Statistical Analysis of Codon Pairs Usage in Prokaryotic Genomes

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Genetic information is coded by the collinear arrangement of four nitrogen bases - adenine (A), guanine (G), cytosine (C) and thymine/uracil (T/U) along with the polynucleotide chains of DNA and RNA. They are combined in triplets called *codons*. Each of the 64 codons, except for UAA, UAG and UGA, codes for one (out of twenty) amino acids. The genetic information is translated/decoded by the help of transfer RNAs (tRNAs). The latter bear complementary triplets, called anticodons and also a single covalently bound amino acid. The place of decoding is the *ribosome*. It contains two sites (A and P) for binding of tRNAs. Therefore the accommodation of two tRNAs, each carrying one amino acid, in these sites is a prerequisite for the sequential formation of dipeptide, tripeptide and *polypeptide* (protein) products. At every moment of translation the two tRNAs in the A and P ribosomal sites are selected on the basis of the two translating codons in mRNA attached to the same ribosome.

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