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The impact nutrigenetics versus the central dogma of molecular biology

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Nutrigenetics, which is ruled by epigenetic mechanisms, specifically studies the modifying effects of inheritance. At the molecular level, what happens is that DNA sequence can be expressed or silenced by epigenetic information, which is directly influenced by environmental conditions. This information system (DNA sequence) is used by the organisms as described by the central dogma of molecular Biology stated by James Watson, co-discoverer of the DNA structure in 1959. This hypothesis predicts that information flows in a single direction from our DNA sequence to RNA through a process called transcription and from RNA to proteins through a process called translation. However, there is another layer of information beyond DNA sequence. From the decade of 1970, a new set of research in genetics gathered in a branch of science called epigenetics (beyond genetic) showed solid evidences that the phenotype is not controlled only by DNA sequence. Environmental conditions will also influence the phenotype by determining regions of DNA sequence that needs to be silenced or expressed. So, there are two types of information that will be used to build a protein. One is the DNA sequence itself and the other will determine what part of DNA sequence will be used by the cell. The influence of epigenetic mechanism is so profound that it can even alters the DNA sequence, since methylation is mutagenic. Methylated cytosine is prone to deamination to thymine. CpG dinucleotides are under-represented in vertebrate genomes. Moreover, the different amount of CpG among organisms shows a solid evidence that methylation also plays an important role in evolution. The difference between the mutagenic effect of methylation and the other types of mutation, which are random is that the methylation tends to be directional and influenced by environmental conditions.

Biography

Levi Ezequiel de Oliveira holds a bachelor's degree in Biological Sciences from the University of Mogi das Cruzes (2004) with the graduation work in bioinformatics finding genes related to Apoptosis in Plant Cells (Model: *Triticum aestivum*). Master's degree in Sciences by University of Sao Paulo (2010). Trainee in the Genome Laboratory of the University of Vale do Paraiba (2004-2005), working with the construction of recombinant vectors containing mitochondrial protein genes obtained from sugarcane to verify in heterologous expression. Doctoral in Sciences at the Biotechnology Program by University of São Paulo (2014), working with various extractive methods of lipid biomolecules for first, second and third generation biodiesel synthesis and lipid raw material characterization by several methods including thermal analysis. In 2017, started the specialization course in Bioinformatics by University of California San Diego. In 2018, started to work for Abepoli Institute, aiming to recover the flora biodiversity preserving native stingless bee.

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