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Diversity of Geminiviruses Causing Cassava Mosaic Disease in Africa

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Abstract

Cassava mosaic disease (CMD) caused by whitefly transmitted geminiviruses occurs wherever cassava is grown in Sub Sahara Africa, presents a serious constraint to cassava production and serious yield losses. The viruses causing CMD reflect a considerable molecular diversity with 6 distinct species so far described resolving in numerous and diverse strains and virus isolates. The cassava mosaic geminiviruses are believed to have initially evolved from indigenous African viruses which adapted to cassava and now occur, either with overlapping distribution over larger geographies, as with African cassava mosaic virus and East African cassava mosaic Cameroon virus or, with a more discrete occurrence as is the case for East African cassava mosaic Zanzibar virus found only in coastal areas of East Africa, Kenya and the island of Zanzibar. The large molecular diversity with viruses from East Africa points to East Africa as the centre of diversification. In addition and more significantly recombination evident in a number of virus genomes is a driving force of geminivirus evolution. Virus diversity and frequent recombination events found in virus genomes provide evidence for continuous evolutionary processes and influence the development of epidemics and the emergence of “new” viruses. The knowledge of virus diversity, the geographic distribution of virus types and the structure of virus populations is a most significant prerequisite to deploy cassava with virus resistance characters. A description of the current status of cassava geminiviruses in Sub Sahara Africa and the diverse phenotypes found in cassava will be presented and discussed in light of putative strategies to challenge CMD in Africa.

Keywords: Cassava mosaic disease, CMD in Sub Sahara Africa, geminivirus diversity