TRANSCRIPTION FACTORS INVOLVED IN GLYCOGEN METABOLISM REGULATION in *Neurospora crassa*

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The end of the Neurospora crassa genome sequence and the availability of a collection of N. crassa mutant strains individually knocked-out in genes encoding transcription factors by the FGSC allowed us to start to perform an investigation of the transcription factors involved in the glycogen metabolism regulation. Glycogen content in N. crassa reaches maximal level at the end of the exponential growth phase however under heat shock glycogen content rapidly drops. Transcription of the gene encoding glycogen synthase (gsn), the regulatory enzyme of glycogen synthesis also decreases after heat shock. A screening was performed with cells of the mutant strains grown under conditions of heat shock or not. The results showed that 10 mutant strains presented changes in glycogen accumulation when compared to the wild type strain. Only two transcription factors have functional roles in biological processes already known: the NCU08000, annotated as the cutinase transcription factor 1a and the NCU06971, annotated as the xylanolytic transcriptional activator XInR. The *gsn* gene expression was analyzed by Northern blot in the selected mutant strains cells under heat shock or not, and the results revealed that some transcription factors might regulate the *gsn* gene transcription. In some strains gene transcription was totally different from the one observed in the wild type strain. Results from preliminary flow cytometry analysis revealed that the absence of some transcription factors results in different conidia size, cell morphology and propidium iodide incorporation in relation to the wild type strain conidia suggesting that some of the selected transcription factors are likely involved in the regulation of other cellular events.

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