

Molecular characterization of a pathogenic integration of the Golfinger Gf species of banana streak virus in the genome of *Musa balbisiana*.

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As several other plants, the genome of banana and plantain suffered integrations of pararetroviral sequences named EPRV (Endogenous pararetrovirus) even though these integrations are not a part of the replication cycle of this virus. An original situation concerns the genome of *Musa balbisiana* which harbours banana streak virus (BSV) EPRV able to reconstitute pathogenic viral genomes under specific conditions.

In order to assess the risk of spreading BSV through the diffusion of micro propagated banana plants and the creation of new lines harbouring EPRVs as well as to understand the evolutionary forces that explain the presence and preservation of EPRVs in *Musa* genome, we proposed to characterise pathogenic BSV EPRVs of the Goldfinger species. The analysing of BAC library of *Musa balbisiana* cv Pisang Klutuk Wulung (PKW) permitted to characterise the integration pattern of BSGfV EPRVs as two similar integrants. Each integrant is composed of back-to-back viral sequences representing more than a whole genome. We developed molecular markers (PCR, PCR-RFLP) to distinguish each others. Then, we analysed the BSGfV EPRV segregation in the triploids hybrid progeny (AAB) resulting from crosses between virus free parents PKW (BB) and IDN110T (AAAA). There are found to be allelic, located as the same locus. Afterwards, we checked for BSGfV expression by searching the presence of virions by IC-PCR in the same AAB progeny in order to precise their allelic origin. Our results confirm that both allelic EPRV could be involved in the restitution of virions. We proposed a model of viral genome releasing based on the number of recombination events necessary to explain the genotype frequency observed between the two alleles.