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Natural history and evolutionary principles of gene duplication in fungi

Friday, November 2, 2007
(4-370)
3:00 – 4:00 PM
Light refreshments served at 2:45 PM

Abstract

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 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 catalogue 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, whereas growth-related genes show selection against such changes. Whole-genome duplication circumvents this constraint and relaxes the dichotomy, resulting in an expanded functional scope of gene duplication. By characterizing the functional fate of duplicate genes we show that 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 after whole-genome duplication. Rather, gene duplication may drive the modularization of functional networks through specialization, thereby disentangling cellular systems.

Host: Alexander van Oudenaarden
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