



## VIROLOGIA

1406

### **Molecular and biological characterization of a new Brazilian begomovirus, *Euphorbia* yellow mosaic virus (EuYMV), infecting *Euphorbia heterophylla* plants**

**Fernandes, F.R.<sup>1</sup>; Albuquerque, L.C. de<sup>1,4</sup>; Oliveira, C.L. de<sup>1,4</sup>; Cruz, A.R.R.<sup>3,4</sup>; Rocha, W.B. da<sup>1,5</sup>; Pereira, T.G.<sup>1,4</sup>; Naito, F.Y.B.<sup>1,4</sup>; Dias, N. de M.<sup>1,4</sup>; Nagata, T.<sup>4</sup>; Faria, J.C.<sup>6</sup>; Zerbini, F.M.<sup>2</sup>; Aragão, F.J.L.<sup>3</sup>; Inoue-Nagata, A.K.<sup>1,4</sup>**

<sup>1</sup>Embrapa Hortaliças; <sup>2</sup>Universidade Federal de Viçosa; <sup>3</sup>Embrapa Recursos Genéticos e Biotecnologia; <sup>4</sup>Universidade de Brasília; <sup>5</sup>Universidade Católica de Brasília; <sup>6</sup>Embrapa Arroz e Feijão. E-mail: fernanda@cnpq.embrapa.br

*Euphorbia heterophylla* is a native species present in the Americas, as well as other tropical regions around the world. To date, no begomovirus has been fully characterized from *E. heterophylla*. Here, we report the complete nucleotide sequence and host range of a new bipartite begomovirus infecting *E. heterophylla* in Brazil and its phylogenetic relationship with other isolates of *Euphorbia mosaic virus*. Ten samples of *E. heterophylla* plants exhibiting symptoms of begomovirus infection were collected in different locations at Goiás state and the Federal District from 2002 to 2009. Total DNA was isolated and the presence of a begomovirus was confirmed by PCR using the universal primers PAL1v1978/PAR1c496. Begomovirus genomic DNA was cloned using rolling-circle amplification. Inserts were sequenced and cognate components were identified based on their high sequence identity at the common region. To determine the host range and infectivity of the cloned viral DNAs, several plants were inoculated via particle bombardment. The 10 collected samples were PCR-positive, and 12 clones corresponding to full-length genomic components (nine DNA-A and three DNA-B), almost identical to each other, were obtained from all samples. The DNA-A sequences share a maximum nucleotide sequence identity of 87.3% with *Euphorbia mosaic Peru virus* (EuMPV), and thus were classified as a novel begomovirus species, tentatively named *Euphorbia yellow mosaic virus* (EuYMV). The EuYMV DNA-B sequences share a maximum nucleotide sequence identity of 56.2% with an *Euphorbia mosaic virus* (EuMV) isolate from Mexico. The clones were able to infect plants of three solanaceous species (*Datura stramonium*, *Nicotiana benthamiana* and *Capsicum annuum*), as well as the original host, *E. heterophylla* (fam. Euphorbiaceae). On *E. heterophylla* plants, the virus caused interveinal chlorosis, yellow mosaic and dwarfing, similar to field infected plants. Phylogenetic analysis demonstrated that this new virus belongs to a different lineage than EuMV isolates from Central America.

Hospedeiro: *Euphorbia heterophylla*

Patógeno: *Euphorbia* yellow mosaic virus (EuYMV)

Doença: virose

Área: Virologia