

Evolution of hazardous integrations of *Banana streak virus* in the genome of the wild banana (*Musa balbisiana*).

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Banana streak virus (BSV) is a plant dsDNA pararetrovirus responsible for banana streak disease. Even though integration is not an essential step in the replication cycle of BSV, the nuclear genome of banana and plantain (genus *Musa*) contains viral integrations called BSV Endogenous Pararetrovirus (BSV EPRV). Triggered by stresses, EPRV found in *Musa balbisiana* reconstitute an infectious viral genome. We showed the wild diploid *M. balbisiana* Pisang Klutuk Wulung (PKW) harbours pathogenic BSV-EPRV and is furthermore resistant to the virus. In these conditions, how to explain the presence of such viral integrants fixed in the host genome in terms of cost and benefits for both plant and virus? In order to highlight this question, we retraced the evolutionary history of infectious EPRV of BSV Golfinger species (BSGfV) integrated at a single locus in the genome of *M. balbisiana* PKW. This integrant was characterized in PKW by sequencing BAC clones containing BSGfV sequences. This BSGfV EPRV is composed of back-to-back viral sequences representing more than a whole genome. We developed molecular markers to explore the polymorphism of BSGfV integration patterns among *M. balbisiana* genotypes and other *Musa* species representing the genetic diversity of the genus. We observed a strong conserved pattern of BSGfV EPRV in all *M. balbisiana* genotypes. Among relative species, we found BSGfV EPRV only in *M. boman* showing a modified pattern. These results suggest that BSGfV integrated its host recently. Phylogenetic analysis of sequence data from both virus and EPRV confirmed this result. The consequences of deleterious viral sequences rapidly fixed in *Musa* genomes will be discussed.

11th Evolutionary Biology Meeting at Marseilles

September 18-21, 2007 – Marseilles, France
<http://ms.eisti.fr/11th-Evolutionary-Biology-Meeting.html>