

**Commercial yeast utilization and genetic structure of vineyard-associated *Saccharomyces cerevisiae* populations revealed by microsatellite analysis**

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Since the beginning of the 1980's, the use of active dried *Saccharomyces cerevisiae* yeast starters has been extensively generalised. Today, the majority of wine production is based on the use of active dried yeast, which ensures rapid and reliable fermentations. The behaviour of these yeasts in the ecosystem of the vineyard is totally unknown as is their potential impact on the natural microflora. The aim of the present study was to evaluate populational structures among fermenting *S. cerevisiae* populations and to assess the impact of active dry yeast usage on the genetic structures of the vineyard microflora.

*Saccharomyces cerevisiae* isolates were obtained from fermentations with grapes from three vineyards of the Vinho Verde Region where commercial yeast strains were used continuously during the last years. Populational genetic analysis was based on six polymorphic microsatellite loci in 361 isolates. Accumulation of small allele-frequency differences across six loci in groups of strains allowed the identification of populational structures. The continuous use of active dry yeast has a very limited impact on the genetic structure of the vineyard microflora. Correlation of genetic differentiation with the distance between sampling points suggested a pattern of isolation-by-distance, where genetic divergence in a vineyard increased with size.

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