Occurrence of fig cryptic virus in fig trees in Iraq

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Fig (*Ficus carica*) belongs to the family Moraceae and is one of the oldest and most important cultivated fruit crops in many countries in temperate regions of the world. The vigor and yield of fig trees are affected by many diseases, the most detrimental of them is fig mosaic disease, which is caused by a complex of viruses. A previous study has shown the presence of fig mosaic virus (FMV) in the northern part of Iraq (Mohammed et al. 2019), but no information is available about the presence of other viruses associated with the disease. The aim of this study is to conduct a survey of major fig viruses, in particular of fig cryptic virus (FCV), in commercial fig orchards in different fig-growing regions in Iraq. A wide range of foliar symptoms including deformations, mosaic, chlorotic mottling, vein banding and clearing, and chlorotic ringspots, were observed on fig trees. One hundred samples were collected from the most important fig cultivars Aswed Dyala (50 samples), Waziri (35 samples) and Sultani (15 samples), and total nucleic acids were extracted from leaf tissue with the silica capture protocol (Foissac et al. 2001). All samples were tested by RT-PCR for the presence of FCV using a specific primer pair designed in the RNA-dependent RNA polymerase region (Elbeaino et al. 2011) to amplify a genomic fragment of 350 bp in size. Results showed that 45% (45 of 100) of the tested samples were infected by FCV.

RT-PCR amplicons of six samples were sequenced and nucleotide sequences were deposited in GenBank under accession numbers OU452323–OU452328. Iraqi isolates shared 96% to 100% nucleotide sequence identity among them, and 96% to 99% with FCV isolate BN13 (FR687854) from Italy. Among the other fig viruses selected for this survey, including FMV, fig fleck-associated virus (FFkAV), and fig leaf mottle-associated virus 2 (FLMaV2), only FMV was detected in 37% (37 of 100) of the samples tested. To our knowledge, this is the first report of FCV in fig trees in Iraq.

Data availability The sequencing data generated in this study were deposited in the GenBank and will be freely available to any researcher.

Declarations

Informed consent All authors have approved the submission of this manuscript.

Conflict of interest The authors declare that they have no conflict of interest.

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