

Infectivity, pseudorecombination and mutagenesis of Kenyan cassava mosaic begomoviruses

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Abstract

Cloned DNA-A and DNA-B components of Kenyan isolates of East African cassava mosaic virus (EACMV, EACMV-UG and EACMV-KE2), East African cassava mosaic Kenya virus (EACMKV) and East African cassava mosaic Zanzibar virus (EACMZV) are shown to be infectious in cassava. EACMV and EACMKV genomic components have the same iteron sequence (GGGGG) and can form viable pseudorecombinants, while EACMZV components have a different sequence (GGAGA) and are incompatible with EACMV and EACMKV. Mutagenesis of EACMZV has demonstrated that open reading frames (ORFs) AV1 (encoding the coat protein), AV2 and AC4 are not essential for a symptomatic infection of cassava, although mutants of both ORF AV1 and AV2 produce attenuated symptoms in this host. Furthermore, ORF AV1 and AV2 mutants were compromised for coat protein production, suggesting a close structural and/or functional relationship between these coding regions or their protein products.