

**PHYLOGENOMICS APPLIED TO *SACCHAROMYCES CEREVISIAE*
STRAINS REVEALS GENES WITH HIGH EVOLUTIONARY
RESOLUTION**

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The quest for genes representing genetic relationships of strains or individuals of a same population and their evolutionary history is acquiring a novel dimension of complexity and novel possibilities with the advancement of NGS technologies. In the past several authors have proposed candidate gene, or combinations of them, that were able to map the diversity of *Saccharomyces cerevisiae* strains, allowing to distinguish and cluster into separate branches closely related strains and therefore to recapitulate the natural diversity of *S. cerevisiae*, both in domesticated and in natural populations. Nowadays, sequencing an entire genome is quite feasible and many genomes of different strains are available to the scientific community. This opens up the possibility to uncover genetic variation in coding and non-coding regions of a population of individuals of the same species. In fact, the knowledge of the sequence variation in a population of strains of the species *S. cerevisiae* offers the ideal model to search a gene or a set of genes representing the evolutionary relations among strains, that could be also inferred from the analysis of their entire genomes. In this work we propose an original strategy aimed at identifying a minimal set of genes able to characterize the population structure of natural yeast strains. By applying a combinatorial approach on gene selection to a pipeline for fast parallel phylogenetic analysis and to an efficient tree-screening strategy, we were able to isolate several genes with sufficient evolutionary resolution to be used in strain characterization and phylogenetic assessment, giving results comparable to those obtained with full genome sequencing.