Glycerol is catabolized by a wide range of microorganisms including Aspergillus species. To identify the transcriptional regulation of glycerol metabolism in Aspergillus, we analyzed data from triplicate batch fermentations of three different Aspergilli (Aspergillus nidulans, Aspergillus oryzae and Aspergillus niger) with glucose and glycerol as carbon sources. Protein comparisons and cross-analysis with gene expression data of all three species resulted in the identification of 88 genes having a conserved response across the three Aspergilli. A promoter analysis of the up-regulated genes led to the identification of a conserved binding site for a putative regulator to be 5′-TGCGGGGA-3′, a binding site that is similar to the binding site for Adr1 in yeast and humans. We show that this Adr1 consensus binding sequence was over-represented on promoter regions of several genes in A. nidulans, A. oryzae and A. niger. Our transcriptome analysis indicated that genes involved in ethanol, glycerol, fatty acid, amino acids and formate utilization are putatively regulated by Adr1 in Aspergilli as in Saccharomyces cerevisiae and this transcription factor therefore is likely to be cross-species conserved among Saccharomycetes and distant Ascomycetes. Transcriptome data were further used to evaluate the high osmolarity glycerol pathway. All the components of this pathway present in yeast have orthologues in the three Aspergilli studied and its gene expression response suggested that this pathway functions as in S. cerevisiae. Our study clearly demonstrates that cross-species evolutionary comparisons among filamentous fungi, using comparative genomics and transcriptomics, are a powerful tool for uncovering regulatory systems.

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