



First report of cassava mosaic geminiviruses and the Uganda strain of *East African cassava mosaic virus (EACMV-UG)* associated with cassava mosaic disease in Equatorial Guinea

A. Valam-Zango^{1,2}, I. Zinga¹, M. Hoareau³, B.K. Tocko-Marabena¹, A.C. Mvila⁴, S. Semballa¹ and J.M. Lett^{3*}

¹ LASBAD, Université de Bangui, BP908 Bangui, Central African Republic; ² Université Marien Ngouabi, Brazzaville, Congo; ³ CIRAD, UMR PVBMT, Pôle de Protection des Plantes, 97410 Saint Pierre, La Réunion, France; ⁴ Institut National de Recherche Agronomique, BP2499, Brazzaville, Congo

*E-mail: lett@cirad.fr

Received: 29 Sep 2015. Published: 12 Dec 2015. Keywords: ACMV, EACMV, EACMCV, *Manihot esculenta*

Cassava mosaic disease (CMD) is one of the main production constraints for cassava (*Manihot esculenta*) in Africa (Patil & Fauquet, 2009). The disease is caused by seven cassava mosaic geminiviruses (CMGs, genus *Begomovirus*). A severe CMD pandemic, caused by the synergistic interaction between *African cassava mosaic virus* (ACMV) and the Uganda strain of *East African cassava mosaic virus* (EACMV-UG), emerged in the 1990's in East Africa and subsequently progressed into neighbouring countries and into Central Africa. EACMV-UG has recently been reported in several Central African countries bordering Equatorial Guinea: Cameroon (Akinbade *et al.*, 2010), the Central African Republic and Chad (Zinga *et al.*, 2012), the Congo Republic and the Democratic Republic of Congo (Neuenschwander *et al.*, 2002) and Gabon (Legg *et al.*, 2004). Although CMD has been reported in Equatorial Guinea, the causal agents have never been identified.

In December 2013, 30 leaves from local cultivars of cassava exhibiting moderate to very severe CMD symptoms were collected at nine different locations in Equatorial Guinea (Table 1). Sixteen leaf samples tested positive by PCR for the presence of CMGs using degenerate and specific primers (Harimalala *et al.*, 2015). Each detection of the virus was confirmed by direct sequencing of the amplification products. Amplification revealed the occurrence of ACMV (30% of the samples), EACMV (27%) and *East African cassava mosaic Cameroon virus* (EACMCV; 13%) in single (ACMV, 27%; EACMV, 10%) and mixed infections (ACMV-EACMV, 3%; EACMV-EACMCV, 13%).

Based on a sample which tested positive by PCR for the presence of EACMV (GQ006), the possible occurrence of EACMV-UG in Equatorial Guinea was investigated. Complete DNA-A and -B molecules were cloned and sequenced using the Phi29 DNA polymerase-based rolling circle amplification strategy. BLASTn analysis showed that the DNA-A sequence (GenBank Accession No. KT780440) shared the highest nucleotide sequence identity (99%) with Central, East and West African isolates of EACMV-UG ([CG:12] JX910240; [UG:Nak] AJ618957; [BF:FaK:08] FM877474). The DNA-B sequence (KT780439) shared the highest nucleotide sequence identity (98%) with Central and East African isolates of EACMV-UG ([CF:CF44B:07] KM885991; [KE:K90:02] AJ704962).

To our knowledge, this is the first report of the occurrence of ACMV, EACMCV and EACMV-UG associated with CMD in Equatorial Guinea. This study confirms the westward spread of the Uganda strain of EACMV.

These results need to be considered during the regional management of cassava diseases and by regulatory phytosanitary bodies.

Acknowledgements

This study was supported by the MAE (PARRAF programme, AIRD), PRASAC-CEMAC (Cassava project-EU), European Union (FEDER) and the *Région Réunion*. A. Valam-Zango is a recipient of PhD fellowships from the ProVeg network and PRASAC-CEMAC.

References

- Akinbade SA, Hanna R, Nguenkam A, Njukwe E, Fotso A, Doumtsop A, Ngeve J, Tenku STN, Lava Kumar P, 2010. First report of the *East African cassava mosaic virus*-Uganda (EACMV-UG) infecting cassava (*Manihot esculenta*) in Cameroon. *New Disease Reports* **21**, 22. <http://dx.doi.org/10.5197/j.2044-0588.2010.021.022>
- Harimalala M, Chiroleu F, Giraud-Carrier C, Hoareau M, Zinga I, Andriamampianina JA, Velombola JA, Ranomenjanahary S, Andrianjaka A, Reynaud B, Lefeuvre P, Lett JM, 2015. Molecular epidemiology of cassava mosaic disease in Madagascar. *Plant Pathology* **64**, 501-507. <http://dx.doi.org/10.1111/ppa.12277>
- Legg JP, Ndjelassili F, Okao-Okuja G, 2004. First report of cassava mosaic disease and cassava mosaic geminiviruses in Gabon. *Plant Pathology* **53**, 232. <http://dx.doi.org/10.1111/j.0032-0862.2004.00972.x>
- Neuenschwander P, Hughes Jd'A, Ogebe F, Ngatse JM, Legg JP, 2002. Occurrence of the Uganda variant of *East African cassava mosaic virus* (EACMV-Ug) in western Democratic Republic of Congo and the Congo Republic defines the westernmost extent of the CMD pandemic in East/Central Africa. *Plant Pathology* **51**, 385. <http://dx.doi.org/10.1046/j.1365-3059.2002.00698.x>
- Patil BL, Fauquet CM, 2009. Cassava mosaic geminiviruses: actual knowledge and perspectives. *Molecular Plant Pathology* **10**, 685-701. <http://dx.doi.org/10.1111/j.1364-3703.2009.00559.x>
- Zinga I, Harimalala M, De Bruyn A, Hoareau M, Mandakombo N, Semballa S, Reynaud B, Lefeuvre P, Lett JM, 2012. *East African cassava mosaic virus*-Uganda (EACMV-UG) and *African cassava mosaic virus* (ACMV) reported for the first time in Central African Republic and Chad. *New Disease Reports* **26**, 17. <http://dx.doi.org/10.5197/j.2044-0588.2012.026.017>

Accession	Strain	Host	Year	Location	GenBank Accession
KT780440	EACMV-UG	Cassava	2013	Equatorial Guinea	KT780440
KT780439	EACMV-UG	Cassava	2013	Equatorial Guinea	KT780439
JX910240	EACMV-UG	Cassava	2009	Uganda	JX910240
AJ618957	EACMV-UG	Cassava	2009	Uganda	AJ618957
FM877474	EACMV-UG	Cassava	2009	Uganda	FM877474
KM885991	EACMV-UG	Cassava	2009	Uganda	KM885991
AJ704962	EACMV-UG	Cassava	2009	Uganda	AJ704962

To cite this report: Valam-Zango A, Zinga I, Hoareau M, Tocko-Marabena BK, Mvila AC, Semballa S, Lett JM, 2015. First report of cassava mosaic geminiviruses and the Uganda strain of *East African cassava mosaic virus* (EACMV-UG) associated with cassava mosaic disease in Equatorial Guinea. *New Disease Reports* **32**, 29. <http://dx.doi.org/10.5197/j.2044-0588.2015.032.029>

©2015 The Authors

This report was published on-line at www.ndrs.org.uk where high quality versions of the figures can be found.