

Genome-wide screening of *Saccharomyces cerevisiae* genes required to foster tolerance towards inhibitory compounds in industrial biomass hydrolysates

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The understanding of the determinants of yeast tolerance to inhibitory compounds present in fermentation media at the genetic level is of essential importance for the improvement of second generation bio-ethanol conversion technology. The aim of this study was to systematically identify, at a genomic scale, the *Saccharomyces cerevisiae* genes required for simultaneous and maximal tolerance to key inhibitors derived from lignocellulose biomass pre-treatment. Based on the screening of the EUROSCARF haploid mutant collection, 242 and 216 determinants of yeast resistance to inhibitory compounds present in industrial wheat straw hydrolysate (WSH) and in inhibitor-supplemented synthetic hydrolysate (SH) were identified, respectively. Twenty-two mutants with deleted genes involved in “Oxidative stress response”, “Lipid Metabolism”, “Aminoacid metabolism”, “Vacuolar acidification”, “Intracellular trafficking and protein sorting”, “Transcription machinery and RNA processing” and “Mitochondrial function” showed a strong susceptibility phenotype in both WSH and SH, 8 of them being for the first time identified as conferring resistance to lignocellulose-derived inhibitors. The intersection of our WSH and SH datasets and those obtained in previous genome-wide studies on single chemical stress resistance, together with results obtained during comparative fermentative performance analysis [1], provided data for further evaluation of the key genes involved in global adaptation to toxic biomass hydrolysates. This study expands our understanding of the genes and underlying molecular mechanisms that are directly involved in yeast response to the multiple stresses occurring during lignocellulose fermentations under industrially relevant conditions.

References:

[1] Pereira FB, Guimarães PMR, Gomes DG, Mira NP, Teixeira MC, Sá-Correia I, Domingues L, “Identification of candidate genes for yeast engineering to improve bioethanol production in Very-High-Gravity and lignocellulosic biomass industrial fermentations”, *Biotechnol. Biofuels*. (2011) 4:57

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