Glycomics and Lipidopics

Extended Abstract

Humans Chromosome 1 Fractal Periods Signature is Highly Correlated with Intelligence and Brain Evolution

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Abstract:

DUF1220 proteins regions show the largest Homo-Sapiens lineage-specific increase in copy number of any protein-coding region in the human genome and map principally to 1q21.1. DUF1220 deletions have been associated with microcephaly and macrocephaly, respectively. DUF1220 copy number has been linked to both brain size in humans and brain evolution among primates. Remarkably, dosage variations involving DUF1220 sequences have now been linked to human brain expansion, autism severity, total IQ, and cognitive and mathematical aptitude scores. We analyzed in chromosome 1q a total of 245 DUF1220 proteins. Finally the method is extended analysing the long 1q21 region from 7 other close primates like Neanderthal, great apes : chimp, gorilla, orangutan and monkeys : macaque, marmoset, vervet. This remarkable property is confirmed by comparing these primates to other mammals such as mice, rabbit, cow, dolphin and Elephant. We then show four classes of multi-periodic fractal structures for all 19 DUF1220 regions and 19 NBPF genes studied cases. The analysis of these spectra of fractal periods[1] reveals a simple linear interdependence, hierarchization and unification between the numerical sequences of each of these 4 spectra and the sequences of Fibonacci and Lucas. Given the evidence of this numerical relationship, we suggest that this discovery may be one of the major causes of a cognitive development of man superior to that of the great primates. Finally the mathematical roots of this whole numbers resonance patterns is discussed. The exact function of the DUF1220 protein is not known. DUF1220 proteins regions show the largest Homo-Sapiens lineage-specific increase in copy number of any protein-coding region in the human genome and map principally to 1q21.1, and partially also in 1p. DUF1220 deletions have been associated with microcephaly and macrocephaly, respectively. In Colorado University Dr Sikela team established that human genome sequences encoding DUF1220, show a dramatically elevated copy number in the human lineage and variation in DUF1220 copy number has been linked to both brain size in humans and brain evolution among primates. Attempts to link genetic and I.Q have been proposed from the 1970s. Now, dosage variations involving DUF1220 sequences have now been linked to human brain expansion, autism severity, total IQ, and cognitive and mathematical aptitude scores. There are many more copies of DUF1220 encoded in the human genome compared to the genome of any other species. Humans have approximately 270 haploid copies, far more than great apes (90–125 copies), monkeys (25–40 copies), and especially prosimians and non-primate mammals (1–9 copies) Dr Sikela Lab. demonstrates the hypothesis that increasing copy number of sequences encoding DUF1220 protein domains is a major contributor to the evolutionary increase in brain size, neuron number, and cognitive capacity that is associated with the primate order. They propose that this relationship is restricted to the anthropoid sub-order of primates. Indeed, thanks to the CRISPR technology, it is now possible to modify locally the genomes, and more particularly the human genome. Especially since it has been established that this region is extremely fragile, difficult to sequence, and often causes severe cerebral disorders. On the other hand, the fractal and global structures of the human genome were demonstrated. For more than 25 years, we have been looking for possible global, even digital, structures that would organize DNA, genes, chromosomes, and even whole genomes. We will analyze here several major sequences containing these proteins DUF1220 according to an original approach highlighting kinds of "fractal periodicities", this method shows evidence of "fractal periods" and "resonance periods" characterizing each of the 24 human chromosomes as well as any partial or complete sequence of any chromosome. below, these resonances make it possible to differentiate the respective genomes of Neanderthal and Sapiens on the global scale of the 1q21.1 DUF1220 main rich region. We introduce here a method of global analysis of the roughness or fractal texture of the DNA sequences at the chromosome scale. To do this, we generalize the method of numerical analysis of the "Master Code of Biology" . Thus, we restructure the sequence into different generic sequences based on "meta codons" no longer triplets of 3 nucleotides but values ranging from 17 to 377 nucleotides, then 360 simulations. This method of analysis will then reveal, in most cases, discrete waves or interferences, most often dissonances. However, sometimes there will emerge kinds of resonances where all scales of analysis appear to be

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in symbiosis. The discrete interferences fields resulting from the analysis of an entire chromosome are therefore a three-dimensional space: Dim y (vertical) restructuring in meta codons of lengths 17 to 377 nucleotides Dim x (horizontal) derived mobile1 such that 1/2 1/3 1/4 ... 1 / n Dim z cumulated populations from the "Master code" operators. The + 1 / -1 derivatives will be of type increase, ie +1 if derivative increasing and will be of type decrease, ie -1 if derived decreasing. In this context we will explore these 3d spaces in 2 forms: -Horizontal, meta codons dimension: curves for a given meta codon dimension, see in the example "resonances" below. -Vertically, spectral differentiation: discrete series d2-d1 is +1 if increase and -1 if decrease. We represent in top the +1 and in low the -1, (see the examples below). Example of three-dimensional interference fields (Neanderthal chromosome 1q21.1 DUF1220 rich region6). The study of the long region6 of more than 5 million base pairs and containing 218 DUF1220 will reveal the spectrum of the following periods: First remark: there are various possible interferences between Fibonacci/Lucas sub-spectrums : Main resonances periods: 5 7 12 19 31 50 81 DUF1220 resonances and periods 5 8 13 21 34 55 89 Fibonacci 0 1 1 2 3 5 8 Fibonacci 5 7 12 19 31 50 81 DUF1220 resonances and periods 2 1 3 4 7 11 18 29 47 Lucas 3 6 9 15 24 39 63... = 3 x (1 2 3 5 8 13..) = 3 times Fibonacci 5 7 12 19 31 50 81,3 4 7 11 Lucas 4 4 8 12 20 = 4 x (1 1 2 3 5...) = 4 times Fibonacci 5 7 12 19 31 50 81, 3 4 7 11 18 Lucas 3 5 8 13 Fibonacci etc...Second remark : There are main resonances periods like 5 7 12 19 31 50... but also secondary resonances periods like : 17 (5+12), 24 (5+19), 26 (7+19), 57 (7+50), 69 (50+19), etc... Main resonances : 5 7 12 19 31 50 81 …/...Harmonic resonances : 17 24 26 36 38 43 48 55 62 74 91 93 98 …/... Finally, we could propose the following rule : The rule is : "The distance between the waves flow periods sequence from DUF1220 region (5 7 12 19 31 50...) and a Fibonacci similar sequence (5 8 13 21 34 55...) is ALSO another shifted Fibonacci sequence (0 1 1 2 3 5...) !" A corollary is: The waves spectrum associated with DUF1220 region (5 7 12 19...) is analog with the INTERFERENCE substraction between TWO Fibonacci waves spectrum shifted (then 5 8 13 21 34... and 0 1 1 2 3 5 8 13 ...)We now study the 16 cases of NBPF genes containing DUF1220 proteins in Homo-Sapiens (HG38), which we will then complete with 3 other representative analogues in Neanderthal. Recall Lucas: 2 1 3 7 11 18 29 47 ...Fibonacci: 0 1 1 2 3 5 8 13 21 34 …Finally, we study the 19 cases of DUF1220 regions, including: the six regions from chromosome1 in Homo-Sapiens, then we concentrate on the long region6 of 1q21.1 in Neanderthal, then in the large apes primates, then in Other primates, and finally in other mammals of which the very small number of DUF1220 is known. Recall :Lucas 2 1 3 7 11 18 29 47, Fibonacci 0 1 1 2 3 5 8 13 21 34. Here are the details of the periods, resonances and dissonances for the 2 long regions6 of 218 DUF1220 in Sapiens (HG38) and in Neanderthal. REGION6 sapiens HG38 vs Neanderthal Recall Resonances: Main resonances : 5 7 12 19 31 50 81 …/..., Harmonic resonances: 17 24 26 36 38 43 48 55 62 69 74 91 93 98 100…/.

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