



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

Stefano Mocali (1), Arturo Fabiani (1), Eiko Kuramae (2), Mattias de Hollander (2), George A. Kowalchuk (2,3,4), Nadia Vignozzi (1), Giuseppe Valboa (1), and Edoardo Costantini (1)

(1) Consiglio per la Ricerca e la Sperimentazione in Agricoltura – Centro di Ricerca per l’Agrobiologia e la Pedologia (CRA-ABP), Firenze, Italy, (2) NIOO-KNAW, Wageningen, The Netherlands, (3) Institute of Ecological Science, Free University of Amsterdam, Amsterdam, The Netherlands, (4) Institute of Environmental Biology, Utrecht University, Padualaan 8, 3584 CH Utrecht, The Netherlands

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 wine final 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 generally lacking. In the current study, soils from two close sites in Central Tuscany (BRO11 and BRO12) cultivated with the same grapevine cultivar Sangiovese, but with contrasting wine quality, were examined. Although the BRO12 site provided a better wine quality than the BRO11, the two soils showed similar physical, chemical, and hydrological properties. Also soil humidity, as determined by FDR (Frequency Domain Reflectometry) sensors, indicated a similar water availability in the first 75 cm during a three years trial (2000-2010). Interestingly, the mean three years value of the ratio between the two stable carbon isotopes $^{13}\text{C}/^{12}\text{C}$, measured in the alcohol of the wines, was significantly higher in BRO12 than in BRO11 (-28,3‰ and -24,4‰ respectively), indicating the presence of a relatively higher water stress in the BRO11 soil. Functional GeoChip microarray analyses revealed higher presence of Actinobacteria in the BRO12 than in the BRO11 soil, where the alfa-Proteobacteria were more abundant. Furthermore, a consistent difference in genes involved in S cycling, with a significant overrepresentation of sulphur-oxidation genes in BRO11 and increased levels of sulphate reduction genes BRO12 was detected. These results are consistent with the high content of sulphates and the abundance of Firmicutes such as *Sulfobacillus thermosulfidooxidans* in the BRO11 soil. Therefore, the different microbiology of the two soils could be related to the different redox conditions of the two soils. The structure of soil microbial communities was assessed using 16S and 18S rRNA genes pyrosequencing and the determination of some soil microbial properties such as microbial respiration, microbial C-biomass were also determined. The role of both genetic and functional diversity of soil bacterial community on grape physiology and wine quality will be discussed.