

2<sup>nd</sup> World Congress on  
**MOLECULAR GENETICS AND GENE THERAPY**  
July 03-04, 2017 Bangkok, Thailand

### Genetic code: Mapping base kinematics in quadruplet codons

**Whyte B Bozegha**  
Nigeria

**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 every one 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 & 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), Fig.1.

**Findings:** Resting patterns are found to be associated with groups of 1 bases, 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 & 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.

wbbozegha@yahoo.com