

Molecular Microbiology and Microbial Physiology

P-313 - SELECTION OF YEAST STRAINS ISOLATED DURING ALENTEJO WINES PRODUCTION TO BE USED AS STARTERS

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Background

The knowledge of new species of yeasts potentialities with fermentative characteristics and/or with specific sensorial properties can be an important tool for the development of oenological processes with higher microbial complexity in a controlled system, conferring a higher wine quality and promoting innovative organoleptic characteristics to the final product.

Identification and characterization of yeasts with certain oenological properties is very important to explore their fermentation potential and improve wine production.

The aim of this study was the identification and characterization of yeast strains with oenological potential, isolated from different grape musts fermentations from Alentejo region.

Method

Initial screening allowed a selection of 16 different yeast strains from grape must from Touriga Nacional, *Cabernet Sauvignon*, Antão Vaz and Síria, at various stages of the fermentation process, to be used in immobilization systems, on the development of new oenological solutions. Batch cultures of these microorganisms were performed in order to characterize kinetic growth, carbohydrate consumption and ethanol production. Selected strains were characterized by their macroscopic and microscopic characteristics. DNA were extracted and amplified for strains identification and characterization [1].

Results & Conclusions

The identification was done by the sequencing of PCR products obtained after amplification of the D1/D2 domain of the large subunit ribosomal RNA gene, and it was possible to identify *Saccharomyces cerevisiae*, *Torulaspora delbrueckii*, *Zygoascus meyeriae*, *Pichia kudriavzevii*, *Rhodotorula mucilaginosa*, *Saccharomyces sp.* and *Hanseniaspora sp.* strains. Molecular analysis by M13-PCR allowed to characterize the genetic profiles for all the isolated yeast strains, showing differences on molecular profiles that allowed grouping according to phylogenetic proximity, both between different species and between strains of the same species.

This approach allows better microbiologic knowledge about the grape must flora and to improve the selection of the most appropriate consortia to be used in the creation of new starters for immobilization solutions.

References & Acknowledgments

References:

[1] Salvador, C. *et al* (2013) *Annals of Microbiology* 64:1179-1187.

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