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The genetic characterization of *Saccharomyces cerevisiae* commercial enological strains: a survey of molecular typing techniques

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Wine production by the addition of active dry wine yeast is today widely accepted, being about 50% of the wine produced in Europe in this way. This enological practice required the development of techniques that were able to distinguish the inoculated strain from the rest of the wild yeast strains present in the must. In the last years, several methodologies based on DNA polymorphisms, have become widely accepted for the discrimination between closely related wine strains. The aim of this study is to validate the usefulness of each typing method (karyotype analysis [1], ∂ sequence typing [2][5], mtDNA restriction analysis [3], and microsatellite genotyping [4]) by studying the degree of polymorphism generated by each of them in 23 commercially available winery yeasts from 5 companies.

The amplification of delta sequence interspersed DNA regions generated only 8 patterns for primer pair A [2] and 20 for primer pair B [5] respectively. The discriminative power of karyotype analysis and mtDNA RFLP (using the restriction enzyme *Hinf*I) was very similar, and generated 21 patterns for the 23 strains. The results obtained by both methods indicated the occurrence of one strain that is commercialized by 3 different active dry yeast producers. Microsatellite typing, using multiplex reactions for six markers on different chromosomes, unequivocally confirmed the results obtained by karyotyping and by mtDNA RFLP.

In global terms, the results show that microsatellite analysis is a very precise and fast method for the typing of *S. cerevisiae* strains. Studies are now underway to type a yeast strain collection and to perform biodiversity studies by this method.

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