



Genome Sequence of *Euphorbia mosaic virus* from Passionfruit and *Euphorbia heterophylla* in Florida

J. E. Polston,^a M. A. Londoño,^{a*} A. L. Cohen,^{b*} M. Padilla-Rodriguez,^{b*} K. Rosario,^b M. Breitbart^b

Department of Plant Pathology, University of Florida, Gainesville, Florida, USA^a; College of Marine Science, University of South Florida, St. Petersburg, Florida, USA^b

ABSTRACT *Euphorbia mosaic virus* (EuMV) was found in a symptomatic passionfruit (*Passiflora edulis*) plant from Homestead, Florida, USA, as well as in the symptomatic weed *Euphorbia heterophylla*. This is the first identification of EuMV in Florida and the United States and the first report of a natural infection of passionfruit by EuMV.

Euphorbia mosaic virus (EuMV) is a species of *Begomovirus* (*Geminiviridae*), a taxon of plant viruses characterized by single-stranded circular DNA genomes (1). EuMV has a bipartite genome consisting of a DNA-A (2,609 to 2,615 nucleotides [nt]) and a DNA-B (2,571 to 2,590 nt).

DNA was extracted from the leaves of a passionfruit plant (*Passiflora edulis* Sims) showing symptoms of leaf distortion and necrotic spots (2). The leaves were collected in 1993 from Homestead, Florida, USA, desiccated, and stored at 4°C. A DNA-A (2,609 nt; KJ647290), and a DNA-B (2,545 nt; KJ647291) were cloned from *EcoRI* and *AvaI*-digestion of rolling-circle amplification products generated using random hexamers. Pairwise scores generated by the Species Demarcation Tool (SDT) indicated that the DNA-A and the DNA-B had the greatest similarity, 98.6% and 97.2%, respectively, to the DNA-A and the DNA-B of EuMV-[CU:Hav:27:07] obtained from *Euphorbia heterophylla* L. in Cuba (HQ896201, HQ896201) (3, 4). The common regions of the DNA components (344 nt) were 97% identical, indicating that these constitute an isolate of *Euphorbia mosaic virus* (EuMV-[US:Fl:PF:313:1993]).

Samples of *E. heterophylla* plants showing symptoms of bright foliar mosaic were collected from Homestead, Florida, in 2013. A DNA-A (2,609 nt; JQ963887) and a DNA-B (2,585 nt; JQ963888) were obtained through cloning and sequencing of *XmnI*-digested rolling-circle amplification products generated using random hexamers. SDT pairwise scores indicated that the DNA-A and the DNA-B had their highest identities, 98.8% and 98.1%, respectively, with those of EuMV-[US:Fl:PF:313:1993]. The common regions of the components (341 nt) were 97% identical, indicating that these constitute a bipartite begomovirus, designated EuMV-[US:Fl:Eu4]. The B component sequences differed in size due to a 40-nt deletion near the iterons in EuMV-[US:Fl:PF:313:1993]. While the presence of a begomovirus in symptomatic *E. heterophylla* has been known in Homestead, Florida, for many years (5), EuMV is the first virus to be associated with those disease symptoms.

DNA-A and DNA-B clones of EuMV-[US:Fl:PF:313:1993] were successfully inoculated to passionfruit 'Liliko'i' and *Phaseolus vulgaris* 'Topcrop' (6). Symptoms in *P. edulis* began as a mild mottling followed by necrotic spots, leaf deformation, and flower abortion. These symptoms are similar to those described for *Passionfruit severe leaf distortion virus* (from Brazil) but different from those of two other partially characterized begomoviruses (7–9). Symptoms in *P. vulgaris*, severe leaf distortion and stunting, were similar to

Received 19 December 2016 **Accepted** 23 December 2016 **Published** 2 March 2017

Citation Polston JE, Londoño MA, Cohen AL, Padilla-Rodriguez M, Rosario K, Breitbart M. 2017. Genome sequence of *Euphorbia mosaic virus* from passionfruit and *Euphorbia heterophylla* in Florida. *Genome Announc* 5: e01714-16. <https://doi.org/10.1128/genomeA.01714-16>.

Copyright © 2017 Polston et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to J. E. Polston, jep@ufl.edu.

* Present address: M. A. Londoño, Universidad Distrital Francisco José de Caldas, Bogotá, Colombia; A. L. Cohen, Department of Microbiology and Immunology, University of California, San Francisco, San Francisco, California, USA; M. Padilla-Rodriguez, Department of Cellular and Molecular Medicine, University of Arizona, Tucson, Arizona, USA.

those described for EuMV-YP from Mexico (10). Whitefly adults (*Bemisia tabaci* Genn. MEAM1) successfully transmitted EuMV from bean to bean, but not from passionfruit to either bean or passionfruit (11). *P. edulis* has been reported to be a poor colonization host for the MEAM1 whitefly (12).

Surveys of passionfruit in Homestead, Florida, from 2011 to 2012 failed to identify any EuMV-infected passionfruit plants, although EuMV-infected *E. heterophylla* plants with whiteflies were readily found. EuMV-[US:Fl:PF:313:1993] may have been transmitted from *E. heterophylla* to passionfruit by a whitefly that was later displaced by *B. tabaci* MEAM1, which first appeared in Florida in the mid-1980s (13, 14).

To our knowledge, this is the first report of EuMV as the causal agent of a disease in passionfruit and the first report of EuMV in the United States.

Accession number(s). The sequences of EuMV-[US:Fl:PF:313:1993] were deposited in GenBank under the accession numbers [KJ647290](#) and [KJ647291](#) (DNA-A and DNA-B, respectively), and the sequences of EUMV-[US:Fl:Eu4] were deposited in GenBank under the accession numbers [JQ963887](#) and [JQ963888](#).

ACKNOWLEDGMENT

We thank H. Capobianco for technical assistance.

REFERENCES

- King AMQ, Adams MJ, Carstens EB, Lefkowitz EJ. 2011. Virus taxonomy: 9th report of the International Committee on Taxonomy of Viruses. Academic Press/Elsevier, London.
- Polston JE, Londoño MA, Capobianco H. 2014. The complete genome sequence of the New World jatropha mosaic virus. *Arch Virol* 159: 3131–3136. <https://doi.org/10.1007/s00705-014-2132-1>.
- Muhire BM, Varsani A, Martin DP. 2014. SDT: A virus classification tool based on pairwise sequence alignment and identity calculation. *PLoS One* 9:e108277. <https://doi.org/10.1371/journal.pone.0108277>.
- Fiallo-Olivé E, Navas-Castillo J, Moriones E, Martínez-Zubiaur Y. 2012. Begomoviruses infecting weeds in Cuba: increased host range and a novel virus infecting *Sida rhombifolia*. *Arch Virol* 157:141–146. <https://doi.org/10.1007/s00705-011-1123-8>.
- Kim KS, Fulton RW. 1984. Ultrastructure of *Datura stramonium* infected with an euphorbia virus suggestive of a whitefly-transmitted geminivirus. *Phytopathology* 74:236–241. <https://doi.org/10.1094/Phyto-74-236>.
- Guenoune-Gelbart D, Sufrin-Ringwald T, Capobianco H, Gaba V, Polston JE, Lapidot M. 2010. Inoculation of plants with begomoviruses by particle bombardment without cloning: using rolling circle amplification of total DNA from infected plants. *J Virol Methods* 168:87–93. <https://doi.org/10.1016/j.jviromet.2010.04.022>.
- Ferreira SS, Barros DR, de Almeida MR, Zerbini FM. 2010. Characterization of passionfruit severe leaf distortion virus, a novel begomovirus infecting passionfruit in Brazil, reveals a close relationship with tomato-infecting begomoviruses. *Plant Pathol* 59:221–230. <https://doi.org/10.1111/j.1365-3059.2009.02205.x>.
- Brown JK, Bird J, Fletcher DC. 1993. First report of passiflora leaf mottle disease caused by a whitefly-transmitted geminivirus in Puerto Rico. *Plant Dis* 77:1264. <https://doi.org/10.1094/PD-77-1264C>.
- Novaes QS, Freitas-Astua J, Yuki VA, Kitajima EW, Camargo LEA, Rezende JAM. 2003. Partial characterization of a bipartite begomovirus infecting yellow passion flower in Brazil. *Plant Pathol* 52:648–654. <https://doi.org/10.1046/j.1365-3059.2003.00878.x>.
- Hernández-Zepeda C, Idris AM, Carnevali G, Brown JK, Moreno-Valenzuela OA. 2007. Molecular characterization and experimental host range of euphorbia mosaic virus-Yucatan Peninsula, a begomovirus species in the *Squash leaf curl virus* clade. *Plant Pathol* 56:763–770. <https://doi.org/10.1111/j.1365-3059.2007.01652.x>.
- Polston JE, Capobianco H. 2013. Transmitting plant viruses using whiteflies. *J Vis Exp* 81:e4332. <https://doi.org/10.3791/4332>.
- Nunes ES, Brown JK, Moreira AG, Watson G, Lourenção AL, Piedade SMS, Rezende JAM, Vieira ML. 2008. First report and differential colonization of *Passiflora* species by the B biotype of *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) in Brazil. *Neotrop Entomol* 37:744–746. <https://doi.org/10.1590/S1519-566X2008000600021>.
- Hoelmer KA, Osborne LS, Yokomi RK. 1991. Foliage disorders in Florida associated with feeding by sweetpotato whitefly, *Bemisia tabaci*. *Fla Entomol* 74:162–166. <https://doi.org/10.2307/3495258>.
- McKenzie CL, Hodges G, Osborne LS, Byrne FJ, Shatters RG, Jr. 2009. Distribution of *Bemisia tabaci* (Hemiptera: Aleyrodidae) biotypes in Florida—investigating the Q invasion. *J Econ Entomol* 102:670–676. <https://doi.org/10.1603/029.102.0227>.