

A novel monopartite begomovirus from Brazil with a broad and unconventional weed host range

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The family *Geminiviridae* comprises circular, single-stranded DNA (ssDNA) viruses that infect a wide range of plant species and pose a significant threat to agriculture. Rapid diagnosis and monitoring of emerging species are crucial for timely management strategies. Plant metagenomics via high-throughput sequencing (HTS) is an increasingly accessible and accurate tool for the detection of these viruses. This study investigated the presence and distribution of a novel begomovirus in leaf samples ($n=72$) from crops and associated weeds collected in the Central region of Brazil. Total DNA was extracted, enriched using Rolling Circle Amplification (RCA), pooled, and sequenced on the Illumina NovaSeq 6000 platform. De Novo Assembly using CLC Genomics Workbench v22.0.1 and Geneious[®] 11.1.5 yielded 34,995,926 reads and 212,435 contigs. A putative new begomovirus genome (2,631 nucleotides in length), sharing 89% nucleotide identity with *Tomato mottle leaf curl virus* DNA–A (ON419897) was recovered and tentatively designated *Begomovirus oleraceus*. Specific primers were designed to amplify the full genome, including restriction enzyme sites for molecular cloning and further infectivity assays in *Solanum* cultivars from Embrapa Hortaliças. PCR screening detected the virus in six of the 72 samples: DF–455 (*Leonotis* sp.), DF–539 (*Malva* sp.), DF–584 (*Oxalis* sp.), GO–585 (*Oxalis* sp.), GO–350 (*Commelina* sp.), and DF–010 (*Sonchus* sp.). Phylogenetic and recombination analyses are currently being performed to elucidate the evolutionary relationships and epidemiological relevance of this new virus.

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