Transcriptome analysis of *Aspergillus niger* grown on sugarcane bagasse

de Souza, W.R.1;Gouvea, P.F.2; Savoldi, M.1; Malavazi, I.3; Goldman, G.H.1*

1- FCFRP, Universidade de São Paulo (USP) and *Laboratório Nacional de Ciência e Tecnologia do Bioetanol (CTBE); 2- FMRP, Universidade de São Paulo (USP), Brazil; 3- Universidade Federal de São Carlos (UFSCar), Brazil

In order to increase bioethanol production, new studies to understand and improve cellulase efficiency and productivity are of paramount importance. Filamentous fungi like *Aspergillus niger* are impressive producers of hydrolytic enzymes already applied in a series of industrial processes. The *A. niger xlnR* transcription factor is a master regulator that activates enzymes of the xylanolytic system, a number of endocellulases and two cellobiohydrolases. The study of transcriptional regulators involved in the activation of genes that encode enzymes responsible for the degradation of cellulose and hemicellulose could provide several advantages for further genetical improvement of biomass-degrading microorganisms. In the present study, we have performed a transcriptional analysis of *Aspergillus niger* wild-type and a deletion mutant strain, Δ*xlnR,* grown on steam-exploded sugarcane bagasse (SESB), a common by-product of ethanol production in Brazilian industrial plants. The transcriptome demonstrated that a broad range of cellulases and hemicellulases were expressed in *A. niger* wild-type strain grown on SESB. As expected, we have found that XlnR is essential to regulate the transcription of many cellulolytic and xylanolytic-encoding genes, since the expression of these genes are much lower in the deleted strain in relation to the wild-type strain. The results have shown that steam-exploded sugarcane bagasse could be a suitable substrate for hydrolytic enzymes production. Future prospects include genetical manipulations in XlnR in order to improve the productivity of hydrolytic enzymes for bioethanol production.

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