LIVING MODIFIED ORGANISM (LMO)

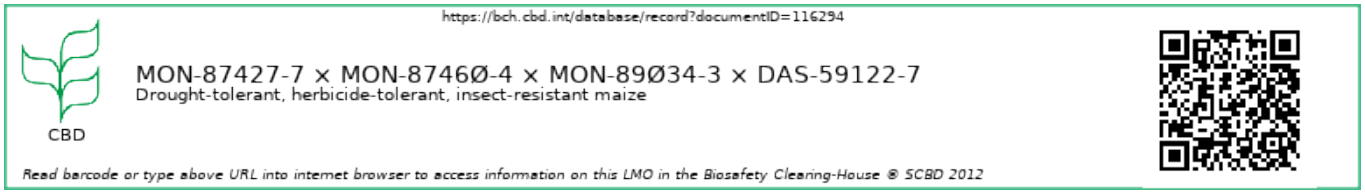
BCH-LMO-SCBD-116294-2

? Decisions on the LMO ? Risk Assessments

LAST UPDATED: 01 OCT 2021

Living Modified Organism identity

The image below identifies the LMO through its unique identifier, trade name and a link to this page of the BCH. Click on it to download a larger image on your computer. For help on how to use it go to the LMO quick-links page.



Name

Drought-tolerant, herbicide-tolerant, insect-resistant maize | EN

Transformation event

MON87427 × MON87460 × MON89034 × 59122

Unique identifier

MON-87427-7 × MON-8746Ø-4 × MON-89Ø34-3 × DAS-59122-7

Developer(s)

- PERSON: DOW AGROSCIENCES GMBH | BCH-CON-SCBD-104809-2

PERSON

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RELATED ORGANIZATION

- PERSON: BAYER CROPSCIENCE | BCH-CON-SCBD-111462-3

PERSON

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RELATED ORGANIZATION

Description

The maize (*Zea mays*) was produced through cross breeding of modified parental maize lines for herbicide tolerance and insect resistance. For abiotic tolerance, the maize expresses *Bacillus subtillus* cold shock protein to enhance natural abiotic (drought) stress responses. For herbicide tolerance, the maize expresses *Agrobacterium tumefaciens* 5-enolpyruvylshikimate-3-phosphate synthase (glyphosate tolerance - enzyme variant) and *Streptomyces viridochromogenes* phosphinothricin N-acetyltransferase (glufosinate tolerance - enzymatic inactivation). The expression of *epsps* is is restricted to the female and vegetative tissues. For Lepidoptera tolerance, the maize expresses *Bacillus thuringiensis* Cry1A.105 and Cry2Ab2. For Coleoptera resistance, the maize expresses *B. thuringiensis* Cry34Ab1 and Cry35Ab1. Additionally, the maize contains an *Escherichia coli* neomycin phosphotransferase II cassette for kanamycin selection, which was used during transformation of a parental line.	EN

Recipient Organism or Parental Organisms

The term “Recipient organism” refers to an organism (either already modified or non-modified) that was subjected to genetic modification, whereas “Parental organisms” refers to those that were involved in cross breeding or cell fusion.

BCH-ORGA-SCBD-246-6 ORGANISM | ZEA MAYS (MAIZE, CORN, MAIZE) |
Crops

BCH-LMO-SCBD-104758-3 LIVING MODIFIED ORGANISM | MON-87427-7 - MAIZE MODIFIED FOR TISSUE SELECTIVE GLYPHOSATE TOLERANCE |
Resistance to herbicides - Glyphosate

BCH-LMO-SCBD-103066-6 LIVING MODIFIED ORGANISM | MON-8746Ø-4 - DROUGHTGARD™ MAIZE |
Resistance to antibiotics - Kanamycin Tolerance to abiotic stress - Cold / Heat, Drought

BCH-LMO-SCBD-43773-18 LIVING MODIFIED ORGANISM | MON-89Ø34-3 - YIELDGARD™ VT PRO™ |
Resistance to diseases and pests - Insects - Lepidoptera (butterflies and moths)

BCH-LMO-SCBD-15165-13 LIVING MODIFIED ORGANISM | DAS-59122-7 - HERCULEX™ RW ROOTWORM PROTECTION MAIZE |
Pioneer Hi-Bred International Inc. | Resistance to diseases and pests (Insects, Coleoptera (beetles)), Resistance to herbicides (Glufosinate)

Characteristics of the modification process

Vector

PV-ZMAP1043; PV-ZMAP595; PV-ZMIR245; PHP17662 | EN

Techniques used for the modification

Cross breeding

Genetic elements construct

Introduced or modified genetic element(s)

Some of these genetic elements may be present as fragments or truncated forms. Please see notes below, where applicable.

BCH-GENE-SCBD-100366-6 CAMV ENHANCED 35S PROMOTER

Promoter

BCH-GENE-SCBD-100359-7 HSP70 INTRON | (MAIZE, CORN)

Intron

BCH-GENE-SCBD-100365-6 CHLOROPLAST TRANSIT PEPTIDE 2 | (THALE CRESS)

Transit signal

BCH-GENE-SCBD-14979-7 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE GENE

Protein coding sequence | Resistance to herbicides (Glyphosate)

BCH-GENE-SCBD-100269-8 NOPALINE SYNTHASE GENE TERMINATOR

Terminator

BCH-GENE-SCBD-101415-9 TI PLASMID LEFT BORDER REPEAT

Plasmid vector

BCH-GENE-SCBD-100364-5 RICE ACTIN 1 GENE PROMOTER | (RICE)

Promoter

BCH-GENE-SCBD-100355-6 RICE ACTIN 1, INTRON | (RICE)

Intron

BCH-GENE-SCBD-103065-7 COLD SHOCK PROTEIN GENE

Protein coding sequence | Tolerance to abiotic stress (Cold / Heat, Drought)

BCH-GENE-SCBD-103067-9 TRANSCRIPT 7 GENE 3' UNTRANSLATED REGION

Terminator

BCH-GENE-SCBD-103069-3 LOXP RECOMBINATION SITE

recombination site

BCH-GENE-SCBD-100287-7 CAMV 35S PROMOTER

Promoter

BCH-GENE-SCBD-15001-5 NEOMYCIN PHOSPHOTRANSFERASE II | (BACTERIA)

Protein coding sequence | Resistance to antibiotics (Kanamycin)

BCH-GENE-SCBD-101416-6 TI PLASMID RIGHT BORDER REPEAT

Plasmid vector

BCH-GENE-SCBD-100354-6 5' UNTRANSLATED LEADER FROM CHLOROPHYLL A/B-BINDING PROTEIN | (WHEAT)

Leader sequence

BCH-GENE-SCBD-43771-9 CRY1A.105 | BACILLUS THURINGIENSIS - BT, BACILLUS, BACTU

Protein coding sequence | Resistance to diseases and pests (Insects, Lepidoptera (butterflies and moths))

BCH-GENE-SCBD-100356-6 HEAT SHOCK PROTEIN 17.3 TERMINATOR | (WHEAT)

Terminator

BCH-GENE-SCBD-101507-5 FMV 34S PROMOTER

Promoter

BCH-GENE-SCBD-100360-4 TRANSIT PEPTIDE AND FIRST INTRON OF RUBISCO SSU | (MAIZE, CORN)

Transit signal

BCH-GENE-SCBD-14988-7 CRY2AB2 | BACILLUS THURINGIENSIS - BT, BACILLUS, BACTU

Protein coding sequence | Resistance to diseases and pests (Insects, Lepidoptera (butterflies and moths))

BCH-GENE-SCBD-100362-7 UBIQUITIN GENE PROMOTER | (MAIZE, CORN)

Promoter

BCH-GENE-SCBD-14994-9 CRY34AB1 | BACILLUS THURINGIENSIS - BT, BACILLUS, BACTU

Protein coding sequence | Resistance to diseases and pests (Insects, Coleoptera (beetles))

BCH-GENE-SCBD-100367-4 PROTEINASE INHIBITOR II GENE TERMINATOR | (POTATO)

Terminator

BCH-GENE-SCBD-100368-6 PEROXIDASE GENE PROMOTER | (WHEAT)

Promoter

BCH-GENE-SCBD-14995-8 CRY35AB1 | BACILLUS THURINGIENSIS - BT, BACILLUS, BACTU

Protein coding sequence | Resistance to diseases and pests (Insects, Coleoptera (beetles))

BCH-GENE-SCBD-15002-4 PHOSPHINOTHRICIN N-ACETYLTRANSFERASE GENE

Protein coding sequence | Resistance to herbicides (Glufosinate)

BCH-GENE-SCBD-100290-6 CAMV 35S TERMINATOR

Terminator

Notes regarding the genetic elements present in this LMO

DNA insert from MON87427 PV-ZMAP1043

Transcription of 5-enolpyruvylshikimate-3-phosphate synthase (*cp4-epsps*) from *Agrobacterium tumefaciens* commences from the *Cauliflower mosaic virus* (CaMV) enhanced 35S promoter and ends at the *A. tumefaciens* nopaline synthase (*nos*) gene terminator. The transcript contains a *Zea mays* heat shock protein 70 (*hsp70*) intron, *Arabidopsis thaliana* N-terminal chloroplast transit peptide sequence, and *cp4-epsps*. The CaMV enhanced 35S promoter-*hsp70* combination promotes gene expression in female and vegetative tissues, but not in male reproductive tissues (pollen microspores and tapetum).

Note:

- Southern blot analyses indicate that a single copy of the T-DNA was inserted at a single site in the parental maize genome and no plasmid vector backbone sequences were detected to have been integrated. DNA sequencing analyses further indicated that the expected T-DNA sequences were integrated.
-The *cp4-epsps* coding sequence is the codon optimized coding sequence of the *aroA* gene from *Agrobacterium sp.* strain CP4 encoding CP4 EPSPS.

DNA insert from MON87460 vector PV-ZMAP595

The T-DNA insert contains the following gene cassettes: *Bacillius subtillus* cold shock protein (*cspB*) and *Escherichia coli* neomycin phosphotransferase II (*nptII*).

Transcription of *cspB* is under control of the *Oryza sativa* actin 1 promoter and *Agrobacterium tumefaciens* transcript 7 gene 3' untranslated region. The transcript initially contains an *O. sativa* actin 1 intron for enhanced gene expression of *cspB*. The sequence is removed (spliced) prior to protein translation. Constitutive expression of *cspB* is expected due to the actin promoter.

Transcription of *nptII* is under control of the *Cauliflower mosaic virus* (CaMV) 35S promoter and *A. tumefaciens* nopaline synthase terminator. High levels of transcription are expected due to the CaMV promoter.

Note:

- The coding sequence of *cspB* has been codon optimized for optimal expression within plant cells.
- Southern blot analysis indicated that no vector backbone sequences were inserted into the parental genome
- Southern blot analysis indicated that the parental genome contains a single insertion
- Sequencing analyses confirm the Southern blot analyses.
- A 22 base pair deletion of genomic DNA at the insert-to-plant DNA junction occurred.
- *loxP* sites can be found in the parental genome and could potentially allow for the excision of the *nptII* cassette by CRE recombinase.

EN

DNA insert from MON89034 vector PV-ZMIR245
Two insecticidal protein expression cassettes were inserted into the genome. *Bacillus thuringiensis cry1A.105* expression is under the control of the CaMV 35S enhanced promoter, which first transcribes wheat (*Triticum aestivum*) 5' untranslated region of the chlorophyll a/b-binding protein (*cab*) and a rice actin 1 intron before transcribing *cry1A.105*. Transcription terminates at the wheat heat shock protein 17.3 terminator. Expression of the *B. thuringiensis cry2Ab2* starts at the *Figwort mosaic virus* 34S promoter, which transcribes the *Zea mays* heat shock protein 70 (*hsp70*), then the *Z. mays* transit peptide and the *cry2Ab2* coding sequence, before terminating at the *nos* terminator.

Note:
- The Cry2Ab2 coding sequence was modified for optimal expression in plants.
- South blot analysis confirmed that single insertions of both *cry2Ab2* and *cry1A.105*, as well as no vector backbone were present and in the parent.
- A deletion removed the duplicated enhancer elements compared to the original CaMV 35S enhanced promoter in PV-ZMIR245.
- The selectable marker, *nptII*, cassette was bred out of the parental line and became not associated with this transformation event.

DNA insert from 59122 vector PHP17662:
Transcription of *Bacillus thuringiensis cry34Ab1* starts at *Zea mays* ubiquitin gene promoter and terminates at the *Solanum tuberosum* proteinase inhibitor II gene terminator. Transcription of *B. thuringiensis cry35Ab1* commences from the (*Triticum aestivum* (wheat) peroxidase gene promoter and stops at another *S. tuberosum* proteinase inhibitor II gene terminator.

Note:
- The coding sequence of *cry34Ab1* and *cry35Ab1* has been adapted to the codon usage in maize as to achieve optimal expression *in planta*.
- The *cry34Ab1* and *cry35Ab1* were cloned from *B. thuringiensis* strain PS149B1.
- Sequence analysis of 59122 done by the European Food Safety Authority indicated that this LMO contains one complete copy of the T-DNA of PHP17662 without internal rearrangements. All three gene cassettes, cry34Ab1, cry35Ab1 and pat, are intact within the transgenic event. The DNA sequences of the genes in 59122 are identical to those in the original plasmid except for two nucleotide differences in the wheat peroxidise promoter. At the 5' T-DNA end a deletion of 22 bp is observed and at the 3' T-DNA end a deletion of 25 bp is observed. The absence of vector backbone in maize 59122 was also demonstrated.

LMO characteristics

Modified traits

Resistance to diseases and pests
- Insects
  - Coleoptera (beetles)
  - Lepidoptera (butterflies and moths)

Resistance to herbicides
- Glufosinate

Glyphosate
Resistance to antibiotics
Kanamycin
Neomycin
Tolerance to abiotic stress
Cold / Heat
Drought

Common use(s) of the LMO

Food
Feed

Detection method(s)

External link(s)

? MON-87427-7 - EU Reference Laboratory for GM Food and Feed (EURL-GMFF) *(English)*

? MON-8746Ø-4 - EU Reference Laboratory for GM Food and Feed (EURL-GMFF) *(English)*

? MON-89Ø34-3 - EU Reference Laboratory for GM Food and Feed (EURL-GMFF) *(English)*

? DAS-59122-7 - EU Reference Laboratory for GM Food and Feed (EURL-GMFF) *(English)*

Additional Information

Other relevant website addresses and/or attached documents

? EUginius - MON87427 x MON87460 x MON89034 x DAS59122 *(English)*

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Further Information

Questions about the Cartagena Protocol on Biosafety or the operation of the Biosafety Clearing-House may be directed to the Secretariat of the Convention on Biological Diversity.

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