

# Complete Sequence of a New Bipartite Begomovirus Infecting Cotton Plants in Brazil

Mariana Martins Severo de Almeida,<sup>a</sup> Sona Jain,<sup>b</sup> Paulo Augusto Vianna Barroso,<sup>c</sup> Lúcia Vieira Hoffmann,<sup>c</sup> Monaliza Gomes de Lucena,<sup>d</sup> Renato de Oliveira Resende,<sup>a</sup> Alice Kazuko Inoue-Nagata<sup>a,e</sup>

Universidade de Brasília, Brasília, Brazil<sup>b</sup>; Universidade Federal de Sergipe, São Cristóvão, Brazil<sup>b</sup>; Embrapa Cotton, Santo Antônio de Goiás, Goiás, Brazil<sup>c</sup>; Universidade Estadual da Paraíba, Paraíba, Brazil<sup>d</sup>; Embrapa Vegetables, Brasília, Brazil<sup>e</sup>

**Begomoviruses are plant viruses responsible for severe losses in important crops, such as beans, cassavas, tomatoes, and cotton, around the world. Here, we report the first full-genome sequence of a bipartite begomovirus species collected from cotton plants in Brazil.**

Received 28 July 2013 Accepted 4 October 2013 Published 7 November 2013

**Citation** de Almeida MMS, Jain S, Barroso PAV, Hoffmann LV, de Lucena MG, Resende RDO, Inoue-Nagata AK. 2013. Complete sequence of a new bipartite begomovirus infecting cotton plants in Brazil. *Genome Announc.* 1(6):e00661-13. doi:10.1128/genomeA.00661-13.

**Copyright** © 2013 de Almeida et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Alice Kazuko Inoue-Nagata, [alice.nagata@embrapa.br](mailto:alice.nagata@embrapa.br).

The begomoviruses (family *Geminiviridae*, genus *Begomovirus*) are circular single-stranded plant DNA viruses, encapsidated in icosahedral geminate particles, and are 18 by 30 nm. The viral genome is characterized by one (monopartite) or two (bipartite) (DNA-A and DNA-B) segments each around 2.6 kb in length. Although begomoviruses are particularly devastating to cotton plants in Asia (1–3), no such reports have been observed in Brazil.

Five cotton plants exhibiting chlorotic spots, interveinal chlorosis, and leaf distortion were collected at Paraíba state in 2009. The begomovirus infection was confirmed by PCR using the universal primers PAL1v1978 and PAR1c496 (4). The full length DNA-A and DNA-B genomes were cloned into pBlueScript vector (Stratagene, La Jolla, California) after rolling circle amplification (5) and digestion with the single cutting enzyme XbaI. Sequencing was performed at Macrogen, Inc. (South Korea) by primer walking. The contigs were assembled using the Staden 4 package (6), and the pairwise distances were calculated by MEGA 5 (7).

From a total of five samples, three similar clones corresponding to the DNA-A segment and six similar clones corresponding to the DNA-B were obtained, and the clones B012-6 and B012-2, corresponding to DNA-A and DNA-B, respectively, from sample B012 were chosen for further analysis. The cloned DNA-A and DNA-B genomes are 2,670 and 2,650 nucleotides long, respectively. They share a common region (CR) of 247 nucleotides with 98% identity, indicating that they are possibly cognate DNA segments of the same virus. The CR of both components contains the known nonanucleotide sequence TAATATTAC that is conserved in geminiviruses. They also contain the likely iteron sequence GGAGT and a G-rich region sequence, known as the “G box.” The genome organization is identical to that of other bipartite begomoviruses.

The DNA-A sequence of this virus, named cotton chlorotic spot virus (CCSV), shares 77.8% nucleotide identity with tomato common mosaic virus (ToCMV) (accession no. NC\_018350), the most related begomovirus, and the DNA-B shares 67.8% nucleotide identity with tomato yellow vein streak virus (ToYVSV) (accession no. NC\_010950).

**Nucleotide sequence accession numbers.** The nucleotide sequences have been deposited into GenBank under the accession no. [KF358470](https://www.ncbi.nlm.nih.gov/nuclot/KF358470) and [KF358471](https://www.ncbi.nlm.nih.gov/nuclot/KF358471).

## ACKNOWLEDGMENTS

This research was sponsored by Embrapa and CNPq. A.K.I.-N. and R.D.O.R. are CNPq fellows.

## REFERENCES

1. Briddon RW. 2003. Cotton leaf curl disease, a multicomponent begomovirus complex. *Mol. Plant Pathol.* 4:427–434.
2. Briddon RW, Markham PG. 2000. Cotton leaf curl virus disease. *Virus Res.* 71:15–159.
3. Mansoor S, Bedford I, Pinner MS, Stanley J, Markham PG. 1993. A whitefly-transmitted geminivirus associated with cotton leaf curl disease in Pakistan. *Pak. J. Bot.* 25:105–107.
4. Rojas MR, Gilbertson RL, Russel DR, Maxwell DP. 1993. Use of degenerate primers in the polymerase chain reaction to detect whitefly-transmitted geminiviruses. *Plant Dis.* 77:340–347.
5. Inoue-Nagata AK, Albuquerque LC, Rocha WB, Nagata T. 2004. A simple method for cloning the complete begomovirus genome using the bacteriophage  $\phi$ 29 DNA polymerase. *J. Virol. Methods* 116:209–211.
6. Staden R. 1996. The staden sequence analyzes package. *Mol. Biotechnol.* 5:233–241.
7. Tamura K, Peterson D, Peterson N, Stencher G, Nei M, Kumar S. 2011. MEGA5: molecular evolution genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Mol. Biol. Evol.* 28:2731–2739.