Biosafety Clearing-House (BCH)

LIVING MODIFIED ORGANISM (LMO)

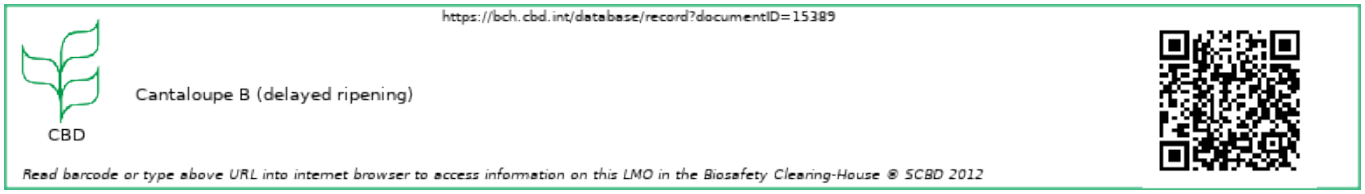
BCH-LMO-SCBD-15389-3

? Decisions on the LMO ? Risk Assessments

LAST UPDATED: 25 JUL 2012

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

Cantaloupe B (delayed ripening) EN

Transformation event

Cantaloupe B

Developer(s)

- ORGANIZATION: AGRITOPE, INC | BCH-CON-SCBD-15386-1

ORGANIZATION

Agritope, Inc
Website: http://www.agritope.com/

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-12124-3 ORGANISM | CUCUMIS MELO (MELON, MELONS) |
Crops

Characteristics of the modification process

Techniques used for the modification

Agrobacterium-mediated DNA transfer

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-15001-5 NEOMYCIN PHOSPHOTRANSFERASE II | (BACTERIA)

Protein coding sequence | Resistance to antibiotics (Kanamycin)

BCH-GENE-SCBD-15017-5 S-ADENOSYLMETHIONINE HYDROLASE GENE

Protein coding sequence | Changes in physiology and/or production (Ripening)

Notes regarding the genetic elements present in this LMO

Canteloupe with delayed ripening due to expression of the SAMase gene from Escherichia coli bacteriophage T3.	EN

LMO characteristics

Modified traits

Resistance to antibiotics

Kanamycin

Changes in physiology and/or production

Ripening

Additional Information

Additional Information

The A and B lines of cantaloupe (Cucumis melo) were developed through a specific genetic modification to express a reduced accumulation of S-adenosylmethionine (SAM) and consequently the trait of delayed ripening. This was accomplished by the introduction of a bacteriophage encoded enzyme, S-adenosylmethionine hydrolase, capable of degrading and thus reducing SAM. The conversion of SAM to 1-aminocyclopropane-1-carboxylic acid (ACC) is the first step in ethylene biosynthesis and the lack of sufficient pools of SAM results in significantly reduced synthesis of this phytohormone, which is known to play a key role in fruit ripening.

These lines were created by Agrobacterium-mediated transformation in which the transfer-DNA (T-DNA) contained the S-adenosylmethionine hydrolase encoding SAMase gene from Escherichia coli bacteriophage T3. The constitutive expression of the SAMase gene was controlled by inclusion of regulatory DNA sequences from A. tumefaciens. In addition, the T-DNA contained sequences encoding the enzyme neomycin phosphotransferase II (NPTII) from the Tn5 transposon of Escherichia coli, strain K12, under the control of the nos promoter from A. tumefaciens. The expression of NPTII activity was used as a selectable trait to screen transformed plants for the presence of the SAMase gene.

Other relevant website addresses and/or attached documents

? Center for Food safety and Applied Nutrition, US FDA *(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.

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