Extended Abstract Journal of Cancer Biology and Therapeutic Oncology 2021
Vol.5 Issue3

Sapiens Mitochondrial DNA Genome Circular Long Range Numerical Meta Structures are Highly Correlated with Cancers and Genetic Diseases mtDNA Mutation

Jean-claude Perez
IBM emeritus, Martignas Bordeaux metropole, France

Introduction

Using the circular nature of the 16k base-pairs human mtDNA genome, we are looking for hypothetical proportions between the C+A and T+G bases. Remarkable proportions are thus discovered, the length of which may be much greater than the length of the genome. We then analyze the impact of evolution on these "numerical resonances" by comparing the referenced mtDNAs of Sapiens, Neanderthal and Denisova. Then, by analyzing 250 characteristic mutations associated with various pathologies, we establish a very strong formal causal correlation between these numerical meta structures and these referenced mutations. To summarize, we should think then research on the following situation: (a) Inputs: 250 cases of mtDNA mutations1 associated with various human diseases. (b) An operator: The exhaustive search for mtDNA genome "Fibonacci resonances" associated with these mutations. (c) A "binary" output: a common behavior of the mtDNA genome resulting from these 250 mutations disorders.

Background of the Research

we showed the existence of specific numerical nucleotides proportions in the DNA of the genes [1,2]. This discovery also applied to small circular genomes such as those of bacteria or mitochondrial DNA genes-rich sequences. On the other hand, it did not work for non-coding DNA sequences regions like human chromosomes. In the cells, mitochondria are known as the powerhouses of the cell. They are organelles that act like a digestive system which takes in nutrients, then breaks them down, and creates energy rich molecules for the cell. The biochemical processes of the cell are known like a cellular respiration..

The genome of the mitochondria or "mtDNA" is a small 16 kb genome whose remarkable feature is the fact that it is looped back on itself forming a circular sequence. This is also true of the genomes of most bacteria. As in prokaryotes, there is a very high proportion of coding DNA and an absence of repeats. It encodes 37 genes: 13 for subunits of respiratory complexes I, III, IV and V, 22 for mitochondrial tRNA (for the 20 standard amino acids, plus an extra gene for leucine and serine), and 2 for rRNA. One mitochondrion can contain two to ten copies of its DNA. Mitochondrial genomes have been extensively studied and identified, especially for many years by Douglas C. Wallace [3-5]. This genome possesses the remarkable hereditary characteristic of being transmitted only by the mother [6], which makes it a privileged tool in the evolution studies of human species. Various heterogeneous genomes copies can be found in the same cell, it is heteroplasmia [7]. It would also appear that the genome of mitochondria and its mutations can play an important role in aging [8,9]. But, above all, simple mutations associated with various diseases (such as LHON) are observed, and somatic mutations are found in cells associated with various diseases such as cancers [10]. Effectvely, it is now emerging that somatic mutations in mitochondrial DNA (mtDNA) are also linked to other complex traits, including neurodegenerative diseases, ageing and cancer.

This work is partly presented 2nd Global Summit on Oncology and Hematology on April 05-06, 2021 | Webinar