

SHIFT 02-207 - EXPLORING THE GENOMIC DIVERSITY OF WILD *S. CEREVISIAE* WINE STRAINS IN SPONTANEOUS FERMENTATION (ID 1930)

Topic

AS03. Evolution, biodiversity and systematics

Authors

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Abstract Body

Modern winemakers commonly inoculate selected *S. cerevisiae* strains in must to obtain controlled fermentations and reproducible products. However, wine has been produced for thousands of years using spontaneous fermentations from wild strains, a practice that is experiencing a revival among small wine producers. Despite the widespread usage of such strains in the past, there is much to know about their ecology, evolution and functional potential. For example, the reciprocal affinities of these strains within the *S. cerevisiae* phylogeny have yet to be discovered, as well as the degree of their genome diversity and impact on wine terroir. To fill this knowledge gap, we have sequenced and studied the genome *S. cerevisiae* present in spontaneously fermented musts sampled across 24 estates of Italy. We set up a protocol based on polyphenols-removing prewashes, followed by both a whole-genome shotgun sequencing and the sequencing of selected *S. cerevisiae* clones to avoid the presence of artefactual chimaeras due to the copresence of strains. We reconstructed 45 genomes of *S. cerevisiae* strains for downstream functional analyses and performed an assembly-free metagenomic analysis to reconstruct the strain-level phylogeny of our *S. cerevisiae* strains. To plan conservation acts in a scenario of continuous climate change, we have isolated and are maintaining strains of interest.