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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

plants with a characterized microbiome, could represent a new system to study microbial interactions and their benefits against abiotic and biotic stresses. For this study, grapevine (*Vitis vinifera* cv. Chardonnay) and lettuce (*Lactuca sativa*) were selected as representative crops for woody and herbaceous systems. Firstly, colonization from selected Biome Agents (BAs) and their efficacy in biocontrol against fungal pathogens were evaluated in controlled conditions. We tested bacterial strains isolated from lettuce leaf endosphere against biotic stress using lettuce plants inoculated with two races of the wilting agent: *Fusarium oxysporum* f. sp. *lactucae*. The efficacy assay was performed *in vivo* by assigning the disease index at 12-, 21- and 28-days post inoculation. The average biomass weight was also evaluated for *in vivo* trials. The identified best performing agents will be evaluated using gnotobiotic conditions. Gnotobiotic plants of both species were obtained by testing different sterilization methods. The gnotobiotic conditions are maintained by using smart boxes able to completely isolate the plants from the external environment while monitoring humidity and plant eco-physiological parameters in real time.

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The GPI-anchored protein HAM-7 regulates root adhesion in *Fusarium oxysporum*

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The fungal cell wall is a dynamic structure protecting cells from environmental stresses, providing cell type-specific morphology and functioning as a physio-chemical rheostat for the transmission of extracellular signals through a large set of cell-wall-anchored proteins. HAM-7 is a highly conserved protein present in all filamentous ascomycetes, and it is known to form a sensor complex at the cell wall/plasma membrane interface for the activation of the MAK-1 cell wall integrity mitogen-activated protein kinase (MAPK) pathway in *Neurospora crassa*. Additionally, absence of the GPI-anchored cell wall protein HAM-7 in *N. crassa* leads to severe defects in cell-to-cell fusion and sexual development. BlastP searches using the *N. crassa* OR74A HAM-7 protein as a bait identified a single 233-amino-acid long orthologue with 64.19% identity in the *Fusarium oxysporum* f. sp. *lycopersici* (*Fol*) genome.

Here, we genetically dissected the contribution of *Fol ham-7* gene in the regulation of stress response, vegetative hyphal fusion, hyphal agglutination, plant root adhesion and virulence. Similarly to *N. crassa*, *Fol ham-7Δ* mutants are severely impaired in vegetative hyphal fusion, but not in vegetative growth under stress conditions (*i.e.* cell wall, hyperosmotic and heat stress). Importantly, despite being unable to undergo hyphal agglutination and plant root adhesion *ham-7Δ* mutants only showed minor however not significant defects in plant virulence.

BNYVV genomic formula changes during host infection and vector transmission

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Multipartite viruses possess genomes split in more than two genomic segments each one packaged into independent particles. One of the benefits of being a multipartite virus is the gene expression modulation via changes of the segment copy number. The soil-borne beet necrotic yellow vein virus (BNYVV) may be considered a model of multipartitism since, with its 4 to 5 genomic RNAs, it has the highest number of genomic segments among RNA viruses infecting plants. In this work, we investigate the ratio of the four genomic segments of BNYVV type B in different host types analyzing tissues from infected roots and leaves by a validated protocol of dual step reverse transcriptase droplet digital (RT-dd)-PCR. BNYVV genome formula was also calculated within the vector *Polymyxa betae* after zoospore purification from infected *Beta vulgaris* roots evaluating the plant rate of contamination. Results showed that some viral gene segments accumulate at low frequency, whereas others dominate. BNYVV segment copy numbers change according to the type of host and organ infected, moreover the virus seems to reach a dedicated set-point genome formula also within its vector. These data together with the biology of this virus raise questions about the genome integrity preservation of BNYVV during the host infection and transmission by the vector.

Current status of *Botryosphaeriaceae*: fourteen years surveys among nursery, urban and agro-ecosystems in Sicily

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