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Comparative transcriptomics and ribo-seq: Looking at *de novo* gene emergence in Saccharomycotina

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Abstract: In *de novo* gene emergence, a segment of non-coding DNA undergoes a series of changes which enables transcription, potentially leading to a new protein that could eventually acquire a novel function. Due to their recent origins, young *de novo* genes have no homology with other genes. Furthermore, *de novo* genes may not initially be under the same selective constraints as other genes. Dozens of *de novo* genes have recently been identified in many diverse species; however, the mechanisms leading to their appearance are not yet well understood. To study this phenomenon, we have performed deep RNA sequencing (RNA-seq) and ribosome profiling (Ribo-seq) experiments on 11 species of yeast from the phylum of Ascomycota in both rich media and oxidative stress conditions. These data have been used to classify the conservation of genes at different depths in the yeast phylogeny. Hundreds of genes in each species were novel (unannotated), and many were identified as putative *de novo* genes; these candidates were then tested for signals of translation using our Ribo-seq data. We show that putative *de novo* genes have different properties relative to phylogenetically conserved genes. This comparative phylotranscriptomic analysis advances our understanding of *de novo* gene origins.

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