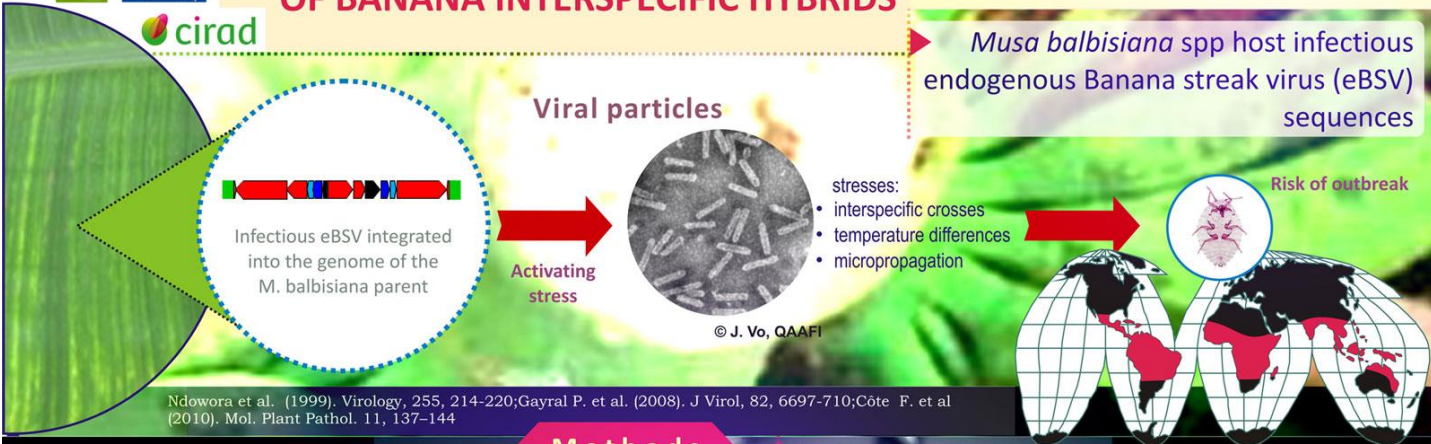


RISK ASSESSMENT OF SPREADING BANANA STREAK VIRUSES (BSV) THROUGH LARGE SCALE DISTRIBUTION OF BANANA INTERSPECIFIC HYBRIDS

Elisa Javer Higginson¹, Reina Teresa Martinez², M.D.L. Reyes³, A. Barahona, M.A. Fonseca³, R.M Garzón³, N. Arencibia³, R. Chinae⁴ & Pierre Yves Teycheney⁵

¹INISAV ejaver@inisav.cu, ²IDIAF, rmartinez@idiaf.gov.do, ³LAPROSAVS, Cuba, ⁴LCCV, Cuba, ⁵CIRAD, Guadeloupe



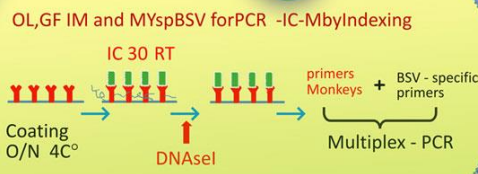
Ndowora et al. (1999). Virology, 255, 214-220; Gayral P. et al. (2008). J Virol, 82, 6697-710; Côte F. et al (2010). Mol. Plant Pathol. 11, 137-144

Methods

1

- Field survey & sample collection
- FHIA 21 (AAAB), MxH (AAB) (DR)
 - FHIA 18 (AAAB), CEMSA ¼ (AAB) (Cuba)
 - Mealybug vector species present
 - Agronomical data

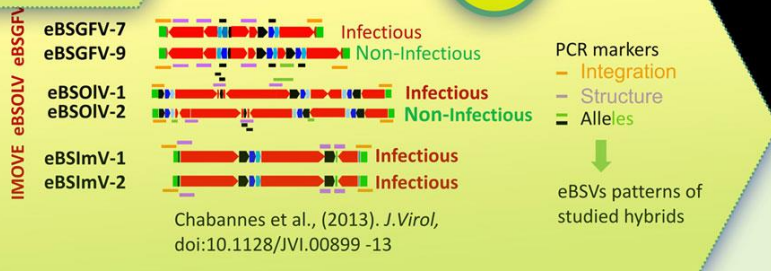
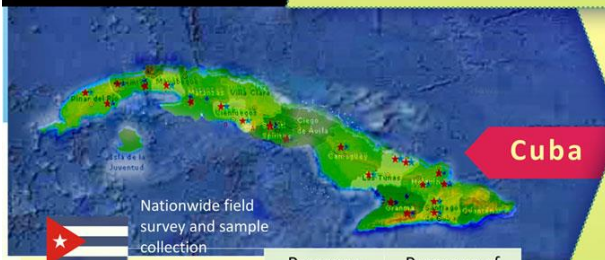
2



Studying the levels of prevalence and molecular diversity of BSV can provide a hint into the risk of spreading BSVs through large scale distribution of interspecific hybrids

Cuba and the Dominican Republic are important producers of interspecific hybrids in the Caribbean

3



Dominican Republic

	Presence symptoms/ Location	Presence of mealybugs/ location
FHIA 18	13/24	18/24
CEMSA 3/4	7/21	9/21

Symptoms based diagnostic is not reliable	No. samples	Infection (%)
Symptomatic	40	32,5%
Asymptomatic	631	2,0%

	Infection % (sucker)	Infection % (in vitro culture)
CEMSA 3/4	3.1%	5%
FHIA 18	4.1%	5.4%

No. of identified samples	<i>D. Brevipes</i>	<i>D.brevipes + P.minor</i>	<i>P. citri</i>
26	23	2	1

3,2% of infected plants were colonized by mealybugs. There is no relationship between presence/absence mealybugs and infection %

	No. samples	Indexing	Total	%	eBSVs pattern				
					eBSOLV	eBSGFV	eBSIMV		
CEMSA3/4	248	8	0	0	8	3.2	OL1	GF7	-
FHIA18	423	17	1	0	18	4.3	OL1/ OL2	GF7/ GF9	-
Total	671	25	0	0	26	3.9			
%		96,1%	3,8%	0					

1. Overall low % of infection by BSV
2. BSOLV causes the 96,1% of all infections
3. BSIMV and BSMYV not detected
4. FHIA 18 has both alleles for eBSGFV and eBSOLV: true AAAB? Technical problem with PCR?

	Symptoms /location	mealybugs /location
FHIA-21	18/21	17/21
MxH	10/21	13/21

	Genotype	No. samples	Indexing		Infection (%)	eBSV patterns	
			BSOLV	BSIMV		eBSOLV	eBSGFV
FHIA-21	AAAB	88	22	0	25	OL1	GF7
MxH	AAB	88	1	0	1,1	OL1	GF7
Total		176	26	0	14,8%		
%			100	0			

1. A significant proportion of FHIA-21 (25%) is infected with BSOLV, the level of infection in MxH is very low (1,1%).
2. Good correlation between indexing results and eBSOLV patterns for both hybrids.
3. BSIMV not detected eBSIMV pattern has not been established yet.

Conclusions

- The levels of prevalence of BSV are low in FHIA 18 and CEMSA ¼ in Cuba and on MxH in Dominican Republic
- High levels of prevalence of BSOLV in FHIA 21 in the Dominican Republic, although both MxH and FHIA21 host infectious eBSOLV alleles: differential expression of infectious eBSOLV allele in FHIA21 and MxH
- Similar infection rates for CEMSA ¼ and FHIA 18 originating from suckers; both harbour similar eBSV allele patterns
- Prevalence levels of BSOLV are higher than those of BSGFV: differential activation levels of infectious eBSOLV and eBSGFV alleles FHIA21 and CEMSA ¼
- FHIA 18 display an unexpected pattern both infectious and non infectious eBSGFV and eBSOLV alleles, and no eBSIMV
- Mealybugs do not seem to play an important role in BSV dissemination

Perspectives

- Study of the impact of plant propagation methods on the activation of infectious eBSV
- Study of the impact of BSV infection on yield and production in plantain and interspecific hybrids
- Characterization of the role of mealybugs in BSV epidemiology