

Abstract of Poster Presentation

Molecular characterisation of integrated sequences of Banana streak virus in the banana plant genome

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The genome of banana (*Musa* sp.) harbours multiple integrations of several species of Banana streak virus (BSV), certainly resulting from illegitimate recombination between host and viral DNA. Surprisingly, this pararetrovirus does not require integration for its replication. Some integrations, only existing in the *Musa balbisiana* genome (denoted B), are infectious by reconstituting a functional viral genome. To date, four widespread species of BSV (Goldfinger -BSGfV, Imové - BSI_mV, Mysore - BSM_{ys}V and Obino l'Ewai - BSOLV) have been reported as integrated into the B genome and as infectious, under stress conditions, resulting in viral infection of the banana plant. In order to study BSV expression from such viral integrants, a characterisation of infectious integrants (eBSV) was undergone by studying both a *Musa* BAC library obtained from the wild diploid *M. balbisiana* cv. Pisang Klutuk Wulung (PKW) containing the four BSV species described above and one interspecific genetic cross using carrier PKW. The organization of eBSGfV was fully characterized recently in our lab (Gayral et al., 2008). eBSGfV results from a single event of integration corresponding to an allelic insertion extensively rearranged, containing at least one full-length viral genome. Although the four BSV species present important differences with each other, the organisation of the three other eBSVs looks like eBSGfV. Indeed, preliminary data indicate that each of them is extensively rearranged in PKW and present as two insertions at the same locus. This suggests an allelic insertion resulting from a single even of integration. Experimental evidences to demonstrate BSV expression and to validate the infectious nature of every eBSV are on the way.