



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

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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.

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Accession	Strain	Host	Country	Year	GenBank
KT780440	UGANDA	Cassava	Uganda	2009	KT780440
KT780439	UGANDA	Cassava	Uganda	2009	KT780439
JX910240	UGANDA	Cassava	Uganda	2009	JX910240
AJ618957	UGANDA	Cassava	Uganda	2009	AJ618957
FM877474	UGANDA	Cassava	Uganda	2009	FM877474
KM885991	UGANDA	Cassava	Uganda	2009	KM885991
AJ704962	UGANDA	Cassava	Uganda	2009	AJ704962
KT780440	UGANDA	Cassava	Uganda	2009	KT780440
KT780439	UGANDA	Cassava	Uganda	2009	KT780439
JX910240	UGANDA	Cassava	Uganda	2009	JX910240
AJ618957	UGANDA	Cassava	Uganda	2009	AJ618957
FM877474	UGANDA	Cassava	Uganda	2009	FM877474
KM885991	UGANDA	Cassava	Uganda	2009	KM885991
AJ704962	UGANDA	Cassava	Uganda	2009	AJ704962

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