

HIGH GENETIC VARIABILITY IN AN RNA PLANT VIRUS, *BANANA MILD MOSAIC VIRUS*

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Background

Banana Mild Mosaic virus (BanMMV) is an unassigned member of the *Flexiviridae* family infecting banana and plantain (*Musa* spp). Vertical transmission by vegetative propagation is currently the only known means of propagation of this virus, since no biological vector has been identified nor has experimental mechanical inoculation on susceptible hosts been successful so far.

Methods

Nucleotide sequences were obtained from BanMMV isolates originating from various locations worldwide. Two distinct regions of the viral genome were targeted : ORF 1, which encodes the viral RNA-dependent RNA polymerase (RdRp), and a region encompassing the 3' end of ORF5, which encodes the coat protein (CP), and the 3' non-coding region (3' NCR). Both regions play a key role in viral replication and are therefore supposedly very conserved.

Results

BanMMV RdRp sequences displayed an extremely high level of molecular diversity when compared to similar sequences obtained from other plant RNA viruses. This situation resulted essentially from a very high ratio of synonymous mutations. A similar analysis performed for a limited selection of banana accessions on the CP/3'NCR region confirmed the high level of diversity observed in the RdRp dataset, characterized by a very high level of synonymous

mutations. Analysis of intra-host diversity indicated the existence of two distinct situations with some plants harbouring only closely related sequence variants while others contained up to three widely divergent isolates. Analyses indicated an absence of structuration of the virus genetic diversity either by the geographical origin of the infected *Musa* accessions or by their genotype. This situation may be, in part, explained by the exchange of banana germplasm between different parts of the world and also by plant-to-plant transmission of the virus, the evidence for which is, for the first time, provided by this study.