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Editorial

Targeting the Gut Microbiota in Obesity?

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Editorial

The association between the human body and the microorganisms that it hosts result from a long coevolution and can be considered mutualistic. Thus, the gut microbiota that colonizes us is responsible for many important functions in maintaining our health, and can be regarded as an additional organ of our body [1]. Therefore, a growing number of studies suggest that dysregulation of this gut microbiota plays a role in the development of many diseases including obesity [2].

The Intestinal Microbiota

While recent studies suggest that the fetus is not sterile, the colonization of the digestive tract really begins at birth. Mother's fecal microbiota is the main source of colonizing bacteria before other bacteria from food, environment or from contact with the parents contribute to the progressive complexity of the child's microbiota [3]. In adults, 1014 microbes live in our gut, as many as the number of eukaryotic cells constituting the human body. The vast majority of intestinal bacteria belong to three phyla: Firmicutes, Bacteroidetes and Actinobacteria. Although a few species constitute a phylogenetic core shared by the human population [4], most of the microbes composing the gut microbiota are specific to each individual. Therefore, it may contribute to modulate the susceptibility of individuals to disease development. The influence of the gut microbiota on its host has particularly been demonstrated through the study of animals devoid of a microbiota (germ-free animals). Recently, studies involving germ-free rodents revealed the role of the gut microbiota in the development of an increasing number of disorders, including obesity.

Intestinal Microbiota and Obesity

Although it was first revealed in 1983 that germ-free rodents needed 30% more calories to maintain their body weight [5], the hypothesis of a contribution of the gut microbiota in obesity has been proposed twenty years later only. It was first shown that germ-free mice had less fat than conventional ones of the same age and strain. Strikingly, the colonization of these germ-free mice with a gut microbiota resulted in a 60% increase in body fat despite reduction in food intake [6]. Subsequently, it was shown that the germ-free mice are resistant to obesity and insulin resistance induced by a high fat diet [7,8]. Moreover, these germ-free mice have less free fatty acids, triglycerides and cholesterol in the blood, and less triglyceride but more cholesterol in the liver. It has been also observed that genetically obese (ob/ob) mice harbored a different microbiota from that of wild type mice with an increased proportion of Firmicutes and a lower proportion of Bacteroidetes [9]. The next step was therefore to investigate whether these microbiota composition differences may play a causal role in the development of obesity. When transplanting the microbiota from lean and obese mice to germ-free mice, the increase in fat mass in recipient mice was higher with the "obese" microbiota [10].

In 2006, the first comparison of the gut microbiota from obese and lean people showed that obese subjects harbored a smaller proportion of Bacteroidetes and more Firmicutes than lean subjects [11], as was previously described in mice. Moreover, weight loss was found to restore a similar bacterial profile to that of lean subjects. However, more recent studies lead to conflicting conclusions pointing out at different groups of bacteria being associated with obesity [12]. Therefore, if a dysbiosis (imbalanced microbiota) is surely present in obese individuals, the data available to date do not establish a type of intestinal microbiota associated with obesity but rather suggest that a combination of environmental and genetic factors contribute to the establishment of a specific microbiota, which could then promote the development of obesity [13]. Furthermore, the presence of a dysbiosis cannot tell whether this imbalanced microbiota is the cause or the consequence of obesity. Causality has been then assessed by transplanting human gut microbiota to germ-free mice. The most convincing study was conducted with the microbiota of twins discordant for obesity. Mice that received the obese humans' microbes gained more body fat, put on more weight, and showed increased level of markers of metabolic disorders than mice that received the microbiota from the lean twin [14]. Strikingly, cohousing mice associated with the human obese or lean microbiota prevents increased adiposity, and it was further demonstrated that bacteria from the lean mice were able to invade the obese microbiota, the best colonizers among the lean communities belonging to the Bacteroidetes phylum. Whether these species were responsible for the lean-like state remains to be proven but it indicates that bacterial species within the human gut microbiota may have the capacity to protect from obesity. This opens the possibility to replace the intestinal microbiota of obese people by a microbiota that could limit the development of obesity. This experiment, called Fecal Microbiota Transplant (FMT), is applied for decades to patients with recurrent *Clostridium difficile* infections, responsible for life-threatening pseudomembranous colitis. Recently, FMT was applied for the first time in obese patients. Patients who received microbiota from lean donors had an increase in peripheral insulin sensitivity 6 weeks after FMT in comparison with peripheral insulin sensitivity prior to FMT, although the body weights and adiposity were not modified [15]. Therefore, if we need to further understand the mechanisms linking the gut microbiota and obesity, these intestinal bacteria should be taken into account to fully apprehend obesity and associated metabolic disorders [16]. Finally, new preventive and therapeutic strategies targeting the microbiota should emerge in the near future to help managing these pathologies.

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References

1. Gérard P, Bernalier-Donadille A. Les fonctions majeures du microbiote intestinal. Cahiers de Nutrition et de Diététique. 2007; 42: 28-36.
2. Clavel T, Desmarchelier C, Haller D, Gérard P, Rohn S, Lepage P, et al. Intestinal microbiota in metabolic diseases: from bacterial community structure and functions to species of pathophysiological relevance. Gut microbes. 2014; 5: 544-551.
3. Palmer C, Bik EM, DiGiulio DB, Relman DA, Brown PO. Development of the human infant intestinal microbiota. PLoS biology. 2007; 5: 177.
4. Tap J, Mondot S, Levenez F, Pelletier E, Caron C, Furet JP, et al. Towards the human intestinal microbiota phylogenetic core. Environ Microbiol. 2009; 11: 2574-2584.
5. Wostmann BS, Larkin C, Moriarty A, Bruckner-Kardoss E. Dietary intake, energy metabolism, and excretory losses of adult male germfree Wistar rats. Laboratory animal science. 1983; 33: 46-50.
6. Backhed F, Ding H, Wang T, Hooper LV, Koh GY, Nagy A, et al. The gut microbiota as an environmental factor that regulates fat storage. Proc Natl Acad Sci USA. 2004; 101: 15718-15723.
7. Backhed F, Manchester JK, Semenkovich CF, Gordon JI. Mechanisms underlying the resistance to diet-induced obesity in germ-free mice. Proc Natl Acad Sci USA. 2007; 104: 979-984.
8. Rabot S, Membrez M, Bruneau A, Gérard P, Harach T, Moser M, et al. Germ-free C57BL/6J mice are resistant to high-fat-diet-induced insulin resistance and have altered cholesterol metabolism. Faseb J. 2010; 24: 4948-4959.
9. Ley RE, Backhed F, Turnbaugh P, Lozupone CA, Knight RD, Gordon JI. Obesity alters gut microbial ecology. Proc Natl Acad Sci USA. 2005; 102: 11070-11075.
10. Turnbaugh PJ, Ley RE, Mahowald MA, Magrini V, Mardis ER, Gordon JI. An obesity-associated gut microbiome with increased capacity for energy harvest. Nature. 2006; 444: 1027-1031.
11. Ley RE, Turnbaugh PJ, Klein S, Gordon JI. Microbial ecology: human gut microbes associated with obesity. Nature. 2006; 444: 1022-1023.
12. Duca F, Gérard P, Covasa M, Lepage P. Metabolic interplay between gut bacteria and their host. Frontiers of hormone research. 2014; 42: 73-82.
13. Gérard P. Gut microbiota and obesity. Cell Mol Life Sci. 2016; 73: 147-162.
14. Ridaura VK, Faith JJ, Rey FE, Cheng J, Duncan AE, Kau AL, et al. Gut microbiota from twins discordant for obesity modulate metabolism in mice. Science. 2013; 341: 1241214.
15. Vrieze A, Van Nood E, Holleman F, Salojärvi J, Kootte RS, Bartelsman JF, et al. Transfer of intestinal microbiota from lean donors increases insulin sensitivity in individuals with metabolic syndrome. Gastroenterology. 2012; 143: 913-916.
16. Dhurandhar NV, Geurts L, Atkinson RL, Casteilla L, Clement K, Gerard P, et al. Harnessing the beneficial properties of adipogenic microbes for improving human health. Obesity reviews: an official journal of the International Association for the Study of Obesity. 2013; 14: 721-735.

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