LIVING MODIFIED ORGANISM (LMO)

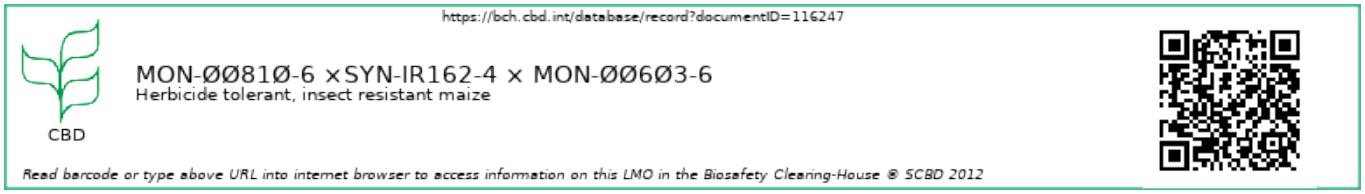
BCH-LMO-SCBD-116247-1

? Decisions on the LMO ? Risk Assessments

LAST UPDATED: 11 AUG 2021

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

Herbicide tolerant, insect resistant maize | EN

Transformation event

MON810 × MIR162 × NK603

Unique identifier

MON-ØØ81Ø-6 ×SYN-IR162-4 × MON-ØØ6Ø3-6

Developer(s)

- ORGANIZATION: SYNGENTA SEEDS GMBH | BCH-CON-SCBD-101875-3

ORGANIZATION

Syngenta Seeds GmbH
Private sector (business and industry)
Syngenta Seeds GmbH Zum Knipkenbach 20
Bad Salzuflen
32107, Germany
Phone: +49 52 22 5308-0
Fax: +49 52 22 5308-12
Email: info.seeds@syngenta.com
Website: http://www.syngenta-seeds.de/de/

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

PERSON

Bayer CropScience
Bayer CropScience AG Alfred-Nobel-Str. 50 40789 Monheim am Rhein
Monheim am Rhein
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 (*Zea mays*) was produced through crossing breeding modified parental lines for insect resistance and herbicide tolerance. For Lepidoptera resistance, the modified maize expresses *Bacillus thuringiensis* Cry1Ab and vegetative insecticidal protein 3Aa20. The protein forms pores in the midgut lining of susceptible pests, leading to cell lysis and septicemia. For glyphosate tolerance, the maize expresses *Agrobacterium tumefaciens* 5-enolpyruvylshikimate-3-phosphate synthase, which encodes a bacterial variant of an endogenous enzyme involved in the essential biosynthesis of aromatic amino acids (shikimate pathway). The bacterial protein does not bind the herbicidal compound with high affinity and thus prevents inactivation of the enzyme. The modified maize also contains an *Escherichia coli* phosphomannose isomerase cassette that was used as a selectable marker during transformation of one parental line.	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

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

BCH-LMO-SCBD-14776-17 LIVING MODIFIED ORGANISM | MON-ØØ6Ø3-6 - ROUNDUP READY™ MAIZE |
Resistance to herbicides - Glyphosate

Characteristics of the modification process

Vector

PV-ZMBK07; pNOV1300; PV-ZMGT32	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-100366-6 CAMV ENHANCED 35S PROMOTER

Promoter

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

Intron

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-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

BCH-GENE-SCBD-100269-8 NOPALINE SYNTHASE GENE TERMINATOR

Terminator

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-14979-7 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE GENE

Protein coding sequence | Resistance to herbicides (Glyphosate)

Notes regarding the genetic elements present in this LMO

DNA insert from MON810 (MON-ØØ81Ø-6) vector PV-ZMBK07 A partial insert containing *Bacillus thuringiensis cry1Ab* was inserted into the parental maize genome. Transcription is directed from the *Cauliflower mosaic virus* 35S enhanced promoter. The transcript contains a *Zea mays* heat shock protein 70 (*ZmHsp70*) intron and the coding sequence of *cry1Ab*. *ZmHsp70* enhances expression of *cry1Ab*. Note: - The coding sequence of *cry1Ab* has been codon optimized for expression in plants. The codon optimization did not result in any changes to the amino acid sequence relative to the native sequence. - Southern blot analysis indicated that a single partial insert is found within the parental genome. - Southern blot analysis did not detect the presence of the *Escherichia coli* neomycin phosphotransferase II gene nor any DNA from plasmid PVZMGT10 (containing genes for glyphosate tolerance - *cp4-epsps*). - ELISA protein analysis and feeding assays indicated expression of Cry1Ab in the parental line. **DNA insert from MIR162 (SYN-IR162-4) vector pNOV1300** In the parental MIR162 maize, a variant of the native *Bacillus 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 a *Z. mays* ubiquitin gene promoter and then transcribes *vip3Aa20* followed by intron 9 of *Z. mays* phosphoenolpyruvate carboxylase, before terminating at the *Cauliflower mosaic virus* 35S terminator. A second expression cassette, containing the *Escherichia coli* phosphomannose isomerase gene, 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 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 maize ubiquitin promoter; (iii) one copy of the *nos* terminator; and (iv) no backbone sequences from transformation plasmid pNOV1300. **DNA insert from NK603 (MON-ØØ6Ø3-6) vector PV-ZMGT32** The plant expression plasmid vector, PV-ZMGT32 contains two adjacent plant gene expression cassettes each containing a single copy of *Agrobacterium tumefaciens* 5-enolpyruvylshikimate-3-phosphate synthase (*cp4-epsps*). In the first (5' end) expression cassette, the *cp4-epsps* gene is under the transcriptional regulation of an *Oryza sativa* actin promoter and an *A. tumefaciens* nopaline synthase (*nos*) terminator. An *O. sativa* actin intron is also present in the transcript for enhanced expression of the coding sequence. The second cassette consists of another *cp4-epsps* gene regulated by a *Cauliflower mosaic virus*	EN

enhanced 35S promoter (containing a duplicated enhancer region) and a *nos* terminator. Similarly, an intron from the maize heat shock protein 70 (*ZmHsp70*) was included for enhancing expression of the coding sequence. Both promoters of the gene cassettes are expected to promoter high levels of transcription.

Note:
- The parental NK603 line contained a single, intact insertion containing both *cp4-epsps* gene cassettes.
- Due to restriction digest prior to particle bombardment, the vector backbone, containing *E. coli* neomycin phosphotransferase II and origin of replication, were not incorporated into the parental genome.

Kindly refer to the parental LMO records for more information.

LMO characteristics

Modified traits

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

Resistance to herbicides
- Glyphosate

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-ØØ81Ø-6 - 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)*

? MON-ØØ6Ø3-6 - EU Reference Laboratory for GM Food and Feed (EURL-GMFF) *(English)*

? MON-ØØ81Ø-6 - GMO Detection method Database (GMDD) *(English)*

? SYN-IR162-4 - GMO Detection method Database (GMDD) *(English)*

? MON-ØØ6Ø3-6 - GMO Detection method Database (GMDD) *(English)*

Additional Information

Other relevant website addresses and/or attached documents

? EUginius - MON810 x MIR162 x NK603 *(English)*

BCH-LMO-SCBD-116247-1

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