

Molecular characterization of Morogoro maize-associated virus, a nucleorhabdovirus detected in maize (*Zea mays*) in Tanzania

David Alan Read, Jonathan Featherston, David Jasper Gilbert Rees, Genevieve Dawn Thompson, Ronel Roberts, Bradley Charles Flett, Kingstone Mashingaidze, Gerhard Pietersen, Barnabas Kiula, Alois Kullaya, Ernest R. Mbega

DOI//doi.org/10.1007/s00705-019-04212-1

Abstract

RNAseq of maize samples collected in Tanzania revealed the presence of a previously undescribed nucleorhabdovirus, tentatively named “Morogoro maize-associated virus” (MMaV), in three samples. The MMaV genome is 12,185-12,187 nucleotides long and shares a 69-70% nucleotide sequence identity with taro vein chlorosis virus. Annotation of the genomes showed a typical nucleorhabdovirus gene organization. PCR was unable to detect the same virus in the remaining 35 samples collected in the region.