The nuclear genome of several plants is invaded by numerous viral sequences. These integrations correspond to accidental events mainly resulting from illegitimate recombination of DNA viruses belonging to the family Caulimoviridae with plant DNA whereas integration into the host genome is not required for viral replication. These integrations are for the most part defective as a result of pseudogenisation driven by the host genome evolution. Conversely, some other integrations named infectious, could release a functional viral genome following activating stresses.

Our aim is to study the integration context of such infectious integrants for Banana streak virus among the diversity of the banana B genome in order to retrace the evolutionary BSV story and understand their impact on host and virus evolution in terms of cost/benefit. To answer this question, we propose to characterize infectious eBSV among a representative sampling of Musa balbisiana diversity and to hypothesize a contribution of eBSV towards plant virus resistance through an RNA interfering mechanism versus a maintain of the virus through interspecific crosses.

**Specific hallmark for each eBSV integration in PKW**
- PCR markers
- Southern blot fingerprints

**Sampling of B genome diversity**
- 20 BB banana plants only  
  - no geographic information
- 69 Inter specific hybrids AB, ABB, AAB  
  - from the 2 areas of interspecific hybridization origin

**BSV eBSV Goldfinger in PKW - allelic integration**

**eBSGJV**
- Infectious allele
- Non infectious allele
- Non eBSGFV allele

**eBSOLV**
- Infectious allele
- Non Infectious allele
- Non eBSGFV allele

**Dendrogram from 78 banana plant samples calculated with NJ algorithm based on eBSGFV hallmarks**
- A strong correlation exists between southern blots and PCR results
- PKW hallmark is strongly conserved among the diploid genotypes
- Positive selection of the infectious allele among the diversity of the banana B genome

**Dendrogram from 69 banana plant samples calculated with NJ algorithm and based on 498 Dart markers**
- A faint correlation exists between southern blots and PCR results
- PKW hallmark is restricted to PKW clade
- Integration loci are highly conserved
- A large area of differentiation with a lot of changes and mutations resulting on identification of novel alleles in the west hybridization area
- Positive selection of the infectious allele

These preliminary results indicate that eBSV could be an adapted marker to precise Musa phylogeography.