

Natural resistance of the diploid *Musa balbisiana* Pisang Klutuk Wulung (PKW) to banana streak virus is probably driven by transcriptional gene silencing

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The genome of banana (*Musa* sp.) harbours multiple integrations of *Banana streak virus* (eBSV), whereas this badnavirus does not require integration for the replication of its ds DNA genome. Some endogenous BSV sequences (eBSV), only existing in the *Musa balbisiana* genome, are infectious by releasing a functional viral genome following stresses such as those existing in in vitro culture and interspecific crosses context. The structure of these eBSV is much longer than a single BSV genome, composed of viral fragments duplicated and more or less extensively rearranged.

Wild *M. balbisiana* diploid genotypes (BB) such as Pisang Klutuk Wulung (PKW) harbour such infectious eBSV belonging to three widespread species of BSV (*Goldfinger* -BSGFV, *Imové* – BSImV and *Obino l'Ewai* - BSOLV) but are nevertheless resistant to any multiplication of BSV without any visible virus particles. In collaboration with the group headed by M. Pooggin (Basel, Switzerland), a deep sequencing of total siRNAs of PKW was performed using the Illumina ultra-high-throughput technology. We obtained for the first time, experimental evidence of virus-derived small RNA (vsRNA) from eBSOLV, eBSGFV and eBSImV by blasting sequences against the 3 BSV species genomes. vsRNA are enriched in 24-nt class thus eBSV in PKW genome are likely silenced at the transcriptional level. Interestingly, we show that hot and cold spots of vsRNA generation do not target similar viral sequences from one eBSV species to the other but are directly correlated with the structure of the integration. All together, those data seem indicate these eBSV induce a natural resistance driven by gene silencing mechanisms based on their complex molecular re-arranged structure which could lead to dsRNA formation.

Mots Clés : Banana Streak Virus, *Musa* sp., Silencing, Resistance, Endogenous Pararetrovirus