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Selection on codon usage and amino acid sequences in prokaryotes

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Abstract

We compared selection pressure that affects synonymous and non-synonymous codon positions in protein-coding sequences of orthologous genes from closely related prokaryotic genomes representing diverse lineages of archaea and bacteria. The analysis employed the Aligned Tight Genome Clusters (ATGC) database where ATGC pairs are built from 1390 prokaryotic species. The codon usage bias in the genes of ATGC pairs is generally low: 90% of the gene-specific Codon Adaptation Index (CAI) values fall within the range of 0.15-0.3. This relatively weak selection on codon usage contrasts the strong purifying selection on amino acid sequences as evidenced by the observation that 66% of dN/dS values are below 0.1. Strong correlations were observed between the CAI values of orthologous genes from most pairs of closely related genomes. For most of the compared genomes, a weak but statistically significant negative correlation between CAI and dN/dS was observed indicative of a weak link between selection affecting protein sequence and selection on codon usage. In parasitic bacteria evolving under weak constraints, this connection disappears altogether. In all analyzed bacteria and archaea, genes that are subject to strong purifying selection on amino acid sequences show a wide spread of codon bias. We investigate in detail the characteristics of genes with exceptionally high CAI values in all compared lineages.