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Red raspberry (*Rubus idaeus*) is considered a crop of global significance and its production has largely increased during the last decade. In Piedmont, the increasing interest in raspberry cultivation has led to a progressive intensification of the production systems and to the adoption of new cultivars to supply the consumer demand. However, the consequent consistent movement of plant materials and fruit, along with the presence of favourable climate conditions, resulted in the emergence of diseases previously not reported in this area. Thus, a monitoring activity was conducted in red raspberry orchards over a three years period (2019–2021) to investigate the etiology and pathogen diversity in association with cane blight, the most common symptom observed and one of the most diffused and serious fungal diseases of raspberry. Isolates were collected from symptomatic plants of the cultivars ‘Diamond Jubilee’ and ‘Grandeur’. Three fungal species were identified: *Paraconiothyrium fuckelii*, *Diaporthe eres* and *Neocosmospora parceramosa*. The identification was achieved through morphological features assessment and multi-locus phylogenetic analyses on four different genomic loci (ITS, *tef1*, *tub2* and *rpb2*). All the species found were confirmed as pathogenic and *P. fuckelii* was the most aggressive. This study provides the first insight on raspberry cane blight in Italy. This preliminary knowledge can be applied to further epidemiological and diagnostic studies in order to adopt effective integrated strategies to control and prevent the disease spread.

Kiwifruit Vine Decline Syndrome: the roles of microbiome and abiotic stress in plant health

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Kiwifruit vine decline syndrome (KVDS) has been threatening kiwifruit cultivation in Italy for the last decade. Symptoms lead to severe root decay leading to irreversible

wilting that develops with the high temperatures of mid-late summer when kiwi vines have the highest transpiration rates. Root symptoms include disappearance of root hairs, breakdown of root cortex, blocked vessels, hypertrophy, and phloem detachment from the cortex. Among the microorganisms involved in the disease development, there are soilborne oomycetes belonging to the genus *Phytophthium*. High summer temperatures and flooding play a key role in the development of the disease. Trials performed in controlled conditions revealed a high virulence for the species *P. helicoides*, which showed a higher temperature tolerance even if the most isolated species is *P. vexans*. The use of a naturally infected soil to reproduce the symptoms revealed higher disease severity compared to the soil inoculation of a single species. For this reason, the soil, rhizosphere, and root microbiota of eight kiwifruit orchards, both healthy and KVDS-affected. Total DNA was extracted, and the population dynamics of fungi, bacteria and oomycetes was analyzed through metabarcoding. Defining the interplay between the factors involved will contribute to the understanding of multifactorial diseases where biotic and abiotic components simultaneously or sequentially affect plant health.

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A gnotobiotic approach to investigate microbiome functions in grapevine and lettuce

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Plant microbiome plays a key role on impacting plant health, however knowledge on the exploitation of certain beneficial microorganisms to improve crops is still partial. The aim of the project is to investigate timing and patterns of the plant microbial colonization and the effect of microorganisms on stress tolerance, fungal pathogenesis and plant growth by using gnotobiotic plants. Gnotobiotic plants, defined as