Diseases Caused by Viruses

First Report of *Capsicum chlorosis virus* Infecting *Chromolaena odorata* in Yunnan, China

Lu Chen,^{1,2} Jianwei Guo,³ Rex Frimpong Anane,^{4,5} Zhe Wang,^{1,2} Zeli Chen,^{2,6} Like Gao,^{1,2} Guosong Wen,^{2,6} and Mingfu Zhao^{1,2,†}

¹ Key Laboratory for Agricultural Biodiversity for Pest Management of China, Ministry of Education, Yunnan Agricultural University, Kunming 650201, Yunnan, China

² Research & Development Center for Health Product, College of Agronomy and Biotechnology, Yunnan Agricultural University, Kunming 650201, Yunnan, China

³ Honghe Innovation Center for Mountain Futures, Kunming Institute of Botany, Chinese Academy of Sciences, Honghe County 654400, Yunnan, China

⁴ Center for Excellence in Animal Evolution and Genetics, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming 650223, Yunnan, China

⁵ State Key Laboratory for Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming 650223, Yunnan, China

⁶ College of Agronomy and Biotechnology, Yunnan Agricultural University, Kunming 650201, Yunnan, China

Lu Chen and Jianwei Guo equally contributed to this study.

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Capsicum chlorosis virus (CaCV) is a negative sense ssRNA virus belonging to the genus *Orthospovirus* in the family *Tospoviridae*. It was first discovered in Australia, and then reported in other places including Thailand, China, India, Greece, and the United States (Abudurexiti et al. 2019; Melzer et al. 2014; Orfanidou et al. 2018; Zheng et al. 2011). CaCV infects plants of the families Amaranthaceae, Apocynaceae, Chenopodiaceae, Cucurbitaceae, Amaryllidaceae, Fabaceae, and Solanaceae (Basavaraj et al. 2017, 2020). *Chromolaena odorata* L. (commonly known as Feiji cao in China) is an invasive weedy herb (family Asteraceae) and is native to Central America. In May 2020, serrated chlorotic rings and chlorotic ringspots resembling symptoms of orthospovirus infection was observed on the leaves of *C. odorata* plants in Honghe County, Yunnan. Three symptomatic leaf samples were collected, and double antibody sandwich enzyme-linked immunosorbent assay (DAS-ELISA) was performed using antisera targeting tomato spotted wilt virus (TSWV), calla lily chlorotic spot virus (CCSV), Capsicum chlorosis virus (CaCV), and tomato zonate spot virus (TZSV) (Proteintech Group, Inc., China). Buffer solution and healthy leaves were used as a blank and negative controls, respectively. All three symptomatic

samples showed positive reactions with only CaCV antiserum (OD₄₅₀ of 0.315 to 0.345 relative to 0.078 and 0.076 for healthy plants and the blank control, respectively). The total RNA extracted from the positive samples were further analyzed by reverse transcription (RT)-PCR using generic primers gL3637 (CCTTTAACAGTDGAAACAT) and gL4435c (CATDGCRCAGARTGRTARACAGA), which were designed to amplify the partial L segment encoding the RNA-dependent RNA polymerase (RdRP) of orthospoviruses (Chu et al. 2001). The expected ~800 bp DNA fragment was amplified from all three positive samples by RT-PCR. The amplified DNA fragments were cloned and sequenced. BLAST search of the sequenced partial L RNA sequences (GenBank accession nos. MW964378 to MW964380) revealed that they shared 86.2 to 97.4% nucleotide (nt) and 97.2 to 100% amino acid (aa) sequence identities with different isolates of CaCV available in GenBank, with CaCV chili isolates (KU941834 to KU941836) from India sharing the highest aa identity of 100%. This confirmed the presence of CaCV in the symptomatic *C. odorata* plants. The 825 bp complete nucleocapsid protein (NP) of CaCV was also amplified from the samples using primers CaCV-F: ATGTCTAMCGTYAGGCAAC and CaCV-R: TYACACYTCWATAGAWGTACTAG (Basavaraj et al. 2020), cloned, and sequenced to obtain complete S fragment-nucleocapsid protein (NP) with a size of 825 bp (MW964381 to MW964383). The pairwise comparisons of three fragments showed 85.1 to 98.3% nt and 87.6 to 99.6% aa sequence identities with different isolates of CaCV. Maximum likelihood phylogenetic trees inferred from the partial RdRP and complete NP aa sequences showed that the *C. odorata* isolates (CaCV-YN) clustered closely with CaCV tomato isolate from Taiwan and tomato (Yuxi-2013) isolate from China, respectively. To our knowledge, this is the first time CaCV has been detected in *C. odorata*. This study will serve as an important reference for the study of host range of CaCV. Further studies will be required to determine whether thrips could transmit CaCV between *C. odorata* and other hosts of the virus.

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[†]Indicates the corresponding author.
M. Zhao; zhaomingfu@163.com