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The Structural Time Biology and Cancer

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Abstract The electromagnetic and gravitational forces are unified in context of time biophysics but intrinsically make a difference. Cell cycle initiates when these two forces coincide and amplified until structural equilibrium. The structural mutations have been clarified towards development of cancer. The molecular point of protein and its corresponding genetic position plays an important role at its disposition.

Keywords TP53, JAK2, Cell cycle, Electromagnetic and Gravitational forces

1. Introduction

Three cancer associated mutations have been considered e.g. G1849T V617F, G469T V157F and C844T R282W for clarification of cancer development. It is seen cancer occurs due to structural breakdown of the system at which electro-magnetic and gravitational 'symmetry breaking' state is concerned. The mass-time transition formula, T (time) = 0.0019M(mass) is essential to proceed [1]. The core values of methionine is derived from its molecular weight i.e. 149*0.0019 – 0.2124(anti-gravitational horizontal time) = 0.0707(hidden time) and so on. The pre-transitional value of Met = 0.2124 – 0.0149 = 0.1975(104) in biology of time. The amino acid glutamine(146.1451) represents the unified electro-magnetic and gravitational structure while Met(149.2124) and Val(117.1469) are two initiating amino acids in protein amplification. We can write '149' assumed to be vertical time while 0.0149 as horizontal time. The intrinsic values after transition or extrusion are the mystery of biophysics. The electromagnetic and gravitational forces are unified in context of time biology. One molecular point or molecular time(0.0001 or 0.0019) values difference is about common in the system.

2. Discussions

Cell cycle and structural biology:

Electro-magnetic(em) and gravitational(g) forces are two category of forces. In context of time or biophysically, em + 103 = g with intra-genic suppression in the structure. The forces act upon cell cycle when these two forces coincide under specific mutations. It is seen molecular point (gravitational point)*3 = genetic position(electromagnetic point) and systematic in dimensional biology. Now I shall describe how electro-magnetic and gravitational structure is co-related in time form.

Glutamine(Q) molecular weight(146.1451) shows pre-transitional values 0.1451 – 0.0146 = 0.1305 = 0.0938 + 0.0367(earth-moon time curvature) where 0.0938 is time form of proton(938.29 Mev/c^2) while 0.0513 is time form of electron(0.511Mev/c^2) with one decimal place change. Again, 0.0513 – 0.0367 = 0.0146 where 12,756 km(diameter of earth)/ 3477 km(diameter of moon) = 3.67 = 0.0367 in time form.

In a complete cycle(positive to negative), (0.0938 + 0.0513) + (0.0938 – 0.0513) = 0.1876.

On gravitational considerations, 0.3477(lunar time) – 0.1605(lunar gravity) = 0.1872 = 0.1876 – 0.0004(adjustable time difference) and in a complete cycle the values stands 0.1605*2 = 0.3210 and 0.3210 – 0.1872= 0.1338 = 0.1235(phe core values) + 0.0103.

The electromagnetic and gravitational forces are unified in a way, 0.1872 = 0.1451 + 0.0421 where 421 = 327 + 94(suppressed values at C844T) causing p53 protein molecule tumor suppressor protein. Under terminal mutational values(0.0327) in R282W causing great impact on suppression values and cell cycle initiates.

The pre-transitional values of Met = 0.2124 – 0.0149 = 0.1975(104) = 0.1875 + 0.0100.

The valine(117.1469) having opposite direction of Met in the structure where 117*0.0019 = 0.2223 = 0.1872 + 0.0351. The Val is related to Met in a way 0.0351 – 0.0104 = 0.0247(AU) and 0.0351 + 0.0047 = 0.0398 = 398(AUG). Although '351' or '0.0351' is not the codon values of Val but an essential structural values where 0.1605 – 0.1254 = 0.0351 = 351 avoiding transitional(10,000) values.

Met and Val can take part as initiating amino acids for cell cycle in turn protein amplification.

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The t-RNA factor 'constancy of distance' $66A^0$ is a complementary time value as 0.1975(104) + 0.1235(65) = 1605*2 where 0.1235 is Phe core values and 0.1235 + 0.0019 = 0.1254(66) shows time-distance-mass are synonymous.

Again, 0.1254 – 0.0513(27) = 0.0741 and 0.0741(39) + 0.0197 = 0.0938. Conversely, 197 – 39 = 158 = 316/2 where 0.1254 – 0.0316 = 0.0938 in the structure.

About p53 and C844T R282W cancer associated mutation:

The p53 protein molecule is a tumor suppressor protein due to suppression of lunar gravity (0.1615) in the protein structure. Lunar gravity plays an essential role in cell cycle and sometimes it is extended by 0.0010 or 10 in the structure. The molecular point 197(val in p53) shows 197*0.0019 = 0.3743 = 0.1872*2 and 197 + 85 = 282(arg) where 85*0.0019 = 0.1615(trp core values). The mutation R282W [2] is a terminal mutation and the suppression values can be calculated since 367(earth-moon time curvature in vertical gravitational form) – 85 = 282. It is seen 0.1615(85) is suppressed causing p53 a tumor suppression protein.

Comparing C844T R282W with G469T V157F, 282 – 157 = 125 and 844 – 469 = 375 = 3*125 = 367 + 8 and correspondingly 938 – 8 = 930 = 844 + 86 that shows genetic position is also suppressed. The total suppression is 86 + 8 = 94 shows lunar gravity plays an important role in cell cycle.

Again, 617 – 282 = 335(UUU – 1) where 335*3 = 1005 = 1849 – 844 in dimensional biology.

Again, 197 + 27(0.0513) = 224(UU) and accordingly 513 – 197 = 316 = 367 – 51 and 197 – 51 = 146(trp) in p53(197*2 = 394) is significant. Mathematically, 146*0.0019 – 0.1615 = 0.1159 = 0.1305 – 0.0146 are the structural matter. The first two bases(UU-224) is co-linear to R282 and intrinsically 617(V) – 336(UUU) = 281. The mutation R282W is a terminal mutation that shows 1451 – 844 = 607 = 281 + 326 where 0.1289(arg core values) – 0.1615(trp core values) = - 0.0326(mutational values) = (-)326 would be added to molecular point. Structurally, 0.1976 + 0.0326 = 0.2301(core values of electromagnetic structure 256.2563) that causes cell cycle [3] and 0.2301 – 0.1545(tyr core values) = 0.0756 = 756 = 425*2 – 94(suppression values).

Furthermore, 1849 – 1451 = 398 and (617 + 481) – 398 = 700 = 607 + 93(suppression values) is co-related with protein amplification. Again, 1451 – 469 = 982 = 607 + 375 shows R282W causes common syndrome for other both deleterious mutations.

The suppression values(94) can be implemented to clarify p53 protein molecule. Now, 94*3 = 282(terminal molecular point) = 375(p53 amplification, 375 + 19 = 394) – 93 = 188 + 94 where 188*2 = 375 + 1 and 326 + 187 = 513(27) electronic values. The core domain of p53 molecule is 94-312(terminal aspects) where 312- 94 = 218 = 393 – 175(E.Coli mutation start-up) is significant.

The core values(C_v) of tyrosin(181.1894) is 181*0.0019 – 0.1894 = 0.1545 and 0.1545 – 0.1254(66) = 0.0291 = 291 = 281 + 10 that aligned to genetic position or electromagnetic point. Now, 0.1872 – 0.1545 = 0.0327(terminal mutational values) and 0.1545 – 0.0938 = 0.0607 = 0.0326 + 0.0281. The genetic position of V617F is 1849 = 938*2 – 27(0.0513) and conversely 938*2 + 513 = 2389 = 1545 + 844(R282W) and (1849 + 469) – 1545 = 773 = 617 + 156 although TP53 and JAK2 genes are different but mathematically systematic is significant.

Again, 1545 – 844 = 701 = 1005 – 304(oxy-time) where 335*3 = 1005 and 617 – 282 = 335. The basic level of codon values may be considered from oxy-time e.g., 398(AUG) – 304 = 94 = 1545 – 1451 = 375 – 281.

V157F and V617F mutations:

Both the mutations are interrelated that impair the t-RNA factor $66A^0$ = 0.1254 time values. The mutational values of V157F = 0.0754 – 0.1235 = - 0.0481 = V617F. Now, 0.1254 – (0.0157 + 0.0481) = 0.0616 = 616 and 0.1254 – (0.0617 + 0.0481) = 0.0156 = 156 with 0.0001 time difference. It is seen 617 – 157 = 460 and the corresponding genetic difference = 1849 – 469 = 1380 = 3*460 and systematically 1380 + 1451 = 2831(149) or 1872 – 460 = 1412(bisection of met time – 3) in the structure. Again, 0.1872 – 0.1254 = 0.0618 and 0.1872 – 0.1098 = 0.0774 = 774 = 617 + 157. Evidently both the mutations impair the fundamental structure liable to cancer development while molecular point or genetic position is a part of structural biology.

The genetic connection in the system can be explained in space-time.

Now, 1849(genetic position) – 1098(i.e. 617 + 481) = 751(val core values with 0.0004 time difference) = 270 + 481 = 481 + 113 + 157 where 270 – 157 = 113. The same mutational values found in F270L and V157F in p53 with opposite direction with 0.0001 time difference.

Again, 1849 – 1615(trp core values avoiding decimal) = 234 = 117*2 and accordingly 234 – 85(opposite impulse) = 149 = 0.2831. Now, 2831 – 1849 = 982 = 1451 – 469(genetic position of V157F) where 469 = 938/2 avoiding decimals.

Oxy-time in biophysics:

Oxy-time(0.0304) is fundamental in amino acid structure where 16(oxygen mass)*0.0019 = 0.0304.

The Val structure can be implemented to clarify the biophysical structure. The values 304(oxy-time) + 47 = 351(val structural data) and 351 + 47 = 398(GUA) would determine the linear oppositeness of Met(AUG) and Val(GUA) where seemingly '47' is a time level for synthesis of amino acids. Again, 850(doubling of gln) – 803(half of lunar gravity) = 47.

Mathematically, 0.1451*2(850) – 0.0893(47) = 0.2008(803) where 2008 = 1254 + 754(val core values) and in a cycle 1254 – 754 = 500 would causes affinity of oxygen to meet 500 + 304 = 804 and correspondingly 547 + 303 = 850(electro-magnetic reach) would be needed for amplification of protein. Now, 1254 + 707 = 1961, 1961 – 803 = 1158 = 1305 – 146.

3. Conclusions

The biology of time motivation would have been revealed out a new cell science. The cancer disease is concerned to structural biology in view of molecular point and genetic position that causes suppression within structural permissibility tends to cell cycle under breakdown of suppression towards mutations. It is explicitly described that the genetic positions are variable electromagnetic positions in time form having no electric charge and synchronized with gravitational time. The terminal mutation C844T R282W is effectual for further investigations.

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