

The Transition Theory in Context of Biophysics

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Abstract Transfer RNA is associated with Earth-Moon time curvature. The amino acids are synthesized by multitude of anti-gravitational influx into acceptor point of t-RNA driven by codon disposition and systematically transit to gravitational arena with a positional motivation. The distance of constancy from the loop of anticodon to the acceptor point possesses a significant acceptance towards structural biology.

Keywords Transfer RNA: P53 protein molecule, Anti-gravity, Anticodon

1. Introduction

This paper involves the cumulative progress of anti-gravitational values with a systematic transition to the gravitational arena urged by the structural positioner. The clarification of t-RNA structure explicit the deterministic time motivation towards amino acid synthesis to some extent. The codon position possesses a parametric structural motivation towards protein amplification.

2. Discussions

Derived from the structural analysis of amino acids molecular weight, it is seen anti-gravitational time values (g^n) extrude or transit to the gravitational arena (g) systematically and that can be mathematically explained. Considering initiating amino acid methionine (149.2124) where 0.2124 is the anti-gravitational values and the naturally infiltrated (codon driven) anti-gravitational values = $0.2124 - 0.0149 = 0.1975$ and $0.1975 + 0.0267$ (a fundamental structural value) = $0.2242 = 0.3496(184) - 0.1254(66)$ where $184 * 0.0019 = 0.3496$ and $66 * 0.0019 = 0.1254$. The 0.0149 is an anti-gravitational values transit to the gravitational arena due to structural thrust into the system but closely interrelated to the anti-gravitational arena. The basic difference of g and g^n i.e. $g = 149 * 0.0019 = 0.2831$ and $0.1975(g^n)$ are of same kind but are opposite in directions of time where $0.0266 / 14 = 0.0019$ [1] and $0.2831 - 0.1975 = 0.0856 = 8 * 0.0107$ where 0.0107 is the unit of anti-gravitational influx.

The anti-gravitational rotations of Met cumulatively reach to 19 rotations $* 0.0107 = 0.2033$ and the transitional value is $414 / 2$ (bisection of codon) = $207 = 149 + 58$ where $58 / 2 = 29 = 0.0552$ exist as negative values of the molecule. While Met

incorporates 19-rotations the anti-codon (UAC) assign to Tyr (181.1894) comprises 16-rotations since $0.1894 - 0.0181 = 0.1713 = 16 * 0.0107$. It is seen gravitational integer values (e.g. 149) is a part of codon. Here the value '149' is assumed to be vertical time (vt) while 0.2124 is assumed to be horizontal time (ht).

The summation of g & g^n for Met = $149 + 112 = 261 = 238 + 23$ where $112 * 0.0019 = 0.2124 + 0.0004$ (a $0.0001 - 0.0004$ time difference found in many places).

238.3059 are in compliance to structural timeline i.e. $0.3059 - 0.0238 = 0.2821$ with 'difference of 10' in the structure since $149 * 0.0019 = 0.2831$.

It is seen $149.2124(\text{met}) + 89.0935(\text{ala}) = 238.3059$, $121.159(\text{cys}) + 117.1469(\text{val}) = 238.3059$ and $131.1736(\text{leu}) + 107.1323 = 238.3059$ where $121.159 - 14.0267 = 107.1323$.

Now, $261 = 238 + 23 = 0.3059 + 0.0437(23) = 0.3496(184)$ that significantly shows $261 - 184 = 77 = 0.1463(\text{val ht})$ exist as hidden time with 0.0006 adjustable time difference in the structure.

Now, $238 - 89 = 149$ and $112 - 23 = 89$ are structural matters.

Systematically, $0.2124 - 0.0935 = 0.1189 = 0.1894(\text{tyr ht}) - 0.0707$ (met core values) and $0.3496 - 0.1894 = 0.1602(\text{lunar gravity})$ and $0.0935 + 0.0437 = 0.1372(72)$ exhibits polymorphic site.

Again, $149.2124 = 149 + 112 = 261 = 238 + 23 = 184 + 77$ is structural matter since $112 * 0.0019 = 0.2124 + 0.0004$ time difference.

Histidine (155.1552) incorporates $13 * 0.0107 = 0.1391 = 0.1552 - 0.0155$ with 0.0006 time difference is a bisected molecule i.e. $2 * 0.1397 = 0.2793(147) = 0.3496(184) - 0.0703(37)$.

Now, $0.2793 - 0.1299 = 0.1494$ (glu core values) thus Glu plays a significant role in the system e.g. E6V mutation in hemoglobin molecule harms the protein system.

The acceptor point CCA of transfer RNA denoting here as 184-CCA accepts multitude of anti-gravitational waves

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synthesized to amino acids with systematic dimensions where $66A^0$ constancy of distance is significantly concerned.

Sometimes valine (117.1469) substitutes Met as initiating amino acid into protein would likely to be since $149.2124 - 117.1469 = 32.0655$ where $47 * 0.0019 - 0.0238 = 0.0655 = 32 * 0.0019 + 0.0047$ constitutes a relation between Met-Val.

The addition of Met-Val core values = $0.0707 + 0.0754 = 0.1461 = 0.2922 / 2$ and the negative part of the molecules $0.0547(\text{met}) + 0.0500(\text{val}) = 0.1047 = 0.1461 - 0.0414$ and $0.1461 - 0.0357 = 0.1104 = 0.0552 * 2$ calculated from $66(0.1254)$ constancy of distance in t-RNA.

The integer gravitational values is a part of codon, $263(\text{GU}) = 117(\text{val vt}) + 146(\text{gln vt})$ and addition of its core values = $0.0754 + 0.1323 = 0.2077$ and $0.2077 - 0.0047(\text{core value differences of met-val}) = 0.2030 = 19 * 0.0107(\text{met rotations})$ with 0.0003 time difference and $0.2033 + 0.1463(77) = 0.3496(184)$.

The mathematically supported explanation above would agree to the synthesis of amino acids by anti-gravitational values and systematically extrude to the gravitational arena where positional motivation (amino acid position) is significantly concerned explained later to some extent. The transit value e.g. 0.0149 to 149 is also a position in space-time extruded urged by the positional structure but the manifestation of molecular weight would lies to the deep meaning of nature.

The g & g^n can be discriminated by 149 and 0.0149 are the part of the structural biology and the transition creates structural equilibrium to exist where both are of same kind but are oppositely directed.

It would be very curious that CCA-184(lunar time termination point) accepts anti-gravitational influx and $266 = 184 + 82$ where $82 * 0.0019 = 0.1558 = 0.1605(\text{lunar gravity}) - 0.0047$ indicates oxygen as a structural value since the interaction of Met-Val at its positive and negative part, where 0.0047 acts as a complementation. According to Tyrosine, $0.3496(184) - 0.1602 = 0.1894(\text{tyr ht})$ while $0.3496 - 0.2124 = 0.1368(72\text{- polymorphic site}) + 0.0004$ and $0.1605 + 0.0608(32) = 0.2213 = 0.2124 + 0.0089$ and $0.2831 - 0.0571(30) = 0.1605 + 0.0655$ in the structure.

About 29.2920 values:

Leu (131.1736) and Asn (132.1184) are assigned to UUA-AAU codon-anticodon complementation.

Now, $0.1736 - 0.1184 = 0.0552(29)$ and $0.1736 + 0.1184 = 0.2920$.

Again, Val-Gln gives $146 - 117 = 29$ and $0.1451 + 0.1469 = 0.2920$.

The core values $29 * 0.0019 - 0.2920 = (-) 0.2369$ generally not being a negative value. So 29 or 0.0551 is a negative value while 0.2920 is a positive.

The acceptor point of transfer RNA is a bisectional point of earth-moon curvature (0.0367) in time form that may be denoted as CCA-184 is a lunar time termination point ($184 * 0.0019 = 0.3477 + 0.0019 = 0.3496$) where $3 * 0.0184 = 0.0552(29)$.

Now, $184 - 29 = 155(\text{His vt})$ and correspondingly $0.2920 - 0.1552 = 0.1368(72)$ exposes polymorphic site-72 as well

as $0.3496(184) - 0.2124(\text{Met ht}) = 0.1372(72)$ with 0.0004 time difference. The difference of core values $0.1393(\text{His}) - 0.0707(\text{Met}) = 0.0686 = 0.1372 / 2$.

Again, $0.3496 - (0.1393 + 0.0707) = 0.1397 = 0.1552 - 0.0155$.

Again, $0.3496 - 0.2920 = 0.0576 = 0.0547 + 0.0029$ (extruded) where $0.0547 + 0.0707 = 0.1254(66)$ meets to $66A^0$ about constant distance of anticodon from the acceptor point in transfer RNA.

Now, $0.292 - 0.1736(\text{bisection of lunar time}) = 0.1184 = 0.1736 - 0.0552(29)$.

Considering $0.0292 = 0.0146 * 2$ with one-step change of decimal position of 0.292 and $0.3496 - 0.2920 = 0.0576 = 0.0146 + 0.0430$ where $0.1881(\text{lys ht}) - 0.1451(\text{gln ht}) = 0.0430$ and $0.3496 - 0.0146 = 0.3350 = 0.1881 + 0.1469(77)$ that disappears would be since $292 - 77 = 215 = 107 * 2(\text{first two unit values of anti-gravity in the structure}) + 1$.

Again, $292 + 29 = 321$ and $292 - 29 = 263 = 146(\text{lys vt}) + 117(\text{val vt})$ are the structural matters into the system.

Lys-Val is closely related explained later on.

Transfer RNA mechanism:

The acceptor point-CCA (357) of transfer RNA is $[367(\text{earth-moon time curvature}) - 10(\text{difference of } 10)] / 2 = 184$ and denoting here as 184-CCA and correspondingly GGU (414) would be the backbone of t-RNA structure. The acceptor point receives anti-gravitational influx at the limit point of lunar time (0.3496).

Now, $357 = 3 * 119$ and like effectiveness of first two bases of codon, $2 * 119 = 238$ is a factor (238.3059) of timeline structure.

Again, $0.3059 - 0.2793(147) = 0.0266$ and $266 + 91 = 357$ where $238 - 147 = 91 = 77(\text{hidden time}) + 14$ and $(238 + 147) = 385 = 414 - 29 = 356 + 29 = 266 + 119$ where transition like 0.0266 to 266 is the structural chemistry of g & g^n .

The constancy of distance ($66 A^0$) [2] in t-RNA is a structural factor while $66 * 0.0019 = 0.1254(\text{anti-gravitational time values})$ where mass-time-distance are synonymous and factor of positional motivation in biophysics.

In Met-Tyr context, $0.1254 - 0.0707(\text{met core values}) = 0.0547(29)$ and $0.1545(\text{tyr core values}) - 0.1254 = 0.0291 = 291 = 357 - 66(\text{met position}) = 184 + 107(\text{tyr codon position according to p53 molecule})$ in the structure. The Met core values $149 * 0.0019 - 0.2124 = 0.0707$ is the hidden time in the gravitational arena while $0.1254 = 0.0707 + 0.547(29)$ exist in the negative part of the molecular structure with 0.0004 time difference).

Previously, it has been shown that Met-Ala structural consistency where $184 - 89 = 95 = 66 + 29$ and correspondingly $0.3496(184) - 0.0935 = 0.2124 + 0.0437(23)$ and $95 * 0.0019 - (0.2124 + 0.0437) = 0.0756(\text{ala core values})$.

In Glu-Val context, $147 * 0.0019 - 0.1299 = 0.1494$ and $0.1494 - 0.1254(66) = 0.0240 = 240 = 184 + 56(\text{codon position according to p53}) = 357 - 117(\text{val vt})$ and $414 - 240 = 174(\text{arg vt})$.

It is seen in this case both the co-ordinations (184 and 240) in the structure is in bisectional form where $240 * 2 = 480 =$

414 + 66.

In Arg-Val context, $117.1469(\text{val}) + 174.2017 = 291.3486$ and $0.2017 - 0.1469 = 0.0548(29)$.

Now, $357 - 291 = 66$ and $117 + 66 = 183$ and correspondingly $0.1469 + 0.1254 = 0.2723 = 0.2017 + 0.0707(\text{met translocation})$ and $0.3496 - 0.2723 = 0.0773 = 0.0754(\text{val core values}) + 0.0019$.

According to codon position in p53, $240 = 174(\text{arg}) + 66(\text{met}) = 0.1289(\text{arg core values}) + 0.0703(\text{met core values with } 0.0004 \text{ time difference}) = 0.1992$ and $75.0669(\text{gly}) + 165.19(\text{phe}) = 240.2569$.

Now, $240 * 0.0019 - 0.2569 = 0.1991$ shows codon position is a part of the system.

Again, $240 = 168(\text{arg}) + 72(\text{pro})$ [3] = $0.1289(\text{arg core values}) + 0.0875(\text{pro core values}) = 0.2164 = 0.1991 + 0.0174$ where $0.1289 - 0.0875 = 0.0414$.

Again, $240 = 168(\text{arg}) + 72(\text{arg}) = 0.1289 + 0.1289 = 0.2578 = 0.1991 + 0.0588$ where $0.0588 = 0.0414 + 0.0174$.

It is seen Trp-Thr combination is in compliance to t-RNA structure assigned by UGG(414)-ACC(357) codon-anticodon composition while the core values of Trp is 0.1615(85) and that of Thr is 0.1064(56) that differentiated by $85 - 56 = 29(0.0551)$.

Now, $0.1615 - 0.1254(66) = 0.0361(0.0357 + 0.0004)$ where UGG(414) is in equilibrium to anti-gravitational codon 0.0357 while $0.1254 - 0.1064 = 0.0190 = 0.0547(29 \text{ with } 0.0004 \text{ time difference}) - 0.0357(\text{ACC})$. The existence of anti-gravitational codon is explicit above where $414 + 266/2 = 547$ shows $0.2261(\text{trp ht}) * 2 - 0.1463(\text{hidden time}) = 0.3059$.

P53 protein molecule (393 codon associated protein) where $393 = 321(\text{lys}) + 72(\text{arg})$ is in timeline structure.

Now, $321 = 146(\text{lys vt}) + 174(\text{arg vt}) + 1$ and according to core values $0.0893(\text{lys } c_v) + 0.1289(\text{arg } c_v) = 0.2182 = 0.2889$ [4] - $0.0707(\text{met } c_v)$ where $707 - 321 = 386 = 320 + 66(\text{met codon position})$ shows structural molecular points and anti-gravitational transition.

Again, $(0.3496 - 0.0393) / 2 = 0.1552(\text{his ht})$ that corresponds to $393 + 184 = 577 = 267 + 2 * 155$ are events of structural biology.

Amino acids relations derived from Lysine (146.1881):

Mathematically, $0.3496(184) + 0.0266 = 2 * 0.1881(\text{lys ht})$ and after transition of 0.0266, $184 + 266 = 450 = 393(\text{p53 amplification}) + 57 = 252(\text{TT}) + 2 * 99$ where $99 * 0.0019 = 0.1881 = 0.171 + 0.0171$ that indicates replication process and correspondingly $0.221 + 0.0221 = 0.2431 = 0.1881 + 0.0551(29)$ since $221 + 171 = 393 - 1$.

Now, $450 + 2 * 146 = 742 = 336(\text{UUU}) + 405(\text{AAA}) + 1$.

In opposite direction, $266 - 184 = 82 = 0.1558 = 0.1881 - 0.0323(\text{extruded for trp-thr})$ and correspondingly $0.1558 + 0.1881 = 0.3439 = 0.3458(\text{trp-thr ht}) - 0.0019$ and $393 - 82 = 311(\text{extruded values for lys-phe})$ and $0.1881 - 0.0330(\text{extruded values for met-tyr}) = 0.1551(\text{his ht})$ are structural matters.

Now, $0.1615(\text{trp } c_v) - 0.0893(\text{lys } c_v) = 0.0722 = 0.0703(\text{met } c_v \text{ with } 0.0004 \text{ time difference}) + 0.0019$ and $0.1064(\text{thr } c_v) + 0.0893 = 0.1957 = 0.2261 - 0.0304(\text{coined as oxy-time a fundamental structural value})$ where $0.0304 + 0.0019 = 0.0323$.

Again, $0.1064 + 0.0893 = 0.1957 = 2 * 0.0703 + 0.0551(29)$ where $0.1615 - 0.1064 = 0.0551$.

Again, $2 * 0.1957 = 0.3914 = 0.3496(184) + 0.0418 = 0.2831(149) + 0.1083(57)$.

In E6V(Hemoglobin-S) and E6K(Hemoglobin-C) mutations, it is seen val-lys(GU = 263 = 146 + 117) are closely related and $184 + 266 = 450 = 292 + 158 = 146 + 304$ and $263 + 158 = 421(\text{GAA}) = 117 + 304$.

Since $0.1494(\text{glu } c_v) - 0.0754(\text{val } c_v) = 0.0740(39)$ and in mutation $\text{GAA}(421) - \text{GUA}(398) = 23$ and consequently $39 - 23 = 16 = 0.0304(\text{oxy-time})$ is absorbed as hidden time causing de-oxygenation in sickle-cell-anemia(SCA).

3. Conclusions

The amino acids are constituted by anti-gravitational values directed by t-RNA mechanism and the anti-gravitational transition is necessarily happening for molecular manifestation. The paper is supported by quantitative and mathematical descriptions and the positional events of coincidence and discrimination in the structure would be an interest of biophysics.

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