Genetic structure of vineyard-associated Saccharomyces cerevisiae populations revealed by microsatellite analysis

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Abstract

The analysis of phylogenetic and microsatellite variability in 306 Saccharomyces cerevisiae isolates collected from 79 Portuguese wineries revealed that a high proportion of isolates showed a similar fermentation profile as well as a high degree of genetic diversity. The microsatellite analysis also revealed sibling isolates within each vineyard, indicating a genetic structure similar to that observed in natural populations. The results support the hypothesis that S. cerevisiae populations are genetically structured at the vineyard level, with a high level of genetic diversity within each vineyard and a lower level of diversity between vineyards.

Introduction

The grape yeasts depend on a large variety of factors such as climatic conditions including temperature, humidity and rainfall, soil type, azores, genotype and adaptation, the fermentative potential, grape variety, the vineyard's exposure to wind and sun, the vineyard's size and the number of vineyards in the area. The selection of the best grape yeast is essential for the establishment of adequate selection control of the fermentation process, concerning the motto “special yeasts for special traits” [4]. The detailed evaluation of the yeasts is an essential step for the establishment of the fermentation process, concerning the yeasts "special yeasts for special traits" [4].

Materials and Methods

Samples

The sampling was carried out at various wineries located in the Vinho Verde region of Portugal, during the 2001–2003 harvest seasons. Among the 93 alleles screened (using mtDNA RFLP) of 1620 isolates of grapes collected in three vineyards of the Vinho Verde region, in northwest Portugal, during the 2001–2003 harvest seasons.

Fermentation

The microsatellite variability

The presence of sibling isolates within each vineyard, indicating a genetic structure similar to that observed in natural populations. The results support the hypothesis that S. cerevisiae populations are genetically structured at the vineyard level, with a high level of genetic diversity within each vineyard and a lower level of diversity between vineyards.

Conclusions

Microsatellite typing with loci SCAYT1-SCAYT6, followed by statistical analysis permitted the recovery of genetic, and therefore the appropriate separation of individual vineyard populations. The present results clarify the existence of grape-yeast diversity, but this knowledge is not enough to explain the formation of genetically isolated subpopulations of grape-yeasts. The genetic diversity within each vineyard is very high, indicating a high degree of genetic variability within each vineyard.

References