POSTER

Molecular analysis of *Banana streak virus* (BSV) in the nuclear genome of *Musa balbisiana*.

Juan-Carlos Noa-Carrazana[1], Magali Lescot[2], Pietro Piffanelli[2],Jan Safar[3], Jaroslav Dolezel[3], T Matsumoto[4], Laura Silva-Rosales[1], Fabrice Lheureux[2], Pierre-Yves Teycheney[6], T. Sasaki[4] and Marie-Line Iskra-Caruana[2]

[1]Cinvestav-IPN Genetic engineering department, Irapuato, Mexico;
[2]CIRAD-BIOS, UMR PIA and UMR BGPI - Campus International de Baillarguet TA A54/K- F-34398 Montpellier Cedex 5, France ;
[3]LMMC Institute of experimental botany Sokolouska 6 - Olomouc, Czech Republic;
[4]NIAS, Tsukuba, Japan,
[5]CIRAD-BIOS UPR75 Station de Neufchâteau, Sainte- Marie, F-97130 Capesterre Belle Eau, Guadeloupe French West Indies,
Tel : 33 499624813
Fax : 33 499624808
Marie-line.caruana@cirad.fr

Banana streak virus (BSV) sequences are integrated in the nuclear genome of *Musa* species. There is strong experimental evidence that some of these BSV integrated sequences, preferentially restricted to *Musa balbisiana* chromosome (noted B) and called BSV endogenous pararetrovirus (BSV EPRVs), can give rise to infectious episomal BSV particles upon stress conditions such as either inter-specific genetic crosses or *in vitro* micro propagation.
As part of an international effort within the *Musa* Genomics Consortium aimed at defining the integration patterns of BSV EPRVs into *Musa* nuclear genome and the mechanisms leading to their activation, three BAC libraries were constructed and characterized from *M. acuminata* Cavendish (AAA), *M. acuminata* Calcutta 4 (AA) and *M. balbisiana* PKW (BB) nuclear genomes, respectively.
Complete genomes of four BSV strains (BSV-OI “Obino L’Ewai”, BSV-Gf “Gold Finger”, BSV-Im “Imove”, BSV-Mys “Mysore”) were used as probes to screen the BAC libraries.
Upon screening of the *M. balbisiana* PKW BAC library, 10 BAC clones positive for BSV-OI, 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 approaches, and 6 selected BACs containing BSV-OI or BSV-Gf EPRV sequences were completely sequenced. Detailed analysis of the nucleotide sequences and chromosomal organization of BSV-OI and BSV-Gf EPRV sequences within these BAC clones will be presented and discussed.
This study represents one of the first steps 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.