



ABSTRACT

Title:

Unveiling the Microbiome Biodiversity and Biogeography of Spontaneous Wine Fermentations through Shotgun Metagenomics

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Presenting:

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Abstract content:

Modern winemakers commonly inoculate grape must with commercial *Saccharomyces cerevisiae* strains to obtain controlled fermentations and reproducible products. However, wine has been produced for thousands of years using spontaneous fermentations (SP) from wild strains, a practice experiencing a revival among small producers. Despite widespread historical usage and some recent geographically scattered metabarcoding studies, much remains to be known about the ecology, evolution, and functional potential of the microbial communities in SP. Here, we investigate the microbial biodiversity of 33 SP must metagenomes from 21 Italian estates and compare them with publicly available shotgun datasets from Germany, Spain and Australia. We reconstructed MAGs for functional analyses, inferred strain-level phylogeny of *S. cerevisiae*, and curated a wine-specific Kraken2 database for taxonomic profiling to overcome the under-representation of oenological taxa in reference databases. We found clear country-level biogeographical structure, with a small global core microbiome within a large variable pan-microbiome. The *S. cerevisiae* phylogeny placed most SP strains within the wine clade and revealed no clear geographic structuring or distinction between spontaneous and commercial strains. We are currently testing the stability of the microbial profiles over time and the ecological origin of *S. cerevisiae* strains (grapevine versus cellar) by analysing multiple time points and microvinified samples. Overall, our results support a *microbial terroir* of spontaneous wine fermentations microbiomes across countries, while *S. cerevisiae* populations are genetically homogeneous within the wine clade.