P18 - Metabolic engineering industrial yeast strains for efficient hemicellulosic bioethanol production

Carlos Costa[1], Aloia Romaní[1], José António Teixeira[1], Björn Johansson[2], Lucília Domingues[1]

[1]CEB – Centre of Biological Engineering, University of Minho, Campus de Gualtar, Braga 4710-057, Portugal; [2]CBMA – Center of Molecular and Environmental Biology, University of Minho, Campus de Gualtar, Braga 4710-057, Portugal. (pg26392@alunos.uminho.pt)

The constant increase of fossil fuels consumption, raising their prices, and environmental concerns derived of its use has stimulated the search for new renewable energy sources. Lignocellulose raw materials (LCMs) derived from agricultural, industrial and forest biomass can be a source of environmental, economic and strategic benefits, avoiding the competition with food production, when used as sustainable feedstock. [1] Nevertheless, lignocellulosic processing to obtain fermentable sugars involves a pretreatment that generates inhibitor compounds of fermentation process and sugars as xylose which cannot be naturally consumed by *Saccharomyces cerevisiae*. Therefore, the pursuit for robust microorganisms in order to design sustainable processes for cellulosic and hemicellulosic bioethanol production is one of the main challenges for a cost-effective lignocellulosic biofuels. The use of natural robust yeast strains can overcome inhibitors effect, as they are known for a higher fermentation capacity and stress tolerance related with harsh industrial processes like high sugar and ethanol concentrations, elevated temperatures, pH variations and presence of toxic compounds. [2] In addition, previous studies from our group have identified key genes necessary for yeast growth and maximal fermentation rate in hydrolysates [3,4]. Strains with robust genetic backgrounds have been shown to already demonstrate enhanced background expression of several genes involved in the detoxification of some of these inhibitors [5], but different genetic backgrounds have shown to present diverse responses. [4] On the other hand, the inhibitory load of lignocellulosic hydrolysates, which varies depending on the raw material and operational conditions of pretreatment [6], has been shown to differentially influence the consequence of genetic manipulations [4], highlighting the importance of evaluating their effect under process-like conditions. In this sense, the aim of this work was to evaluate the effect of xylose metabolic engineering on different background yeast strains isolated from industrial environments ("cachaça" distilleries and first and second bioethanol industries) using several pretreated lignocellulosic feedstocks.

REFERENCES: [1] Ruiz HA, Rodríguez-Jasso RM, Fernandes BD, Vicente AA, Teixeira JA. (2013). Renew. Sust. Energy Rev., (21): 35; [2] Pereira FB, Guimarães PMR, Teixeira JA, Domingues L. (2011). J. Biosci. Bioeng., 112 (2): 130; [3] Pereira FB, Romaní A, Ruiz HA, Teixeira JA, Domingues L. (2014). Bioresource Technology, (161): 192; [4] Cunha JT, Aguiar TQ, Romaní A, Oliveira C, Domingues L. (2015). Bioresource Technology, (191): 7; [5] Liu ZL, Ma M, Song M. (2009). Mol. Genet. Genomics, (282): 233; [6] Chandel AK, da Silva SS, Singh OV. (2013). Bioenerg. Res., (6): 388.