

**Prevalence of BSV resulting from an endogenous origin in the outbreak and maintain of the banana streak disease.**

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The biodiversity of banana streak virus results from two phenomenons, the natural spreading of the disease and the “wake up” of the endogenous pararetrovirus (EPRV) sequences present in the *Musa balbisiana* genome, denoted B. Two contrasted BSV epidemic situations occurring in field conditions in Equator and Colombia were studied in order to estimate the relative importance of both phenomenons.

In Equator, the field plantation was constituted by virus free banana triploids *M. acuminata* (denoted A) AAA suspected to be contaminated by BSV infected inter-specific triploids AAB located as a test plot inside the total plantation. In Colombia, the field plantation was constituted by inter-specific triploid hybrids (AAB) suspected to be themselves at the origin of the infection due to the presence of BSV EPRV in their genome.

The virus was checked in 40 samples per location by immuno capture PCR (IC-PCR) and direct binding (DB) PCR using both specific BSV and degenerate badnavirus primers. We studied the existing molecular diversity by sequencing the end part of ORF3 containing the reverse transcriptase gene. Southern blot analyses were performed in order to precise the origin of the virions, either endogenous or exogenous.