Diseases Caused by Viruses

First Report of *Bean common mosaic virus* Infecting Heavenly Bamboo (*Nandina domestica*) in China

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Heavenly bamboo (*Nandina domestica*) is an evergreen ornamental plant with worldwide distribution. In May 2018, seven out of 20 *N. domestica* plants showing virus-like symptoms, such as yellow mosaic and curling, were observed in Lin'an, Zhejiang province. To determine the causal agent, a small RNA library was constructed using the Small RNA v1.5 Sample Prep Kit (Illumina, San Diego, CA) with total RNA extracted from leaves of a symptomatic plant. The library was sequenced by the Solexa platform at BGI Genomics (Shenzhen, China). A total number of 21,071,675 high-quality reads of 17 to 28 nucleotides (nt) in length remained after trimming adapter sequences and quality control. Reads were assembled using Velvet 0.7.31 and Oases 0.2.07 with the *k-mer* value of 17 (Schulz et al. 2012). BlastN and BlastX search against the GenBank viral nonredundant sequence databases revealed 56 contigs homologous to bean common mosaic virus (BCMV; genus *Potyvirus*, family *Potyviridae*). No contig homologous to the genomic sequence of other plant-infecting viruses was identified. These contigs were further assembled into a 9,315-nt fragment by SeqMan Pro 7.1.0 in Lasergene package (DNASTAR, Madison, WI), which covered 92.68% of the genome of BCMV strain CT (BCMV-CT; GenBank accession no. KM076650). The genome of this BCMV isolate (BCMV-NTZ1) was amplified by reverse transcription polymerase chain reaction (RT-PCR) and rapid amplification of cDNA ends (RACE) using primers designed based on assembled contigs with the Phusion High-Fidelity DNA Polymerase (New England Biolabs, Beijing, China) and

the FirstChoice RLM-RACE Kit (Invitrogen, Carlsbad, CA), respectively. Amplicons were cloned and Sanger sequenced with three independent clones per amplicon. The genome is 10,052 nt in length excluding the poly-A tail (GenBank accession no. MZ670770) and shared the highest nt sequence identities with BCMV-CT (88.46%). The putative polyprotein shared 93.36% amino acid (aa) sequence identity with that of BCMV-CT. BCMV-NTZ1 also clustered with BCMV-CT in phylogenetic trees based on BCMV full genomes and aa sequences of coat protein. Five-leaf-stage seedlings of *Nicotiana tabacum*, *N. benthamiana*, *Glycine max* (L.) Merr., and *Capsicum frutescens* were mechanically inoculated with sap of BCMV-infected *N. domestica* leaves at 15 plants per species. Seedlings of *G. max* developed virus-like (mosaic and leaf deformity) symptoms (7/15) at 15 days postinoculation, whereas other plants remained symptomless throughout the experiment. Subsequent RT-PCR on all the plants using primers 27F1/14Rter and sequencing confirmed the presence and absence of BCMV-NTZ1 in all symptomatic *G. max* seedlings and other asymptomatic indicator plants, respectively. Subsequent RT-PCR survey further confirmed the association of BCMV with symptomatic heavenly bamboo samples but not asymptomatic plants (7/20). To the best of our knowledge, this is the first report of BCMV naturally infecting heavenly bamboo in China. *N. domestica* is susceptible to many viruses (e.g., cucumber mosaic virus, Plan-tago asiatica mosaic virus, nandina stem pitting virus, apple stem grooving virus, and alternanthera mosaic virus) (Ahmed et al. 1983; Barnett et al. 1973; Hughes et al. 2002, 2005; Tang et al. 2010; Wei et al. 2015). Our results indicate that *N. domestica* can also serve as an overwinter reservoir for BCMV, and special attention should be paid to the damage it may cause.

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