LIVING MODIFIED ORGANISM (LMO)

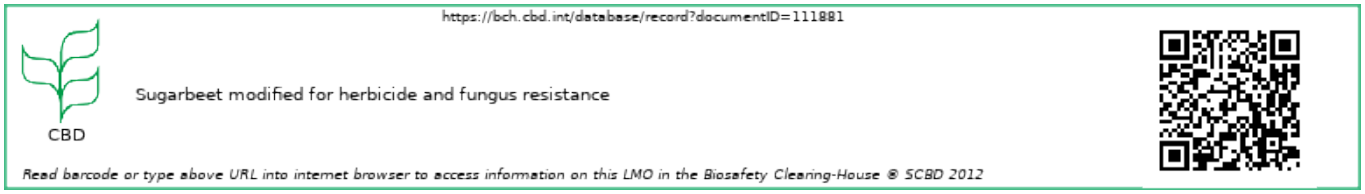
BCH-LMO-SCBD-111881-2 EN DE

? Decisions on the LMO ? Risk Assessments

LAST UPDATED: 18 MAY 2017

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

Sugarbeet modified for herbicide and fungus resistance	EN

Transformation event

TAD13, TAD 18, TAD28, TAD33 and TAD44.

Developer(s)

- PERSON: DIECKMANN SEEDS | BCH-CON-DE-109234-2

PERSON

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RELATED ORGANIZATION

Description

Sugarbeets were modified to constitutively express phosphinothricin acetyltransferase (pat) gene. As a result of the genetic modification the resulting sugarbeet is tolerant to L-phosphinothricin-containing herbicides.	EN

Furthermore, the plants were also modified to constitutively express the defensin-like protein 1 gene (AMP1) of *Dahlia merckii*. Defensins have antimicrobial properties, therefore the introduction of the AMP1 gene confers a resistance to pathogenic fungi to the plants.

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-12097-4 ORGANISM | BETA VULGARIS (COMMON BEET, SUGARBEET, BETMA)

Crops

Characteristics of the modification process

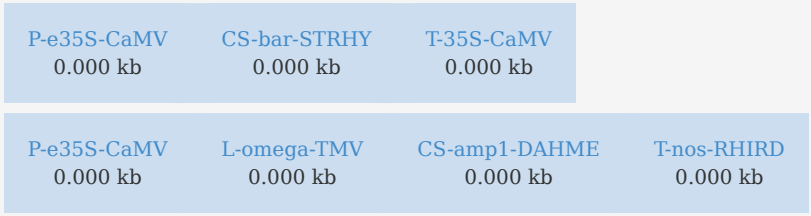
Vector

pIG35SDM EN

Techniques used for the modification

Direct DNA transfer

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-100290-6 CAMV 35S TERMINATOR

Terminator

BCH-GENE-SCBD-104820-3 OMEGA 5' UNTRANSLATED LEADER | (TMV)

Leader

BCH-GENE-SCBD-111875-2 DEFENSIN-LIKE PROTEIN 1 GENE | DAHLIA MERCKII (BEDDING DAHLIA, DAHME)

Protein coding sequence | Resistance to diseases and pests (Fungi)

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

Terminator

BCH-GENE-SCBD-111876-2 IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE PROMOTER | (YEAST)

Promoter

BCH-GENE-SCBD-111877-2 IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE GENE | (YEAST)

Protein coding sequence | Selectable marker genes and reporter genes

BCH-GENE-SCBD-111878-2 IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE TERMINATOR | (YEAST)

Terminator

BCH-GENE-SCBD-45875-7 BETA-GALACTOSIDASE GENE | (BACTERIA)

Protein coding sequence | Selectable marker genes and reporter genes

BCH-GENE-SCBD-111879-2 LAC OPERON PROMOTER | (BACTERIA)

Promoter

BCH-GENE-SCBD-111880-2 LAC OPERON REPRESSOR GENE | (BACTERIA)

Protein coding sequence

BCH-GENE-SCBD-111872-2 PMB1 ORIGIN OF REPLICATION | (BACTERIA)

Plasmid Vector

BCH-GENE-SCBD-14972-12 PHOSPHINOTHRICIN N-ACETYLTRANSFERASE GENE

Protein coding sequence | Resistance to herbicides (Glufosinate)

Notes regarding the genetic elements present in this LMO

The pIG35SDM plasmid was transferred into the plants as naked DNA via protoplast transformation. As a result, some of the transformation events have the entire transformation vector integrated into their genome while others only contain parts thereof. In addition to the genetic elements listed above, the pIG35SDM plasmid also contained the following sequences which were also transferred into the modified sugarbeet but are non-functional in plants: * The imidazoleglycerol phosphate dehydratase (his3) gene from *Saccharomyces cerevisiae* which is expressed as a selection marker in bacteria under the control of its native promoter and terminator sequences. Furthermore, due to the close proximity of these genes within the yeast genome, the transcription initiation site of the yeast ATP-dependent RNA helicase (ded1) gene and the first 6 bp of the ded1 coding sequence are included with of the 3‘ sequence of the his3 gene. * Portions of the Lac operon from *Escherichia coli*, specifically: a 12 bp sequence of the N terminus of the lacZ gene, the promoter/operator region of the lacZ gene and 88 bp of the sequence of the C terminus of the lacI gene. * The origin of replication of the pMB1 plasmid from *E. coli*. Each of the transformation events contain up to three copies of the genes integrated into their respective genomes. There is no extrachromosomal replication of the genetic material.	EN

LMO characteristics

Modified traits

Resistance to diseases and pests

Fungi

Resistance to herbicides

Glufosinate

Common use(s) of the LMO

Research

BCH-LMO-SCBD-111881-2

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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