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A Brief Account of Hematopoiesis

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Abstract The proteolytic cleavage is due to gravitational and electromagnetic conflicts in stem cell biology that related to oxy-time. The system goes to super suppressions (900 or multiple of 900) causing some deletions and the structure of SCF and c-Kit receptor has been discussed to some extent with GNNK and serine sub-types in the processes of hematopoiesis.

Keywords SCF, c-Kit receptor, Hemoglobin, Alanine, Serine

1. Introduction

Analysing G1849T V617F and G469T V157F, it is seen the mutational values at genetic level 151(G) – 126(T) = 25 = 0.0475 = 475 (under transition) = 252(TT) + 224(UU) with '1' or 0.0001 time difference and mutational values at protein level, 0.0754 (val core values) – 0.1235 (phe core values) = - 0.0481 which would be added to corresponding molecular point [1]. Now, TT(252) and UU(224) would not exists at a place until implement of vertical gravitational values or suppressions and it is significant that 481 – 475 = 6 = 0.0114 (factor of opposite). Moreover, 1849 – 469 = 1380 = 460*3 and 1849 + 469 = 2318(122), the mid-values of 61*3 = 183 or 0.3477 (lunar time). A time difference of 0.0001(1) - 0.0002(2) is about common in the system which is not specifically clarified and would be adjustable. Decimals have been avoided somewhere as there are so many transitions in the system.

Mathematically, 0.1605 (lunar gravity) – 0.0225 (UU) = 0.1380 = 1380 and 1605 + 252 (TT) = 1857 = 2318 (122) – 461 in triplet mechanism. Again, 2318 + 252 = 2570 = (1605 + 1031) – 66 (i.e., 0.1254, a t-RNA factor) and 570 + 461 = 1031 (an electromagnetic component) and also 2000 = 1031 + 969 = 1380 + 620 (i.e., 62*10) = 1651 + 349 are interrelated. It is seen 224 (UU) + 154 (factor of opposite) = 378 (TTT).

The values 14.0267 (a common inter-protein values somewhere) where 267 = 154 + 113(6) would not exists at a place until implementation of gravitational vertical values '14' or suppression where 900 – 267 = 633 = 1601 – 969 and conversely 1601 + 969 = 2570 with a 0.0001(1) time difference where 0.0004 acts as 0.0076 in a suppressed form.

The genetics deals with some important values of amino acids e.g., core values of arginine (174.2017) = 174*0.0019 – 0.2017 = 0.1289, pre-transitional values = 0.2017 – 0.0174 = 0.1843 and ultimate values = 0.1843 – 0.1289 = 0.0554 = 554.

Hematopoiesis is governed by cytokines SCF and c-Kit receptor that binds together. It is a biological stage where the system contracts by 1000 to 100 and the effective contraction = 1000 – 100 = 900 or multiple of 900 where positive and negative values come together and some deletion occurs non-withstanding the suppression. There are some striking points while p53 contains arg or pro in polymorphic site (72 or 0.1368), human hemoglobin alpha and beta strand contains ser and his. The total expansion of duplicate strands, 141*2 + 146*2 = 574 = 1605 – 1031 and the iron containing 'heme' portion (54.845) is related to alanine (89.0935).

The midpoints of lunar time (0.1736*2 = 0.3472 with 2*0.0002 time difference) = 1736 = 836 (under suppression) = 705 (suppressed form of lunar gravity) + 131 (suppressed form of electro-magnetic component) and 969*2 = 1938 = 1849 + 89 and also 1849 = 1876 (i.e., 938*2) – 27 (0.0513) are important under super-suppressions(900 or multiple of 900).

The lunar time is significant where gravity and electromagnetics co-exists and fundamentalism of genetics.

There would be migration of '27' and '62' coupled to form alanine (89.0935) where 1031 – 62 = 969 and 935 – 836 = 100 (app.) and related to iron containing 'heme' portion and would be related to valine mechanism towards proliferation. The proteolytic cleavage is due to the gravitational and electromagnetic conflicts that related to oxy-time.

The amino acids or base pairs are units of the system and core values and molecular points are related in hematopoiesis.

2. Discussions

Hematopoiesis is governed by some cytokines, SCF and c-Kit receptor where 248 (soluble SCF expansion) + 976 (c-Kit receptor expansion) = 1224 and 976 Aa = 519 (extracellular domain) + 23 (transmembrane domain) + 433

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(an intracellular tail consisting of a juxta-membrane domain) and a tyrosine kinase domain inserted by about 80 amino acids where 976 = 574 (i.e., 1605 – 1031= 574) + 402 (hydrophobic domain in SCF). The '519' is a gravitational component while '433' is an electromagnetic component that intrinsically differed by '574' values. The significant structure of SCF, the portion 149-177 (exon 6) and 190-212 segments where 149 + 177 = 326 and 190 + 212 = 402 (hydrophobic transmembrane domain) are applicable to the system where 402 + 326 = 728 = 165 + 563 that equivalent to 814*2 = 1628 gives 728 under super-suppressions and where 814 = 487 (deoxyribonucleotide tri-phosphates avg. MW in g/mol) + 327 (deoxyribonucleotide mono-phosphates avg.MW) exists at a place under suppression in stem cell biology.

The difference of 487 – 327 = 160 gives 728 + 160 = 888 = 563 + 326 where 0.1463 or 77 of fundamental molecular equation $270^{+}.3667^{-}$(193) [2] suppressed to 563 while 270 + 193 = 463. The segment 190-212 comply with 190 + 3 = 193 and 212 + 58 (3 app.) = 270.

Previously, I described 333 (CCC) + 154 (factor of opposite) = 487 and 333 (CCC) – 6 (factor of opposite) = 327 i.e., under suppressions positive and negative values comes together. The differential values of lunar gravity and electromagnetic component, 1605 – 1031 = 574 are more suppressed or would goes to opposite side where 574 + 154 = 728 and lunar gravity (1605) suppressed to 705 while electromagnetic values (1031) suppressed to 131 and correspondingly 1736 (about halved of lunar time) suppressed to 836 = 705 + 131 while '62' migrates from 969 where 1031 – 62 = 969.

The deletion of exon 6 (i.e., 149-177) in SCF^{248} is due to suppression since 574 + 326 = 900.

The SCF/c-Kit receptor is an expression or freedom of two linked anti-directional amino acids his and pro core values or hidden time goes parallel under super-suppressions (900 or multiple of 900). Derived from lunar time '184'(or, 0.3496), 184 = 115 + 69 (or, 0.1311) gives proline 115.1311 and 184 = 155 + 29 (or, 0.0551) gives histidine 155.1552 with a '1000' structural factor where 115 = 114(6) + 1 and 155 = 154 + 1 are two factors of opposite and core values and molecular point are co-related.

Under super-suppressions, the two anti-directional amino acids meets together and bisects where 326*2 = 652 (or, 1552), 402*2 = 804 and 206*2 = 412 (or, 0.1311 app.). According to fundamental molecular equation $270^{+}.3667^{-}$ (193), 155 + 115 = 270 and correspondingly, 0.1552 + 0.1311 = 0.2863 where 0.3667 – 0.2863 = 0.0804 = 804 = 402*2 (bisects) and in opposite direction 155 – 115 = 40 and 1552 – 1311 = 241 (i.e. cys pairing) where 121*2 = 242 and 0.1590*2 = 0.3180 where 0.3667(193) – 0.3180 = 0.0487 = 487 (de-oxy-nucleotide) and 0.3496(184) – 0.3180 = 0.0316 (oxy-time under suppression) = 0.1216 = 0.0608(32)*2 shows the affinity of oxygen raises under suppression. That is why hemoglobin functions as oxygen respiration.

The cys (121.1590) pairing is significant for full biological activity in haematopoiesis. The cys^{4}-cys^{89} and cys^{43}-cys^{138} that can be clarified as 89 + 4 = 93 = 274 – 181 where 43 + 138 = 181 = 242 – 61 where 154 = 93 + 61. The values '242' and '272' derived from 121*2 = 242 and 1605 – 136 = 1469 = 0.1590 – 0.0121 with 0.0002 time difference.

The pre-transitional values of pro = 0.1311 – 0.0115 = 0.1196 (or, 296) where 1605 (lunar gravity) – 0.1196 = 0.0409 = 409 = 574 – 165 (proteolytic cleavage Ala^{165}, would be exon 6) and pre-transitional values of his = 0.1552 – 0.0155 = 0.1397 = 1397 = 1605 – 208 where 574 – 208 = 366 = 183*2 (bisects) where 183 – 165 = 18 (about one-step and would be exon 7).

Now, the core values of his = 155*0.0019 – 0.1552 = 0.1393 (or, 493) and that of pro = 115*0.0019 – 0.1311 = 0.0874 where 1393 – 874 = 519 (extracellular domain) and in opposite direction, 1393 + 874 = 2267 (or, 467) where 519 – 467 = 52 = 26*2 (tyr26) and the difference of 519 – 433 = 86 = 43*2 (cys) would be 86 + 52 = 138 = 115 (factor of opposite app.) + 23, taking negative part under consideration and the intrinsic difference of 519 and 433 would be 574 while it is derived from gravitational and electromagnetic aspects and 574 – 437(23) = 138 – 1. The cys^{4}-cys^{89} and cys^{43}-cys^{138} would thus strengthen the cytokines structure.

The pro206 (i.e., 0.1311 suppressed to 411 = 206*2 (app.) is significant in the structure where 206 = 185 + 21, sub-divided according to proteolytic cleavage where 185 – 21 = 164 and the oxy-time = 316 = 165 + 151 where 574 = 423 (NN) + 151 and 749(GK) + 151 = 900 clarified later on.

In the processes of hematopoiesis, the system would be reached out at 0.1368 (72) and 0.3667(193) for cell growth or proliferation. It is seen the position 72 occupies arg-pro (i.e., 415, the difference of arg-pro core values) in p53 tumor suppressor protein while the position 72 occupied by his-ser (i.e., 328, the difference of his-ser core values) in alpha & beta strands of human hemoglobin and 415 – 328 = 87 = 89 -2 with a 0.0002(2) time difference. The alpha strand possesses 44pro-his45 while p53 possesses 177pro-his178 and 295pro-his296 is significant. Mathematically, (295 + 296) + (177 + 178) = 946 = 554 (arg ultimate values) + 392 (p53 expansion – 1) and conversely 591 – 355 = 236 = 393 – 157 where 322(pro ultimate values) = 165(proteolytic cleavage) + 157.

About $GNNK^{+/-}$ and $ser^{+/-}$ sub-types:

The GK and NN shows a difference of '100' while 756 (core values of gly) + 893 (lys) = 1649 that suppressed to 749 and 1324 (asn)*2 = 2648 (or, suppressed to 848) and 1023 is applicable for molecular point where '511' is highly significant. The negative impact of NN is zero while 893 – 756 = 137 and 1023 – 749 = 274 = 137*2 and 749 – 511 = 238 = 326 – 88 where 511 – 424 = 87 and 511 + 424 = 935 since the core values of ala and gly are same and 511 – 88 = 423. It is seen 900 – 749 = 151 = 574 – 423 that would suggest GK is an opposite direction of NN. It is seen 848 – 574 = 274 = 1023 – 749, 848 – 415 = 433 (juxta membrane domain) and 848 – 329 = 519 (extracellular domain) that also suggest GNNK acts as a mediator between arg-pro and his-ser in the processes of hematopoiesis.

The molecular point 511 (electronic time) is highly significant and GNNK acts as a mediator between 415 (i.e., arg-pro core values difference in polymorphic site 72 in p53 protein) and 328 (i.e., his-ser core values difference in molecular point 72 in alpha and beta strand of haemoglobin). Mathematically, 415 – 328 = 87 where 511 – 87 = 424(N) and conversely 415 + 328 = 743 = 749 – 6 (factor of opposite). The point of bisection 0.3667(193) shrinks to 0.0967(51) with 0.0002 time difference where 193 – 51 = 142 = 415 – 273 (i.e.,131 + 142 = 273) and conversely 193 + 51 + 328 = 572 where 705-131 = 574 and 705 + 143 = 848(NN) and also 705 – 142 = 563 where the fundamental molecular equation $270^{+}.3667^{-}$(193) shrinks to 563 since 270 – 193 = 77 = 0.1463 (i.e., 77*0.0019 = 0.1463 that shrinks to 563) and also 270 + 193 = 463 with a 1000 structural factor.

The other point of bisection 72 (or, 0.1368 that shrinks to 468 = 234*2) where 234 – 51 = 183 = 511 – 328 and also 328 + 234 = 562 = 563 -1 shows 415 exists in upper level while 328 exists in lower level but interrelated. It is seen 234 + 51 = 285 = 848 – 563 and conversely 848 + 563 = 1411 that equivalent to electronic time 511.

The serine (105.0930) subtype shows 715 – 574 = 141(alpha strand –arg141) where 1289 (arg core values) – 715 = 574 and 715 – 389 = 326. Conversely, 574 + 487 = 1061 and 1061 – 493 (his) = 568 and 568 + 146 = 714. The serine molecular point 715 is suppressed form of 1615(85) where 900 – 715 = 185.

The GNNK and serine are related by 1023 – 715 = 308 = 154*2 (factor of opposite) and correspondingly 715 + 114*2 (factor of opposite) = 943, suppressed form of arg pre-transitional values (0.1843) where 943 = 554 (i.e. 0.1843 – 0.1289= 0.0554 = 554) + 389 (suppressed form of arg core values) and where 554 – 389 = 165 (proteolytic cleavage). The ser pre-transitional values = 0.0930 – 0.0105 = 0.0825 = 825 = 402 + 423 = 804 + 21 while 825 + 749 = 1574 and 1065 – 749 = 316 (oxy-time in suppressed form) and also 715 + 511 = 1226 that equivalent to 326. Considering oxy-time, 316 = 165 + 151 where 574 – 151 = 423(NN) and 574 + 165 = 739 = 749(GK) – 10 and also 554 + 10 = 564 while the values 10(0.0190) arises from 378 (TTT) – 368 = 10, the two points of bisection. It is seen 756 – 511 = 245 = 326 – 81 (would be tyrosine kinase domain).

The glu6val mutation shows 943 – 118 = 825 (ser pre-transitional values) and 825 + 569 (i.e., 0.1469) = 1394 (his core values) are significant with 0.0001(1) time difference. The glu6val and glu6lys mutations are associated where the total mutational values = 740 + 601 = 1341 (or, 441) where 441 – 154 = 287 = 574/2 and 1494 (glu core values) – 154 = 1340 and also 441 + 139 (negative values) = 580 = 574 + 6 that shows directional change of beta strand on mutations causing de-oxygenation while 1605 – 1031 = 574.

Fe-Ala complex:

The molecular weight of Fe is 55.845 g/mol that aligned to hematopoiesis where 845 + 55 = 900 and 845 – 55 (or, 27*2 + 1) = 790 = 728 + 62 and 900 + 728 = 1628 that suppressed to 728. It is seen 790 – 487 = 303 (oxy-time) and correspondingly 790 + 326 = 1116 or 216 where 216 – 154 = 62 and 278 – 154 = 124 = 62*2 since 62*0.0019 = 1178 that suppressed to 278. Again, the pre-transitional values of ala = 0.0935 – 0.0089 = 0.0846 where 89*0.0019 = 0.1691 = 0.0845 + 0.0846 with a decimal factor exists where 89*10 – 900 = 10 and 55 – 10 = 45 (or, 0.0855) where 855 – 846 = 10 (app.) compared with Fe molecular weight.

It is seen 117 + 27 = 144 = 72*2 = 55 + 89 and 89 – 55 = 34 where 144 – 34 = 110 = 55*2 and also 117 – 62 = 55 where 117 + 76 = 193 and 270 – 117 = 153 would be the valine (117.1469) mechanism towards proliferation that aligned to fundamental molecular equation. Furthermore, 117*2 = 234 and 1469 suppressed to 569 = 285 (app.)*2 where 234 + 51 = 285 and 234 – 51 = 183 = 511 – 328 = 117 + 66 where 117 – 66 = 51.

3. Conclusions

The genetics is electro-gravitational chemistry or interactions where lunar gravity (1605) and electro-magnetic component (1031) co-exists in lunar time. In stem cell biology SCF and c-Kit receptor are two complementary cytokines experiencing super-suppressions (900 or multiple of 900) causes gravitational and electromagnetic conflicts results proteolytic cleavage (Ala^{165}) and an expression of his-pro core values in directional biology. In course of hematopoiesis cell growth the system would be reached out at 72 (or, 0.1368) and 193 (or, 0.3667) towards proliferation while his-ser in molecular point 72 is significant for alpha and beta strands in human hemoglobin. The GNNK would acts as a mediator between arg-pro and his-ser of polymorphic site 72 of p53 protein and alpha-beta strands of human hemoglobin. The super-suppressions causing positive and negative values meet together and results raising the affinity of oxygen. The blood molecular disease sickle cell anaemia would be due to directional change upon glu6val and glu6lys mutations in beta strand so release oxygen (de-oxygenation). The system maintains dimensionally correct otherwise influx of electro-gravitational or anti-gravitational waves (0.0107 unit) through cell processes towards equilibrium.

REFERENCES

[1] American Journal of Medicine and Medical sciences 2023, 13(3): 224 – 226.