

Biosafety Clearing-House (BCH)

LIVING MODIFIED ORGANISM (LMO)

BCH-LMO-SCBD-260556-1

[? Decisions on the LMO ? Risk Assessments](#)

LAST UPDATED: 07 JUN 2022

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.



MON-87427-7 × MON-95379-3 × MON-87411-9 × MON-87419-8
Insect-protected, herbicide-tolerant maize

<https://bch.cbd.int/database/record?documentID=260556>



Read barcode or type above URL into internet browser to access information on this LMO in the Biosafety Clearing-House © SCBD 2012

Name

Insect-protected, herbicide-tolerant maize

EN

Transformation event

MON87427 × MON95379 × MON87411 × MON87419

Unique identifier

MON-87427-7 × MON-95379-3 × MON-87411-9 × MON-87419-8

Developer(s)

- [ORGANIZATION: MONSANTO COMPANY](#) | [BCH-CON-SCBD-46324-3](#)

ORGANIZATION

Monsanto Company
800 N. Lindbergh Blvd. St. Louis, MO 63167, USA
Phone: +1 314 694-1000
Website: <http://www.monsanto.com/>

Description

The maize (*Zea mays*) was produced through crossing modified parental lines for resistance to insect pests and tolerance to herbicides. For protection from Lepidoptera insects, the maize expresses synthetic Cry1B.868 and Cry1Da_7 proteins, which have pore-forming mode of action that is independent of the receptors that other Bt toxins interact with. For protection from Coleoptera insects, the maize expresses *Bacillus thuringiensis* Cry3Bb1, which has a pore-forming mode of action. In addition, the maize contains an RNA interference cassette that specifically targets *Diabrotica virgifera virgifera* Snf7, an essential cellular component of

EN

endosomal sorting complex required for transport and thus confers resistance to this pest. For tolerance to glyphosate, the maize expresses *Agrobacterium tumefaciens* 5-enolpyruvylshikimate-3-phosphate, which has a low binding affinity for the herbicidal compound and allows for the continued synthesis of aromatic amino acids through the shikimate pathway. For tolerance to glufosinate, the maize expresses *Streptomyces viridochromogenes* phosphinothricin N-acetyltransferase, which inactivates phosphinothricin through acetylation.

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-258895-1 LIVING MODIFIED ORGANISM | MON-95379-3 - INSECT-PROTECTED MAIZE |

Bayer CropScience Deutschland GmbH | Resistance to diseases and pests (Insects, Lepidoptera (butterflies and moths), Cotton bollworm (*Helicoverpa* spp.), European corn borer (*Ostrinia nubilalis*), Fall armyworm (*Spodoptera frugiperda*))

BCH-LMO-SCBD-108881-1 LIVING MODIFIED ORGANISM | MON-87411-9 - MAIZE MODIFIED FOR HERBICIDE TOLERANCE AND INSECT RESISTANCE |

Monsanto | Resistance to diseases and pests (Insects, Coleoptera (beetles), Western corn rootworm (*Diabrotica virgifera*), Northern corn rootworm (*Diabrotica barberi*)), Resistance to herbicides (Glyphosate)

BCH-LMO-SCBD-111531-4 LIVING MODIFIED ORGANISM | MON-87419-8 - DICAMBA AND GLUFOSINATE TOLERANT MAIZE |

Resistance to herbicides - Glufosinate

Characteristics of the modification process

Vector

PV-ZMAP1043; PV-ZMIR522223; PV-ZMIR10871; PV-ZMHT507801

EN

Techniques used for the modification

Cross breeding

Genetic elements construct

P-e35S-CaMV
0.620 kb

I-hsp70-MAIZE
0.803 kb

TP-ctp2-ARATH
0.227 kb

CS-CP4epsps-RHIRD
1.367 kb

T-nos-RHIRD
0.252 kb

V-LB-RHIRD
0.182 kb

V-loxP
0.035 kb

T-ltp-ORYS
0.300 kb

CS-cry1Be2_1Ca_1Ab3-SY
3.600 kb

I-1_ubi1-M
1.053 k

L-ubi-MAIZE
0.078 kb

P-ubi1-MAIZE
0.877 kb

L-35s-CMoVb 0.537 kb	P-tip1-SETIT 0.981 kb	I-1_act15-ORYSA 1.293 kb	CS-Cry1Da1_CryAb3-SYNTH 3.501 kb	T-gos2-ORYSA 0.468 kb
P-e35S-CaMV 0.620 kb	I-hsp70-MAIZE 0.800 kb	CS-Snf7_RNAi_u-DIAVI 0.239 kb	CS-Snf7_RNAi_u-DIA 0.239 kb	T-rbcS_E9-PEA 0.632 kb
P-pHIG-MAIZE 0.948 kb	L-cab-WHEAT 0.060 kb	I-1_act1-ORYSA 0.479 kb	CS-Cry3Bb1-BACTU 1.961 kb	T-hsp17_3-WHEAT 0.209 kb
P-TubA-ORYSA 2.180 kb	TP-ctp2-ARATH 0.227 kb	CS-CP4epsps-RHIRD 1.367 kb	T-TubA-ORYSA 0.581 kb	
P-ubq-ANGER 1.640 kb	L-ubq-ANGER 0.100 kb	I-ubq-ANGER 1.040 kb	CS-pat-STRVR 0.550 kb	T-RA5B-ORYSA 0.210 kb

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-103069-3 LOXP RECOMBINATION SITE |

recombination site

BCH-GENE-SCBD-258891-1 LIPID TRANSFER PROTEIN-LIKE TERMINATOR | ORYZA SATIVA (RICE, ORYZA) |

Terminator

BCH-GENE-SCBD-258889-1 CRY1B.868 | BACILLUS THURINGIENSIS (BT, BACILLUS, BACTU) |

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

BCH-GENE-SCBD-103627-5 UBIQUITIN INTRON 1 | (MAIZE, CORN) |

Intron

BCH-GENE-SCBD-103927-2 UBIQUITIN 5' UNTRANSLATED REGION | (MAIZE, CORN) |

Leader

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

Promoter

BCH-GENE-SCBD-105196-2 FMV 35S ENHANCER |

Leader

BCH-GENE-SCBD-258892-1 TONOPLAST INTEGRAL PROTEIN 1 PROMOTER | SETARIA ITALICA - FOXTAIL MILLET, ITALIAN MILLET |

Promoter

BCH-GENE-SCBD-258893-1 RICE ACTIN 15 INTRON | ORYZA SATIVA (RICE, ORYZA) |

Intron

BCH-GENE-SCBD-258890-1 CRY1DA_7 | BACILLUS THURINGIENSIS (BT, BACILLUS, BACTU) |

Protein coding sequence | Resistance to diseases and pests (Insects, Lepidoptera (butterflies and moths), Cotton bollworm (*Helicoverpa* spp.), European corn borer (*Ostrinia nubilalis*), Fall armyworm (*Spodoptera frugiperda*))

BCH-GENE-SCBD-258894-1 GOS2 TERMINATOR | ORYZA SATIVA (RICE, ORYZA) |

Terminator

BCH-GENE-SCBD-108875-2 SNF7 CODING SEQUENCE | (WESTERN CORN ROOTWORM) |

Protein coding sequence | Resistance to diseases and pests (Insects, Coleoptera (beetles), Western corn rootworm (*Diabrotica virgifera*))

BCH-GENE-SCBD-101877-5 RBCS-E9 GENE TERMINATOR | (GARDEN PEA) |

Terminator

BCH-GENE-SCBD-108876-1 PIIG GENE PROMOTER | (MAIZE, CORN) |

Promoter

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

Leader sequence

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

Intron

BCH-GENE-SCBD-14993-5 CRY3BB1 | BACILLUS THURINGIENSIS - BT, BACILLUS, BACTU |

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

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

Terminator

BCH-GENE-SCBD-108877-1 ALPHA TUBULIN GENE PROMOTER | (RICE) |

Promoter

BCH-GENE-SCBD-108880-1 ALPHA TUBULIN GENE TERMINATOR | (RICE) |

Terminator

BCH-GENE-SCBD-111526-2 UBIQUITIN GENE PROMOTER | ANDROPOGON GERARDII (BIG BLUESTEM, TURKEYFOOT, TALL BLUESTEM, BLUEJOINT, ANGER) |

Promoter

BCH-GENE-SCBD-111527-2 UBIQUITIN LEADER SEQUENCE | ANDROPOGON GERARDII (BIG BLUESTEM, TURKEYFOOT, TALL BLUESTEM, BLUEJOINT, ANGER) |

Leader Sequence

BCH-GENE-SCBD-111528-2 UBIQUITIN INTRON SEQUENCE | ANDROPOGON GERARDII (BIG BLUESTEM, TURKEYFOOT, TALL BLUESTEM, BLUEJOINT, ANGER) |

Intron

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

Protein coding sequence | Resistance to herbicides (Glufosinate)

BCH-GENE-SCBD-111529-1 RA5B GENE TERMINATOR | (RICE) |

Notes regarding the genetic elements present in this LMO

DNA insert from MON87427 PV-ZMAP1043

The MON87427 genome contains one gene cassette *Agrobacterium tumefaciens* 5-enolpyruvylshikimate-3-phosphate synthase (*cp4-epsps*). Transcription of *cp4-epsps* 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.
- The expression of *cp4-epsps* from the MON87411 parental genome is expected to overcome the tissue specific expression from the MON87427 genome.

DNA insert from MON95379 vector PV-ZMIR522223

The MON95379 genome contains two gene cassettes: synthetic *cry1B.868* and synthetic *cry1Da_7*.

The *cry1B.868* coding sequence is under control of a *Zea mays* ubiquitin promoter and an *Oryza sativa* lipid transfer-like protein terminator. The promoter contains the promoter, leader and intron sequences from the maize ubiquitin gene. High levels of transcription are expected in all tissues due to the constitutive nature of the promoter.

The *cry1Da_7* coding sequence is under control of a *Setaria italica* promoter and an *O. sativa* *gos2* terminator. The first intron of the rice actin 15 gene was also included and likely improves expression of the gene.

Note:

- Both *cry1B.868* and *cry1Da_7* sequences are derived from *Bacillus thuringiensis* sequences. Refer to the genetic element records for more information.
- During development of the modified maize, a *c4-epsps* cassette (rice tubulin A terminator; *cp4-epsps*; *Arabidopsis thaliana* chloroplast transit peptide 2; and rice tubulin A promoter) was removed using Cre-lox excision. The T-DNA right border was also truncated (lost) during transformation.
- Next-generation sequencing indicated that a single, intact copy of the the intended DNA insertion was present in the parental genome. No backbone or other unexpected sequences were detected.

DNA insert from MON87411 vector PV-ZMIR10871

The MON87411 genome contains three cassettes: an RNA interference (RNAi) cassette targeting *Diabrotica virgifera virgifera*, *Bacillus thuringiensis cry3Bb1* and *Agrobacterium tumefaciens* 5-enolpyruvylshikimate-3-phosphate synthase (*cp4-epsps*).

Transcription of the RNAi cassette commences from the *Cauliflower mosaic virus* 35S enhanced promoter and terminates at the *Pisum sativum* ribulose biphosphate carboxylase small chain 2 terminator. The transcript initially contains a *Zea mays* heat shock protein 70 intron, which contributes to enhanced expression in vegetative tissues of the plant, and two partial coding sequences of the *D. virgifera virgifera* Snf7p gene, which encodes the SNF7 subunit of the ESCRT-III complex. The two Snf7p sequences are in an inverted orientation, separated by a 150-nucleotide intervening sequence, which allows base pairing between the inverted sequences and hairpin RNA formation post-transcription, which then triggers an RNAi response. Due to RNAi processing, small interfering RNA molecules (roughly 21-23 nucleotides in length) will be produced and thus no translation into protein will occur from this cassette.

Transcription of the *cry3Bb1* is under control of the *Z. mays* physical impedance induced protein promoter and *Triticum aestivum* (wheat) heat shock protein 17.3 terminator. The transcript also contains a wheat 5' untranslated leader from chlorophyll a/b-binding protein and *Oryza sativa* actin 1 intron for enhanced expression of the transgene. Expression of *cp4-epsps* is under control of an *O. sativa* alpha tubulin promoter and terminator. The transcript additionally contains *Arabidopsis thaliana* chloroplast targeting peptide 2 to sequester the protein to the chloroplast.

Note:

- Sequencing, PCR and bioinformatic analyses indicate that a single, intact insertions of the three gene cassettes occurred in the parental line.
- No plasmid backbone was detected.

DNA insert from MON87419 vector PV-ZMHT507801

The MON87419 genome contains two gene cassettes: *Streptomyces viridochromogenes* phosphinothricin N-acetyltransferase (*pat*) and *Stenotrophomonas maltophilia* dicamba monooxygenase (*dmo*).

The *pat* coding sequence is under the control of the *Andropogon gerardii* ubiquitin promoter and the *Oryza sativa* alpha-amylase/trypsin inhibitor terminator. The transcript includes the *A. gerardii* 5' untranslated leader sequence and an intron from ubiquitin before (5') coding sequence of *pat*.

The *dmo* coding sequence is under control of the *Peanut chlorotic streak caulimovirus* (PC1SV) full-length transcript promoter and the *Triticum aestivum* (wheat) heat shock protein 17 terminator. The transcript produced contains a wheat chlorophyll a/b-binding 5' untranslated leader sequence (for improved gene expression), an *O. sativa* actin 1 untranslated region and intron (for improved gene expression), the untranslated and

targeting region of *Petunia hybrida* chloroplast transit peptide 4 (for chloroplast targeting of the protein) and *dmo*.

Note:

- Originally, the plasmid vector contained two T-DNA elements that were inserted during the initial transformation event: one containing the *dmo* and *pat* expression cassettes, and a second containing an *Agrobacterium tumefaciens* 5-enolpyruvylshikimate-3-phosphate synthase (*cp4-epsps*) expression cassette. The *cp4-epsps* expression cassette is regulated by the *O sativa* actin 1 promoter and 5' untranslated leader, *O. sativa* intron, the *Arabidopsis thaliana* chloroplast targeting peptide 2 targeting sequence, and the *A. tumefaciens* nopaline synthase 3' untranslated region. Subsequent traditional breeding, segregation, selection, and screening were used to isolate those plants that contain the *dmo* and *pat* expression cassettes (T-DNA I) and do not contain the *cp4-epsps* expression cassette (T-DNA II).
- Molecular characterization of MON87419 indicated that a single copy of T-DNA I was integrated into the maize genome at a single intact locus that includes all expected elements within the insert, with the exception of incomplete Right and Left Border sequences. These analyses also showed no PV-ZMHT507801 backbone elements or T-DNA II sequences were present in the event.

For more information, kindly refer to the parental LMO records.

LMO characteristics

Modified traits

Resistance to diseases and pests

Insects

Coleoptera (beetles)

Western corn rootworm (*Diabrotica virgifera*)

Northern corn rootworm (*Diabrotica barberi*)

Lepidoptera (butterflies and moths)

Cotton bollworm (*Helicoverpa* spp.)

European corn borer (*Ostrinia nubilalis*)

Fall armyworm (*Spodoptera frugiperda*)

Resistance to herbicides

Glufosinate

Glyphosate

Detection method(s)

External link(s)

? [MON-87419-8 - EU Reference Laboratory for GM Food and Feed \(EURL-GMFF\)](#) (JRC) [English]

? [MON-87427-7 - EU Reference Laboratory for GM Food and Feed \(EURL-GMFF\)](#) (JRC) [English]

? [MON-87427-7 - CropLife International Detection Methods Database](#) (CropLife) [English]

? [MON-87411-9 - CropLife International Detection Methods Database](#) (*CropLife*) [*English*]

[BCH-LMO-SCBD-260556-1](#)

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.

**Secretariat of the Convention
on Biological Diversity**

413 rue Saint-Jacques, suite 800
Montreal, Québec, H2Y 1N9
Canada
Fax: +1 514 288-6588
Email: secretariat@cbd.int