

Biosafety Clearing-House (BCH)

LIVING MODIFIED ORGANISM (LMO)


BCH-LMO-SCBD-14797-15

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

LAST UPDATED: 08 MAY 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.



SYN-BTØ11-1
YieldGard™ maize

CBD

<https://bch.cbd.int/database/record?documentID=14797>



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

Name

YieldGard™ maize

EN

Transformation event

Bt 11 (X4334CBR, X4734CBR)

Unique identifier

SYN-BTØ11-1

Developer(s)

- **ORGANIZATION:** SYNGENTA | [BCH-CON-SCBD-14926-2](#)

ORGANIZATION

Syngenta

Website: <http://www.syngentaseeds.com>

Description

Insect-resistant and herbicide tolerant maize produced by inserting the cry1Ab gene from *Bacillus thuringiensis* subsp. *kurstaki* to confer resistance to the European corn borer (*Ostrinia nubilalis*), and the phosphinothricin N-acetyltransferase (PAT) encoding gene from *Streptomyces viridochromogenes* to confer tolerance to phosphinothricin (PPT) herbicide, specifically glufosinate ammonium.

EN

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

Related LMO(s)

BCH-LMO-SCBD-45400-3 | Bt-10 Maize | Syngenta | Resistance to antibiotics (Ampicillin), Resistance to diseases and pests (Insects, Lepidoptera (butterflies and moths), European corn borer (*Ostrinia nubilalis*)), Resistance to herbicides (Glufosinate)

[Show detection method\(s\)](#)

Characteristics of the modification process

Vector

pZO1502 Derived from pUC18

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Techniques used for the modification

Direct DNA transfer

Genetic elements construct

P-35S-CaMV 0.510 kb	I-ADH1 intron 6 0.470 kb	CS-Cry1Ab-BACTU 1.850 kb	T-nos-RHIRD 0.250 kb
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P-35S-CaMV 0.420 kb	I-ADH1 intron 2 0.180 kb	CS-pat-STRVR 0.550 kb	T-nos-RHIRD 0.250 kb
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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-15002-4 PHOSPHINOTHRICIN N-ACETYLTRANSFERASE GENE |

Protein coding sequence | Resistance to herbicides (Glufosinate)

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-100269-8 NOPALINE SYNTHASE GENE TERMINATOR |

Terminator

BCH-GENE-SCBD-100287-7 CAMV 35S PROMOTER |

Promoter

BCH-GENE-SCBD-103625-2 ALCOHOL DEHYDROGENASE 1, INTRON 6 | (MAIZE, CORN) |

Intron

BCH-GENE-SCBD-103867-1 ALCOHOL DEHYDROGENASE 1, INTRON 2 | (MAIZE, CORN) |

Intron

Notes regarding the genetic elements present in this LMO

Maize line Bt11 was genetically modified to contain two novel genes, cry1Ab and pat, for insect and herbicide tolerance respectively. Both genes were introduced into a maize line by particle acceleration (biolistic) transformation.

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Information on the inserted DNA sequences:

- 35S promoters derived from cauliflower mosaic virus (CaMV) and 35S-1 originated from the CM1841 isolate of CaMV as a 500 Ddel to Ddel fragment, subsequently converted to SacI sites and 35S-2 originated from the Cabb-S strain of CaMV as a n AluI to Ddel fragments (ca 425bp), whose ends were subsequently modified.
- introns derived from the maize alcohol dehydrogenase 1S gene and were used to enhance heterologous gene expression.
- Btk gene which is an altered version of the full length cry1A(b) gene of *Bacillus thuringiensis* var *kurstaki* HD-1. The Btk was obtained as a 1.8kb Nco-Bg/II fragment. The truncated Btk protein is identical to the N-terminal 615 amino acids of the native Btk protein of 1155 amino acids.
- pat gene (phosphinotricin acetyl transferase) cloned from the soil microorganism, *Streptomyces viridochromogenes* strain Tu494. Alteration did not result in any amino acid sequence changes.
- nos terminator consisting of 423-678 of the nopaline synthase gene of *Agrobacterium tumefaciens* plus added restriction sites.

Vector information

Plasmid pZO1502 is the vector used for the transformation of Bt maize. This is a derivative of plasmid pUC18. The plasmid has a molecular weight of 2.7 kb and contains the following sequences:

- the prokaryotic gene bla (also called ampR) under a prokaryotic promoter encoding β -lactamase, which confers resistance to ampicillin; it is used as a bacterial selectable marker;
- the gene lac Z, encoding a portion of a β -galactosidase, this gene is not functional;
- the pUC origin of replication derived from the plasmid pBR 322 carrying a mutation.

LMO characteristics

Modified traits

Resistance to diseases and pests

Insects

Lepidoptera (butterflies and moths)

European corn borer (*Ostrinia nubilalis*)

Resistance to herbicides

Glufosinate

Common use(s) of the LMO

Food

Feed

Detection method(s)

External link(s)

? [SYN-BTØ11-1 - EU Reference Laboratory for GM Food and Feed \(EURL-GMFF\)](#) (English)

? [SYN-BTØ11-1 - CropLife International Detection Methods Database](#) (English)

Additional Information

Other relevant website addresses and/or attached documents

? [BT11 - OECD](#) (*English*)

[BT11 - CERA](#) (*English*)

? [Bt11 Petition.pdf](#) (*English*)

[BCH-LMO-SCBD-14797-15](#)

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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