

## Biosafety Clearing-House (BCH)

LIVING MODIFIED ORGANISM (LMO)


BCH-LMO-SCBD-116256-2

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

LAST UPDATED: 01 OCT 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.



**MON-87427-7 × MON-87460-4**  
Drought-tolerant maize with tissue-specific herbicide tolerance

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

<https://bch.cbd.int/database/record?documentID=116256>



Name

Drought-tolerant maize with tissue-specific herbicide tolerance

EN

Transformation event

MON 87427 × MON 87460

Unique identifier

MON-87427-7 × MON-87460-4

Developer(s)

- [PERSON: BAYER CROPSCIENCE](#) | [BCH-CON-SCBD-111462-3](#)

#### PERSON

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#### RELATED ORGANIZATION

Description

The maize (*Zea mays*) was modified for tissue-specific herbicide tolerance and drought tolerance through cross breeding of modified parental lines. For glyphosate tolerance, the maize expresses *Agrobacterium tumefaciens* 5-enolpyruvylshikimate-3-phosphate synthase

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(*cp4-epsps*), which is a bacterial variant of the endogenous gene involved in the biosynthesis of aromatic amino acids (shikimate pathway). The bacterial protein does not bind the herbicide with high affinity and thus allows for the continued biosynthesis of essential aromatic amino acids. Due to the combination of promoter and intron genetic elements (see 'Notes regarding the specific genetic elements' below), *cp4-epsps* is expressed in vegetative and female-specific tissues, thus allowing for glyphosate-treated maize to serve as the female parent during the production of hybrid seed. For drought tolerance, the maize expresses *Bacillus subtilis* cold shock protein, which binds RNA and maintains cellular functions under water-limited conditions (improvement of natural abiotic stress responses, also to cold stress). The maize also contains an *Escherichia coli* neomycin phosphotransferase II cassette, which allowed for kanamycin selection during transformation of a parental line.

#### 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-104758-3](#) LIVING MODIFIED ORGANISM | MON-87427-7 - MAIZE MODIFIED FOR TISSUE SELECTIVE GLYPHOSATE TOLERANCE |

Resistance to herbicides - Glyphosate

[BCH-LMO-SCBD-103066-6](#) LIVING MODIFIED ORGANISM | MON-87460-4 - DROUGHTGARD™ MAIZE |

Resistance to antibiotics - Kanamycin Tolerance to abiotic stress - Cold / Heat, Drought

### Characteristics of the modification process

#### Vector

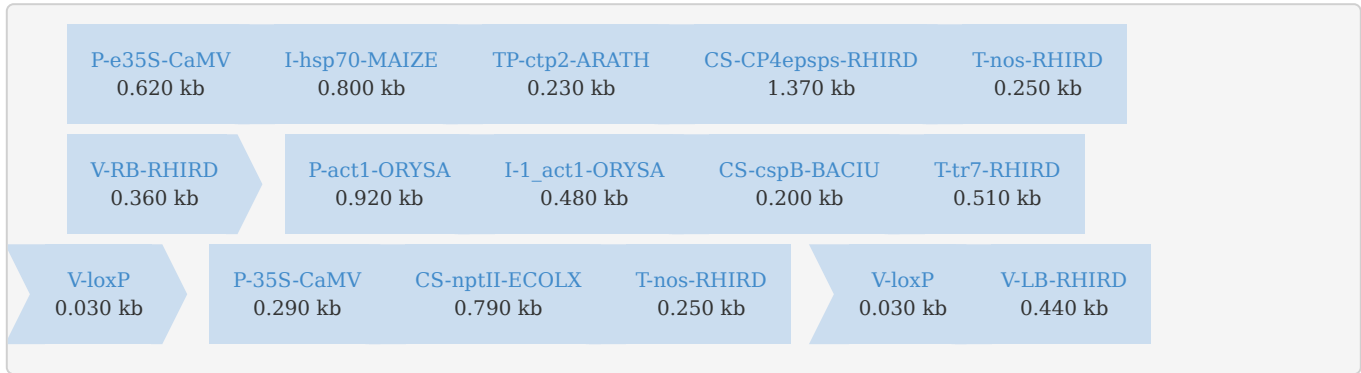
PV-ZMAP1043; PV-ZMAP595

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-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)

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

Terminator

**BCH-GENE-SCBD-101415-9** TI PLASMID LEFT BORDER REPEAT |

Plasmid vector

**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-103065-7** COLD SHOCK PROTEIN GENE |

Protein coding sequence | Tolerance to abiotic stress (Cold / Heat, Drought)

**BCH-GENE-SCBD-103067-9** TRANSCRIPT 7 GENE 3' UNTRANSLATED REGION |

Terminator

**BCH-GENE-SCBD-103069-3** LOXP RECOMBINATION SITE |

recombination site

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

Promoter

**BCH-GENE-SCBD-15001-5** NEOMYCIN PHOSPHOTRANSFERASE II | (BACTERIA) |

Protein coding sequence | Resistance to antibiotics (Kanamycin)

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

Plasmid vector

Notes regarding the genetic elements present in this LMO

#### **DNA insert from MON87427 PV-ZMAP1043**

Transcription of 5-enolpyruvylshikimate-3-phosphate synthase (*cp4-epsps*) from *Agrobacterium tumefaciens* commences from the *Cauliflower mosaic virus* (CaMV) enhanced 35S promoter and ends at the *A. tumefaciens* nopaline synthase (*nos*) gene terminator. The transcript contains a *Zea mays* heat shock protein 70 (*hsp70*) intron, *Arabidopsis thaliana* N-terminal chloroplast transit peptide sequence, and *cp4-epsps*. The CaMV enhanced 35S promoter-*hsp70* combination promotes gene expression in female and vegetative tissues, but not in male reproductive tissues (pollen microspores and tapetum).

#### Note:

- Southern blot analyses indicate that a single copy of the T-DNA was inserted at a single site in the parental maize genome and no plasmid vector backbone sequences were detected to have been integrated. DNA sequencing analyses further indicated that the expected T-DNA sequences were integrated.

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-The *cp4-epsps* coding sequence is the codon optimized coding sequence of the *aroA* gene from *Agrobacterium sp.* strain CP4 encoding CP4 EPSPS.

#### **DNA insert from MON87460 vector PV-ZMAP595**

The T-DNA insert contains the following gene cassettes: *Bacillus subtilis* cold shock protein (*cspB*) and *Escherichia coli* neomycin phosphotransferase II (*nptII*).

Transcription of *cspB* is under control of the *Oryza sativa* actin 1 promoter and *Agrobacterium tumefaciens* transcript 7 gene 3' untranslated region. The transcript initially contains an *O. sativa* actin 1 intron for enhanced gene expression of *cspB*. The sequence is removed (spliced) prior to protein translation. Constitutive expression of *cspB* is expected due to the actin promoter.

Transcription of *nptII* is under control of the *Cauliflower mosaic virus* (CaMV) 35S promoter and *A. tumefaciens* nopaline synthase terminator. High levels of transcription are expected due to the CaMV promoter.

#### Note:

- The coding sequence of *cspB* has been codon optimized for optimal expression within plant cells.
- Southern blot analysis indicated that no vector backbone sequences were inserted into the parental genome
- Southern blot analysis indicated that the parental genome contains a single insertion
- Sequencing analyses confirm the Southern blot analyses.
- A 22 base pair deletion of genomic DNA at the insert-to-plant DNA junction occurred.
- *loxP* sites can be found in the parental genome and could potentially allow for the excision of the *nptII* cassette by CRE recombinase.

*For more information, kindly refer to the parental LMO records.*

### **LMO characteristics**

#### Modified traits

Resistance to herbicides  
    Glyphosate  
Resistance to antibiotics  
    Kanamycin  
Tolerance to abiotic stress  
    Cold / Heat  
    Drought  
Selectable marker genes and reporter genes

#### Common use(s) of the LMO

Food  
Feed

## Detection method(s)

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External link(s)

- ? [MON-87427-7 - EU Reference Laboratory for GM Food and Feed \(EURL-GMFF\)](#) ( *English* )
- ? [MON-87460-4 - EU Reference Laboratory for GM Food and Feed \(EURL-GMFF\)](#) ( *English* )
- ? [MON-87427-7 - GMO Detection method Database \(GMDD\)](#) ( *English* )
- ? [MON-87460-4 - GMO Detection method Database \(GMDD\)](#) ( *English* )

## Additional Information

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Other relevant website addresses and/or attached documents

- ? [EUginus - MON-87427-7 x MON-87460-4](#) ( *English* )

[BCH-LMO-SCBD-116256-2](#)

## 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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