Integrations of *Banana streak virus* sequences in the genome of the banana *Musa balbisiana* - Endogenous viruses or host genes?

Philippe Gayral, Nathalie Laboureau, Marie-Line Iskra-Caruana.
CIRAD BIOS - UMR BGPI
TA A-54/K, Campus international de Baillarguet
F-34398 MONTPELLIER Cedex 5
Philippe.gayral@cirad.fr

*Banana streak virus* or BSV (*Badnavirus*) is a double stranded DNA pararetrovirus causing leaf streak mosaic disease. Recently, numerous outbreaks of the disease occurred in all banana producing areas in interspecific *Musa* hybrids (*M. acuminata* x *M. balbisiana*) originating from virus-free parents. These infections correlated with BSV DNA sequences integrated in the *M. balbisiana* genome only, called endogenous pararetroviruses (EPRVs). Although integration is not needed for the replication cycle, some BSV EPRVs could become infectious under stress conditions by reconstituting a replication-competent genome after homologous recombination events. Surprisingly, even though the wild *M. balbisiana* Pisang Klutug Wulung (PKW) harbours pathogenic BSV EPRV, it is resistant to the virus. In these conditions, how to explain 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 EPRVs of Golfinger species (BSGfV) integrated at a single locus in the genome of PKW. The structure of this EPRV was characterized in PKW by sequencing BAC clones containing BSGfV EPRVs. The integrant 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. BSGfV EPRVs showed the same integration pattern as PKW in all *M. balbisiana* and a modified pattern in the relative species *M. boman*. Any BSGfV EPRV was observed in the other *Musa* species. We assume that BSGfV integrated its host recently. Phylogenetic analysis combining sequence data from both virus and EPRV confirmed this result. The consequences for *Musa* harbouring potentially deleterious sequences which have rapidly been fixed will be discussed.