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The Analysis of Protein Molecular Point

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Abstract The molecular points in protein possess a structural biology. The molecular point symmetry has been shown in light of valine-tryptophan structural relation. The impairment of fundamental molecular point in the structure causes cancer. The molecular point is a sensitive point of amino acid structure in space-time.

Keywords Molecular point, JAK2 gene, TP53, Hidden time

1. Introduction

Two types of molecular point in protein amplification would be existed i.e. fixed and variable that lies in gravitational arena. The molecular points are sensitive point of amino acid structure and possess a structural biology. The one fundamental cause of cancer is impairment of molecular point towards mutations. The molecular point would be measured from lunar gravity in the structure. The single mutation JAK2 G1849T V617F indicates the arena of cell cycle and protein amplification in context of electro-magnetic structure.

2. Discussions

Structural analysis of initiating amino acids:

The discovery of the formula T = M*0.0019 have far-reaching implications in bio-physics. [1].

The V617F mutation gives a clear understanding of time motivation towards protein amplification. The molecular weight of valine(117.1469) is structurally interesting as follows.

The core values of valine = 117*0.0019 – 0.1469 = 0.0754 = 0.1254(66 A^0 t-RNA factor) – 0.0500 and the pre-transitional values = 0.1469 – 0.0117 = 0.1352 = 0.1605(lunar gravity) – 0.0253 where 66*0.0019 = 0.1254. While 0.1254 meets to lunar gravity(0.1605) the value of difference = 0.1605 – 0.1254 = 0.0351 transit to gravitational arena with addition of 0.0010 i.e. 0.0351 + 0.0010 = 0.0361 = 0.0304(oxy-time) + 0.0057 = 19. In p53(393 amino acid protein standard molecule) it is seen 107(tyr) + 19 = 126(tyr).

Now, 0.1254 – 0.0754 = = 0.0500 = 0.0754 – 0.0253 = 0.0551(29) – 0.0051 where 0.1605 – 0.1352(pre-transitional values) = 0.0253 = 0.0304 – 0.0051 provides an interesting relation in the structure while leu or ile(131.1736) exists in zero level from lunar gravity i.e. 0.1736 – 0.0131 = 0.1605. Occasionally, val would be substituted by leu.

One molecule or molecular point difference is about common in the system.

Evidently, in course of protein amplification, ‘500’(anti-gravitational values) goes to gravitational arena as molecular point makes V(117 + 500) = V617. Conversely, 500 – 107(reduced by 10) = 393(p53 protein molecule) so there is a structural relation between TP53 and JAK2 gene and correspondingly of their proteins. Cell cycle or protein amplification initiates when anti-gravitational time penetrates to gravitational field and vice versa.

For methionine(149.2124), the core values = 149*0.0019 – 0.2124 = 0.0707 and the pre-transitional values 0.2124 – 0.0149 = 0.1975(104) = 0.1605 + 0.0370 where 104*0.0019 = 0.1976.

Now, 0.1254 – 0.0707 = 0.0547 = 0.0370 + 0.0177 where 0.0370 = 0.0304(oxy-time) + 0.0066 = 0.0481(mutational values in V617F) – 0.0111(C) = 0.0193 + 0.0177 and in gravitational arena 193 – 177 = 16(oxygen) or 193 + 111 = 304 are internal structure. It is significant met initiation point is 149 + 29 = (178 – 1) where 370 + 29 = 398(AUG) since ‘29’ represents anti-gravitational (0.0107 unit) approaching values meets to lunar gravity(0.1605).

The met-val relations are as follows.

117 + 126(T) = 243(met) and 361 – 244 = 117 and correspondingly 500 + 117 = 617.

Moreover, 361 + 126(T) = 487(de-oxy-nucleotide average molecular weight) and 500 + 487 = 987(52) = 1605 – 617 where 243 – 66 = 177 and 66 + 51 = 117.

About ‘193’ fundamental values:

The difference of 193(earth-moon time curvature) – 183(lunar time) = 10 and 193 is a time limit in the system and after that there would be directional change of time e.g. 204 – 193 = 11 = 0.0209 = 0.0414(UGG-Trp codon values) –

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0.0205 for tryptophan(204.2261) and accordingly 204 + 85(trp core values) = 289.

The anti-gravitational influx(0.0107 unit) is determined by 193*0.0019 = 0.3667, 0.3667 – 0.2124(met ht) = 0.1543(tyr core values) and 0.1545 + 0.0228 = 0.1773 = 0.3667 – 0.1894(tyr ht) where 193 – 181 = 12 = 0.0228.

Again, 0.3667 – 0.1552(his ht) = 0.2115 = 0.1393(his core values) + 0.0722 where 193 – 155 = 38 = 0.0722.

Again, 193 = 146(lys vt) + 47 and 47*0.0019 = 0.0893(lys core values breaks up into time).

Again, 500 = 193 + 307 where 307 = 304 + 3 = 304 + 57 = 361 where 3*0.0019 = 0.0057.

A symmetry between gravitational and anti-gravitational values that we can write 0.0361 = 361, 0.0500 = 500 etc.

About p53 protein molecule:

P53 protein molecule(393 amino acids associated) is a tumor suppressor protein because of lunar gravity(0.1605) and oxygen(0.0304) suppression in the molecule. Simultaneously, there would be other suppression like lys-trp appearance side-by-side in the molecule. It is seen molecular points 23 and 24 are occupied by trp and lys respectively i.e. suppression of 19*2 = 38 = 32 + 6 at this molecular point shows oxy-time(16*0.0019 = 0.0304) also suppressed causing p53 tumor suppression protein. Lunar gravity and oxy-time are two important components for cell cycle and protein amplification.

Now, 393 = 169 + 224(UU) where 169 = 2*85(trp core values 0.1615) – 1 = 0.321(lunar gravity*2) = 321 and 336(UUU) + 32(oxygen) = 368(earth-moon time curvature).

Again, 282 – 117 = 165 = 617 – 452 where '452' is a trp factor since 0.2057(trp pre-transitional values) – 0.1605 = 0.0452 = 452 = 2301 – 1849 where the core values of electro-magnetic structure(256.2563) is 256*0.0019 – 0.2563 = 0.2301 = 2301 is related to JAK2 G1849T V617F are mathematically consistent.

The molecular point '282' is a sensitive point since 617 – 336(UUU) = 281 and R282W is a cancer associated mutation. The mutational values of R282W = 0.1289 – 0.1615 = -0.0326 = (-) 326 = 378(TTT) – 52 where 256 – 204 = 52. The negative mutational values would be added to the molecular point i.e. 282 + 326 = 608 and consequently 608 + 378 = 986(52) and 0.1605 – 0.0988 = 0.0617 = 617.

Again, 326(mutational values) + 87 = 413 = 500 – 87 where 282 – 87 = 195(I195T) = 608 – 413 where 165 – 79 = 86. The both mutations appeared as 326(R282W) + 311(I195T) = 637 = 157 + 481 in V157F. Correspondingly, 282 + 87 = 369 = 617(V617F) – 248(G248Q) are structural mutations.

Again, mutational values '326' is a bisectional values and 326*2 = 652 = 552(29) + 100 = 129 causing break-up of suppression in p53 and 197(val) + 129 = 326 where 197 + 85 = 282 = 367 -85. In case of V157F, mutational values = 481*2 = 962, 962 – 651 = 311(I195T). Correspondingly, 962 – 129 = 833 = 393(p53) + 440 where 440 = 282 + 158 = 203 + 237 = 168 + 272 are structural mutational points and 440 = 193 + 247(AU) = 323 + 117 = 203 + 237 = 547 – 107 = 617 – 177 = 421 + 19 = 361 + 79 where 500 – 79 = 421 = 861 – 440 are structural matters in space-time.

Here are two reciprocal mutations in p53 have been discussed i.e. H168R/R273H and V157F/F270L according to mutational values. [2].

The values 361 – 193 = 168 makes 168 a sensitive structural point and mutation at this point is detrimental. The mutational values(104) for both mutations coincides to space-time values i.e. 273 – 168 = 105.

Secondly, 270 – 157 = 113 = 110 + 3 = 110 + 57 = 167 and 270 + 3 = 273.

The mutation V157F is a cancer associated mutation. Structurally, 203 + 158 = 361 where 79*2 = 158 and 79*0.0019 = 0.1501 = 0.1605(lunar gravity) – 0.0104 where 0.1501 – 2*0.0481 = 0.0639 – 0.0100. Again, 639 = 158 + 481(mutational values) = 500 + 139 = 336(UUU) + 304(oxy-time) are structural matters.

Again, 617 + 2*481 = 1579 = 1849 – 270 where 1849 – 481 = 1368(72 polymorphic site).

The Valine-Tryptophan relation in terms of molecular point:

In p53 protein molecule, tryptophan is found in 23, 53, 91 and 146 positions. The values 0.0361(19) is derived from 0.1615(trp core values) – 0.1254(66A^0 t-RNA factor) = 0.0361.

Now, 361 + 23(trp) = 384, 500(val virtual codon values) – 384 = 116(val fixed molecular point); 361 + 53 = 414(trp codon values), 500 – 414 = 86 = 203(val) – 117(val); 361 + 91 = 452, 500 – 452 = 48, 204 – 48 = 156(val); 361 + 146 = 507, 507 – 500 = 7, 204 – 7 = 197(val) shows val and trp systematic disposition. The molecular point V203 is significant where val and trp assigns side-by-side. It is seen V157 is a fundamental values since 361 – 158 = 203 and 500 + 203 = 703(met core values with 0.0004 time difference).

Now, 203 + 146 = 349 is not a mutation point but 349 – 100 = 249 is a destabilizing mutation point (R249S) and accordingly 500 – 349 = 151 is a highly destabilizing mutation point(P151S) that shows structural mutation since 861 – 513 = 349 – 1.

Again, 203 + 91 = 294 = 282 + 12 and mutation shows at 282 – 12 = 270(F270L) since 414 – 335 = 79 = 91 – 12. Now, 204 + 52 = 256 shows highly destabilizing mutation I255F. It is seen 393 – 165(Q165K) = 228(D228E) = 12*0.0019 under suppression.

The val-trp are also related by 0.1615(trp) – 0.0754(val) = 0.0861 = 0.0500 + 0.0361 and 0.1254(66) – 0.0861 = 0.0393 = 393(p53) and correspondingly (0.1254 + 0.0861) – 0.0617 = 0.1498 where 1849 – 1498 = 351 = 266 + 85.

Since 0.1254 – 0.0893(lys core values) = 0.0361, the molecular point 500 – 361 = 139 is occupied by lys in p53 and also 117 + 256 = 373(lys).

In normal beta chain of human hemoglobin, trp is found in 15 and 37 positions.

Now, 361 + 15 = 376, 500 – 376 = 124, 124 – 87 = 37; 361 + 37 = 398, 500 – 398 = 102, 117 – 102 = 15(trp) where 500 – 413 = 87 = 204 – 117.

It is seen molecular point constitutes a structural biology and impairment of molecular point causes diseases. The impairment of molecular point '6' in beta hemoglobin causes sickle-cell-anemia(SCA). The molecular point '6' occupies glutamic acid(147.1299) in beta hemoglobin changes to valine or lysine.

Now, mutational values = 0.1494(glu) – 0.0754(val) = 0.0740(39), 0.0741 – 0.0551(29) = 0.0190, 0.0190 + 6*0.0019 = 0.0304(oxy-time) causes de-oxygenation.

Another mutational values = 0.1494(glu core values) – 0.0893(lys core values) = 0.0601 where 0.0601 + 0.0551(29) = 0.1152(glu pre-transitional values) = 0.1299 – 0.0147 that shows impairment of '6' and '147' variable and fixed molecular point respectively.

About JAK2 G1849T V617F mutations:

It is a single acquired somatic mutation present in the majority of patients with myeloproliferative cancer. The JAK2 V617F is an oncogenic event present in 95% to 98% of polycythemin vera(PV). This led to the production of uncontrolled too many blood cells.

Mathematically, JAK2 G1849T is measured from lunar gravity(0.1605) where 0.1605 – 0.0617 = 0.0988(52) and 0.0988 + 0.0861 = 0.1849.

The difference of core values = 0.1615(trp) – 0.0754(val) = 0.0861 = 0.0500(val) + 0.0361(trp).

Again, 0.1849 – 0.1605 = 0.0244(M243 + 1) = 0.0861 – 0.0617 that lies into val-trp complex and also 500 – 244 = 256 and 361 – 244 = 117 completes a cycle.

In terms of molecular point, 617 = 500 + 117 = 204 + 414(UGG-trp codon values).

The mutational values of V617F = 0.0754 – 0.1235 = -0.0481 = (-) 481. The negative mutational values would be added to the molecular point i.e. 617 + 481 = 1098 = 1849 - 751(val core values with '3' difference). Correspondingly, 1849 – 475(25) = 1374 = 617 + 757(val core values with '3' difference) where 151(G) – 126(T) = 25 = 0.0475 = 475.

Moreover, 617*3 = 1849 + 2; 361 – 117 = 244 gives 500 + 244 = 744 where 744*2 = 1849 – 361; 617 + 244 = 861 and 617 – 244 = 373(lys); 617*2 = 1234(phe core values).

The mutations V157F and V617F are interrelated in dimensional biology.

The values, 617 – 157 = 460, 460 + 361 = 821 = 500 + 321(lys), 861 = 460 + 401 where 883(lys core values with 0.0010 difference) – 481(mutational values) = 402 and 883 – 304 = 579 can be derived from R282W where 361 – 282 (opposite direction) = 79 = 579 - 500; 861 – 481 = 380 = 361 + 19 that proportionate to 500 – 19 = 481.

Again, 425 – 157 = 268 and 1849 + 268 = 2117 = 1500(79) + 617 where 617 – 79(negative impulse) = 538 = 393 + 145 and 146*0.0019 = 0.2774 = 2774 = 1849 + 925 where 925 – 393 = 532 = 538 – 6(displacement of six values).

A mathematical relation has been established between gene and protein mutation point. This single mutation impairs the fundamental structure leads to blood cancer. The V617F mutation is significant for JAK2 and TP53 gene interrelation, penetration of anti-gravitational values to the gravitational arena would be causing cell cycle or protein synthesis. Obviously the single mutation JAK2 G1849T V617F is the area of activity for cell cycle and protein amplification in context of electro-magnetic structure associated with val-trp relation where 513 – 413 = 100 and 256 – 204 = 52.

Electro-magnetic Structure of Space-time:

In HVQ complex, it is seen electro-magnetic and gravitational co-existence in the structure. The values 155(his vt) + 358(CAU his codon values) = 513(electron mass 0.511 Mev/c^2) bisects in the structure to form 256.2563 electro-magnetic structure [3] following anti-gravitational influx where 256 = 117(val vt) + 139 that derived from 0.1393(his core values) – 0.1254(66) = 0.0139 = 139.

Again, 0.0938(proton mass 938.29 Mev/c^2) + 0.0513 = 0.1451(gln ht) and 938 – 513 = 425 = 169 + 256(I255F) = 321 + 104(Q molecular point in p53). The mechanism of cell cycle and protein amplification would exist in HVQ complex since V617F is the single mutation in JAK2 gene. Mathematically, 425 – 393(p53) = 32(oxygen) where 32*0.0019 = 0.0608 = 608 and 608(negative impulse) + 425 = 183(lunar time 0.3477) and correspondingly 617 – 425 = 193(earth-moon time curvature) – 1 = 224 – 32 = 159 + 32 + 1. The mutation R282W shows 282 + 326(mutational values) = 608 extruded that release of suppressed oxygen causes cancer associated mutation.

The amino acid gln(146.1451) where the horizontal time(0.1451) equipoises electro-magnetic structure and 146*0.0019 = 0.2774 = 3*0.0925(equal triplet values where 925 = 500 + 425) and 2*925 = 1849(JAK2).Correspondingly, 925/3 = 308 and 308*2 = 617(V617F) with 0.0001 time difference. Again, 117 = 3*39 i.e. 1849 – 741*2 = 367 = 373(lys) – 6.

Again, 146(trp) + 91(trp) = 237(met) = 3*79 where 79*2 = 158(V157F) and 158*3 = 474(25) = 2*237 that shows mutational displacement of 0.0006 = 0.0481 – 0.0475 corresponds to gene mutation 151(G) – 126(T) = 25 = 0.0475 = 475 in JAK2. The '6' displacement i.e. 111(C) + 6 = 117(val fixed molecular point), 151(G) + 6 = 157(V157F), 475(25) + 6 = 481, 475 – 6 = 469(V157F) are found in the system.

Again, 0.0545 = 0.0551(29) – 0.0006 that gives 0.0545 + 0.0425(electro-magnetic difference) = 0.0970 = 970 = 1451 – 481(mutational values) and 1849 – 1305(pre-transitional values of gln) = 544. It is seen 938 + 367 = 1305 and 513 – 367 = 146.

Arginine(174.2017) gives pre-transitional values 0.2017 – 0.0174 = 0.1843 = 0.1849 – 0.0006 and 0.1849 – 0.1605 = 0.0244 = 244 = 500 – 256 = 361 - 117 that lies into electro-magnetic structure.

The mutation of electro-magnetic structure I255F is highly destabilizing(likely one step-down mutation) since 500 + 255 = 755(val core values) and 754 – 393 = 361 impairs the fundamental structure. Also 617 – 255 = 362, 425 = 256 + 169, 256 – 117 = 139, 255 + 139 = 394 lies into fundamental structure.

Obviously, JAK2 G1849T V617F the single mutation is the area of activity for blood cancer in the electro-magnetic

structure. The codon values of electro-magnetic structure(256.2563) can be attributed as follows.

The difference of core values = 0.1615(trp) – 0.0707(met) = 0.0908 and the difference of codon values = 414(UGG) – 398(AUG) = 16 = 0.0912/ 3 = 0.0304(16) with 0.0004 time difference. Similarly the difference of core values = 0.2301(electro-magnetic structure) – 0.1393(his core values) = 0.0908 so the attributive codon values of electro-magnetic structure(256.2563) = 358(CAU his codon) + 16 = 374(GUC) which is val codon values.

Now, 0.0374 + 0.0100 = 0.0474(25) corresponds to JAK2 G1849T where G – T = 25 = 0.0475 = 475. The addition of '100' bisects in cell cycle activating 425(proton-electron difference what is 374 + 50 = 425 - 1) + 50 = 475 that causing cell cycle and protein amplification. The values 938 (proton time or mass values) + 50 = 988 = 0.0988 = 52*0.0019 and 425 – 52 = 373. Previously it is seen 0.0267(14) + 100 = 114 or 0.0367 causes bisection and '57' is a bisection factor in trp where bisection and cell cycle co-exists.

Again, 374 + 19 = 393(p53) and (374 + 361) – 617 = 117(val) + 1 and 1849 – 735 = 639(V157F) + 475 and the values 256 – 117 = 139(lys) = 500 – 361 = 513 – 374 are mathematically consistent.

This would be the cause for single mutation tends to blood cancer and change of codon level towards mutation causing gravito-motive force to produce uncontrolled too many blood cells under infiltration of anti-gravitational values.

3. Conclusions

The single mutation JAK2 G1849T and its corresponding mutation V617F is the hotspot for blood cancer and the rectifying area in context of electro-magnetic structure derived from anti-gravitational influx and related to val-trp complex. Lunar gravity(0.1605) would be existed at the anti-gravitational arena but the extrusion of lunar gravity(204 = 119 + 85) at the gravitational arena would have deep impact tends to cell cycle and protein amplification.

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