Plasticity of the Yeast Transcription Network After the Whole-genome Duplication

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Motivation

Gene duplication is a key mechanism in evolution for generating new functionality, and is known to have produced large proportions of genes of sequenced genomes. Reported duplication mechanisms include local events such as unequal crossing over , retroposition, together with global events, such as chromosomal or whole genome duplication (WGD). One of such "whole-genome duplication" (WGD) events has been proven among the Ascomycota fungi, in the branch of S.cerevisiae. The genes duplicated during this event are shown to have functional and interaction properties different from the conventional (local) duplicates, indicating that the WGD is free of some of the constraints affecting local duplications.

Methods

We studied the evolution of transcriptional interactions triggered by the yeast WGD with a combined methodology including
i) transcription network data analysis and graph-growth modelling, and
ii) cis-regulatory sequence analysis comparing pre- and post- WGD yeasts.

Results

Our results uncover the WGD as a major source for the evolution of complex pathways in the transcriptional regulation of yeast. The inheritance of interactions among WGD duplicates does not occur independently, but follows elementary "duplication subgraphs", that relate ancestral interactions with newly formed ones. Moreover, duplication subgraphs are strongly dependent on their network neighborhood and give rise to higher order circuits with two elementary properties: newly formed transcriptional pathways are not broken and preferentially crossconnected with older ones. In contrast, local duplications involve mainly target genes (and not transcription factors). Growth by local duplication has created a few cross-connected interaction subgraphs by successive duplications, but only over hundred million years. Based on these observations, we develop a quantitative "oneshot" evolutionary graph duplication model for the WGD with predictive power, and use it on the data to estimate quantities that are not observable directly, such as the probability of loosing transcriptional interactions. At the cis-regulatory sequence level, we observe large plasticity in the promoters of WGD duplicates. A comparative analysis of regulatory motifs shows a marked tendency for regulatory sub-functionalization, i.e. motifs that were present before the WGD are divided between the promoters of WGD duplicates, and tend not to be present on both. Post-WGD paralogs are less subject to this sub-functionalization than WGD paralogs. In conclusion, network-based an sequence-based approaches highlight differences between local and global duplications.

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