IDENTIFICATION OF *Neurospora crassa* TRANSCRIPTION FACTORS REGULATING GLYCOGEN METABOLISM

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A search for transcription factors involved in glycogen metabolism regulation in N. crassa has been performed in our laboratory. It is known that in N. crassa glycogen content reaches maximal level at the end of the exponential growth phase and under heat shock condition it rapidly drops. This process might result from the regulation at transcriptional level of enzymes involved in the carbohydrate metabolism, since transcription of the gene encoding glycogen synthase (gsn) decreases under this condition. With the availability of a collection of N. crassa transcription factor knockout strains by the FGSC we started selecting the mutant strains showing a different profile of glycogen accumulation in comparison to the wild type strain. Among the selected strains are those mutants in genes encoding the transcription factors NIT2, involved in nitrogen metabolism regulation, PAC, involved in pH response regulation and RCO-1, a general transcriptional repressor. Most of the other strains are mutants in genes annotated as encoding hypothetical proteins. The expression of the gene *gsn* was analyzed by Northern blot in the selected mutant strains during normal growth and after exposure to heat shock (from 30°C to 45°C). The selected strains showed different patterns in the *gsn* gene expression; while in some of them the transcription was down-regulated after heat shock, as it is in the wild type strain, loss on the gene transcription regulation and up-regulation were also observed. This analysis allowed us to identify transcription factors involved in glycogen metabolism regulation by acting directly in the *qsn* gene transcription regulation. Analysis of the promoter *qsn* sequence identified the presence of *cis* regulatory DNA elements for some transcription factors.

Key words: transcription factors, gene expression, Neurospora

Supported by FAPESP and CNPq