

Biosafety Clearing-House (BCH)

LIVING MODIFIED ORGANISM (LMO)


BCH-LMO-SCBD-116312-1

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

LAST UPDATED: 06 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.



<https://bch.cbd.int/database/record?documentID=116312>

MON-87427-7 × MON-87411-9 × DAS-59122-7
Herbicide-tolerant, insect-resistant maize



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

Name

Herbicide-tolerant, insect-resistant maize

EN

Transformation event

MON87427 × MON87411 × 59122

Unique identifier

MON-87427-7 × MON-87411-9 × DAS-59122-7

Developer(s)

- [PERSON: BAYER CROPSCIENCE](#) | [BCH-CON-SCBD-111462-3](#)

PERSON

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RELATED ORGANIZATION

- [PERSON: DOW AGROSCIENCES GMBH](#) | [BCH-CON-SCBD-104809-2](#)

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 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). For Coleoptera resistance, the maize expresses *B. thuringiensis* Cry3Bb1, Cry34Ab1 and Cry35Ab1. The maize contains an RNA interference cassette targeting *Diabrotica virgifera virgifera* Snf7 for specific resistance against *D. virgifera virgifera*.

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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-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-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-ZMIR10871; PHP17662

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Techniques used for the modification

Cross breeding

Genetic elements construct

P-e35S-CaMV 0.620 kb	I-hsp70-MAIZE 0.800 kb	TP-ctp2-ARATH 0.230 kb	CS-CP4epsps-RHIRD 1.370 kb	T-nos-RHIRD 0.250 kb
P-e35S-CaMV 0.620 kb	I-hsp70-MAIZE 0.800 kb	CS-Snf7_RNAi_u-DIAVI 0.240 kb	CS-Snf7_RNAi_u-DIA 0.240 kb	T-hsp17_3-WHEAT 0.210 kb
P-pIIG-MAIZE 0.950 kb	L-cab-WHEAT 0.060 kb	I-1_act1-ORYSA 0.480 kb	CS-Cry3Bb1-BACTU 1.960 kb	T-hsp17_3-WHEAT 0.210 kb
P-TubA-ORYSA 2.180 kb	TP-ctp2-ARATH 0.230 kb	CS-CP4epsps-RHIRD 1.370 kb	T-TubA-ORYSA 0.580 kb	
P-ubi1-MAIZE 1.990 kb	CS-cry34Ab1-BACTU 0.370 kb	T-pinII-SOLTU 0.320 kb		
P-pox-WHEAT 1.300 kb	CS-cry35Ab1-BACTU 1.150 kb	T-pinII-SOLTU 0.320 kb		
P-35S-CaMV 0.550 kb	CS-pat-STRVR 0.550 kb	T-35S-CaMV 0.200 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-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-100356-6](#) HEAT SHOCK PROTEIN 17.3 TERMINATOR | (WHEAT) |

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

Promoter

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

Terminator

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-100287-7 CAMV 35S PROMOTER |

Promoter

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.
- 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 MON87411 vector PV-ZMIR10871

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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 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 peroxidase 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.

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

LMO characteristics

Modified traits

Resistance to diseases and pests

Insects

Coleoptera (beetles)

Resistance to herbicides

Glufosinate

Glyphosate

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-87411-9 - 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 MON87411 x DAS59122](#) (*English*)

[BCH-LMO-SCBD-116312-1](#)

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

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