DIFFERENTIAL EXPRESSION ANALYSIS OF CELLULASES FROM GLYCOSILHYDROLASE FAMILY OF \textit{PENICILLIUM ECHINULATUM} S1M29 IN INDUCTION AND REPRESSION CONDITIONS

Nora, L. C.\textsuperscript{1}, Persinoti, G. F.\textsuperscript{2}, Gonçalves, T. A.\textsuperscript{2}, Squina, F.\textsuperscript{2}, Dillon, A. J. P.\textsuperscript{1}, Camassola, M.\textsuperscript{1}

\textsuperscript{1} Instituto de Biotecnologia, Universidade de Caxias do Sul, Rio Grande do Sul, Brazil
\textsuperscript{2} Laboratório Nacional de Ciência e Tecnologia do Bioetanol (CTBE), São Paulo, Brazil

The fungus \textit{Penicillium echinulatum} S1M29 arouses interest of study for producing enzymes that hydrolyze lignocellulosic biomass to obtain ethanol. In order to analyze the transcriptional profile of glycosyl hydrolases from \textit{P. echinulatum} grown both in bagasse sugarcane (BCA) and glucose, a large-scale RNA sequencing was performed. The paired-end reads generated using Illumina HiSeq 2500 were quality filtered using Trimmomatic and assembled into transcripts using Trinity. EdgeR/Bioconductor package was used for differential expression analysis. Transcriptome annotation was achieved according to the pipeline suggested by Trinotate, integrating information of transcripts with differential expression data and proteins predicted by the program Transdecoder. In addition, BLASTp and BLASTx analysis were conducted to identify possible gene functions. The resulting predicted proteins were classified into families according to dbCAN, such that 59 proteins were found to belong to AA family (auxiliary protein), 128 with domains of CBM family (carbohydrate binding modules), 407 proteins of GH family (glycosil hydrolases), 155 of GT family (glycosyltransferases), and 17 of PL
family (polysaccharide lyases). Among the GH family, four endoglucanases were identified, wherein three were down-regulated in glucose and up-regulated in BCA and one did not show differential expression. Moreover, 15 beta-glucosidases were identified, wherein seven were down-regulated in glucose and up-regulated in BCA and 6 presented no differential expression. Among cellobiohydrolases, one was down-regulated in glucose and one had no differential expression. Three alpha-glucosidases were down-regulated in glucose and up-regulated in BCA. It is perceivable that, when the carbon source changes, the mutant *P. echinulatum* S1M29 expresses its genes differently, in order to adapt to environmental conditions. Most genes encoding cellulolytic enzymes were expressed in a positively manner in BCA media, suggesting that this biomass can be used as a carbon source to induce the production of cellulases in *P. echinulatum*.

**Key words:** cellulases, RNA-seq, *Penicillium echinulatum*. 