

## The genetics of molecular evolution

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A team of scientists researching the effect of long-term molecular evolution (the study of DNA, RNA and proteins) have produced findings which suggest most amino-acid substitutions have different fitness effects in different species. This is an important breakthrough as there is now evidence to show that a genetic background determines whether a modification, which is the main factor regulating evolution at the level of proteins, is beneficial, harmful or inconsequential.



The work was supported by grants from the Spanish Ministry of Science and Innovation, and through the EU's Quantomics ('From sequence to consequence - tools for the exploitation of livestock genomes') project, which is under the 'Food, agriculture and fisheries, and biotechnology' Theme of the EU's Seventh Framework Programme (FP7). The findings are published in the science journal *Nature*.

The team of scientists was led by research Professor Fyodor Kondrashov, who is the head of the Evolutionary Genomics group at the Centre for Genomic Regulation in Barcelona, Spain. The Professor uses computers for most of his work, analysing vast quantities of experimental data to see how different versions of genes arise. He studies genomes of organisms from fish to birds to humans, to investigate the speed, effect and mechanisms of gene variance and evolution. In previous studies, he has found that <u>mutations</u> which cause disease in one type of organism, may be harmless in another, and has been trying to work out the molecular details behind such differences.

Most scientists have assumed that in the short term having two identical copies of a gene has no effect on an organism's biology. However, Professor Kondrashov has always thought that such duplications are far more likely to be beneficial or harmful to an organism. This theory has now been confirmed with this latest research where scientists studied multiple alignments of at least 1,000 orthologues (different genes) with 16 proteins from species from a diverse evolutionary background.

The study of the factors determining the tempo and mode of molecular evolution continues to be at the forefront of evolutionary biology. Many studies have focused on the role of selection versus genetic drift in the fixation of amino-acid substitutions. Scientists are now certain that both, selection and genetic drift, contribute to a substantial fraction of all amino-acid substitutions in the course of evolution.



The study of molecular evolution is not a new area of research. In fact, it started in the early 20th century with 'comparative biochemistry'. However, molecular evolution only came into its own in the 1960s and 1970s, following the rise of molecular biology. After the 1970s, nucleic acid sequencing allowed <u>molecular evolution</u> to reach beyond proteins to highly conserved ribosomal RNA sequences, the foundation of a reconceptualisation of the early history of life.

**More information:** Breen, M. S., Kemena, C., Vlasov, P. K. Notredame, C. and Kondrashov, F. A., 'Epistasis as the primary factor in molecular evolution', *Nature*, 2012, 490, 535-538. <u>doi:10.1038/nature11510</u>

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