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First report of the *East African cassava mosaic virus*-Uganda (EACMV-UG) infecting cassava (*Manihot esculenta*) in Cameroon

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Cassava mosaic disease (CMD) is a major constraint of cassava (*Manihot esculenta*) in Cameroon. Previous studies confirmed the occurrence of *African cassava mosaic virus* (ACMV), *East African cassava mosaic Cameroon virus* (EACMCV) and *East African cassava mosaic virus* (EACMV) in CMD etiology (Fondong *et al.,* 2000). In this study, surveys were conducted for EACMV-Uganda (EACMV-UG), a recombinant virus responsible for severe CMD epidemics in East and Central Africa, which occurs in adjoining Republic of Congo (RC) and Gabon (Legg *et al.,* 2004). Surveys were conducted during March to November 2009 in 156 fields in 37 administrative divisions (Fig. 1). Six to eight samples from each field were collected from plants with distinct symptoms and severity, and analysed with the polymerase chain reaction (PCR) using primers UV-AL1/F1 and ACMV-CP/R3 specific for EACMV-UG (Zhou *et al.* 1997), ACMV and EACMV/ EACMCV (Alabi *et al.,* 2008). Viruses were identified based on the amplification of diagnostic fragments for ACMV (368 bp), EACMV/EACMCV (650 bp), and EACMV-UG (1630 bp).

Out of 1159 samples, single infections of ACMV and EACMV/EACMCV, and mixed infections of ACMV with EACMV/EACMCV were detected in, respectively, 57.1%, 4.2% and 23.0% of the total. EACMV-UG, as a mixed infection with ACMV (Fig. 2) and/or EACMV/EACMCV, was detected in 57 (33.9%) out of 168 samples from a total of 21 fields in Kadey, Boumba-and-Ngoko, Lom-and-Djerem and Mbere divisions (Figs. 1). Incidence in fields ranged from 11.1% (Mbotoro) to 83.3% (Boyere). To further confirm the virus identity, the 1630 bp PCR product from Gamago (Kadey) was sequenced (GenBank Accession No. GU395301). Comparison with sequences in GenBank revealed the highest identity (98%) with the DNA-A sequence of EACMV-UG (Fig. 3). To our knowledge, this is the first report of EACMV-UG in Cameroon. Its occurrence in areas bordering EACMV-UG affected countries suggests the spread of the virus by whiteflies or infected cuttings. Urgent deployment of resistant varieties in the affected regions is necessary to prevent severe CMD epidemics and further spread of this virus into West Africa.

Acknowledgements

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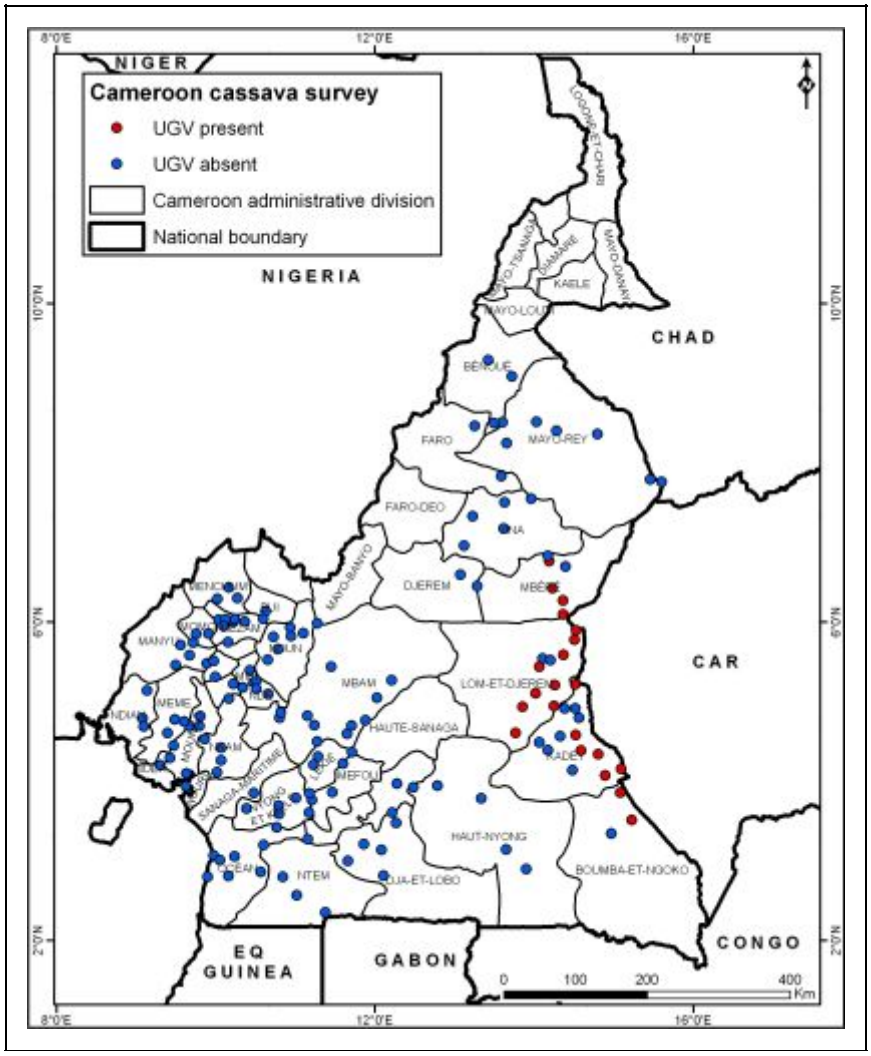

Figure 1: Geographic distribution of EACMV-UG in Cameroon. All the sampled locations are indicated by circles as follows: areas of EACMV-UG occurrence, red circles; areas where only ACMV and/or EACMV/EACMCV were detected, blue circles.

Figure 2: CMD symptoms in cassava plant infected with ACMV and EACMV-UG in Letta, Kadey division, Cameroon.

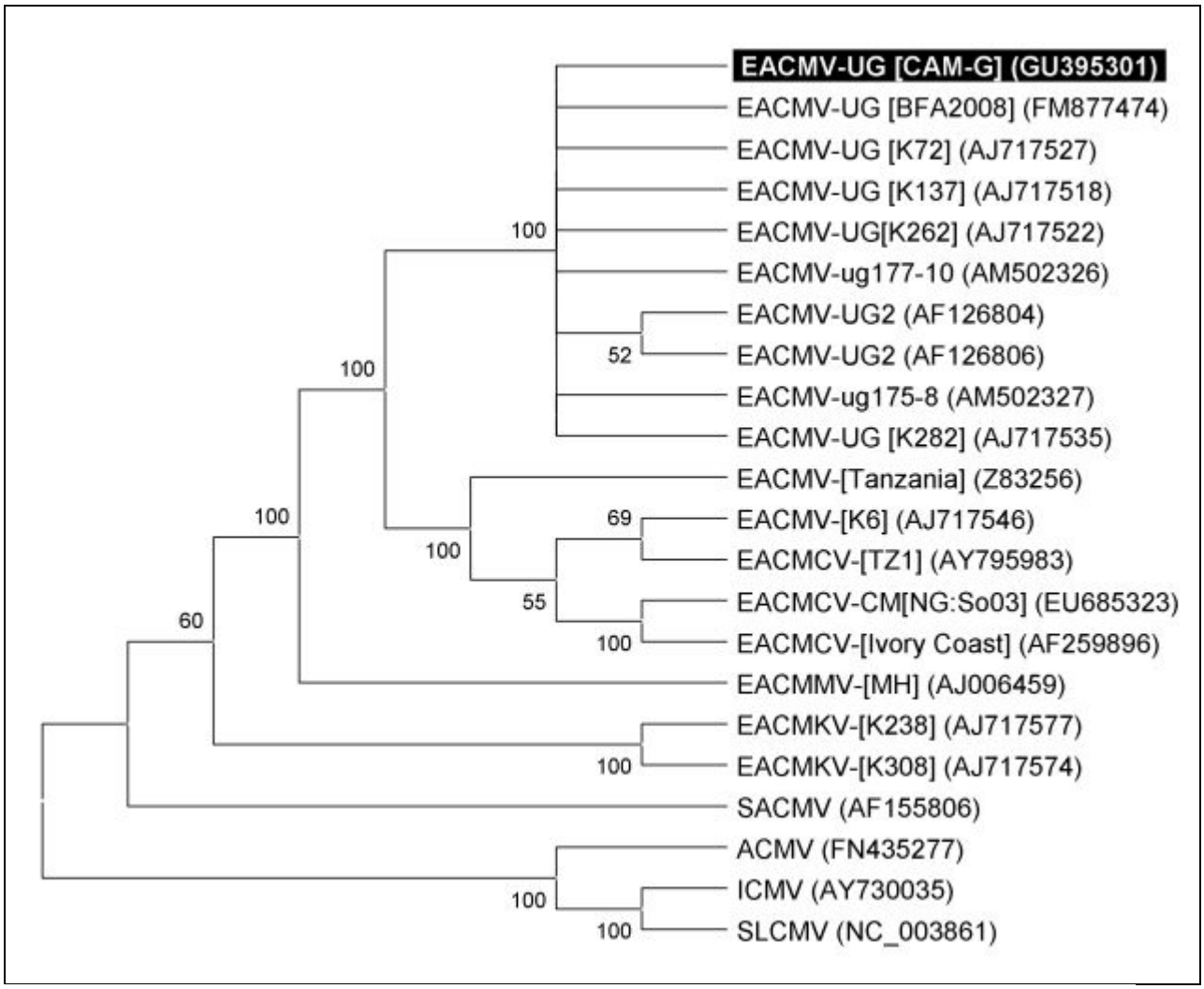

Figure 3: Phylogenetic relationship of EACMV-UG Cameroon isolate (highlighted) relative to various GenBank isolates inferred by the neighbour-Joining method using MEGA4 software based on the ClustalW alignment of the 1630 base pairs of DNA-A segment. Bootstrap values (1,000 replications) are shown as percentages at the branch points. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed.