BİRUNİ ÜNİVERSİTESİ "Bilimin Geleceği" BİRUNİ UNIVERSITY "Future of Science"

Biruni Health and Education Sciences Journal (BHESJ)

ISSN: 2687-5608

Volume 4/2 Fall

2021 p. 38/41

Epigenetik ve Beslenme

Epigenetics and Nutrition

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Abstract

DNA methylation, histone modification and "epigenetic changes" occurring through non-coding RNAs play a role in the regulation of chromatin and gene expression.Epigenetic mechanisms affect cellular gene expression levels independently from DNA sequence. Epigenetic modifications can cause heritable phenotypic changes by the influence of environmental factors such as toxicants, nutrition and stress. Specific epigenetic marks that escape embryonic epigenetic reprogramming may have a role in obesity, insulin resistance, Type 2 diabetes, inflammation, cardiovascular diseases, neurodegenerative diseases and immune system diseases susceptibility through subsequent generations. Nutrients physiologically and pathologically affect epigenetic mechanisms important for gene expression throughout life. Based on this information, regulation of these mechanisms with diet or special nutritional components can provide protection from diseases and increase the quality of life. More scientific studies are needed to have precise information on this subject.

Key words: Nutrition, epigenetic,nutrient.

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After the completion of the Human Genome Project, it has come to the fore that inheritance has a new dimension beyond genes, and it has been revealed that important changes can occur in the work of genes without changing the structure of DNA during life. In this new dimension of inheritance, which is called epigenetics, it has been proven that environmental factors, especially nutrition, have important effects, and even the changes that occur can be transferred to new generations. These changes are thought to be effective in many areas of health, from maternal development to aging processes and chronic diseases. As our knowledge about epigenetic mechanisms and the effect of nutrition on it increases, it is clear that many diseases can be prevented and treated with individualized dietary recommendations.

Phenotypic changes that occur as a result of the relationship between genes and gene products that are not inherited, without any change in DNA sequence, are called “epigenetic” (Waddington, 2012: 10). It is known that environmental factors including nutrition, smoking, lifestyle, air pollution, microbial infections and maternal nutrition have an effect on epigenetic changes.

Foods and bioactive nutrient contents cause epigenetic changes on DNA and change gene expressions at the transcription level (Choi, 2010: 8). One of these mechanisms, DNA methylation is the addition of methyl groups to cytosine groups on DNA as a covalent (Niculescu, 2012: 270). DNA that receives methyl group is normally inactive, while DNA that does not take methyl group is the DNA regions that actively participate in transcription (Daniel, 2015: 59). Honey bees are a clear example of nutrition-mediated DNA methylation. The larvae fed with royal jelly Apis continue their lives as a queen bee with the increase of DNA methylation in the synactin p62 gene; Those fed with pollen live a short life as worker bees. It has been reported that this gene regulates lipid regulation, hormonal regulation, posttranslational modifications, energy transfer and some other physiometabolic events (Kucharski et al., 2008: 1827). A similar study was conducted by Dolinoy et al. With dietary changes in mice, hypomethylation was induced on the agouti gene and ectopic agouti gene expression was silenced. It has been observed that there are differences in coat color, body weight and susceptibility to chronic diseases (Waterland et al. 2006: 401-6).

Methyl groups used in DNA methylation are taken into the body with dietary sources. Studies conducted in experimental models show that micronutrients such as folic acid, B_6, B_{12}, choline and betaine, which change during pregnancy, can have significant effects on methylation processes of the fetus, which is in the process of rapid cell proliferation and differentiation, and these effects can be transferred to adulthood (Padmanabhan et al 2013: 637). The best known of these is the Dutch Winter Hunger Cohort. During the German occupation of the Netherlands, with the Nazis cutting off their food and fuel support, the daily intake of energy fell below 700 calories. In individuals in this region, as a result of starvation in the early stages of maternal development, cardiovascular problems including atherogenic lipid profile and decreased cognitive functions, nutrient deficiency, kidney and lung function disorders in the middle periods, and glucose intolerance in adulthood in individuals exposed to hunger in the last period of pregnancy (Roseboom et al. 2006: 485). Histone modifications and miRNA are other mechanisms induced by dietary factors.

Various studies have shown that different foods, macro and micronutrients, and dietary components such as polyphenols are effective on epigenetic mechanisms (Kabasakal et al, 2019: 9). However, it is very difficult to determine a specific nutrient or bioactive nutrient component for each epigenetic change. Because foods are in a complex relationship with other genes, nutritional components and systems in the body. Our knowledge of nutritional epigenetics is currently limited. However, we can say that we will be able to benefit more from epigenetic changes in individualized dietary recommendations with future studies, and thus, we will make an important way in the prevention of diseases. On the other hand, it is important that positive changes can be made at the genetic level and healthier generations can be raised in every period of life, especially starting from the period before pregnancy, by providing the parents with adequate and balanced nutrition and diversity.

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