Functional analysis of the transcription factors XlnR and CreA involved in the regulation of transcription of cellulases- and hemicellulases-encoding genes in *Aspergilli*

Gustavo H. Goldman
Laboratório Nacional de Ciência e Tecnologia do Bioetanol – CTBE, Caixa Postal 6170, 13083-970 Campinas, São Paulo, Brazil and Faculdade de Ciências Farmacêuticas de Ribeirão Preto, Universidade de São Paulo, São Paulo, Brazil

The high cost of hydrolyzing biomass polysaccharides to fermentable sugars remains a major obstacle to be overcome before cellulosic ethanol can effectively be commercialized. The costs of cellulases and hemicellulases contribute substantially to the price of bioethanol. New studies to understand and improve cellulase efficiency and productivity are of paramount importance. The study of transcriptional regulators involved in the regulation 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. The *Aspergilli* transcription factors XlnR and CreA are regulators that activate and catabolite repress enzymes of the xylanolytic system, a number of endocellulases and two cellobiohydrolases. We are interested in understanding how *Aspergilli* senses the presence of cellulose, hemicelluloses, and the catabolite repressor glucose and transduce this signal to the transcription factors XlnR and CreA. Here, we describe a screening of a collection of *A. nidulans* null mutations of genes encoding about 100 protein kinases and 40 F-box proteins for the presence or absence of growth in minimal medium supplemented either with xylose or glucose and inhibitory concentrations of the glucose analogue 2-deoxy-glucose or allyl alcohol. Growth and reduced growth of growth in these media made possible to identify mutants which are either catabolite repression resistant or sensitive. We were able to identify several mutants that correspond to genes that encode protein kinases as catabolite sensitive and one F-box protein as catabolite resistant. Further molecular characterization of these mutants and their corresponding genes will be shown and discussed. Financial support: FAPESP and CNPq, Brazil.