

Editorial

The Intersection of Nutrigenetics, Nutrigenomics, and the Microbiome in Human Health

Giuseppe Merra *

Section of Clinical Nutrition and Nutrigenomics, Department of Biomedicine and Prevention, University of Rome Tor Vergata, 00133 Rome, Italy; E-Mail: giuseppe.merra@uniroma2.it

* **Correspondence:** Giuseppe Merra; E-Mail: giuseppe.merra@uniroma2.it

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1. Introduction to Nutrigenetics, Nutrigenomics, and the Microbiome

Human assistance in solving these issues requires the implementation of nutrition recommendations in the general population in the framework of personalized nutrition, as well as the development of a new generation of genetically validated functional foods. It is, however, crucial to face technical barriers that still hamper the clinical use of nutrigenomic tests since comprehensive models integrating co-genomic resources and dietary inputs from food metabolomics could be the key elements to impact the applied reliability of genomics findings for personalized diet. The present review has been organized into separate sections, each dealing with main advances and broad knowledge applications significant in disease reduction or healthy aging, covering research activity launched during this century [1, 2].

Summing up, many opportunities and challenges lie ahead in the application of advanced knowledge in genomics to the public and all stakeholders, particularly in the exploration of the vast world of interactions between human, nutrition, and microbiome-related genomics and the integration of "omics" techniques, where expertise is needed in the multidisciplinary fields [3].

Nutrigenomics studies the genome-scale effects of food, which can have applications in treating diseases or combating the aging effect. In contrast, nutrigenetics is a narrower research field



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focusing on gene-variant-diet interactions. New molecular technologies have enabled the discovery of the human microbiome - the assemblage of microbiota, the host, and their environmental interactions, supporting genomics research. The enormous complexity and variety of commensal microbes that inhabit the human body emerge as a new series of endogenous genomes influencing nutritional and health outcomes, impacting variability in people's responses to diet intervention [4].

Interest in the relationship between diet and health has existed for thousands of years. Hippocrates, also known as the "Father of Medicine," stated, "Let food be thy medicine and medicine be thy food." The 20th and 21st centuries have significantly increased the field's knowledge base. The advance of molecular biology has, especially in the last two decades, culminated in the onset of a new era of personalized nutrition [5].

2. Genetic Variability and Nutrient Metabolism

Wild-type alleles of fatty acid desaturase 1 (FADS1) and desaturase 2 (FADS2) are associated with a more efficient desaturation and elongation of dietary ALA. Conversely, individuals carrying a specific FADS haplotype are more responsive to dietary ALA and have higher levels of circulating long-chain LC-PUFA compared to carriers of FADS haplotypes that are less efficiently converted. Metabolic conditions proposed to influence the conversion of ALA to longer-chain omega-3 LCPUFA include intakes of omega-3 and omega-6 fatty acids and single nucleotide polymorphisms (SNPs) in the FADS gene cluster. Other inherited and epigenetic variations in the enzymes metabolizing fatty acids and other metabolic pathways have also been reported. In light of the evidence for discrepancies in nutrient metabolism, there is increasing interest in identifying nutrient metabolism-related genes and personalizing nutrition [5, 6].

The nutritional needs of individuals are unique due to complex interactions among genetic, physiological, and environmental factors. Within the last three decades, the influence of genetic variability (including mutations that lead to loss of enzyme function, gene duplications, and additional genetic variations that cause increased or decreased metabolic activity) on nutrient metabolism has been appreciated. The long-chain omega-3 long-chain polyunsaturated fatty acids (LCPUFA), eicosapentaenoic acid (EPA, C20:5n-3), and docosahexaenoic acid (DHA, C22:6n-3) are reduced from alpha-linolenic acid (ALA, C18:3n-3) through the action of fatty acid desaturases 1 and 2 (FADS1 and FADS2, respectively) [5].

3. Microbiome Diversity and Function

The human microbiome resides throughout the body, with distinct niches that harbor unique and diverse microbial communities. The microbiome has a variety of nutritional, metabolic, physiological, and immune functions to contribute to human health. Humans have utilized various strategies to care for the microbes, including diet, lifestyle, and medication. As a result of these interactions, humans have co-evolved with their microbes. Genetics, environmental exposures, diet, and lifestyle have shaped the microbiome composition and functions. When the microbiome composition and function are disrupted, various diseases can occur.

Furthermore, the diversity and stability of the microbiome are important indicators of health. These findings have opened the door to the role of the microbiome in human health. In response, more research has been conducted to understand different groups in more detail and correctly

establish the means to maintain or return microbiome balance to support overall health, cure diseases, and ensure the earth's sustainability [7].

4. Impact of Nutrigenetics and Nutrigenomics on the Microbiome

Epidemiological and intervention studies have confirmed a causal relationship between human microbiome functionality and host health status. When considering future personalized nutrition strategies, it is, however, expected to focus on the genetic identity of the host or the sensitivity to individual nutrients, overlooking the high genetic potential of our gut microbiota. The present review aims to analyze the potential outcomes of the human microbiota clad in light of mechanistic evidence in nutrigenetics and nutrigenomics, to which it brings an added not fully exploited value toward precision nutrition and public health [7].

In the 21st century, nutrigenetics and nutrigenomics have focused predominantly on incorporating genetic diversity into personalized nutrition advice to promote healthy aging and improve the global obesity issue. Both aspects are well described at the individual level. However, how an individual's genetic diversity modulates their gut microbiota composition and metabolic activities independently of a controlled diet and lifestyle is an understudied field of nutrigenetics and nutrigenomics. This review highlights this critical knowledge gap and encourages an integrated perspective on tackling both personal nutrition together. The functionality of the human gut microbiota is primarily involved in microbiota-host co-metabolism and in converting some otherwise ingesta-resistant polysaccharides into small-chain fatty acids, produced as a by-product of the microbiome, or other molecules such as vitamins or cryptic phytochemicals. These functions evidence a high potential of the gut microbiota to affect our health status [5-8].

5. Therapeutic Applications and Future Directions

Mounting evidence implicates alterations in the gut microbiome during pregnancy, at birth, and during the first few years of life with a risk for genetically predisposed future metabolic dysregulation or immune dysfunction. Pregnancy with the earliest exposure to food after birth and the acquisition of a stable adult gut microbiome contains the "first 1000 days" which appears to be an ideal time to test the microbiogenomic personalized interventions developed for people suffering from or susceptible to chronic diseases of adulthood. Interventions or screening at this early stage are significantly more feasible when no severe clinical problems occur. The appropriate food to correct for each problematic microbiome deemed formed may deliver permanent health or decrease the risk of subsequent disease [6, 9].

This editorial was focused on the possibilities for using dietary modulation of microbiome-host molecular cross-talk to prevent, mitigate, or manage a variety of chronic diseases affecting 21st-century populations, particularly in complex individuals who may be the most genetically susceptible or resistant to such diseases. The two principal interventions for modulating the microbiome are targeted food-derived dietary components to promote the growth of health-associated species or limit the activities of disease-associated species. Nutrigenetic and nutrigenomic data have and will continue to identify the best nutritional candidates for consumption, likely shortly for a given individual, to prevent or manage chronic diseases. In addition to helping clarify the intricate molecular interactions between an individual's microbiome and other molecular components in its diet, gut microbiota in feces and/or metabolites in fecal water will

increasingly find applications as inexpensive, noninvasive, objective clinical tools for quantifying health status and disease progression and/or response to therapy [7-10].

Author Contributions

The author did all the research work for this study.

Competing Interests

The author has declared that no competing interests exist.

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