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NEW DISEASE REPORT

# First report of *Ti ringspot-associated virus* infecting peach in Greece

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*Emaravirus*, high throughput sequencing, *Prunus persica*

In summer 2023, a sample of clingstone peach (*Prunus persica* cv. PI-A37) from Ampeleies (regional unit of Pella, Greece) exhibiting virus-like symptoms, i.e., mosaic and chlorotic spots on the leaves, bud failure and severe fruit deformity, was analysed with High Throughput Sequencing (HTS). Total RNA was extracted from leaves with an RNeasy Plant Mini Kit (Qiagen, Germany) and was subjected to RNA-Seq in an Illumina Novaseq 6000 platform. The HTS analysis resulted in approximately 40 million, paired-end 150 bp reads that were *de novo* assembled with Geneious (v. 11.1.5). A BLASTn analysis revealed the presence of viruses known to occur in Greece, namely *Plum pox virus* (*Potyvirus* genus), *Prunus necrotic ringspot virus* (*Ilarvirus* genus), *Nectarine stem pitting-associated virus* (*Luteovirus* genus) and *Peach latent mosaic viroid* (*Pelamoviroid* genus). Five contigs were annotated as the genome of a *Ti ringspot-associated virus* isolate (TiRSaV, *Emaravirus* genus), which was recently identified in Hawaii and was associated with an emerging disease of ornamental plants of ti (*Cordyline fruticosa*) (Olmedo-Velarde et al., 2019).

The TiRSaV genome consists of five single stranded, negative sense RNA segments. Analysis of the obtained sequences showed that the highest nucleotide (nt) identity (93.5%) was recorded between the RNA 1 of the Greek (7137 bp; GenBank Accession No. OR713125) and Hawaiian isolates (NC_055641). RNA 2 (2310 bp; OR713126), RNA 3 (1107 bp; OR713127) and RNA 4 (1306 bp; OR713128) sequences showed 91.2, 89.8 and 91.7% nt identity with the respective RNA segments of the Hawaiian isolate (NC_055642, NC_055643 and NC_055644). Unlike the other four identified RNA segments, RNA 5 segment of our isolate (OR713129) covered only 43% of the Hawaiian RNA 5 and had 95.3 % nt identity. RT-PCR (Olmedo-Velarde et al., 2019) was used for the amplification of a short fragment of RNA 3 from both the RNA used in the HTS analysis as well as from a new RNA preparation derived from the same tree. The PCR products were analysed with Sanger sequencing and the resulting sequences were identical to that obtained from RNA-Seq analysis. To investigate whether TiRSaV could be associated with the observed symptoms we tested with RT-PCR four different peach samples exhibiting similar symptoms as well as two asymptomatic samples. All the additional samples tested negative.

To the best of our knowledge this is the first report of TiRSaV in Greece and in Europe. So far, the virus was only found in nature in ti plants and was mechanically transmitted to several herbaceous species (Olmedo-Velarde et al., 2019). This is the first report of the virus in an important woody host and shows that its host range is more extensive than described previously. Although TiRSaV was not associated with the symptoms observed in peach, its presence in peach and the potential for its transmission by eriophyid mites, suggests that further investigation is needed to evaluate the putative risk this virus could pose in cultivated plants.

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## REFERENCE

Olmedo-Velarde, A., Park, A.C., Sugano, J., Uchida, J.Y., Kawate, M., Borth, W.B., Hu, J.S. et al. (2019) Characterization of ti ringspot-associated virus, a novel emaravirus associated with an emerging ringspot disease of *Cordyline fruticosa*. *Plant Disease*, 103, 2345–2352. https://doi.org/10.1094/PDIS-09-18-1513-RE

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