Identification of Genomic Targets for the *Neurospora crassa* Hypothetical Transcription Factor NCU04390 by ChIP-sequencing

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The mechanisms by which glycogen content is controlled in microorganisms are intricate, involving co-regulation of many proteins. In *Neurospora crassa*, glycogen reaches maximal levels at the end of the exponential growth phase. However, under heat shock, glycogen content and transcription of the glycogen synthase gene (*gsn*) rapidly decrease. A NCU04390 deletion strain showed a drastic increase in glycogen levels and up-regulation of the *gsn* transcript after heat shock when compared to the wild-type strain, which suggests that NCU04390 is directly involved in the regulation of glycogen metabolism. Because the product of this ORF is annotated as a hypothetical transcription factor (TF) with an N-terminal zinc-finger and a central fungal-specific TF domain, chromatin immunoprecipitation followed by high throughput DNA sequencing (ChIP-seq) is expected to reveal genes that are directly regulated by NCU04390. First, GFP or V5 tags were translationally fused to the 3’-end of NCU04390 by gene replacements. ChIP was performed with NCU04390-GFP and -V5 strains at 30 °C and at 45 °C with commercial antibodies against the GFP or V5 tags. ChIP-libraries were sequenced on a HiSeq2000 Illumina genome analyzer. Data from both ChIP experiments, as well as validation by region-specific ChIP-PCR and RNA analyses will be presented.

Keywords: *Neurospora crassa*, transcription factor, ChIP-Seq

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