Introduction

Fermentations by yeasts and fungi have a longstanding cultural and historical tradition in most societies and the economic interest of fermentation technologies is constantly increasing. Saccharomyces cerevisiae is one of the world’s premier fermenting microorganisms. Yeasts are predominately found in association with human activities, particularly the production of alcoholic beverages. Whether the vineyard is the natural environment of S. cerevisiae, or whether it is a matter of contamination, recent studies have shown that specific strains can be isolated from the populations of alcoholic beverages that have been fermented. The vineyard is thus subject to the influence of the brewing process, which can change the microbiological composition of the vineyard. The objectives of the present study were to evaluate the population distribution among S. cerevisiae isolates isolated from some of the most important grape varieties in different Portuguese regions, using polymorphic microsatellites.

Materials and Methods

Samples

The sampling plan included 20 vineyards and 4 grape varieties in several Portuguese apppellations of origin. In each region, representative specific microsatellite markers were selected for the purpose of comparing grape varieties, and for the generations (5 randomly selected isolates) of yeast strains obtained from spontaneously fermenting grape juice (100 ml) in 2001, 2003, and 2006. The number of isolates per grape variety was limited to 225. In each vineyard, samples were collected from the same variety and grape variety at different grape varieties are also predominant in the fermenting fermenting-yeast flora of grapes from the Vinho Verde and Bairrada Regions. However, in the central region of Portugal, the fermenting yeast flora is dominated by S. cerevisiae. The distribution of the most frequent alleles among vineyards is shown in the Table 1. The ten markers revealed a high degree of genetic variability, being ScAAT1, C5 and ScAAT5 the most polymorphic markers with 62, 20 and 20 alleles, respectively.

Allelic frequencies

Distribution of the most frequent microsatellite alleles

The colored circles mark the three most frequent alleles among the different grape varieties of the Vinho Verde and Bairrada Regions. Five alleles were shared by more S. cerevisiae populations, whereas alleles 20X(AAT1), 20X(C), 22X(C) and 23X(C) can be considered as characteristic of the vineyards from where these isolates were obtained. The colored circle marks the three most frequent alleles among the different isolates from each vineyard. The ten markers revealed a high degree of genetic variability, being ScAAT1, C5 and ScAAT5 the most polymorphic markers with 62, 20 and 20 alleles, respectively.

Conclusions

The fermenting yeast flora of grapes from the Vinho Verde and Bairrada Regions is dominated by S. cerevisiae and is characterized by a strong genetic diversity. The distribution of the most frequent alleles among the different grape varieties of the Vinho Verde and Bairrada Regions is shown in the Table 1. The ten markers revealed a high degree of genetic variability, being ScAAT1, C5 and ScAAT5 the most polymorphic markers with 62, 20 and 20 alleles, respectively.

References