EFFECT OF THE MUTANT *ΔTRBTF3* OF *TRICHODERMA REESEI* IN THE TRANSCRIPTIONAL RESPONSE BY MICROARRAYS

SAENZ, E.C.T., FERREIRA, A.J., RAMOS, A., DORRY, H.F.

Instituto de Química, Universidade de São Paulo.

This filamentous fungus is a microorganism that has been used by some laboratories around the world for the study of diverse basic biological questions due to its great biotechnological importance. We had established a data base of ESTs for this microorganism and, through the technique of cDNA microarray, we had determined the transcriptional response of *T. reesei* to oxygen and glucose availability, as well as some environmental stresses. Based on such studies we chose some transcripts affected by oxygen limitation such as the *btf3* gene, for more detailed investigations. This gene codes for the BTF3 regulatory protein (RNA Polymerase B Transcription Factor 3), a conserved transcriptional factor among eukaryotes that is involved in the transcription of several class II promoters and is part of the nascent polypeptide-associated complex (NAC). In order to study the functionality of the *btf3* gene in normal conditions, a large-scale transcriptional comparative analysis between *T. reesei* wildtype strain QM9414 and the *btf3* knockout mutant was executed. The expression of approximately 2,000 genes was analyzed using microarrays. The knockout of *btf3* produces the increment of the expression of genes involved with the primary metabolism pathways (ND4 and FBA), cellular defense (DnaJ, HSP70 and RCI), cell wall (ACT) and protein synthesis (eIF2); whereas it repressed genes related to the structure cell (HFBII), protein synthesis (eIF1) and RNA synthesis (ATF21).