



First report of jujube yellow mottle-associated virus infecting jujube (*Ziziphus jujuba* Mill.) in Korea

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Jujube yellow mottle-associated virus (JYMaV) in the genus *Emaravirus* was recently identified from Jujube trees in China and found to be associated with jujube yellow mottle disease (JYMD) (Yang et al. 2019). JYMaV is a negative-stranded RNA virus with a multi-segmented genome comprising six RNA segments. Jujube (*Ziziphus jujuba* Mill.) belongs to the family Rhamnaceae and grows in Asia and Europe. In June 2022, several jujube plants (Cultivar King) displaying yellowing and mottling on their leaves were observed growing around a rice paddy in Hoengseong, Korea. To identify pathogens infecting jujube plants, five leaves showing disease symptoms from a single jujube plant were collected, and total RNA was extracted using the RNeasy Plant Mini Kit (Qiagen, Hilden, Germany). Ribosomal RNA-depleted library with 100 bp pair-end reads was sequenced on NovaSeq 6000 system (Macrogen, Seoul, Korea). Seventeen contigs (167,404 reads) associated with JYMaV were identified by *de novo* transcriptome assembly using Trinity assembler, followed by a BLASTX search against a plant viral database (Jo et al. 2021). Final data assembly resulted in six contiguous contigs that represent the complete genome of the JYMaV isolate Won. The length of these segments is for RNA1 7119 nts, RNA2 2212 nts, RNA3 1171 nts, RNA4 1320 nts, RNA5 1270 nts and RNA6 888 nts (GenBank OP204206–OP204211). The amino acid identities of the six RNAs of JYMaV isolate Won were 98.27% (RNA1 of HZ isolate), 98.78% (RNA2 of HZ isolate), 99.66% (RNA3 of AKS-6

isolate), 99.47% (RNA4 of HZ isolate), 94.24% (RNA5 of AKS-6 isolate), and 98.45% (RNA6 of YGQ-2-3-2 isolate). RNA was extracted from a symptomatic plant used for RNA sequencing and three asymptomatic plants. RT-PCR was conducted using JYMaV-RNA1 specific primers (JYMaV-7330F1_5'-GGCATTATGCAGGACACCT-3' and JYMaV-8076R1_5'-TCAAATCTTGGCATTTCGTTG-3'). A 751 bp fragment was amplified from four jujube plants. A 751-bp PCR product from the symptomatic plant was cloned, followed by Sanger sequencing. The partial sequence of JYMaV isolate Won shared 96.54% nucleotide identity with the known JYMaV isolate HZ (GenBank MT953011). The jujube cultivar King was originally derived from China and distributed in Korea by grafting. Therefore, JYMaV might be introduced to Korea with JYMaV infected jujube plants. To date, none of viral pathogens infecting jujube plants in Korea have not been identified. To our knowledge, this is the first report of JYMaV infecting jujube plants in Korea.

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