Chapter 12

Gut Microbiome and Diet Interaction

Odangowei Inetiminebi Ogidi
https://orcid.org/0000-0002-9961-893X
Bayelsa Medical University, Yenagoa, Nigeria

Iniebiyo Felagha
University of Africa, Toru-Orua, Nigeria

ABSTRACT

The survival of hosts is contingent upon the gut microbiota, an ecosystem composed of billions of microorganisms residing in the intestinal space. Microbial colonization is a concurrent process with immune system maturation that impacts gastrointestinal function. Diet influences the composition of the microbiota in the intestines. For the maintenance, restoration, and development of bodily tissues, humans require carbohydrates, protein, lipids, and an assortment of other nutrients on a consistent basis. The progression and initiation of diseases may be impacted by alterations in the feeding patterns of the intestinal microbiota, which subsequently influence the physiological state of the host. Changes in the quantity and functionality of intestinal bacteria are hallmarks of chronic noncommunicable diseases. A greater comprehension of the influence that bacteria and their metabolites have on the onset and/or progression of various human diseases can be attained through an analysis of the interaction among the gut microbiota, diet, and host as discussed in this chapter.

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INTRODUCTION

Ten trillion microbial cells are estimated to reside in the human gastrointestinal (GI) tract. This tract is inhabited by an extensive array of mutualistic microorganisms. Specialised metabolites, among other bioactive compounds, are generated by these microbes. These metabolites are critical for stimulating the immune system and metabolic pathways of the host. Due to its metabolic capacity being similar to that of the liver, the gastrointestinal microbiota (GM) is commonly referred to as a "metabolic organ" (O'Hara & Shanahan, 2006). The advancements in the fields of metabolomics and metagenomics have facilitated the identification of numerous small compounds generated by microorganisms, along with the corresponding genes associated with their synthesis (Martinez et al., 2017). Therefore, the mutually beneficial relationship between genetically modified organisms (GM) and their hosts results in a wide range of metabolic patterns. The advancements in GM metabolomics are gradually unravelling the metabolic interaction between the host and the microbes (Yadav et al., 2018). Genetic modification (GM) facilitates the production of primary metabolites, which are subsequently transformed into secondary metabolites referred to as "specialised metabolites" (Hooper et al., 2012; Sharon et al., 2014).

Certain specialised metabolites are linked to metabolic pathways that are unique to a particular taxonomic group. The integration of metagenome and metatranscriptome sequencing enables insights into the classification and functions of these metabolites (Quinn et al., 2014). The comprehension of the interaction between the host and microbiome, which is facilitated by the specialised metabolites implicated, can be enhanced further by employing computational methodologies, molecular networking analysis, and high-resolution mass spectrometry (Sharon et al., 2014). Microbial communities have the ability to swiftly adapt their functionality in reaction to alterations in dietary patterns, hence augmenting the adaptability of human diets (Sheflin et al., 2017). Several environmental factors influence the regulation of GM physiology, including both short-term and long-term dietary patterns and interventions (Portune et al., 2017).

The metabolic processes associated with the breakdown of nutrients and xenobiotics have an impact on various mechanisms. This category includes the following mechanisms: (i) the exchange of chemical information between metabolic compounds produced by humans and microbes; (ii) the regulation of the immune system and protection against pathogens; (iii) the regulation of the enteric nervous system and the development of resistance to colorectal cancer; (vi) the impact on neurological behaviour; and (vii) the reduction of lipid levels in the bloodstream and the adjustment of cholesterol levels (Delzenne & Williams, 2002). Environmental factors such as location, diet, social dynamics, and behaviour influence the genetic composition of the host, as the concepts become more complex. Crosstalk is the

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