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The genotypic and pheno-metabolomic landscape of *a Saccharomyces cerevisiae* strain collection

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Genome sequencing is essential to understand individual variation and to study the relationship between genotype and phenotype. Recently, large-scale sequencing projects of *Saccharomyces cerevisiae* revealed the existence of a few well defined lineages and some mosaics of that lineages, suggesting two domestication events during the history of association to human activities, one for sake strains and one for wine strains. Nevertheless, scarce information is available regarding phenotypic variability among strains used for different biotechnological applications.The objective of the present work was to undertake high-throughput approaches for a combined genetic, phenotypic and metabolomic evaluation of 187 *S. cerevisiae* strains. 100793 data points were generated and data analysis was performed using Principal Component Analysis (PCA).Phenotypic screening considered 28 physiological traits with biotechnological relevance. Resistance to ethanol (14 and 16% v/v), growth in the presence of potassium bisulfite and sulfur dioxide and the capacity to grow at 40°C contributed most to the highest variance (strain variability). Genetic characterization was performed using eleven highly polymorphic *S. cerevisiae* specific microsatellite loci. More than 200 different alleles were obtained, being around 30 responsible for the highest strain variability. All strains were used for fermentations with must of the grape variety Loureiro. When glucose concentration was below 5 g/L, samples were collected and used for fiber optics spectroscopy and bioanalytical analysis. HPLC was used to quantify primary fermentation products and organic acids. Fructose, glucose and ethanol concentrations contributed to the highest variance. Relevant volatile compounds that account for inter-strain differences were determined by GC-MS. PCA revealed ethyl acetate, 1-hexanol and 2-methylpropanol as the ones with highest weight. Globally, only spectral analysis (UV-VIS-NIR) showed correspondence between PCA segregation of strains and their technological use. Computational analyses are now underway to combine the strain's metabolic signatures with phenotypic and genetic data, to obtain a holistic overview of the pheno-metabolomic landscape and to develop tools for the prediction of a strain's biotechnological potential.

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