SURVEY OF MOLECULAR METHODS FOR THE TYPING OF WINE YEAST STRAINS

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Wine production by the use of selected *Saccharomyces cerevisiae* strains, commercially available as active dry yeast is widely accepted, being an enological practice extensively applied nowadays. The use of techniques that enable to distinguish the inoculated strain from the remaining yeast flora present in the grape must is regarded with great practical interest. In the last years, several methodologies of typing based on DNA polymorphisms have been developed which allowed the discrimination among closely related yeast strains.

A survey of the genetic polymorphisms produced by distinct methods was performed in 23 commercial winery yeast strains. The microsatellite typing, using 6 different *loci*, an optimized interdelta sequence analysis and RFLP of mitochondrial DNA generated by the enzyme *Hinf* I had the same discriminatory power: among the 23 commercial yeast strains, 21 distinct patterns were obtained. Karyotype analysis originated 22 patterns, thereby allowing the discrimination of one of the three strains that were not distinguished by the other methods. Due to the equivalence of the results obtained in this survey, any of the methods can be applied at the industrial scale.

[1] Blondin, B. and Vezinhet, F. 1988. Rev. Fr. Oenol. 28: 7-11.

[2] Ness, F., Lavallée, F., Dubourdieu, D., and Aigle, M. 1993. J. Sci. Food Agric. 62: 89-94.

[3] Querol, A., Barrio, E., and Ramón, D. 1992. System. Appl. Microbiol. 15: 439-446.

[4] Pérez, M.A., Gallego, F.J., Martinez, I. and Hidalgo, P. 2001. Lett. Appl. Microbiol. 33, 461-466.

[5] Legras, J.L. and Karst, F. 2003. FEMS Microbiol Lett 221(2):249-55.

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