

## ABSTRACT

The focus of the study is to analyze the bacterial genome sequences for understanding the pattern of the differential codon usage in bacterial genomes. The genome sequence were taken from "Genome Information Broker (<http://www.gib.genes.nig.ac.jp>) site ". Synonymous codons in a family box of genetic code have the same nucleotides at the 1<sup>st</sup> and 2<sup>nd</sup> positions. Since any of the four nucleotides can occur at the 3<sup>rd</sup> nucleotide position in these codons, analysis of synonymous codon usage pattern in different family boxes of genetic code will reveal if there is any preference for the occurrence of a particular nucleotide in a family box. The preferred nucleotide can be correlated with the genome G + C% and the tRNA occurrence which are considered as the evolutionary forces acting on the codon usage pattern of an organism. Moreover, comparative analysis of codon usage pattern across the genomes might reveal the presence of any other common factor playing important role in determining codon usage in these organisms. In this study we have found out that in leucine family box codons occurrence of a keto nucleotide is preferred over an amino nucleotide, and in arginine family box codons occurrence of pyrimidine nucleotide is preferred over purine nucleotides at the 3<sup>rd</sup> nucleotide position.