New Disease Reports

First report of Pepo aphid-borne yellows virus on zucchini in Cote d'Ivoire

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Cucurbits are very important crops for West African farmers, in particular in Côte d'Ivoire, ensuring self-sufficiency and the generation of income. However, plant viral diseases are a major constraint to cucurbit production (Lecoq & Katis, 2014). During a virus survey in the dry (January to March 2014) and wet (June to August 2014) seasons, about 80% of cucurbit plants presented virus-like symptoms. A total of 757 leaf samples were collected from cucumber (*Cucumis sativus*), squash and zucchini (*Cucurbita pepo*), watermelon (*Cirullus lanatus*), calabash gourd (*Lagenaria siceraria*) and melon (*Cucumis melo*) in 16 regions of Côte d'Ivoire representing six agricultural environments. Samples were selected from leaves with viral symptoms including mosaic, leaf distortion, shoe-string, blister, narrowing, leaf curling and yellowing (Fig. 1). Samples were dried over calcium chloride for later analysis. All samples were tested by double-antibody sandwich-ELISA for *Cucumber mosaic virus* (CMV), *Moroccan watermelon mosaic virus* (MWMV), *Papaya ringspot virus* (PRSV), *Watermelon mosaic virus* (WMV) and *Zucchini yellow mosaic virus* (ZYMV) with antisera from DSMZ (Braunschweig, Germany). A total of 399 samples tested positive in ELISA for CMV, PRSV and ZYMV in either single or mixed infections. To check for species of the genus *Polerovirus* (family *Luteoviridae*) that are reported to occur frequently in mixed infections with other aphid-borne viruses, RT-PCR screening was done (Knierim *et al*., 2013; Knierim *et al*., 2014). Samples totalling 68 representative for the growing regions, seasons and crops were selected. Total RNA was extracted (QIAGEN RNeasy kit) from the dried leaf material and screened by RT-PCR with the universal polerovirus primer pair Gen1 and Gen2 in combination with an internal control (Knierim *et al*., 2013).

The expected 325 bp dsDNA band indicative of polerovirus presence was amplified from 13 samples and subsequently sequenced. Sequences analysis revealed that all sequences shared 93.8% to 99.6% nt identity with one another and subsequent BLAST analysis of each sequence against GenBank confirmed close identity to Pepo aphid-borne yellows virus (PABYV) isolates from Mali (95-97%; KF427698-KF427700) and to PABYV isolates from South Africa (93-97%; KJ789897, KJ789900, KJ789902-KJ789904 and KJ789911). Of the 13 samples that tested positive for PABYV, all were from zucchini and were found in the locations Agokro, Dabou, Daoukro, Divo, Duekoue, Korhogo, Kpokhankro, Man, Songo-te and Tombokaha. We also demonstrated the existence of PABYV in the dry season (eight samples) and wet seasons (eight samples). For four of the 13 PABYV samples, longer sequence fragments (1376 nts) were obtained with another universal polerovirus primer pair (Knierim *et al*., 2014) and sequence analysis confirmed the first results (GenBank Accession Nos. KR054131-KR054134). Other cucurbit-infecting polerovirus species were not detected during this study.

This is the first report of PABYV from Côte d'Ivoire and the virus is now reported from three countries in Africa (Côte d'Ivoire, Mali and South Africa) since its first description in 2008. It seems to be widely distributed in Côte d'Ivoire, occurring in dry and in wet season crops. Although PABYV was only found in mixed infections in this study and the direct impact on the yield is not known, it should be considered in strategies to manage virus diseases particularly when zucchini is cultivated.

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Figure 1

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