

Towards the elimination of infectious endogenous *Banana streak virus* sequences from *Musa balbisiana*

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Infectious endogenous sequences of at least 3 distinct *Banana streak virus* species are present in the genome of *Musa balbisiana* spp [1, 2], which are important progenitors for breeding improved banana varieties. Once activated by biotic or abiotic stresses, these sequences can cause infection in natural and synthetic interspecific hybrids harbouring the *M. balbisiana* genome [3]. Therefore, infectious endogenous BSV (eBSV) sequences are currently the main constraint for breeding much needed banana and plantain interspecific hybrids and for exchanging *Musa* germplasm.

The full genomic and genetic organization of eBSV sequences present in diploid *M. balbisiana* cultivar Pisang Klutuk Wulung (PKW) was recently elucidated [1, 4], showing that endogenous BSGFV, BSOLV and BSImV sequences in PKW result from a single integration event. This work also showed that integration of infectious eBSGFV and eBSOLV is di-allelic whereas that of infectious eBSImV is monoallelic. In the case of eBSGFV and eBSOLV, only one allele is infectious.

Taking advantage of recently designed primer sets [1, 3; Baurens, unpublished], we have undertaken the characterization of eBSOLV, eBSGFV and eBSImV in the *M. balbisiana* accessions of CIRAD Guadeloupe's germplasm collection. This work unveiled important differences between accessions, which were shown to harbor all combinations of infectious and non infectious alleles for one or several distinct BSV species. Some accessions were even found to be exempt from eBSImV. These results were confirmed biologically, by following the kinetics of expression of infectious eBSV sequences in various genotypes during cell culture, which is the most potent abiotic stress activating infectious eBSV sequences. Based on these results, breeding improved *M. balbisiana* progenitors devoid of infectious eBSGFV and/or BSOLV sequences was undertaken by segregating the corresponding infectious and non infectious alleles. This was achieved in several selfed and/or double haploid lines.

This work paves the way to the elimination of infectious eBSV sequences from *M. balbisiana* progenitors, and to the safe use of *M. balbisiana* genitors for creating interspecific banana and plantain hybrids.

Keywords : endogenous pararetrovirus; infectious; Banana streak virus; segregation

References

- [1] Gayral P., Noa-Carrazana J.-C., Lescot M., Lheureux F., Lockhart B.E.L., Matsumoto T., Piffanelli P., Iskra-Caruana M.-L. (2008). *J. Virol.* **82**: 6697-6710.
- [2] Iskra-Caruana ML, Baurens FC, Gayral P, Chabannes M. (2010). A four-partner plant-virus interaction: enemies can also come from within. *Mol Plant Microbe Interact.* **23**:1394-402
- [3] Côte F, Galzi S., Folliot M., Lamagnère Y., Teycheney P.-Y., and Iskra-Caruana M.-L. (2010). *Mol. Plant Pathol.* **11**: 137–144
- [4] Gayral P., Blondin L., Guidolin O., Carreel F., Hippolyte I., Perrier X., Iskra-Caruana M.-L. (2010). *J. Virol.* **84**: 7346-59