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Diversity of Cassava Mosaic Begomoviruses and the Complex Structure of the Cassava Mosaic Disease in Cameroon

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Abstract

The impact of the Cassava mosaic disease CMD on the reduction of cassava production in Africa in the last two decades has been very dramatic. From the late 1980's a highly severe CMD epidemic emerging in north-central Uganda expanded to affect cassava plantings in much of the Lake Victoria Basin and westwards to the Democratic Republic of the Congo, DRC. The severe decline of the cassava in CMD is implicated with the occurrence of a new recombinant virus, the East African cassava mosaic virus Uganda variant (EACMV-UG), occurring in single and in mixed infection with other begomoviruses in cassava. The greatest challenge posed by the CMD pandemic is its westward expansion to Central and West Africa raising concerns that it may eventually spread to West Africa with Nigeria being the world's largest cassava producing country. Consequently, the virus situation in cassava growing areas in the countries neighbouring DRC requires frequent monitoring, to provide an up-to-date overview on the existing virus populations and on newly invading or evolving virus types. In Cameroon, two begomoviruses, the East African cassava mosaic Cameroon virus, EACMCV, and the African cassava mosaic virus, ACMV, have been reported so far. Single and mixed infections exist with EACMCV infections leading to serious disease phenotypes. Consequently, a virus survey to resolve the complex cassava virus situation Cameroon was conducted. In January/February 2006, cassava with severe CMD symptoms was collected from 21 locations across five agroecological zones of Cameroon. Cassava cuttings were rooted and maintained at the DSMZ virus department to observe developing virus symptoms. Virus infections were studied using a novel PCR approach, the rolling circle amplification, RCA, using the bacteriophage phi 29 DNA polymerase. RCA amplified viral DNA was characterised by restriction fragment length polymorphism, RAPD, resolving a number of polymorphic patterns indicating for further virus variants and/or mixed virus infections. Exact identification of the begomoviruses by sequence analysis further provided information on diversity and distribution of the begomoviruses in Cameroon. Details of the begomovirus populations infecting Cassava in Cameroon will be presented.

Keywords: ACMV, Cameroon, cassava mosaic disease, EACMCV, mixed begomovirus infection, virus population structure