This study reports the identification of hop latent viroid (HLVd) in commercial hop (Humulus lupulus L.) plants in the Pazaryeri region, Bilecik province, in Turkey. Hop plants without clear symptoms were randomly collected during 2015 and 2016 surveys. A total of 210 samples were collected from commercial cultivars Erciyes, Brewers Gold, Aroma and Ege. RNA was extracted using the GeneJET Plant RNA Purification Mini Kit and used in one step RT-PCR with specific HLVd primer pair 5’-CCACCGGTAGTTTC-CAACT-3’ and 5’-ATACAACTCTTGAGCGCCGA-3’ and protocols described by Eastwell and Nelson (2007). HLVd was detected in 20 out of 210 plant samples. The amplified DNA products of the expected size (ca. 260 nts) were purified and directly sequenced. Direct sequencing of the PCR products (Molgantec, Turkey) confirmed the presence of HLVd in these plants. Blast analyses and dendograms of HLVd sequences performed using the Mega 7 (Kumar et al., 2016) showed 97% to 98% maximum nucleotide identity with GenBank accession numbers KT600318 (Belgium) and EF613181 (China). Four HLVd isolates were graft transmitted from infected to healthy hop plants. All inoculated plants were found to be positive for HLVd in the RT-PCR tests and none of them exhibited any specific symptoms. To our knowledge, this is the first report of HLVd on hop plants in Turkey.


In September 2016, two apple trees (Malus domestica Borkh) of cv. Shinano Sweet showing bright cream spot and mosaic patterns on leaves were observed in Pocheon, South Korea. Mosaic symptoms have been found commonly on leaves of apple trees infected with apple mosaic virus (ApMV). Symptomatic leaves were tested by enzyme-linked immunosorbent assay (ELISA) and reverse transcription (RT)-PCR for ApMV but this virus was not detected in either of the samples. Apple necrotic mosaic virus (ApNMV) is a recently described novel ilarvirus isolated from apple trees in Japan and China (Noda et al., 2017) and correlated with a mosaic disease similar to that caused by ApMV. The presence of ApNMV was confirmed by RT-PCR with specific primer pairs ApNMV-CP+1 and ApNMV-CP-1 (Noda et al., 2017). Expected PCR fragments of ca. 650bp were amplified and directly sequenced. BLASTn results showed 94% nucleotide sequence identity with the CP gene region of the previously published ApNMV (LC108995). The consensus sequence of Korean strain KO (LC276940) was deposited in GenBank. The ApNMV-positive samples were also infected with apple chlorotic leaf spot virus (ACLSV), apple stem grooving virus (ASGV) and apple stem pitting virus (ASPV) as detected by RT-PCR (Han et al., 2016). To our knowledge, this is the first report of ApNMV infecting apple trees in Korea. Further research is needed to establish the relationship between ApNMV and ApMV causing mosaic disease on apple trees.

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