

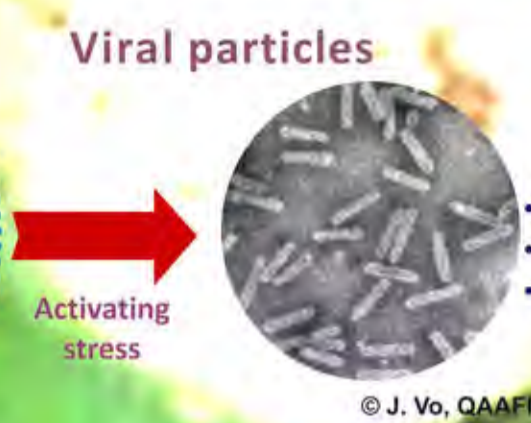
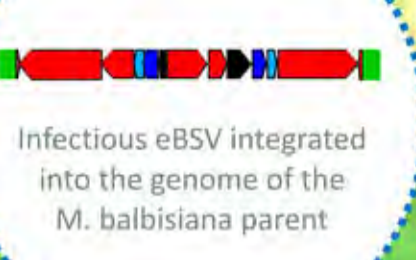
RISK ASSESSMENT OF SPREADING BANANA STREAK VIRUSES (BSV) THROUGH LARGE SCALE DISTRIBUTION OF BANANA INTERSPECIFIC HYBRIDS

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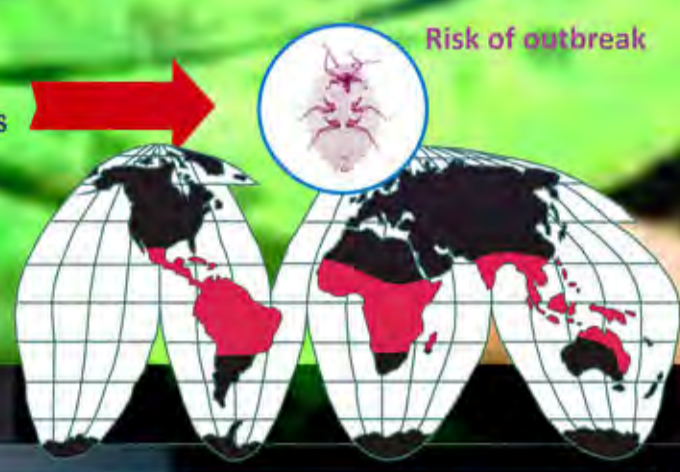
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Musa balbisiana spp host infectious endogenous Banana streak virus (eBSV) sequences



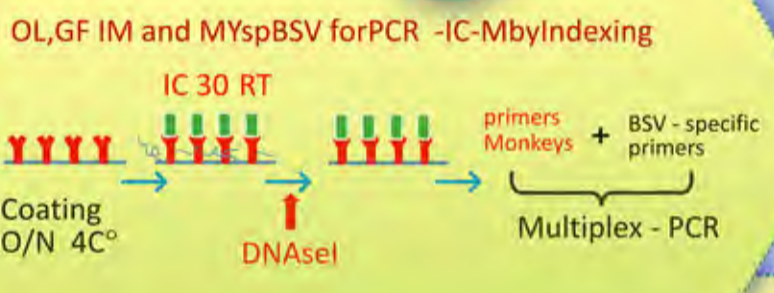
- stresses:
- interspecific crosses
 - temperature differences
 - micropropagation



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 3/4 (AAB) (Cuba)
 - Mealybug vector species present
 - Agronomical data



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



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

	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. brevipus + P. minor</i>	<i>P. citri</i>
26	23	2	1

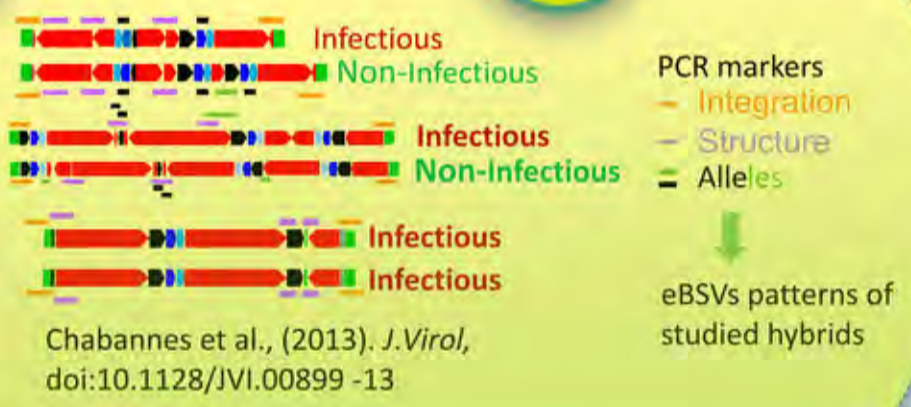
3,2 % of infected plants were colonized by mealybugs. There is no relationship between presence/absence mealybugs and infection %

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

Cuba

Dominican Republic



Genotype	No. samples	Indexing BSOLV	Indexing BSIMV	Infection (%)	eBSV patterns
FHIA-21	88	22	0	25	OL1 GF7
MXH	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 3/4 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 3/4 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 3/4
- 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 eBSVs
- 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