

Biodiversity bioprospecting for xylitol production: selection, physiological and genetic characterization of new yeast strains

Débora Trichez¹, Clara V. G. C. Carneiro, Carlos E. V. F. Soares^{1,2}, Andrei S. Steindorff, ,
Eduardo F. Formighieri and João R. M. Almeida^{1,2}

¹Embrapa Agroenergy, Brasília, Brazil

²University of Brasilia, Brasília, Brazil

joao.almeida@embrapa.br

Growing demand for chemical products and environmental friendly processes has motivated the search for alternative solutions and renewable raw materials to replace some conventional processes. In this way, the lignocellulosic biomass has a great potential to be used for production of biofuels and value added chemicals. Xylitol is a five-carbon polyol with a wide-range of applications in odontologic pharmaceutical and food industries. At industrial scale, it is produced chemically by an expensive process of xylose hydrogenation at high temperatures and pressures, using nickel metal as catalyst. Since some yeast are able to convert xylose to xylitol, microbiological fermentation processes can be an interesting alternative to produce xylitol with lower cost. Considering this context, we prospected 400 yeast strains from Brazilian biodiversity for their ability to utilize xylose for growth. Following, the best performing strains were characterized physiologically. Xylose consumption profile and xylitol production by these cells were determined during cultivation in bioreactors using mineral medium and sugarcane bagasse hydrolysate under different aeration conditions. Sequencing of 26S r-DNA demonstrated that these strains are close related to the clade *Spathaspora* sp. and *Meyerozyma* sp. The new strains did not produce significant quantities of ethanol from xylose, but the xylitol production reached yields up to 0,70 g.g⁻¹, showing similar performance with strains commonly used for xylitol production. To better understand the genetic background of two yeasts, whole genome sequencing was performed and a comparative analysis was carried out. Data on genomes size, annotation and gene synteny will be presented and discussed.