





Biosafety Clearing-House (BCH)

LIVING MODIFIED ORGANISM (LMO)

BCH-LMO-SCBD-46299-13

? Decisions on the LMO ? Risk Assessments

LAST UPDATED: 06 APR 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.

https://bch.cbd.int/database/record?documentID=46299



MON-89Ø34-3 X MON-88Ø17-3 Genuity⊗ VT Triple Pro™ Maize



Read barcode or type above URL into internet browser to access information on this LMO in the Biosafety Clearing-House @ 5CBD 2012

Name

Genuity® VT Triple Pro™ Maize

ΕN

Transformation event

MON89034 x MON88017

Unique identifier

MON-89Ø34-3 x MON-88Ø17-3

Developer(s)

- ORGANIZATION: MONSANTO EUROPE S.A. | BCH-CON-EUR-43679-1

ORGANIZATION

Monsanto Europe S.A. Avenue de Tervuren 270-272 Brussels B-1150, Belgium

Description

The modified maize was produced through traditional cross-breeding of two modified parental lines MON89034 and MON88017, resulting in a stacked event with resistance to insects and tolerance to herbicides. The maize expresses Lepidopteran-specific CRY1A.105 and CRY2Ab2, as well as Coleopteran-specific CRY3Bb1, insecticidal proteins from *Bacillus thuringiensis*. Additionally, the modified maize includes EPSPS from *Agrobacterium tumefaciens* strain CP4 for tolerance to glyphosate.

ΕN

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-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-15106-10 LIVING MODIFIED ORGANISM | MON-88Ø17-3 - YIELDGARD™ VT™

ROOTWORM/RR2™ MAIZE

Resistance to diseases and pests - Insects - Coleoptera (beetles) Resistance to herbicides - Glyphosate

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

Crops

Characteristics of the modification process

Vector

PV-ZMIR245 and PV-ZMIR39

ΕN

Techniques used for the modification

Cross breeding

Genetic elements construct

V-LB-RHIRD P-e35S-CaMV L-cab-WHEAT I-1 act1-ORYSA CS-cry1A 105-SYNTH 0.240 kb 0.300 kb 0.060 kb0.480 kb 3.530 kb T-hsp17 3-WHEAT 0.210 kb P-34S-FMV I-hsp70-MAIZE TP-rbcS-MAIZE CS-Cry2Ab2-BACTU T-nos-RHIRD 0.560 kb0.800 kb 0.400 kb 1.910 kb 0.250 kbV-RB-RHIRD 0.230 kb P-act1-ORYSA T-nos-RHIRD I-1 act1-ORYSA TP-ctp2-ARATH CS-CP4epsps-RHIRD 0.260 kb 0.930 kb 0.460 kb 0.230 kb 1.370 kb P-e35S-CaMV L-cab-WHEAT I-1 act1-ORYSA CS-Cry3Bb1-BACTU T-hsp17 3-WHEAT 0.610 kb 0.070 kb 0.460 kb 1.960 kb 0.230 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-14979-7 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE GENE

Protein coding sequence | Resistance to herbicides (Glyphosate)

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-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-14988-7 CRY2AB2 | BACILLUS THURINGIENSIS - BT, BACILLUS, BACTU Protein coding sequence | Resistance to diseases and pests (Insects, Lepidoptera (butterflies and moths)) BCH-GENE-SCBD-100364-5 RICE ACTIN 1 GENE PROMOTER | (RICE) Promoter BCH-GENE-SCBD-100355-6 RICE ACTIN 1, INTRON | (RICE) BCH-GENE-SCBD-100365-6 CHLOROPLAST TRANSIT PEPTIDE 2 | (THALE CRESS) Transit signal BCH-GENE-SCBD-100269-8 NOPALINE SYNTHASE GENE TERMINATOR BCH-GENE-SCBD-100366-6 CAMV ENHANCED 35S PROMOTER BCH-GENE-SCBD-100354-6 5' UNTRANSLATED LEADER FROM CHLOROPHYLL A/B-BINDING PROTEIN | (WHEAT) Leader sequence 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) BCH-GENE-SCBD-100360-4 TRANSIT PEPTIDE AND FIRST INTRON OF RUBISCO SSU | (MAIZE, CORN) Transit signal BCH-GENE-SCBD-101415-9 TI PLASMID LEFT BORDER REPEAT Plasmid vector BCH-GENE-SCBD-101416-6 TI PLASMID RIGHT BORDER REPEAT Plasmid vector

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 the *Bacillus thuringiensis* genes cry1A.105 and cry2Ab2.

Transcription of cry1A.105 begins are the Cauliflower Mosaic Virus (CaMV) 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 expression of cry1A.105.

ΕN

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 Rubsico and cry2Ab32. The Hsp70

regulates and enhances gene expression, while the transit peptide targets cr2Ab2 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 nptll 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 MON88017 vector PV-ZMIR39

Maize line 88017 contains *A. tumefaciens* 5-enolpyruvylshikimate-3-phosphate (epsps) and *B. thuringiensis* cry3Bb1.

Transcription of epsps starts from the rice Actin 1 promoter and terminates at the *A. tumefaciens* nos terminator. The transcript initially includes (5' to 3'): a rice Actin 1 intron for enhanced gene expression, *Arabidopsis thaliana* chloroplast transit peptide 2 for chloroplast targeting of the EPSPS protein and epsps.

Transcription of the cry3Bb1 commences from the CaMV 35S enhanced promoter and terminates at the wheat heat shock protein 17.3 terminator. The transcript initially includes (5' to 3'): wheat 5' untranslated leader from chlorophyll a/b-binding, rice Actin 1 intron and cry3Bb1. The wheat untranslated leader and the rice actin intron regulate and enhance expression of the downstream cry3Bb1 element.

Note:

- The wild-type cry3Bb1 coding sequence was modified to encode six specific amino acid substitutions, resulting in the synthetic cry3Bb1 coding sequence present in the vector. The differences at the six positions are: 2A (insertion), H232R, S312L, N314T, E318K, Q349R.
- Molecular analyses of MON 88017 confirmed that single copies of the cp4 epsps and cry3Bb1 genes are integrated at a single locus in the corn genome with all expression elements intact and no plasmid bacterial backbone present. Plasmid PV-ZMIR39 contains the left and right transfer DNA (T-DNA) border sequences that facilitate transformation.

For additional information on this LMO, please refer to the records of the parental LMOs.

LMO characteristics

Resistance to diseases and pests

Insects

Coleoptera (beetles)

Lepidoptera (butterflies and moths)

Resistance to herbicides

Glyphosate

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)

? MON-88Ø17-3 - EU Reference Laboratory for GM Food and Feed (EURL-GMFF) (<code>English</code>)

Additional Information

Other relevant website addresses and/or attached documents

? FAO GM Foods Platform: MON-89Ø34-3 x MON-88Ø17-3 (<code>English</code>)

? EUginius: MON89034 x MON88017 (English)

BCH-LMO-SCBD-46299-13

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