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The Biophysical Structure and Analysis of Some Molecular Diseases

Ratan Kumar Sarkar

Janhavi, Keota, Hooghly, West Bengal, India

Abstract Methionine-Tyrosine constitutes an electro-gravitational structure that related to insulin receptor. The biophysical system works on two domains 900 and the reverse domain 109 in Earth-Moon space-time structure. The structural analysis of cancer mutational values with intermediate values has been made and aspartic acid (133.1032) might be a resolution in a specific cancer but needed through investigation. The Tyrosine-Arginine duo should be investigated towards diabetes mellitus.

Keywords Insulin, Glucagon, Insulin receptor, Auto-phosphorylation, Point mutation

1. Introduction

Two important parameters of biophysical structure are ‘900’ and the reverse domain ‘109’ with a difference of ‘1’ associated with directional biology. The values beyond 900 and the intermediate values would be added to 109 but not restricted in the structure.

The core values (C_v) of tyrosine (181.1894) = 181*0.0019 – 0.1894 = 0.1545 or 645(under suppression) where 900 – 645 = 255 and 645 – 255 = 390 (intermediate values) and where 390 + 109 = 499(reverse to 0.1894 or 994) and 390 – 109 = 281 = 900 – 619 creates structural conflicts 94*61 = 5734 (molecular weight of insulin in g/mol) where core values of glucose (180.1558) is 962 (under suppression) or 619 in opposite direction with a difference of 1 that related to Y960 in insulin receptor. The two values 499 and 619 (ending with 9) blocking time in directional biology results structural conflicts and transits to masses since time is indomitable and cannot be stopped.

The core values is an important parameter that related to molecular point of amino acids in protein and needed for mutational evaluation applying the formula T(ht) = 0.0019*M(vt) derived from 14.0267 an inter amino acid factor found somewhere e.g. 119.1197 (thr) – 105.0930 (ser) = 14.0267 where T and M are assumed to be horizontal and vertical time respectively.

The molecular weight of amino acids is sophisticated time values possesses a biophysical structure.

Previously I have shown 183(lunar time) – 117(val vt) = 66, a distance of constancy factor in tRNA [1] where 66 = 15 + 51 = 24 + 42 in directional biology. The histidine (155.1552) is an fundamental values where 155 – 117 = 38 and correspondingly 1552 – 1469 = 83 i.e. reverse to 38 and 183 – 155 = 28 and so 1552 + 82 = 1634 would be the corresponding ht of Earth’s time (184) where 1634 – 1605 (lunar gravity) = 29 = 23 + 6 since 711 (reverse of 117) – 6 = 705 and 711 + 23 = 734 and the reverse values 437(23).

The core values of 184.1634 = 0.1862 or 962 align to glucose (180.1558) core values where 900 – 731 (insulin receptor alpha subunit) = 169(structural reverse of 962). The systolic-diastolic nature would be arising from Earth-Moon time-gravity interactions where 183 + 551(29) = 734 and 183 – 29 = 154 (factor of opposite) = 705 – 551.

In context of 66, after 15 the reverse action initiates where 15*0.0107 (influx of electro-gravitational impulses unit) = 0.1605 (lunar gravity) and in framework of 19 = 15 + 4 where 0.0107*4 = 0.0428 = 425 + 3 avoiding decimals where 938 – 513(27) = 425. Again, 131(or 1031)*15 = 1965 or 165 (under suppression) and 131*4 = 524(reverse of 425) where 42 (reverse of 24)*4 = 168 = 165 + 3 in the structure and where 131 – 107 = 24 and also 24*15 = 360 shows electro-gravitational impulses would differs by angle (360) in the structure where 701 (reverse of 107) + 76(4) = 777(183) under suppression. It is seen 360 + 540 = 900 and correspondingly 540 – 360 = 180 (intermediate values) = 289 – 109 where 994 (tyr ht) – 705 = 289 = 229 + 60 (beyond 900) and 886(94) = 705 + 181 in the structure.

The electro-gravitational chemistry is in equilibrium while 3477(183) – 1451*2 = 575 = 1605 – 1031 with a difference of 1 where 938 + 513(27) = 1451. If it appears 575 = 475 + 100 (with a difference), the electro-gravitational chemistry activates towards equilibrium.

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* Corresponding author:
rksarkar36@gmail.com (Ratan Kumar Sarkar)
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The values ‘575’ in context of tRNA can be clarified as 900 – 575 = 325 and 575 – 325 = 250 = 359 – 109 where 359 is complementary values of 135(A) and 250 = 141 + 109 where 949 – 808 = 141 is related to Tyr-Met chemistry clarified later on. It is seen 359 – 15 = 344 = 222*2(CC) – 100 where 49 + 51 (insulin length) = 100 = 69 + 31 and where 51*0.0019 = 0.0969 or 969 in the structure.

The values ‘9’ (0.0171 or 171) is the factor of directionality [2] where 15 + 9 = 24 or 51 – 42 = 9 in the system. The system is associated with 27 and 72 (polymorphic site) where 27 = 15 + 12 or 51 + 21 = 72 where 12* 0.0107 = 0.1284 or 384 and where 705 + 384 = 1089 or 189 = 900 – 711 and correspondingly 705 – 384 = 321 (reverse of 123) where 777(183) + 123 = 900 in the structure.

The electro-gravitational structure can be clarified as:

183 (lunar time or terrestrial time with a difference of 1) + 734 (would be earth’s gravity) = 917 where 109 + 17 = 126 (T) and correspondingly 900 – 513(27) = 387 where 513 – 387 = 126 (T) shows electro-gravitational directional biology.

The curvature of time = 12760(Earth’s diameter in Km) / 3477 (Moon’s diameter in Km) = 3.67 or 367 = 183 + 184 = 361(19) + 6 where 34 + 19 = 53 = 705 – 652 and 184 – 155 = 29 and also 734 – 579 = 155 that associated with histidine (155.1552).

As the transitions prevail in the system decimals have been avoided in many places.

2. Discussions

Sickle-cell anemia (SCA):

The mutational values of glu6val = 1494 – 754 = 740 = 594 + 146 (length of human beta-hemoglobin) = 1348 (or 448) – 608 (oxy-time) and in opposite direction 1494+ 754 = 2248 or 448 (under suppression) = 594 – 146.

The mutational values of glu6lys = 1494 – 893 = 601(79) = 47 (or 0.0893) + 32 (oxygen) and in opposite direction 1494 + 893 = 2387 or 587 = 608 (oxy-time) – 21 and also 608 + 146 = 754.

The mathematical and structural interpretation may be helpful for implementation.

About Cancer:

The cancer causes due to blocking of time by ‘factor of directionality’ 9 or 171 and curving of time by factors of opposite 154 or 6 clarified in this context. The mutational values are calculated from core values (C_V) of amino acids and negative mutational values would be added to respective molecular point and avoided due to structural complicacy.

Considering structural symmetry to clarify cancer where 900 – 575 (electro-gravitational difference) = 325 and 575 – 325 = 250 (intermediate values) = 359 – 109 = 141 + 109 where 356 + 3 = 359 and 138 + 3 = 141. The other structural matter 900 – 645 (tyr core values) = 255 where 645 – 255 = 390 (intermediate values) = 499 – 109 = 281 + 109 where 141*2 = 282 = 281 +1 and also 578 – 3 = 575 and 808 + 230 = 578 + 460 =1038 or 138 = 69*2 derived from Met-Tyr chemistry.

Previously I have shown, in JAK2 G1849T V617F and TP53 G469T V157F [3] the mutational values 151(G) – 126(T) = 25 where 25*0.0019 = 0.0475 or 475 = 900 - 425 where 754 (val core values) – 475 = 279 and 754 + 475 = 1229 or 329 shows blocking of time and time is indomitable that can’t be blocked causes structural conflicts where 27*32 = 864 = 900 - 36 and 864 – 289 (tyrosine kinase factor) = 575 tranquilizes cancer in electro-gravitational structure.

In directional biology, 32*0.0019 – 0.0171(9) = 0.0437(23) thus blocking time and 0.0513(27) – 0.0171 = 0.0342(18) and 342 + 468(72) = 810 = 809 +1 and otherwise 513(27) + 171 = 684 = 900 – 216 where 468(72) + 216 = 684 considering from positive and negative segment.

It is seen 900 – 645(tyr core values) = 255 = 754(val core values) – 499(a tyr component that reverse of 994) and 1545 (tyr core values) – 754 = 791 = 900 – 109(suppressed) is a crucial arena for cancer structural analysis.

The C844T R282W [4] causes cancer would exists in opposite direction of above clarified. Here the mutational values = 126(T) – 111(C) = 285(15) and 389(arg core values) – 285 = 104 and 389 + 285 = 674 = 574 + 100 where 754 + 104 = 858 (molecular point in lung cancer) and 900 – 499 = 401 (reverse of 104).

Considering EGFR mutations T2573G L858R, T790M and C797S where 858*3 = 2574. The mutational values of L858R = 1289 – 753 = 536 = (179*3 – 1) and that of T790M = 1064 – 707 = 357 = 179*2 -1 goes to cysteine line where 900 – 797 = 103 = 281 – 178 where 420 – 242 = 178 and 858 – 797 = 61 = 480 – 420 with a difference of 1. Cysteine (121.1590) has two core values 709 (normal) and 518 (after disulphide bonds) where 709 – 518 = 191 = 179 + 12 = 900/3 – 109 and 709 + 518 = 1227 or 327 = 109*3.

C797S: The mutational values = 1065 – 709 = 356 = 900 – 544 where 544 – 356 = 188 and 188 + 109 = 297 = 796 – 499 and 578 = 297 + 281 and also 188 – 109 = 79 = 578 – 499 and 281 – 79 = 202. It is found 202 + 109 = 311 (factor of opposite in reverse) and 359 – 188 = 171(9) and 188 + 141 = 329 thus blocking time and 595 (asp core values) + 202 = 797, so aspartic acid may be a resolution to intercept molecular signalling towards cancer but needed investigations.

L858R: Here 900 – 858 = 42 where 42*0.0019 = 0.0798 or 798 = 797 + 1 and 858 = 359 + 499 and correspondingly 141 + 281 = 422 = 858 – 436 making a difference of 100 with the mutational values 1289 - 753 = 536 and 536 + 436 = 972 aligns to structural intermediate values 172 where 900 – 536 = 364 and 536 – 364 = 172 where 172 + 109 = 281 and 172 – 109 = 63 = 499 – 436 goes reverse. It is found 63*0.0019 = 0.1197 or 297 where 595(D) = 297 + 298 bisected.

T790M: The structural values ‘109’ is suppressed since 900 – 109 = 791 with a difference of 1 a directional factor. The mutational values = 1064 – 707 = 357 where the intermediate structural values 186 = 576 – 390 (tyr intermediate values) = 390 - 204 since 109 is suppressed and 858 – 790 = 68 where 68*0.0019 = 1292 or 392 and where 595 (D) – 204 = 391 = 186*2 + 19 and also 900 – 881 (reverse of 188) = 19.

The cysteine-aspartate structure shows 709 – 595 = 114 and 595 – 518 = 77 = 154/2 that aligned to factors of opposite.

Diabetes Mellitus:

The molecular weight of insulin is 5734g/mol (334 under suppression) while that of glucagon is 3483g/mol (783 under suppression) which are products of structural conflicts and related to glucose (180.1558 g/mol, 962 core values) and glycogen (666 daltons). It is found 783 – 334 = 449 and conversely 783 + 334 = 1117 or 217. A difference of 100 exists where 900 -666 (glycogen unit) = 234 = 334 – 100 and 783 – 666 = 117.

Since 888 = 4*222(CC) and 135(A)*4 = 540 = 900 -360 are parameters of the system, '4' is a factor of the system where 4*783 (glucagon) = 3132 or 432 = 666 – 234 (reverse of 432) and 900/2 - 1 = 449 and conversely 109*2 – 1 = 217 where '1' is associated with the directional biology.

Again, 575 (electro-gravitational difference) = 900 - 325 where 325 + 9 = 334 and 575 – 9 = 566 = 666 -100 where 100 is an activation values. The positive and negative structural interactions maintain the glucose homeostasis in blood.

The Tyr-Met chemistry is associated with insulin receptor structure. It is seen 0.2124(met ht) – 0.1605 = 0.0519 or 519 and 0.1894 (tyr ht) – 0.1605 = 0.0289 or 289 where 519 + 289 = 808 and 519 – 289 = 230 and doubling the both quantities 230*2 = 460 (lys cooperativity) = 617 – 157 (split) and 808*2 = 1616 or 716 (reverse of 617) = 774(i.e. 617 + 157) - 58 that complemented by insulin (i.e. 109 – 51 = 58) and activates tyrosine kinase domain mediated by insulin receptor since 900 – 774 = 126 =109 + 17 (beyond 900) and 774 = 617 + 157 would not co-exist.

The values 808 – 230 = 578 = 289*2 = 153 + 425 that shows an electro-gravitational structure where 938 – 513 = 425.

The insulin receptor is composed of two alpha and two beta subunits connected by disulphide bonds. The alpha subunit comprises 719 or 731 amino acids which is extracellular while beta subunit comprises 620 amino acids where a 194 -Aa extracellular domain, a 23- Aa transmembrane domain and a 403-Aa cytoplasmic sequence with a well-preserved tyrosine kinase domain.

The beta subunit would be organised as 194*2 = 388 = 900 – 512 where 512 – 388 = 124 = 23 + 101 and 403 = 289 (tyrosine kinase factor) + 114 (factor of opposite) where 403 – 194 = 209 and 620 + 209 = 829 (rotational values of 289). The values 209 = 109 + 100 where 99 = 524 – 425 is suppressed and goes to opposite side and makes 99 + 1 = 100 while 524-524 disulphide bond occurs. The other bonds at 435, 468 can be clarified as 717 – 183 = 534 (reverse of 435) and 468 – 33 = 435 while 524 – 425 = 99 = 3*33.

It is found 512 + 209 = 721 = 719 + 2 = 731 – 10 makes a difference 2 + 10 = 12 while 403 + 388 = 791 = 719 + 72 and 731 – 15 = 716 = 808*2 where 403 – 388 = 15 = 27 – 12. Again, 888 – 719 = 169(glucose core values in reverse direction) = 900 - 731 and 731 = 522 (i.e. 513 + 9) + 209 in lunar time-lunar gravity context. Again, 222 (CC) = 304(reverse of 403) – 82 = 194 + 28 and correspondingly 719 + 403 = 1122 = 731 + 391(reverse of 193) and also 437(23) – 222 = 215 (reverse of 512) where 437 + 113 = 550 = 1450 (expressed) = 731 + 719 and where 620 – 437(23 or reverse of 734) = 183 and 620 + 114 = 734 in the structure.

Derived from 14.0267, where 154 – 114 = 40 = 149 – 109 and 149 curved to 194 and 267 + 113 = 380 = 403 – 23. The values 900 – 267 = 633 = 779(41) – 146 where 146.1451 (gln) and 146.1882 (lys) are associated since 1451 + 1882 = 3333 or 633 under suppression and 267 = 154 + 113 = 121 + 146 while 690 (cys ht) – 633 = 57 = 89 – 32 where 210 – 121 = 89.

The values '14' curved to 41 (a directional values of oxy-time where 41 = 32 +9) where 41*0.0019 = 0.0779 or 779 where 770 – 608 = 162 = 148 (i.e. 524 + 524 = 1048 or 148) + 14 and 770 + 608 = 1378 or 478 = 578 – 100 in the structure. It is seen 779 + 121 = 900 and 779 – 121 = 658 = 690 (or 1590) – 32 that related to cysteine (121.1590) and 658 - 480 = 178 where 242 + 178 = 420 = 900 – 480 and also 193 – 14 = 179. It is seen 779 – 777(183) = 2 and 779 – 10 = 769(reverse of 967 i.e. 193) makes a difference 2+ 10 = 12.

It is seen 146*0.0019 = 0.2774 or 974 where 705 + 74 =779 and correspondingly 183 = 146 + 37 and 109 + 37 = 146 in the structure.

The binding of insulin to INSR causes phosphorylation in tyrosine residues in tyrosine kinase domain. The mutations F382V, R735S, L1018A, Y960F causes insulin resistance are clarified below.

R735S: The core values of tyr is 1545 or 645 = 900 – 255 where 255 or 1155 is a molecular point of R1155. It is seen 537 (reverse of 735) + 109 = 646 and 1155 – 735 = 420 = 900 – 480 where 480 and 420 are positive and negative paths (either or) of cysteine (121.1590) or 242.3180 after disulphide bond in the system. Glucose is structurally linked to cysteine where 480 – 420 = 60 = 169 – 109. Now, 900 – 735 = 165 (ser core values) where 735 – 165 = 570 = 679 – 109 and 679 – 579 = 100 would activates electro-gravitational structure that causes insulin resistance.

F382V: There are two effective core values of cysteine 709 (normal) and 518 (after bonding) where 709 – 518 = 191 = 900 – 709 and 900 – 518 = 382 = 191*2 and conversely 709 + 518 = 1227 or 327 = 109*3 and where 327*2 = 654 = 754 (val core values) – 100 would causes insulin resistance.

L1018A: The electromagnetic values i.e. 524 – 425 = 99 goes opposite side under suppression and makes 100. Here the mutational values is 893 (lys) – 756 (ala) = 137 where 137 + 342(18) = 479 = 579 – 100 would causes insulin resistance.

Y960F: The mutational values = 1545 – 1235 = 310 = 479 – 169 where 479 = 579 -100 would causes insulin resistance. In opposite direction, 1545 + 1235 = 2780 or 980 and correspondingly 109 + 80 = 189 = 289 – 100 would causes insulin resistance.

The glucagon would be the product of structural conflicts where 3483 g/mol = 81*43 where 819 – 439 = 380 = 390 – 10 = 267 + 113 where 645 – 255 = 390 and 819 – 552 = 267 and 552 – 439 = 113 (factor of opposite).

It is interesting that the summation of values beyond 900 shows 258 + 262 + 263 = 783 (glucagon) and 246 + 251 + 252 = 749 of tyrosine trio Y1146, Y1151, Y1152 and Y1158, Y1162, Y1163.

The values '749' represents part of insulin where 5734g/mol = 94*61 = 47(749)*122 where '122' is beyond 900 and 122 +110 = 232 or 1132 (expressed), the molecular point where conserved Asp (133.1032) exists and also 122 + 133 = 255 or conserved 1155Arg exists a lunar time-lunar gravity chemistry where 705 – 595 (asp core values) = 110 and 74 + 109 = 183 (lunar time).

The Asp-Arg chemistry shows 122 + 133 = 255 and correspondingly 2017 (arg ht) – 1032(asp ht) = 985 where 389 (arg core values) + 595 (asp core values) = 984 = 985 – 1.

The molecular signalling of insulin activates tyrosine kinase domain mediated by insulin receptor. The insulin comprises ‘51’ amino acids where 51*0.0019 = 0.0969 or 969 and correspondingly 109 – 51 = 58 that activates tyrosine kinase domain. Here, 69*2 = 138 = 578(289*2) + 460 (under suppression) and 58*2 = 116 where 900 – 289 = 611 (reverse of 116) and 578 + 611 = 1189 or 289 where 289 = 79*2(158) + 131 actuates for biological processes. The infiltration of electro-gravitational impulses (0.0107 or 107) shows 131 = 107 + 24 and 158 = 107 + 51 where 15 + 9 = 24 and 42 + 9 = 51 and 107*51 = 5457 or 957 = 735 + 222 (CC) and 116*15 = 1740 or 840 = 705 + 135(A) in the structure. Again, 957 – 579 = 378 = 900 – 522 where 705 – 522 = 183 = 378 – 195. The tyrosine kinase factor shows 900 - 289 = 611 = 601(79) + 10 = 621 (reverse of 126) – 10 and 289 = 116 + 173 where 739(181) is complementary values of 173 are significant.

3. Conclusions

The biophysical structure works in two domains 900 and the reverse domain 109 in Earth-Moon space-time structure. There would be infiltration of electro-gravitational impulses of 0.0107 values into the system following 33 = 12 + 21, 66 = 15 + 51 = 24 + 42 and 99 = 27 + 72 framework and would be differed by an angle. The ‘values of directionality’ 9 or 0.0171 blocking indomitable time e.g. 279 or 329 causes structural conflicts transit to masses. The core values of amino acids are important parameter to evaluate mutational values and linked to molecular point of protein. The positive and negative interactions in the structure maintain the glucose homeostasis in blood. The Tyr-Arg duo would be important towards diabetes mellitus. The tyrosine kinase factor 289 and its respective values 611 or 116 possess profound implications in biochemistry. The aspartic acid might be investigated and would be a resolution for specific cancer.

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