

Evidence for a soil microbial terroir in the Chianti Classico district in Tuscany (Italy)

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Originally developed for wine, the terroir concept is becoming popular throughout agri-environmental sciences in many parts of the world, linking the uniqueness and quality of agricultural products to the environment where they are produced. Even though it is well known that geology, morphology and microclimate influence and diversify the wine characters within a wine district (macro-terroir), recent literature suggests that different soil features can drive wine characters also within the same macro-terroir, at both farm and vineyard scale. However, the drivers beyond these differences remain elusive, and the potential contribution of soil microbes has been ignored until recently. Therefore, in this multidisciplinary work we have tried to assess the possible role of soil microbial communities in vineyards on defining the quality of the wine produced.

Soils from 4 different macro-terroir areas located within the Barone Ricasoli farm in Brolio (SI), Tuscany (Central Italy), characterized by different geology and cultivated with the grapevine cultivar Sangiovese, were collected: Fattoio (feldspathic sandstone), Leccio (marine sands), Agresto (limestone), and Ceni (fluvial deposits). Within each terroir, two areas homogeneous for soil features were delimited (Basic terroir unit, BTU) and monitored over 3 years for the soil physico-chemical and biological parameters as well as viticultural parameters. In this work we report the results of the analysis of microbial communities in the 8 BTUs, determined through molecular (PCR-DGGE), metabolic (BIOLOG) and biochemical (microbial respiration, biomass C) techniques.

The results showed that each vineyard is characterized by a well defined bacterial community whose structure varies both as a function of different BTUs and terroir areas, depending on soil features. In fact, the vineyards Fattoio 1 and 2 exhibit a very similar bacterial composition between them and stable over time, even for the low total organic matter content. In contrast, Leccio 1 is very different from Leccio 2 (much more than Agresto 1 compared to Agresto 2) and shows values of biological fertility and bacterial diversity always lower than Leccio 2. Ceni 1 and 2, however, even though quite distinct from each other, do not show many similarities with other vineyards. Interesting to note that the values of the Sangiovese performance index, which estimate the quality of the wine produced are well correlated with the bacterial diversity of different BTU. In conclusion, despite soil bacterial community composition was shown to be strictly related to the quality of grapes, further investigation is still required in order to better highlight the effect of such microbial communities on vine physiology and wine quality.