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The RNA virome of the medfly: a necessary step to optimize medfly control

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Insect specific viruses (ISVs) are known to specifically infect insect hosts causing no apparent effects on their fitness. The discovery of ISVs has largely increased during recent decades thanks to Next Generation Sequencing techniques, especially in insects with industrial interest. For instance, some RNA viruses were recently discovered in the agricultural pest *Ceratitis capitata*, also known as the Mediterranean fruit fly (medfly). Medfly infestations are mainly counteracted by the sterile insect technique (SIT), which requires the production of tons of sterile medfly males. Mass-rearing facilities offer a controlled way to rear large quantities of insects for different purposes. However, such mass-reared insects are threatened by viral diseases, coming from viruses introduced via horizontal transmission or from already present covert infections that are triggered into overt infections.

Understanding the interaction between covert RNA viruses and the medfly host requires the description and characterization of the RNA virome of the fly host. To do so, we have applied bioinformatics approaches to discover RNA viruses in the transcriptomes of four different medfly populations originating from multiple captures in the citriculture area in Spain. The obtained medfly virome is composed of twelve RNA viruses, five of which are new to medflies. Nine of the detected viruses belong to six known virus families while three are unclassified RNA viruses. Finally, we have defined the genomic structure, the phylogenetic classification, and the relative abundance of the discovered covert RNA viruses in four different laboratory and wild populations of *C. capitata*, including the V8A population used for SIT applications.