

# HIGHLIGHTS

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## EVOLUTION

# Same rates for neighbours



Property taxes (or ‘rates’ as they used to be called in the UK) tend to be the same for houses in the same region. Now it has been found that similar rates — in this case, rates of evolution — also apply to proteins encoded by neighbouring genes.

The data sample in this study consists of 176 pairs of linked mouse–rat orthologous genes. Williams and Hurst asked whether these linked genes, and the proteins that they encode, evolve at a different rate, on average, from all (10,000) randomly chosen pairs of the same genes. The answer was a resounding yes, as none of the random pairs of genes evolved more closely than the linked pairs.

Linked genes evolve at a similar rate at the amino-acid sequence level (which is a reflection of the non-synonymous rate of gene evolution,  $K_a$ ) and, to a similar but less striking degree, at the nucleotide sequence

level (indicated by the background rate of evolution,  $K_s$ ). This correlation between  $K_a$  and  $K_s$  shouldn’t be surprising, as it is intuitive that, if linked genes evolve at a similar rate to each other, then so should the proteins that they encode. In fact, the story is more complicated, as the correlation between the evolution rate of linked proteins occurs independently of the similar evolution rate of their encoding genes. The mouse genome seems to be a mosaic of “protein rate domains”, each characterized by proteins with a defined rate of evolution.

So, if there is no mechanistic connection between protein evolution rate and that of their genes, why should proteins encoded by linked genes co-evolve? An untested explanation is that genes with a common function, which tend to have comparable rates of evolution, are clustered in the genome.

A second explanation, one that the authors have addressed, is that protein rate domains are preserved by stabilizing selection, whose job it is to extinguish any deviation from the status quo. Stabilizing selection would efficiently wipe out any change in the evolution rate of proteins in a given genetic region — strong stabilizing selection would enforce a low rate of evolution. Previous work had indicated a possible link between the intensity of stabilizing selection and G+C content. It follows that a high G+C content would correlate with a high level of stabilizing selection and, consequently, with a low evolution rate ( $K_a$ ). This inverse relationship between G+C content and  $K_a$  was observed, and supports the theory that the co-evolution of linked genes is caused by a variation in the intensity of stabilizing selection around the genome.

This second model still needs to be refined. For instance, the G+C-rich domains are longer than the co-evolving protein domains, which are predicted to be 1 to 2 cM in length. On the other hand, the correlation observed in this study could be fortuitous, and simply reflect the particular kind of genes that inhabit G+C-rich regions.

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## References and links

**ORIGINAL RESEARCH PAPER** Williams, E. J. B. & Hurst, L. D. The proteins of linked genes evolve at similar rates. *Nature* **407**, 900–903 (2000)

**WEB SITES** Laurence Hurst’s lab | HOVERGEN: Homologous Vertebrate Genes Database