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Title: Evolution of tryptophan biosynthetic pathway in microbial genomes: a comparative genetic study

Authors: Sinha, Somdatta (/jspui/browse?type=author&value=Sinha%2C+Somdatta)

Keywords: Pathway evolution

Tryptophan biosynthetic pathway

Relative synonymous codon usage (RSCU)

Relative amino acid usage (RAAU)
Codon adaptation index (CAI)
Principal component analysis (PCA)

Cluster analysis

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Abstract:

Biosynthetic pathway evolution needs to consider the evolution of a group of genes that code for enzymes catalysing the multiple chemical reaction steps leading to the final end product. Tryptophan biosynthetic pathway has five chemical reaction steps that are highly conserved in diverse microbial genomes, though the genes of the pathway enzymes show considerable variations in arrangements, operon structure (gene fusion and splitting) and regulation. We use a combined bioinformatic and statistical analyses approach to address the question if the pathway genes from different microbial genomes, belonging to a wide range of groups, show similar evolutionary relationships within and between them. Our analyses involved detailed study of gene organization (fusion/splitting events), base composition, relative synonymous codon usage pattern of the genes, gene expressivity, amino acid usage, etc. to assess inter- and intra-genic variations, between and within the pathway genes, in diverse group of microorganisms. We describe these genetic and genomic variations in the tryptophan pathway genes in different microorganisms to show the similarities across organisms, and compare the same genes across different organisms to find the possible variability arising possibly due to horizontal gene transfers. Such studies form the basis for moving from single gene evolution to pathway evolutionary studies that are important steps towards understanding the systems biology of intracellular pathways.

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