

ABSTRACT

Fourteen archaeal genomes with varying G+C % have been analysed to determine the abundance of encoded amino acids and the codon usage. The frequencies for various amino acids have been observed to occur following a common trend similar in all the genomes irrespective of the genome G + C % variations. Codon usage pattern for eight amino acids encoded by synonymous codons revealed that genome G + C % has a direct correlation with the relative frequencies of the synonymous codons.