19. Prevalence and diversity of *Banana streak virus* species in Cuba

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Banana streak virus (BSV) species are widespread in *Musa* spp worldwide. They are naturally transmitted either horizontally by several mealybug species or vertically by vegetative propagation of infected germplasm. They are also transmitted through the expression of infectious BSV endogenous sequences (BSV EPRVs) integrated into the genome of *Musa balbisiana*, one of the progenitors of synthetic and natural banana hybrid species. Expression of infectious BSV EPRVs occurs in interspecific hybrid species, whether natural or synthetic, harbouring both the *M. acuminata* and *M. balbisiana* genomes. Expression process is activated by biotic and abiotic stresses including *in vitro* culture. Therefore, BSV is currently the main viral constraint to *Musa* genetic improvement, germplasm movement, ex-situ conservation and mass propagation.

The risk of spreading BSV through large scale distribution of interspecific banana hybrids has never been assessed. Such a study was initiated in Cuba in 2007. Risk assessment studies rely primarily on the study of the prevalence and diversity of BSV species in distinct *Musa* genotypes and under various cultural conditions, which both affect the activation of infectious BSV EPRVs. Nationwide field surveys, sample collection and indexing are being performed in Cuba. So far, a total of 1321 leaf samples have been collected from symptomatic and asymptomatic plants of various genotypes (AAA, AAAA, AAB, AAAB, AABB and ABB). They were indexed separately for four BSV species, Goldfinger (BSGFV), Imové (BsImV), Mysore (BSMysV) and Obino l'Ewaï (BSOLV) by multiplex immunocapture PCR (M-IC-PCR). All four species were identified for the fist time in Cuba. Overall, results show an important level of prevalence (>40%) of BSV species in cultivars and hybrids harbouring the B genome. On the contrary, less than 0.5% of Giant Dwarf Cavendish (AAA) samples were indexed positive for BSV.
In order to identify new BSV species, all samples were also indexed by M-IC-PCR using degenerate primers. PCR products obtained from *M. acuminata* samples otherwise indexed negative using species-specific primers were selected, cloned and sequenced. Phylogenetic analyses suggest that some of these sequences may correspond to new BSV species.