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The Mole-structural Biology in Electromagnetic Structure of Space-time

Ratan Kumar Sarkar

Janhavi, Keota, Hooghly, West Bengal, India

Abstract The evaluation of electromagnetic structure of space-time has been facilitated to determine synthesis of amino acids under codon-anticodon assignment and have been shown in different aspects. The events of amino acid synthesis in the polypeptide chain are specified by the molecular points or space-time points in the structure can be complemented in terms of codon. The infiltration of anti-gravitational impulses into electromagnetic structure of space-time concerned to methionine involvement, bisectional processes and structural mutations in p53 are mathematically shown towards predictability of directional gravity.

Keywords Space-time, Codon-anticodon, P53 protein, Structural & Molecular biology

1. Introduction

In this paper 'electro-magnetic structure' refers to space-time structure that in compliance with sub-atomic particles masses i.e. electron ($e^- = 0.511Mev/c^2$) and proton ($p^+ = 938.29Mev/c^2$) in the context of biology. The mole-structural biology refers to molecular and structural biology is integrated and it would be structural biology acts as a template for molecular biology. Derived from TP53 gene, p53 protein molecule is a standard molecule that exhibits points in space-time and shows systematic structural mutations.

2. Discussion

The position where directions of time is in equilibrium i.e. 27*0.0107 = 0.2889 = 0.321 – 0.0321 = 152*0.0019 is a significant position where gravitational and anti-gravitational time are sustained [1].

This also satisfies p53 protein manifestation like 152(pro) + 27(pro) = 179(his) = 358(CAU) / 2.

0.0875(pro core values)*2 = 0.1750 = 0.1393 (his core values) + 0.0357.

Again, 27*0.0019 = 0.0513 or, 270 space-time point or molecular point = 0.513 meets to electronic mass with 0.0020 i.e. approximately one molecule (0.0019) time difference.

Again, 270(0.513) / 3 = 90(0.171) in triplet structural mechanism of biology. Space-time point and its corresponding mass or time has been shown side by side. Considering one molecule difference the values actually represents 89(0.1691) where 0.1691 = 0.1602 (lunar gravity) + 0.0089.

Amino acids starts with Gly(75.0669) and on structural considerations, 75.0669 – 2*14.0267 = 47.0135. Now, 2*47.0135 = 94.0270 that can be represented as 940.270.

270(0.513) and 940(0.270) may be called a mathematically devised electromagnetic structure of space-time.

It is significant that the molecular weight of alanine is 89.0935 g/mol where 0.0935 is the time form of proton mass $938Mev/c^2$ with 0.0003 time difference.

Now, 938 – 513 = 425 = 367(earth-moon curvature) + 57 with one molecule difference that makes '57' a significant bisection and replication factor since 367 = 2*183(lunar time) + 1.

It is a general tendency that time runs to reach 0.0367(earth-moon time curvature) but attaining in this point time bisects since 14 + 100 = 0.0267 + 0.0100 i.e. 114.0.0367 where 114 = 2*57 and 0.0367 = 2*0.0183 where 183*0.0019 = 0.3477(lunar time).

In the loop of t-RNA the anti-codon maintain a constant distance of $66A^0$ from the acceptor point C-C-A(357) [2] that would conforms to electromagnetic structure of space-time since 937 – 513 = 424 = 357 + 66 = 367 + 57 with one molecule difference and also 357 – 66 = 291 is a significant structural value where 938 – 357 = 581 = 291*2.

Correspondingly, 414(GGU) + 66 = 480 = 936 – 456(GGG + 3)) and 414 – 66 = 348 where 936 – 348 = 588 = 333(CCC) + 255.

Again, 480 = 423 + 57 = 225(bisection of GGG – 3) + 255 are structural values found in oncogenic mutations of p53.

* Corresponding author:
rksarkar36@gmail.com (Ratan Kumar Sarkar)
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Both negative and positive side calculation has a meaningful value in the structure.

SAR codon-anticodon complex:

A serine (105.093)-alanine (89.0935)-Arginine (174.2017) interrelation is in consensus to electromagnetic structure of space-time.

The core value (C_v) of serine = 105*0.0019 – 0.0930 = 0.1065 while that of alanine = 89*0.0019 - 0.0935 = 0.0756 and 0.1065 – 0.0756 = 0.0309 is bisection of 0.0618 = 0.0513 + 0.0105.

Now, 49*0.0019 = 0.0931 that shows 105 – 49 = 56 (bisection factor) for serine.

The trans-gravitational value (T_V) of alanine = 0.0935 – 0.0089 = 0.0846 and 0.0846 / 2 = 0.0423 = 0.0936 – 0.0513 while alanine core values = 0.0756 = 0.0423 + 0.0333.

The climax where the anti-gravitational influx torn out and transit to gravitational arena is said to be trans-gravitational value (T_V).

The bisection of serine core values = 0.1066 / 2 = 0.0533 = 0.1289(core values of Arg) – 0.0756 (core values of Ala). The bisection of Arg core values = 0.1290 / 2 = 0.0645 where 0.0645 + 0.0423 = 0.1068.

A time difference of 3 or 0.0003 or 0.0057 has been found in many places both in positive or negative side in the structure.

Methionine nexus to electromagnetic structure of space-time:

According to p53 protein F270, 165.19(phe) + 105.093(ser) = 270.2830 where 149(met vt)*0.0019 = 0.2831.

Again, 149.2124(met) + 121.1590(cys) = 270.3714 where 270*0.0019 – 0.3714 = 0.1416 = 0.2832/ 2(bisected).

Again, 181.1894(tyr) + 89.0935(ala) = 270.2830.

Again, 155.1552(his) + 115.1310(pro) = 270.2862 where 0.2862 = 0.2830 + 0.0032(oxygenation).

The above calculation shows 267 + 3 = 270 possess a timeline in the electronic space-time structure and 0.0938*3 = 0.2830 – 0.0016(de-oxygenation) in the system.

938 – 513 = 425 = 273 + 152(i.e. 149 + 3) = 304(oxy-time) + 120(difference of gly-pro) is significant in the structure.

About p53 protein molecule and structural mutations:

P53 is a bisected molecule of ($453^{GGG} + 333^{CCC}$) / 2 = 393 where (453 – 333) + 393 = 513.

It is seen 453 – 333 = 120 = 0.0875(core values of pro) – 0.0756(core values of gly) with one molecule difference.

P53 would be called an oxygenated molecule since 393 = 304 + 89 or 571 = 304 + 267 where 571 – 393 = 179 – 1 and 179 = 27 + 152 = 252(TT) – 73 (polymorphic site in p53) are structural matters and would liable to respiration of oxygen into the system while gravity or anti-gravity possess contraction and expansion properties e.g. 16*0.0019 = 0.0304 = 304 = 178 + 126(T). Again, 393 = 304 + 89 gives 16 + 89 = 105 = 178 – 73 and 89 – 16 = 73 are structural matters.

'72' = 73 – 1 = 393 - 321 is called polymorphic site where 72 = 56(bisection or replication factor) + 16(oxygenation) makes the site special.

P53 is an ideal protein molecule which exhibits molecular points or space-time points which would be possessed negative and positive interactions causing deletions.

P53 molecule has been found in cancerous cell where oncogenic mutations breaks down the fundamental structure of the molecule and would impair the oxygenation system tends to lethality. M133L, R282W etc. are some mutations where molecular point-133 is specified for methionine (149.2124) and so on and mutations in these sites results structural distortion. The M133 can be shown as follows in the structure.

266(gly) / 2 = 133 follows 89*2 = 178 = 267 – 89(pro) = 152(pro) + 27(pro) – 1.

Now, core values of Gly = 75*0.0019 – 0.0669 = 0.0756 while core values of Met stands 149*0.0019 – 0.2124 = 0.0707 that differed by 0.0756 – 0.0707 = 0.0049 = 49 and would corresponds to GGG(454) / 2 – 49 = 178 in the structure.

The mutational values of M133L is 0.0707(met c_v) – 0.0753(leu c_v) = (-) 0.0046 = (-) 46 that would be added to molecular point-133 yielding 133 + 46 = 179 shows mutational possibility. The Met vt-149 is concerned to 133 + 16 (oxygenation) in p53 molecule shows thermo-stability.

The mutational values of R282W also gives negative values as (-) 326 and gives 282 + 326 = 608 = 2*304 = 393 + 107*2 + 1 where 393 – 215 = 178.

It is revealed out mutational values, mutated amino acid distances, p53 amplification (393) is interrelated. It is seen the mutation in bisectional site is detrimental likely in most of the cases.

R249S, H168R, R273H are associated with molecular point distances or space-time points [3].

Mutational site-249*2 – 393 = 105 which corresponds to 273 – 168 = 105 and also with mutational values 0.1393(HC_V) – 0.1289(RC_V) = 0.0105 with 0.0001 time difference.

The bisection of (453 – 3) / 2 = 225 is a significant site occupied by Val and correspondingly (333 + 3) / 2 = 168 occupied by His. It is seen 225 – 57 = 168(mutation point) and 225 + 57 = 282(mutation point) are structural mutations where 393 + 57 = 450(GGG – 3) and 393 - 57 = 336(CCC + 3).

M133L / V203A / N239Y / N268D are super-stable quadruple mutants [4] clarified as follows.

The mutational values of M133L and V203A are respectively (-) 46 and (-) 2.

Stabilized mutation means oxygenation(+16) of the site while destabilization means (-) 16 developing the concept of real and apparent site.

Now, 133 + 16 = 149(site and met vertical time coincides) while 133 + 46 = 179 = 152 + 27.

Now, 203 + 2 = 205 = 221 – 16 and 393 - (133 + 203) = 57.

Again, 171 + 16 = 187(apparent site) = 203 – 16 shows 179 + 187 = 367(earth-moon curvature) – 1.

The mutational values of N23Y and N268D are respectively (-) 221 and (-) 171.

Now, 221 + 171 = 393(p53 amplification) and (268 + 239) – 393 = 114 = 2*57.

Again, 268 – 239 = 29 and 393 + 29 = 423 – 1 that stabilizing the electromagnetic structure.

Here are some highly destabilizing mutations have been clarified.

V157F provides mutational values (-) 481 = 225 + 255(would be associated with I255F) and it is significant that bisection of (453 – 3) / 2 = 225 is not a mutation point in the structure.

Again, 393 – 157*2 = 79 where 225 – 79 = 146 would be associated with L145Q and 255 – 79 = 176 would be associated with R175H.

Again, 481 – 79 = 402 = 146 + 256 are related to L145Q and I255F.

V143A provides the mutational values (-) 2 and thus would associated with 143 + 2 = 145(L145Q).

The mutational values of L145Q = (-) 0.0570 = (-) 570.

Now, 145 + 570 = 715 = 393 + 321 + 1 where 393 – 321 = 72(polymorphic site) and 72 + 73 = 145 i.e. L145Q.

I shall discuss here about same mutations but in different sites e.g. F134L & F270L and R175H & R273H and I195T & I232T.

It is seen that 482 = 304 + 178 = 225 + 255 + 2 and also 304 – 178 = 126(T) are structural matters in the system.

F270L and F134L are related as follows.

Here, 270 – 134 = 136 = 79 + 57 in the structure and mutational values provides 482 = 304 + 178.

Now, 482 + 136 = 618 = 393 + 225 and 393 – 225 = 168 (H168R) and also 304 – 168 = 136.

R175H & R273H are related as follows.

Here, 273 – 175 = 98 and the mutational values provides (-)104.

Now, 175 + 104 = 279 and 273 + 104 = 377.

393 – 279 = 114 = 2*57 and 393 – 16 = 377 makes R273H a hotspot mutation.

Moreover, 393 – 73 = 320 = 377 – 57 and 393 + 73 = 466 = 377 + 89 where 105 – 16 = 89.

I195T & I232T are related as follows.

Here, 232 – 195 = 37 and the mutational values provides (-) 311.

Now, 195 + 311 = 506, 506 – 393 = 113 = 2*57 – 1 and (232 + 311) – 393 = 150 where 150 + 37 = 187 = 336(CCC – 3) – 149 and 150 – 37 = 113 = 450 – 337.

Impact of electro-magnetic space-time structure on amino acids synthesis:

It is significant that when ‘values of difference’ between electronic molecular point (270) and designated codon appears to ‘89’ then influx of anti-gravitational (0.0107 unit) rotations shows a complete one or in approximation. The amino acids are taken on designated codon-anticodon sequence.

UUA(359)-Leu(131.1736)-AAU(382)-Asn(132.1184):

359 – 270(AA) = 89 and correspondingly 0.1736 – 0.0131 = 0.1605 = 15*0.0107.

Again, 382 – 270 = 112, 112*0.0019 = 0.2128 = 0.1324(core values of asn) + 0.1608 / 2.

AUG(398)-Met(149.2124)-UAC(358)-Tyr(181.1894):

358 - 270 = 88 and correspondingly 0.1894 – 0.0181 = 0.1713 = 16*0.0107.

Again, 398 - 270 = 128 = 112 + 16 that corresponds to 398 – 16 = 382 and 382 – 270 = 112 = 0.2124(met ht with adjustable 0.0004 time difference).

Now, 0.1545(Tyr core values) – 0.0707*2(Met core values*2) = 0.0131 = 131 = 128 + 3.

It is seen there are time sharing between Met-Tyr as follows.

(149*0.0019 + 0.2124) – 0.1605*2 = 0.1745 = 0.1894 – 0.0149.

Again, (181*0.0019 + 0.1894) – 0.1605*2 = 0.2124.

AAA(405)-Lys(146.1881)-UUU(336)-Phe(165.19):

336 - 270 = 65 +1 where 65*0.0019 = 0.1235(core values of Phe).

405 – 270 = 134 + 1, 134 = 87 + 47 where 47*0.0019 = 0.0893(core values of Lys) and 87 = 69(codon-anticodon difference) + 18(Phe-Lys core values difference).

UGG(414)-Trp(204.2261)-ACC(357)-Thr(119.1197):

357 – 270 = 87 and correspondingly 0.1197 – 0.0119 = 0.1078 = 10*0.0107 + 0.0008.

Again, 414 – 270 = 144 = (204 – 63) + 3 = 56 + 88 where 85*0.0019 = 0.1615(core values of Trp) with difference of ‘3’.

The codon-anticodon difference = 414 – 357 = 56 + 1 where 56*0.0019 = 0.1064(core values of Thr) and 0.1064 – 0.0513 = 0.0551 = 29 in contraction form related to 29 + 56(values of difference) = 85 = 0.1615(core values of Trp).

Trp-Thr combination is clearly related to GGG(453)-CCC(333) structure since 453 - 333 = 119 + 1 and Trp-Thr possess 119*0.0019 = 0.2261 in positive and negative side. Otherwise, 453 + 333 = 786 = 414 + 357 + 16(oxygenation) with one molecule difference.

It is seen 204.2261 = 89.0935(ala) + 115.1310(pro) + 0.0016.

3. Conclusions

Digital amplification of molecular points in protein is concerned to space-time points in structural foundation to molecular manifestation lies to deep meaning of nature. An in-vitro experimental concept may be carried out as ‘cancer cell in zero-gravity region’ to probe development of cancer.

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