



Although different genes evolve at different rates, when complete sets of orthologous genes are considered across taxa, the distribution of rates is remarkably conserved. That is, the differences in the rates of evolution among genes in a genome remain consistent. A potential explanation for this observation is the molecular clock, which is a model that has been used widely in phylogenetics. Now, Koonin and colleagues show that available phylogenetic data are more compatible with an alternative model that they propose termed the universal pacemaker (UPM).

Under the molecular clock model, the rate of evolution of a particular gene remains constant, and therefore this could explain why relative rates of evolution between genes also remain constant. However, the data do not fit a strict molecular clock model, and a 'relaxed' molecular clock model is now more widely used. The alternative, more general UPM model proposes that the rate of evolution of a gene may vary arbitrarily, but changes in gene-specific rates are correlated. That is, evolutionary rates of all genes in a genome in a particular lineage increase or decrease together.

To test the models, the authors used phylogenetic trees for 2,294 orthologous gene families, including data from 41 archaeal genomes and 59 bacterial genomes. Under the constraints of the molecular clock model or the UPM model, they fitted these gene trees to 'supertrees', which reflect the dominant trend in the evolution of these species. They then assessed how good the fit is between the gene trees and the supertree under each of the models and found that the fit for the UPM model was significantly better. The authors concluded that the UPM is sufficient to explain the correlations in evolutionary rates across genes in a genome. This work on bacteria and archaea also fits previous observations of lineage-specific changes in evolutionary rate in mammals.

So how might the UPM model relate to biological events? Factors that might cause the 'pace' in a particular lineage to increase or to decrease include changes in population structure or lifestyle that alter the effective population size; investigating such changes will be an interesting research direction.

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ORIGINAL RESEARCH PAPER Snir, S., Wolf, Y.I. & Koonin, E. V. Universal pacemaker of genome evolution. *PLoS Comput. Biol.* **8**, e1002785 (2012)

FURTHER READING Yang, Z. & Rannala, B. Molecular phylogenetics: principles and practice. *Nature Rev. Genet.* **13**, 303–314 (2012)