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The Analysis of P53 Protein Molecule Oncogenic Mutation

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Abstract The proteins are synthesized on the basis of electromagnetic structure of space-time under variable codon that measured from earth-moon time curvature. The symmetry of gravitational and electromagnetic waves is synchronized towards molecular manifestation in the biophysical structure. The highly destabilizing mutation in p53 protein molecule is the breakdown of amplified electromagnetic structure of protein molecule. Some parametric values in the structure explicit the mode of destabilization.

Keywords P53 protein molecule, Electromagnetic waves, Oncogene

1. Introduction

This paper involves symmetry of gravitational and electromagnetic waves in terms of amino acid synthesis in biophysics. Electromagnetic structure exposes ambiguity of gravitational vertical time and molecular point in protein amplification. The oncogenic mutations follows breakdown of electromagnetic structure of p53 tumor suppressor protein has been discussed herewith.

2. Discussions

Before entering to p53 oncogenic mutations I shall discuss how gravitational and electromagnetic waves are unified in the space-time structure.

The mass of proton 938.2900 Mev/c^2 is related to electronic mass 0.511 Mev/c^2 as follows [1].

Avoiding decimals, 938 – 268 = 670 = 2900*2 – 5130 where 270*0.0019 = 0.5130 = 0.5110 + 0.0019 (one molecule) with 0.0001 time difference since decimal makes a difference between gravitation and anti-gravitation and '670' arises from 75.0669(gly) assigned by GGU(414) and 414 + 256 = 670, a structural network.

Again, 0.513 – 0.0268 = 0.4862(256) = 0.2900*2 – 0.0938 where 256 is bisection of electronic time while anti-gravitational segment of proton is a bisected value.

On structural considerations, CCA(357) the acceptor point of t-RNA is correspondingly related to GGU(414) and 357 – 100 = 257 while 414 +100 = 514 where '100' is a structural factor arising from 14.0267 fundamental values originated from 0.0367 earth-moon time curvature towards structural equilibrium.

One molecule (0.0019 or 0.0001) difference is about common in the system.

The corresponding anti-gravitational value of '256' is 149.2124(met) + 107.1323 = 256.3447 where 0.2900 + 0.0547(29) = 0.3447 and 181.1894(tyr) + 75.0669(gly) = 256.2563 where 0.3447 – 0.2563 = 0.0884 = 0.0547 + 0.0336(UUU anti-gravitational codon) with 0.0001 time difference. Here, 121.159(cys) – 14.0267 = 107.1323 and 29*0.0019 = 0.0547 with 0.0004 time difference in the system that applicable to Met-Val interrelation will be discussed later.

The values '29' (i.e. 0.0029 or 0.0551) is an essential complementary factor in the structure that would be 30 identifiable spots found in hemoglobin electrophoresis treatment.

The one step-up of electromagnetic structure (256.2563) = 256.2563 + 14.0267 = 270.2830 where 149*0.0019 = 0.2831 and 165.19(phe) + 105.093(ser) = 270.2830. The values 270.283 shows structural timeline [2] e.g. 149.2124(met) + 121.159(cys) = 270.3714 where 0.513(270) – 0.3714 = 0.1416(bisection of 0.2831). In p53 molecule 270 occupies phenylalanine and 270 + 66 = 336(UUU) where '66' is 'distance of constancy' in t-RNA shows structural synchronization.

Codons would be measured from 367 or 0.0367(earth-moon time curvature) and Met-Phe have symmetry from codon level like 336(UUU) + 31 = 367 = 398(AUG) – 31 and correspondingly 0.1235(phe c_v) – 0.0707(met c_v) = 0.0528 = 0.0547(29) – 0.0019(one molecule) and 0.0547 + 0.0207 = 0.0754(val c_v) where 0.0207 is bisection of GGU(0.0414 or 414).

The impact of codon level is effectiveness on codon-anticodon complementation. It is seen the core value of Phe = 165*0.0019 – 0.19 = 0.1235 = 66 – 1 where 66 + 3 = 69 = AAA(405) – UUU(336) and also 69 – 29(extruded to complement val) = 40 = AUG(398) – UAC(358).

Codon level also systematic to Leu-Asn, 367 – 8 =

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359(UUA) and 367 + 2*8 = 383(AAU).

Now, 0.0753(leu c_v)*2 – 0.1324(asn c_v) = 0.0182(lunar time 183*0.0019 = 0.3477 with one molecule difference concerned to codon).

It is seen codon and anticodon are differentiated by upper and lower level codon considering 0.0367 earth-moon curvature. The influx of anti-gravitational waves is determined by codon level in respect of 0.0367 or 367 causing gravito-motive force towards amino acid synthesis.

The gravitational and electromagnetic waves are unified in a way as follows.

0.2563 – 0.0256 = 0.2307 = 19*0.0107 (19 rotations of anti-gravitational unit) + 0.0256 + 0.0019 shows electronic time is bisected.

In context of Met-Phe symmetry, the one step-down structural value would be 242.3135 where 165*0.0019 = 0.3135. Systematically, 0.3135 – 0.2563 = 0.0572 = 0.0267(14) + 0.0305(coined as oxy-time a structural value) where 0.0547 – 0.0305 = 0.0242 = 242, a structural network.

Again, in Met-His context, 0.2124(met ht) – 0.1552(his ht) = 0.0572 and 0.0149 + 0.0155 = 0.0304 = 304 on transition.

The core value(c_v) of electro-magnetic structure 256.2563 is 256*0.0019 – 0.2563 = 0.2301 is effective into the structural system.

0.2301 – 0.1235(phe c_v) = 0.1066(thr c_v) = 0.0707(met c_v) + 0.0357(CCA);

0.2301 – 0.1545(tyr c_v) = 0.0756(gly c_v);

0.2301 – 0.1393(his c_v) = 0.0908 = 0.1615(trp c_v) – 0.0707(met c_v).

Obviously 256.2563 is a fundamental electromagnetic structure synchronized with the amino acid synthesis.

From molecular standpoint, 256.2563 values resembles to 155.1552(his) and correspondingly 358(CAU) + 155 = 513 = 367 + 146(trp position in p53).

Accordingly, 0.1615(trp c_v) – 0.1393(his c_v) = 0.0222 = 222(CC) and 513 – 66 = 447 = 302(GG) + 145 in the structure.

146W is found in p53 where 146 is Lys vertical time. It is seen 414(trp-UGG) – 367 = 47 where 47*0.0019 = 0.0893(lys c_v) that would be the cause of 146W in p53. Again, 0.1254(66) – 0.0893 = 0.0361 = 0.1615(trp c_v) – 0.1254(t-RNA factor) and 367 – 47 = 320 occupies Lys in p53. The Lys codon 405(AAA) – 320 = 85 = 0.1615(trp c_v).

Note that 256 + 111(C) = 367(earth-moon time curvature) is a structural matter.

The codons and core values are interrelated as follows.

0.2301 – 0.1393 = 0.0908 = 0.1615 – 0.0707 and codon difference $414(UGG)^{trp} – 398(AUG)^{met} = 16$ and accordingly the attributable codon of 256.2563 would be $358(CAU)^{his}$ + $16 = 374(GUC)^{val}$ and 0.2301 = 0.0754(val c_v) + 0.1547(tyr core value with 0.0002 time difference).

The electromagnetic structure (256.2563) is discussed here in context of Cys-Met.

121(cys vt)*0.0019 = 0.2299 = Core values of electromagnetic structure(256.2563) with 0.0002 time difference.

Now, 0.2563 – 0.1590(cys ht) = 0.0973 = 0.0707 + 0.0266 = 0.2296 – 0.1323(gln or asn c_v).

Note that the core values of Cys-Met is differentiated by 0.0002 time values and 256.2563 – 14.0266 = 242.2297 where 242 = 121*2.

Accordingly, 0.1590*2 – 0.2563 = 0.0617 = 0.0884 – 0.0267.

Again, 149 – 121 = 28 = 0.0532 and 0.2563(A) – 0.0532 = 0.2031(19-rotations of anti-gravitational unit) or 135 – 28 = 107 and 532 – 256 = 276 = 552/2 in the structure.

Conversely, 298(i.e. 149*2) – 256 = 42 = 0.0798 = 0.0532 + 0.0266 where 149 – 121 = 28 and 0.2124*2 – 0.2563 = 0.1685 = 0.1415(bisection of 149) + 0.0270, a structural network.

The values 149*0.0019 = 0.2831 found in 270.2830 whereas 121*0.0019 = 0.2299 found in core values of 256.2563 shows structural cycle between positive and negative arena.

The transitions 0.159 – 0.0121 = 0.1469(val ht) is related to 0.1736(leu ht) – 0.0146 = 0.1590 where 121 + 146 = 267.

The unfolding of gravitational vertical time i.e. 149 for 149.2124(met) is necessarily happening for amino acid mutation. The core values shows the status of the molecule derived from assumed vertical time(149*0.0019) and negative horizontal time(0.2124) in the structure. The detrimental mutation would defects the oxygenation system in the structure.

In case of SCA, Hemoglobin S, glutamic acid(147.1299) is mutated to valine(117.1469) causing core value difference, 0.1494 – 0.0754 = 0.0740 = 39 = 23 + 16 where 16 or 0.0304 is absorbed and '23' is adjusted by the codon change, 421(GAA) – 398(GUA) = 23.

On Hemoglobin C, 0.0740 + 0.0153(oxy-time bisected) = 0.0893(lys c_v) or 0.0754(val c_v) – 0.0153 = 0.0601 = 0.1494 – 0.0893 and from codon level 421(GAA) – 405(AAA) = 16.

From electromagnetic structure standpoint, 0.2301 – 0.1494 = 0.0807 = 807 and 807 – 66 = 741 and correspondingly 0.1254(66) = 0.0754 + 0.0500 where 0.0807 – 0.0500 = 0.0304(oxy-time) with 0.0003 time difference.

Again, 0.2301 – 0.0893 = 0.1408 = 0.1254 + 0.0154 (bisected oxy-time).

In this way we find existence of oxy-time(0.0304) in the electromagnetic structure (256.2563).

3. Structural Pre-conditions

Codons works on structural pre-conditions until amino acids attains to equilibrium state. While core values(c_v) of amino acids are an equilibrium state of molecules core values and codons are closely related in the structure. The basic structure are concerned to some parametric values will be discussed here.

GGU(414) – CCA(357) = 56 + 1 and Trp(UGG)-Thr(ACC) falls on this structure with dispositional variations. This also satisfies 367(earth-moon time curvature) and lunar gravity where 82 – 16(oxy-time) = 66(a constant distance factor in t-RNA).

Now, 414 – 367 = 47 and 367 – 357 = 9 + 1.

For Phe-Lys, 56 + 9 = 65 = 0.1235(phe c_v) and 56 – 9 = 47 = 0.0893(lys c_v);

For Met-Tyr, 414 – 398(AUG) = 16 = 0.0304 = 304(oxy-time) and 358(UAC) = 357 + 1.

In structural aspects Met is concerned to oxy-time the initiating amino acid in protein and 149(met vt or 149*0.0019 = 0.2831, a structural parameter) – 82 = 67 = 37(met c_v with 0.0004 time difference) + 29(extruded to complement val) with one molecule difference. It is seen 367 – 304 = 63 = 47 + 16 in the structure.

The lunar gravity 0.1605 – 0.1558(82) = 0.0029(complementary factor) + 0.0019(one molecule) and conversely 0.0547(29) + 0.0082 = 0.0629(reciprocal of lunar gravity with 0.0004 time difference) shows interaction between vertical and horizontal time.

It is significant that 112(U) = 83 + 29, a mixing of vertical and horizontal time in context of lunar gravity.

4. P53 Protein Oncogenic Mutation

P53 protein is recognized as tumor suppressor protein undergoes oncogenic mutations cease to normal function of p53 protein molecule discussed herewith.

The amplification of protein occurs on the basis of variable codon (393 for p53) while the gravitational part of amino acid is a part of codon. P53 amplifies to 393 amino acids within the biophysical structure where codon-anticodon may be side by side e.g. tyr(236)-met(237) for p53. I shall discuss about highly destabilizing mutations of p53 protein considering very oncogenic mutations of cancer cell breakdown the fundamental structure of p53 although I255F indicates electromagnetic structure (256.2563) might not be mutated and mutation occurs one step-down molecular point. Here is structural analysis of highly destabilizing mutations of p53 viz. F134L/V143A /L145Q/P151S/V157F/H168R/R175H/I195T/Y220C/I232T /M237I/C242S/G248Q/I255F/F270C/F270L/R282W.

P53 protein molecule is 393-amino acid long where 393 can be treated as variable codon. Some structural parameters arose from 393 – 367 = 26, 367 – 336(UUU) = 31 and 31 + 26 = 57, 367 – 256 = 111(C) etc. determines the mutation point e.g. 256 – 31 = 225 where 225 – 57 = 168 & 225 + 57 = 282 = 393 – 111.

The one step-up (14.0267) position of electromagnetic structure is 270.2830 where '270' is molecular point as well as gravitational vertical time is subjecting to mutation F270C/F270L.

F270L & I255F: Here, 393 – 270 = 123(a mutational point) and mutational value is 0.0482 = 482 = 256 + 225 = 513 – 31, according to core values and transition in the gravitational arena.

The corresponding mutation F134L shows 390 – 134 = 256 and 'difference of three' regarding molecular point found in many places since 3*0.0019 = 0.0057 = 57 = 414 – 357 in the structure.

The mutational values of F270C = 0.1235 – 0.0709 = 0.0526 = 526(on transition) = 270 + 256.

The R282W with the conformation of 393 – 111 = 282 while earth-moon curvature 367 = 256 + 111. Moreover, the mutational values = 0.1289 – 0.1615 = (-) 0.0326 = (-) 326 = 393 – 66 with one molecule difference. Moreover, 282 + 326 = 608 = 393 + 215 where 367 – 215 = 152(oxy-time bisected).

The mutations C242S and P151S would be trans-activated since 242 + 151 = 393 and mutational values for C242S = (-) 0.0356 = (-) 356 and for P151S = 170 and resultant values = 356 – 170 = 186 where 393 – 186 = 207(bisection of 414) and 183(lunar time) +3 = 186.

The oncogenic mutations L145Q and G248Q are in systematic timeline since 393 = 145 + 248 where the mutational values are systematic.

R175H is significant in p53 molecule since 174 is a molecular point as well as gravitational vertical time not generally seen such phenomenon. The molecular weight of arginine is 174.2017 which related to 0.2017 + 0.0547(29) = 0.2564 and 256 – 174 = 82 where 83*0.0019 = 0.1577 = 0.1605(lunar gravity) – 0.0029 and correspondingly 0.2563 + 0.0029 = 0.2592 = 0.1577 + 0.1015 where 0.1605 – 0.0589(reciprocal of 17) = 0.1016 with one molecule difference.

V143A: 256 – 143 = 112 + 1 and according to horizontal time 0.2563(135) – 0.1469(val ht) = 0.1094 meets to lunar gravity(0.1605) when complemented by 0.0571(30).

Again, 0.2124(met ht) – 0.0547(29) = 0.1577(83) and 149 – 83 = 66 in the structure.

Likely in this way mutation in the structural parameter 143 is detrimental.

Note that 14.0266 is a fundamental value where 266 = 183(lunar time) + 83(lunar gravity) in the structure.

Now I shall discuss about '36' molecular point, a bisectional site.

In p53 protein molecule regarding molecular point, 393 = 321(lys) + 72(arg) = 357(lys) + 36(pro) = 221(glu) + 172(val) = 257 + 136 and 256 = 184(asp) + 72(arg) where '100' is a structural factor.

Now, according to core values, $(0.1495^{asp\ cv} + 0.1289^{arg\ cv}) – 0.2563 = 0.0221 = 221$ and $0.1289 – 0.0875^{pro\ cv} = 0.0414 = 414$ where 414 – 221 = 193 = 146(lys vt) + 47 where $47*0.0019 = 0.0893^{lys\ cv}$ and $(0.1494^{glu\ cv} + 0.0754^{val\ cv}) – 0.2563 = 0.0315 = 315 = 414 – 100$ with one molecule difference.

Again, 321 – 193 = 128 = 0.2432 = 0.1881(lys ht) + 0.0551(29).

There is no basic difference between Asp and Glu core values except 0.0001 time difference.

The molecular point-256 is a combination of lunar time(184*0.0019 = 0.3496) and polymorphic site-72.

The mutation Y220C is concerned to 184 + 36 = 220 = 256 – 36.

The mutations M237I and V157F would be trans-activated since mutational values for both the cases (0.0707 – 0.0753) = (-) 0.0046 = (-) 46 and (0.0754 – 0.1235) = (-) 0.0481 = (-) 481 respectively and the resultant values = (-) 527 where 527 – 367 = 160 = 553(29) – 393.

The mutations M237I and V157F also shows 240(glu factor) – 3 = 237 and 240 – 83(lunar gravitational factor) = 157 where 393 – 83 = 310(mutational values of I195T) are structural matters.

The negative mutational values would be added to respective molecular point.I195T & I232T: The resultant mutational values = (-) 0.0311*2 = (-) 622 and adding it to molecular points (506 + 543) = 1049 = 367 + 682(bisection of polymorphic site-72) and 622 – 427 = 195 = 393 – 198.

A structural symmetry has been found in H168R/R273H/R249S [3] mutations like molecular point*2 – 393 that applicable to H168R/R273H/R249S.

Here, 393 – 168*2 = 57(codon difference of basic structure); 249*2 – 393 = 105 and 273*2 – 393 = 153(oxy-time bisected) = 336 – 183(lunar time) and correspondingly 456 – 183 = 273.

The mutational value of H168R, 0.1393 – 0.1289 = 0.0104 = 104 = 273 – 168 with one molecular point difference. Again, 393 – 183 = 210 = 105*2 and 249 – 183 = 66 shows the structural symmetry.

5. Translocation 147(Glu Vertical Time)

V225 is a non-mutation point in p53 having significant implication in biophysics.

V225 = 224(UU) + 1 and 117.1469(val) + 107.1323 = 224.2792 = 149.2124(met) + 75.0669(gly) where 147*0.0019 = 0.2793 and 121.159(cys) – 14.0267 = 107.1323. Now, 0.2792 – 0.1299(glu ht) = 0.1494(glu c_v coincidence) = 0.1254(66) + 0.0240 = 306(oxy-time) on transition and on codon basis 306 – 224(UU) = 82 = 66 + 16(oxy-time) in the structure. Systematically, 225 + 30 = 255 and 225 – 30 = 195 are mutation points and 333(CCC) + 3 = 336(UUU) = 2*168(mutation point) but 453(GGG) – 3 = 2*225 where 225, a non-mutation point is significant.

Again, (393 – 3) / 2 = 195 makes I195T a significant mutation where 393 = 168 + 225 and 225 – 168 = 57. The mutational value of I195T = (-) 0.0311 = (-)311 where 394 – 311 = 83 = 0.1577 meets to lunar gravity when complemented by 0.0029. Now, 112(U) - 29 = 83 and 195 + 311 = 506 = 394 + 112(U). Conversely, 0.1577 – 0.1494 = 0.0083 = 83 and 0.1605 – 0.1494 = 0.0111 = 111(C) on transitions.

6. Conclusions

While the biophysical system is concerned to lunar time or gravity the anti-gravitational influx is symmetrical to electromagnetic waves for molecular manifestation lies to deep meaning of nature. Codons determines the structural level with respect to earth-moon time curvature (0.0367 or 367) causing gravito-motive force urges to flow anti-gravitational waves for synthesis of amino acids or protein. Derived from P53 gene, p53 protein molecule possessed an intrinsic characteristic. The oncogenic mutation shows how it is affecting the fundamental protein structure analyzed to some extent. The clarification on p53 mutations made within structural conformation.

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