Description of a new Fabaceae-infecting *Begomovirus* species in Central Brazil

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Members of the genus *Begomovirus* (family *Geminiviridae*) can infect a wide range of dicot and monocot hosts, including tomatoes (*Solanum lycopersicum*) and other vegetable crops as well as non-cultivated weed and native plants. These viruses display a remarkable ability for generating genetic variation through mutations, recombination, and pseudorecombination events. This diversity drives the emergence of new species and their adaptation to different hosts and environments. Elucidating the diversity and host range is essential for the analyses of epidemiological dynamics of the members from this group of pathogens. The present study aimed to catalog the diversity of *Begomovirus* species infecting non-cultivated plants associated with tomato fields, which may act as reservoirs of viruses from this crop in Brazil. Total DNA was extracted individually from 94 symptomatic foliar samples (from 11 botanical families). The DNA samples were subjected to Rolling Circle Amplification (RCA) pooled, and sequenced on the Illumina NovaSeq 6000. A total of 16,079,516 reads were obtained, from which 38,901 contigs were assembled, leading to the recovery of 153 virus-like genomes. Fourteen (14) contigs displayed nucleotide identities below 91% with previously characterized *Begomovirus* species. The Contig #16 exhibited 86% to identity to *Begomovirus solanumtenuimusivi* (GenBank accession EU710752). A specific primer pair (EAFC16/EARC16) was designed, and PCR assays confirmed the presence in a sample (DF–520) of a putative new *Begomovirus* species. The isolate DF–520 was collected from a symptomatic Fabaceae plant in Central Brazil. Complete genomic characterization of this novel virus is in progress. The detection of *Begomovirus* species in Fabaceae hosts reinforces the role of non-cultivated plants in maintaining viral diversity and facilitating the persistence and spread of diseases that might affect economically important crops.

Keywords: *Geminiviridae*, High Throughput Sequence, Polymerase Chain Reaction, Host range, tomatoes.

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