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Obesity and Gut Microbiota

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ABSTRACT

INTRODUCTION

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.

KEYWORDS

Microbiota, Obesity, Gut, Dysbiosis.

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 millions genes while the human genes count only 23000, thus the very rich functional potential [4]. In individuals with the 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.

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].

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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].

LINK WITH OBESITY

The link between gut microbiota and obesity came initially from studies on mice. Even though 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 the 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 the 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 the 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 developping 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. [40] showed that Akkermansia and Faecalibacterium negatively correlate with obesity and with the introduction of any of these microorganisms, a decrease in body weight occurs. A study by HJ Zuo et al., [41] 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 perfingens in obesity compared to normal body weight.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 studies 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 lacting obese mothers an increase in *Lactobacillus* and *Staphylococcus* in colostrum, and a decrease in Bifidobacterium is observed [46], this translates in the infants gut microbiota

through translocation and puts him at high risk for obesity [47].

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 [49]. Perturbation of Primary bile acids [49] and choline [50] metabolisms by the perturbated 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.

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.

REFERENCES

1. Ardatskaya MD, Bel'mer SV, Dobritsa VP, et al. (2015) Disbiosis (dysbiosis) of the intestine: Current status, problems, comprehensive diagnosis and therapeutic correction. Experimental and Clinical Gastroenterology (5): 13-50.
2. Ley RE, Turnbaugh PJ, Klein S, et al. (2006) Human gut microbes associated with obesity. Nature 444(7122): 1022-1023.
3. Leser TD, Mølbak L (2009) Better living through microbial action: the benefits of the mammalian gastrointestinal microbiota on the host. Environmental Microbiology 11(9): 2194-2206.
4. Qin J, Li R, Raes J, et al. (2010) A human gut microbial gene catalogue established by metagenomic sequencing. Nature 464(7285): 59-65.
5. Holmes E, Li JV, Marchesi JR, et al. (2012) Gut microbiota composition and activity in relation to host metabolic phenotype and disease risk. Cell Metabolism 16(5): 559-564.
6. Nicholson JK, Holmes E, Kinross J, et al. (2012) Host-gut microbiota metabolic interactions. Science 336(6086): 1262-1267.
7. Turnbaugh PJ, Ley RE, Mahowald MA, et al. (2006) An obesity-associated gut microbiome with increased capacity for energy harvest. Nature 444(7122): 1027-1031.
8. Kasubuchi M, Hasegawa S, Hiramatsu T, et al. (2015) Dietary gut microbial metabolites, short-chain fatty acids, and host metabolic regulation. Nutrients 7(4): 2839-2849.
9. Zhang C, Zhang M, Wang S, et al. (2010) Interactions between gut microbiota, host genetics and diet relevant to development of metabolic syndromes in mice. The ISME Journal 4(2): 232-241.
10. Martínez I, Muller CE, Walter J (2013) Long-term temporal analysis of the human fecal microbiota revealed a stable core of dominant bacterial species. PloS One 8(7) : e69621.
11. Turnbaugh PJ, Hamady M, Yatsunenko T, et al. (2009) A core gut microbiome in obese and lean twins. Nature 457(7228): 480-484.

12. Macfarlane GT, Macfarlane S (1997) Human colonic microbiota: ecology, physiology and metabolic potential of intestinal bacteria. Scandinavian Journal of Gastroenterology 32: 3-9.
13. Falk PG, Hooper LV, Midtvedt T, et al. (1998) Creating and maintaining the gastrointestinal ecosystem: what we know and need to know from gnotobiology. Microbiology and Molecular Biology Reviews 62(4): 1157-1170.
14. Ouwehand A, Isolauri E, Salminen S (2002) The role of the intestinal microflora for the development of the immune system in early childhood. European Journal of Nutrition 41(1): i32-i37.
15. Bäckhed F, Ley RE, Sonnenburg JL, et al. (2005) Host-bacterial mutualism in the human intestine. Science 307(5717): 1915-1920.
16. DiBaise JK, Young RJ, Vanderhoof JA (2006) Enteric microbial flora, bacterial overgrowth, and short-bowel syndrome. Clinical Gastroenterology and Hepatology 4(1): 11-20.
17. Gill SR, Pop M, DeBoy RT, et al. (2006) Metagenomic analysis of the human distal gut microbiome. Science 312(5778): 1355-1359.
18. Hooper LV, Midtvedt T, Gordon JI (2002) How host-microbial interactions shape the nutrient environment of the mammalian intestine. Annual Review of Nutrition 22(1): 283-307.
19. Dominguez-Bello MG, Blaser MJ, Ley RE, et al. (2011) Development of the human gastrointestinal microbiota and insights from high-throughput sequencing. Gastroenterology 140(6): 1713-1719.
20. Lepage P, Leclerc MC, Joossens M, et al. (2013) A metagenomic insight into our gut's microbiome. Gut 62(1): 146-158.
21. Bäckhed F, Ding H, Wang T, et al. (2004) The gut microbiota as an environmental factor that regulates fat storage. Proceedings of the National Academy of Sciences 101(44): 15718-15723.
22. Aron-Wisnewsky J, Gaborit B, Dutour A, et al. (2013) Gut microbiota and non-alcoholic fatty liver disease: new insights. Clinical Microbiology and Infection 19(4): 338-348.
23. Ley RE, Bäckhed F, Turnbaugh P et al. (2005) Obesity alters gut microbial ecology. Proceedings of the National Academy of Sciences 102(31): 11070-11075.
24. Ravussin Y, Koren O, Spor A, et al. (2012) Responses of gut microbiota to diet composition and weight loss in lean and obese mice. Obesity 20(4): 738-747.
25. Delzenne NM, Neyrinck AM, Cani PD (2013) Gut microbiota and metabolic disorders: how prebiotic can work?. British Journal of Nutrition 109:81-85.
26. Kasai C, Sugimoto K, Moritani I, et al. (2015) Comparison of the gut microbiota composition between obese and non-obese individuals in a Japanese population, as analyzed by terminal restriction fragment length polymorphism and next-generation sequencing. BMC Gastroenterology 15(1): 1-10.
27. Sommer F, Ståhlman M, Ilkayeva O, et al. (2016) The gut microbiota modulates energy metabolism in the hibernating brown bear Ursus arctos. Cell Reports 14(7): 1655-1661.
28. Martens EC (2016) Fibre for the future. Nature 529(7585): 158-159.
29. Santacruz A, Marcos A, Wärnberg J, et al. (2009) Interplay between weight loss and gut microbiota composition in overweight adolescents. Obesity 17(10): 1906-1915.
30. Million M, Lagier JC, Yahav D, et al. (2013) Gut bacterial microbiota and obesity. Clinical Microbiology and Infection 19(4): 305-313.
31. Le Chatelier E, Nielsen T, Qin J, et al. (2013) Richness of human gut microbiome correlates with metabolic markers. Nature 500(7464): 541-546.

32. Serino M, Luche E, Gres S, et al. (2012) Metabolic adaptation to a high-fat diet is associated with a change in the gut microbiota. Gut 61(4): 543-553.
33. Finucane MM, Sharpton TJ, Laurent TJ, et al. (2014) A taxonomic signature of obesity in the microbiome? Getting to the guts of the matter. PloS One 9(1): e84689.
34. Haro C, Rangel-Zúñiga OA, Alcalá-Díaz JF, et al. (2016) Intestinal microbiota is influenced by gender and body mass index. PloS One 11(5): e0154090.
35. Kalliomäki M, Carmen Collado M, Salminen S, et al. (2008) Early differences in fecal microbiota composition in children may predict overweight. The American Journal of Clinical Nutrition 87(3): 534-538.
36. Karlsson CL, Önnerfält J, Xu J, et al. (2012) The microbiota of the gut in preschool children with normal and excessive body weight. Obesity 20(11): 2257-2261.
37. Million M, Maraninchi M, Henry M, et al. (2012) Obesity-associated gut microbiota is enriched in Lactobacillus reuteri and depleted in Bifidobacterium animalis and Methanobrevibacter smithii. International Journal of Obesity 36(6): 817-825.
38. Angelakis E, Armougom F, Carrière F, et al. (2015) A metagenomic investigation of the duodenal microbiota reveals links with obesity. PloS One 10(9): e0137784.
39. Schwiertz A, Taras D, Schäfer K, et al. (2010) Microbiota and SCFA in lean and overweight healthy subjects. Obesity 18(1): 190-195.
40. Remely M, Hippe B, Geretschlaeger I, et al. (2015) Increased gut microbiota diversity and abundance of Faecalibacterium prausnitzii and Akkermansia after fasting: a pilot study. Wiener klinische Wochenschrift 127(9): 394-398.
41. Zuo HJ, Xie ZM, Zhang WW, et al. (2011) Gut bacteria alteration in obese people and its relationship with gene polymorphism. World Journal of Gastroenterology 17(8): 1076.
42. Goodrich JK, Waters JL, Poole AC, et al. (2014) Human genetics shape the gut microbiome. Cell 159(4): 789-799.
43. Ghoshal S, Witta J, Zhong J, et al. (2009) Chylomicrons promote intestinal absorption of lipopolysaccharides. Journal of Lipid Research 50(1): 90-97.
44. Trasande L, Blustein J, Liu M, et al. (2013) Infant antibiotic exposures and early-life body mass. International Journal of Obesity 37(1): 16-23.
45. Cromwell GL (2002) Why and how antibiotics are used in swine production. Animal Biotechnology 13(1): 7-27.
46. Cabrera-Rubio R, Collado MC, Laitinen K, et al. (2012) The human milk microbiome changes over lactation and is shaped by maternal weight and mode of delivery. The American Journal of Clinical Nutrition 96(3): 544-551.
47. Martín R, Langa S, Reviriego C, et al. (2003) Human milk is a source of lactic acid bacteria for the infant gut. The Journal of Pediatrics 143(6): 754-758.
48. Vangay P, Ward T, Gerber JS, et al. (2015) Antibiotics, pediatric dysbiosis, and disease. Cell host & Microbe 17(5): 553-564.
49. Tremaroli V, Bäckhed F (2012) Functional interactions between the gut microbiota and host metabolism. Nature 489(7415): 242-249.
50. Dumas ME, Kinross J, Nicholson JK (2014) Metabolic phenotyping and systems biology approaches to understanding metabolic syndrome and fatty liver disease. Gastroenterology 146(1): 46-62.
51. Collado MC, Engen PA, Bandín C, et al. (2018) Timing of food intake impacts daily rhythms of human salivary microbiota: a randomized, crossover study. The FASEB Journal 32(4): 2060-2072.

52. David LA, Maurice CF, Carmody RN et al. (2014) Diet rapidly and reproducibly alters the human gut microbiome. Nature 505(7484): 559-563.
53. Tremaroli V, Bäckhed F (2012) Functional interactions between the gut microbiota and host metabolism. Nature 489(7415): 242-249.