New Disease Reports

Occurrence of *Banana bunchy top virus* in banana and plantain (*Musa* sp.) in Benin

B. Lokossou [1], D. Gnanvossou [2], O. Ayodeji [3], F. Akplogan [4], A. Safiore [5], D.Z. Migan [6], A.M. Pefoura [7], R. Hanna [8] and P. Lava Kumar [3]*

[1] *Institut National des Recherches Agricoles du Bénin (INRAB), Niaouli, Benin*; [2] *International Institute of Tropical Agriculture (IITA), BP 08-0932, Cotonou, Benin*; [3] *IITA, PMB 5320, Oyo Road, Ibadan, Nigeria*; [4] *Centre Communal pour la Promotion Agricole (CeCPA), Dangbo, Benin*; [5] *Centre Régional pour la Promotion de l'Agriculture (CeRPA), Porto-Novo, Benin*; [6] *Centre Communal pour la Promotion Agricole (CeCPA), Avrankou, Benin*; [7] *Centre Africain de Recherches sur Bananiers et Plantains (CARBAP), Njombe, Cameroon*; [8] *IITA, BP 2008 (Messa), Yaoundé, Cameroon*

*E-mail: L.kumar@cgiar.org

Received: *29 Dec 2011.* ***Published:*** *02 Mar 2012.* ***Keywords:*** *Babuvirus, banana aphid, Africa*

Banana bunchy top virus (BBTV; genus *Babuvirus,* family *Nanoviridae*), is one of the most serious pathogens of banana (AAA genome) and plantain (AAB genome) (*Musa* spp). BBTV is well established in central and southern sub-Saharan Africa (Kumar *et al*., 20011). It is transmitted by the banana aphid, *Pentalonia nigronervosa* (Homoptera: Aphididae), in a persistent manner. In July 2011, banana and plantain that displayed stunting and leaf symptoms typical of banana bunchy top disease were observed to be widespread in Dangbo Commune, Ouémé Department, Benin. To identify the cause of the disease, a roving survey was conducted in December 2011 in nine locations in Avrankou, Dangbo, Akpro-Missérété and Porto-Novo Communes, in Ouémé (Fig. 1). In each location, incidence of symptom-bearing plants was estimated from counts of 15 mats, and samples were collected for BBTV assessment. About 60% of the 94 banana mats assessed had plants exhibiting typical symptoms of BBTV infection - chlorotic leaf margins, dark green streaks on petioles, narrow leaves that bunched at the top and severe stunting (Fig. 2).

Total DNA was extracted from 25 leaf samples collected from plants with symptoms; they were then tested for BBTV by polymerase chain reaction (PCR) according to the published protocols. Two oligonucleotide primer pairs, mREP-F and mREP-R, specific for a ~240 bp conserved domain of BBTV DNA-mRep segment (Mansoor *et al.,* 2005), and Scp-F and Scp-R specific for a ~1075 bp BBTV DNA-S that encodes coat protein gene (Amin *et al*., 2008) were used for PCR amplification. The amplicons of expected size were obtained from 23 of the 25 samples analysed suggesting the presence of BBTV in the affected plants (Fig. 3). The PCR products of DNA-mRep segment amplified from the BBTV-infected banana samples collected in Zoungue (GenBank Accession No. JQ437548) and Mitro (JQ437549) were sequenced in both directions directly from the purified PCR products. These two sequences showed 100% nucleotide sequence identity with a BBTV isolate from Cameroon (FJ580970) and 99-100% identity with several other BBTV isolates from the GenBank database belonging to the South Pacific group, comprised of BBTV isolates from Africa, Australia, India and South Pacific (Fig. 4). This finding confirmed that the virus isolate associated with the diseased plants in Benin indeed was of the BBTV South Pacific type. This finding constitutes the first report of BBTV in Benin. The disease is widespread in all the four communes surveyed (Fig. 1). Further surveys are necessary to assess the extent of BBTV occurrence in Benin. Until now, Cameroon was the western most frontier of BBTV presence in sub-Saharan Africa (Oben *et al*., 2009). This finding confirms spread of the disease into West Africa, and underscores an urgent need for intensive surveys in neighbouring countries and implementation of strict phytosanitary measures to prevent movement of planting material from the infected zones and to prevent further spread of BBTV.

Acknowledgements

This work was funded by the IITA core donors. We thank Mr. Saka Bachirou (CeRPA, Porto-Novo, Benin) and T. Oviasuyi (IITA, Ibadan, Nigeria) for their support of this survey.

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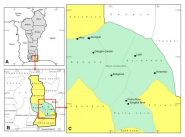

Figure 1

Figure 2

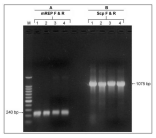

Figure 3

Figure 4

To cite this report: Lokossou B, Gnanvossou D, Ayodeji O, Akplogan F, Safiore A, Migan DZ, Pefoura AM, Hanna R, Lava Kumar P, 2012. Occurrence of *Banana bunchy top virus* in banana and plantain (*Musa* sp.) in Benin. *New Disease Reports* **25**, 13. [doi:10.5197/j.2044-0588.2012.025.013]

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