LIVING MODIFIED ORGANISM (LMO)

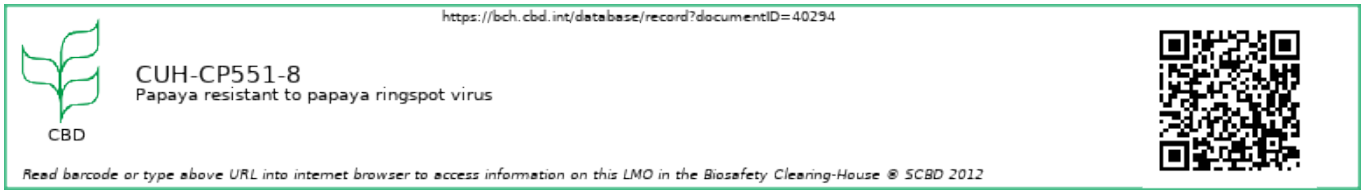
BCH-LMO-SCBD-40294-8

? Decisions on the LMO ? Risk Assessments

LAST UPDATED: 17 JAN 2014

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

Papaya resistant to papaya ringspot virus | EN

Transformation event

55-1

Unique identifier

CUH-CP551-8

Developer(s)

- ORGANIZATION: CORNELL UNIVERSITY AND UNIVERSITY OF HAWAII | BCH-CON-SCBD-40290-1

ORGANIZATION

Cornell University and University of Hawaii
United States of America

Description

Papaya lines 55-1 was developed using recombinant DNA techniques to resist infection by papaya ringspot virus (PRSV), a major limiting factor in papaya production.

This papaya line was developed by inserting virus-derived sequences that encode the PRSV coat protein (CP). The introduced viral sequences do not result in the formation of any infectious particles, nor does their expression result in any disease pathology.

PRSV belongs to the potyvirus group and is an aphid-transmissible RNA virus that commonly

EN

infects papaya, causing serious disease and economic loss.

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-12085-4 ORGANISM | CARICA PAPAYA (PAPAYA, PAWPAW, PAPAW, CARPA) |
Crops

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

Cultivar: Sunset EN

Related LMO(s)

BCH-LMO-SCBD-40296-11 | CUH-CP631-7 - Papaya resistant to papaya ringspot virus | Cornell University | Resistance to antibiotics (Kanamycin), Resistance to diseases and pests (Viruses, Papaya ringspot virus (PRV)), Selectable marker genes and reporter genes
Show detection method(s)

Characteristics of the modification process

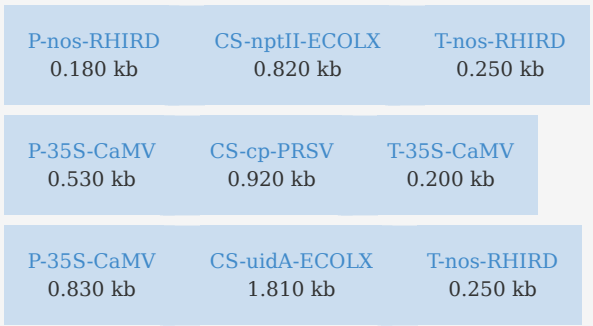
Vector

pGA482GG/cpPRV-4 EN

Techniques used for the modification

Biolistic / Particle gun

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-15026-6 PRSV COAT PROTEIN |
Protein coding sequence | Resistance to diseases and pests (Papaya ringspot potyvirus resistance)

BCH-GENE-SCBD-15001-5 NEOMYCIN PHOSPHOTRANSFERASE II | (BACTERIA) |
Protein coding sequence | Resistance to antibiotics (Kanamycin)

BCH-GENE-SCBD-46004-7 BETA-GLUCURONIDASE CODING SEQUENCE | (BACTERIA) |
Protein coding sequence | Selectable marker genes and reporter genes

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

Promoter

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

Terminator

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

Promoter

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

Terminator

Notes regarding the genetic elements present in this LMO

The Agrobacterium tumefaciens binary plasmid pGA482GG/cpPRSV-4 used for the transformation contained three plant-expressible genes, the PRSV CP, neo, and uidA genes. The plasmid also had two genes encoding resistance to tetracycline and gentamycin antibiotics, respectively, but their associated DNA regulatory sequences enabled expression only in bacteria. The plasmid included the right- and left-border regions derived from the A. tumefaciens T-DNA. Expression of the PRSV CP gene was controlled by including promoter and transcription termination and polyadenylation signal sequences derived from the 35S transcript of cauliflower mosaic virus (CaMV). In addition, the CP gene sequences were fused to the 5' untranslated sequence and the first 39 nucleotides from the cucumber mosaic virus (CMV) CP to enhance translation of the transgene mRNA. The inclusion of these additional sequences was necessary because PRSV naturally encodes its CP as part of a polyprotein and, therefore, the CP coding region normally lacks a translation initiation ATG codon. Expression of the neo gene was under control of the promoter and terminator sequences from the nopaline synthase (nos) gene of A. tumefaciens. The second marker gene, uidA, was modified for plant expression by the addition of 35S promoter region from CaMV and the nos 3'-termination region.	EN

LMO characteristics

Modified traits

Resistance to diseases and pests
- Viruses
  - Papaya ringspot virus (PRV)

Resistance to antibiotics
- Kanamycin

Selectable marker genes and reporter genes

Common use(s) of the LMO

Food

Detection method(s)

External link(s)

? Detection of GM Papaya Event 55-1 in Fresh and Processed Papaya using Duplex PCR.pdf *(English)*

Additional Information

Southern blot analyses of genomic DNA from line 55-1 verified that it contained the PRSV CP gene, intact copies of two plant-expressible marker genes encoding NPTII and GUS, respectively, and a partial copy of the tetracycline resistance marker gene. Genomic DNA did not hybridize with probes to the gentamycin marker genes or to the origin of bacterial replication (Ori V/Tet) region. The partial tetracycline resistance gene was not expressed in plants, due both to the fact that the gene was incomplete and under the regulatory control of a bacterial promoter.	EN

Additional Information

Other relevant website addresses and/or attached documents

? 55-1/63-1 - CERA *(English)*

? OECD BioTrack Product Database *(English)*

? Transgenic papaya: A case for managing risks of Papaya ringspot virus in Hawaii. *(English)*

? Papaya resistant to papaya ringspot virus - Japan BCH.pdf *(English)*

? Virus Resistant Papaya Plants Derived from Tissues Bombarded with the Coat Protein Gene of Papaya Ringspot Virus *(English)*

? 55-1/63-1 - APHIS *(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
413 rue Saint-Jacques, suite 800
Montreal, Québec, H2Y 1N9
Canada
Fax: +1 514 288-6588
Email: secretariat@cbd.int