Diseases Caused by Viruses

Macroptilium erythroloma (Fabaceae): A Natural Weed Host of Bean Golden Mosaic Virus in Brazil

J. G. Batista,¹ R. C. Pereira-Carvalho,^{1,†} M. F. Malheiros,¹ D. V. Rezende,¹ L. N. A. Reis,¹ M. E. N. Fonseca,² and L. S. Boiteux²

¹ Plant Pathology Department, Universidade de Brasília (UnB), Brasília–DF, Brazil

² National Center for Vegetable Crops Research (CNPV), Embrapa Hortaliças, Brasília–DF, Brazil

Funding: This research had financial support from grants from Empresa Brasileira de Pesquisa Agropecuária, Fundação de Apoio à Pesquisa do Distrito Federal, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior, and Conselho Nacional de Desenvolvimento Científico e Tecnológico. Plant Dis. 104:3270, 2020; published online as <https://doi.org/10.1094/PDIS-12-19-2669-PDN>. Accepted for publication 18 July 2020.

Bean golden mosaic virus (BGMV) is a widely distributed *Begomovirus* species (family *Geminiviridae*) responsible for severe yield losses in the bean (*Phaseolus vulgaris* L.) crop in Brazil. Isolates of BGMV infecting cultivated as well as weed hosts have been also reported (Bracero et al. 2003; Sobrinho et al. 2014). *Macroptilium erythroloma* ([Mart. ex Benth.] Urban) leaves displaying golden mosaic-like symptoms were collected from the Brasília–DF area in 2016. Total DNA extraction was performed from three symptomatic plants using a CTAB protocol (Boiteux et al. 1999). Sanger dideoxy sequencing of the maturase (*matK*) gene (99.11% identity) and morphological analyses confirmed the symptomatic plants as being *M. erythroloma*. Purified DNA was also submitted to rolling circle amplification (Inoue-Nagata et al. 2004) and sequenced on an Illumina HiSeq 2500 platform (Macrogen, South Korea). Sequence analysis of the isolate RDF_327 JB_09 was performed in the CLC Genomics Workbench program after manually refining and assembling the reads in higher quality contigs. Contigs were imported into the Geneious software and compared via the BLASTn algorithm to a GenBank viral database. The Illumina-derived viral contigs for full-length DNA-A from symptomatic *M. erythroloma* (MN822294) displayed high identity levels ($\approx 99\%$) with DNA-A components from an array of BGMV isolates. This DNA-A sequence was also obtained by direct Sanger dideoxy sequencing of overlapping PCR amplicons employing a primer walking strategy. The final sequence (MT319763) was identical to the original Illumina-derived contigs and displayed nucleotide identities above 99% with a collection of BGMV isolates from common beans (e.g., KJ939798) and *M. lathyroides*

(e.g., KJ939766), indicating the absence of artifactual chimeric sequences. The 2,617 nt of the DNA-A component displayed all six open reading frames (ORFs): AV1 (CP) in the viral sense, and AC1 (Rep), AC2 (TrAP), AC3 (Ren), AC4, and AC5 in the complementary sense. The contigs for full-length DNA-B (MN822293) displayed 98.2% identity to one bean BGMV isolate from Minas Gerais State, Brazil (MG334553). The 2,594 nt of the DNA-B component displayed two ORFs: BV1 (NSP) in the viral sense and BC1 (MP) in the complementary sense. Plants of bean (*P. vulgaris* cv. Carioca), soybean (*Glycine max* cv. Monsoy 9144), peanut (*Arachis hypogaea* cv. BRS Havana), cowpea (*Vigna unguiculata* cv. Seridó), and tomato (*Solanum lycopersicum* cv. Santa Clara) were employed in infectivity assays. One week before, a BGMV-infected *M. erythroloma* plant (one of the plants previously employed in the molecular BGMV characterization) was caged with aviruliferous adults of *Bemisia tabaci* MEAM 1. These whiteflies were subsequently transferred to cages with five plants of each plant species. Noninoculated plants of each species were employed as negative controls (i.e., BGMV-free plants of bean, soybean, cowpea, and tomato that were exposed to aviruliferous adult whiteflies). One apical leaf sample per test plant was collected at 21 days after inoculation, and the presence of BGMV was studied employing PCR assays with specific primers. PCR results indicated that BGMV isolate from *M. erythroloma* was transmitted to all five plant species. In the genus *Macroptilium*, BGMV has been reported thus far infecting only the species *M. lathyroides* (L.) Urban (Bracero et al. 2003; Sobrinho et al. 2014). However, *M. erythroloma* was assigned in the early 1980s as a putative BGMV host based solely upon symptoms and biological tests (Chagas et al. 1981). Therefore, we provide here the first formal confirmation of *M. erythroloma* as a natural BGMV host. The BGMV isolate from *M. erythroloma* was able to infect accessions of bean, soybean, peanut, cowpea, and tomato under our experimental conditions. Therefore, the presence of *Macroptilium* weeds in association with commercial bean fields might be a major epidemiological concern, because they may serve as year-round sources of BGMV inoculum for this crop.

References:

- Boiteux, L. S., et al. 1999. J. Am. Soc. Hortic. Sci. 124:32.
- Bracero, V., et al. 2003. Plant Dis. 87:1022.
- Chagas, C. M., et al. 1981. Arq. Inst. Biol. (Sao Paulo) 48:113.
- Inoue-Nagata, A. K., et al. 2004. J. Virol. Methods 116:209.
- Sobrinho, R. R., et al. 2014. J. Gen. Virol. 95:2540.

The author(s) declare no conflict of interest.

Keywords: virus, BGMV, *Macroptilium erythroloma*, pathogen detection, etiology

[†]Indicates the corresponding author.

E-mail: carvalhorcp@gmail.com (R.C.P.-C.)