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The Structural Analysis of Mutation and Methylation

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Abstract Methylation and mutation are structurally interrelated. P53 protein mutations impair intra-genic or intra-protein molecular suppression causing structural perturbation while methylation is concerned to negative gravitation. The etiology of cancer implies to transformation of valine-histidine complex to tryptophan-threonine complex through structural mutations of p53 protein molecule undergoes cell cycle based on differentiated molecular point structural level and extrusion of suppressed gravitational values in the structure.

Keywords P53 protein molecule, Mutation, Methylation, Molecular point, Intra-genic suppression

1. Introduction

This paper involves how p53 mutations impair the suppression of lunar time (0.3496) and lunar gravity (0.1605) coincidence. P53 protein is a 393-amino acid long valine-oriented protein molecule and accordingly concerned to Histidine assigned by its designated anticodon. The molecular points of the p53 protein molecule possess a structural biology. The oppositely directed transformation to Tryptophan shows extrusion of suppressed gravitational values in specific mutations. Methylation is associated with negative gravitation while core values would not be negative values.

2. Discussions

Amino acids are synthesized by influx of gravitational waves determined by the codon level in context of earth-moon time curvature (367 or 0.0367) in association with $66A^0$ (66*0.0019 = 0.1254) a positioner factor of t-RNA.

Here is a pre-transitional and pro-transitional account of gravitational waves in context of lunar gravity. The pre-transitional values of Met(149.2124) is 0.2124 – 0.0149 = 0.1975 and pro-transitional core values (C_v) or hidden time = 149*0.0019 – 0.2124(negative cumulative gravitation) = 0.0707.

Now, 0.1975 – 0.0707 = 0.1268 = 0.1605(lunar gravity) – 0.0337(UUU) with 0.0001 time difference assigned to Phe(165.1900). Conversely, 0.1900 – 0.0165 = 0.1735 and 0.1735 – 0.1235(phe C_v) = 0.0500 and 0.1605(lunar gravity) – 0.0500 = 0.1105 = 0.0707 + 0.0398(AUG).

Note that 398(AUG) – 31 = 367 = 336(UUU) + 31.

Accordingly, 0.1894(tyr ht) – 0.0181 = 0.1713 and 0.1713 – 0.1545(tyr C_v) = 0.0168 and 0.1605 – 0.0168 = 0.1437 = 0.1105 + 0.0336 with 0.0004 systematic time difference.

Again, 0.1605 + 0.0168 = 0.1773 = 0.1415 + 0.0358 where 149*0.0019 / 2 = 0.1415 and 0.1605 – 0.1415 = 0.0190 = 190 = 358 – 168 (molecular point of his).

Moreover, 405(AAA) – 358(UAC) = 47 = 0.0893(lys core values).

Conversely, 0.1881(lys ht) – 0.0146 = 0.1735 and 0.1735 – 0.0893(lys C_v) = 0.0842 and 0.1605 – 0.0842 = 0.0763 = 763 = 405(AAA) + 358(UAC).

Interestingly, 0.1552(his ht) – 0.0155 = 0.1397 and core values of His = 155*0.0019 – 0.1552 = 0.1393 and 0.1397 – 0.1393 = 0.0004 time difference shows non-existence of lunar gravity.

Conversely, 0.1469(val ht) – 0.0117 = 0.1352 and 0.1352 – 0.0754(val C_v) = 0.0598 and 0.1605 – 0.0598 = 0.1007 = 0.0513(electronic time)*2 – 0.0019. The amplification of p53 is concerned with electronic structure of space-time. P53 is a Val-oriented (GUA) molecular amplification concerned to its designated anticodon (CAU) product His synthesized by gravitational influx.

On intragenic or intra-protein suppression of p53, lunar time (0.3496) and lunar gravity (0.1605) equipoises i.e., 0.3496 – 0.1605 = 0.1891 that differs with His core values by 0.1891- 0.1393 = 0.0498 and 0.1007(val complementation) + 0.0498 = 0.1505 = 0.1605(lunar gravity) – 0.0100(100) and 0.1605 – 0.0754(val c_v) = 0.0851(45*0.0019 – 0.0004).

In contrast, Trp-Thr complex gains '100' factor in p53(e.g. 493 + 146 = 639) and bisects in many aspects and tends to cell cycle since bisection and cell cycle co-exists. Analyzing Trp-Thr complex, it is seen 414(UGG) – 357(ACC) = 57 and 57/2 = 29 = 0.0551 = 0.1615(trp c_v) – 0.1064(thr c_v). Under intra-protein suppression of p53, Trp gravitational vertical time(204) goes down to 146(trp molecular point) which is actually Lys vertical time(146) consensus with 0.1254($66A^0$

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t-RNA factor) – 0.0893(lys C_v) = 0.0361(19) = 0.1615(trp C_v) – 0.1254. Mathematically, 204 – 146 = 58 and 58 – 2*19 = 20 where 0.2261(119) – 0.1881(99) = 20, the difference of Trp & Lys horizontal time(ht). The molecular points of p53 cause a structural biology with original and apparent position of amino acids under suppression.

The horizontal time segment of Trp-Thr shows 182*0.0019 = 0.3458 = 0.2261(trp ht) + 0.1197(thr ht) and after gaining '100' the mutation reflects on R282W where 282 – 204 = 78 = 58 + 20 and 282 + 45 = 327(extruded mutational values) in the structure.

The fundamental values 267*0.0019 = 0.5073 = 0.3496(184) + 0.1605 – 0.0029(complementary values) with 0.0001 time difference. Under lunar gravitational suppression, 183 - 83 = 100 and correspondingly (204 – 146) – 20 = 38 that gives 183 – 38 = 145 in the complex and accordingly 83 = 45 + 38 where 45*0.0019 = 0.0855 = 0.0304(oxy-time) + 0.0551(29) in the structure.

One molecule difference is about common in the system.

Now, I shall discuss about the molecular point level of the complex.

The values 117(val vt) + 29 = 146(trp molecular point in p53) and 125(thr molecular point) + 29 = 154(his vt – 1) can be derived from core values of corresponding amino acids. Now, 0.1615(trp c_v) – 0.0754(val c_v) = 0.0861 where 0.0861 – 0.0551(29) = 0.0310 = 310 = 184(lunar time) + 125(thr). Note that molecular point would be measured from lunar time (184). Conversely, 0.1615 – 0.1393(his c_v) = 0.0222 where 0.0222 + 0.0310 = 0.0532 = 0.0551(29) – 0.0019. Again, 0.1064(thr c_v) – 0.0754 = 0.0310 and 0.1393 – 0.1064 = 0.0329 = 329 = 146(trp) + 183 = 204 + 125 where 146 + 125 = 271(his-val vt - 1) = 117 + 155 where '29' is concerned to oxygenation in the system. Moreover, 367 + 29 = 396 = 1289(arg c_v) – 893(lys c_v) avoiding decimals and 639 = 367 + 272(his-val vt).

Lys-Phe complex is associated with Val-His complex since the core values of Phe = 0.1235 = 66 – 1 and '66'(t-RNA factor) acts as a structural positioner. Accordingly, 0.2033(i.e. 107*0.0019) – 0.1615 = 0.0418 = 0.0361 + 0.0057.

Again, (0.3496 + 0.1605) – 204(trp vt)*0.0019 = 0.1225 = 0.1254 – 0.0029.

It is seen (0.1545 + 0.0707) - 0.0361 = 0.1891(lunar time and gravity suppressive coincidence) where 0.0361 – 0.0004 = 0.0357(CAC) and correspondingly 414(GUG) would be concerned to oxygenation in the suppressed system where 414 = 398 +16 = 304 + 111 and 111 + 57 = 168(molecular point for his) is highly destabilizing on mutation.

P53 protein possess a Val-oriented (GUA) molecular amplification when codon difference of Met(237)-Tyr(236) is suppressed i.e. 40*0.0019 = 760 = 367 (earth-moon time curvature) + 393 and 393 – 367 = 26 where 26*0.0019 = 0.0494 = 494 = 393 + 100 with one molecule difference.

The p53 amplification generates according to Val-398(GUA) with 0.0004 time difference.

Etiology of Cancer:

P53 mutation is associated with more than 50% human cancer is recognized as tumor suppressor protein. Lunar gravity plays an important role for cell cycle and we found Trp core values 0.1615 as a lunar gravity with difference of '10' is extruded. While lunar time and gravity are suppressed, cell cycle is arrested and Trp is not found in p53 after Trp-146 (suppressed) and highly destabilizing mutation occurs at L145Q and also R282W shows incidence of tryptophan(W) in the structure. Evidently, the etiology of cancer is a transformation of His-Val complex (p53) to Trp-Thr complex in association of Lys-Phe complex through structural mutations that concerned to extrusion of gravitational or anti-gravitational values. The values 367 (earth-moon time curvature) – 85(trp c_v) = 282, a mutation point that gives Trp and R282W gives mutational values 0.1289 – 0.1615 = (-) 0.0326 and consequently 326 + 282 = 2*304 = 393 + 215 and 327 = 282 + 45 where 215 – 58 = 157 and 215 + 58 = 273 are two highly destabilizing mutational point in the complex.

The transformation of His-Val(cys) complex to Trp-Thr(tyr) complex can be explained as follows. The His-Val complex having molecular weight 155.1552 + 117.1469 = 272.3021 g/mol where 0.3021 = 159*0.0019 would concerned to Cys(121.159) while that of Trp-Thr complex 204.2261 + 119.1197 = 323.3458 where 182*0.0019 = 0.3458 would concerned to Tyr(181.1894) with one molecule difference. Interestingly, (121 + 181) = 302 and (0.1894 – 0.1590) = 0.0304(oxy-time) in the structure. Now, 0.1545(tyr core values) – 0.0709(cys core values) = 0.0836 = 0.0551(29) + 0.0304 – 0.0019 and 0.0639(his-val core values difference) – 0.0551(trp-thr core values difference) = 0.0088 = 88 = 393(p53) – 304 = 88 + 1. There would not be basic difference between Met and Cys except 0.0002 time difference. Accordingly, 0.3458(182) – 0.1545(tyr core values) = 0.1913 = 0.1590(cys ht) + 0.0323(extruded) where 204 = 159 + 45 that shows opposite direction of transformation with structural complexities. The Trp-Thr complex shows no such suppression where lunar time or Tyr vt at anti-gravitational segment with '1' difference and lunar gravity (0.1605) with 0.0010 time difference is extruded.

The system gets complicated by the biophysical processes of transition or extrusion, suppression, translocation, expansion or contraction of gravitational values in the curvature, molecular point positioning etc. towards equilibrium.

P53 protein structural mutations:

Here are discussions of some p53 mutations while molecular point manifests a biophysical structure.

The V157F/M237I/R282W mutations are interrelated described herewith.

The mutational values (derived from core values) of three mutants are – 0.0481, -0.0046 and -0.0326 respectively. The negative mutational values would be added to respective molecular point while the molecular point difference (distance) is also accountable.

Now, 157 + 481 = 638, 237 + 46 = 283 and 282 + 326 = 608 on transitions. These mutations shows parametric values like 393 – 282 = 111(leu), 282 – 157 = 125(thr) and 283 – 157 = 126(tyr) and 237 + 157 = 394(p53).

The V157F mutation is crucial in the system since 0.1891(lunar time & gravity coincidence) – 0.1254(t-RNA factor) = 0.0637 = 0.1393(his c_v) – 0.0754(val c_v) with 0.0002 time difference and 0.1393(his core values) – 0.1235(phe core values) = 0.0158 = 157 + 1.

Now, 639 = 146(trp) + 493 = 500 + 139 = 357 + 282 = 336(UUU) + 304(oxy-time) etc. in the structure.

Again, 0.0639(his-val c_v) – 0.0551(trp-thr c_v difference) = 0.0088 = 88 = 393 – 305(oxy-time) where 88 + 16 = 104(a mutation point). The gravitational values '639' can be a suppressed form of 153 since 153 = 126 + 27 = 126 + 513 = 639. So according to suppressions gravitational values can be exists in different forms.

The mutations V157F and F270L are structurally systematic. The mutational values of both mutants are 0.0481 with 0.0001 time difference where 270 – 157 = 113 = 480 – 367.

The highly destabilizing mutations L145Q and G248Q are interrelated while 145 + 248 = 393(p53).

Now, the mutational values for both mutations are – 570 and – 567 while 248 – 145 = 103(one step down of mutation point). Accordingly, 145 + 570 = 715 = 393 + 322(extrusion of trp-thr complex) and 248 + 567 = 815 = 323 + 393 + 100.

Again, 1891 – 567 = 1324(Q c_v) avoiding decimal.

The mutations T123A/ H168R are highly destabilizing [1].

The mutational values are 0.1064 – 0.0756 = 0.0308 = 308 and 0.1393 – 0.1289 = 0.0104 = 104 and molecular point difference = 168 – 123 = 45.

Now, 308 – 104 = 204(trp vt) = 125 + 79 = 282 – 78 = 249 – 45 are structural matters.

The mutations V143A/N268D are destabilizing [2].

The mutational values are – 2 and – 171 respectively and molecular point difference = 268 – 143 = 125. Now, (143 + 2) + (268 + 171) – 125 = 459 = 393 + 66 in the structure.

The mutations P151S/ C242S are highly destabilizing in Val –His complex where mutational values are -189 and -355 respectively.

Now, 151 + 189 = 340, 242 + 355 = 597 and 242 – 151 = 91 that shows (340 + 597) – 91 = 846 = 639 + 207(bisection of 414).

A brief account of methylation:

14.0267 is a fundamental value in biophysics [3] that comprises one carbon atom and two hydrogen atoms. Although methyl group (CH_3) replaces one hydrozen atom (0.0019) but intrinsically methylation is not addition of 14.0267 and possess negative gravitation. The molecular weight of methyl group (CH_3) is 15.0350 g/mol that gives core values = 15*0.0019 – 0.0350 = (-) 0.0065 thus the resultant core values would be 0.0350 + 0.0015 = 0.0415 = 415 that equipoised to UGG(414)-Trp with one molecule difference.

Previously I have shown 238.3059 is a systematic values [4] in biophysics where 415 – 238 = 177 and 238 – 77 = 161(0.3059) where '100' is a structural factor.

Now, 238.3059 = 126.1995 + 112.1064 where 0.1995 – 0.1064 = 0.0931(ser ht) and 105(ser vt) + 14 = 119 and accordingly 0.1197 – 0.0931 = 0.0266 = 14. These are concerned to gene expression of DNA to messenger-RNA with directional and T-U changes.

The Lysine (146.1881) methylation shows 146.1881 + 15.0350 = 161.2231 and 119*0.0019 – 0.2231 = 0.0030 that would exerts opposite direction of 238.3059 with bisection of '238' in the structure that would silencing the gene expression of DNA to m-RNA due to directional conflicts.

Again, Arginine (174.2017) methylation shows 174.2017 + 15.0350 = 189.2367 and 189.2367 – 161.2231 = 28.0136 that gives core values 0.0415 with one molecule difference. Here, 0.2367 – 0.2261(119) = 0.0106 = 106 where 267 – 29 = 238 and 106 + 161 = 267 in the structure and also 238 – 161 = 77 = 106 – 29 and 106 + 77 = 183. Note that 267 = 184(lunar time) + 83 that meets to lunar gravity (0.1605) when complemented by 0.0029.

The Arg-Lys core values shows 0.1289 – 0.0893 = 0.0396 = 396 = 415 – 19(one molecule difference) concerned to Arg-Lys methylation.

According to Trp-Thr complex, 323(trp-thr vt) = 161*2 + 1 and 119 + 56(thr core values 0.1064) = 175(arg vt + 1) in the structure. Now, 282 – 146 = 136 = 107 + 29 where 282 – 175 = 107, 175 – 146 = 29, 551 – 136 = 415 and anti-gravitational difference 0.2017(arg ht) – 0.1881(lys ht) = 0.0136 shows gravitational and anti-gravitational chemistry.

3. Conclusions

Lunar gravity is suppressed in Val-His complex so causes anti-proliferative nature while Trp-Thr complex would having not such suppression and lunar gravity(0.1615 with 0.001 time difference) is extruded and exists in upper level(0.0361) from t-RNA factor($66A^0$) causes cell cycle. The molecular points of p53 protein constitute a structural biology causing gravito-motive force by differentiated level in the complex on mutations while mutations in specific points are significant. The V157F[551(29) – 157 = 394] mutation especially exhibits the transformation of Val-His complex to Trp-Thr complex by extrusion of suppressed gravitational values(639) in the structure.

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