

Editorial

The Role of Nutrigenomics in Food Safety: The Future Perspective in Personalized Foods

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Functional food is a food that beyond the normal benefits for health could also reduce the risk of a disease. There are several methods to produce functional food, including reduction of food components or the complete elimination of it, addition of components as supplements such as probiotics and antioxidants, replacing a component, and/or increasing food stability.

It is important to have a deep knowledge about the safety of these added compounds and the real benefits of their addition. Nevertheless, as compound assimilation by the body during nutrition is a complex process, the common biochemical and physiological methodologies are usually limited to describing the great complexity of the effects from a genomics point of view. Nutrigenomics, one of the new fields in the "omics" branches, could be able to explore the broader spectrum of the effects of these added compounds and, therefore, help in the design of functional foods based on individual health/genome profiles with the aim of reducing the risk of specific diseases (Keijzer et al., 2010). Also, with this new field, scientists can develop specific and individualized nutrient rich diets as a key tool to help or "cure" certain health problems.

Nutrigenomics, derived from the words "nutrition" and "genomics", analyzes the interaction between nutrient's bioactive components and the genome, describing the influences of genetic variation on nutrition by a direct correlation between the nutrient's absorption, gene expression and metabolism (Kato, 2008).

The quality and safety of food certainly have a huge effect on health, but genetics also play an important role in different type of diseases, including inheritance or health problems derived from gene-environment interactions. A variety of environmental signals can change the gene expression profiles, and as a consequence, generate health problems. Nutrition is one of the main components of the

environmental conditions, which can change the phenotype. Some of the important diseases that could be caused by changing the gene expression patterns include cancer, cardiovascular problems, digestive and inflammatory diseases, allergies and diabetes among others (Jones and Baylin, 2002; Multhaup et al., 2015; Prescott and Saffery, 2011). Therefore, nutrigenomics can certainly contribute to personalized medicine.

Personalized nutrition along with detailed individual genome information enables researchers using nutrigenomics to predict cellular and molecular events after consuming food and these results can be used to reduce the hazards associated with some compounds (Fenech et al., 2011). Any processed food can result in various patterns of gene expression and therefore different metabolite production. Nutrigenomics describes these different patterns and presents them as a dietary signature that is specific for each cell, tissue and organism. All of these changes can influence homeostasis and metabolic pathways (Muller and Kersten, 2003). So, it could enable us to design supplemented food and food processing systems to prevent chronic diseases such as obesity and type-2 diabetes. Nutrigenomics has different phases including finding the effective markers related to food compounds, intervention, seeking the gene expression profile and recommendation of a personalized diet for a patient.

In complementary alternative medicine (CAM) treatment, such as consumption of herbal preparations, addition of dietary supplements and etc., we could use nutrigenomics (Richardson et al., 2000) to predict the effects of each compound on gene expression and therefore metabolic pathway in an individual.

Therefore, information about the interaction mechanisms of food components on gene expression would help patients not only to avoid consumption of certain food as

prevention but also to include compounds into the food that will definitely improve their lives. In addition, knowing the necessary nutrients would positively help scientists to manage the disease outcome in patients (Muller and Kersten, 2003; Ouhtit, 2014).

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