

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

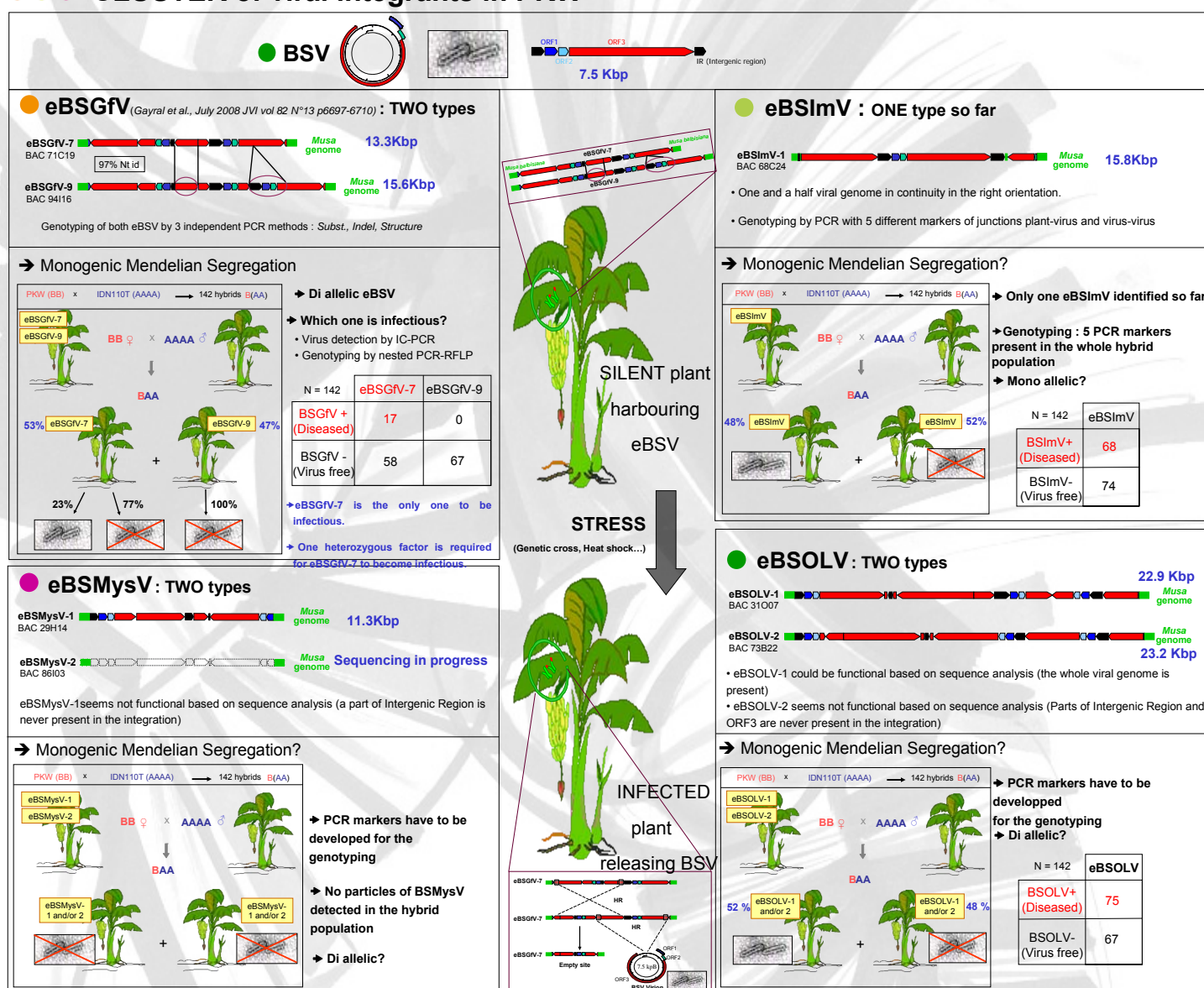
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The genome of banana (*Musa* sp.) harbours multiple integrations of several species of *Banana streak virus* (BSV) known as endogenous pararetrovirus (EPRV) named eBSV in banana. Surprisingly, this pararetrovirus does not require integration for its replication. Some integrations, only existing in the *Musa balbisiana* genome (denoted B), are infectious by releasing virions in interspecific hybrids. Here we describe and analyze the organization of the integration for four BSV species (Goldfinger - BSGfV, Imové - BSmV, Mysore - BSMysV and Obino l'Ewai - BSOLV) present in the wild diploid *M. balbisiana* cv. Pisang Klutuk Wulung (PKW) where virus expression never occurred. This was undergone by studying both a *Musa* BAC library obtained from PKW and one interspecific genetic cross using PKW as female parent.

CLUSTER of viral integrants in PKW



The four eBSV described in PKW genome suggest an allelic insertion resulting from a single integration event. Although we found only one eBSmV so far, the presence of the 5 PCR markers in the whole hybrid population suggest an allelic insertion too. Every eBSV is extensively rearranged except for eBSmV where one and a half viral genome is present in continuity in the right orientation. *In vivo* validation of the infectious nature of each eBSV allele is under way. Finally, we are currently working on the mechanisms underlying EPRV activation by testing experimentally a model of activation based on homologous recombination (HR).

