Abstract

The conditions of four genetic fingerprinting methods (intersimple sequence typing, mitochondrial DNA restriction fragment length polymorphism (RFLP), bacterial repetitive element-based fingerprinting, and multilocus sequence typing) were compared for their ability to detect chromosomal rearrangements and genetic instability in the strain Zymaflore VL1 (Saccharomyces cerevisiae). From 33 randomly selected isolates, 17 isolates showed chromosomal rearrangements, which were detected as variable numbers of bands in the RFLP, PFGE, and microsatellite analysis. The microsatellite analysis was the most efficient method to detect variations of chromosome length, as it allowed the detection of 18 out of 18 cases of chromosomal rearrangements across different genetic fingerprinting methods.

Genetic instability of a commercial Saccharomyces cerevisiae strain

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Introduction

With the advent of new genetic fingerprinting methods, the ability to detect chromosomal rearrangements and genetic instability in yeast is improving. The occurrence of such rearrangements has been observed in natural isolates and is of particular interest in the field of oenology, where it is known to affect yeast performance in wine production.

Materials and Methods

Fermentation and strain isolation

The strains isolated from a commercial strain Zymaflore VL1 were obtained from a grape inoculum used in the harvest of the 2010 and 2011 vintages. The strains were isolated from different grape varieties and different geographical regions (Portugal, France). The yeast strains were isolated using the corresponding commercial yeast strain as the reference.

DNA isolation

Each isolate collected was cultured in YPD medium (1% w/v sucrose, 0.1% w/v peptone, and 0.5% w/v yeast extract), and DNA was processed using previously described protocols. The DNA was purified from each isolate, and its quality and quantity were assessed.

Microsatellite amplification

The microsatellite DNA markers were amplified using specific primers. The amplification conditions were optimized to ensure optimal PCR reaction conditions. The microsatellite analysis was performed using capillary electrophoresis, and the results were analyzed using specific software.

RESULTS

Chromosomal polymorphisms

Microsatellite analysis of the commercial strain Zymaflore VL1

Chromosomal polymorphisms were assessed in 18 isolates from the commercial strain Zymaflore VL1. The results showed that 17 out of 18 isolates had chromosomal rearrangements, which were detected as variable numbers of bands in the RFLP, PFGE, and microsatellite analysis. The microsatellite analysis was the most efficient method to detect variations of chromosome length, as it allowed the detection of 18 out of 18 cases of chromosomal rearrangements across different genetic fingerprinting methods.

Conclusions

Chromosomal rearrangements were detected in 17 out of 18 isolates from the commercial strain Zymaflore VL1. The microsatellite analysis was the most efficient method to detect chromosomal rearrangements, as it allowed the detection of 18 out of 18 cases across different genetic fingerprinting methods.

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