

P003 Codon pair bias in prokaryotic and eukaryotic genomes

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In many organisms codon usage is biased, with certain synonymous codons preferred over others. Codon pairing is also subject to significant bias, which is additional to that of dipeptide bias. In this study the hypothesis was tested that the influence of tRNA structure within the translating ribosome is the selective force driving codon pair bias. A series of bioinformatic tools was created to analyse codon pairing within bacterial and eukaryotic genomes. Cluster analysis was used to identify P site (5') and A site (3') codons with similar pairing preferences. This revealed that the identity of the third P site nucleotide and the first A site nucleotide exerts a key influence over codon pair bias. In addition to this dinucleotide bias, cluster analysis revealed that in some genomes, a significant influence is exerted by the combination of the P site codon third nucleotide and the identity of the tRNA in the ribosomal A site. Multivariate analysis was used to identify individual sequence elements within these A-site tRNAs that affect codon pairing. This analysis suggests a translational origin for codon pair bias. We propose that optimal tRNA juxtaposition within the ribosome is a driving factor in selecting codon pairing, which may be associated with the fidelity or kinetics of translation.