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Abstract – SY36

ADDRESSING THE CORRELATION BETWEEN COPPER LEVELS AND MICROBIOME DIVERSITY IN THE RHIZOSPHERE OF TWO GRAPEVINE CULTIVARS

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Grape (*Vitis vinifera* L.) is one of the most widely cultivated fruit crops with a great economic impact. The interaction between microorganism and grapevine is an important aspect in sustainable agriculture and it could affect plant yield, taste and health. Copper (Cu) is the most used fungicide in both conventional and organic viticulture systems for controlling fungal (e.g. Peronospora) and bacterial diseases of plants. Copper accumulates in soils mainly via agronomic treatments and by leaf fall. Although Cu is an essential micronutrient, it might become toxic to living organisms when it is present in excess. This study was aimed at developing and implementing next-generation sequencing (NGS) protocols to evaluate the effect of bioavailable soil Cu on rhizosphere microbial and fungi communities' composition of two grapevine cultivars (Pignoletto and Alionza). Soil carrots of 15 cm length were collected in proximity of grapevine root systems. On rhizosphere soils, total Cu content was determined by ICP-OES on wet acid digested samples. Potentially bioavailable-to-plant Cu was assessed by DTPA method. NGS libraries were prepared after rhizospheric soil DNA preparation and PCR amplification targeting the 16S rRNA gene and ITS region aiming to characterize bacterial and fungi community compositions, respectively. The following sequences were used: 16S- 341F and 16S-805R and ITS1 and ITS4 for the 16S and ITS locus, respectively. Libraries were sequenced on MiSeq instrument (Illumina, San Diego, CA) using 300-bp paired-end. The diversity of microorganisms across soil samples and their dependence on total and bioavailable Cu levels were evaluated using QIIME2 (Quantitative Insights Into Microbial Ecology). Under the conditions of this experiment, there was no correlation between the bioavailable copper level and the whole microbiota diversity.