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THE MICROBIAL CONTINUITY ACROSS CHANGING ECOSYSTEMS

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PROGRAM



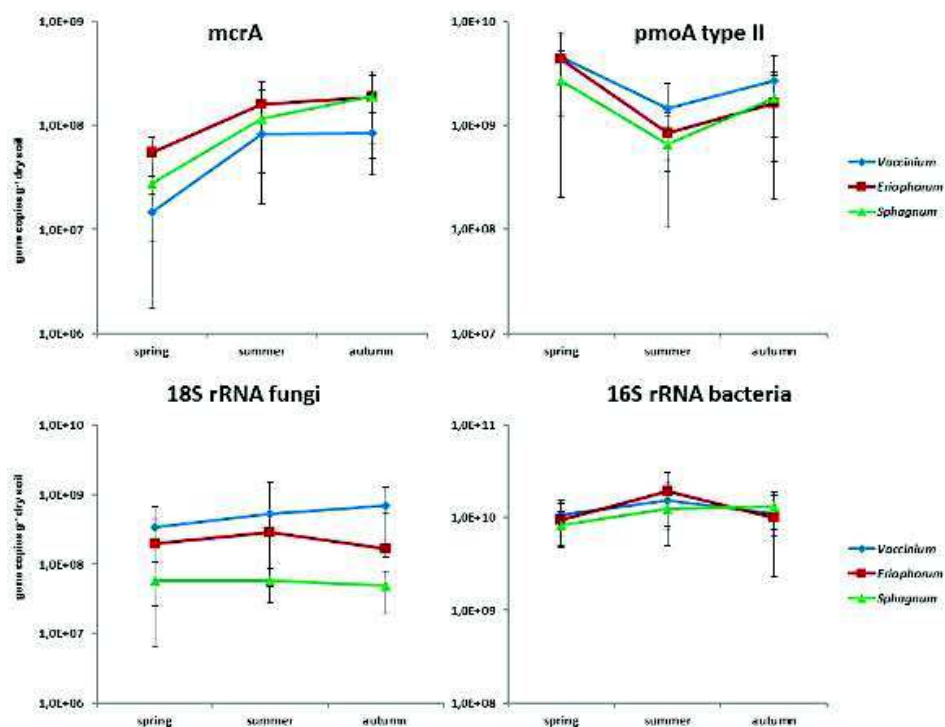
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Figure 2



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Comparison of bacterial soil communities between vineyards and their surrounding semi-natural areas.

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Soil microbial processes play important roles in maintaining soil structure and ecosystem functions where microbiota is influenced by management, plant cover and invertebrates. Comparing the extent of divergence between soil bacteria in vineyards and in semi-natural margins in the same areas was the key objective of this work. Soil samples were collected in 12 vineyards and in their non-cropped surroundings. Farms were located in two neighbouring groups of hills, renowned for their wine quality: the Euganean Hills, with soils of prevalent volcanic origin, and the Berici Hills, with marine sedimentary genesis. Soil bacterial communities were determined based on the 16S rRNA gene analysis through the 454 pyrotag sequencing of the V1-V3 hypervariable region. Soil physical and chemical parameters, fungal communities, and macro- and meso-fauna of the vineyards were also studied, and statistical analyses highlighted interesting correlations between some bacterial taxa and soil characteristics, including the presence of different species of earthworms. Weighted UniFrac distance between soil bacterial communities was calculated, and the related UPGMA tree and PCoA plot showed that the majority of the semi-natural secondary deciduous woodlot soils clustered together, indicating that these, although geographically distant, presented more similar bacterial communities comparing to their respective nearest vineyard soil. Some groups were present with significantly different abundances in vineyard and semi-natural soils: Alphaproteobacteria, Acidobacteria, Bacteroidetes, Chloroflexi, Gammaproteobacteria, Gemmatimonadetes, and few other phyla. Within these, some families were decisive in determining differences. Overall, more than 800 bacterial genera and more than 4000 bacterial species were approximated through rarefaction curves. This study provides novel insights into how environment and soil management can affect and

Microbial diversity and functioning in the soil ecosystem

shape soil microbial community composition. This work was carried out within the 'Veneterroir' project, PSR 2007-2013 of the EU funding to Veneto Region.

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Soil archaeal community changes associated with oil palm fatal yellowing using pyrotags

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Palm oil is considered a potential feedstock for biodiesel production in Brazil due to its high productivity. Fatal Yellowing (FY), of unknown etiological origin, has decimated oil palm plantations in the Amazon region. Little is known about archaeal communities in the Amazon and relative to FY. In this study, soil archaeal communities of oil palm plants with and without FY symptoms were compared using high-throughput sequencing of 16S ribosomal RNA gene (pyrotags). Nine soil samples, grouped according to disease stage (0, 5 and 8), were studied. The Mothur software package was used for quality control of sequences and remaining analysis; the Silva database was used for taxonomic classification. Only two archaeal phyla, Euryarchaeota and Thaumarchaeota were present in all soils studied, regardless of disease stage, with Euryarchaeota being the main phylum in all samples. Euryarchaeota had significant higher representation in soils from plants displaying the most advanced disease stage (Group 8). Soil from Group 8 plants also showed higher archaeal diversity, and the highest number of OTUs. Increasing FY symptoms correlated with a higher representation of genus *Candidatus Nitrosotalea* (Thaumarchaeota) and *Rice Cluster I* (Euryarchaeota) in soil. Although to date there are no reports of pathogenic *Archaea*, this study found an increase in archaeal diversity and an increase in the abundance of specific archaeal in soil from plant with FY. This is the first work to explore a potential role of *Archaea* in plant disease.

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Soil organic matter mineralization depends on microbial diversity

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Human activities and climatic changes are leading to a rapid and significant reduction of biodiversity, referred to as "the sixth extinction". As a consequence, understanding the effect of diversity on ecosystem functioning and stability is now a central issue in ecological sciences. In this context, we investigated the link between microbial diversity and mineralization of organic matter in soil, which is a major function for soil fertility, environment quality and global changes. To simulate an erosion of soil microbial diversity, microcosms of a soil previously sterilized by gamma irradiation have been inoculated with three different dilutions of a suspension of the same but non sterile soil. By this way, three series of microcosms representing a gradient of soil diversity have been obtained, with D1>D2>D3. After microbial communities have colonized and stabilized, microcosms have been amended with ¹³C labelled wheat residues. Decomposition of wheat residues and of indigenous organic matter have been assessed during 60 days by measuring ¹³CO₂ and ¹²CO₂ fluxes, respectively. Results show that intensity of the soil respiration as well as of the priming-effect induced by the addition of plant residues was strongly linked to microbial diversity, with the highest values observed where diversity is greatest. These results illustrate the importance of considering the microbial diversity as a predictive variable of organic carbon storage/release in soils.

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Non-conventional pretreatments mitigate the inhibitory effect of 5-hydroxymethylfurfural in dark fermentation process.

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Introduction: In dark fermentation process based on mixed cultures, the production of hydrogen (H₂) is carried out by the H₂ producing bacteria (HPB). However, the existing technologies are extremely unreliable and not cost effective. Functional stability and microbial diversity seem to be positively correlated in natural and engineered ecosystems. Thus, understanding