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Posters

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METAGENOME OF SOILS FROM FRUIT TREE ORCHARDS IN NE SPAIN AS A PREDICTIVE TOOL OF PHYTOSANITARY STATUS IN PERENNIAL AGROECOSYSTEMS

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A high percentage of agricultural soils in the European Union cope with degradation processes, mainly because of unsustainable management practices, such as intensive tillage, excessive fertilization, erosion, etc. Under this scenario, soil microbiological diversity is crucial for the productivity and sustainability of agricultural systems since microbial communities (prokaryotes and eukaryotes) support and modulate basic and essential services for their functioning. The abundance and population structure of the microbiome informs us about aspects such as the phytosanitary status of crops, the capacity for resilience against disturbances, or the presence/absence of microorganisms that allows the plant to cope with biotic or abiotic stresses. In this sense, it has been commonly accepted that detailed studies of the microbial diversity associated with different compartments (soils, rhizospheres, accompanying floras, etc.) are a very useful indicator of the sustainability and functioning of the whole agroecosystem. This study has characterized by means of high-throughput sequencing methods, the microbial biodiversity (fungi and bacteria) from soils of pome and stone fruit trees (apple, pear, peach, fig, plum and cherry) crops in different productive areas of the province of Zaragoza (NE Spain), in the frame of a broader study to evaluate some soil indicators related with its health and sustainability, including their phytosanitary status. The results obtained suggest that the microbial communities associated with the soil of the surveyed plots have, in general terms, a medium-high degree of biodiversity, taking as reference diversity values observed in studies of this type (bare soil of woody agroecosystems). Considering the fungal taxonomic composition globally, most of these soils presented a certain degree of microbiological exhaustion, defined by the major presence of soil-borne pathogens in relation to the rest of the saprophytic or symbiotic microorganisms characterized.

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METAGENOMIC INSIGHTS INTO THE GRAPEVINE ENDOPHYTIC MICROBIOME-PHAEOMONIELLA CHLAMYDOSPORA INTERACTIONS: IDENTIFICATION OF TAXA CORELATED TO HEALTH STATUS OF PROPAGATION MATERIAL

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In the metagenomics era, the development of next generation sequencing technologies has led to extensive investigations of the interactions between microbiomes and plant pathogens, in several pathosystems. In grapevine, a few studies have been conducted that associate the beneficial microbiome with plant health status, concerning grapevine fungal diseases. This study aimed to investigate the fluctuation of *Phaeomonilla chlamydospora* biomass from the nursery to the field and to explore alterations in the endophytic microbiome between vines with low and high pathogen concentration, throughout the propagation process. Quantification of the pathogen's biomass was carried out in three types of propagation material (canes, grafted unrooted and grafted rooted vines in various rootstock/scion combinations), using a dual-labeled probe assay. Subsequently, next generation sequencing was carried out in selected vines with low and high pathogens' concentrations. The qPCR assays showed that *P. chlamydospora* biomass was highly increased in grafted vines compared to canes, hypothesizing that the production process negatively affects the beneficial microorganisms present in the initial propagation material. Bioinformatic analysis including non-metric multidimensional scaling followed by differential abundance analysis in fungi and yeasts, revealed that several Amplicon Sequence Variants (ASVs) such as *Aureobasidium* and *Filobasidium*, two taxa widely used in biological control of plant pathogens, were more abundant in canes compared to the grafted rooted vines. Furthermore, *Clonostachys rosea* and *Filobasidium* were significantly more abundant in vines with low biomass compared to those with high concentrations. A specific pattern was observed regarding the bacterial microbiome, with *Pseudomonas*, being consistently more abundant in vines with low pathogens' biomass in almost all rootstock/scion combinations. These findings suggest that the propagation material production process highly impacts the composition of the grapevine microbiome and could stimulate research regarding the discovery of effective biological control agents and the development of microbial consortia against trunk pathogens.

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