

28-How eBSV polymorphism could enlighten BSV and banana evolution story?

Duroy PO.¹, Perrier X.², Laboureau N.¹, Jacquemoud-Collet JP.², Iskra-Caruana ML.¹

¹ CIRAD, UMR BGPI, F-34398 Montpellier Cedex 5.

² CIRAD, UMR AGAP, F-34398 Montpellier Cedex 5.

pierre-olivier.duroy@cirad.fr

The nuclear genome of banana plants is invaded by numerous viral sequences of banana streak viruses (BSV), a DNA virus belonging to the family *Caulimoviridae*. These integrations are mostly defective as a result of pseudogenisation driven by the host genome evolution. Conversely some named infectious, can release a functional viral genome following activating stresses. We characterized the infectious endogenous BSV (eBSV) for three BSV species (BSOLV, BSGFV and BSimV) present within the *Musa balbisiana* B genome of the seedy diploid Pisang Klutuk Wulung (PKW). Our aim is to study PKW-related BSV integrations among the diversity of the banana B genomes in order to retrace the evolutionary BSV and banana stories

We extended on purpose the *M. balbisiana* diversity by the addition of interspecific hybrids with *M. acuminata* showing different levels of ploidy for the B genome (ABB, AAB, AB) of the banana sample in order to include unsampled or extinct *M. balbisiana* resources. We also based the analysis referring to the two areas of sympatry between *M. acuminata* and *M. balbisiana* and the centers of origin for the most largely cultivated AAB cultivars. One was in India and the other one in East Asia going from Philippines to New Guinea (Perrier et al, 2009).

We characterized the PKW-related eBSV allelic polymorphism using PCR markers (described in poster Galzi & Duroy et al.) and Southern blots on 77 accessions. We codified the results of Southern blot and PCR in order to calculate a common dissimilarity matrix and interpret the eBSV distribution. As a result, three dendrograms of PKW-related eBSV made with the Neighbor Joining (NJ) method on the 77 banana accessions, for each BSV species, are presented as well as one dendrogram resulting of NJ analysis for the three BSV species all together . We show that the known phylogeny of banana accessions can enlighten the eBSV structure diversity and that eBSV polymorphisms can help to understand the particularly unresolved *M. balbisiana* diversity. An evolutionary scheme of BSV/eBSV banana evolution will be proposed.

Keywords: Banana Streak Virus, *Musa sp.*, Phylogeny, Viral Evolution, Endogenous Pararetrovirus.

References:

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