



Genetic and functional diversity of soil microbial communities associated to grapevine plants and wine quality

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Introduction

Despite the economic importance of vineyards in Italy, the wine sector is facing severe challenges from increased global competition and climate changes. The quality of the grape at harvest has a strong direct impact on final wine quality and the strong relationship between wine composition, aroma, taste and soil properties has been outlined in the “Terroir concept”. However, information on the impact of soil microbial communities on soil functions, grapevine plants and wine quality is still lacking.

Objectives

The aim of this study was to explore the composition and the potential functions of soil microbial communities associated to grapevine plants grown in two soils which showed similar physical, chemical and hydrological properties but which provided a different wine quality.

Materials and Methods

Soils from two sites of the Chianti region in Tuscany (BRO11 and BRO12) cultivated with the grapevine cultivar Sangiovese with contrasting wine quality were examined by means of a structural and functional approach: specifically, GeoChip microarrays, pyrosequencing of 16S rRNA and 18S rRNA genes, enzyme assays and measurements of some soil biological properties, such as microbial biomass C and soil respiration, were carried out.

Results

Enzyme assays and soil biological analyses revealed a higher biological activity in BRO11 as compared to BRO12. The structure of soil microbial communities, assessed using 16S and 18S rRNA gene-targeted pyrosequencing, revealed a higher presence of Actinobacteria in the BRO12 than in the BRO11 soil where, in contrast, the alfa-Proteobacteria are more abundant. GeoChip microarray analyses revealed a consistent difference in genes involved in S cycling, with a significant overrepresentation of sulfur-oxidation genes in BRO11 and increased levels of sulfate reduction genes BRO12. These results are consistent with the high content of sulfates and the abundance of Firmicutes such as *Sulfobacillus thermosulfidooxidans* in the BRO11 soil.

Conclusion

The preliminary results of this work suggested an active role of microbial communities on grape physiology and “Terroir concept”. In particular, the biological oxidation of sulphur in BRO11 appeared to be one of the factors which determines the wine quality. However further studies are needed to confirm this indication.