First report of Corchorus golden mosaic virus (CoGMV) infecting ramie (Boehmeria nivea) in India

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DISEASE NOTES

First Report of *Corchorus golden mosaic virus*(CoGMV) Infecting Ramie (*Boehmeria nivea*) in India

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ABSTRACT

Ramie (*Boehmeria nivea*) is a perennial herbaceous plant that produces strong and lustrous bast fiber. It is native to East Asia and is mainly grown in China, India, Taiwan, Philippines, Thailand, Brazil, and South Korea (Sarkar et al. 2012). In May 2013, ramie plants exhibiting yellow mosaic symptoms were noted in experimental fields of the CRIJAF research farm, Barrackpore, India. In young green leaves, vein-clearing was prominent, whereas older leaves showed complete yellowing. Plants were stunted and bushy. The incidence of the disease varied from 2 to 10%. Five symptomatic and five asymptomatic samples were collected from the field and DNA was extracted using the CATB method (Biswas et al. 2013). DNA samples were tested for begomovirus infection by PCR using universal primer pair PAL1v1978B/PAR1c715H (Rojas et al. 1993). Only the symptomatic samples showed amplification of a 1.5-kb product suggesting that plants were infected by a begomovirus. Furthermore, circular DNA was amplified by rolling circle amplification (RCA) with Illustra TempliPhi Kit (GE Healthcare, UK) according to the manufacturer's instructions. RCA product was digested with *EcoRI*, *BamHI*, *EcoRI*, *KpnI*, *Hind III*, and *PstI*(New England Biolabs) respectively. The fragments of 2.1 kbp (with *BamHI* digestion) and 1.5 kbp (with *KpnI* digestion) were cloned and sequenced. The sequence of the 2.1-kbp fragment showed similarity with published sequences of begomovirus DNA-A component. From the 2.1-kbp sequence, a pair of primers was designed to obtain full-length DNA-A component, namely JAF1 (5′-CTTCATCGTTTCTCAGCATCAT-3′) and JAR1 (5′-CACTTGCACACGATCTCTAAGA-3′). The full-length DNA-A was 2686 bp nucleotides and encoded six putative ORFs (GenBank Accession No. KF962542). The sequence of the 1.5-kbp fragment shared similarity with DNA-B. The begomoviral circular DNA-B was amplified using the pair of primers JBF1 (5′-GTAACACCCGAAGTGCACG-3′) and JBR1 (5′-AAAGGAGAGACACCAGTCTGCC-3′) designed from the 1.5-kbp sequence. PCR yielded a full-length DNA-B sequence of 2666 bp nucleotides and encoded two putative ORFs (GenBank Accession No. KF962543). BLASTn analysis revealed that DNA-A from the ramie begomovirus isolate has 100% nucleotide sequence identity with the complete sequence of DNA-A component of *Corchorus golden mosaic virus* (Accession No. FJ463902). Similarly, DNA-B also has 100% identity with complete sequence of CoGMV DNA-B component (Accession No. FJ455448). Based on BLASTn analysis and sequence analysis using MEGALIGN (DNASTAR), the virus causing symptoms in ramie appears to be CoGMV, which is a New World begomovirus from the Old World infecting jute (*Corchorus capsularis*) (Ha et al. 2006). To our knowledge, this is the first report that CoGMV infects

ramie plants. The incidence of CoGMV in ramie is relatively low, but in the future it may negatively affect the yield.

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