

Risk assessment of spreading Banana streak viruses in the Dominican Republic through large scale cultivation of plantain cultivars and hybrids harbouring infectious eBSVs

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Most cultivated plantains are interspecific cultivars or hybrids: they harbour *Musa acuminata* (A) genomes and *Musa balbisiana* (B) genomes which hosts infectious endogenous *Banana streak virus* sequences (eBSVs). Spontaneous infections can arise in plantains following activation of these sequences by biotic and abiotic stresses, such as tissue culture and temperature differences, while several mealybug species can transmit BSV horizontally. The level of activation of infectious eBSVs by tissue culture has been quantified for several plantain cultivars and hybrids [1, 2], but virtually nothing is known about activation levels under field conditions, thus preventing the assessment of the risk of spreading BSV through large scale cultivation of plantains. This question was addressed in the Dominican Republic, using the most widely cultivated plantain types in the country: triploid AAB cultivar Macho x Hembra (MxH) and tetraploid AAAB hybrid FHIA21. Both carry infectious eBSV alleles OL1 and GF7 of the two distinct BSV species BSOLV and BSGFV, respectively, but are devoid of infectious eBSVs of species BSIMV.

Firstly, a nationwide survey was conducted throughout all Dominican banana growing areas. A total of 590 leaf samples of FHIA21 and MxH were collected from 36 locations reflecting the diversity of banana cultivation conditions in the country (temperature, irrigation, type of planting material, presence of mealybugs...). Samples were indexed for viral species BSOLV, BSGFV and BSIMV. Based on these results, two locations were selected for an in depth survey: 100 FHIA21 and 100 MxH leaf samples were collected from nearby plots in each location, and mealybug samples were also collected on sampled plants. All plant samples were indexed for viral species BSOLV, BSGFV and BSIMV, whereas total DNA was extracted from mealybugs and used to type mealybug species and search for BSV in mealybugs. Results from indexings and molecular analyses were used in a multifactorial statistical analysis taking into account environmental factors. Overall, results suggest that in the Dominican Republic, BSV infections in plantains MxH and FHIA21 result from the activation of infectious eBSVs rather than from horizontal transmission by mealybug vectors. They show that infection levels are significantly more important in FHIA21 than in MxH, highlighting the importance of genetic background in eBSV activation processes.

Activation of infectious eBSVs was also assessed experimentally in FHIA21 and MxH. To this end, an experimental plot was set up under field culture conditions, using FHIA21 and MxH plants produced either by tissue culture or by suckers. Mealybugs and ants were controlled by insecticide treatment throughout the experiment, therefore ensuring that BSV infections could only arise from the activation of infectious eBSVs. All 484 plants of the plot were indexed regularly for BSV species BSOLV, BSGFV and BSIMV. Indexing results were used in a multifactorial statistical analysis, providing the first comparative risk assessment of spreading Banana streak viruses through cultivation of plantain cultivars and hybrids originating from tissue culture or suckers.

Mots-clés : Plantain; *Banana streak virus*; eBSVs; risk assessment.

Références :

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