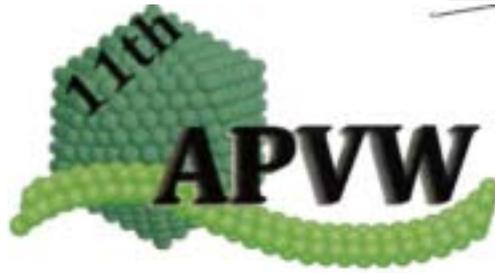


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HANDBOOK



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Taming infectious endogenous *Banana streak virus* sequences for breeding and growing new banana interspecific hybrids

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Infections of banana and plantain by three species of *Banana streak virus* (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 only, which are important progenitors for breeding improved banana varieties. Once activated by biotic or abiotic stresses, these viral integrants cause spontaneous infections in both natural and synthetic interspecific hybrids harbouring the *M. balbisiana* (B) genome. Therefore, infectious eBSVs within B genomes are the main constraint for breeding new banana and plantain interspecific hybrids, for distributing existing interspecific hybrids harbouring infectious eBSVs and for exchanging *Musa* germplasm.

The sequence and organization of eBSVs in the diploid *M. balbisiana* genitor Pisang Klutuk Wulung (PKW) was elucidated for the three BSV species Obino l'Ewai (BSOLV), Goldfinger (BSGFV) and Imové (BSIMV). This work showed that both integrations of BSGFV and BSOLV are di-allelic, with one infectious and one non-infectious allele each, 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, paving the way to the safe use of *M. balbisiana* for breeding improved banana and plantain hybrid varieties.

The risk of spreading BSV through large scale distribution of interspecific hybrid FHIA21 (AAAB) and natural interspecific selection Macho X Hembra (AAB), which both harbour infectious eBSOLV and eBSGFV alleles, was assessed in the Dominican Republic. Results suggest that monitored BSV infections may result from the activation of eBSV infectious alleles rather than vector transmission and that the level of expression of infectious alleles is significantly higher in FHIA21 than in MxH.