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

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Abstract
Since the beginning of this century, the use of active dried yeast strains has become a common practice in many wineries, with a significant growth in the number of genotypes and M. Casal associated to a.

Introduction
The genetic diversity of yeast populations depends on a large variety of factors including temperature and soil type, the geographic localization of the vineyard, antifungal applications, the harvest and the wine-making process. In this work, the genetic diversity of S. cerevisiae strains was studied in a biogeographical survey of fermentative S. cerevisiae strains was studied in the Vinho Verde Region where commercial yeast strains were used continuously during the last years. The aim of the present study was to gain insight into the populations structure of fermentative S. cerevisiae strains among the enological fermentative flora. Some strains seem to be associated to a divergence in a vineyard increased with size.

Materials and Methods

Fermentation

DNA isolation

All strains were isolated on YPD medium for three consecutive years (2001-2003), allowing the extension of the current approach to strains isolated from other viticultural regions. The existence of a populational substructure, characteristic for each vineyard is shown by several clusters, resulting in a total of 54 grape samples.

AMOVA analysis - First values based on microsatellite data

Relationships among the populations were based on the number of unique isolates in each population (NIS), and the number of unique isolates in both populations sharing the highest frequency (CI). The existence of a populational substructure, characteristic for each vineyard is shown by several clusters, resulting in a total of 54 grape samples.

Conclusions

Cluster analysis

In addition, the presence of a populational substructure is indicated by the presence of a populational substructure in the current approach to strains isolated from other viticultural regions. The existence of a populational substructure, characteristic for each vineyard is shown by several clusters, resulting in a total of 54 grape samples.

References


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