

**BANANA VIRUS X (BVX), A NOVEL FLEXIVIRUS HARBOURING DEFECTIVE RNAs,
DEFINES A NEW GENUS WITHIN THE FLEXIVIRIDAE FAMILY**

**Pierre-Yves TEYCHENEY¹, Armelle MARAIS², Laurence SVANELLA-DUMAS²
& Thierry CANDRESSE²**

¹CIRAD-FLHOR, Capesterre Belle-Eau, Guadeloupe, FWI

²Equipe de virologie, UMR GD2P, INRA-Université Bordeaux 2, Villenave d'Ornon Cedex,
France
teycheney@cirad.fr

Background

Banana and plantain (*Musa* spp) are an essential staple food and account for one of the most widely exported fruits in the world. This crop is susceptible to numerous pests and pathogens, including five reported and characterized viruses which are severe constraints to exchanges of *Musa* germplasm. A study of the molecular variability of *Banana mild mosaic virus* (BanMMV) isolates infecting banana in Guadeloupe lead to the identification of a short nucleotide sequence belonging to a distinct viral species.

Methods

The partial nucleotide sequence of the RNA genome of this agent was determined from double stranded RNA following 3' RACE amplification.

Results

Five open reading frames were identified from the analysis of the last 2917 nucleotides of RACE-amplified sequence. They correspond, from 5' to 3', to a truncated ORF encoding replication-associated protein, three ORFs encoding a movement-associated triple gene block (TGB) and a capsid protein (CP) gene. This deduced genome organization is similar to that of some members of the *Flexiviridae* family such as Potexviruses and Foveaviruses. Sequence comparisons suggest that this virus is a new virus species in the *Flexiviridae* family, for which the name Banana virus X (BVX) is proposed. Sequence comparisons also showed that BVX is only distantly related to other members of the *Flexiviridae* family, in which it does not appear to belong to any existing genus. There is currently no evidence that infection by BVX can cause any visible symptoms in *Musa* sp. Furthermore, it was shown that BVX produces defective RNAs derived from its genomic RNA by non-homologous recombination. Three distinct pairs of donor/acceptor recombination sites involving short direct nucleotide repeats were characterized. Contrary to the situation encountered for the Potexviruses, these recombination sites are located within the TGB1 and CP genes and the recombination event results in a truncated TGB1 protein.

A small scale study of the molecular variability of BVX was performed on *Musa* samples collected in different locations in Guadeloupe. It showed that BVX is reasonably distributed in *Musa* plants

in Guadeloupe and displays a very low level of molecular variability, which is in marked contrast to the situation encountered for BanMMV, another member of the *Flexiviridae* family infecting *Musa* spp.