MOLECULAR ANALYSIS OF BANANA STREAK VIRUS (BSV) "INTEGRANTS" INTO THE NUCLEAR GENOME OF *MUSA BALBISIANA*.

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Background

Banana streak virus (BSV) sequences are integrated into the nuclear genome of *Musa balbisiana.* There is strong experimental evidence that some of these BSV integrated sequences, called BSV endogenous pararetroviruses (BSV EPRVs), can give rise to infectious episomal BSV genomes upon stress conditions. Such stresses include interspecific genetic crosses, therefore this phenomenon represents a serious limitation to the creation of novel *Musa* hydrids between A (*Musa acuminata*) and B (*Musa balbisiana*) genomes and to the diffusion of such hybrids.

Methods

As part of an international effort within the *Musa* Genomics Consortium aimed at defining the integration patterns of BSV EPRV sequences into the nuclear genome of *Musa* species and the mechanisms leading to the activation of such BSV EPRVs, we have constructed and characterised three BAC libraries from *M. acuminata* Cavendish (AAA), *M. acuminata* Calcutta 4 (AA) and *M. balbisiana* PKW (BB) nuclear genomes, respectively.
Complete genomes of four different BSV strains (BSV-Ol "Obino L'Ewai", BSV-Gf "Gold Finger", BSV-Im "Imove", BSV-Mys "Mysore") were used as probes to screen the BAC libraries and FISH experiments were carried out to test for the presence of integrated viral sequences in *Musa* B chromosomes.

Results

Upon screening of the *M. balbisiana* PKW BAC library, 10 BAC clones positive for BSV-Ol, 9 for BSV-Gf, 26 for BSV-Mys and 24 for BSV-Im were identified. All positive BAC clones were distinct from each other. On the other hand, screening of either *M. acuminata* Calcutta 4 or *M. acuminata* Cavendish BAC libraries with the four complete viral sequences revealed that no BSV EPRVs related to the four analyzed strains were present in any of the two *Musa* A genomes analyzed.
BAC clones found positive upon screening were further characterized by BAC-end sequencing and RFLP-fingerprinting, and selected BACs containing BSV-Ol or BSV-Gf EPRV sequences were completely sequenced. Detailed analysis of the nucleotide sequences and chromosomal organization of BSV-Ol and BSV-Gf EPRV sequences within these BAC clones will be presented and discussed. This study represents the first step towards the characterization of the mechanisms leading to the activation of BSV EPRV sequences in *Musa* and the implementation of novel strategies to counteract this phenomenon.