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

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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.