

Abstract

Abundance values of codons belonging to eight family boxes of genetic code were found out in amino acid biosynthesis genes of twelve different bacterial genomes. The abundance of the four nucleotides at the 3rd position of these codons were studied in each family box codons under three different groups such as (i) purine-pyrimidine bases (A, G and C, T); (ii) amino-keto (A, C and G, T); and (iii) complementary base (A, T and G, C). Apart from the already known AT/GC biases, biases for amino-keto and purine-pyrimidine nucleotides were observed for certain family box codons in all the genomes. A comparative analysis of the abundance frequencies of the three groups of nucleotides suggests that variability among family box codons within a ORF is greater than the variability among different genes for a particular family box codons. This indicates a role of the 1st and the 2nd nucleotide of a codon influencing the occurrence of a nucleotide at the 3rd position.