GENOME EVOLUTION

An innovative look at duplication

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Gene duplication and loss have long been appreciated as powerful forces in genome evolution, but little is known about their influences on different types of biological innovation. This issue has now been addressed in a study that traces the history of gene duplication and loss in a set of fungal genomes.

Wapinski and colleagues previously devised a powerful computational tool, SYNERGY, which can predict the ancestry of all genes from multiple genomes. Genes from related species are divided into 'orthogroups', which contain all the genes that are derived from a single ancestral gene, resulting in a large number of gene trees that show all duplication and loss events. The same group has now applied this approach to the genomes of 17 species of ascomycete fungi.

After generating orthogroups for these species, the authors looked at individual gene losses and duplications in relation to function. These processes seem to be restricted in terms of the types of gene they can operate on: genes with key cellular functions (such as in meiosis or the cell cycle) had rarely been modified by duplication or loss. By contrast, genes that are active in environmental stress conditions show more frequent duplications and losses. However, a different pattern was seen for the whole-genome duplication (WGD) event that took place during ascomycete evolution. Many orthogroups that experienced few, if any, individual duplications seem to be more likely to retain such gains and losses following the WGD, suggesting that such large-scale events release genes from the constraints against these processes.

What types of functional innovation can duplications bring about? Strikingly, classifying genes according to broad functional categories showed that paralogous pairs seldom evolve to carry out unrelated biochemical functions. Looking at the properties of paralogues in terms of their interactions within molecular networks revealed more subtle innovations. Nearly half of the paralogous pairs show significant conservation in their interacting partners, whereas the rest share no interactions at all, suggesting high levels of neofunctionalization, with paralogues taking on new but related functions, or subfunctionalization, where the two paralogues each take on a subset of the functions of the ancestral gene.

Duplications also provide opportunities for changes in gene regulation. The authors revealed that such regulatory divergence is an important mode of innovation following duplication. In 70% of cases, sets of genes that share regulatory sequences or that are controlled by the same transcription factor contained no paralogous pairs. So, paralogues diversify most frequently in terms of their regulation, rather than through innovation in terms of biochemical function.

Finally, the authors examined what happens when several genes from a particular class — in terms of function, regulation or expression — are duplicated simultaneously. Could such events contribute to the modularity of biological networks by producing paralogous modules, as suggested by previous studies? Surprisingly, in the vast majority of cases this is not the case; duplicated genes in fact tend to disperse into different classes, even in the case of paralogues produced following the ascomycete WGD. Instead, the authors suggest that duplication contributes to modularity when subfunctionalization occurs, and paralogous pairs each interact with only a subset of the partners of the ancestral gene.

SYNERGY has already provided several new insights into how gene duplications lead to biological innovation and shape molecular networks. As more genome sequences of related groups of species become available, similar approaches will provide the opportunity to determine whether these principles apply more generally.

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