Fitosanidad
ISSN: 1562-3009
fitosanidad@inisav.cu
Instituto de Investigaciones de Sanidad Vegetal
Cuba

Javer Higginson, Elisa; Font, Caridad; Quiala, Idilio; Gonzalez, Gloria; Fonseca, Maria A.; Echemendía, Ana Lidia; Yves Teycheney, Pierre
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Fitosanidad, vol. 20, núm. 2, agosto, 2016, pp. 93-94
Instituto de Investigaciones de Sanidad Vegetal
La Habana, Cuba

Comunicación corta

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Presencia de especies de *Banana streak virus* en el cultivar FHIA 23 en Cuba

Elisa Javer Higginson[1], Caridad Font[1], Idilio Quiala[1], Gloria Gonzalez[1], Maria A. Fonseca[2], Ana Lidia Echemendía[1] and Pierre Yves Teycheney[3]

[1] *Instituto de Investigaciones de Sanidad Vegetal, Calle 110 no. 514 entre 5ta. B y 5ta. F, Playa, CP11600, La Habana, Cuba. ejaver@inisav.cu*
[2] *Laboratorio Provincial de Sanidad Vegetal Granma, Carretera central vía Holguín, no. 371, Bayamo*
[3] *Centre International de Recherche en Agronomie pour le Développement, UPR75, Station de Neufchateau, Sainte-Marie, 97130 Capesterre Belle-Eau, Guadeloupe, FWI.*

Bananas and plantains (*Musa*. sp) play a significant role in food security in Cuba. Tetraploid interspecific hybrids (AAAB, AABB, and AAAA) and dessert/cooking bananas (AAA, AAB, and ABB) are between the most cultivated varieties. *Banana streak viruses* (BSVs) form a complex of badnaviruses from the family *Caulimoviridae* known to infect *Musa* sp. worldwide (Bhat *et al*., 2016). Several species of BSV have been fully characterized and are now recognized by the International Committee on Taxonomy of Viruses (ICTV) (King *et al*., 2012; Adams *et al*., 2015).The most widespread species are *Banana streak OL virus* (BSOLV), *Banana streak GF virus* (BSGFV), *Banana streak IM virus* (BSIMV), *Banana streak MY virus* (BSMYV) (Iskra-Caruana *et al*., 2014 a, b).

Infections with BSOLV, BSGFV and BSIMV, in AAAB and AAB genotypes, can arise from activation of its endogenous counterparts integrated in *Musa balbisiana* genome (B) (Dallot *et al*., 2001; Cote *et al*., 2010; Chabannes *et al*., 2013) and could be subsequently spread in the field by mealybugs vectors (Meyer *et al*., 2008; Kubiriba *et al*., 2013) or by vegetative propagation (Daniells *et al*., 2001).

This has motivated a nationwide field survey in which several species of BSV were found infecting some FHIA hybrids and dessert bananas (Javer-Higginson *et al*., 2009, 2014). In an effort to continue the exploration of the genetic diversity and incidence of these badnaviruses in other banana cultivars; additional surveys were undertaken on the dessert-type tetraploid (AAAA) hybrid FHIA 23.

With this purpose, leaf samples were collected at random from symptomatic and/or non-symptomatic plants in four FHIA 23 plots located at El Mambí in Ciego de Avila province, Bayamo in Granma, Quivicán in Mayabeque and Santo Domingo in Villa Clara provinces; Collected samples were processed and indexed for the presence of BSV species BSOLV, BSGFV, and BSIMV by multiplex immunocapture PCR (M-IC-PCR), following the protocol of Le Provost *et al*. (2006). A total of 84 samples were collected. Only one plant at El Mambí was symptomatic with symptoms consisting in slight chlorotic leaf streaks.

While BSOLV and BSGFV species were detected in 12% of the 84 indexed FHIA 23 samples, the specie BSIMV does not appeared in any sample of this cultivar. Infected FHIA 23 samples were only detected in the eight-month plantation of El Mambí in Ciego de Avila. The 17 % (9/52) of the samples were identified infected by BSOLV in this location, including the plant displaying the chlorotic leaf streaking. An additional FHIA 23 non-symptomatic sample of the same location was infected by BSGFV.

Recibido: 6/2/2016
Aceptado: 19/4/2016

To validate these results, the nucleotide sequences of some amplicons were determined. The GenBank accession numbers of the sequences are KX880510-KX880512. Blast analysis showed that cloned sequences share 99% of nucleotide identity with reference sequences BSOLV AJ002234.1 or KJ013507.1 (BSGFV). This report confirms the presence of BSOLV and BSGFV species in the tetraploid hybrid FHIA 23 in Cuba.

Although present in the country, the sanitary status of FHIA 23 plantations regarding species of BSV had never been assessed. In the present work we found that the majority of BSV infected FHIA 23 samples were non-symptomatic consistent with previous observations made by Péréfarres *et al*. (2009) in Guadalupe, Javer-Higginson *et al*. (2014) in Cuba, and Martinez, 2015 in the Dominican Republic, showing that non-symptomatic BSV-infections are frequent. Hence, symptoms based diagnostic is ineffective.

Whether these infections arose from mass propagation of infected plant materials or from mealybug transmission from neighboring infected plants, is unknown. In any case, it would be necessary to implement accurate and sensitive diagnostic methods to monitor the status of planting material. If *in vitro* culture is used, the meristem micropropagation combined with cryotherapy procedures will assure the removal of contaminating viruses, as recommended by Thomas *et al*. (2015).

ACKNOWLEDGEMENTS

This work was supported by the Centre of Genetic Engineering and Biotechnology (CIGB), Havana, Cuba, the Guadeloupe Region through its Fonds de Coopération Régionale program and the French Embassy in Cuba. Authors are grateful to Professor B.E.L. Lockhart for kindly providing the antiBSV antiserum.

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