LIVING MODIFIED ORGANISM (LMO)

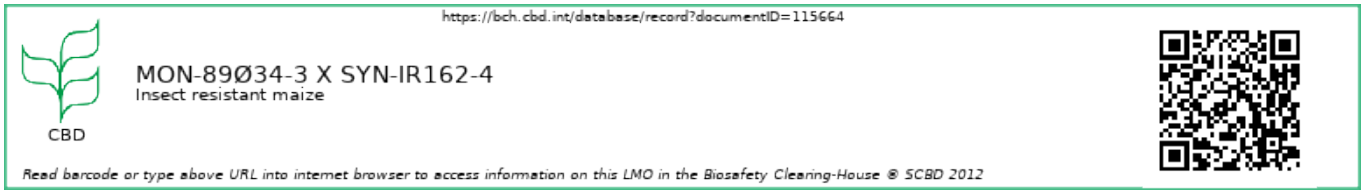
BCH-LMO-SCBD-115664-1

? Decisions on the LMO ? Risk Assessments

LAST UPDATED: 31 JUL 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.



Name

Insect resistant maize | EN

Transformation event

MON89034 x MIR162

Unique identifier

MON-89Ø34-3 x SYN-IR162-4

Developer(s)

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

PERSON

Bayer CropScience
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40789, Germany
Phone: +49 21 73 - 38-0
Website: https://www.cropscience.bayer.com/en, https://www.cropscience.bayer.de/de-DE

RELATED ORGANIZATION

Description

The modified maize was produced through the cross breeding of two modified parental lines for Lepidoptera resistance through the expression of *Bacillus thuringiensis* Cry1A.105, Cry2Ab2 and Vegetative insecticidal protein 3Aa20. The modified maize also contains a | EN

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-43773-18 LIVING MODIFIED ORGANISM | MON-89Ø34-3 - YIELDGARD™ VT PRO™

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

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

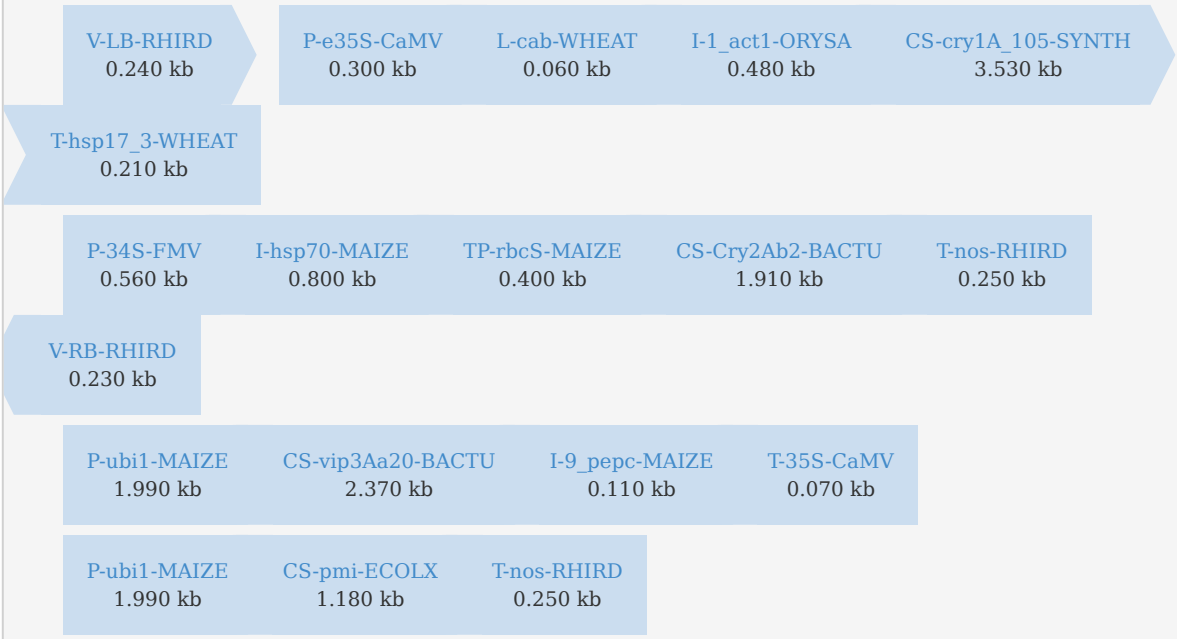
Vector

PV-ZMIR245; pNOV1300 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-101415-9 TI PLASMID LEFT BORDER REPEAT

Plasmid vector

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

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-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-100359-7 HSP70 INTRON | (MAIZE, CORN)

Intron

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-100269-8 NOPALINE SYNTHASE GENE TERMINATOR

Terminator

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

Plasmid vector

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

DNA insert from MON89034 vector PV-ZMIR245: Maize line MON89034 expresses two Bt-toxins encoded by *Bacillus thuringiensis cry1A.105* and *cry2Ab2*. Transcription of *cry1A.105* begins at the Cauliflower Mosaic Virus (CaMV) Enhanced 35S promoter and finishes at the wheat (*Triticum aestivum*) wheat heat shock protein 17.3 terminator. The transcript initially includes (5' to 3'): wheat 5' untranslated leader from the chlorophyll a/b-binding protein, *Oryza sativa* (rice) actin 1 intron and *Cry1A.105*. The wheat 5' untranslated leader sequence and the rice intron enhance the expression of *cry1A.105*.	EN

Transcription of *cry2Ab2* commences from the Figwort Mosaic Virus (FMV) 35S promoter and terminates at the *Agrobacterium tumefaciens* nopaline synthase (*nos*) terminator. The transcript initially includes (5' to 3'): maize heat shock protein 70 (*hsp70*) intron, maize transit peptide and first intron from the small subunit of Ribulose-1,5-bisphosphate carboxylase/oxygenase and *cry2Ab32*. The *hsp70* regulates and enhances gene expression, while the transit peptide targets Cry2Ab2 to the chloroplast.

Note:
- The viral promoters are expected to be constitutively active and promote high levels of transcription.
- The coding sequence of *cry2Ab2* was codon-optimized for expression within plant systems.
- A second T-DNA insertion (containing CaMV 35S promoter, *Escherichia coli* neomycin phosphotransferase and *A. tumefaciens nos* terminator) was initially inserted into the genome for kanamycin selection during transformation. However, once transformants were regenerated, the selectable marker was bred out of the parental line using convention breeding techniques.
- Southern blot analyses indicated a single copy of the *cry1A.105* and the *cry2Ab2* cassettes. No backbone plasmid DNA or *nptII* sequences were detected. PCR and DNA sequence analyses provided the complete DNA sequence of the insert and confirmed the organization of the elements within the insert. Furthermore, sequence analysis indicated that MON 89034 no longer has the duplicated enhancer elements compared to the original e35S promoter in PV-ZMIR245, possibly due to a recombination event that resulted in its deletion.

DNA insert from MIR162 vector pNOV1300
In the parental MIR162 maize, a variant of the native *B. thuringiensis* vegetative insecticidal protein 3Aa (*vip3Aa*), termed *vip3Aa20*, was inserted into the transformation cassette. 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. The intron enhances expression of the transgene.

A second expression cassette, containing *E. coli* phosphomannose isomerase (*pmi*), was 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 (*nos*) terminator.

Note:
- Southern blot analyses demonstrated that the T-DNA insert contains: (i) single copies of *vip3Aa20* and *pmi* gene; (ii) two copies of the maize ubiquitin promoter; (iii) one copy of the *nos* terminator; and iv) no backbone sequences from transformation plasmid pNOV1300.
- *vip3Aa20* is a variant of the native *vip3Aa*, which has codon changes that result in M129I (methionine to isoleucine at position 129) and K284Q (lysine to glutamine at position 284) amino acid substitutions.

LMO characteristics

Modified traits

Resistance to diseases and pests
Insects
Lepidoptera (butterflies and moths)
Selectable marker genes and reporter genes
Other
Tolerance to mannose

Common use(s) of the LMO

Food
Feed

Detection method(s)

External link(s)

? MON-89Ø34-3 - 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

? EUginius - MON89034 x MIR162 *(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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