DETECTION AND CHARACTERIZATION OF FIG VIRUSES IN GREECE

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Introduction

Fig is infected by a high number of viruses and virus-like agents; however the data on the presence and spread of these pathogens in Greece are rather limited. The aim of this study was to identify and characterize fig viruses occurring in the country using conventional molecular methods along with Next Generation Sequencing (NGS) of small interfering RNAs (siRNAs).

Materials and Methods

During 2014-2016, samples were collected from fig trees in gardens, isolated areas or from commercial orchards exhibiting leaf mosaic, chlorotic mottling and deformation. Samples were tested by RT-PCR for the presence of *Fig mosaic virus* (FMV), *Fig badnavirus 1* (FBV-1), *Fig cryptic virus* (FCV) and *Fig fleck associated virus* (FFKaV). Moreover, generic nested RT-PCR assays for the detection of Closteroviridae and Betaflexiviridae members were used (1). One sample was also subjected to high-throughput sequencing of siRNAs and the generated data were analysed using Geneious.

Results and Discussion

The results revealed a high incidence of FBV-1 and FMV throughout the country, while FCV and FFKaV were identified for the first time in Greece in a limited number of samples. Some trees were tested positive for the presence of a clostero- and/or betaflexivirus and sequencing of the generic RT-PCR products showed the presence of *Fig leaf mottle associated virus* 1 (FLMaV-1) and a putative new member of the genus *Tepovirus*. The presence of both viruses was confirmed by species-specific RT-PCR assays developed afterwards. Analysis of the NGS data allowed the reconstruction of almost the complete genomes of FBV-1 and FMV. Also, partial sequences of FLMaV-1, *Fig mild mottle virus* (FMMV) and the new tepovirus were obtained. Molecular characterization of the new identified viral agents is underway. Further large scale surveys are needed to evaluate their incidence and geographical distribution in different regions in Greece.

References

1. Dovas and Katis, 2003. *Journal of Virological Methods* 107: 99-106.