

Obesity and Gut Microbiota

El Darazi E^{1*}, Sacre Y², El-Khoury E^{3*} and Nour AMA⁴

¹First and corresponding author. Faculty of Arts and Sciences, The Holy Spirit University of Kaslik USEK, Lebanon

²Faculty of Arts and Sciences, The Holy Spirit University of Kaslik, Lebanon

³Department of surgery, Central Military Hospital, Beirut, Lebanon

⁴School of Engineering, The Holy Spirit University of Kaslik, Lebanon

*Corresponding author:

Elias El-Khoury,
Department of surgery, Central Military Hospital,
Beirut, Lebanon, E-mail: efkhoury@gmail.com

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1. Abstract

The human microbiota is an extremely large system with its majority inhabiting the colon. In this review we study the relation between the gut microbiota composition and obesity.

2. Introduction

Human microbiota is the system englobing more than 100 trillion microorganisms living in symbiosis with the hosting body [1, 2]. The majority of the human microbiota inhabits the gastrointestinal tract especially the colon [3]. The microbiota gene composition, the microbiome, is composed of 10 million genes while the human genes count only 23000, thus the very rich functional potential [4]. In individuals with same eating habits and activity, different body weight changes are noted, a possible cause can be the intestinal microbiota [5, 6]. Thus, the state of intestinal microbiota can be classified as one of the multiple causes of obesity [7]. In fact, the development and progression of obesity can be due to an imbalance in the microbiota [8], and changes in the diet can lead to changes in the composition of the intestinal microflora [9]. Multiple documents confirm the association between gut microbiota and obesity. The knowledge of the mechanism is limited. This review summarizes the link between gut microbiota and obesity.

3. Function

Due to its diversity, the microbiota has a high stability against various environmental factors [10] and can perform similar metabolic

functions by different microorganisms at the same time [11]. Thus its important role in gastrointestinal [12, 13] motility, drug interaction and immune modulation [14, 15].

It inhibits pathogenic bacteria colonization of the gut [16] and increases the energy value of food [17]; it also ferments alimentary debris, breaks down their toxins, and absorbs their minerals [12, 18].

4. Colonization

The microbiota colonization of the gut starts at birth. The initial gut microbiota can resemble the mother's vaginal microbiota (Lactobacillus, Prevotella, and Sneathia) for infants that are vaginally delivered or the mother's skin microbial community (Staphylococcus, Corynebacterium, and Propionibacterium) in case of caesarean section [19]. When the individual reaches adulthood, the gut microbiota becomes composed mainly of Firmicutes and Bacteroidetes [20].

5. Link with Obesity

The link between gut microbiota and obesity came initially from studies on mice. Eventhough germ free mice eated more and moved less, they were resistant to obesity; when conventionalized they became obese [21]. Moreover, transplanting microbiota from obese animal to germ-free mice increased their body fat.7 Different studies demonstrated that in obesity the number of Firmicutes increases while the number of Bacteroidetes decreases despite the same nutrition and motor activity [22-26]. In the same concept, a

study showed that mice treated with summer microbiota of bears, which is rich in Firmicutes and depleted in Bacteroidetes, developed an increase in body weight [27]. Eating food high in fat has the same effect in augmenting the Firmicutes/ Bacteroidetes ratio [2, 28]. Weight loss in adolescents due to restriction of the fat component in the diet was accompanied by a significant increase in the content of Bacteroidetes in feces [29]. This ratio can be explained by the fact that Bacteroidetes have fewer genes for enzymes involved in lipid and carbohydrate metabolism than Firmicutes [30], resulting in higher adiposity compared with those with a high gene count [31]. Surprisingly, Serino et al. showed that intestinal microbiota in mice with obesity was characterized by a decrease in the number of Firmicutes in favor of Bacteroidetes [32], and Finucane et al. showed no difference between obese and lean individuals in their relative abundance of Bacteroidetes or Firmicutes [33]. A peculiar study done by Haro et al. found that in men, Bacteroidetes genus decreased with obesity, but no changes were observed in women [34].

Other microbiota changes have also been observed. The work of Kalliomaki et al. showed that infants with high *Staphylococcus aureus* in feces are at risk for developing obesity in school age [35]. Another study showed that obese preschool microbiota was characterized by an increase in Enterobacteriaceae while a decrease in *Akkermansia muciniphila* [36]. Million et al. showed a high content of *L. reuteri* with high BMI and low incidence of *Bifidobacterium animalis* and *Methanobrevibacter smithii* [37]. Another study showed that obese population, presents a higher proportion of anaerobes, mostly *Veillonella*, *Bulleidia*, and *Oribacterium* [38]. *Bifidobacterium* is found to have a negative correlation with obesity in another study [39]. Remely et al. showed that *Akkermansia* and *Faecalibacterium* negatively correlate with obesity and with the introduction of any of these microorganisms, a decrease in body weight occurs [40]. A study by HJ Zuo et al., aimed at identifying differences in the composition of the microbiota between people with normal weight and obesity, revealed a significant decrease in the level of *Clostridium perfringens* in obesity compared to normal body weight [41]. In another study, another specific microorganism associated with obesity was identified: Christensenellaceae, this microorganism is negatively associated with obesity [42].

It has been concluded that antibacterial therapy in the first months of life, may be a risk factor for obesity, through violation of the normal composition of the gut microbiota [31, 43, 44]. Same study was done on animals where antibacterial drugs accelerated growth rates; moreover, the earlier antibiotic therapy is used, the more pronounced the growth process is [45]. Interestingly, in lactating obese mothers an increase in *Lactobacillus* and *Staphylococcus* in colostrum, and a decrease in *Bifidobacterium* is observed [46], this translates in the infant's gut microbiota through translocation and puts him at high risk for obesity [47].

6. Mechanisms

Well balanced symbiosis between gut microbiota and the human system is essential for the maintenance of a healthy state. Dysbiosis however is often associated with disease. Multiple theories, based on animal experimental studies, try to explain the relation between gut microbiota dysbiosis and obesity.

Dysbiosis can reduce the diversity by the loss of keystone species and the increase in pathogens, this results in modification of the metabolic capacities by increasing inflammation in adipose tissues and reduction of fatty acid oxidation by muscles [48]. A reduction in satiety is observed, due to impaired secretion by enteroendocrine cells of neurotensin. Perturbation of Primary bile acids [49] and choline [50] metabolisms by the perturbed gut microbiota can cause accumulation of fat and obesity. Also, increased energy extraction from food [51], altered fermentation of fibers [52], and increased endotoxaemia [53], all caused by dysbiosis can induce obesity.

7. Conclusion

Obesity has been linked to different gut microbiota changes. This is due essentially to dysbiosis through different mechanisms of action in humans that remain to be deciphered. The role of the gut microbiota in the development and chronicity of obesity still needs to be clarified.

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