

Genetic Code: Mapping Base Kinematics in Quadruplet Codons

WB Bozegha*

Numeration Science Literature Development Project, Department of Combinatorial Computation, Yenizue-Gene, Yenagoa, Bayelsa State, Nigeria

***Corresponding Author:** WB Bozegha, Numeration Science Literature Development Project, Department of Combinatorial Computation, Yenizue-Gene, Yenagoa, Bayelsa State, Nigeria.

Received: March 15, 2018; **Published:** June 07, 2018

Abstract

Statement of the Problem: The 24-quadruplet genetic code structure is new and yet to be spelt in order to be rendered fit for coding application in protein studies. Tracing the base kinematics in everyone, of the 24 quadruplets is a possible ingredient of the experimental spelling exercise, so the presentation of this paper conveying the diagrammatic information on base movement/non-movement per quadruplet codon is part of the solution.

Methodology and Theoretical Orientation: The one-dimensional linear disposition of the four bases per codon is rendered in two-dimensional setting of a square in which the bases are located at the corners at one per corner to facilitate indication of movement/non-movement per base type. The input set square carrying the four base types at one per corner is reproduced in 24 places at one per codon.

The mapping of base kinematics is per base type per codon, relative to its forebear in the input square; in case of movement by an arrow to the new position (corner), and in case of non-movement by encirclement in its existing position (corner), Figure 1.

Findings: Resting patterns are found to be associated with groups of 1 base, 2 bases, and 4 bases; while movement patterns are by groups of 2 bases, 3 bases and 4 bases. The movements/non-movements of the mapping of base kinematics for three different genetic code sequences are tabulated and analyzed and six laws are observed and stated in the text.

Conclusion and Significance: The new 24-quadruplet genetic code is rendered in pictorial form by mapping of base kinematics in quadruplet codons with 24 distinct base-type arrangements justifying the genetic code engagement in protein synthesis.

Recommendations: This new 24-quadruplet genetic code should be publicized vigorously to attract experimental experts to spell it so as to render it fit for coding application in protein studies.

Keywords: Genetic Code; Kinematics; Quadruplet Codons

Introduction

Figure 1 is carrying the genetic code base kinematics in three streams, each headed by model GA CU in respect of the unique genetic code sequence produced by the named three independent combinatorial computational techniques; Neo-digibreed (SCP), SSMA (PSI), SSMA (DSI) respectively from left to right with a common input set of the RNA four bases A, U, G, C (Adenine, Uracil, Guanine, Cytosine).

Each stream of base kinematic mapping (diagramatisation) runs from codons 1 - 24 covering five pages in all, featuring patterns of base movement and rest in unique sequence of its own, but sharing a common index of movement or rest with the rest, as conveyed in table 1 for rest, and table 2 for movement.

The first column per technique carries the output of factorial complements of permutations for the given input set of 4 from 4 i.e. $4P4 = 4! = 4 \times 3 \times 2 \times 1 = 24$ quadruplets which are subjected to mapping in respect of base kinematics in the adjoining column.



Figure 1: Genetic Code: Mapping Base Kinematics in Quadruplet Codons.**Key to Figure 1**

Stationary to New Position

SSMA: Solid State Mixing Algorithm; SCP: Successive Collateral Posting; PSI: Place-Skipped Input Mixing Scheme; DSI: Digit-Skipped Input Mixing Scheme

Notes

- a) Set of three arrows making a triangle are unidirectional; either all clockwise or all anticlockwise.
- b) Set of four arrows making a rectangle are unidirectional; either all clockwise or all anticlockwise.
- c) Circles are free from arrows.

Discussion

The newly derived 24-quadruplet genetic code structure can be arranged in two basic shapes: one rectangular, where the 24 codons are placed side by side in a column fig. 1, and the other linear, where the 24 codons are placed end to end. This body of 24-quadruplets either in oblong or linear shape is referred to as litomorphology; it is stationary. The 24quadruplet codons derived from an input quadruplet set have diverse base sequences relative to the input set, except one, and are stationary or motionless. The changes in base sequence per codon are due to base movements and mapping the base movements/non-movements per codon for the 24 constituent quadruplets of the genetic code sequence renders the genetic code in kinomorphology, and it is pictorial and seems to be animated.

The pictorial rendition of the three different genetic code sequences derived from three different methods is presented in Figure 1.

Two Tables, 1 and 2 of analysis of base movement/non-movement covering the three genetic code sequences convey identical patterns of movement (Movement Pattern Index 113355442211, Table 1) and identical patterns of rest or non-movement (Resting Pattern Index 122112222, Table 2).

Results

Base kinematics characteristics per codon show performance of activities of movement and rest by bases in groupings of 2,3, and 4 for movement, ref. Table, 1 and 1,2, and 4 for rest (stationary) ref. Table 2.

Table 1: Resting patterns in three kinematics systems.**Key to Table 1**

V: Vertical; H: Horizontal; LD: Leading Diagonal; CD: Companion Diagonal; UE: Upper End; LE: Lower End; ✓: Present; ✓T: Present Top; ✓B: Present Bottom; ✓R: Present Right; ✓L: Present Left

Table 2: Movement patterns in three kinematics systems.**Key to Table 2**

UPD: Unpaired; PD: Paired; C: Clockwise; CC: Counter Clockwise; V: Vertical; H: Horizontal; LD: Leading Diagonal; CD: Companion Diagonal; ✓: Present; ✓N: Present Northern; ✓S: Present Southern; ✓E: Present Eastern; ✓W: Present Western; ✓TR: Present Top right; ✓TL: Present Top left; ✓T: Present Top; ✓B: Present Bottom; ✓R: Present Right; ✓L: Present Left; ✓BR: Present Bottom right; ✓BL: Present Bottom left

Six laws governing base kinematics affecting movement (motility) and rest (stationary) centred on movement and resting patterns and their indices-Movement Pattern Index (MPI) and Resting Pattern Index (RPI) are evident in the regularity and plurality of common occurrence of certain salient factors that warrant their formal statement as laws as follows:

Law 1: A group of 1 base can rest but cannot move

Law 2: A group of 3 bases can move but cannot rest

Law 3: A group of 2 bases can either move or rest

Law 4: A group of 4 bases also can either move or rest

Law 5: All true genetic code sequences of 24 quadruplet codons have the same movement pattern index (MPI) of 113355442211, ref. Table 2

Law 6: All true genetic code sequences of 24 quadruplet codons have the same resting pattern index (RPI) of 12211 2222, ref. Table 1

Conclusion and Significance

Mapping base kinematics in quadruplet codons has transformed the morphology of the 24-quadruplet genetic code structure from litomorphology (stationary), to kinomorphology (motile) that is pictorial and animated. This pictorial rendition of this new 24 quadruplet genetic code structure is a veritable facility for the spelling exercise yet to be done in order to render it fit for adoption in coding application in protein studies. Also the six laws of base kinematics governing the grouping of bases in strengths of 1, 2, 3 and 4 are significant as phenomenal indication of membership cohesion per group in Science. As Science and Scripture are but the two faces of the coin of Creation membership cohesion may well be taken for ethical lesson concerning attitudes of families in human experience.

Recommendation

Let this 24 quadruplet genetic code structure be widely publicized for the challenge of spelling it to confront as many spelling experts as possible.

Bibliography

1. Jason W Chin. "Reprogramming the Genetic Code: From Triplet to Quadruplet Codes". *Angewandte Chemie International Edition* 51.10 (2012): 2288-2297.
2. J Christopher Anderson. "An Expanded Genetic Code with A Functional Quadruplet Codon". *Proceedings of the National Academy of Sciences of the United States of America* 101.20 (2004): 7566-7571.
3. Dieter Soll. The genetic code - Thawing the "Frozen accident". *Journal of Biosciences* 31.4 (2006): 459-463.
4. Agris PF. "Decoding the genome: A modified view". *Nucleic Acids Research* 32.1 (2004): 223-238.
5. Nirenberg M and Leder P. "RNA codewords and proteins synthesis: The effect of trinucleotides upon the binding of sRNA to ribosomes". *Science* 145 (1964): 1399-1407.
6. Becker WM. "The World of the cell". The Benjamin and Cummings Publishing Company, Inc (1986).
7. Crick FRC. "The genetic code II". *Scientific American Journal* (1962).
8. Crick FRC. "The genetic code III". *Scientific American Journal* (1966).
9. Roberts MBV. "Biology, A Functional Approach". The English Language Book Society and Nelson (1971).
10. Yanofsky Charles. "The Gene Structure and Protein Structure". *Scientific American Journal* 216.5 (1967): 80-94.

Volume 1 Issue 7 July 2018

© All rights are reserved by WB Bozegha.