

EVOLUTION

The birth of new genes

“some open reading frames (ORFs) in transcribed non-genic sequences can be translated, which would provide adaptive potential”

This paper presents and tests a model for the evolution of new genes from non-genic sequences.

The evolutionary model put forward by Carvunis *et al.* is that some open reading frames (ORFs) in transcribed non-genic sequences can be translated, which would provide adaptive potential. Occasionally, some of these translated non-genic ORFs (which the authors term ‘proto-genes’) would be retained over evolutionary time and would evolve the characteristics of genes. This model means that there would be a continuum from non-genic ORFs through to genes.

The authors tested this model by analysing the *Saccharomyces cerevisiae* genome. First, they categorized *S. cerevisiae* ORFs into 11 groups on the basis of their degree of conservation

throughout the Ascomycota phylum. The most weakly conserved ORFs (namely, groups 0–4) were taken as candidate proto-genes. ORFs_{1–4} are annotated ORFs that are only found in the four closely related *Saccharomyces sensu stricto* species, and the ORFs₀ group comprised ~100,000 unannotated ORFs.

The authors then analysed a genome-scale ribosome footprinting data set and found that 1,139 of the ORFs₀ showed evidence of translation. When the authors examined translation under different nutritional conditions, they found differential translation to be more prevalent among ORFs_{0–4} than it was among ORFs_{5–10} (which are considered as genes). Thus, the newly emerged ORFs might provide adaptive stress-response functions. A subset of the candidate proto-genes (namely, 3% of translated ORFs₀ and 9–25% of ORFs_{1–4}) showed evidence of purifying selection, with the proportion increasing with increased conservation,

as would be expected under the model of an evolutionary continuum.

In total, the authors designated 1,891 ORFs as proto-genes, but they emphasize that these lie on a continuum between non-genic and genic sequences. In terms of the contribution of proto-genes to genome evolution, there are more ORFs₁ that have arisen since the split of *S. cerevisiae* and *Saccharomyces paradoxus* and that are under purifying selection than there are genes generated through sporadic gene duplications since that split. Therefore, it may be necessary to re-evaluate the evolutionary contribution of *de novo* gene birth.

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ORIGINAL RESEARCH PAPER Carvunis, A.-R. *et al.* Proto-genes and *de novo* gene birth. *Nature* 24 June 2012 (doi:10.1038/nature11184)

FURTHER READING Tautz, D. & Domazet-Lošo, T. The evolutionary origin of orphan genes. *Nature Rev. Genet.* **12**, 692–702 (2011).

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