The asymmetric phenotypic graphs of codons and anticodons of the Standard Genetic code determine the mode of evolution of proteins

Marco V. José *, Gabriel S. Zamudio

Theoretical Biology Group, Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, CDMX CP 04510, Mexico City; gazaso92@gmail.com

*Correspondence: marcojose@biomedicas.unam.mx

Abstract: The Standard Genetic Code (SGC) is written in an alphabet of four letters (C, A, U, G), grouped into words three letters long, called triplets or codons. Each of the 64 codons specifies one of the 20 amino acids or else serves as a punctuation mark signaling the end of a message. The SGC is implemented via the transfer RNAs that bind each codon with its anticodon. These molecules define the genetic code, by linking the specific amino acids and tRNAs with the corresponding anticodons. To understand the meaning of symmetrical/asymmetrical properties of the Standard Genetic Code (SGC), we designed synthetic genetic codes with known symmetries and with the same degeneracy of the SGC. We determined their impact on the substitution rates for each amino acid under a neutral model of evolution. We prove that the phenotypic graphs of the SGC for codons and anticodons for all the possible arrangements of nucleotides are asymmetric. Both the SGC and symmetrical synthetic codes exhibit a proportional probability of occurrence of the amino acids according to their degeneracy. Unlike the SGC, the synthetic codes display a constant probability of occurrence of the amino acid according to their codonicity. The asymmetry of the phenotypic graphs of codons and anticodons of the SGC, has important implications on the evolutionary processes of proteins by preferring specific amino acids irrespective of their codonicity.

Keywords: Standard Genetic Code; Anticodon code; Phenotypic graphs; Protein