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Gut morphology and gene expression in obesity: Short review and perspectives

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SUMMARY

Obesity, a multifactorial and polygenic condition, is considered one of the great global public health problems of our time. The intestinal microbiome should be considered as a set of genetic factors that, together with the host genotype and lifestyle (consumption and energy expenditure), contribute to the pathophysiology of obesity. Increasing evidence showed an increased proportion of bacterial phylum Firmicutes and reduced concentrations of Bacteroidetes in obese as compared to normal weight humans. Studies report that DNA methylation patterns in the blood are associated with intestinal microbiota profiles and suggest that the microbiota and its metabolites influence genomic reprogramming. Investigations of the intestinal microbiota and its impact on genomic changes and their relationship to the risk of developing obesity provide opportunities to establish the basis for incorporating biological individuality into recommendations with significant therapeutic potential.

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1. Introduction

The prevalence of overweight and obesity has reached epidemic proportions worldwide. Obesity is a multifactorial and polygenic condition considered to be one of the great public health challenges, especially since excess adiposity is associated with medical complications and comorbidities [1,2].

Changes in eating habits, such as the increase in the consumption of foods high in fat and sugar, appear to be related to the alteration of the genetic composition and metabolic activity of the resident microorganisms – the human gut microbiome. Such diet-induced changes may be related to the increasing prevalence of chronic diseases, including obesity [3,4].

The intestinal microbiome can be considered as a set of genetic factors that, together with the host genotype and lifestyle (consumption and energy expenditure), contribute to the pathophysiology of obesity [4].

Rankinen et al. [5] studied genotypes positively associated with obesity and identified 22 candidate genes for obesity. The authors found 5 phenotypes related to obesity: energy expenditure, low lipid oxidation, adipogenesis, sedentary lifestyle, and hyperphagia (i.e., regulation of hunger, appetite and satiety).

In this review article, we will discuss hypotheses about the association between gene expression and obesity, as well as aspects related to the intestinal microbiota.

2. Human intestinal microbiota in obesity

In recent years there has been increased interest in the study of the human intestinal microbiota since intestinal microorganisms appear as potential contributors to the increased prevalence of obesity [4].

The ecosystem consists mainly of bacteria, but also viruses, protozoa, fungi and archaea. The microbiota of the human intestine is mainly composed of Bacteroidetes, Firmicutes and Proteobacteria, as a minor but important component. The intestinal microbiota plays an important role in host health, shaping the development of the immune system, metabolizing dietary nutrients (such as fatty acids, glucose and bile acids) and drugs, digesting complex polysaccharides, and synthesizing vitamins and bioactive molecules [6,7].

The mechanisms by which the intestinal microbiome can influence energy metabolism and homeostasis include regulating the use of energy from food, interacting with signaling molecules involved in the metabolism of microorganisms, modifying intestinal permeability, releasing intestinal hormones, and chronic inflammation [4,8].

Diversity in intestinal microbial ecology among humans may be an important factor affecting energy homeostasis; that is, individuals predisposed to obesity may have intestinal communities that promote the extraction and/or storage of energy from a particular diet. Studies have reported that the prevalence of obesity was lower in individuals with greater microbial diversity. This hypothesis that intestinal microbial diversity is linked to obesity deserves further exploration in humans since it may generate new treatment strategies [9].

Most of the findings on the relationship between the microbiome and obesity are based on studies with rodents. However, increasing evidence shows an increased proportion of bacteria of the phylum Firmicutes and reduced concentrations of Bacteroidetes in obese as compared to normal weight

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