



**Metagenomics analysis of soil prokaryote  
community composition and diversity  
at 22 Barossa Valley vineyard sites**

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## ABSTRACT

**ABSTRACT** Soil is one of the influential factors that defining a wine's terroir or the uniqueness of a wine produced by vines grown in specific conditions and also by different winery process (e.g., oak process). Recent data shows that the diversity, distribution and composition of soil microbial communities may play important roles in determining wine quality and indirectly affect its economic value. Here, we evaluated the impact of environmental factors on microbial composition and diversity of 22 Barossa Valley vineyard sites using metagenomics tools based on the 16S rRNA gene hypervariable region 4. In this study, we report that environmental heterogeneity (rainfall, temperature, soil moisture, soil P content) in different regions caused more phylogenetic dissimilarity than geographic distance. Eden Valley and Western Ridge showed lower diversity and a higher ratio of dominant taxa, and this was correlated with a correlated with higher rainfall. The coldest region, Eden Valley, had the lowest diversity. Combined with functional analysis of metagenomics data, soil microbial community composition and diversity has the potential to be useful biological indicators of grape berry and wine characteristics. Importantly, these features significantly associated with changes in the microbial communities, highlighting the influence of microbiome on the grape plants. Our results suggest that environmental factors affect wine terroir and this may be mediated by changes in microbial structure, thus providing a basis understanding of the mechanistic interactions between plants and growing conditions.