO-A-2007023719 and WO-A-2007023764



(S-XI)



(S-XII)

in which

R_N^1 is halogen, (C_1-C_4)-alkyl, methoxy, nitro, cyano, CF_3, OCF_3

Y, Z independently of one another are O or S,

n_N is an integer from 0 to 4,

R_N^2 is (C_1-C_{16})-alkyl, (C_2-C_6)-alkenyl, (C_3-C_6)-cycloalkyl, aryl, benzyl, halobenzyl,

R_N^3 is hydrogen, (C_1-C_6)alkyl,

O) one or more compounds from the group consisting of:

1,8-naphthalic anhydride,

O,O-diethyl S-2-ethylthioethyl phosphorodithioate (disulfoton),

4-chlorophenyl methylcarbamate (mephenate),

O,O-diethyl O-phenyl phosphorothioate (dietholate),

4-carboxy-3,4-dihydro-2H-1-benzopyran-4-acetic acid (CL-304415, CAS Reg. No.: 31541-57-8),

2-propenyl 1-oxa-4-azaspiro[4.5]decane-4-carbodithioate (MG-838, CAS Reg. No.: 133993-74-5),

methyl [(3-oxo-1H-2-benzothiopyran-4(3H)-ylidene)methoxy]acetate (from WO-A-98/13361; CAS Reg. No.: 205121-04-6),

cyanomethoxyimino(phenyl)acetonitrile (cyometrinil),

1,3-dioxolan-2-ylmethoxyimino(phenyl)acetonitrile (oxabetrinil),

4'-chloro-2,2,2-trifluoroacetophenone O-1,3-dioxolan-2-ylmethyloxime (fluxofenim),

4,6-dichloro-2-phenylpyrimidine (fenclorim),

benzyl 2-chloro-4-trifluoromethyl-1,3-thiazole-5-carboxylate (flurazole),

2-dichloromethyl-2-methyl-1,3-dioxolane (MG-191),

including the stereoisomers, and the salts customary in agriculture.

A mixture 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts to be applied in connection with other known active compounds, such as fungicides, insecticides, acaricides, nematicides, bird repellents, plant nutrients and soil structure improvers to transgenic plants containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more

preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705, US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a

mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342 (named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and

being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), is likewise possible.

Some of the safeners are already known as herbicides and accordingly, in addition to the herbicidal action against harmful plants, also act by protecting the crop plants. The weight ratios of herbicide (mixture) to safener generally depend on the herbicide application rate and the effectiveness of the safener in question and may vary within wide limits, for example in the range from 200:1 to 1:200, preferably from 100:1 to 1:100, in particular from 20:1 to 1:20. The safeners may be formulated analogously to the compounds of the formula (I) or their mixtures with other herbicides/pesticides and be provided and used as a finished formulation or as a tank mix with the herbicides.

The required application rate of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts to areas where such transgenic plants containing one or more chimeric gene(s) (I) comprising a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms, consisting of (a) Avena, preferably Avena sativa, more preferably comprising a DNA sequence identical to SEQ ID No. 1 encoding HPPD defined by SEQ ID No. 2, (b) Pseudomonas, preferably Pseudomonas fluorescens, more preferably comprising a DNA sequence identical to SEQ ID No. 3 encoding HPPD defined by SEQ ID No. 4, (c) Synechococcoideae, preferably Synechococcus sp., more preferably comprising a DNA sequence identical to SEQ ID No. 6, encoding HPPD defined by SEQ ID No. 7, (d) Blepharismidae, preferably Blepharisma japonicum, more preferably comprising a DNA sequence identical to SEQ ID No. 8 encoding HPPD defined by SEQ ID No. 9, (e) Rhodococcus, preferably Rhodococcus sp. (strain RHA1), isolate ro03041 more preferably comprising a DNA sequence identical to SEQ ID No. 10 encoding HPPD defined by SEQ ID No. 11, or Rhodococcus sp. (strain RHA1), isolate ro02040, more preferably comprising a DNA sequence identical to SEQ ID No.12 encoding HPPD defined by SEQ ID No. 13 , (f) Picrophilaceae, preferably Picrophilus torridus, more preferably comprising a DNA sequence identical to SEQ ID No. 14 encoding HPPD defined by SEQ ID No. 15, (g) Kordia, preferably Kordia algicida, more preferably comprising a DNA sequence identical to SEQ ID No. 16 encoding HPPD defined by SEQ ID No. 17, or (II) comprising one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, preferably mutants as described in WO 2010/085705,

US6,245,968, WO 2009/144079, WO2011/076877, WO2011/076882, WO2011/076892, WO2011/076885, WO2011/076889, WO 2012/021785, according to the latter, comprising more especially one or more mutated DNA sequences of HPPD encoding genes obtained from maize (Zea mays) or soybean (Glycine max), or (III) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas fluorescens HPPD protein (i) comprising an E (Glu) -> P (Pro) replacement at position 335 and a G (Gly) -> W (Trp) replacement at position 336 (named PfHPPDEvo33 and being disclosed under SEQ ID No:6 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 254), (ii) comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named PfHPPDEvo40 and being disclosed under SEQ ID No:8 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 275), or (iii) comprising an E (Glu) -> P (Pro)replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 296), or (IV) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas (=Comamonas) testosteroni HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> S (Ser) replacement at position 352, and an A (Ala) -> E (Glu) replacement at position 356 (named Axmi428H-Evo40 and being disclosed under SEQ ID No 55 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 32), (ii) comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33), or (V) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas aeruginosa strain ATX22717 HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> S (Ser) replacement at position 338, and an A (Ala) -> E (Glu) replacement at position 342

(named Axmi305H-Evo40 and being disclosed under SEQ ID No 51 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 40), (ii) comprising a E (Glu) -> P (Pro) replacement at position 337, a G (Gly) -> W (Trp) replacement at position 338, a K (Lys) -> A (Ala) replacement at position 341 and an A (Ala) -> Q (Gln) replacement at position 342 (named Axmi305H-Evo41 and being disclosed under SEQ ID No 52 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 41), or (VI) comprising a mutated DNA sequence described in PCT/US2013/59598 (WO2014/043435), more specifically a mutated sequence of the Pseudomonas agarici HPPD protein (i) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> S (Ser) replacement at position 336, and an A (Ala) -> E (Glu) replacement at position 340 (named Axmi309H-Evo40 and being disclosed under SEQ ID No 53 in PCT/US2013/59598 (WO2014/043435), and being disclosed in present application as the HPPD protein sequence under SEQ ID No 36), (ii) comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37), are growing varies depending, inter alia, on external conditions such as temperature and humidity It can vary within wide limits, for example between 0.001 and 10 000 g/ha or more of active substance; however, it is preferably between 0.5 and 5000 g/ha, particularly preferably between 0.5 and 1000 g/ha and very particularly preferably between 0.5 and 500 g/ha.

SEQUENCES LISTING

SEQ ID No. 1: Nucleic acid sequence encoding *Avena sativa* HPPD optimized for the expression in E. coli cells

SEQ ID No. 2: Protein encoded by SEQ ID No. 1

SEQ ID No. 3: Nucleic acid sequence encoding *Pseudomonas fluorescens* HPPD mutated at position 336; mutation Gly => Trp (Pfw336)

SEQ ID No. 4: Protein encoded by SEQ ID No. 3 (PfHPPD336W)

SEQ ID No. 5: Nucleic acid sequence encoding *Pseudomonas fluorescens* HPPD mutated at at position 336; mutation Gly => Trp; optimized for the expression in soybean and cotton

SEQ ID No. 6: Nucleic acid sequence encoding *Synechococcus sp. HPPD*

SEQ ID No. 7: Protein encoded by SEQ ID No. 6

SEQ ID No. 8: Nucleic acid sequence encoding Blepharisma japonicum *HPPD* (FMP37)

SEQ ID No. 9: Protein encoded by SEQ ID No. 8

SEQ ID No. 10: Nucleic acid sequence encoding Rhodococcus sp. (strain RHA1), isolate ro03041 HPPD (FMP22)

SEQ ID No. 11: Protein encoded by SEQ ID No. 10

SEQ ID No. 12: Nucleic acid sequence encoding Rhodococcus sp. (strain RHA1), isolate ro02040 HPPD

SEQ ID No. 13: Protein encoded by SEQ ID No. 12

SEQ ID No. 14: Nucleic acid sequence encoding Picrophilus torridus *HPPD*

SEQ ID No. 15: Protein encoded by SEQ ID No. 14

SEQ ID No. 16: Nucleic acid sequence encoding Kordia algicida HPPD (FMP27)

SEQ ID No. 17: Protein encoded by SEQ ID No. 16

SEQ ID No. 18: Nucleic acid sequence encoding Synechococcus sp. HPPD optimized for the expression in soybean and cotton

SEQ ID No. 19: Nucleic acid sequence encoding Blepharisma japonicum HPPD optimized for the expression in soybean and cotton

SEQ ID No. 20: Nucleic acid sequence encoding Rhodococcus sp. (strain RHA1), isolate ro0341 HPPD optimized for the expression in soybean and cotton

SEQ ID No. 21: Nucleic acid sequence encoding Rhodococcus sp. (strain RHA1), isolate ro0240 HPPD optimized for the expression in soybean and cotton

SEQ ID No. 22: Nucleic acid sequence encoding Picropphilus torridus HPPD optimized for the expression in soybean and cotton

SEQ ID No. 23: Nucleic acid sequence encoding Kordia algicida HPPD optimized for the expression in soybean and cotton

SEQ ID No 24 Nucleic acid sequence encoding Pseudomonas fluorescens HPPD (PfHPPD-Evo33)

mutated at position 335, mutation Glu => Pro;
and mutated at position 336; mutation Gly => Trp

SEQ ID No 25 Protein encoded by SEQ ID No 24.

SEQ ID No 26 Nucleic sequence encoding Pseudomonas fluorescens HPPD (PfHPPD-Evo40) mutated at position 335, mutation Glu-->Pro, mutated at position 336, mutation Gly-->Ser, and mutated at position 340, mutation Ala-->Glu

SEQ ID No 27 Protein encoded by SEQ ID No 26.

SEQ ID No 28 Nucleic acid sequence encoding Pseudomonas fluorescens HPPD (PfHPPD-Evo41)
mutated at position 335, mutation Glu-->Pro,
mutated at position 336, mutation Gly-->Trp,
mutated at position 339, mutation Lys-->Ala,
and mutated at position 340, mutation Ala-->Gln

SEQ ID No 29 Protein encoded by SEQ ID No 28.

SEQ ID No 30 Nucleic acid sequence encoding Pseudomonas (=Comamonas) testosterone Axmi428H HPPD

SEQ ID No 31 Protein encoded by SEQ ID No 30.

SEQ ID No 32 Protein sequence of Pseudomons (=Comamonas) testosteroni Axmi428H HPPD (Axmi428-Evo40)
Mutated at position 351, mutation Glu-->Pro,
mutated at position 352, mutation Gly--> Ser, and
mutated at position 356, mutation Ala -->Glu

SEQ ID No 33 Protein sequence of Pseudomonas (=Comamonas) testosteroni Axmi428H HPPD (Axmi428-Evo41)
mutated at position 351, mutation Glu-->Pro,
mutated at position 352, mutationGly--> Trp,
mutated at position 355, mutation Lys-->Ala, and
mutated at position 356, mutation Ala -->Gln

SEQ ID No 34 Nucleic acid sequence encoding Pseudomonas agarici Axmi309H HPPD.

SEQ ID No 35 Protein encoded by SEQ ID No 34.

SEQ ID No 36 Protein sequence of Pseudomonas agarici Axmi309H HPPD (Axmi309-Evo40)
mutated at position 335, mutation Glu-->Pro,

mutated at position 336, mutation Gly--> Ser, and
mutated at position 340, mutation Ala -->Glu

SEQ ID No 37 Protein sequence of Pseudomonas agarici Axmi309H HPPD (Axmi309-Evo41)
mutated at position 335, mutation Glu-->Pro,
mutated at position 336, mutation Gly--> Trp,
mutated at position 339, mutation Lys-->Ala, and
mutated at position 340, mutation Ala -->Gln

SEQ ID No 38 Nucleic acid encoding of Pseudomonas aeruginosa Axmi305H HPPD.

SEQ ID No 39 Protein encoded by SEQ ID No 38.

SEQ ID No 40 Protein sequence of Pseudomonas aeruginosa Axmi305H (Axmi305-Evo40)
mutated at position 337, mutation Glu-->Pro,
mutated at position 338, mutation Gly--> Ser, and
mutated at position 342, mutation Ala -->Glu

SEQ ID No 41 Protein sequence of Pseudomonas aeruginosa Axmi305H (Axmi305-Evo41)
mutated at position 337, mutation Glu-->Pro,
mutated at position 338, mutation Gly--> Trp,
mutated at position 341, mutation Lys-->Ala, and
mutated at position 342, mutation Ala -->Gln

SEQ ID NO 42 HPPD protein encoded by Avena sativa

SEQ ID No 43 HPPD protein as of SEQ ID No 42 having a deletion at position 109 (Avena sativa Δ A109).

SEQ ID No 44 HPPD protein encoded by Zea mays.

SEQ ID No 45 Nucleic acid encoding of Pseudomonas fluorescens HPPD (PfHPPD).

SEQ ID No 46 Protein encoded by SEQ ID No 45.

Examples

A. Cloning of Avena HPPD (according WO02/46387)

A1- Cloning for expression in E. coli cells

cDNA coding for Avena sativa HPPD (AvHPPD; SEQ ID No. 1) was ordered at GeneArt (Regensburg, Germany) using the codon usage optimized for the expression of the gene in Escherichia coli cells. Upstream to the start codon ATG, was added the sequence corresponding to the recognition site of the restriction enzyme BamHI, and downstream to the stop codon was added the sequence stretch corresponding to the recognition site of the enzyme HindIII. The synthesized fragment was cloned using the restriction enzymes BamHI and HindIII in the previously opened vector pET32a (Novagen, Darmstadt, Germany), in order to obtain a fusion with the HisTag present in the vector at the N-Terminal extremity from the AvHPPD protein (SEQ ID No. 2). The resulting vector was named pET32a-AvHPPDe.

The protein was produced in E.coli and isolated following the standard protocol (as described for example in WO2009/144097).

A2- Cloning of the AvHPPD gene in the pBin19 binary vector for expression in plants

The cDNA corresponding to the gene coding for AvHPPD protein was cut out from the plasmid pET32a-AvHPPDe using the restriction enzymes NcoI and NotI. The overhang sequence resulting from the NotI restriction was filled up, and the consequent fragment was then cloned in the vector pRT100-OTPc (see for example Töpfer (1987), Nucleic Acids Res. 15: 5890, and PCT/EP2010/070561) previously restricted with the enzymes NcoI and SmaI. The resulting plasmid was named pBin19-CaMV35S-OTPc-AvHPPDe-35S, and was used to transform Agrobacterium tumefaciens strain ATHV (see for example PCT/EP2010/070561).

B Cloning of PfHPPD-G336W

B1- Cloning of PfHPPD-G336W for the expression in E. coli cells

The gene coding for the mutant HPPD G336W (SEQ ID No. 3) (US 6,245,968) from Pseudomonas fluorescens in the plasmid pKK233-2 (Clontech) (US 6245968) was

used as template for a PCR to add to the sequence at it 5' extremity the sequence corresponding to the recognition site of the enzyme NcoI and at its 3' extremity the sequence corresponding to the recognition site of the enzyme XbaI. (see WO 2009/144079). The cloning was made in order to obtain a His tag fusion protein at the N-terminal extremity of the Pseudomonas HPPD G336W (SEQ ID No. 4) named "pSE420(RI)NX-PfG336W".

B2 - Cloning of PfHPPD-G336W for the expression in plants

A binary vector for tobacco or soybean transformation is, for example, constructed with the CaMV35 promoter driving the expression of the gene PfHPPD-G336W (SEQID No 5), with a codon usage optimized for the expression in dicotyledoneous plants and at its 5'extremity was added a sequence coding for an OTP, and further upstream a sequence TEV (Tobacco etch virus) to improve the stability of the mRNA in plants followed by the CaMV35S terminator. Additionally, the transformation vector also contains a PAT gene cassette in which the gene is driven by a CaVM35S promoter and followed by a CaMV35S terminator for glufosinate based selection during the transformation process and a 2mEPSPS gene cassette in which the gene is driven by an histone promoter from Arabidopsis to confer tolerance to the herbicide glyphosate to the transformed plants. The binary vector was called pFCO117.

All other mutated Pseudomonas genes and genes obtained from other organisms according to this invention can be cloned in analogy to the above.

B3 – Alternative approach for cloning of HPPD genes into a plant expression cassette.

For each of the HPPD genes described herein, the open reading frame (ORF) is amplified by PCR from a full-length DNA template. Hind III restriction sites are added to each end of the ORFs during PCR. Additionally, the nucleotide sequence ACC is added immediately 5′ to the start codon of the gene to increase translational efficiency (Kozak (1987) Nucleic Acids Research 15:8125-8148; Joshi (1987) Nucleic Acids Research 15:6643-6653). The PCR product is cloned and sequenced using techniques well known in the art to ensure that no mutations are introduced during PCR.

The plasmid containing the PCR product is digested with Hind III and the fragment containing the intact ORF is isolated. This fragment is cloned into the Hind III site of a plasmid such as pAX200, a plant expression vector containing the rice actin promoter (McElroy et al. (1991) Molec. Gen. Genet. 231:150-160) and the PinII terminator (An et

al. (1989) The Plant Cell 1:115-122). The promoter – gene – terminator fragment from this intermediate plasmid is then subcloned into plasmid pSB11 (Japan Tobacco, Inc.) to form a final pSB11-based plasmid. These pSB11-based plasmids are typically organized such that the DNA fragment containing the promoter – gene– terminator construct may be excised by double digestion by restriction enzymes, such as Kpn I and Pme I, and used for transformation into plants by aerosol beam injection. The structure of the resulting pSB11-based clones is verified by restriction digest and gel electrophoresis, and by sequencing across the various cloning junctions.

The plasmid is mobilized into Agrobacterium tumefaciens strain LBA4404 which also harbors the plasmid pSB1 (Japan Tobacco, Inc.), using triparental mating procedures well known in the art, and plating on media containing spectinomycin. The pSB11-based plasmid clone carries spectinomycin resistance but is a narrow host range plasmid and cannot replicate in Agrobacterium. Spectinomycin resistant colonies arise when pSB11-based plasmids integrate into the broad host range plasmid pSB1 through homologous recombination. The cointegrate product of pSB1 and the pSB11-based plasmid is verified by Southern hybridization. The Agrobacterium strain harboring the cointegrate is used to transform maize by methods known in the art, such as, for example, the PureIntro method (Japan Tobacco).

C Mutation of the various HPPD enzymes

C1- First generation point mutant library (as described in detail in PCT/US2013/59598 (WO2014/043435)).

The Pfw336 mutant was further mutagenized at several positions. Randomization of these positions was carried out using the QUIKCHANGE® lightning kit. The theoretical diversity of the library was about 300. Mutants were pooled and transformed into DH5α E. coli cells. Six hundred individual clones were screened for tolerance to the HPPD inhibitor tembotrione (TBT). The clones were grown in LB media plus kanamycin at 37 degrees C in a shaker until an OD600 nm of 0.3 was reached. Cultures were then switched to 30 degrees C and incubated for an additional 17 hours. Cultures were spun down and cell pellets resuspended in 10 mM Hepes/KOH pH 7.6, 4 mM MgCl2, 1 mM DTT. The cells were lysed by bead beating and soluble cell extracts were obtained after centrifugation.

The mutants were analyzed using a brown color assay. Specifically, the HPPD extracts were assayed in 96 well format for HPPD inhibitor tolerance by spotting on solid media containing LB-agar, kanamycin, 5 mM tyrosine, 42 mM succinate and an HPPD inhibitor. In the primary screen, 20 ul extract was spotted in triplicate on plates containing 250 uM tembotrione. Plates were covered with airpore tape and incubated at 37 degrees C. After 24 hours, brown pigment formation was visually compared to a sample containing PfHPPD336W. Variants showing increased pigment formation in the presence of TBT were re-assayed on 250 uM TBT and 250 uM diketonitrile (DKN) active compound of isoxaflutole (IFT). Those variants that again showed improved inhibitor tolerance were again expressed, and extract was titrated on 250 uM TBT and 250 uM DKN to determine the extent of improvement. Extract samples were also analyzed by SDS-PAGE and the extracts were found to contain equal amounts of HPPD protein.

C2 - Second generation permutational library screening (as descrived in detail in PCT/US2013/59598 (WO2014/043435))

The sequences of the top performing first-generation variants were analyzed and a second generation permutational library in the region combining positions 335, 336, 339, 340 was generated. Screening was carried out as described under C1, above. Titration data below shows variant PfHPPDEvo40 had improved tolerance to TBT and DKN compared to PfHPPD336W. SDS-PAGE analysis was carried out and showed no differences in HPPD expression levels between variants.

Variants were also tested by plating whole E. coli cells expressing HPPDs on media containing various HPPD inhibitors. For these experiments, DH5α cells containing HPPD expressing plasmids were grown in LB media + kanamycin until an OD600nm=0.5 was reached. Serial dilutions of cells were prepared in LB media + kanamycin corresponding to OD600 values of 0.016, 0.008, 0.004, and 0.002. Ten microliters of each dilution were plated in triplicate on plates containing no HPPD inhibitor, 250 uM TBT, 250 uM DKN and 250 uM mesotrione (MST). Plates were incubated for 18 hours at 37 degrees C. SDS-PAGE analysis was carried out and showed no differences in HPPD expression levels between variants.

C3 - Preparation of Pseudomonas fluorescens HPPD mutant G336W (Pfw336) and kinetic characterization of the HPPD enzymes.

The native *Pseudomonas fluorescens* HPPD nucleotide sequence (PfHPPD, 1077 bp, as described in WO2009144079), which encodes the amino acid sequence listed herein as SEQ ID No 45, and as described in WO2009144079, WO 96/38567, and in Rüetschi et al. (*Eur. J. Biochem*., 205, 459-466, 1992), was initially cloned into the unique NcoI site of the expression vector pKK233-2 (Pharmacia) that provides a start codon.

At the 5' end, directly downstream to the ATG, a nucleic acid sequence encoding an alanine amino acid and a nucleic acid sequence encoding a N-terminal HIS6-Tag was inserted. Upstream to the ATG, two additional cysteine base pairs were added in order to obtain a sequence corresponding to the recognition site of the restriction enzyme NcoI and downstream to the stop codon the sequences corresponding to the recognition site of the restriction enzyme XbaI were added. The DNA sequence corresponding to the gene, including the sequence encoding the HIS-TAG, was cut with the restriction enzymes NcoI and XbaI, and then cloned into the modified expression vector pSE420(RI)NX (5261 bp).

The cloning and expression vector pSE420(RI)NX (5261 bp) is based on the plasmid pSE420 by Invitrogen (Karlsruhe, Germany). Modifications of this vector include the addition of a nptII gene (neomycin phosphotransferase; Sambrook and Russell, 2001, Molecular Cloning: a laboratory manual (Third edition)) conferring tolerance to the antibiotic kanamycin and which is missing the majority of the superlinker region (multiple cloning site).

The plasmid possesses the trp-lac (trc) promoter and the $lacI^q$ gene that provides the lac repressor in every *E. coli* host strain. The lac repressor binds to the lac operator (lacO) and restricts expression of the target gene; this inhibition can be alleviated by induction with Isopropyl β-D-1-thiogalactopyranoside (IPTG).

The resulting vector was called pSE420(RI)NX-PfHPPD and it was used to transform *Escherichia coli* BL21 cells (Merck, Darmstadt, Germany).

The plasmid pSE420(RI)NX-PfHPPD was subjected to PCR-mediated site-directed mutagenesis to alter a defined codon at corresponding sites of the PfHPPD gene. The codon encoding Glycine (G) at position 336 was replaced by a codon encoding tryptophan (W). The resulting mutant was called Pfw336, and the resulting vector pSE420(RI)NX-Pfw336.

Expression of HPPD was carried out in *E. coli* K-12 BL21 containing pSE420(RI)NX-PfHPPD or pSE420(RI)NX-Pfw336. Cells were allowed to grow until OD reached 0.5, then expression was initiated from the trp-lac (trc) promoter by induction with 1 mM

IPTG which binds to the lac repressor and causes its dissociation from the lac operon. Expression was carried out over 15 h at 28 °C.

To prepare the pre-starter culture, 2 mL of TB medium (100 µg*mL^{-1} carbenicillin) were inoculated with 50 µL of an *E. coli* K-12 BL21 glycerol stock. The pre-starter culture was incubated at 37 °C with shaking at 140 rpm for 15 h. 200µl of the pre-starter culture was used to initiate the starter culture (5mL TB supplement with 100 µg*L^{-1}), which was incubated 3 h at 37°C.

To prepare the main culture, 400 mL of TB medium (100 µg*mL^{-1} carbenicillin) were inoculated with 4 mL of the starter culture. This starter culture was incubated at 37 °C with shaking at 140 rpm until OD_{600} 0.5 was reached. Then recombinant protein expression was induced with 400 µl of 1M IPTG solution. The cells were allowed to grow for an additional hour under these conditions, then the temperature was lowered to 28°C and the culture was shaken at 140 rpm for 15 h. Cells were harvested by centrifugation at 6000 x g for 15 min at 4 °C. Then cell pellets were stored at -80 °C.

D - Production of HPPD protein in E coli, purification via His-Tag

The *Arabidopsis thaliana* AtHPPD coding sequence (1335 bp; Genebank AF047834; WO 96/38567) was initially cloned into the expression vector pQE-30 (QIAGEN, Hilden, Germany) in between the restriction sites of BamHI and HindIII. The obtained vector was called “pQE30-AtHPPD” (see WO 2009/144079).

The plasmid possesses the trp-lac (trc) promoter and the *lac*I^q gene that provides the *lac* repressor in every *E. coli* host strain. The *lac* repressor binds to the *lac* operator (*lac*O) and restricts expression of the target gene; this inhibition can be alleviated by induction with Isopropyl β-D-1-thiogalactopyranoside (IPTG).

All above defined E. coli expression vectors were used to transform *Escherichia coli* BL21 cells (Merck, Darmstadt, Germany).

For the AtHPPD (*Arabidopsis thaliana* HPPD) that was used as reference see WO 2009/144079.

Expression of HPPD was carried out in *E. coli* K-12 BL21 containing pQE30-*AtHPPD*, pET32a-AvHPPDe, pSE420(RI)NX-Pfw336 , pSE420(RI)NX-FMP27 or pSE420(RI)NX-FMP37. Cells were allowed to grow until OD reached 0.5, then expression was initiated from the trp-lac (trc) promoter by induction with 1 mM IPTG

which binds to the *lac* repressor and causes its dissociation from the *lac* operon. Expression was carried out over 15 h at 28 °C.

To prepare the pre-starter culture, 2 mL of TB medium (100 µg*mL^{-1} carbenicillin) were inoculated with 50 µL of an *E. coli* K-12 BL21 glycerol stock. The pre-starter culture was incubated at 37 °C with shaking at 140 rpm for 15 h. 200µl of the pre-starter culture was used to initiate the starter culture (5mL TB supplement with 100 µg*L^{-1}), which was incubated 3 h at 37°C.

To prepare the main culture, 400 mL of TB medium (100 µg*mL^{-1} carbenicillin) were inoculated with 4 mL of the starter culture. This starter culture was incubated at 37 °C with shaking at 140 rpm until OD_{600} 0.5 was reached. Then recombinant protein expression was induced with 400 µl of 1M IPTG solution. The cells were allowed to grow for an additional hour under these conditions, then the temperature was lowered to 28°C and the culture was shaken at 140 rpm for 15 h. Cells were harvested by centrifugation at 6000 x g for 15 min at 4 °C. Then cell pellets were stored at -80 °C.

D1 - Isolation and purification of His_6-tagged HPPD in native form

Lysis of cells

Cells were lysed using Lysozyme, an enzyme that cleaves the 1,4-β-linkages between N-acetylmuramic acid and N-acetyl-D-glucosamine residues in peptidoglycan which forms the bacterial cell wall. Cell membranes were then disrupted by the internal pressure of the bacterial cell. In addition, the lysis buffer contained Benzonase® Nuclease, an endonuclease that hydrolyzes all forms of DNA and RNA without damaging proteins and thereby largely reduces viscosity of the cell lysate. Lysis under native conditions was carried out on ice.

For purification of His_6-tagged proteins the QIA*express*® Ni-NTA Fast Start Kit was used following the user manual instruction.

D2 - Purification of His_6-tagged proteins by immobilized metal ion affinity chromatography (IMAC)

The cleared cell lysate (10 mL) obtained after centrifugation of the lysis reaction was loaded onto a Ni-NTA Fast Start Column from the QIA*express*® Ni-NTA Fast Start Kit (Qiagen, Hilden, Germany) and purification was carried out according to the instruction manual. The His_6-tagged protein was eluted with 2.5 mL of elution buffer.

D3 - Desalting of HPPD solutions by gel filtration

HPPD solutions eluted from a Ni-NTA Fast Start Column with 2.5 mL of elution buffer were applied to a Sephadex G-25 PD-10 column (GE Healthcare, Freiburg, Germany) following the user manual instruction. After the whole sample had entered the gel bed, elution was performed with 3.5 mL of storage buffer.

The HPPD solutions eluted from the desalting column were frozen at -80 °C in 1 mL aliquots.

D4 - Determination of HPPD protein concentration using the Bradford protein assay

Protein concentration was determined using the standard Bradford assay (Bradford, (1976), Anal Biochem 72: 248-254).

D5 - Determination of purity of HPPD solutions using SDS-PAGE

The integrity of the eluted protein was checked by SDS-PAGE protein gel electrophoresis using the gel NuPAGE® Novex 4-12 % Bis-Tris Gels (Invitrogen, Karlsruhe, Germany), approximately 10 µg of protein were loaded. 10 µL of Laemmli Sample Buffer was added to 1-10 µL of protein solution and the mixture was incubated at 90 °C for 10 min. After short centrifugation step, the whole mixture was loaded into a slot of an SDS gel previously fixed in a XCell *SureLock*™ Novex Mini-Cell gel chamber filled with NuPAGE® MOPS SDS Running Buffer (diluted from the 20 x-solution with ddH_2O). A voltage of 150 was then applied to the gel chamber for 1 h. For staining of protein bands, the gel was immersed in Coomassie Brilliant Blue R-250 Staining Solution. For destaining of the polyacrylamide gel, it was immersed in Coomassie Brilliant Blue R-250 Destaining Solution until protein bands appear blue on a white gel.

E - Determination of HPPD activity in presence of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide

pI50-values (the log value of the concentration of inhibitor necessary to inhibit 50% of the enzyme activity in molar concentration, see 3rd column of Table 1) for 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide were determined from dose-response plots of HPPD activity versus inhibitor concentration using the the so-called HGD assay and the 4 Parameter Logistic Model or Sigmoidal Dose-Response Model of the ID Business Solutions Ltd. XLfit software suite. With the HGD assay HPPD activity was measured at room temperature by adding appropriate

amounts of HPPD to a solution of 200 mM Tris-HCl pH 7.6, 10 mM ascorbate, 20 µM FeSO4, 650 units of catalase, 8 µg HGA dioxygenase (HGA: homogentisate) and 600 µM HPP in a total volume of 1 ml. Initial reaction rates were determined from the increase in absorbance at 318 nm due to the formation of maleylacetoacetate (ε318 = 11,900 M-1 cm-1).

In cases, the symbol “>” is used this means that the value was far higher than the one indicated but could not be precisely calculated within in the range of concentration of inhibitor tested.

In the 1st column of Table 1, the HPPD employed in the assay is named and in the 2nd column of Table 1, the corresponding SEQ ID No of present invention is disclosed.

In the 4th column of Table 1, the inhibition of the enzyme activity of the resepective enzyme at the 0.2µM concentration of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide is disclosed.

All results are shown in Table 1.

Table 1

HPPD	SEQ ID No	pI_{50}	% inhibition at 0.2 µM
PfHPPD	46	7,0	76
PfHPPD336W	4	6,7	76
PfHPPD-Evo33	25	6,6	39
PfHPPD-Evo40	27	6,6	40
PfHPPD-Evo41	29	6,7	50
Axmi428H	31	7,0	71
Axmi428H-Evo40	32	5,6	8
Axmi428H-Evo41	33	6,0	25
Axmi309H	35	7,1	78
Axmi309H-Evo41	37	6,5	26
FMP22	11	5,9	0
FMP27	17	6,5	29
FMP37	9	5,3	0
Avena sativa Δ A109	43	5.7	8

These data show that the HPPD derived from various organisms do show an acceptable tolerance to 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide (see PfHPPD, Axmi309H, FMP22, FMP27, FMP37) and certain mutants of some of the before (see PfHPPD336W, PfHPPD-Evo33, PfHPPD-Evo40, PfHPPD-Evo41, Axmi428H-Evo40, Axmi428H-Evo41, Axmi309H-Evo41) are even less sensitive to 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide.

F - Soybean transformation

Soybean transformation is achieved by using methods well known in the art, such as the one described using the Agrobacterium tumefaciens mediated transformation soybean half-seed explants using essentially the method described by Paz et al. (2006), Plant cell Rep. 25:206. Transformants are identified using various HPPD inhibitors as selection marker. The appearance of green shoots can be observed, and documented as an indicator of tolerance to the respective herbicide. The tolerant transgenic shoots will show normal greening comparable to wild-type soybean shoots not treated with the respective HPPD inhibitor, whereas wild-type soybean shoots treated with the same amount of the respective HPPD inhibitpr will be entirely bleached. This indicates that the presence of the HPPD protein enables the tolerance to HPPD inhibitor herbicides.

Tolerant green shoots are transferred to rooting media or grafted. Rooted plantlets are transferred to the greenhouse after an acclimation period. Plants containing the transgene are then sprayed with HPPD inhibitor herbicides, as for example with tembotrione at a rate of 100g AI/ha. Ten days after the application the symptoms due to the application of the herbicide are evaluated and compared to the symptoms observed on a wild type plants under the same conditions.

Soybean plants obtained according to the above are used for collecting field trial data.

G - Cotton T0 plant establishment and selection.

Cotton transformation is achieved by using methods well known in the art, especially preferred method in the one described in the PCT patent publication WO 00/71733. Regenerated plants are transferred to the greenhouse. Following an acclimation

period, sufficiently grown plants are sprayed with HPPD inhibitor herbicides as for example tembotrione equivalent to 100 gAI/ha supplemented with ammonium sulfate and methyl ester raps oil. Seven days after the spray application, the symptoms due to the treatment with the herbicide are evaluated and compared to the symptoms observed on wild type cotton plants subjected to the same treatment under the same conditions.

H - Transformation of Maize Plant Cells by Agrobacterium-Mediated Transformation

Constructing the plant expression cassette for stable expression in the maize plant and maize transformation are well known in the art and in this particular example the methods were described and used from the PCT patent publication W02014/043435 and WO2008/100353. The polynucleotide sequences encoding the HPPD variants (PCT/US2013/59598 (WO2014/043435)) have been stacked with a DNA sequence encoding an EPSPS protein to confer tolerance to herbicides, which target the EPSPS. The EPSPS gene was isolated from Arthrobacter globiformis (WO2008/100353) and joined in-frame to a transit peptide sequence to guide translocation of the translated protein to the chloroplast. Stable expression was achieved with an ubiquitous promoter (Ubiquitin 4 promoter from sugarcane, U.S. Patent 6,638,766), and a 35S terminator sequence from Cauliflower Mosaic Virus, which was cloned upstream and downstream of the EPSPS gene, respectively.

The corresponding HPPD variants were cloned with the same promoter, chloroplast transit peptide, and terminator sequence as described for the EPSPS gene expression cassette. The coding sequences for both genes have been codon optimized for maize expression.

For maize transformation ears were best collected 8-12 days after pollination. Embryos were isolated from the ears, and those embryos 0.8-1.5 mm in size were preferred for use in transformation. Embryos were plated scutellum side-up on a suitable incubation media, and incubated overnight at 25°C in the dark.However, it is not necessary per se to incubate the embryos overnight. Embryos were contacted with an Agrobacterium strain containing the appropriate vectors having a nucleotide sequence of the present invention for Ti plasmid mediated transfer for about 5-10 min, and then plated onto co-cultivation media for about 3 days (25°C in the dark). After co-cultivation, explants were transferred to recovery period media for about five days (at 25°C in the dark). Explants were incubated in selection media with glyphosate for up to eight weeks, depending on the nature and characteristics of the particular selection

utilized. After the selection period, the resulting callus was transferred to embryo maturation media, until the formation of mature somatic embryos was observed. The resulting mature somatic embryos were then placed under low light, and the process of regeneration was initiated as known in the art. The resulting shoots were allowed to root on rooting media, and the resulting plants are transferred to nursery pots and propagated as transgenic plants. Plants were routinely analyzed for the expression and presence of the transgenes using the ELISA protein detection method. Only plants recovering in the selection media and having a detectable HPPD transgene protein expression were used for the herbicide tolerance analysis.

I – Herbicide tolerance evaluation of transgenic plants expressing mutated HPPD protein variants

I1 – Greenhouse trials with transgenic maize T0 plants

Regenerated T0 events from tissue culture were transplanted into two inch square pots with synthetic soil (Fafard® Mix) and controlled-released fertilizer (Haifa Multicote™; polymer-coated controlled-release fertilizer, NPK Pro 18-6-12 + Micronutrients) and cultivated in the greenhouse (GH) under supplementary high pressure sodium light for 12 days at a maximum of 30°C during the day and a minimum of 22°C at night. Fully recovered plants were transferred into five inch square pots filled with synthetic soil and control released fertilizer under the same environmental conditions. After seven days the T0 plants have been sprayed with 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide either at 25g AI/ha (with “g AI/ha” meaning “gram of active ingredient per hectare”), 50g AI/ha, or 100g AI/ha prepared from a WP20 (wettable powder 20%) formulation supplemented with esterified vegetable oil mixture (Hasten™ spray adjuvants, 0.578% v/v) and ammonium sulphate (AMS, 0.97% w/v). All herbicide treatments were conducted in a DeVries Tracker Sprayer system with standard application protocols, which are well known in the art. As a spray control T0 events have been sprayed with the adjunvant mixture lacking the herbicide. All T0 events sprayed with this mixture did not show bleached leaves.
If not stated otherwise, six days after treatment (DAT) of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide the damage of transgenic T0 events were evalutated.

T0 events, which express the EPSPS selectable marker gene and do not possess a HPPD variants type, were used as control maize plants and exhibited 100% leaf damage already at 25 g AI/ha of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide.

Non-transformed maize plants also exhibited 100% leaf damage already at 25 g AI/ha of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide.

Table 2 summarizes results of transgenic maize plants expressing mutants of the *Pseudomonas fluorescens* HPPD protein comprising an E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named PfHPPDEvo41 and being disclosed under SEQ ID No:16 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application under SEQ ID No. 29), or a mutated sequence of the *Pseudomonas* (=*Comamonas*) *testosteroni* HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 351, a G (Gly) -> W (Trp) replacement at position 352, a K (Lys) -> A (Ala) replacement at position 355 and an A (Ala) -> Q (Gln) replacement at position 356 (named Axmi428H-Evo41 and being disclosed under SEQ ID No 56 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 33) or a mutated sequence of the *Pseudomonas agarici* HPPD protein comprising a E (Glu) -> P (Pro) replacement at position 335, a G (Gly) -> W (Trp) replacement at position 336, a K (Lys) -> A (Ala) replacement at position 339 and an A (Ala) -> Q (Gln) replacement at position 340 (named Axmi309H-EVO41 and being disclosed under SEQ ID No 54 in PCT/US2013/59598 (WO2014/043435) and being disclosed in present application as the HPPD protein sequence under SEQ ID No 37).

Control maize plants express the EPSPS selectable marker gene and do not possess a HPPD protein variant. Plants classified with a rating of “0” showed severe bleaching of the leaf at a range of 41% to 100% damage of the total leaf area. A rating of “1” was assigned to plants having a moderate tolerance with 16% to 40% damage of total leaf area. A rating of “2” was assigned to plants with good tolerance within the range of 6% to 15% damage of total leaf area. Plants with a rating of “3” showed almost no bleaching with 5% or less of the leaf area damaged by the herbicide treatment.

The results in Table 2 show that the tested maize events expressing transgenic HPPD proteins are more tolerant to the HPPD herbicide 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide at agronomically relevant doses compared to control plants.

All control events exhibited severe bleaching symptoms already at a herbicide concentration of 25g of AI/ha. In contrast ~70 % of tested events expressing PfHPPDEvo41 (n=21) and Axmi428H-Evo41 (n=29) showed a high tolerance with 5% or less bleached leaf area after treatment with a 100g AI/ha herbicide concentration of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide. Also 60% of the tested HPPD variant Axmi309H-Evo41 confer acceptable resistance with 15% or less bleached leaf area after the same treatment with 100g AI/ha.

Table 2

Evaluation of leaf area damage from maize control plants and maize transgenic T0 events six days after the application of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide at a rate of 25 – 100 g AI/ha. Following herbicide tolerance classes have been defined: “0”= marginal tolerance; 41% - 100% damaged leaf area; “1”= moderate tolerance; 16% - 40% damaged leaf area; “2”= good tolerance; 6% - 15% damaged leaf area; “3”= high tolerance; 0% - 5% damaged leaf area.The herbicide were applied to plants originated from 9, 12, and 1 independent transgenic events for PfHPPDEvo41, Axmi428H-Evo41, and Axmi309H-Evo41, respectively.

Maize Events	Herbicide tolerance classes				Total number events
	0	1	2	3	
2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide concentration: 25 g AI/ha					
Control	5*	0	0	0	5
PfHPPDEvo41	6	0	1	28	35
2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide concentration: 50 g AI/ha					
Control	4	0	0	0	4
PfHPPDEvo41	1	0	2	28	31
Axmi428H-Evo41	0	0	0	7	7
2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide concentration: 100 g AI/ha					
Control	50	0	0	0	50
PfHPPDEvo41	4	0	2	15	21
Axmi428H-Evo41	3	4	1	21	29
Axmi309H-Evo41	5	9	16	6	36

Note: *evaluation 9 days after treatment

I1 – Greenhouse trials with transgenic soybean T1 plants

Wild type soybean (Merlin and Thorne) and transgenic soybean T1 plants expressing the variant of the *Pseudomonas fluorescens* HPPD protein PfHPPD-G336W (WO99/24585), or PfHPPD-Evo33, or PfHPPD-Evo40, or PfHPPD-Evo41 (PCT/US2013/59598(WO2014/043435)) were sprayed at the V2-V3 stage of soybean development with 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide of formulation type WP20 (concentration range of 6.25g AI/ha – 75g AI/ha) supplemented with ammonium sulfate and methylated rape seed oil (Actirob). As a spray control, wild type soybean (Merlin and Thorne) and transgenic soybean T1 plants have been sprayed with the adjunvant mixture lacking the

herbicide. Herbicide tolerance was evaluated 21 days after spraying. The following herbicide tolerance classes have been defined for scoring: “0”= marginal tolerance; 41% - 100% damaged leaf area; “1”= moderate tolerance; 16% - 40% damaged leaf area; “2”= good tolerance; 6% - 15% damaged leaf area; “3”= high tolerance; 0% - 5% damaged leaf area.

Table 3 summarizes the results of the *in planta* HPPD inhibitor tolerance analysis. All plants (including the wild type soybean events), which have been treated with the control adjuvant mixture without herbicide, did not develop bleached leaf area. The wild type soybean plants (Merlin and Thorne) already showed a severe bleaching of 45%-50% of the total leaf area at a concentration of 6.25 g of AI/ha of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide followed by 90-100% damaged leaf area at a higher concentration of 25 g of AI/ha. Most of the transgenic soybean T1 plants expressing the variant of the *Pseudomonas fluorescens* HPPD protein PfHPPD-G336W, or PfHPPD-Evo33, or PfHPPD-Evo40, or PfHPPD-Evo41 conferring high tolerance to a concentration of 25 g AI/ha.

Several transgenic soybean T1 plants expressing the variant of the *Pseudomonas fluorescens* HPPD protein PfHPPD-Evo41 also exhibit high tolerance to 50 g AI/ha with less than 5% damaged leaf area. Hence PfHPPD-Evo41 events were more tolerant to 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide than events expressing PfHPPD-G336W.

Table 3

Evaluation of the HPPD inhibitor tolerance from wild type (wt) soybean plants (Merlin and Thorne) and T1 soybean transgenic events expressing the variant of the *Pseudomonas fluorescens* HPPD protein PfHPPD-G336W (WO99/24585), or PfHPPD-Evo33, or PfHPPD-Evo40, or PfHPPD-Evo41 (PCT/US2013/59598 (WO2014/043435)). Plants were treated with 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide with a final concentration of 6.25, 25, 50, or 75 g AI/ha. Herbicide tolerance has been scored after 21 days of treatment. As a control wild type soybean and transgenic soybean T1 plants were treated with the spray mix lacking the herbicide 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide. All these control plants did not show bleached leaf area. Following leaf area damage classes have been defined for herbicide tolerance scoring: “0”= marginal tolerance; 41% - 100% damaged leaf area; “1”= moderate tolerance; 16% - 40% damaged leaf area; “2”= good tolerance; 6% - 15% damaged leaf area; “3”= high tolerance; 0% - 5% damaged leaf area.

Soybean Events	Herbicide tolerance classes				Total number events
	0	1	2	3	
2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide concentration: 6.25 g AI/ha					
Merlin (wt)	4	0	0	0	4
Thorne (wt)	4	0	0	0	4
PfHPPD-Evo33	1	0	0	11	12
PfHPPD-Evo40	0	0	0	4	4
PfHPPD-Evo41	0	0	0	12	12
PfHPPD-G336W	0	0	0	12	12
2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide concentration: 25 g AI/ha					
Merlin	4	0	0	0	4
Thorne	4	0	0	0	4
PfHPPD-Evo33	1	0	2	13	16
PfHPPD-Evo40	2	7	1	6	16
PfHPPD-Evo41	2	8	1	21	32
PfHPPD-G336W	0	0	0	16	16
2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide concentration: 50 g AI/ha					
PfHPPD-Evo33	0	4	0	0	4
PfHPPD-Evo40	0	4	0	0	4
PfHPPD-Evo41	0	1	0	3	4
PfHPPD-G336W	0	4	0	0	4
2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide concentration: 75 g AI/ha					
PfHPPD-Evo33	0	4	0	0	4
PfHPPD-Evo40	0	4	0	0	4
PfHPPD-Evo41	0	4	0	0	4
PfHPPD-G336W	0	3	1	0	4

J Field Trials

Field Trials concerning weed efficacy of various combinations of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide (component (A) and other herbicidal active compounds (component (B))

J A) Test-method

The experiments were conducted as post applied field trials with an application volume of 200 liter water per hectare and two repetitions.

The evaluation 14 days after application was assessed visually.

Treated plants were compared to untreated plants (0-100% scale).

The results (as a mean of 2 replicates) are reported in the tables below.

The application rates of the herbicidal active ingredients when used alone or in combinations are given in the tables below.

As a standard, the adjuvant system Stefes Mero® was used

J B) Abbreviations used in Tables 4 - 7

Dose g ai/ha = Application rate in grams of active ingredient per hectare

EC = Expected value according to Colby (E^C = A+B)

Δ = Difference (%) of measured value -% - to the expected value -% (measured value minus expected value)

Assessment = measured values: for each (A) + (B) in%

Evaluation: - Measured value (%) is greater > than E^C > synergism (+ Δ)

Measured value (%) is equal to or E^C > Additive effect (Δ +_0)

J C) Field data results for 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide in combination with other herbicidal compounds are shown in Tables 4 to 7, below.

All these data demonstrate the syngerstic effects of such combinations on various weeds.

Table 4: 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide plus Atrazine

Active ingredient(s)	Dose g ai/ha	Efficacy [1)] (%)
		Euphorbia heterophylla
(A) 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide	75	35
(A) 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide	25	15
(B) Atrazine	1000	74
(A) + (B)	75+1000	100 (E^C = 83 ; Δ +17)
(A) + (B)	25+1000	92 (E^C = 78 ; Δ +14)

Application at 5 leaf stage; Assessment 14 days after application

Table 5: 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide plus Glufosinate-ammonium

Active ingredient(s)	Dose g ai/ha	Efficacy [1)] (%)
		Amaranthus retroflexus
(A) 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide	50	65
(B) Glufosinate-ammonium	500	33
(A) + (B)	50+500	90 (E^C = 77 ; Δ +13)

Application at 6 leaf stage; Assessment 14 days after application

Table 6: 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide plus Glyphosate

Active ingredient(s)	Dose g ai/ha	Efficacy [1)] (%)
		Ipomoea aristolochiaefolia
(A) 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide	50	15
(A) 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide	25	10
(B) Glyphosate	960	70
(A) + (B)	50+960	89 (E^C = 75 ; Δ +14)
(A) + (B)	25+960	85 (E^C = 73 ; Δ +12)

Application at 6 leaf stage; Assessment 14 days after application

Table 7: 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide plus Metribuzin

Active ingredient(s)	Dose g ai/ha	Efficacy [1)] (%)
		Digitaria horizontalis
(A) 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide	50	70
(B) Metribuzin	480	35
(B) Metribuzin	240	15
(A) + (B)	50+480	100 (E^C = 81 ; Δ +19)
(A) + (B)	50+240	90 (E^C = 75 ; Δ +15)

Application at 2 tillers; Assessment 14 days after application

Comparable results have been obtained by the application of further combinations according the invention.

All publications and patent applications mentioned in the specification are indicative of the level of skill of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

Claims

1. The use of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts for controlling unwanted plants in areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides by containing one or more chimeric gene(s) comprising (I) a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, (b) Pseudomonas, (c) Synechococcoideae, (d) Blepharismidae, (e) Rhodococcus, (f) Picrophilaceae, (g) Kordia, or (II) one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms, or (III) one or more DNA sequences encoding mutated maize (Zea mays) or soybean (Glycine max) HPPD each being mutated as described in WO 2012/021785.

2. The use of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts according to claim 1, wherein at least one of the chimeric genes contained in the transgenic crop comprises a DNA encoding a hydroxyphenylpyruvate dioxygenase (HPPD) selected from the group consisting of SEQ ID No.2, SEQ ID No. 4, SEQ ID No. 7, SEQ ID No. 9, SEQ ID No. 11, SEQ ID No. 13, SEQ ID No 15, SEQ ID No. 17, SEQ ID No, 25, and SEQ ID No 27, SEQ ID No. 29, SEQ ID No 31, SEQ ID No 32, SEQ ID No 33, SEQ ID No 35, SEQ ID No 36, SEQ ID No 37, SEQ ID No 39, SEQ ID No 40, SEQ ID No 41, SEQ ID No 43, SEQ ID No 46.

3. A method for controlling unwanted plants comprising the application of 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts according to claim 1 in areas of transgenic crop plants being tolerant to HPPD inhibitor herbicides by containing one or more chimeric gene(s) comprising (I) a DNA sequence encoding hydroxyphenylpyruvate dioxygenase (HPPD) derived from a member of a group of organisms consisting of (a) Avena, (b) Pseudomonas, (c) Synechococcoideae, (d) Blepharismidae, (e) Rhodococcus, (f) Picrophilaceae, (g) Kordia, or (II) one or more mutated DNA sequences of HPPD encoding genes of the before defined organisms or (III) or (III) one or more DNA sequences encoding mutated maize (Zea mays) or soybean (Glycine max) HPPD each being mutated as described in WO 2012/021785., and in which the application is performed to (a) the

unwanted plants, (b) to the seeds of unwanted plants, and/or (c) to the area on which the plants grow.

4. A method according to claim 3, wherein at least one of the chimeric gene contained in the transgenic crop comprises a DNA encoding a hydroxyphenylpyruvate dioxygenase (HPPD) selected from the group consisting of SEQ ID No.2, SEQ ID No. 4, SEQ ID No. 7, SEQ ID No. 9, SEQ ID No. 11, SEQ ID No. 13, SEQ ID No 15, SEQ ID No. 17, SEQ ID No, 25, and SEQ ID No 27, SEQ ID No. 29, SEQ ID No 31, SEQ ID No 32, SEQ ID No 33, SEQ ID No 35, SEQ ID No 36, SEQ ID No 37, SEQ ID No 39, SEQ ID No 40, SEQ ID No 41, SEQ ID No 43, SEQ ID No 46.

5. A method according to claim 3 or 4, in which the transgenic crop plant belongs to the group of dicotyledonous crops consisting of Arachis, Beta, Brassica, Cucumis, Cucurbita, Helianthus, Daucus, Glycine, Gossypium, Ipomoea, Lactuca, Linum, Lycopersicon, Nicotiana, Phaseolus, Pisum, Solanum, and Vicia, or to the group of monocotyledonous crops consisting of Allium, Ananas, Asparagus, Avena, Hordeum, Oryza, Panicum, Saccharum, Secale, Sorghum, Triticale, Triticum, Zea.

6. A method according to any one of claims 3, 4 or 5, in which 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts is applied in combination with one or more HPPD inhibitor herbicides selected from the group consisting of triketone or pyrazolinate herbicide in mixed formulations or in the tank mix, and/or with further known active substances which are based on the inhibition of acetolactate synthase, acetyl-CoA carboxylase, cellulose synthase, enolpyruvylshikimate-3-phosphate synthase, glutamine synthetase, p-hydroxyphenylpyruvate dioxygenase, phytoene desaturase, photosystem I, photosystem II, protoporphyrinogen oxidase, or act as growth regulators.

7. A method according to claim 6, in which2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-yl)-4-(trifluoromethyl)benzamide or its salts is applied in combination with one or more other HPPD inhibitor herbicides selected from the group consisiting of tembotrione, mesotrione, bicyclopyrone, tefuryltrione pyrasulfotole, pyrazolate, diketonitrile, benzofenap, or sulcotrione.

8. Composition comprising 2-chloro-3-(methylsulfanyl)-N-(1-methyl-1H-tetrazol-5-

yl)-4-(trifluoromethyl)benzamide or its salts (component (A)) and one or more, preferably one, component(s) (B) selected from the sub-groups B1 to B11, with:

B1 consisting of 1,3-diketo compounds, comprising
prohexadione, prohexadione-calcium, trinexapac-ethy,
alloxydim, alloxydim-sodium, butroxydim, clethodim, cycloxydim,
ketospiradox, profoxydim, sethoxydim, tepraloxydim, tralkoxydim,
mesotrione, sulcotrione, tefuryltrione, tembotrione, bicyclopyrone,
fenquinotrione, SL-261,
pinoxaden,

B2 consisting of (sulfon)amides, comprising
beflubutamide, bromobutide, dimethenamide, dimethenamide-P,
diphenamide, napropamide, pethoxamid, N-[3-chloro-4-(1-methylethyl)-phenyl]-2-methylpentanamide,
naptalam, propyzamide,
diflufenican, etobenzanid, flufenacet, mefenacet, mefluidide,
pentanochlor, picolinafen, propanil, N-phenylphthalamic acid,
acetochlor, alachlor, amidochlor, butachlor, butenachlor, dimethachlor,
metazachlor, metolachlor, S-metolachlor, pretilachlor, propachlor,
propisochlor, (2-chloro-6'-ethyl-N-isopropoxymethylaceto-o-toluidide),
thenylchlor,
asulam, carbaryl, carbetamide, chlorpropham, desmedipham,
phenmedipham, propham,
butylate, cycloate, dimepiperate, EPTC, esprocarb, methasulfocarb,
molinate, orbencarb, pebulate, prosulfocarb, pyributicarb, thiobencarb, tri-allate, vernolate,
amidosulfuron, azimsulfuron, bensulfuron, bensulfuron-methyl,
clorimuron, chlorimuron-ethyl, chlorsulfuron, cinosulfuron,
cyclosulfamuron, ethametsulfuron, ethametsulfuron-methyl,
ethoxysulfuron, flazasulfuron, flucetosulfuron, flupyrsulfuron-methyl-sodium, foramsulfuron, halosulfuron-methyl, imazosulfuron, iodosulfuron,
iodosulfuron-methyl-sodium, mesosulfuron, mesosulfuron-methyl,
metazosulfuron, methiopyrsulfuron, metsulfuron, metsulfuron-methyl,
monosulfuron, monosulfuron-ester, nicosulfuron, orthosulfamuron,

oxasulfuron, primisulfuron-methyl, propyrisulfuron, prosulfuron, pyrasulfuron, pyrazosulfuron-ethyl, rimsulfuron, sulfometuron, sulfometuron-methyl, sulfosulfuron, thifensulfuron, thifensulfuron-methyl, triasulfuron, tribenuron, tribenuron-methyl, trifloxysulfuron, trifloxysulfuron (sodium), triflusulfuron, triflusulfuron-methyl, tritosulfuron, (benzoic acid, 2-[[[[[4-methoxy-6-(methylthio)-2-pyrimidinyl]amino]carbonyl]amino]sulfonyl]methyl ester), flucarbazone, flucarbazone-sodium, ipfencarbazone, propoxycarbazone, propoxycarbazone-sodium, thiencarbazone, thiencarbazone-methyl, cloransulam, cloransulam-methyl, diclosulam, florasulam, flumetsulam, metosulam, penoxsulam, pyroxsulam, 3-chloro-N-[(4,6-dimethoxypyrimidin-2-yl)carbamoyl]-1-methyl-4-(5-methyl-5,6-dihydro-1,4,2-dioxazin-3-yl)-1H-pyrazole-5-sulfonamide,

B3 consisting of arylnitriles, comprising bromoxynil, bromoxynil-butyrate, bromoxynil-potassium, bromoxynil-heptanoate, bromoxynil-octanoate, detosyl-pyrazolate (DTP), dichlobenil, ioxynil, ioxynil-octanoate, ioxynil-potassium, ioxynil-sodium, pyraclonil,

B4 consisting of azoles, comprising benzofenap, pyrazolynate (pyrazolate), pyrazoxyfen, pyroxasulfone, topramezone, pyrasulfotole, tolpyralate, 3-(3-chloro-5-{[1-methyl-3-(trifluoromethyl)-1H-pyrazol-5-yl]oxy}phenoxy)-1-methyl-5-(trifluoromethyl)-1H-pyrazole, 3-(3-iodo-5-{[1-methyl-3-(trifluoromethyl)-1H-pyrazol-5-yl]oxy}phenoxy)-1-methyl-5-(trifluoromethyl)-1H-pyrazole, 1-ethyl-3-(3-fluoro-5-{[1-methyl-3-(trifluoromethyl)-1H-pyrazol-5-yl]oxy}phenoxy)-5-(trifluoromethyl)-1H-pyrazole, pyraflufen, pyraflufen-ethyl, fenoxasulfone, fluazolate, isouron, isoxaben, isoxaflutole, imazamethabenz, imazamethabenz-methyl, imazapic, imazapic-ammonium, imazapyr, imazapyr-isopropyl-ammonium, imazaquin, imazaquin-ammonium, imazethapyr, imazethapyr-ammonium azafenidin, methazole, oxadiargyl, oxadiazon, amicarbazone, bencarbazone, carfentrazone, carfentrazone-ethyl, sulfentrazone, ,

amitrole, paclobutrazol, uniconazole, uniconazole-P, cafenstrole, fentrazamide,

B5 consisting of other herbicides, comprising allidochlor, aminocyclopyrachlor, aminocyclopyrachlor-potassium, aminocyclopyrachlor-methyl, N-acetylthiazolidine-4-carboxylic acid, acrolein, aminopyralid, ammonium pelargonate, ammonium sulfamate, aviglycine, benazolin, benazolin-ethyl, benfluralin, benfuresate, bentazone, benzobicyclon, 6-benzylaminopurine, borax, brassinolide, bromofenoxim, butralin, carvone, catechin, chlorfenac, chlorfenac-sodium, chlorfenprop, chlorflurenol, chlorflurenol-methyl, chloridazon, chlormequat chloride, chloroacetic acid, chlorphthalim, chlorthal-dimethyl, cinidon, cinidon-ethyl, cinmethylin, clofencet, clomazone, cloxyfonac, cyanamide, cyclanilide, cyclopyrimorate, 6-isopentylamino-purin, kinetin, zeatin, dalapon, daminozide, dazomet, n-decanol, difenzoquat metilsulfate, 2,6-diisopropylnaphthalene, dikegulac, dikegulac-sodium, dimethipin, dimethylarsenic acid, dinitramine, dinoterb, diquat, diquat dibromide, dithiopyr, DNOC, endothal, endothal-dipotassium, endothal-disodium, endothal-mono(N,N-dimetylalkylammonium), ethafluralin, ethofumesate, ethylchlozate, ferrous sulfate, flamprop, flamprop-M-isopropyl, flamprop-M-methyl, fluchloralin, flufenpyr, flufenpyr-ethyl, flumetralin, flumiclorac, flumiclorac-pentyl, flumioxazin, flupropanate, flurenol, flurenol-butyl, flurenol-dimetylammonium-metyl, fluridone, flurochloridone, flurtamone, fluthiacet, fluthiacet-metyl, gibberillic acid, halauxifen, halauxifen-methyl, halauxifen salts, indanofan, isopropalin, isoprothiolane, maleic hydrazide, mepiquat chloride, metam, methiozolin, methylarsonic acid, 1-methylcyclopropene, methyl isothiocyanate, nitrophenolate mixture, nonanoic acid, norflurazon, oleic acid, oryzalin, oxaziclomefone, paraquat, paraquat dichloride, pendimethalin, pentachlorophenol, pentoxazone, petroleum oils, prodiamine, n-propyl dihydrojasmonate, pyridafol, pyridate, quinoclamine, sintofen, sodium chlorate, sulfuric acid, tar oils, TCA, TCA sodium, tecnazene, thiazopyr, triacontanol, triafamone, trifluralin and urea sulfate,

B6 consisting of (het)arylcarboxylic acids, comprising chloramben, dicamba, dicamba salts, 2,3,6-TBA, clopyralid, fluroxypyr, fluroxypyr-methyl, inabenfide, picloram, triclopyr, quinclorac, quinmerac, indol-3-ylacetic acid, 4-indol-3-ylbutyric acid, 2-(1-naphthyl)acetamide, 1-naphthylacetic acid, 2-naphthyloxyacetic acid,

B7 consisting of organic phosphorus compounds, comprising anilofos, bensulide, bilanafos, bilanafos-sodium, butimafos, clacyfos, fosamine, glufosinate, glufosinate salts, glufosinate-ammonium, glufosinate-sodium, glufosinate-P, L-glufosinate-ammonium, L-glufosinate-sodium, glyphosate, glyphosate salts, glyphosate-isopropyl-ammonium, glyphosate-ammonium, glyphosate-dimethylammonium, glyphosate-trimesium (=sulfosate), glyphosate-diammonium, glyphosate-potassium, glyphosate-sodium, piperophos, ethephon and tribufos,

B8 consisting of phenyl ether, comprising acifluorfen, acifluorfen-sodium, aclonifen, fluoroglycofen, fluoroglycofen-ethyl, fomesafen, fomesafen-sodium, halosafen, lactofen, oxyfluorfen, bifenox, ethoxyfen-ethyl, clomeprop, cloprop, dichlorprop, dichlorprop-P, mecoprop, mecoprop-sodium, mecoprop-butotyl, mecoprop-P, mecoprop-P-butotyl, mecoprop-P-dimethylammonium, mecoprop-P-2-ethylhexyl, mecoprop-P-potassium, 4-CPA, 2,4-D, 2,4-D-butotyl, 2,4-D-butyl, 2,4-D-choline, 2,4-D-dimethylammonium, 2,4-D-diolamin, 2,4-D-ethyl, 2,4-D-2-ethylhexyl, 2,4-D-isobutyl, 2,4-D-isooctyl, 2,4-D- iso-propyl-ammonium, 2,4-D-potassium, 2,4-D-triisopropanolammonium, 2,4-D-trolamine, MCPA, MCPA-butotyl, MCPA-dimethylammonium, MCPA-2-ethylhexyl. MCPA-isopropylammonium, MCPA-potassium, MCPA-sodium, MCPA-thioethyl, 2,4-DB, MCPB, MCPB-methyl, MCPB-ethyl-sodium, clodinafop-ethyl, clodinafop-propargyl, cyhalofop, cyhalofop-butyl, diclofop, diclofop-methyl, diclofop-P, diclofop-P-methyl, fenoxaprop, fenoxaprop-P, fenoxaprop-P-ethyl, fluazifop, fluazifop-butyl, fluazifop-P, fluazifop-P-butyl, haloxyfop, haloxyfop-P, metamifop, propaquizafop,

quizalafop, quizalafop-ethyl, quizalafop-P, quizalafop-P-ethyl, quizalafop-P-tefuryl,

B9 consisting of pyrimidines, comprising
ancymidol, flurprimidol, pyrimisulfan,
bispyribac, bispyribac-sodium, pyribenzoxim, pyriminobac, pyriminobac-methyl, pyribambenz, pyribambenz-isopropyl, pyribambenz-propyl, pyriftalid, pyrithiobac, pyrithiobac-sodium,
benzfendizone, bromacil, butafenacil, lenacil, saflufenacil, terbacil, tiafenacil,
2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]-N-[methyl(1-methylethyl)-sulfamoyl]benzamide,
ethyl[(3-{2-chloro-5-[2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]-4-fluorophenoxy}pyridin-2-yl)oxy]acetate

B10 consisting of (thio)ureas, comprising
cumyluron,
chlorbromuron, chlorotoluron, chloroxuron, daimuron, diflufenzopyr, diflufenzopyr-sodium, dimefuron, diuron, fluometuron, forchlorfenuron, isoproturon, karbutilate, linuron, methyldymron, metobromuron, metoxuron, monolinuron, neburon, siduron, terbucarb, thidiazuron,
methiuron,
tebuthiuron,
methabenzthiazuron,

B11 consisting of triazines, comprising
triaziflam, indaziflam,
atrazine, cyanazine, cyprazine, propazine, simazine, terbumeton, terbuthylazine, trietazine,
prometon,
ametryn, dimethametryn, prometryn, simetryn, terbutryn,
ethozin, hexazinon, metamitron, metribuzin,
trifludimoxazin.

9. Composition according to claim 8, further comprising one or more safeners (component (C)) selected from the group consisting ofbenoxacor (C1), cloquintocet-mexyl (C2), cyprosulfamide (C3), dichlormid (C4), fenclorim (C5), fenchlorazole (C6), furilazole (C7), isoxadifen-ethyl (C8),mefenpyr-diethyl (C9), 4-(dichloroacetyl)-1-oxa-4-azaspiro[4.5]decane of CAS 71526-07-3 (C10), 2,2,5-trimethyl-3-(dechloroacetyl)-1,3-oxazolidine of CAS 52836-31-4 (C11). 2-methoxy-N-({4-[(methylcarbamoyl)amino]phenyl}sulfonyl)benzamid der CAS 129531-12-0 (C12).

10. Composition according to any one of claims 8 and 9, wherein one or more, preferably one, component(s) (B) is/are selected from the sub-groups B1 to B11, with:

B1 consisting of clethodim, mesotrione, sulcotrione, tefuryltrione, tembotrione and bicyclopyrone,

B2 consisting of acetochlor, diclosulam, diflufenican, flumetsulam, foramsulfuron, nicosulfuron, S-metolachlor, thiencarbazone-methyl, dimethenamide-P, rimsulfuron, alachlor, chlorimuron-ethyl, florasulam, flucarbazone-sodium, flufenacet, iodosulfuron-methyl-sodium, ethoxysulfuron, ipfencarbazone, metsulfuron-methyl, propoxycarbazone-sodium and tribenuron-methyl,

B3 consisting of bromoxynil and ioxynil,

B4 consisting of amicarbazone, carfentrazone-ethyl, imazapyr, imazethapyr, isoxaflutole, oxadiargyl, oxadiazon, pyrasulfotole, pyroxasulfone and topramezone,

B5 consisting of paraquat dichloride, pendimethalin, aminopyralid, flumioxazin, flurtamone, halauxifen, halauxifen-methyl, halauxifen salts, pyridate, bentazone, cinidon-ethyl, clomazone and trifluralin,

B6 consisting of dicamba, dicamba salts and fluroxypyr,

B7 consisting of glufosinate, glufosinate-ammonium, L-glufosinate-ammonium, glyphosate, glyphosate-isopropyl-ammonium

B8 consisting of 2,4-D, 2,4-D-butotyl, 2,4-D-butyl, 2,4-D-choline, 2,4-D-dimethylammonium, 2,4-D-diolamin, 2,4-D-ethyl, 2,4-D-2-ethylhexyl, 2,4-D-isobutyl, 2,4-D-isooctyl, 2,4-D- iso-propyl-ammonium, 2,4-D-potassium, 2,4-D-triisopropanolammonium, 2,4-D-trolamine, fenoxaprop-P-ethyl, lactofen, fluazifop-P-butyl, aclonifen and haloxyfop-P,

B9 consisting of saflufenacil

B10 consisting of diuron, diflufenzopyr and fluometuron, and

B11 consisting of atrazine, indaziflam, terbuthylazine and metribuzin.

11. Composition according to any one of claims 7 and 8, wherein one or more, preferably one, component(s) (B) is/are selected from the sub-groups B1 to B11, with:

B1 consisting of clethodim mesotrione, bicyclopyrone and tembotrione,

B2 consisting of acetochlor, diclosulam, diflufenican, foramsulfuron, nicosulfuron, S-metolachlor, thiencarbazone-methyl, dimethenamide-P, rimsulfuron, alachlor, chlorimuron-ethyl, florasulam, flucarbazone-sodium, flufenacet and iodosulfuron-methyl-sodium,

B3 consisting of is bromoxynil,

B4 consisting of carfentrazone-ethyl, imazapyr, imazethapyr, isoxaflutole, oxadiargyl, oxadiazon and pyroxasulfone,

B5 consisting of paraquat dichloride, pendimethalin, aminopyralid, flumioxazin, flurtamone, halauxifen, halauxifen-methyl, halauxifen salts and pyridate,

B6 consisting of dicamba and dicamba salts,

B7 consisting of glufosinate-ammonium and glyphosate,

B8 consisting of 2,4-D, 2,4-D-butotyl, 2,4-D-butyl, 2,4-D-choline, 2,4-D-dimethylammonium, 2,4-D-diolamin, 2,4-D-ethyl, 2,4-D-2-ethylhexyl, 2,4-D-isobutyl, 2,4-D-isooctyl, 2,4-D- iso-propyl-ammonium, 2,4-D-potassium, 2,4-D-triisopropanolammonium, 2,4-D-trolamine, fenoxaprop-P-ethyl, lactofen and fluazifop-P-butyl,

B9 consisting of saflufenacil,

B10 consisting of diuron and diflufenzopyr, and

B11 consisting of are atrazine, indaziflam, terbuthylazine and metribuzin.