



HOW GENOMICS FUEL BREEDING : UNRAVELING THE STRUCTURE OF INFECTIOUS eBSV LEAD TO THE END OF THE BSV CONSTRAINT FOR BREEDING BANANA INTERSPECIFIC HYBRIDS

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Infections of banana and plantain by banana streak viruses (BSV) can occur in the absence of vector-mediated transmission, through the activation of infectious endogenous BSV sequences (eBSVs). Such infectious eBSVs are present in the genome of *Musa balbisiana* spp, which are important progenitors for breeding improved banana varieties. Once activated by biotic or abiotic stresses, these viral integrants cause spontaneous infection in both natural and synthetic interspecific hybrids harbouring the *M. balbisiana* (B) genome. Therefore, the presence of infectious eBSVs within B genomes is the main constraint for breeding banana and plantain interspecific hybrids and for exchanging *Musa* germplasm.

The sequence and organization of eBSVs in the diploid *M. balbisiana* genitor Pisang Klutuk Wulung (PKW) was elucidated for BSV species Obino l'Ewaï (BSOLV), Goldfinger (BSGFV) and Imové (BSIMV). This work showed that integration of BSGFV and BSOLV is di-allelic, with one infectious and one non-infectious allele, whereas that of BSImV is monoallelic. Allele-specific molecular markers were developed and used to genotype *M. balbisiana* germplasm, unveiling important differences between accessions and the presence of modified eBSV alleles in several accessions. Breeding improved *M. balbisiana* progenitors devoid of infectious eBSGFV and/or eBSOLV alleles was achieved through self-pollination and chromosome doubling of haploid lines. Both approaches lead to *M. balbisiana* cultivars devoid of infectious eBSOLV and/or eBSGFV resulting from the segregation of eBSOLV and eBSGFV alleles. These results pave the way to the safe use of *M. balbisiana* in breeding programs, and open new perspectives for breeding improved banana and plantain hybrid varieties.