Comparison of vineyard-associated Saccharomyces cerevisiae populations by microsatellite analysis

Dorit Schuller1, Eva Valero2,3, Brigitte Cambon2, Sylvie Dequini2, Margarida Casal2

1 Departamento / Centro de Biologia, Universidade do Minho, Braga, Portugal
2 UMR Sciences pour l’Oenologie, INRA, Montpellier, France
3 Present address: Departamento de Agroalimentação, IMIDRA, Madrid, Spain

Abstract

Herein, we present the first results of an extensive study performed during several harvest seasons on the diversity of Saccharomyces cerevisiae populations associated with vineyards. The study was carried out in the Vinho Verde Wine Region of Portugal and the Rhone Valley (South France) during the 2001–2003 harvest seasons. Among the 93 isolates obtained, 52 new alleles were identified. For all microsatellites analyzed, heterozygosity was three times two or less than the expected value, probably due to a strong population substructuring. Population structures were identified based on the accumulation of small allele-frequency differences among sites in groups of vineyards. The present work is the first large-scale approach allowing that microsatellites typing results in a new large population resolution of Saccharomyces cerevisiae strains isolated from vineyards.

Introduction

The grape’s fruit juice is a large variety of factors such as climatic conditions including temperature and rainfall, the geographic isolation of the vineyard, its viticulture, oenological practices, the vintner technique, grape variety, the vineyard’s age as well as the soil type.

Materials and Methods

Samples

The sampling plan included four vineyards in the North of Portugal (Barcelos, Vila Verde, Vila Real and Guimarães) and one vineyard in the Languedoc Region (South France) during the 2001–2003 harvest seasons. Among the 93 isolates obtained, 52 new alleles were identified. For all microsatellites analyzed, heterozygosity was three times two or less than the expected value, probably due to a strong population substructuring. Population structures were identified based on the accumulation of small allele-frequency differences among sites in groups of vineyards. The present work is the first large-scale approach allowing that microsatellites typing results in a new large population resolution of Saccharomyces cerevisiae strains isolated from vineyards.

Abstract

The aim of the present study was to gain insight into the populational structure of vineyard-associated Saccharomyces cerevisiae strains from spontaneous fermentations of grapes collected in three vineyards of the Vinho Verde Wine Region of Portugal.

The C2 population lies within the P-cluster, indicating that genetic differences do not delimit specific populations belonging to each vineyard. The highest Saccharomyces biodiversity was observed in winery M (323 isolates, 73 patterns) followed by C (26 isolates, 3 patterns) and P (20 isolates, 4 patterns), respectively.

Saccharomyces species that may be present in spontaneous fermentations are characterized by unique specific microsatellite patterns.

This poster is available at http://repositorio.sdum.uminho.pt

Acknowledgements

The authors wish to thank all wine production facility representatives, especially the three vineyard managers and the wine producers from the three vineyards.

References

[10] Software for population genetics, Alcalde de la Reconquista, Spain.

RESULTS

A two-way analysis of variance (ANOVA) was performed on the data using the statistical package STATISTICA 8.0 (Statsoft, Tulsa, OK).

Conclusions

Microsatellites of Saccharomyces cerevisiae strains were found to be neutral markers of variability in a large population of grapevine-associated yeasts isolated from vineyards. The presence of these neutral markers in grapevine-associated yeasts can be used to evaluate the genetic diversity and population structure of Saccharomyces cerevisiae strains. Genetic differentiation among S. cerevisiae populations derived mainly from grapevine in whole-race frequencies rather than from demographic ‘dispersal’ patterns, and the accumulation of small allele-frequency differences among sites in groups of vineyards. The presence of these neutral markers in grapevine-associated yeasts can be used to evaluate the genetic diversity and population structure of Saccharomyces cerevisiae strains. The extant of the current approach to strains isolated from other viticultural regions is currently underway, since a preliminary comparison reveals major differences in both climatic conditions and viticultural practices (unpublished data).

Molecular identification

In Portugal, yeast populations isolated from different sites within the same vineyard were identified using the following techniques.

The six markers revealed a high degree of genetic variability, being ScAAT1 and ScAAT7 the most polymorphic markers with 31 and 19 alleles, respectively.

The number of genotypes was further characterized by six microsatellites, ScAAT2, ScAAT5, ScAAT6, ScAAT3, ScAAT4 and ScAAT1. Each microsatellite revealed a high degree of genetic variability, with ScAAT1 and ScAAT3 being the most polymorphic markers with 31 and 19 alleles, respectively.

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