First report of fig mild mottle-associated virus in Iran

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Fig mild mottle-associated virus (FMMAV) is a putative member of the genus *Closterovirus* in the family *Closteroviridae*. This virus is thought to be disseminated through propagation and grafting in fig orchards, as no vectors are known and seed transmission is not suspected. In a survey of major fig growing regions of Mazandaran province in the north of Iran for FMMAV in June 2016, leaf samples from fig trees showing symptoms typical of fig mosaic disease were collected. Forty four samples were randomly collected in 10 fig gardens and tested for the presence of FMMAV by RT-PCR using total RNA and specific primers LM3s 5'-AAGGGGAATCTACAAGGGTCG -3' and LM3a 5'-TATTACGCGCTTGAGGATTGC -3' designed in the heat shock protein 70 homologue (HSP70h) gene (Elbeaino et al. 2010). The expected 311 bp DNA fragment was amplified from five (11%) symptomatic fig

samples. No association between a specific symptomatology and the presence of FMMAV was found, suggesting co-infection with other viruses. A FMMAV amplicon was purified, cloned into pTZ57R/T (MBI Fermentas, Germany) and sequenced. The corresponding sequence of the partial HSP70h gene was deposited in GenBank under accession No. MG242131. BLAST alignment showed that the 311 bp amplicon from the Iranian FMMAV isolate shared 88% nucleotide sequence identity with a FMMAV isolate from Tunisia (LN850113) and 97% with an isolate from Spain (KC914283). FMMAV is known to occur in fig trees in different countries worldwide (Bayoudh et al. 2017), however, to the best of our knowledge, this is the first report of FMMAV in Iran.

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