

Biosafety Clearing-House (BCH)

LIVING MODIFIED ORGANISM (LMO)


BCH-LMO-SCBD-115663-4

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

LAST UPDATED: 05 AUG 2020

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 × SYN-IR162-4
Herbicide tolerant, Insect resistant maize

CBD

<https://bch.cbd.int/database/record?documentID=115663>



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

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Transformation event

MON87427 × MIR162

Unique identifier

MON-87427-7 × SYN-IR162-4

Developer(s)

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

PERSON

Bayer CropScience

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RELATED ORGANIZATION

Description

The modified maize was produced through the cross breeding of two modified parental lines for herbicide tolerance and insect resistance. For Lepidoptera resistance, the maize expresses *Bacillus thuringiensis* Vegetative insecticidal protein 3Aa20. For herbicide

EN

tolerance, the maize expresses *Agrobacterium tumefaciens* 5-enolpyruvylshikimate-3-phosphate synthase, which encodes a variant of the endogenous enzyme involved in aromatic amino acid synthesis and confers glyphosate tolerance in female and vegetative tissues. The tissue specificity additionally allows for glyphosate-treated plants to serve as a female parent in the production of hybrid lines. The modified maize also contains a selectable, *Escherichia coli* phosphomannose isomerase, for mannose selection during parental transformation.

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-100885-13](#) LIVING MODIFIED ORGANISM | SYN-IR162-4 - AGRISURE™ VIPTERA MAIZE |

Syngenta Crop Protection AG | Resistance to diseases and pests (Insects, Lepidoptera (butterflies and moths))

Characteristics of the modification process

Vector

PV-ZMAP1043; pNOV1300

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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-ubi1-MAIZE 1.990 kb	CS-vip3Aa20-BACTU 2.370 kb	I-9_pepc-MAIZE 0.110 kb	T-35S-CaMV 0.070 kb	
P-ubi1-MAIZE 1.990 kb	CS-pmi-ECOLX 1.180 kb	T-nos-RHIRD 0.250 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-100362-7 UBIQUITIN GENE PROMOTER | (MAIZE, CORN) |

Promoter

BCH-GENE-SCBD-100887-5 VEGETATIVE INSECTICIDAL PROTEIN 3AA20 |

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

BCH-GENE-SCBD-101406-4 PHOSPHOENOLPYRUVATE CARBOXYLASE, INTRON 9 | (MAIZE, CORN) |

Intron

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

Terminator

BCH-GENE-SCBD-15003-7 PHOSPHOMANNOSE ISOMERASE GENE | (BACTERIA) |

Protein coding sequence | Mannose tolerance, Selectable marker genes and reporter genes

Notes regarding the genetic elements present in this LMO

Genetic elements from 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.

Genetic elements from pNOV1300

In the parental MIR162 maize, a variant of the native *B. thuringiensis* vegetative insecticidal protein 3Aa (*vip3Aa20*), named *vip3Aa19*, which has codon changes that result in a single M129I amino acid substitution was inserted into the transformation cassette. During the transformation process an additional DNA mutation resulted in a K284Q amino acid substitution. This final form was designated the name *Vip3Aa20*. Transcription of *vip3Aa20* commences at the *Z. mays* ubiquitin gene promoter and then transcribes *vip3Aa20* followed by intron 9 of *Z. mays* phosphoenolpyruvate carboxylase, before terminating at the CaMV 35S terminator.

A second expression cassette, containing the *E. coli* phosphomannose isomerase gene, was

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also inserted into the parental genome. The gene is under the control of another ubiquitin promoter and transcription terminates at the *Agrobacterium tumefaciens* nopaline synthase gene (*nos*) terminator.

Note:

- Southern blot analyses demonstrated that the T-DNA insert contains: i) single copies of a *vip3Aa20* gene and a *pmi* gene; ii) two copies of the ZmUbi1nt promoter; iii) one copy of the *nos* terminator; and iv) no backbone sequences from transformation plasmid pNOV1300.

LMO characteristics

Modified traits

Resistance to diseases and pests
Insects
Lepidoptera (butterflies and moths)
Resistance to herbicides
Glufosinate
Selectable marker genes and reporter genes
Other
Mannose tolerance

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)
? [SYN-IR162-4 - EU Reference Laboratory for GM Food and Feed \(EURL-GMFF\)](#) (English)

Additional Information

Other relevant website addresses and/or attached documents

? [EUGenius - MON87427 x MIR162](#) (English)

[BCH-LMO-SCBD-115663-4](#)

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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on Biological Diversity**

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