American Journal of Biochemistry 2021, 11(2): 15-17
DOI: 10.5923/j.ajb.20211102.01

The Analysis of Directional Genetics

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Abstract In-depth analysis of amino acids molecular weight has been made that revealed up electro-gravitational chemistry of biology. There are curvatures and transitions in biology of time make the system flexible. Polymorphic site in context of genetics mathematically described.

Keywords Gravity, Antigravity, Co-linearity, Molecular point, Tryptophan

1. Introduction

Time or antigravity cannot be stopped. Biology, in this context, are natural phenomena towards macro-molecular assemblies to stop time but ultimately failed. Some processes are curvatures, transfer time to opposite direction etc. The time values 0.1451 (electro-magnetic), 0.1736 (lunar time) runs in same direction while 0.1605 (lunar gravity) runs in opposite direction clarified in my previous paper [1]. In directional biology, 0.1254 ($66A^0$, t-RNA distance of constancy factor where 66*0.0019 = 0.1254 manifests distance and mass are synonymous) is away from polymorphic site by 72 – 66 = 6 (i.e. 0.0114) in p53 fundamental protein are structural components. The formula, Time = 0.0019*integer mass (gravitational time) would be a threshold to enter electro-gravitational chemistry of biology. The pre-transitional values, core-values or hidden time are highly impacted in biochemistry. Considering methionine (149.2124), the transitional values at deflection point is 0.2124 – 0.0149 = 0.1975(104) and hidden time or core-values (C_v) = 149*0.0019 – 0.2124 = 0.0707. The transition from anti-gravitional (0.0149) to 149 (gravitional) is a cause to counter time by changing direction where gravitational time would be necessarily greater than anti-gravitational time to produce hidden time and to give constant values of amino acids.

A relation between lunar gravity (0.1605) and oxy-time (0.0608 or 0.0032) can be explained as 0.01605 + 0.0003(57) = 0.1608 where 0.0425 (electro-magnetic time in opposite direction) + 0.0183 (lunar time in opposite direction where 183*0.0019 = 0.3477 = 0.1736*2 with systematic 0.0005 time difference) = 0.0608 and 0.0425 - 0.0057 = 0.0368 (earth-moon curvature of diameter). For regeneration or replication the system appears at oxy-time (0.0608).

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Received: Oct. 27, 2021; Accepted: Nov. 17, 2021; Published: Dec. 15, 2021
Published online at http://journal.sapub.org/ajb

Nucleotides are building blocks of DNA. The systematic average molecular weight of deoxy-ribo-nucleotide triphosphate is 487.0 g/mol and that of monophosphate is 327.0 g/mol. The average MW is effective into the system. In anti-parallel strands the difference is 487 – 327 = 160 = 154 (factor of opposite) + 6 (difference of polymorphic site and t-RNA factor i.e., 72 – 66 = 6 = 0.0114 in time form). The summation = 487 + 327 = 814 = 0.0814 in time form constitutes the genetics of electro-gravitational chemistry.

2. Discussions

I have considered methionine (149.2124), leucine or isoleucine (131.1736), glutamine (146.1451) and arginine (174.2017) to clarify electro-gravitational biochemistry to some extent.

Methionine is an initiating amino acid for its characteristics and is aligned to fundamental molecular structure 238+.3059-(161+). The pre-transitional values of fundamental molecular structure = 0.3059 – 0.0238 = 0.2821 = 0.2831(149) – 0.0010 (or 0.0190). A bio-molecule (164.1380), probably non-existed, but significant is introduced here having core values or hidden time 0.1736 which is aligned to histidine (155.1552) by +/- 9(0.0171) in both sides. The addition of pre-transitional values of arginine (174.2017) and likely non-existed bio-molecule (164.1380) = 0.1843 + 0.1216 = 0.3059 and correspondingly 174 + 164 = 338 = 238+ 100 = 148 + 190(or 0.0010 lies in curvature absorbed in the system) with 1 or 0.0001 time difference. Structurally, 0.1605 (lunar gravity) + 0.1216 = 0.2821 and 0.1605 – 0.1216 = 0.0389 = 0.0399 – 0.0010 where 0.0238 + 0.0161 = 0.0399 in the structure.

The pre-transitional values of leucine = 0.1736 – 0.0131 = 0.1605 (lunar gravity) appears at deflection point by 0.0107*15 rotations and deflects to stop anti-gravitational lunar time (0.1736) which is about halved of 0.3477(183) where 0.1736 can be expressed as curvatures 0.1736 = 0.1368 (72, polymorphic site at p53 protein) + 0.0368 (earth-moon curvature) making leucine molecular weight

a fundamental constant [2], nevertheless, leucine zipper would be an outcome of gravity-antigravity conflicts. The bio-particles are formed (e.g. tumor) by the conflicts of gravity-antigravity under mutations.

The glutamine (146.1451) is comprises proton (0.0938) and electron (0.511) at anti-gravitational values with 0.0002 time difference. The values 0.1451 = 0.0938 + 0.0513 in time form with one place decimal change where 0.1451 – 0.1605 = 0.0154 (factor of opposite). A time difference 0.0001-0.0002 is found in many places. The values 146 – 131 = 15 = 0.0285 = 0.0131 + 0.0154 that absorbed in the system indicates lunar gravity and lunar time runs in opposite direction and lunar time and electro-magnetic values runs in same direction. The pre-transitional values of glutamine, 0.1451 – 0.0146 = 0.1305 = 0.1605 – 0.0300 making 0.0446 (i.e., 0.0300 + 0.0146) an important values in system where 0.0446 = 0.0425 + 0.0021 (or 0.0399) = 0.0814 – 0.0368 (curvature) and 0.0446*2 = 0.0892 (lysine core values with 0.0001 time difference). The difference, 0.1882 – 0.1451= 0.0431 = 0.0425 (electro-gravitational values in opposite direction) + 0.0006 (or, 6, a structural values) = 0.0146 + 0.0285. It is seen 0.0446 = 0.0389 + 0.0057(3) and 0.1323 (gln core values) – 0.1254 = 0.0069 = 0.0066 + 0.0003 in the structure.

Moreover, 0.1323 (gln C_v) – 0.0707 (met C_v) = 0.0616 (V617F) and in opposite direction, 0.1323 + 0.0707 = 0.2030 = 0.1216 + 0.0814 and correspondingly 0.1216 – 0.0814 = 0.0402 = 0.0212 (about halved of electro-magnetic values in opposite direction) + 0.0190 (curvature).

The fundamental molecular structure $238^{+}.3059^{-}$(161) gives 270.3667 (i.e., 193 = 183 + 10) by adding oxygen or oxy-time (32= 0.0608) values in both side would be a place for regeneration or replication. The values 0.3477 – 0.3059 = 0.0418 and 0.0418 + 0.0190(10) = 0.0608(32) would be a bisecting place as 14.0267 when added by '100' in both sides gives 57 (a structural values) and 183*0.0019 = 0.3477 (lunar time). The values '100' or '1000' are commonly found in the structure developed in directional biology of genetics e.g., 0.3477 – 0.1026(0.0513*2) = 0.2451 = 0.1451 + 0.1000, 0.3477 – 0.1876(0.0938*2) = 0.1601 = 0.1605 – 0.0004.

By adding '154' in fundamental molecular structure 271 + 154 = 425 (electro-magnetic values in opposite direction) and correspondingly 0.3059 – 0.1451 = 0.1608 that can be expressed as 0.0608 (oxy-time) + 1000 or 0.1605 + 0.0003(57) in the structure.

The values, 425 – 57 = 368 (earth-moon curvature i.e., 12756 km (earth's diameter)/3477 km (moon's diameter) = 0.367) and correspondingly 0.1451 – 0.1083(57) = 0.0368 and 425 + 183 (lunar time in opposite direction since 183*0.0019 = 0.3477) = 608 (oxy-time) and correspondingly 0.3477 – 0.1451*2 = 0.0575 = 0.0608 – 0.0033 with 0.0001 time difference in the structure. Obviously oxygen acts as a defender to counter time.

In the structure, 183 = 154 (factor of opposite) + 29(0.0551) would be structural components. The values, 0.1605 – 0.1254 = 0.0351 and correspondingly 0.1605+ 0.1254 = 0.2859 = 0.3059 – 0.0200 shows 0.0551(29) is a structural component. While 238 + 313 = 551 and correspondingly 161+ 313 = 474 = 237 makes a cycle.

Moreover, 0.3477 – 0.1083(57) = 0.2394(126) that would be component of p53, a fundamental protein in human life. The values 0.2033(107) – 0.1605 = 0.0428 = 0.0425 + 0.0003 in the structure.

Structural labyrinth in directional biology:

Likely, a non-existed molecular weight 164.1380 is clarified in a way where the hidden time = 164*0.0019 – 0.1380 = 0.1736 (lunar time) and pre-transitional values = 0.1380 – 0.0164 = 0.1216 while the hidden time of tryptophan is 0.1615(85) = 0.1605 + 0.0010. The bio-molecule possessed molecular weight 164.1380, if fabricated, may be helpful to counter anti-gravitational time. Moreover, 0.0354 – 0.0190 (curvature) = 0.0164 and 0.1216 – 0.0190 = 0.1026 (electron time*2). It is seen 164.1380 is analogical to phe-lys amino acids. Also, these values are expansion factors in protein where 460*3 = 1380 and 164*3 – 32 = 460.

The molecular structure 238.3059(161) where 0.3059 – 0.0238 = 0.2821 = 0.2831 (met 149) - 0.0010 and 0.1605 + 0.1216 = 0.2821 where 0.1605 – 0.1216 = 0.0389 = 0.0399 – 0.0010 in the structure.

The values 164.1380 is symmetrical to hidtidine (155.1552) where 164 – 155 = 9 = 0.0171 = 0.1552 – 0.1380 with 0.0001 time difference.

The values 164.1380 can be related to tryptophan (204.2261) in a way 0.1380 – 0.0190 (curvature) = 0.1190 = 0.1615 – 0.0425 and 0.2261 – 0.1190 = 0.1071 where 0.1261 – 0.0190 = 0.1071 and 0.1261 + 0.0190 = 0.1451 and 0.2261 – 0.1646 = 0.0615 = 0.0425 + 0.0190.

The methionine time structure is compatible to values of genetics 0.0814 in the system. In the structure, 0.1608 – 0.1254(66) = 0.0354 = 0.0177*2 = 0.0707/2 = 0.0164 + 0.0190 (curvature) and correspondingly 0.1608 + 0.1254 = 0.2862 = 0.1431*2 where 0.1431 – 0.1451 = 0.0019 + 0.0001. A time difference of 0.0001 or 0.0019 found equivalent to 14.0266 in the system and 0.1975 (met pre-transitional values) – 0.1605 (lunar gravity) = 0.0370 = 0.0547 – 0.0177 where 0.1254 – 0.0707 (met core values) = 0.0547. From the genetic point of view, 814 – 177 = 637(V617F) and 814 – 354 = 460 (expansion factor) avoiding decimals. Again, 0.2831(149) = 0.1451 + 0.1380 and correspondingly 425 – 164 = 261 = 149 + 112 where 112*0.0019 = 0.2128 = 0.2124 (met horizontal time assumed) + 0.0004 (time difference) and also 0.0551(29) – 0.0004 = 0.0547.

From genetic point of view, 0.0814 = 0.0425 + 0.0389 and correspondingly 0.2821 – 0.1451 = 0.1370 = 0.1380 – 0.0010 and 0.1370 – 0.0814 = 0.0556 = 0.0547 (met) + 0.0010 with 0.0001 time difference.

Polymorphic site and molecular point:

In p53 protein, the molecular point '72' (i.e., 72*0.0019 = 0.1368) is polymorphic site where arginine (174.2017) or proline (115.1311) can be evolved. It is seen 333 (CCC) + 154 (factor of opposite) = 487 (avg. MW of de-oxyribo-nucleotide triphosphate) and 421 (AGA) + 66

(t-RNA factor) = 487.

In the structure, 0.2821 – 0.0814 = 0.2007 = 0.2017 (arg ht) – 0.0010 and 0.2017 + 0.0814 = 0.2831(149) and correspondingly 174 + 149 = 323 is associated with proline and 174 – 149 = 25 = 0.0475 where 0.0475 + 0.0814 = 0.1289 (arg C_v) and 0.1843(arg pre-transitional values) – 0.0475 = 0.1368(72). In case of proline, 0.1196 – 0.0874 = 0.0322 where 0.3059 /2 – 0.0333 (CCC) = 0.1196 in the structure. Moreover, 0.0814 – 0.0554 = 0.0260 and 0.0684(bisection of polymorphic site) – 0.0130 = 0.0554 = 0.1843 – 0.1289.

In p53 protein tryptophan (204.2261) is found in positions 23, 53, 91 and 146. The pre-transitional values of trp = 0.2261 – 0.0204 = 0.2057 = 0.1605 + 0.452. Now, 91*0.0019 = 0.1729 where 0.1729 – 0.1368 = 0.0361 = 0.0452 – 0.0091. Again, 0.2774(146) – 0.1605*2 = 0.0436(23) and 0.2774 – (0.1605 + 0.1368) = 0.0199 = 0.0146 (molecular point) + 0.0053. The values 0.2774(146) – 0.1368*2 = 0.0038 shows when structural values rise to 0.0361(19) and correspondingly lowered by 0.0038 in fundamental molecular structure and also rises to 238 + 200 = 438 = 0.0438(23). The difference of core values 0.1615(trp) – 0.1323(gln) = 0.0292 = 2* 0.0146 in the structure is significant. In p53 protein, 72 + 19 = 91(trp) and 72 – 19 = 53(trp) is something special.

V157F and V617F mutations:

The mutations G469T V157F(p53) and G1849T V617F (JAK 2) have been considered for clarification. The mutational values for both mutations is 0.754 (val C_v) – 0.1235 (phe C_v) = - 0.0481 which would be added to respective molecular point on transition e.g., 157 + 481 = 638. Following mutations (0.1097 + 0.0638 = 0.1735) the system would reaches to 0.1735(lunar time) where 0.1254 (t-RNA factor) – 0.1735 = - 0.0481 makes detrimental. From genetic point of view, 1735 – 814 = 921 = 460*2 + 1, 814 + 637 = 1451, 814 – 637 = 177 = 637 – 460 (expansion factor) and 177*3 = 531 = 1000 - 469 where 1380 (i.e., 1849 – 469 = 1380 = 460*3) – 531 = 849 = 1849 (genetic point) – 1000. It is seen 0.1254 – 0.0157 = 0.1097 (JAK 2 mutation i.e. 0.0617 + 0.0481 = 0.1098) and 0.1254 – 0.0617 = 0.0637 (p53 mutation). The mutations goes bisectional stage since 814 – 368 = 446 = 354 + 92 (i.e., 184/2) avoiding decimals in the structure. It is seen 814 – 707 = 107 (rotational unit) and 425 – 354 = 71 (polymorphic site – 1) would be active while 107 + 71 = 177 in the structure.

3. Conclusions

The molecular biology has been clarified in view of genetics to some extent from oxy-time to polymorphic site that would be opened up the scope of implementation. The molecular point is not simply a number but a structural component. The biophysical chemistry lies in the arena of gravitational and anti-gravitational implications.

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