

XIX CONGRESO DE LA SOCIEDAD ARGENTINA DE MICROBIOLOGÍA GENERAL

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PROKARYOTIC DIVERSITY IN THE RHIZOSPHERE OF ARGENTINEAN WINE-PRODUCING REGIONS

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Argentina ranks as the seventh-largest wine producer. In this geographically and climatologically diverse country, each region has its own unique set of features that imparts special characteristics to its wines. Microorganisms associated with vines play a key role in determining wine quality, as they can impact sensory attributes and contribute to the distinct regional terroir. Recent research has uncovered notable differences in microbial communities across grape varieties and vineyard locations. In this study, we examined the diversity of prokaryotic microorganisms in the rhizosphere of vineyards situated in three wine regions of Argentina: Patagonia (Río Negro), Cuyo (Mendoza and San Juan), and the Northwest (Salta). The soil physicochemical properties of the vineyards were assessed using principal component and clustering analysis. It was observed that the sand/clay ratio, sodium, potassium, and carbonate concentrations were the main variables that defined regional groups, clustering sampling sites in accordance with their geographical location. Using 16S next-generation sequencing methods, we focused our analysis on two key cultivars: Malbec and Cabernet Sauvignon. These varieties have garnered considerable attention in recent studies due to their distinctive attributes, which may vary depending on the geographic region where they are grown. Although no significant variations were observed between Malbec and Cabernet Sauvignon vineyards, substantial differences in microbial diversity were found across the regions studied. Taxonomic identification revealed distinct microbial compositions between regions, with significant variations in abundance at the family level. Canonical correspondence analysis demonstrated correlations between soil physicochemical properties and microbial families, underscoring the influence of soil characteristics on microbiota composition. Soils with high sand content, such

as those in Salta, were enriched with bacteria from the families *Pseudomonadaceae*, *Moraxellaceae*, *Bacillaceae* and *Paenibacillaceae*. In contrast, soils rich in lime, clay, sodium, potassium, and carbonate, such as those in Mendoza and San Juan, were enriched in bacterial families like *Rhizobiaceae*, *Chlamydomonadaceae* and *Xanthomonadaceae*. These differences in microbial populations establish a site-specific prokaryotic profile that could serve as an identifying signature. This comprehensive analysis provides insight into the intricate relationship between soil characteristics, microbial diversity, and the concept of terroir in Argentine vineyards. Understanding these interactions is crucial for enhancing vineyard management practices, ultimately influencing the organoleptic properties of wines produced in different regions.

Palabras clave: Rizosphere - Wine - Prokaryotic Diversity