Transcription Factors in Fungi: TFome Dynamics, Three Major Families, and Dual-Specificity TFs.

Shelest E (2017) Transcription Factors in Fungi: TFome Dynamics, Three Major Families, and Dual-Specificity TFs. *Front Genet* 8, 53.

Details



Abstract

Transcription factors (TFs) are essential regulators of gene expression in a cell; the entire repertoire of TFs (TFome) of a species reflects its regulatory potential and the evolutionary history of the regulatory mechanisms. In this work, I give an overview of fungal TFs, analyze TFome dynamics, and discuss TF families and types of particular interest. Whole-genome annotation of TFs in more than 200 fungal species revealed ~80 families of TFs that are typically found in fungi. Almost half of the considered genomes belonged to basidiomycetes and zygomycetes, which have been underrepresented in earlier annotations due to dearth of sequenced genomes. The TFomes were analyzed in terms of expansion strategies genome- and lineage-wise. Generally, TFomes are known to correlate with genome size; but what happens to particular families when a TFome is expanding? By dissecting TFomes into single families and estimating the impact of each of them, I show that in fungi the TFome increment is largely limited to three families (C6 Zn clusters, C2H2-like Zn fingers, and homeodomain-like). To see whether this is a fungal peculiarity or a ubiquitous eukaryotic feature, I also analyzed metazoan TFomes, where I observed a similar trend

(limited number of TFome-shaping families) but also some important differences connected mostly with the increased complexity in animals. The expansion strategies of TF families are lineage-specific; I demonstrate how the patterns of the TF families' distributions, designated as

Beteiligte Forschungseinheiten

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doi: 10.3389/fgene.2017.00053

PMID: 28523015