First report of cucumber mosaic virus infecting bahizi (*Angelica dahurica*) in China

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Baizhi (*Angelica dahurica*, family Apiaceae), an important traditional medicine, is widely planted in China, Korea and Japan. Tobacco ringspot virus and angelica bushy stunt virus have been reported to infect baizhi (Lim et al. 2017; Wei and Wu 1988). In May 2018, baizhi with ringspot and chlorotic spot symptoms was found in Haidian District of Beijing, China. To identify the causal agent(s), total RNA was extracted from the symptomatic leaves using mirVana miRNA isolation kit (Ambion, Austin, USA) according to manufacturer's instructions. Small RNA library was prepared using TruSeq small RNA library preparation kit (Illumina, San Diego, USA) and sequenced from both ends (paired-end) on an Illumina HiSeq 2500 platform. The sequence reads were assembled using Velvet algorithms with a *k*-mer of 19 and a total of 47 assembled contigs ranging from 82 to 107 bp were obtained. Then, the assembled contigs were annotated against the GenBank Virus Reference Database annotated using a local BLASTn program. Analysis results revealed 19 contigs shared high nucleotide sequence identity (86%–99%) with cucumber mosaic virus (CMV) from the genus *Cucumovirus*, family *Bromoviridae*. To confirm the high-throughput sequencing results, RT-PCR was performed with CMV-specific primers (CMVCPf: 5'- ATGGACAAATCTGA ATCAACCA-3' /CMVCPr: 5'-TCAGACTGGGAGCA

CCCCAGACGT-3'). A fragment of 657 bp (GenBank accession No. MN557856) was obtained. Sequencing and BLASTn analysis revealed that this fragment included complete coat protein gene and shared 99.54% nucleotide identity and 98.62% amino acid identity with CMV isolate HX from *Agastache rugosa* in China (MG754206). To our knowledge, this is the first report of CMV infecting *A. dahurica*.

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