First Report of Pea as a Natural Host of *Tomato mottle mosaic virus* in China

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Tomato mottle mosaic virus, a new species in the genus *Tobamovirus* and family *Virgaviridae*, was first reported on tomato in Mexico in 2013 (Li et al. 2013). Subsequently, tomato mottle mosaic virus (ToMMV) was found infecting pepper and eggplant in China (Chai et al. 2018; Li et al. 2014). ToMMV was thought to pose a serious risk to solanaceous crops due to its potential to break resistance and numerous means of transmission (Li et al. 2020); meanwhile, some plant species in the families of *Amaranthaceae*, *Brassicaceae*, *Cucurbitaceae*, and *Verbenaceae* were found as hosts of ToMMV under experimental conditions (Li et al. 2020; Sui et al. 2017). To clarify the occurrence of ToMMV in Yunnan Province of China, 395 plant samples, including tomato (*Solanum lycopersicum* L.), pepper (*Capsicum annuum* L.), and pea (*Pisum sativum* L.), exhibiting viral-like symptoms, were collected in major crop plantations in Yunnan Province in 2020. Total nucleic acids were extracted from the diseased samples using a CTAB method (Li et al. 2008) and tested by reverse transcription polymerase chain reaction (RT-PCR) with ToMMV specific primers, ToMMVMPF (5'-ATGGCTCTAACTGTTAGTGGT-3') and ToMMVMPPR (5'-TTAATACGAATCAGATCCCGCG-3'), which were designed based on the movement protein gene sequence of ToMMV YYMLJ isolate (KR824950). ToMMV was detected in 13 symptomatic samples (11 cherry tomato and two pea plants) with a total detection rate of 3.29%. An 807-bp fragment was amplified from two out of 86 pea samples showing foliar chlorosis, mosaic, and malformation and necrosis symptoms, and the amplicons were cloned

and sequenced. Sequences obtained from the two pea samples were identical. Therefore, one sequence was deposited in GenBank (accession no. MW561348). A BLAST search result showed that the nucleotide sequence had the highest identity of 99.88% with the ToMMV TiLhaLJ isolate (KR824951). The ToMMV infection on the two pea samples was also verified by dot-enzyme immunoassay (Dot-ELISA) using ToMMV monoclonal antibody (kindly provided by Dr. Jianxiang Wu, Zhejiang University, China). To determine the pathogenicity of ToMMV on pea, a ToMMV infectious cDNA clone was used to inoculate healthy 3-week-old pea plants via an *Agrobacterium*-mediated method (Tu et al. 2021). Mottle or slight mosaic, chlorosis, and malformation symptoms were observed on the upper leaves of eight out of 12 inoculated plants 8 days postinoculation, and ToMMV could be detected by RT-PCR from the eight symptomatic plants but not from the asymptomatic and healthy control pea plants with the above described ToMMV specific primer pair. ToMMV has now been detected in Mexico, China, Spain, the U.S.A., Israel, and Netherlands on tomato, pepper, and eggplant (Ambrós et al. 2017; Lovelock et al. 2020; Turina et al. 2016; Webster et al. 2014). To the best of our knowledge, this is the first report of natural infection of ToMMV in pea as well as the natural infection of ToMMV on plants outside of the family *Solanaceae*. The result also implies that ToMMV has a potential risk to more crops in the field. Since pea, pepper, and tomato are economically important cash crops in China, proper virus management strategies for the cultivation of these crops should be adopted.

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