

Section «Bioengineering Bioinformatics»

The effect of lateral gene transfer on rate of subsequent evolution of
protein-coding genes

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Each genome is a collection of genes that widely differ with respect to their histories and characteristic rates of evolution. It is usually assumed that the characteristic rate of evolution of a protein-coding gene depends primarily on the structural-functional constraints that are intrinsic to the encoded protein. However, age classes possess systematic differences in short-term evolutionary rates and selection pressures [4].

The mechanisms that lead to birth of new genes are not fully understood. The most common route of innovation is thought to be gene duplication followed by a major acceleration of evolution so that the similarity to the ancestral genes becomes undetectable. In prokaryotes, a major source of genes is the phenomenon of lateral gene transfer (LGT). In gene age-related analyses, however, it is often assumed that new genes typically emerge as a result of gene duplication, and the contribution of other sources is negligible (e.g., [4]). Furthermore, radical changes in the genetic environment of a sequence segment may cause subsequent accumulation of compensatory substitutions in a process of adaptive walk; such “trails” of compensatory substitutions had been previously observed, e.g., in evolution of eukaryotic protein-coding genes after of indels [2], or of viral genes after reassortments [3].

Here, we asked whether the genes that had appeared in a genome via LGT differ systematically in the rate of subsequent evolution from their ancestors, or from other genes in the recipient genome. We used data on LGT events among 144 prokaryotes [1] to study sequence evolution rate of genes involved in LGT before and after the LGT event. We ordered the genes in the donor and the recipient genomes by their dN/dS values, and compared the ranks of transferred genes in the donor and the recipient genome. 19 LGT events affecting more than one donor and recipient species with unambiguous direction of gene transfer have been observed; among those, 5 LGT events were accompanied by an increase in dN/dS, and 3 LGT events, by a decrease in dN/dS. Overall, this preliminary analysis suggests that the effect of LGT on subsequent rate of evolution is minor, probably because the subset of LGT-prone genes is itself biased towards the fast evolving ones.

References

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