

## Biosafety Clearing-House (BCH)

LIVING MODIFIED ORGANISM (LMO)


BCH-LMO-SCBD-114651-2

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

LAST UPDATED: 12 JUL 2019


### 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.



DP-305423-1 X MON-87708-9 X MON-89788-1  
High oleic acid, herbicide tolerant soy

<https://bch.cbd.int/database/record?documentID=114651>



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

Name

High oleic acid, herbicide tolerant soy

EN

Transformation event

DP-305423-1×MON87708×MON89788

Unique identifier

DP-305423-1 x MON-87708-9 x MON-89788-1

Developer(s)

- [ORGANIZATION: DUPONT POINEER](#) | [BCH-CON-SCBD-106199-2](#)

#### ORGANIZATION

Dupont Poineer  
Private sector (business and industry)  
Chestnut Run Plaza 720/1S5 974 Centre Road  
Wilmington,, Delaware  
19805, United States of America

Description

The soybean has been modified to produce increased levels of monounsaturated fatty acid (oleic) and decreased levels of polyunsaturated fatty acids (linoleic and linolenic). The additional inserted genes (acetolactate synthase, dicamba monooxygenase, and cp4 epsps) confer tolerance to herbicides (sulfonyleurea, 3,6-dichloro-2-methoxybenzoic acid, and glyphosate, respectively).

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-10453-6** ORGANISM | GLYCINE MAX (SOYBEAN, SOYA BEAN, SOYA, SOYBN) |

Crops

#### Related LMO(s)

**BCH-LMO-SCBD-49073-9** | DP-3Ø5423-1 - TREUS™ Plenish™ Soybean | Pioneer Hi-Bred Production Inc. | Changes in quality and/or metabolite content (Lipid and fatty acids), Resistance to herbicides (Sulfonylurea)

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

**BCH-LMO-SCBD-104665-6** | MON-877Ø8-9 - Dicamba Tolerant Soybean | Resistance to herbicides

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

**BCH-LMO-SCBD-40284-18** | MON-89788-1 - Roundup Ready2Yield™ soybean | Monsanto | Resistance to herbicides (Glyphosate)

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

### Characteristics of the modification process

#### Vector

PHP19340 and PHP17752; PV-GMHT4355; PV-GMGOX20

EN

#### Techniques used for the modification

Cross breeding

#### Genetic elements construct

P-KTi3  
2.080 kb

FAD2-1  
0.600 kb

T-KTi3  
0.200 kb

P-SAMS  
1.300 kb

CS-ahas-SOYBN  
1.970 kb

T-ahas-SOYBN  
0.600 kb

P-PC1SV-PCSV  
0.430 kb

L-5UTR-TEV  
0.130 kb

TP-rbcS-PEA  
0.240 kb

CS-DMO  
1.020 kb

T-rbcS\_E9-PEA  
0.640 kb

L-35s-CMoVb  
1.040 kb

P-TSF1  
0.000 kb

L-TSF1  
0.050 kb

I-TSF1  
0.620 kb

TP-ctp2-ARATH  
0.230 kb

CS-CP4epsps-RHIRD  
1.370 kb

T-rbcS\_E9-PEA  
0.640 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-103893-1** KUNITZ TRYPSIN INHIBITOR GENE PROMOTER | (SOYBEANS) |

Promoter

**BCH-GENE-SCBD-103894-1** KUNITZ TRYPSIN INHIBITOR GENE TERMINATOR | (SOYBEANS) |

Terminator

[BCH-GENE-SCBD-103895-2](#) SAMS PROMOTER | (SOYBEANS) |

Promoter

[BCH-GENE-SCBD-100268-6](#) ACETOHYDROXY ACID SYNTHASE GENE | (SOYBEANS) |

Protein coding sequence | Resistance to herbicides (Sulfonylurea)

[BCH-GENE-SCBD-103896-5](#) ACETOHYDROXY ACID SYNTHASE GENE TERMINATOR | (SOYBEANS) |

Terminator

[BCH-GENE-SCBD-104662-2](#) PC1SV PROMOTER | (PCSV, PCLSV) |

Promoter

[BCH-GENE-SCBD-104664-2](#) TEV 5' UNTRANSLATED REGION | (TEV) |

Leader

[BCH-GENE-SCBD-103616-4](#) RBCS TRANSIT PEPTIDE | (GARDEN PEA) |

Transit signal

[BCH-GENE-SCBD-100728-2](#) DICAMBA MONOOXYGENASE GENE |

Protein coding sequence | Resistance to herbicides

[BCH-GENE-SCBD-101877-5](#) RBCS-E9 GENE TERMINATOR | (GARDEN PEA) |

Terminator

[BCH-GENE-SCBD-105196-2](#) FMV 35S ENHANCER |

Leader

[BCH-GENE-SCBD-103903-1](#) ELONGATION FACTOR EF-1ALPHA PROMOTER | (THALE CRESS) |

Promoter

[BCH-GENE-SCBD-103904-1](#) ELONGATION FACTOR EF-1ALPHA LEADER | (THALE CRESS) |

Leader

[BCH-GENE-SCBD-103905-1](#) ELONGATION FACTOR EF-1ALPHA INTRON 1 | (THALE CRESS) |

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-115046-3](#) OMEGA-6-DESATURASE | (SOYBEANS) |

Protein coding sequence | Changes in quality and/or metabolite content (Lipid and fatty acids)

Notes regarding the genetic elements present in this LMO

#### **Genetic elements associated with PHP19340 and PHP17752:**

Microprojectile bombardment was used to co-transform secondary plant cell embryos with two purified linear DNA fragments: a 2924 base pair fragment (PHP19340A fragment) containing the gm-fad2-1 cassette, and the 4512 base pair fragment (PHP17752A fragment) containing the gm-hra cassette. The gm-fad2-1 cassette includes the promoter region from the *Glycine max* (soybean) Kunitz trypsin inhibitor gene (KTI3), a fragment of the omega(6)-fatty acid dehydrogenase (FAD2-1) gene that corresponds to approximately 40% of the middle portion of the FAD2-1, and the 3' untranslated region of the KTI3 gene (KTI3 terminator). The gm-hra cassette contains the gm-hra gene, which is an optimized form of the endogenous Acetohydroxy acid Synthase (als) gene from soybean, with transcription

EN

regulated by the S-adenosyl-L-methionine synthetase (SAMS) constitutive promoter from soybean and with transcription terminated by the endogenous als gene terminator from soybean.

Note: Sequence characterization of the inserted DNA in 305423 soybean confirms that it contains four insertions that comprise:

- \* Insertion 1: one truncated PHP19340A fragment with a truncated KTi3 terminator and intact gm-fad2-1 gene fragment and intact KTi3 promoter, one intact PHP19340A fragment, one intact PHP17752A fragment, one truncated PHP19340A fragment with an intact KTi3 promoter and a truncated gm-fad2-1 gene fragment, and one truncated PHP19340A fragment with a truncated KTi3 promoter and truncated gm-fad2-1 gene fragment.

- \* Insertion 2: one truncated PHP19340A fragment with a truncated KTi3 promoter and with intact gm-fad2-1 gene fragment and intact KTi3 terminator.

- \* Insertion 3: one truncated copy of the KTi3 promoter with a nonfunctional 495 bp fragment of the plasmid backbone; and

- \* Insertion 4: two truncated PHP19340A fragments in an inverted repeat configuration, both with a truncated KTi3 promoter and intact gm-fad2-1 gene fragment and KTi3 terminator.

#### **Genetic elements associated with PV-GMHT4355:**

Expression of the *Stenotrophomonas maltophilia* dicamba monooxygenase (DMO) gene is controlled by the peanut chlorotic streak virus Full-Length transcript promoter and the *Pisum sativum* (pea) small subunit of rubulose-1,5- bisphosphate carboxylase terminator. The transcript contains 5' untranslated region of the tobacco etch virus (to improve gene expression), pea N-terminal chloroplast transit peptide (for chloroplast localization), and DMO.

Note:

- Southern blot analysis indicated that the second 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) expression cassette was not integrated into the MON87708 line and neither were any elements of the vector backbone. The cassette contained the following elements in an antisense orientation to the dicamba expression cassette: P-FMV>> L-DnaK>> TS-CTP2>> CS-C4 EPSPS>> T-E9.
- Southern blot analysis and sequencing analysis indicated that a single intact dicamba expression cassette was integrated into the MON87708 line. Southern blot analysis indicated that the vector backbone was not present in the parental line.

#### **Genetic information associated with PV-GMGOX20:**

Information on the inserted DNA sequences:

The DNA inserted into the soybean genome contains:

- Codon optimized coding sequence of the aroA (epsps) gene from the *Agrobacterium sp.* strain CP4 encoding the CP4 EPSPS protein.
- a chimeric transcriptional promoter (P-FMV/Tsf1) consisting of chimeric sequence derived from *Arabidopsis thaliana* Elongation factor 1 alpha (Tsf1) gene promoter and enhancer sequences from the 35S of the Figwort Mosaic Virus.

Located between the promoter and the cp4epsps coding sequence are:

- the non-translated leader sequence (L-Tsf1) and the I-Tsf1 non translated intron;
- a chloroplast transit peptide sequence (TS-CTP2), derived from the *A. thaliana* epsps gene and placed before the cp4 epsps gene encoding sequence in the gene insert;

- a polyadenylation sequence from RbcS2 gene (T-E9), derived from *Pisum sativum* (pea) containing the 3' non translated region of the pea ribulose-1,5 biphosphate carboxylase small sub unit E9.

Note:

- Southern blot analyses indicated that the parental MON 89788 contained a single intact cp4 epsps expression cassette integrated at a single locus within the soybean genome. DNA sequencing analyses of the MON 89788 insert confirmed the expected coding region of the cp4 epsps gene cassette, is identical to that transformed in the T-DNA cassette. No backbone sequences from the transformation plasmid were detected and no partial genetic elements, linked or unlinked to the inserted expression cassette were detected.

The genetic material that is inserted in 305423 soybean is genetically linked and segregates following a typical pattern of Mendelian inheritance expected for a single, genetically-linked insertion locus.PV-GMGOX20

## LMO characteristics

### Modified traits

Resistance to herbicides

Glyphosate

Sulfonylurea

Changes in quality and/or metabolite content

Lipid and fatty acids

Other

Tolerance to dicamba (3,6-dichloro-2-methoxybenzoic acid) herbicide.

### Other gene(s) whose expression was affected by the transformation

[BCH-GENE-SCBD-115046-3](#) OMEGA-6-DESATURASE | (SOYBEANS) |

Protein coding sequence | Changes in quality and/or metabolite content (Lipid and fatty acids)

### How the expression of the gene(s) was affected

Transcription of the gene fragment under the control of a seed-preferred KTi3 promoter acts to silence the expression of the endogenous soybean omega-6 desaturase, which results in an increased level of oleic acid and decreased levels of linoleic and linolenic acids in the soybean seed.

EN

### Common use(s) of the LMO

Food

Feed

Biofuel

## Detection method(s)

### External link(s)

? [MON-89788-1 - EU Reference Laboratory for GM Food and Feed \(EURL-GMFF\)](#) ( English )

- ? [DP-3Ø5423-1 - EU Reference Laboratory for GM Food and Feed \(EURL-GMFF\)](#) ( *English* )
- ? [MON-877Ø8-9 - GMOMETHODS](#) ( *English* )

Additional Information

Please refer to the parental organism records for additional information on detection and identification.

EN

## Additional Information

Additional Information

Please refer to the parental organism records for more additional information.

Other relevant website addresses and/or attached documents

- ? [MON-89788 - Monsanto](#) ( *English* )
- ? [MON 87708- APHIS](#) ( *English* )
- ? [DP-3Ø5423-1 - Pioneer](#) ( *English* )

[BCH-LMO-SCBD-114651-2](#)

## 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.

**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](mailto:secretariat@cbd.int)