



First report of tomato yellow Leaf curl virus and cucumber mosaic virus infecting Huoxiang (*Agastache rugosa*) in CHINA

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Abstract

Huoxiang (*Agastache rugosa*, family Labiatae) is used as a traditional Chinese medicine. In 2017, Huoxiang with stunted, chlorotic, and mosaic symptoms were found in Haidian District of Beijing, China. To identify the causal agent(s), total RNA of symptomatic leaves was extracted and further analyzed by high-throughput sequencing (HTS). Sequence analyses revealed nine contigs with high nucleotide sequence identity (93%–100%) with tomato yellow leaf curl virus (TYLCV) from the genus *Begomovirus*, family *Geminiviridae* and seventeen contigs with high nucleotide sequence identity (85%–100%) with cucumber mosaic virus (CMV) from the genus *Cucumovirus*, family *Bromoviridae*. To confirm the HTS results, RT-PCR was performed with TYLCV-specific primers and CMV-specific primers, respectively. Two fragments of 651 bp (GenBank accession No. MG775386) and 657 bp (MG754206) were obtained, respectively. Sequencing and BLASTn analysis revealed that the 651 bp fragment shared 100% nucleotide identity with TYLCV isolate ZJHZ (MF590742), and the 657 bp fragment shared 98.9% nucleotide identity with CMV strain K (AF127977). To our knowledge, this is the first report of TYLCV and CMV infecting *A. rugosa*.

Keywords Huoxiang · Tomato yellow leaf curl virus · Cucumber mosaic virus · High-throughput sequencing · RT-PCR

Huoxiang (*Agastache rugosa*, family Labiatae) is used as a traditional Chinese medicine. In May 2017, Huoxiang with stunted, chlorotic, and mosaic symptoms were found in Haidian District of Beijing, China. To identify the causal agent(s), total RNA was extracted from the symptomatic leaves using TRNzol reagent (Tiangen, Beijing, China) according to manufacturer's instructions and further analyzed by high-throughput sequencing (HTS) on an Illumina HiSeq 2500 platform. The sequence reads were assembled using Velvet algorithms and annotated using a local BLASTn program. Sequence analyses revealed nine contigs with high nucleotide sequence identity (93%–100%) with tomato yellow leaf curl virus (TYLCV) from the genus *Begomovirus*, family *Geminiviridae* and seventeen contigs with high nucleotide sequence identity (85%–100%) with cucumber mosaic virus (CMV) from the genus *Cucumovirus*, family *Bromoviridae*. TYLCV and CMV cause serious disease in many economically important crops and have a wide host range (Jacquemond 2012;

Moriones and Navas-Castillo 2000). To confirm our HTS results, RT-PCR was performed with TYLCV-specific primers (TY315F: 5'-GCGACCAGGCGATATAATCATT-3' / TY947R: 5'-TTGGCTGCCTCCTGATGATT-3') and CMV-specific primers (CMVCPf: 5'-ATGGACAAATCTGATCAACCA-3' / CMVCPr: 5'-TCAGACTGGGAGCA CCCAGACGT-3'), respectively. Two fragments of 651 bp (GenBank accession No. MG775386) and 657 bp (MG754206) were obtained, respectively. Sequencing and BLASTn analysis revealed that the 651 bp fragment shared 100% nucleotide identity with TYLCV isolate ZJHZ (MF590742), and the 657 bp fragment shared 98.9% nucleotide identity with CMV strain K (AF127977). To our knowledge, this is the first report of TYLCV and CMV infecting *A. rugosa*.

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