

Role of Nutrigenomics in Treatment of Non-Communicable Diseases

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DESCRIPTION

The relationship between diet, nutrients, and gene expression is what is meant to be meant by the term "nutrigenomics," which is also known as "nutritional genomics." Genes can respond to environmental factors, one of which is nutrition, in addition to having an effect on the phenotype—the physical manifestation of genetic traits. Vitamin A, which controls gene expression, and folate, choline, vitamins B2, B6, and B12, all of which are involved in the one-carbon cycle, is notable key nutrients. Gene expression has also been linked to more general dietary patterns like diets with a high Glycaemic Index (GI) load. For instance, a high GI diet is linked to an increased polymorphism in the Adiponectin gene, which can lead to insulin resistance and type II diabetes.

The development of cutting-edge technologies that make it possible to process a large amount of data pertaining to gene variants has a significant impact on the field of research known as nutritional genomics. These technologies, which are called "omic," we are able to simultaneously identify and measure many different kinds of molecules thanks to genomic, proteomic, metabolomic, transcriptomic, and other methods. This is important because the majority of chronic diseases are caused by complex interactions among a very large number of distinct gene variants rather than by single genetic effects influenced by a single dietary exposure (like phenylalanine and PKU), as in the case of leptin deficiency.

Nutrigenomics investigates how nutrients affect gene expression, expanding strategies for the prevention and treatment of Non-Communicable Diseases (NCDs) such as obesity, type 2 diabetes, Inflammatory Bowel Disease (IBD), and cancer, as well as the perspective of designing and prescribing customized diets based on the individual genetic makeup. It aims to observe the variations of genetic polymorphisms that are involved in the absorption, metabolism, and excretion of nutrients and bioactive compounds. These variations are viewed in conjunction with other subfields of research, such as metabolomics, transcriptomics, and proteomics. Together, these subfields enable the discovery of the effects that nutrients have on the epigenome or genome and how they can affect each individual.

Epigenetic changes can be caused by diet alone or in conjunction with other environmental factors. These changes in the genes have a big impact on cellular processes like hormonal balance, cell signaling, carcinogen metabolism, apoptosis, controlling the cell cycle, changing energy levels, and angiogenesis. In addition, the development of the offspring and their long-term health can be impacted. As a result, it is essential to comprehend the individual's health status and link it to their nutritional requirements.

The term "functional food" refers to foods that, in addition to their fundamental nutritional function, contain physiologically active components that have a health-enhancing effect. These components are known as bioactive compounds, and even if they are present in trace amounts, taking them on a regular basis has the potential to lower the risk of developing chronic diseases. It is suggested that these compounds should be obtained naturally. We can think of polyphenols like resveratrol, quercetin, curcumin, and genistein as examples of bioactive compounds.

In addition, the inherited individual genetic sequence can also influence diet, leading to the suppression of nutrients and risks for NCDs. During intrauterine life, the nutrients and other food compounds can modulate gene expressions or even change the nucleotide sequence, modifying the organism's response to toxic and infectious compounds. Through personalized diets, understanding these interactions between the genome and food contributes to health promotion and lowers the risk of Noncommunicable Diseases (NCDs).

There is a dearth of information regarding these bioactives' mode of action in the majority of studies, which focus solely on determining whether or not there is a change in the level of gene expression. Last but not least, the majority of genes have a direct connection to the metabolism of glucose or insulin. However, there is a pressing need to investigate genes that are involved in other significant metabolic processes, such as oxidative stress, apoptosis, inflammation, and apoptosis, which may have an indirect connection to the treatment and prevention of disease. It is also essential to recognize that the genetic variants of each gene may respond differently to the compounds.

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