First Report of Fig Mosaic Virus on Fig in Russia

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Fig mosaic virus (FMV) (genus *Emaravirus* in the family *Fimoviridae*) is considered the etiological agent of fig mosaic disease (FMD), which is recorded in most of the fig-growing areas with an average global infection rate of 33%. The multipartite FMV genome is composed of six negative monocistronic ssRNAs, each of which is separately encapsidated (Preisling et al. 2021). Although FMD-like symptoms, which include mosaic, chlorotic ringspots, and oak leaf patterns, were observed in approximately a third of 400 fig accessions in the Nikita Botanical Gardens, Yalta, Russia (Mitrofanova et al. 2016), FMV has not been identified as the causal agent of the disease. In June of 2020, total RNA was isolated from symptomatic leaves of 59 trees (32 years old) representing 31 local and 27 introduced *Ficus carica* L. cultivars and a single *F. pseudocarpa* Miq. tree using an RNeasy Plant Mini kit (Qiagen, U.S.A.). FMV was tested by reverse transcription PCR using primer sets E5 (Elbeaino et al. 2009) and EMARAVGP (Walia et al. 2009), which amplify a 302-bp fragment of RNA1 and a 468-bp fragment of RNA2, respectively. PCR products of the expected sizes were generated in all samples, indicating a high FMV incidence in the plantings. The genome sequences of FMV isolates from *F. carica* cultivars Bleuett, Kraps di Hersh, Smena, and Temri and *F. pseudocarpa* were determined by high-throughput sequencing on a MiSeq Illumina platform. Double-stranded RNA was isolated from FMV-positive leaves using a Viral Gene-spin Viral DNA/RNA Extraction Kit

(iNtRON, Korea), followed by cDNA library preparation with the NEBNext Ultra II RNA Library Prep Kit (New England Biolabs, U.S.A.). On average, 695,000 quality-filtered 150-bp pair-ended reads per a library were produced and used in a de novo assembly using the metaSpades program version 3.14 (Nurk et al. 2017). In each of five samples, BLASTn analysis found six FMV-related contigs. The contigs spanned 99 to 100% of corresponding genomic segments of the most closely related isolates. In addition to FMV, fig cryptic virus-related contigs were also detected in some samples. The FMV contigs covering RNA1 to RNA6 had the highest identity to corresponding genomic segments of isolates AM941711 (96.5 to 96.6%), FM864225 (94.4 to 94.6%), FM991954 (97.9 to 98.2%), AB697863 (96.4 to 96.6%), AB697879 (93.3 to 93.4%), and AB697895 (95.4 to 97.0%), respectively. Five Russian isolates shared 99.2 to 100% nucleotide sequence identity, depending on the genomic segment. Their sequences were deposited in GenBank under accession numbers MW201216 to MW201230 and MW208662 to MW208676. Phylogenetic analysis of six open reading frames (ORFs) showed that ORF1 to ORF3 and ORF6 of the Russian isolates clustered with FMV isolates from Italy, whereas ORF4 grouped with the isolate JTT-Pa (AB697863) from Japan. ORF5 of the Russian isolates formed a separate cluster with the isolates SB1 and SB2 from Serbia and JTT-Vi from Japan (AB697879 to AB697884). Incongruity of phylogenetic relationship among the genomic segments suggests reassortment among ancestors of the Russian FMV isolates. In addition, similar to SB1, SB2, and JTT-Vi, ORF5 of the Russian isolates encodes a protein of 486 amino acid (aa) residues, in contrast to the corresponding protein of Italian isolates consisting of 502 aa. To the best of our knowledge, this is the first report of FMV in Russia. This finding not only expands the information on the geographical distribution of FMV but also extends knowledge on *F. pseudocarpa* as a natural host of the virus.

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