

# Evolution of specific codon usage patterns in particular microbial species

Wenfa Ng

Unaffiliated researcher, Singapore, Email: [ngwenfa771@hotmail.com](mailto:ngwenfa771@hotmail.com)

## Abstract

mRNA sequence encodes the protein sequence with the codon table as decoder. Specifically, different groups of three nucleotides encode different amino acids and help translate a mRNA sequence into a protein sequence. In the process of decoding the mRNA sequence and translating it into a protein code, tRNA plays an important role in mediating the codon recognition and amino acid transfer process to a nascent peptide chain. Given that there are 64 codons and 20 natural amino acids, different codons could encode for the same amino acid, thereby, resulting in a degenerate protein code. More importantly, different microbial species have different complement of tRNAs. Hence, different microbes use different types of tRNA to ferry degenerate amino acids, and this phenomenon is known as codon usage pattern of a microbe, and holds important implications to the efficiency in which a heterologous gene would be expressed in a foreign host. Specifically, if a heterologous gene is encoded by codons not commonly used by the expression host, expression of the gene would either fail or protein production would be low. This arises because the necessary tRNA that decode the codon and ferry the amino acid for chain elongation is not present in high concentration in the expression host. However, what causes the evolution of different codon usage patterns in different microbial species? Specifically, why specific tRNAs are of higher relative abundance compared to others in a microbe? And, more importantly, which arise first, changes in codon usage pattern or relative abundance of tRNA? For example, a microbe should be able to decode every codon used in its genome in order to survive and propagate. Hence, tight coordination must be present between the repertoire of tRNA it carries in its genome with the codons used to encode different amino acids used by the cell. Serious consequences would arise if there is a mismatch between the codons used and tRNA available to decode the codons. Genome mining has revealed that individual microbial species carry a specific set of tRNA for decoding the codons used in the genome sequence. Consider the case that mutations result in changes in codon usage for which the cell does not have the necessary tRNA for decoding, gene expression would thus be affected and this may translate into a loss of fitness phenotype placing the strain at a survival disadvantage. Such a strain would lose out to the wildtype and the altered genetic complement eliminated from the population. Similar logic applies to the case of altered tRNA available for decoding the codons used in a genome. Hence, translation of altered codon usage pattern or tRNA complement into a growth deficit would effectively curtail the evolutionary space for codon usage pattern in a microbe; thereby, ensuring that the bare minimum tRNA complement is available for decoding the codons used in a species.

**Keywords:** codon table, protein sequence, DNA sequence, transfer RNA, amino acid, codon, codon usage pattern, growth deficit, selection advantage, heterologous expression, expression host,

***Subject areas:*** biochemistry, molecular biology, biotechnology, synthetic biology, microbiology,

**Conflicts of interest**

The author declares no conflicts of interest.

**Funding**

No funding was used in this work.