The Methionine and Structural Genetics

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Abstract Methionine has been implemented to go through the structural genetics. The genetics is basically electro-gravitational chemistry where molecular point possesses essential role. The polymorphic site and t-RNA distance of constancy factor are two essential components in the structure. The genetic suppression has been clarified to some extent for p53 tumor suppressor protein where lysine-tryptophan complex is significant.

Keywords De-oxy-nucleotide, Genetic suppression, Molecular point, Lysine, p53

1. Introduction

Methionine generally is an initiating amino acid of protein. Starting from methionine I shall enter into structural genetics. The genetics is basically electro-gravitational chemistry and the foundation stands on lunar gravity, lunar-terrestrial time (0.0368 curvature or 193*0.0019 = 0.3667 curvature) and electro-magnetics (0.1451 or 0.0425 in opposite direction). The basic structure is originating from 183 (0.3477, diameter of our moon) = 154 + 29(0.0551) where 0.0551*3 = 0.1653 = 0.0839 + 0.0814 = 0.0803 (halved of lunar gravity) + 0.0850(electro-magnetic values in opposite direction) and 0.0551 - 0.0477 = 0.0074 and 0.3000 - 0.2900 (i.e. 0.1450*2) = 0.0100 = 0.0174 - 0.0074 = 100. A systematic time difference of 0.0001-0.0002 has been found in many places will not be mentioned specifically in directional biology.

The processes are so organized that there is scope of doubling and bisection in the system. The t-RNA factor $(66^{\circ} = 0.1254)$ and polymorphic site (72 = 0.1368) are components of structural genetics and would be anti-parallel that differentiated by 0.1368 - 0.1254 = 0.0114(6). The lunar gravity runs in opposite direction of electro-magnetic since 0.1605 - 0.1451 (i.e. 0.0938 + 0.0513) = 0.0154 (factor of opposite) [1]. The electro-magnetic values in opposite direction i.e. $0.0938(p^+) - 0.0513(e^-) = 0.0425$ significantly transit to 425 = 183 + 242 where 242 = 121*2 and where 487 - 327 = 160 = 121 + 39 in the structure. The average molecular weight (g/mol) of de-oxy-ribonucleotides are effective in structural genetics. The addition of avg. MW = 487.0 + 327.0 = 814.0 and correspondingly the subtraction = 487 - 327 = 160 = 154 (factor of opposite) + 6 (i.e. difference of polymorphic site-72 and t-RNA distance of constancy factor-66 = 72 - 66 = 6) that can be shifted to 160

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The de-oxy-ribonucleotide triphosphate (avg. MW 487.0 g/mol) exists in opposite direction of proline codon (CCC) = 333 + 154 = 487 where 487 - 44 = 443 = 222(CC)*2 that can be applied to methionine (149.2124) structure where 149 + 29 = 177 = 111 + 66. Although 0.0399 (AUG) is a structural component of methionine but another intrinsic structural component is 0.0399 = 0.0333(CCC) + 0.0066 and correspondingly 0.0453(GGG) is a factor where 0.0453 (GGG) + 0.0154 = 0.0607 (oxy-time) and 0.0302(GG) + 0.0154 = 0.0456 (GGG + 3). The addition of first two bases gives 0.0247(AU) + 0.0222 (CC) = 0.0469 (i.e. p⁺/2, a hotspot genetic point G469) and the rest 0.0151(G) + 0.0111(C) + 0.0066 = 0.0328 (mono-de-oxy-ribonucleotide) where 0.0328 - 0.0171 = 0.0157 (molecular point, V157).

The DNA or protein expansion is an outcome of electro-gravitational chemistry and the expansion values is determined by molecular point in DNA and protein as well.

The values, 0.3477 - 0.2831(149, met integer values) = 0.0646 (trp factor) = 0.575 + 0.0071 and 0.2902 - 0.2831 = 0.0071 and 0.3477 - 0.2902 = 0.0575 and also 646 + 354 (complementary factor) = 1000 in the structure where 0.1608 - 0.1254 = 0.0354. Again, 575 - 184 = 391 = 851 - 460 (expansion unit would have negative impact) and 0.0190(10) + 0.0171(9) = 0.0361 and correspondingly 0.0190 - 0.0171 = 0.0019 in the structure.

In lunar time (0.3477 = 0.2831 + 0.0646), both are bisectional factors where 0.2831 = 0.1451 + 0.1380 (460*3, expansion factor) or 0.1451 - 0.0357 (119*3, expansion factor in opposite direction) = 0.1094 = 0.0547*2 and where 0.1254 - 0.0707 (met C_v) = 0.0547. Since 183 = 154 + 29(0.0551) an opposite factor exists within lunar time, the dual bisection of lunar time would occur under electro-magnetic interference since bisection would not happen until positive and negative segment do meets. Mathematically, 0.0354 + 0.0071 = 0.0425

(electro-magnetic values) where 0.0646 + 0.0354 (i.e. 0.1608 - 0.1254, complementary factor) = 1000 where 0.2902 (0.1451*2) - 0.2831 = 0.0071 and 0.0646(34) - 0.0500 = 0.0146 and 0.0500 - 0.0146 = 0.0354 in directional biology. Again, 0.1415 (i.e. 0.2831/2) - 0.1000 = 0.0415 = 0.0425 - 0.0010 (i.e. 0.0190 = 0.0184 + 0.0006) and 149(0.2831) + 5 = 154 and 0.0850(0.0425*2) - 0.0665(35 = 29 + 6) = 0.0185. It is seen 0.1605 - 0.1415 = 0.0190(10) and $0.1615(trp C_v) - 0.1605 = 0.0010$.

Three factors 0.0646 (trp factor), 0.0547 (met factor) and 0.0446 (gln factor) found in the system where 0.0646 = 0.0323*2 where 0.0323 = 323 = 204 + 119(0.2261). The met factor derived from 0.1254(66) - 0.0707 = 0.0547 and glutamine (146.1451) shows pre-transitional values 0.1451 - 0.0146 = 0.1305 = 0.1605 - 0.0300 and from electro-magnetic and lunar gravity context 0.0300 + 0.0146 = 0.0446.

There are transitions like 0.0425 to 425 in the system, so decimals have been avoided somewhere.

2. Discussions

The core-values or hidden time of met = 149*0.0019 - 0.2124 = 0.0707 and pre-transitional values = 0.2124 - 0.0149 = 0.1975(104). The scenario changes when 0.0149 is added to core-values = 0.0149 + 0.0707 = 0.0856(45) and bisects since 149*0.0019 = 0.2831 = 0.1415*2. The values 0.1415 - 0.0855 = 0.0560 = 0.0532 + 0.0028 where positive meets to negative and bisects. The difference, 0.1975 - 0.0707 = 0.1268 = 0.1368(72) - 100 in the structure where 0.1268 - 0.0708 = 0.0560 = 0.1415 - 0.0855(45). The values 0.0560 (or, 28.0532) can be taken from cys (121.1590) where 121.1590 + 28.0534 = 149.2124. Again, 121*0.0019 = 0.2299 = 0.1415 + 0.0884 where 0.0884 = 0.0814 + 0.0070 = 0.894 (lys core values) - 0.0010. The values, 0.0814 = 0.0487 (tri) + 0.0327(mono) and also the average values 0.0407 (di) is effective in the system.

From genetic point of view, 977 (i.e. 487*2 + 3) – 562 = 415 and 1000 – 977 = 23 = 0.0437 (in time form) where 438 + 562 = 1000 (a structural values) and 1000 – 707 (met core values) = 293 where 562 + 293 = 855. Again, 0.0977 + 0.0707 = 0.1684 = 0.1000 + 0.0684(36, halved of polymorphic site) where 684 + 293 = 977. It is seen 0.0855 – 0.0171 = 0.0684 and 0.0874 (pro core values) – 0.0190(10) = 0.0684 = 0.0977 – 0.0293.

Again, 487 = 44 + 443 where 443 is linked to 380 in a way 443 = 154 + 289 where 289 + 91(about halved to lunar time where 183 = 91*2 + 1) = 380 = 425 - 45(0.0856) and the values '469' directly fall to '425' since 469 - 44 = 425 and 469 + 425 = 894 (lys core values). The expansion units 460 and 104 that would be negative impact where 1000 + 380 = 460*3 and correspondingly 1045 = 855(45) + 190 and 104 + 45 = 149 where 460 - 312 (i.e. 104*3) = 148 avoiding decimals. The expansion unit can be derived from G1849T V617F and G469T V157F and from reciprocal mutations H168R and R273H.

The pre-transitional values of met = 0.1975 = 0.1605 + 0.0370 and from bisectional point of view, 0.1975 = 0.1415 + 0.0560(0.0280*2). The lunar gravity is significantly linked to oxy-time (32*0.0019 = 0.0608) and also linked to polymorphic site where 0.1605 - 0.1368(72) = 0.0237 and 0.0237 + 0.0370 = 0.0607. It is seen 0.0370 + 0.0469 = 0.0839 = 0.0280*3 and correspondingly 0.0839 + 0.0814 (i.e. 0.0487 + 0.0327) = 0.1653(87) and 1000 - 840 = 160 (i.e. difference of 487 - 327 = 160) in the structure.

The electro-gravitational structure, 1876 (i.e. 938*2) - 1368(72) = 508 = 977 - 469 (i.e. 938/2) = 608 (oxy-time) - 100 and 0.1608 (i.e. 0.1605 + 0.0003) - 0.1254(66) = 0.0354= 0.0508 - 0.0154 i.e. lies in opposite direction where 117*3 = 351 = 354 - 3 and 117*2 = 234 where 0.1605 - 0.1368 = 0.0237 = 0.0234 + 0.0003 and where 3 or 0.0057 is a complementary factor in the system.

The hotspot '469' is a bisectional point where 560 - 469 = 91 (lunar time bisected) and correspondingly 560 + 469 = 1029 (trp factor) where 1029 + 154 = 1183 = 100 + 57 = 157 (hotspot, V157) in a suppressed form. It is seen 1381 - 469 = 912 = 304*3 and 1735 (about halved to lunar time) – 912 = 823 = 469 + 354 in the structure.

Conversely, 1876 - 1254 = 622 = 469 + 153 where 312(104*3)*2 = 624 and where 912 - 623 = 289 = 840 - 551(29) in the structure.

The value and lysine would be in opposite direction of met in different way since met codon is AUG while value-GUA and lysine (AAA) – met (AUG) = 405 - 399 = 6 (would be values of opposite). It is seen 0.0803 + 0.0091 = 0.0894 (lys core values) while 0.0803 - 0.0091 = 0.0712 = 0.0707 (met core values) + 0.0005 and 0.0754 (val core values) – 0.0707 = 0.0047 = 47 = 0.0893.

Measuring core values from 0.1254(66), 0.1254 - 0.0707 = 0.0547 and 0.1254 - 0.0893 = 0.0361 and 0.0547 - 0.0361 = 0.0908 in upper level hitting the tryptophan where 0.0707 + 0.908 = 0.1615 (trp core values) and 0.0707 + 0.0323 (i.e. 0.0204 + 0.0119) = 0.1030 (about halved of trp pre-transitional values). It is also associated with tyrosine (181.1894) since 893 - 707 = 186 = 181 + 5 and 0.1894 = 0.1800 + 0.0094(5) = 0.1713 + 0.0181 where 0.2261(119) - 0.0461(119, opposite direction) = 0.1800.

From electro-magnetic point of view, $1876(p^{+*2}) - 893(lys core values) = 983 = 360 + 623$ and correspondingly 983 + 623 = 1606 (lunar gravity) where 623 = 469 + 154 (factor of opposite) shows system works from upper level to lower level and 1415 - 623 = 792, a valine factor will be clarified later.

Again, 1876 - 1254(66) = 622 and 1254 + 153 = 1407 = 1000 + 407(di) = 894 + 513 and 1368(72) + 154 = 1522 = 2902 (i.e. 1451*2) - 1380 (electro-magnetic expansion, 460*3).

The electron values exists in upper level i.e. 487 + 26 = 513 (i.e. 27*0.0019 = 0.0513) while expansion unit lies in lower level i.e. 487 - 27 = 460 where 469 + 44 = 513 and 560 + 47 = 607 (oxy-time) and 560 - 47 = 513 where 47*0.0019

= 0.0893 (lys core values) and 487 + 513 = 1000, an intrinsic structural values.

The genetic structure originates from basic structure 183 = 154 + 29 where 0.0551*3 = 0.1653 = 0.0803 (halved of lunar gravity) + 0.0850 (i.e. 0.0425*2, electro-magnetic values in opposite direction). As a result, 0.2902 (i.e. 0.1451*2) - 0.1653 = 0.1249 = 0.1254 (66) - 0.0005. It is seen 0.1249 - 0.0446 (i.e. 0.0223*2) = 0.0803 and 0.1249 + 0.0357 = 0.1606 where 357 = 119*3 and 119 = 100 + 19(0.0361) = 0.0461 (expansion unit would be having negative effect) and 461 - 104 (expansion unit) = 357. The system works from electro-magnetic upper level '1876' to lower level '469' where 1876 - 223 = 1653(87) and 1653 - 623 = 1030 (about halved of trp pre-transitional values).

It is seen for value, 0.1469 + 0.0117 = 0.1586 = 0.0793*2where 0.0977 - 0.0184 (lunar time in opposite direction) = 0.0793 since 117 + 66 = 183. Mathematically, 793 - 57(3) = 736 = 1736 (about halved of lunar time) - 1000 and $793 + 1083(57) = 1876(p^{+}*2)$ in the structure. Interestingly, 0.0370 + 0.0253 = 0.0623 = 0.0469 + 0.0154 that measured pre-transitional values from level of lunar gravity of met and val. It is seen 0.0469 - 0.0285 (mutational values, C843T) = 0.0184 and correspondingly 0.0469 + 0.0285 = 0.0754 (val core values) and the mutational values calculated from 0.1368(72) - 0.1083(57) = 0.0285 = 0.0351 - 0.0066. It is seen 117*0.0019 = 0.2223 = 0.1586 - 0.0637 where 0.0637 + 0.0154 = 0.0791.

The above describes electro-gravitational chemistry of genetics to some extent where expansion and tryptophan also are structural components. The electro-magnetic values in opposite direction would be of gravitational characteristic.

Mathematical interpretation of G1849T V617F mutation and SCA:

While the met values 0.0547 meets to 0.0391 it bisects i.e. $0.0547 + 0.0391 = 0.0938(p^+) = 0.0469*2$ and the values of difference, 0.0547 - 0.0391 = 0.0156(V157) = 0.0312(expansion values)/2 and can be applied to G1849T V617F. Considering expansion values 460*3 = 1380 = 690*2and 690 = 617 + 73 (polymorphic site) = 684 (halved of polymorphic site) + 6 and 1368(72) - (690 + 617) = 61 = 66 - 5.

There are analogical system in trp (204.2261) and glu (147.1299) like 0.1605 - 0.1152 (glu pre-transitional values) = 0.0453 = 0.2058 (trp pre-transitional values) - 0.1605 that measured from lunar gravity. The mutations glu6val and glu6lys in Hemoglobins gives mutational values 0.1494 (glu C_v) - 0.0754 (val C_v) = 0.0740 and 0.1494 - 0.0893 (lys C_v) = 0.0601 where 740 - 601 = 139 and 740 + 601 = 1341 = 1646 (trp factor) - 305(oxy-time) causing de-oxygenetion to

complement where 1646 - 1415 = 231 (halved of expansion factor) and 323 - 139 = 184 and also 462 - 139 = 323 in the structure.

Genetic suppression:

Genetic suppression for p53 tumor suppressor protein has been measured from molecular point 139-lys where 139 =67 + 72 and where polymorphic site and t-RNA factor have been coincides causing block proliferation. Lysine (146.1881) is a significant amino acid where lunar gravity, lunar time and electro-magnetic values are closely exists. The glutamine (146.1451) and leucine (131.1736) shows 146 - 131 = 15 = 0.0285 = 0.0154 + 0.0131 and 0.1882 - 0.1451 = 0.0431 = 0.0425 + 0.0006 and 0.1882 - 0.1736 = 0.0146. The molecular point-139 exists about middle where 131 + 8 = 139 = 146 - 7 and lysine core values (0.0893) is significant since 0.0893 - 0.0285 = 0.0608 = 0.0469 + 0.0139 and 0.0469 + 0.0424 = 0.0893. The values 0.1876 - 0.1368 = 0.0508 = 0.0254*2 where 0.0254 + 0.0139 = 0.0393 and 0.0508 - 0.0394 = 0.0114(6) = 0.1368 - 0.1254.

The genetic suppression of p53 tumor suppressor protein can be evaluates from molecular point of lys-trp complex. It is seen 0.1615(85, trp core val;ues) – 0.1254 = 0.0361(19) = 0.1254 - 0.0893(47, lys core values). The trp is found in molecular points 23, 53, 91 and 146 in p53 protein while I shall consider 139, 321 for lysine. It is seen 72 + 19 = 91 and 72 - 19 = 53 indicates 0.1254(66) takes the position of polymorphic site. Again, 47 + 6 = 53, 85 + 6 = 91 and 323 (trp factor, 204 + 119 = 323) - 321 = 2 = 0.0038 shows 0.0361 suppressed to 0.0019.

3. Conclusions

The methionine structure has been drawn from genetic point of view associated with tryptophan while two bisectional segment part of lunar time. Apart from methionine codon (AUG) an intrinsic structural component has been found differently read also linked to molecular or genetic point. There are genetic suppression and anti-parallel moving makes the system somewhat complicated. The genetic suppression described might be helpful for further development.

REFERENCES

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