



UNRAVELLING THE STRUCTURE OF INTEGRATED BANANA STREAK VIRUS SEQUENCES (eBSV) ALLOW MARKERS ASSISTED SELECTION OF MUSA GERmplasm DEVOID OF INFECTIOUS eBSV

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ABSTRACT

The *Musa balbisiana* banana genome (B genome) forms part of the genotype of many important banana cultivars, such as the famous plantain subgroup that is a staple food for millions of people in Africa and Latin America. Moreover, it is often associated with desirable traits of agronomic interest such as vegetative vigour, biotic and abiotic stress tolerance. However, it became recently the main constraint for breeding banana and plantain interspecific hybrids and for exchanging *Musa* germplasm as it harbors integrated copies of *Banana streak virus* (BSV) named endogenous BSV (eBSV) that are able to release infectious virus.

We recently fully characterized integrants of three BSV species—*Goldfinger* (eBSGFV), *Imové* (eBSImV) and *Obino l'Ewai* (eBSOLV)—in the seedy *Musa balbisiana* Pisang klutuk wulung (PKW) by studying their molecular structure, genomic organization, genomic landscape and infectious capacity [1 ; 2]. This



thorough characterisation led to the production of eBSV specific molecular markers which are used to widely screen banana hybrids, genitors and germplasm to future crop-oriented breeding programmes aimed at producing safe interspecific banana hybrids but also to estimate and limit the risk of BSV outbreak on natural hybrids spread intensively in developing countries as a food source.

References :

[1] Gayral P. et al., (2008). *J. Virol.* **82**, 6697-6710.

[2] Chabannes M., et al., (2013). *J. Virol.* **87**, 8624-37.