Codon usage bias study in cyanobacteria

Codon is a series of three nucleotides (a triplet) that encodes a specific amino acid residue in a polypeptide chain. There are 61 codons encoding different amino acids and 3 stop codons but only 20 different amino acids are translated by them. The overabundance in the number of codons allows many amino acids to be encoded by more than one codon. Genetic code of organisms shows higher bias towards one codon than the other for same amino acid. Codon usage bias is the way by which different synonymous codon of the same amino acid get inserted in the coding DNA sequence (Fig. 1).

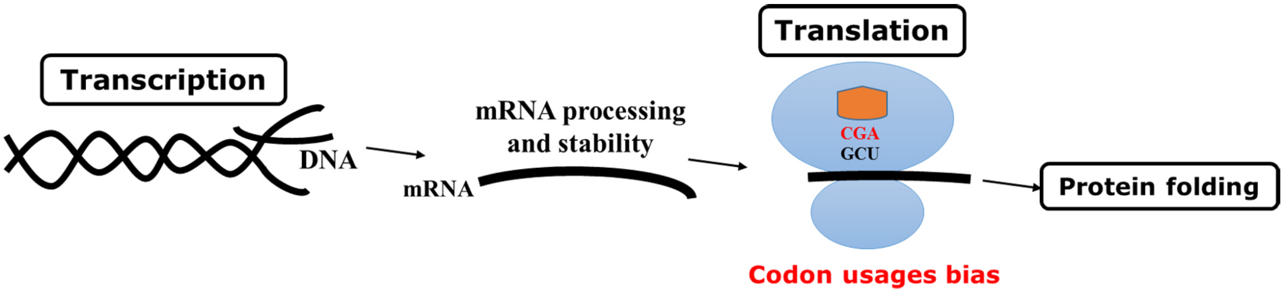

Fig. 1. Codon usages bias analysis controlling processes in organisms.

Reasons behind such bias and factors affecting bias are much debated area in the field of molecular evolution. Individual genes and the entire genome of an organism can vary significantly in nucleotide composition (Bernardi and Bernardi 1986; Muto and Osawa 1987). Genome of some organisms is disproportionately rich in guanine and cytosine (GC), while others have adenine and thymine (AT) rich genome. The variation in nucleotide composition is mostly found in the synonymous codon positions of genes and because of these variations, DNA content may have little effect on the amino acid content of the encoded proteins (Loomis and Smith 1990; Lockhart et al. 1992). Nucleotide and amino acid compositions of photolyase gene were studied to determine their genomic and structural relationship in freshwater, marine and hot spring cyanobacteria. Photolyase encoding genes from hot spring cyanobacteria showed highest GC content. The genomic GC content was found to influence the codon usage and amino acid variability in photolyases. The third position of codon was found to have more effect on amino acid variability in photolyases than the first and second positions. The variation of amino acids Ala, Asp, Glu, Gly, His, Leu, Pro, Gln, Arg and Val in photolyases of three different habitats was found to be controlled by first position of codon (G1C1). However, second position (G2C2) of codon regulates variation of Ala, Cys, Gly, Pro, Arg, Ser, Thr and Tyr contents in photolyases. Third position (G3C3) of codon controls incorporation of amino acids such as Ala, Phe, Gly, Leu, Gln, Pro, Arg, Ser, Thr and Tyr in photolyases from three habitats. Photolyase encoding genes of hot spring cyanobacteria have 85% codons with G or C at third position, whereas marine and freshwater cyanobacteria showed 82 and 60% codons respectively, with G or C at third position. Principal component analysis (PCA) showed that GC content has a profound effect in separating the genes along the first major axis according to their RSCU (relative synonymous codon usage) values, and neutrality analysis indicated that mutational pressure has resulted in codon bias in photolyase genes of cyanobacteria. This study provides novel insights into the codon usages bias of photolyase encoding genes in different cyanobacteria. This has relevance in expression study of photolyase encoding genes in other organisms. Detailed analysis of photolyase encoding genes reveals that G3C3 content can affect codon usage bias in cyanobacteria. ‘C’ ending codons were more preferred in all studied cyanobacteria. This study reveals that GC mutational bias influence the codon usage of photolyase encoding genes in all studied cyanobacteria (Rajneesh et al. 2017). Photolyases are important for cosmetic industry as addition of photolyase containing liposome (EC4.1.99.3) to traditional sunscreen was found to significantly reduce the UV-induced damage of human skin by reducing the pyrimidine dimers (Stege et al. 2000; An et al. 2013). This information could be further utilized for commercial/laboratory scale production of cyanobacterial photolyases for their structural studies and/or the development of new class of sunscreens.

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