





Biosafety Clearing-House (BCH)

LIVING MODIFIED ORGANISM (LMO)

BCH-LMO-SCBD-116035-3

? Decisions on the LMO ? Risk Assessments

LAST UPDATED: 02 FEB 2022

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.

https://bch.cbd.int/database/record?documentID=116035



Drought tolerant sugarcane



Read barcode or type above URL into internet browser to access information on this LMO in the Biosafety Clearing-House @ 5CBD 2012

Name

Drought tolerant sugarcane

ΕN

Transformation event

NXI-4T

Developer(s)

- ORGANIZATION: PT PERKEBUNAN NUSANTARA XI | BCH-CON-SCBD-116034-1

ORGANIZATION

PT Perkebunan Nusantara XI

Surabaya

60175, Indonesia

Phone: +62 031 3524596

Email: sekretariat@ptpn11.co.id Website: https://ptpn11.co.id/

Description

The sugarcane (*Saccharum officinarum*) was modified for abiotic (drought, salt) stress tolerance through the expression of *Rhizobium meliloti* choline dehydrogenase, which leads to increased glycine betaine biosynthesis. Glycine betaine maintains a cell's water potential by osmotic adjustment. The expression of choline dehydrogenase may also increase sugar content and promote early maturing.

ΕN

The sugarcane also contains *Escherichia coli* neomycin phosphotransferase II and hygromycin B phosphotransferase for kanamycin and hygromycin resistance, respectively.

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-115592-1 ORGANISM | SACCHARUM OFFICINARUM L. - SUGARCANE, SUGAR CANE

Point of collection or acquisition of the recipient organism or parental organisms

Sugarcane cultivar BL579

ΕN

Related LMO(s)

BCH-LMO-SCBD-116038-1 | Drought tolerant sugarcane | Changes in physiology and/or production - Yield, Growth rate, Ripening Resistance to antibiotics - Hygromycin, Kanamycin Selectable marker genes and reporter genes Tolerance to abiotic stress - Drought, Salinity

BCH-LMO-SCBD-259084-1 | Drought-tolerant sugarcane | Changes in physiology and/or production (Ripening, Yield), Resistance to antibiotics (Hygromycin, Kanamycin, Neomycin), Selectable marker genes and reporter genes, Tolerance to abiotic stress (Drought, Salinity)

Characteristics of the modification process

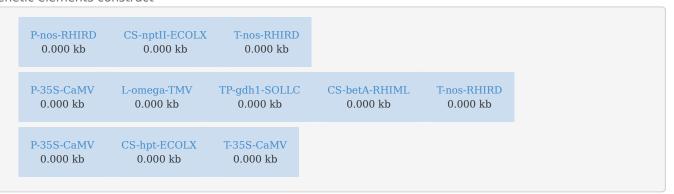
Vector

pMLH2113 EN

Techniques used for the modification

Agrobacterium-mediated 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-100287-7 CAMV 35S PROMOTER

Promoter

BCH-GENE-SCBD-116036-1 GLUTAMATE DEHYDROGENASE MITOCHONDRIAL TRANSIT PEPTIDE - SOLANUM LYCOPERSICUM - TOMATO, SOLLC

BCH-GENE-SCBD-116039-1 CHOLINE DEHYDROGENASE - SINORHIZOBIUM MELILOTI - RHIML

Changes in physiology and/or production - Yield, Ripening Tolerance to abiotic stress - Drought, Salinity

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

Terminator

BCH-GENE-SCBD-14991-8 HYGROMYCIN B PHOSPHOTRANSFERASE GENE | (BACTERIA)

Protein coding sequence | Resistance to antibiotics (Hygromycin), Selectable marker genes and reporter genes

BCH-GENE-SCBD-100290-6 CAMV 35S TERMINATOR

Terminator

BCH-GENE-SCBD-100270-6 NOPALINE SYNTHASE GENE PROMOTER

Promoter

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

Protein coding sequence | Resistance to antibiotics (Kanamycin)

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

Leader

Notes regarding the genetic elements present in this LMO

The modified sugarcane contains three gene cassettes: *Rhizobium meliloti* choline dehydrogenase (*betA*); *Escherichia coli* neomycin phosphotransferase (*nptII*) and *E. coli* hygromycin B phosphotransferae (*hph*).

The betA sequence is under control of a Cauiflower mosaic virus (CaMV) 35S promoter and Agrobacterium tumefaciens nopaline synthase (nos) terminator. At the 5' end of the betA coding sequence is a Tobacco mosaic virus omega 5' leader to enhance translation and a Solanum lycopersicum glutamate dehydrogenase mitochondrial transit peptide, which directs the translated protein to the mitochondria.

ΕN

The *hph* coding sequence is under transcriptional control of a CaMV 35S promoter and terminator.

The *nptll* coding sequence is under transcriptional control of a *nos* promoter and terminator.

Important notes:

- The CaMV promoter associated with the *betA* coding sequence may have two tandem repeats of -419 to -90.

LMO characteristics

Modified traits

Resistance to antibiotics

Hygromycin

Kanamycin

Tolerance to abiotic stress

Drought

Salinity

Changes in physiology and/or production

Ripening

Yield

Selectable marker genes and reporter genes

Common use(s) of the LMO

Biofuel Food

Additional Information

Additional Information

The events NXI-1T and NXT-6T were developed while producing NXT-4T.

Other relevant website addresses and/or attached documents

- ? EUginius NXI-4T sugarcane (English)
- ? ISAAA NXI-4T sugarcane (English)
- ? Biotechnology of Drought-Tolerant Sugarcane.pdf (English)
- ? Beating the heat (Nature Biotechnology).pdf (English)
- ? Application No AU 200059458 B2 Early-maturing sugarcane with high sugar content.pdf (English)
- ? Efficient Promoter Cassettes for Enhanced Expression of Foreign Genes in Monocot and Dicot plants.pdf (English)
- ? Sugarcane Water Stress Tolerance Mechanisms and Its Implications on Developing Biotechnology Solutions.pdf (English)
- ? Powerpoint July 2019 Jember University Biosafety Certification.pdf (English)

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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

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