



Obesity and Gut Microbiota



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Abstract

The prevalence of overweight and obesity among children and adolescents has risen dramatically increasing and is considered a high-income country problem. Different trials surgical and medical have been tried over years. Recently, the link of gut microbiota to overweight and obesity has been documented in many literatures. In our mini review we will explore this relation ship

Significance: Obesity; Gut microbiota

Introduction

Approximately 35% of adults aged 20 to 50 are overweight (BMI > 25 k/m²) [1]. Gut microbiota in relation to obesity has become a major focus of recent research. It may provide an effective treatment for obesity. Here, we will discuss how this relates to obesity.

Main Text

As a group of microbial species, intestinal microbiota plays a critical role in the health and disease of the host. These bacteria coexist with the host during their lifetime. The literature was reviewed in several ways show that gut microbiota has a tight association with host metabolism via the production of gut microbiota-derived metabolites, such as short-chain fatty acids (SCFAs) which can supply energy for colonic epithelial cells, trimethylamine-N-oxide (TMAO) which is associated with the formation of white adipose tissue and inosine-5-monophosphate (IMP) which has been found involved in the metabolism of lipids. Moreover, gut microbiota can affect digestion and metabolism, as well as the immune system and bile acid profile. It is believed that a link exists between gut microbiota and obesity and other metabolic diseases in hosts caused by the microbiota-derived toxic metabolites, extra energy derived from gut bacteria, and low-grade inflammation caused by endotoxemia. Moreover, certain dietary plants may influence gut microbiota to affect weight gain through their effect on metabolism [2]. The gut microbial composition of 100 women from Ghana and the US was compared (50 lean women and 50 obese women) and it was found that lean women had more Bacteroides, and the westerners had more butyrate-producing gut bacteria [3].

Gut microbiota species obesity related

A number of the species in this group are defined as obesity-related, which includes Firmicutes and Bacteroidetes. The propensity of obese humans and mice have a higher Firmicutes/ Bacteroidetes ratio [4]. A meta-analysis, including 17 randomized controlled trials (RCTs) in humans, 51 studies on farm animals, and 14 studies on experimental models, reported that Lactobacillus acidophilus administration was associated with weight gain in humans, and Lactobacillus fermentum and Lactobacillus ingluviei would cause weight gain in animals [5]. 100 women from Ghana and the US (50 lean and 50 obese) were examined for gut microbiota composition, and the lean women had more Bacteroides, and the lean Ghanaians had more butyrate-producing bacteria. Mice transplanted with feces from the lean Ghanaians were resistant to obesity induced by 6-weeks high-fat diet feeding ($p < 0.01$) [5].

Treatment strategies for obesity

In (morbid) obesity, bariatric surgery (weight loss surgery) is another, more drastic approach to improving metabolic function. A higher satiety signal after bariatric surgery may account for the weight loss caused by increased peptide YY (PYY) and the incretin glucagon-like peptide 1 (GLP-1) levels after surgery. The increase in fecal and plasma bile acids was associated with higher satiety signals. Bariatric surgery has been shown in smaller studies to alter gut microbiota composition in humans, Proteobacteria increased and Firmicutes decreased after the procedure. It has been proposed that an increase in Oxygen after ileostomy surgery could result in an increase in Proteobacteria. A higher

pH in colonic lumen may also be a result of decreased gastric acid production after surgery. Higher pH can inhibit bacteria from the Bacteroidetes and Firmicutes phylas [6]. In conclusion, bariatric surgery changes not only the intestinal physiology, but also the microbial composition of the host, with some benefits [3].

Author's Contribution

Both authors have contributed to the writing and the review of the manuscript.

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