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Short Communication
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A New Dimension of Codons for Protein Synthesis

Jacob Varghese B*, Khai Bui, Naomi Divall, Alexander Egan, Ali Kermani, Adam Lodge and Daniela Vollmer
Institute for Cell and Molecular Bioscience, Newcastle University, United Kingdom

Abstract

Protein synthesis is a series of codon–anticodon interactions to buildup the polypeptide chains. The corresponding rule is that out of 64 codons in mRNA, 61 codons have recognizing ability of the 20 amino acids based on degeneracy except methionine and tryptophan which are coded by single codon. The remaining three are stop codons of mRNA sequence, which does not decode any amino acids in the protein synthesis mechanism. A fascinating study is how many amino acids are recognizing the high guanine-cytosine or adenine-uracil rich triplet codons. These data would be useful to find the copy numbers of transfer RNA that encode the amino acids having high guanine-cytosine triplet codons or adenine-uracil rich triplet codons in three domains of life (Bacteria, Archeae and eukaryotes). The four types of nucleotides compositions (guanine, cytosine, adenine and thymine or uracil) have distinctly playing a central role in amino acid composition of protein sequences.

Keywords: Codon; Anti-codon; Amino acids; tRNA

Introduction

Transfer Ribonucleic acids (tRNA) is a polymer of four different types of nucleotides such as guanine and adenine cytosine and uracil. Each nucleotide is made of an invariant phosphorylated sugar to which is attached one of the four standard nucleic acids [1]. tRNA has the clover leaf secondary structure with the acceptor, anticodon, D-arm and T-arm which are folded into the L-shaped tertiary structure. tRNA structure have nearly 79 modifications that have been identified and characterized in all three domains. The modified tRNA's function is to improve the fidelity and efficiency in protein synthesis by maintains the reading frame [2]. tRNA anticodon is unique on each tRNA because triplet anticodons (combination of G, C, A, U) buildup a polypeptide chain by adding 20 different amino acids (Table 1). Possibly, high GC ratios of tRNA anticodon synthesis the polypeptide chain have high percentage of proline, arginine, alanine and glycine in protein molecules. However, high AU ratio of tRNA anticodons synthesis the protein molecules which have been more number of phenylalanine, Leucine, Isoleucine, Methionine, Tyrosine, Asparagine and Lysine. For example, high GC content organism have distinct synonymous of codon usages and tRNA subsets that results as high frequency number of positively charged (Arginine and Lysine), aromatic residues (Phenylalanine, Tryptophan, Tyrosine).

1st position (5' end)	2nd position								3rd position (3'end)
	U		C		A		G		
U	UUU	PHE	UCU	SER	UAU	TYR	UGU	CYS	U
	UUC	PHE	UCC	SER	UAC	TYR	UGC	CYS	C
	UUA	LEU	UCA	SER	UAA	STOP	UGA	STOP	A
	UUG	LEU	UCG	SER	UAG	STOP	UGG	TRP	G
C	CUU	LEU	CCU	PRO	CAU	HIS	CGU	ARG	U
	CUC	LEU	CCC	PRO	CAC	HIS	CGC	ARG	C
	CUA	LEU	CCA	PRO	CAA	GLN	CGA	ARG	A
	CUG	LEU	CCG	PRO	CAG	GLN	CGG	ARG	G
A	AUU	IIE	ACU	THR	AAU	ASN	AGU	SER	U
	AUC	IIE	ACC	THR	AAC	ASN	AGC	SER	C
	AUA	IIE	ACA	THR	AAA	LYS	AGA	ARG	A
	AUG	MET	ACG	THR	AAG	LYS	AGG	ARG	G
G	GUU	VAL	GCU	ALA	GAU	ASP	GGU	GLY	U
	GUC	VAL	GCC	ALA	GAC	ASP	GGC	GLY	C
	GUA	VAL	GCA	ALA	GAA	GLU	GGA	GLY	A
	GUG	VAL	GCG	ALA	GAG	GLU	GGG	GLY	G

High GC nucleotides codon bases were colored in blue whereas AU rich nucleotides codons were colored in red. According GC rich and AU rich triplet codons the amino acids were colored accordingly.

Table 1: Separation of tRNA codons based on high GC and AU rich nucleotides.

S. No	A.A	3nt GC	5' and middle position G/C, 3' is A/U	S. No	A.A	3nt UA	5' and middle position A/U, 3' is G/C
1	PRO	CCC	CCU	1	PHE	UUU	UUC
		CCG	CCA	2	LEU	UUA	UUG
2	ARG	CGC	CGU	3	IIE	AUU AUA	AUC
		CGG	CGA	4	MET	NIL	AUG
3	ALA	GCC	GCU	5	TYR	UAU	UAC
		GCG	GCA	6	TRP	UAA(STOP)	UAG
4	GLY	GGC	GGU	7	ASN	AAU	AAC
		GGG	GGA	8	LYS	AAA	AAG

Four types of 8 codons were separated (Table 2) by high GC and AU rich nucleotides The first type 8 codons are GC triplet nucleotides means that 5' base, middle base and 3' bases (colored in blue). The 2nd one is 5' and middle bases are CG the last 3' base is U or A. Third type of 8 codons are AU triplet nucleotides,. The fourth type of 8 codons contains 5' and middle bases are AU, the last 3' base is C or G.

Table 2: Segregation of GC rich, AU rich codons and its amino acids.

Methodology

In all 64 codons the four nucleotides (G, C, A or U) were equally distributed in the codons. Thus an interesting objective is how many amino acids code more numbers of high GC/AU bases codons. On this view, Proline, Arginine, Alanine and Glycine these four amino acids are unique features among 20 amino acids. In total 64 codons these four amino acids (P, R, A and G), each one have two numbers of triplet GC codons (Table 2). Whereas only one amino acid Isoleucine have two numbers of triplet AU codons other amino acids like Phenylalanine, Leucine, Tyrosine, Asparagine and Lysine have sole number of triplet AU codons.

Corresponding author: Jacob Varghese B, Institute for Cell and Molecular Bioscience, Newcastle University, Richardson Road, Newcastle upon Tyne, NE2 4AX, United Kingdom, E-mail: vbjacob6@gmail.com

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S. No	A.A	5' have G/C middle and 3' have A/U	Middle Base A/U ntd	A.A	Middle Base G/C ntd	5' have A/U, middle and 3' have G/C
1	LEU	CUU	CUC	SER	UCU	UCC
	LEU	CUA	CUG	SER	UCA	UCG
2	VAL	GUU	GUC	THR	ACU	ACC
	VAL	GUA	GUG	THR	ACA	ACG
3	HIS	CAU	CAC	CYS	UGU	UGC
	GLN	CAA	CAG	STOP	UGA	UGG
4	ASP	GAU	GAC	SER	AGU	AGC
	GLU	GAA	GAG	ARG	AGA	AGG

Another four types of 8 codons were separated on the basis of GC/AU bases distribution on the respective amino acids. L, V, H, Q, D, E, S, T, C, R these 10 amino acids shares the equal distribution of G, C, A and U nucleotides including two stop codons.

Table 3: Segregation of AU and GC rich triplet codons and its amino acids.

Among 64 codons, two forms of 32 codons are separated on bases of high GC or AU rich nucleotide distribution. The first forms of 32 codons are segregated into four types of 8 codons.

Discussion

In this method 32 codons are separated by four types of 8 codons on the basis of GC/AU nucleotides allocation. All four types of 8 codons has equal number of GC/AU units which decode the 10 different amino acids decoded Leu, Val, His, Gln, Asp, Glu, Ser, Thr, Cys, Arg including two stop codons (Table 3). Serine has six triplet codons (6 codons) which contain equal numbers of GC and AU nucleotides. Leu, Val, Thr these three amino acids have four triplet codons (12) with equal sharing of GC and AU nucleotides. His, Gln, Asp, Glu, Cys, Arg amino acids has two triplet codons (12) an equal sharing of GC and AU nucleotides. A stop codon has contains an equal share of two GC and AU triplet codons (2 codons).

Conclusion

The conclusion is G/C triplet codons encode just 4 amino acids but the A/U codons encode 7 amino acids and one stop codon. Obviously these finding suggests that A/U triplet codons encode more amino acids including stop codons. For example, *E. coli* has six codons of arginine that varies from 1.4 to 24.1 per 1000 codons that this codon bias is the difference among identical codon usage [3]. Glutamic acid, asparagines, isoleucine, phenylalanine and tyrosine are all encoded by A/T rich codons and are used significantly less often in *M. tuberculosis*, whereas alanine, arginine, tryptophan and proline are much more frequent. It is conceivable that biased amino acid composition, which is a reflection of the skewed codon usage imposed by the high G/C content of the genome [4].

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