

EVOLUTIONAL MEANING OF GENE NEIGHBORING IN PROKARYOTES:
DIHYDROFOLATE REDUCTASE AND THYMIDYLATE SYNTHASE GENES AS
A CASE OF STUDY.

Vitor Hugo Moreau

Núcleo de Biotecnologia (NuBioTec), Faculdade de Tecnologia e Ciências (FTC),
Salvador, BA, Brazil

Study of gene order became a promise area since the sequencing of numerous genomes from the 1990s. Conservation of gene order follows a common trend for prokaryotes: gene order is preserved at close phylogenetic distances and is lost as phylogenetic distance increases. Proposed explanations for selection of the gene ordering include the interaction between proteins encoded by neighbor genes. The correlation between phylogenetic distance and gene neighboring in prokaryotes was studied. I have measured the genomic distance between dihydrofolate reductase (DHFR) and thymidylate synthase (TS) genes in bacteria genomes. DHFR and TS are enzymes that work together in successive reactions of folate biosynthesis. These proteins exist, in some protozoan, as bifunctional enzyme, what could be important in channeling the substrate between active sites. These genes are neighbors in some bacteria, while they are found to be located millions of basepairs apart in others (5.5×10^6 bp in *Pseudomonas siringae*). I have performed multiple alignments and calculated phylogenetic distance between 129 bacteria. It was possible to observe a significant correlation between DHFR and TS genes distance and their phylogenetic distance from *P. siringae*. It is possible to suppose that DHFR-TS genes may be evolutionarily driven to get closer in bacteria genomes. This phenomenon could be important for increasing performance of the folate metabolism in prokaryotes.

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