

ABSTRACT

The focus of the study is to analyze the bacterial genome sequences for in-frame dinucleotide abundance and amino acid abundance. The genome sequences were taken from "Genome Information Broker (<http://www.gib.genes.nig.ac.jp>) site". A comparative analysis of in-frame dinucleotide abundance and amino acid in several bacterial genomes has been done in this study. Dinucleotide abundance studies revealed that the abundance value of a dinucleotide at the 1st position of codons is less variable than its abundance at the 2nd or the 3rd position in different bacterial genomes. This is correlated with the similarities observed in the relative abundance patterns of different amino acids in different bacterial proteomes.