

### Thousand cankers disease of walnut threatens the walnut groves of the Italian peninsula

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Thousand cankers disease (TCD) of walnut is an emerging new disease of walnut caused by the ascomycete fungus *Geosmithia morbida* (Hypocreales, Bionectriaceae) and its vector insect, the walnut twig beetle *Pityophthorus juglandis* (Coleoptera, Curculionidae, Scolytinae). TCD is a disease of North American origin (USA), which in the last decade has spread to some Italian areas: first reported in the Veneto region in 2013, the disease was subsequently found in various regions of northern Italy and in 2019 it was reported in Tuscany, in the province of Florence. Main host of TCD is the black walnut (*Juglans nigra*) but in some situations the common walnut (*Juglans regia*) can also be attacked, e.g. in mixed stands with the two species growing adjacently. There is currently a strong concern that the disease may spread to other regions of our country, because the black walnut has been extensively used in tree plantations since the early nineties of the last century, with the financial support of the European Union (EU Regulation 1992/2080) aimed at boosting the cultivation of valuable hardwoods. But, being Italy the only country in which TCD is currently reported outside the USA, the concern is also high at the European level. Indeed, there is a strong fear that the disease could spread to other EU countries, where black walnut plantations have also been established with similar financial measures. For this reason, both the fungal pathogen and its insect vector have been included in the EPPO A2 List of quarantine pests. Given this alarming situation, molecular diagnostic tools have been developed to be used in phytosanitary surveillance at sensitive sites (ports, airports, etc.) and over the territory (nurseries, plantations, etc.). Such diagnostic protocols revealed the capacity to detect the DNA of the two organisms from a variety of matrices, such as necrotic areas (cankers) around insect holes, infected internal tissues (galleries), adults and insect larvae, insect frass. They therefore constitute a promising tool to try to counter the epidemic spread of the disease.

### Survey of Kiwifruit Vine Decline Syndrome in Lazio region

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Kiwifruit Vine Decline Syndrome (KVDS) is a disease that affects *Actinidia chinensis* (kiwifruit) causing plant decline. Symptoms appear as root rot and branch wilting. The disease spread out in Lazio (central Italy) in 2017, while in northern Italy appeared as early as 2012. The disease probably is caused by abiotic and biotic factors. In this study, we aim to investigate the aetiological agents causing the symptoms, using both traditional, molecular and Next Generation Sequencing (NGS) approaches. Root and rhizosphere samples were collected from 20 kiwifruit orchards localized in Lazio region. Isolation from symptomatic roots revealed the presence of *Cylindrocarpon* sp. and oomycetes such as *Phytophthora* sp. In order to understand whether there is a clear difference in microbiome between kiwifruit plants affected or not by KVDS, we set up a DNA extraction method and a metabarcoding analysis using ITS2 for fungi and oomycetes. Preliminary results show that the DNA extraction method from root and soil samples works properly despite the high polysaccharides content in roots. Furthermore, NGS sequencing confirms the differences in the microbial community of asymptomatic and symptomatic samples. The next step is to analyse the other soil and root samples to confirm the difference between the symptomatic and asymptomatic plants to associate a pool of potential pathogens to the disease and a pool of microorganism to the healthy root and rhizosphere.

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### Spread of *Olea europaea* geminivirus (OEGV) in olive trees in Sicily

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