

Natural history and evolutionary principles of gene duplication in fungi

Gene duplication and loss is a powerful source of functional innovation. However, the general principles that govern this process are still largely unknown. With the growing number of sequenced genomes, it is now possible to examine these events in a comprehensive and unbiased manner. Here, we develop a novel procedure that resolves the evolutionary history of all genes in a large group of species. We apply our procedure to seventeen fungal genomes to create a genome-wide catalog of gene trees that determine precise orthology and paralogy relations across these species. We show that gene duplication and loss is highly constrained by the functional properties and interacting partners of genes. In particular, stress-related genes exhibit many duplications and losses while growth-related genes show selection against such changes. This dichotomy is relaxed following whole-genome duplication. Duplicated genes rarely diverge with respect to biochemical function, but typically diverge with respect to regulatory control. Surprisingly, paralogous modules of genes rarely arise, even following whole-genome duplication. Rather, gene duplication drives the modularization of functional networks through specialization, thereby disentangling cellular systems.