

Report of novel Euphorbiaceae and Fabaceae hosts of *Cnidoscolus* Mosaic Leaf Deformation Virus.

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Begomoviruses are widely distributed in Brazil and often infect both cultivated and native plants. Their high mutation and adaptation capacity enables frequent host shifts, as shown by previous studies on begomovirus diversity. This study aimed to detect *Cnidoscolus* mosaic leaf deformation virus (CnMLDV) in Brazil in order to evaluate host range and the potential risks that this virus may pose to economically important crops. Total DNA was individually extracted from 49 plant samples, enriched by Rolling Circle Amplification (RCA), pooled, and subjected to sequencing on the Illumina NovaSeq 6000 platform. Assembly generated 26,858,704 reads and 106,635 contigs. PCR using a CnMLDV-specific primer pair (CnMLDV-F/CnMLDV-R) confirmed the presence of CnMLDV in two samples: AL-006 from *Canavalia* sp. (Fabaceae) and AL-001 from *Manihot* sp. (Euphorbiaceae). Further purification, complete genome recovery, and molecular characterization of the viral DNA from these samples are underway. This was previously detected in Euphorbiaceae hosts, but it seems to be first report in members of the Fabaceae family. The detection of CnMLDV in *Manihot* sp. is particularly concerning, as it highlights the host-range plasticity and evolutionary potential of begomoviruses, including recombination and adaptation events that may facilitate future crop infections.

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