

Biosafety Clearing-House (BCH)

LIVING MODIFIED ORGANISM (LMO)


BCH-LMO-SCBD-15374-8

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

LAST UPDATED: 24 JUL 2013

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-88Ø17-3 X MON-ØØ81Ø-6
YieldGard™ VT Triple

CBD

<https://bch.cbd.int/database/record?documentID=15374>



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

Name

YieldGard™ VT Triple

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Transformation event

MON88017 x MON810

Unique identifier

MON-88Ø17-3 x MON-ØØ81Ø-6

Developer(s)

- [ORGANIZATION: MONSANTO](#) | [BCH-CON-SCBD-14925-3](#)

ORGANIZATION

Monsanto
800 North Lindbergh Blvd.
St. Louis, MO
63167, United States of America
Phone: + 1 314 694-1000
Fax: +1 314 694-3080
Website: <http://www.monsanto.com>

Description

A stacked insect-resistant maize derived from conventional cross-breeding of MON-88Ø17-3 and MON-ØØ81Ø-6. Resistance to insect attack is conferred through expression of a truncated form of the cry1Ab gene and cry3Bb1 gene from *Bacillus thuringiensis* subsp. *kurstaki* HD-1 and tolerance to glyphosate-herbicides is produced through introduction of the

EN

epsps gene from *Agrobacterium tumefaciens* which confers tolerance to the herbicide Roundup, with the active ingredient glyphosate.

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-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-LMO-SCBD-14750-19 LIVING MODIFIED ORGANISM | MON-ØØ81Ø-6 - YIELDGARD™ MAIZE |

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

Characteristics of the modification process

Vector

PV-ZMIR39, PV-ZMBK07 and PV-ZMGT10

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Techniques used for the modification

Cross breeding

Genetic elements construct

P-e35S-CaMV
0.610 kb

I-hsp70-MAIZE
0.800 kb

CS-Cry1Ab-BACTU
3.460 kb

P-act1-ORYSA
0.930 kb

I-1_act1-ORYSA
0.460 kb

TP-ctp2-ARATH
0.230 kb

CS-CP4epsps-RHIRD
1.370 kb

T-nos-RHIRD
0.260 kb

P-e35S-CaMV
0.610 kb

L-cab-WHEAT
0.070 kb

I-1_act1-ORYSA
0.460 kb

CS-Cry3Bb1-BACTU
1.960 kb

T-hsp17_3-WHEAT
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-14985-12 CRY1AB | BACILLUS THURINGIENSIS - BT, BACILLUS, BACTU |

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

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

Promoter

BCH-GENE-SCBD-100359-7 HSP70 INTRON | (MAIZE, CORN) |

Intron

[BCH-GENE-SCBD-100364-5](#) RICE ACTIN 1 GENE PROMOTER | (RICE) |

Promoter

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

Intron

[BCH-GENE-SCBD-100365-6](#) CHLOROPLAST TRANSIT PEPTIDE 2 | (THALE CRESS) |

Transit signal

[BCH-GENE-SCBD-100269-8](#) NOPALINE SYNTHASE GENE TERMINATOR |

Terminator

[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

Notes regarding the genetic elements present in this LMO

DNA insert from MON810, vectors PV-ZMBK07 and PV-ZMGT10

MON810 contains a truncated portion of a synthetic form of the cry1Ab gene from *Bacillus thuringiensis* subsp. *kurstaki*. Two constructs PV-ZMBK07 and PV-ZMGT10 have been used for transformation, but molecular analyses showed that MON810 does not contain any element from PV-ZMGT10 construct and only the elements from construct PV-ZMBK07 have been integrated into its genome. MON810 contains one integrated DNA consisting of P-e35S, I-Hsp70 and cry1Ab. The terminator of the nopaline synthase (nos) gene was lost due to a truncation at the 3' end of the gene cassette during genome integration and is, therefore, not present in MON810.

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DNA insert from MON88017 vector PV-ZMIR39

MON88017 expresses the cry3Bb1 gene encoding a Coleopteran-specific insecticidal protein to control infestation with corn root worm, and the cp4 epsps gene.

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

LMO characteristics

Modified traits

Resistance to diseases and pests

Insects

Coleoptera (beetles)

Lepidoptera (butterflies and moths)

European corn borer (*Ostrinia nubilalis*)

Resistance to herbicides

Glyphosate

Common use(s) of the LMO

Food

Detection method(s)

External link(s)

- ? [MON-88Ø17-3 - EU Reference Laboratory for GM Food and Feed \(EURL-GMFF\)](#) (*English*)
- ? [MON-ØØ81Ø-6 - EU Reference Laboratory for GM Food and Feed \(EURL-GMFF\)](#) (*English*)

Additional Information

Additional Information

MON88017 x MON810 is resistant to insect attack and tolerant to use of the herbicide glyphosate. The cry3Bb1 gene encodes a Coleopteran-specific insecticidal protein from *Bacillus thuringiensis* (subsp. *kumamotoensis*) in order to control infestation with corn root worm, the cry1Ab gene produces the insect control protein Cry1Ab, a delta-endotoxin which is insecticidal to lepidopteran insects, and the cp4 epsps gene from the soil bacterium *Agrobacterium* ssp. strain CP4 provides tolerance to the herbicide glyphosate.

The cry3Bb1 gene encodes the insect control protein Cry3Bb1, a delta-endotoxin, The toxin protects the plant from the Coleopteran insects western corn rootworm (*Diabrotica virgifera*), northern corn rootworm (*D. barberi*), and Mexican corn rootworm (*D. virgifera zea*). The cry1Ab gene produces the insect control protein Cry1Ab and protects the plant against lepidopteran insects such as the european corn borer (ECB).

Cry proteins act by selectively binding to specific sites localized on the lining of the midgut of susceptible insect species. Following binding, pores are formed that disrupt midgut ion flow, causing gut paralysis and eventual death due to bacterial sepsis. Cry3Bb1 is lethal only when eaten by Coleopteran species, including corn root worm, and its specificity of action is directly attributable to the presence of specific binding sites in the target insects. Cry1Ab is insecticidal only when eaten by the larvae of lepidopteran insects (moths and butterflies). There are no binding sites for the delta-endotoxins of *B. thuringiensis* on the surface of mammalian intestinal cells, therefore, livestock animals and humans are not susceptible to these proteins.

The cp4 epsps gene encodes for a form of the plant enzyme 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) that is highly tolerant to inhibition by glyphosate.

This line is a product of traditional plant breeding, and therefore is not automatically subject to regulation in all jurisdictions as are transgenic plants resulting from recombinant DNA technologies. Certain jurisdictions may request notification in advance of the release of a stacked hybrid, or may request information to conduct an environmental and food safety assessment.

Other relevant website addresses and/or attached documents

- ? [MON-88Ø17-3 x MON-ØØ81Ø-6 - CERA](#) (*English*)
- ? [MON-88Ø17-3 x MON-ØØ81Ø-6 - OECD](#) (*English*)

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