

Invited Talk

Control of translation: comparative genomics and mechanistic aspects

Yitzhak Pilpel and Orna Man

Department of Molecular Genetics
Weizmann Institute of Science
Rehovot 76100, Israel
pilpel@weizmann.ac.il

Abstract

A major challenge in comparative genomics is to understand how phenotypic differences between species are encoded in their genomes. Phenotypic divergence may result from differential transcription of orthologous genes, yet less is known about the involvement of differential translation regulation in species phenotypic divergence. In order to assess translation effects on divergence, we analyzed approximately 2,800 orthologous genes in nine yeast genomes. For each gene in each species, we predicted translation efficiency, using a measure of the adaptation of its codons to the organism's tRNA pool. Mining this data set, we found hundreds of genes and gene modules with correlated patterns of translational efficiency across the species. One signal encompassed entire modules that are either needed for oxidative respiration or fermentation and are efficiently translated in aerobic or anaerobic species, respectively. In addition, the efficiency of translation of the mRNA splicing machinery strongly correlates with the number of introns in the various genomes. Altogether, we found extensive selection on synonymous codon usage that modulates translation according to gene function and organism phenotype. We conclude that, like factors such as transcription regulation, translation efficiency affects and is affected by the process of species divergence.