

P036 The strength of selected codon usage bias in archaea
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While the nature and causes of synonymous codon usage bias have been extensively studied in Bacteria and Eukaryotes, little is known about the codon usage of Archaea. Deviations from random codon usage can be explained by unequal mutation rates and natural selection for translationally optimal codons. Within genomes where translational selection is effective, it is the highly expressed genes that require to be translated most efficiently, and thus display the greatest bias towards a subset of codons best recognised by the most abundant tRNA species. Here we investigate the codon usage in the genomes sequences of 50 species of Archaea. We quantify the strength of selected codon usage bias, which indicates the extent to which patterns of codon usage within a genome have been influenced by natural selection, by comparing the codon frequencies found in sets of highly expressed genes with those found across entire genome sequences. We find that whilst some species of Archaea show a strong degree of selected codon usage bias, this is never as strong as that observed in some Bacterial species. Patterns of codon usage in Archaea are largely consistent with those observed in Bacteria, where the strength of selected codon usage bias is positively correlated with the numbers of ribosomal RNA operons, the number of transfer RNA genes, and growth rate.