

East African cassava mosaic-like viruses from Africa to Indian Ocean Islands: molecular diversity, evolutionary history and geographical dissemination of a bipartite begomovirus

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Cassava (*Manihot esculenta*) is a major food source for over 200 million sub-Saharan Africans. Unfortunately, its cultivation is severely hampered by cassava mosaic disease (CMD). Caused by a complex of bipartite cassava mosaic geminiviruses (CMG) species (Family: Geminiviridae; Genus: Begomovirus) CMD has been widely described throughout Africa and it is apparent that CMGs are expanding their geographical distribution. Determining where and when CMG movements have occurred could help curtail its spread and reveal the ecological and anthropic factors associated with similar viral invasions. We applied Bayesian phylogeographic inference and recombination analyses to available and newly described CMG sequences to reconstruct a plausible history of CMG diversification and migration between Africa and South West Indian Ocean (SWIO) islands.

The isolation and analysis of 114 DNA-A and 41 DNA-B sequences demonstrated the presence of three CMG species circulating in the Comoros and Seychelles archipelagos (East African cassava mosaic virus, EACMV; East African cassava mosaic Kenya virus, EACMKV; and East African cassava mosaic Cameroon virus, EACMCV). Phylogeographic analyses suggest that CMG's presence on these SWIO islands is probably the result of at least four independent introduction events from mainland Africa occurring between 1988 and 2009. Amongst the islands of the Comoros archipelago, two major migration pathways were inferred: One from Grande Comore to Mohéli and the second from Mayotte to Anjouan. Numerous re-assortments events were detected between EACMV and EACMKV, which seem to almost freely interchange their genome components.

Rapid and extensive virus spread within the SWIO islands was demonstrated for three CMG complex species. Strong evolutionary or ecological interaction between CMG species may explain both their propensity to exchange components and the absence of recombination with non-CMG begomoviruses. Our results suggest an important role of anthropic factors in CMGs spread as the principal axes of viral migration correspond with major routes of human movement and commercial trade.

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