Unraveling metabolically active fungal-bacterial diversity in commercial organic vineyard soils

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OBJECTIVES

To assess the impact of phenology (pre-bloom and post-harvest periods) on the diversity of metabolically active soil-rhizosphere microbiota in a commercial vineyard in Sant Sadurní d’Anoia, a typical cava and wine producing region (Penedès DO, Catalonia, Spain).

Location of Catalonia (dark green)

Plot coordinates: 41°49’N 1°28’E

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• *Vitis vinifera* variety ‘Macabeu’, grafted onto 41-B (*V. berlandieri* x *V. vinifera*), 18 years old.
• Total Surface 6 ha, vine spacing: 1.0 x 2.6 m.
• Organic and rainfed farming.
• Fertilizer: 20 tones (composted cow manure)/ha every 4 years.
• Permanent cover crop and *silt loam* soil in Zone 1 and tillage and *sandy loam* soil in Zone 4.

Mediterranean climate (SMC)

**Temperature**
- Summer: 23–24 ºC
- Winter: 6–8 ºC

**Rainfall**
- Annual 550 mm
- Maximum rate in fall and minimum rate in summer

Adapted from Andreu 2019
Soil water content

RESULTS

Rainfall and ETo

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Microbial assessment: Quantitative PCR

In post-harvest period, bacterial and fungal population were more enriched and active, specially in zone 4.

In zone 1, active bacterial population increased 2 orders of magnitude.

In zone 4, metabolically active bacteria increased 5 orders of magnitude.

The harvest and climate conditions promoted this activity.

Bacteria and Archaea Ammonia Oxidizers (AOB and AOA), were detected in, post-harvest period.

*Nitrospirales* presence and activity (MiSeq data), could hamper ammonia-oxidizers activity.
Total and functional bacterial diversity in Z4 is more homogeneous in postharvest period than Z1 zone.

- **Actinobacteria** (mainly by Actinomycetales order), **Proteobacteria** (mainly by Rhizobiales and Pseudomonadales orders) were the most predominant phylotypes.

- **Clostridiales** (Firmicutes phylum) phylotypes were completely replaced during post-harvest season.

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Fungal Diversity

April 2018: Pre-harvest

October 2018: Post-harvest

- Alpha Fungal diversity was lower than bacterial diversity in both plots.
- Fungal alpha and beta diversity was smaller and less uniform in both periods than bacterial diversity

Ascomycota, Basidiomycota and Zygomycota were the most predominant phyla.
CONCLUSIONS

• Soil bacterial and fungal communities were more metabolically active during post-harvest than pre-harvest season season in both zones.

• No metabolically-active fungal community was detectable in pre-harvest period. Fungal populations were less diverse than bacterial diversity.

• Both environmental conditions and the mechanical harvest may promote microbial growth due to sugar availability in soil (-30 cm) linked to rainy periods. The vineyard, in post-harvest period, could be more exposed to phytopathogens, so this could be an interesting period to control these communities and consequently the potential infection for the next productivity period.

• High throughput sequencing analysis (16S/ITS MiSeq) revealed that the microbial diversity was specific both for each plot, each plant and time period.

• The diversity of bacterial and fungal populations increased during post-harvest season.

• Simultaneous RNA/DNA-based molecular biology tools could improve the knowledge of metabolically active microbial populations in soils at different seasons and phenological stages of rainfed vineyard.

• These can be important in order to study and evaluate the potential and real emissions of greenhouse gases from vines in Mediterranean conditions under climate change.

• This information must be used to accomplish the compromises developed in COP 21 and COP 22, related to mitigation strategies.