

Integrated sequences of Banana streak virus (BSV) in banana plantain: how does gene silencing-based plant defense system work?

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The majority of cultivated bananas are intra and interspecific hybrids of the two main species *Musa acuminata* (denoted genome A) and *Musa balbisiana* (denoted genome B). The Banana streak virus (BSV) is responsible of the banana streak mosaic disease and causes severe damage on the *Musa acuminata* hybrids, which are extremely susceptible. The virus is mealybugs- vector transmitted from plant to plant. Curiously, BSV also exists as endogenous sequences named (eBSV) within all B genomes and can give rise active viruses leading to a systemic infection in banana plants. The banana plantain is a natural triploid interspecific hybrid AAB and harbors viral sequences for two BSV species within its B genome. It spontaneously develops BSV infections following abiotic stresses by releasing active viral genome from eBSVs. However, no epidemic has been reported so far, whereas several plantains regularly show infections in the fields. We suspected that the banana plantain regulates such endogenous viral infections by a gene silencing-based plant defense mechanism resulting from a co-evolution process.

Our project aims understanding how this pathosystem works by following after an endogenous infection the kinetic of the virus distribution in the plant *via* molecular (IC-PCR, qPCR) and histologic (serological detection) markers as well as the small viral RNA profiles involved in gene silencing (TGS, PTGS) *via* Northern blots, NGS and LNA probes.