PROSPECTING GENES OF XYLOSE METABOLISM IN YEASTS ISOLATED FROM ROTTING ENERGY CANE AND PLAGUE INSECTS

Borelli, G.¹; Santos, L.V.¹; Pereira, G.A.G.¹
¹Laboratório de Genômica e Expressão, Departamento de Genética, Evolução e Bioagentes, Instituto de Biologia, Universidade Estadual de Campinas, Campinas, Brazil

Commercial instability and the ecologically costly use of petroleum subproducts are the main reasons for the increase of research in biocompounds area. The second-generation ethanol (2G) production from sugarcane bagasse or straw is an alternative to avoid these obstacles. However, the yeast strains used industrially for production of ethanol in Brazil do not consume pentoses present in sugarcane bagasse, being xylose the most common sugar in biomass. Despite several attempts to obtain strains that consume these sugars, the lineages still do not have a satisfactory performance for ethanol production in industrial scale. Thus, this work explores a yeast collection built from degraded energy cane and plague insects collected from energy cane. The primary targets are xylose reductases and transporters. Through prospection of these genes, we expect an efficient expression in industrial strains obtaining a yeast with high performance in ethanol production. We built the collection directionally inducing isolation of yeasts that consume xylose. Almost 800 isolates are being identified by sequencing using ITS and D1/D2 from large ribosomal subunit, and some of the species are being characterized through fermentation assays with xylose and lignocellulosic biomass hydrolysate, in order to find a robust platform for production of renewable chemicals, which is of great industrial interest. Two species have exhibited high rate of xylose uptake when compared with the other strains and have no published genomes. We are sequencing their genomes to obtain the genes of interest. One of the yeasts isolated presented a higher xylitol yield in synthetic media and biomass hydrolysate even when compared with known strains in literature. Finally, some of genes of xylose pathway will be expressed in industrial Saccharomyces cerevisiae strains to evaluate the production of 2G ethanol.

We acknowledge National Council for Scientific and Technological Development (CNPq) for funding.

Keywords: Xylose, xylitol, second generation ethanol (2G).