11-Marker-assisted genotyping of eBSV alleles in banana

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The genome of banana (*Musa* sp.) harbours multiple integrations of *Banana streak viruses*(eBSVs), although integration is not required for the replication of cognate viruses. In the past 20 years, BSV outbreaks monitored in banana-producing areas resulted mostly from the activation of infectious eBSVs in newly created interspecific banana hybrids. Recently, we established that these problematic infectious eBSVs are present in the*Musa balbisiana* genomes,one of the main group of progenitors used for breeding hybrid varieties [1-4]. We also elucidated the sequence and organization of eBSVs in the model diploid *M. balbisiana* cultivar PisangKlutukWulung (PKW), showing that integration of infectious eBSGFV[5] and eBSOLV is di-allelic, with one infectious and one non-infectious allele, whereas that of infectious eBSImV is monoallelic[6].Based on the sequences and the structure of these eBSV we have developed several PCR and Derived Cleaved Amplified Polymorphic Sequences (deCAPS) markers for genotyping eBSVs[4 ; 6].To this aims, different markers were developed: (i) integration markers targeting eBSV insertion sites, (ii) structure markers targeting internally reorganized eBSV structures and (iii) allelic markers allowing the distinction between alleles of the same eBSV species.
Markers were assessed by screening the same banana genotypes in two different laboratories located in Montpellier and Guadeloupe respectively. A larger scale validation was undertaken through the screening ofall *Musa balbisiana* genotypes available fromCIRAD *Musa* collection in Guadeloupe, newly created hybrids from CARBAP in Cameroon and germplasm collection provided by Bioversity International in Belgium.
The use of these molecular tools is now a prerequisite not only for future crop-oriented breeding programmes aimed atproducing safe interspecific banana hybrids but also for assessing the risk of BSV outbreaksresulting from the activation of infectious eBSVs in natural hybrids that have been widely distributed in developing countries.

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