

## **Evolution of African cassava mosaic virus by recombination between bipartite and monopartite begomoviruses**

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Cassava mosaic disease (CMD) is a major constraint on cassava cultivation in Africa. The disease is endemic and is caused by seven distinct cassava mosaic geminiviruses (CMGs), some of them including several variants. From cassava leaf samples presenting CMD symptoms collected in Burkina Faso, four DNA-A begomovirus components were cloned and sequenced, showing 99.9% nucleotide identity among them. These isolates are most closely related to African cassava mosaic virus (ACMV) but share less than 89% nucleotide identity (taxonomic threshold) with any previously described begomovirus. A DNA-B genomic component, sharing 93% nucleotide identity with DNA-B of ACMV, was also characterized. Since all genomic components have a typical genome organization of Old World bipartite begomoviruses, this new species was provisionally named African cassava mosaic Burkina Faso virus (ACMBFV). Recombination analysis of the new virus demonstrated an interspecies recombinant origin, with major parents related to West African isolates of ACMV, and minor parents related to Tomato leaf curl Cameroon virus and Cotton leaf curl Gezira virus. This is the first report of an ACMV-like recombinant begomovirus arisen by interspecific recombination between bipartite and monopartite African begomoviruses.

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