

Genetic structure of vineyard-associated *Saccharomyces cerevisiae* populations revealed by microsatellite analysis

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The analysis of six polymorphic microsatellite loci was performed in 361 *Saccharomyces cerevisiae* isolates obtained from spontaneous fermentations. This population derived from a previous screening (using mtDNA RFLP) of 1620 isolates of grapes collected in three vineyards of the Vinho Verde Region, in northwest Portugal, during the 2001 – 2003 harvest seasons. Among the 93 alleles obtained, 52 new alleles were identified. For all loci analyzed, observed heterozygosity was three to four times lower than the expected value, probably due to a strong populational substructuring. Populational structures were identified based on the accumulation of small allele-frequency differences across six loci in groups of strains. Genetic differentiation in the same vineyard in consecutive years was of the same order of magnitude as the differences verified among sampling sites within each vineyard. Correlation of genetic differentiation with the distance between sampling points suggested a pattern of isolation-by-distance, where genetic divergence in a vineyard increased with size. The present work is the first large-scale approach showing that microsatellite typing reveals a very fine population resolution of indigenous *S. cerevisiae* strains isolated from vineyards.