





# **Biosafety Clearing-House (BCH)**

## LIVING MODIFIED ORGANISM (LMO)

BCH-LMO-SCBD-115622-1

# ? Decisions on the LMO ? Risk Assessments

LAST UPDATED: 26 JUN 2020

# **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=115622



Cassava mosaic disease resistant cassava



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

Name

Cassava mosaic disease resistant cassava

ΕN

Transformation event

pCRNAi-dsAC1dsAV1 tripleintron

Developer(s)

- PERSON: PROF. HASSAN KARAKACHA WERE | BCH-CON-SCBD-115618-2

**PERSON** 

Prof. Hassan Karakacha Were

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**RELATED ORGANIZATION** 

Description

The cassava was modified for resistance to Cassava mosaic disease (CMD) by introducing an RNA interference cassette that targets *African cassava mosaic virus* (ACMV) replication associated disease AC1 and capsid protein (AV1). The production of hairpin RNA by the host cells trigger an RNAi response that is expected to target viral transcripts and prevent viral replication and thus further infection. Due to conservation between AC1 and AV1 sequences in ACMV and *East african cassava mosaic virus*, the modified cassava is expected to resistant

ΕN

to both viruses, which can cause CMD. A selectable marker, *Escherichia coli* hygromycin B phosphotransferase, was additionally included for hygromycin selection during transformation.

## 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-112539-1 ORGANISM | MANIHOT ESCULENTA (CASSAVA, BRAZILIAN ARROWROOT, YUCA, MANIOC, MANDIOCA, MANES) |

#### Related LMO(s)

BCH-LMO-SCBD-115625-1 | Cassava mosaic disease resistant cassava | Prof. Hassan Karakacha Were Resistance to antibiotics - Hygromycin Resistance to diseases and pests - Viruses Selectable marker genes and reporter genes

BCH-LMO-SCBD-115621-1 | Cassava mosaic disease resistant cassava | Prof. Hassan Karakacha Were Resistance to antibiotics - Hygromycin Resistance to diseases and pests - Viruses Selectable marker genes and reporter genes

BCH-LMO-SCBD-115623-1 | Cassava mosaic disease resistant cassava | Prof. Hassan Karakacha Were Resistance to antibiotics - Hygromycin Selectable marker genes and reporter genes

BCH-LMO-SCBD-115624-1 | Cassava brown streak disease resistant cassava | Prof. Hassan Karakacha

Were Resistance to antibiotics - Hygromycin Selectable marker genes and reporter genes

## Characteristics of the modification process

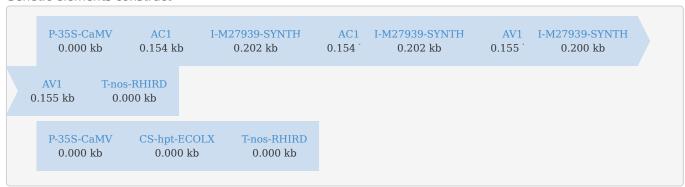
Vector

pCAMBIA1300 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-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-112601-1 M27939 INTRON SEQUENCE

Intron

BCH-GENE-SCBD-114697-1 REPLICATION ASSOCIATED GENE | AFRICAN CASSAVA MOSAIC VIRUS (ACMV)

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

BCH-GENE-SCBD-115619-1 CAPSID PROTEIN - AFRICAN CASSAVA MOSAIC VIRUS - ACMV

Notes regarding the genetic elements present in this LMO

## RNA interference cassette

The modified cassava contains an RNA interference (RNAi) cassette designed to target *African cassava mosaic virus* replication associated gene (AC1) and capsid protein (AV1). Transcription is initiated from the *Cauliflower mosaic virus* (CaMV) 35S promoter and terminates at the CaMV 35S terminator. The transcript contains two segments (sense and antisense) of AC1 separated by a plant synthetic intron. Following the AC1 portion, the transcript contains another synthetic intron and then AV1 antisense and sense sequences separated another synthetic intron. Post-transcription, the introns between the sense and antisense sequences function as loops, allowing the sense and antisense segments of AC1 and AV1 to base pair, forming hpRNA. Two hpRNA structures separated by a synthetic intron are expected to be formed: one corresponding to the AC1 segment and one corresponding to the AV1 segment. The hpRNA acts as double stranded RNA (dsRNA), which triggers an RNAi response and the host cell machinery will target *AC1* and *AV1* viral transcripts for degradation.

ΕN

#### Note:

- The segment of AC1 corresponds to position 1690 to 1844 of the ACMV DNA 1 (DNA A) (GenBank accession AJ427910).
- The segment of AV1 corresponds to position 492 to 647 of the ACMV DNA 1 (DNA A) (GenBank accession AJ427910).
- The source of the AC1 and AV1 sequences is ACMV strain Nigeria-Ogo.
- Due to the RNAi response, no protein translation is expected to occur from the transcript produced from the RNAi cassette.

## Selectable marker

Transcription of *Escherichia coli* hygromycin B phosphotransferase is under transcriptional control of the CaMV 35S promoter and *Agrobacterium tumefaciens* nopaline synthase terminator.

## LMO characteristics

Modified traits

Resistance to diseases and pests

Viruses

Resistance to antibiotics

Hygromycin

Selectable marker genes and reporter genes

Other

Resistance to African cassava mosaic virus

Common use(s) of the LMO

Food

## **Additional Information**

Additional Information

#### RNA interference

An RNAi response is an anti-viral response triggered by the recognition of dsRNA. Host DICER recognizes dsRNA, cleaving the dsRNA into small interfering RNA (siRNA), roughly 21-23 bp long (size is host dependent). The siRNA is then bound by ARGONAUTE family proteins, which unwind the duplex, leaving a single strand of the siRNA, and activating the RISC complex. The RISC complex targets transcripts with homology to the siRNA and degrades them.

Other relevant website addresses and/or attached documents

? GenBank: African cassava mosaic virus-[Nigeria-Ogo] AC1 gene, AC2 gene, AC3 gene, AC4 gene, AV2 gene and AV1 gene ( English )

BCH-LMO-SCBD-115622-1

# **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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