First reports of Cotton leaf curl Gezira virus and Okra yellow crinkle virus associated with okra leaf curl disease in Côte d’Ivoire

K. Séka 1,2, A. Ouattara 3,4, K.P. Assiri 2, K.D. Kra 2, M. Hoareau 1, P. Lefeuvre 1, H. Atta Diallo 2 and J.M. Lett 1*

1 CIRAD, UMR PVBMT, Pôle de Protection des Plantes, 97410 Saint-Pierre, Ile de La Réunion, France; 2 Université Nangui Abrogoua, 02 BP 801 Abidjan, Côte d’Ivoire; 3 Université de Ouagadougou, 03 BP 7021, Ouagadougou 03, Burkina Faso; 4 INERA, LMI Patho-Bios, 01 BP 476, Ouagadougou 01, Burkina Faso

*E-mail: lett@cirad.fr

Received: 02 Jun 2016. Published: 23 Aug 2016.

Okra leaf curl disease (OLCD) is commonly observed in okra (Abelmoschus esculentus) crops in several African countries (N’Guesan et al., 1992). Affected plants are severely stunted with apical leaf curl (upward or downward), distortion and thickening of the veins. In Africa, OLCD is associated with a complex of several strains of two begomovirus species: Cotton leaf curl Gezira virus (CLCuGV; Idris & Brown, 2002) and Okra yellow crinkle virus (OYCv; Shih et al., 2007). In 2012 and 2013, severe symptoms of leaf curling, deformation, and vein thickening (Fig. 1), resembling those of okra leaf curl disease were observed on okra in four localities in south-eastern Côte d’Ivoire (Table 1).

Fourteen leaf samples with symptoms were collected and tested for the presence of begomoviruses using a polymerase chain reaction (PCR) assay with a set of degenerate primers designed to amplify the coat protein gene of Old World begomoviruses (Clust4CP-F342, 5′-TATMATCATTTCCACBCCVG-3′; Clust4CP-R1032, 5′-GCATGAGTACATGCCATATAC-3′). PCR products of the expected sizes were obtained for nine samples suggesting the presence of Old World monopartite begomoviruses in all four localities (Table 1).

PCR positive samples were further processed and full-length viral genomes were amplified from four samples (Table 1) by rolling-circle amplification, cloned using the BamHI restriction enzyme and sequenced. One complete genome sequence (GenBank Accession No. KX100570) showed the highest pairwise sequence identity of 99% (100% coverage) with isolates of the Niger strain of CLCuGV from Niger (CLCuGV-NE[NE:Sad:NG2FL:Ok:07], FJ469627) and Burkina Faso (CLCuGV-NE[NE:Bam:Ok4:08], FN54524). The other three sequences (KX100571 to KX100573) showed the highest pairwise sequence identity of 98-99% (100% coverage) with isolates of the Mali strain of OYCv from Mali (OYCv-ML[ML:Mom1:09], DQ902715; OYCv-ML[ML:Bam4:06], EU024119). A maximum likelihood phylogenetic tree, produced from the complete genome sequence (GenBank Accession No. KX100570) showed the highest pairwise sequence identity of 98-99% (100% coverage) with isolates of the Mali strain of OYCv from Mali (OYCv-ML[ML:Mom1:09], DQ902715; OYCv-ML[ML:Bam4:06], EU024119). A maximum likelihood phylogenetic tree, produced from alignments of publicly available begomovirus sequences (MEGA6; Tamura et al., 2013), confirmed the genetic relationship of Ivorian CLCuGV and OYCv isolates with isolates from three neighbouring countries, Burkina Faso, Mali and Niger (Fig. 2).

To our knowledge, this is the first report of CLCuGV and OYCv implicated in OLCD in Côte d’Ivoire. Our results confirm that OLCD is associated with a complex of several strains of CLCuGV and OYCv in sub-Saharan Africa (Tiendrébéogo et al., 2010) and show that Ivorian isolates are genetically closely related to strains described in West Africa.

Acknowledgements

This study was funded by the Région Réunion, the European Union (FEDER) and the CIRAD.

References


