

## MALVAVISCUS YELLOW MOSAIC VIRUS, A BEGOMOVIRUS CARRYING A NANOVIRUS-LIKE NONANUCLEOTIDE AND A MODIFIED STEM-LOOP STRUCTURE

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### Resumo

Begomoviruses (family *Geminiviridae*) are whitefly-transmitted viruses with a circular, ssDNA genome encapsidated in twinned icosahedral particles. In Brazil, a high number of begomoviruses infecting non-cultivated plants have been described. These plants may act as natural begomovirus reservoirs and as sources of genetic variability. Here we describe a novel bipartite begomovirus infecting *Malvaviscus arboreus* (Malvaceae) plants showing a bright yellow mosaic, collected at Campinas, São Paulo state in May 2005 and Rio de Janeiro, Rio de Janeiro state in August 2009 and February 2011. Total DNA was extracted and the viral genome was amplified by RCA, cloned and sequenced. Sequence analysis indicated that the virus corresponds to novel species, for which the name Malvaviscus yellow mosaic virus (MalYMV) is proposed. Successful infection by biolistic of *Nicotiana benthamiana* and *Malvaviscus arboreus* was confirmed by PCR, RCA and Southern blot hybridization. Symptoms observed in infected *Malvaviscus arboreus* plants consisted in bright yellow mosaic while in *N. benthamiana* showed slight mosaic and leaf deformation. The progeny virus population present in biolistic infected plants was isolated and identity to the original isolate was confirmed by sequencing. Therefore, Koch's postulates were fulfilled. Strikingly, MalYMV has a nanovirus- and alphasatellite-like nonanucleotide (5'-TAGTATTAC-3'). Moreover, a short sequence located 5' of the nonanucleotide potentially forms a minor hairpin structure embedded in the major hairpin. Intramolecular interactions involving the sequence of the atypical nonanucleotide were predicted. To biologically characterize the replication origin of this distinct begomovirus, three different mutants were obtained. The mutant that rescues the begomovirus nonanucleotide (TAATATTAC) was able to infect *N. benthamiana* plants, showing that the point mutation at the nonanucleotide does not disrupt MalYMV replication. On the other hand, the short sequence located 5' of the nonanucleotide seems to be essential for infection. Although MalYMV has been collected in Brazil, it is phylogenetically closer to viruses from Central and North America. The *M. arboreus* plant at Campinas has been displaying the observed yellow mosaic symptoms since at least the 1960's, which suggests that MalYMV may be poorly transmitted (or not transmitted at all) by local whitefly populations.

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**Palavras-chaves:** Geminiviridae, Malvaceae, replication origin, hairpin structure