GENE EVOLUTION

How to teach an old gene a new trick

Essential biological functions are thought by many to be evolutionarily ancient. By scrutinizing the origin and evolution of a new essential gene in *Drosophila melanogaster*, Karr and colleagues show that evolution of novel and important functions is, in fact, a continuing process.

Evolution of novelty is poorly understood, but looking at recently evolved genes is likely to provide important insights. Male-specific genes are thought to be among the genes that evolve fastest, so Loppin *et al.* chose *K81*, a fly gene that affects male fertility, as a case study.

Intriguingly, database searches, genomic dot blots and PCR failed to identify any *K81*-related sequences outside the *melanogaster* subgroup, within which *K81* sequence and expression pattern are conserved, indicating functional conservation. Clearly, *K81* must have evolved less than ~30 Mya ago, when the *melanogaster* subgroup diverged, but how? On the basis of DNA sequence analysis and its genomic location, it is most likely that *K81* arose by random retroposition of mRNA from an ancestral locus. The second step towards evolving its new function involved *K81* expression coming under the control of a promoter of an upstream gene that is expressed only in the male germline; the ancestral locus is ubiquitously expressed. The final step might have involved adaptive evolution at the *K81* locus as the gene acquired new function.

As well as new insights into the evolution of novelty, Loppin *et al.* provided the first molecular identification of a *Drosophila* paternal effect gene — its wild-type function is required for zygote viability. These are fascinating topics, and for insights into both the authors recommend turning to essential male-specific genes.

Magdalena Skipper

References and links

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WEB SITE

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GENE REGULATION

Back-up circuits: paralogues lend a hand

Why do so many severe mutations not show a phenotype? Paralogues are thought to step in and rescue the function of the mutated gene, although new research shows that this back-up is — perhaps paradoxically — only seen between paralogues that have dissimilar expression patterns.

Duplicated pairs of genes — paralogues — do not exist without a good reason, as genes with identical functions are usually dealt with by forcing one gene copy to diversify or die. A recent study takes its cue from the observation that some diversified gene copies can remember their original function, and can lend support when their paralogues are compromised. By analysing two sets of data for *Saccharomyces cerevisiae* — mutant viability and mRNA expression — researchers show that this back-up is most efficent when the expression pattern of the paralogues is largely non-overlapping, and they have developed a molecular model for how a paralogue fills in for its mutated relative.

It is intuitive that paralogues that are functionally similar are also more likely to substitute for each other in times of need, and it stands to reason that it helps if the two paralogous proteins localize to the same part of the cell: this is indeed the case for *S. cerevisiae*. The unexpected news, from studying mRNA-expression profiles under 40 growth conditions, was that the best back-up systems involve paralogues with mRNA expression that is only partially correlated. This indicates that, on mutation, the transcription profile of non-mutated paralogues is reprogrammed to match that of the mutated copy. The predictions of this idea were borne out by several experiments; for example, paralogues that show low transcriptional correlation were transcriptionally activated when one copy was mutated. How paralogues might achieve reprogramming was indicated by the architecture of their promoters. Optimal back-up occurs when genes feature a mix of regulatory motifs: unique ones, which would govern the differential expression of paralogues in the wild-type, and common ones, which would come into play during back-up.

Perhaps the most captivating questions that arise from this study — How exactly does a mutation trigger the reprogramming of gene expression? Can back-up circuits be selected for? — are still at the modelling stage, but could nevertheless refocus our views of genetic robustness in yeast and beyond.

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