

Metaviromic analysis reveals coinfection of papaya in western Kenya with a unique strain of Moroccan watermelon mosaic virus and a novel member of the family Alphaflexiviridae

Abstract

Severe mottling symptoms were observed on *Carica papaya* L. in Koyonzo, Kakamega County, Kenya. Total RNA was sequenced via an RNAtag-seq workflow. Assembled contigs indicated the presence of a divergent strain of Moroccan watermelon mosaic virus (genus *Potyvirus*) with a complete genome length of 9,733 nt (GenBank accession no. MN418119). Additionally, the complete genome sequence of a novel member of the viral genus *Allexivirus* was determined (GenBank accession no. MN418120). The genome contains six open reading frames (ORFs) that show varying degrees of sequence similarity to members of the genus *Allexivirus*; however, it appears to lack an ORF encoding a nucleic-acid-binding homolog. The tentative name “papaya virus A” (PaVA) has been proposed for this virus.

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