The 24-Quadruplet genetic code thriving on codon potency, codon integrity, codon uniqueness and codon compatibility.

Bozegha WB*

Department of Numeration Science Literature, Development Research Project, Yenagoa, Bayelsa State, Nigeria

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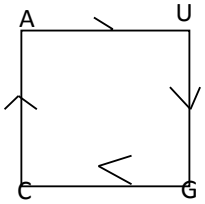
Introduction

The scientific observation by Molecular Biologists in 1953 that the sequence of the RNA four bases A, U, G, C (Adenine, Uracil, Guanine, Cytosine) in the nucleus of a cell influenced the sequence of the 20 amino acids of protein in the surrounding cytoplasm of the cell led to the search for what is responsible for the correlation between the two entities: 4 bases and 20 amino acids. In 1954 the answer emerged in the name of genetic code of 64 triplets derived from the four RNA bases by successive collateral posting to digitality 3 level, otherwise described as base crossing method anchored on the formula, 4^3, where 4 is the number of bases available and 3 is the number of bases per combination [1].

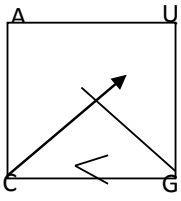
This genetic code derivation formula of 4^3 is now changed to 4^4, meaning permutation of 4 from 4 which by tower multiplication of 4, gives $4! = 4 \times 3 \times 2 \times 1 = 24$ quadruplets. The formula 4^3 can also be modified to 4^4 to produce 256 quadruplets by successive collateral posting method to digitality 4 level. 24 of these alone are permutations, while 232 are non-permutations and must be deleted to obtain the genetic code of 24 permutation quadruplets [2]. So here we have the 24-quadruplet genetic code to be what is responsible for the aforesaid Molecular Biologists' observation of 1953. A combinatorial input/output multiplicative replication system, using an input set of the four bases in the sequence A, U, G, C in Square Kinematics View Mixing Scheme, Figure 1 yields the output sequence of the 24-quadruplet genetic code as shown in Figure 1.

The 24 quadruplets in lines 1-24 of Figure 1 constitute the genetic code derived from the input sequence A, U, G, C of the RNA four bases. So with A, U, G, C as the input sequence of the four bases, the output sequence is the genetic code of 24 quadruplet codons in the sequence shown in Figure 1. The 20 amino acids of the protein type in the cytoplasm of the cell also would stand in sequence corresponding to that of the codons



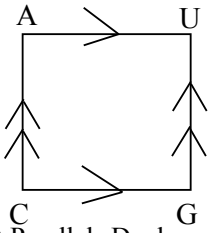
(a) Sides Deployment

From A clockwise	AUGC	Line 1
Fro	CGCA	Line 2
From U clockwise	UGCA	Line 3
Fro	ACGU	Line 4
From G clockwise	GCAU	Line 5
Fro	UACG	Line 6
From C clockwise	CAUG	Line 7
Fro	GUAC	Line 8



(b) Diagonals Deployment

From A clockwise	AGCU	Line 9
Fro	UCGA	Line 10
From G clockwise	GCUA	Line 11
Fro	AUCG	Line 12
From C clockwise	CUGA	Line 13
Fro	AGUC	Line 14
From U clockwise	UCAG	Line 15
Fro	GACU	Line 16



(c) Parallels Deployment

Parallels AU//CG Becomes	AUCG	Line 17
Fro	GCUA	Line 18
Parallels UA//GC Becomes	UAGC	Line19
Fro	CGAU	Line 20
Parallels CA//GC Becomes	CAGU	Line 21
Fro	UGAC	Line 22
Parallels GC//UA Becomes	GCUA	Line 23
Fro	AUCG	Line 24

Figure 1. *Square kinematics view mixing scheme with input sequence A, U, G, C*

in Figure 1. Whence a change of the sequence of the input set of four bases, out of the 24 possible sequences (permutations), there will be a corresponding change of sequence of the codons of the genetic code output which in turn leads to a change of sequence of the 20 amino acids of the resultant protein type. This is a demonstration of co-linearity between the genetic code of 24 quadruplet codons and protein type of 20 amino acids, where the 20 amino acids are individually engaged for placement in a sequence by 20 codons, with four spare codons for four place and time based start/stop control signals in protein synthesis [3].

The 24 quadruplets listed in Figure 1, being the product of one RNA quadruplet, reflects the potency of the quadruplet codons of this new 24-quadruplet genetic code. So codon potency is the strength of the 24-quadruplets genetic code for protein type proliferation and diversification, duly facilitated by codon compatibility, that is to say codons without neighborhood claims, nor restrictions in sequential alignment [4]. Examination of the 24 quadruplet codons listed in Figure 1 will show (i) That the sequences of the four bases per codon are all different, meaning the codons possess uniqueness in sequence, and (ii) That the four base types are present in each of the 24 codons as in the input set thereby reflecting codon integrity. Codon integrity is the unifying factor of the 24-quadruplet genetic code as the presence of all four bases in all 24 quadruplet codons guarantees codon potency and codon uniqueness. Codon uniqueness ensures individualized functional disposition of codons where 20 of the 24 codons individually engage 20 amino acids for placement in a sequence corresponding to theirs and the rest 4 codons serve as four signals for four place and time-based start/stop controls in protein synthesis geared to protein type proliferation and diversification in an atmosphere of codon compatibility [5].

Conclusion

This 24-quadruplet genetic code equipped with 24 quadruplet codons characterized by potency, integrity, uniqueness and compatibility in addition to collinearity with protein types is the true genetic code with a workforce of strength 24 for ably servicing protein synthesis in Nature since Creation.

Recommendations

Let this 24-quadruplet genetic code be widely publicized to attract experimental experts in genetics to spell it in order to render it fit for coding application in protein synthesis studies.

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***Correspondence to:**

Bozegha WB
Department of Numeration Science Literature Development Research Project
No. 9 Otiotio Road
Yenagoa, Bayelsa State
Nigeria
Tel: +2348068029860
E-mail: wbbozegha@yahoo.com