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Review

The effect of diet on the fluctuations of human gut microbiota

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Abstract: It was previously thought that the establishment of the gut microbiota was completed within the first two years of life, and this community maintains fairly stable throughout the adult lifetime thereafter. However, recent evidence shows that the gut microbiota composition is constantly changing in the gut environment and is heavily influenced by diet. The individual differences responding to diets would root on the fluctuations of gut microbiota if dietary fluctuations affect the composition of gut microbiota so significantly.

Keywords: Gut microbiota, dietary intervention; dietary patterns.

1. INTRODUCTION

The gut microbiota, known to be an enormous community of trillions of microbes, has co-evolved with the human host [1]. Given the intimate and complex interactions between gut microbiota and its host, it is not surprising that the gut microbiota plays many determinant roles in the metabolic activities of human to affect various traits and diseases [2, 3]. Indeed, the complex interaction of gut microorganisms shapes the metabolic environment rich in enzymes to modulate nutrient metabolism and energy balance. Therefore, the stability and dynamics of the gut microbiota will have, not only local but also systemic effects that may determine the health and well-being of the host [4]. Current opinion suggests that the complete establishment of the gut microbiota that is considered as a profile characteristic of adult microbiota takes the first two years of life typically and once this process completed, the community structure of the gut microbiota maintains relatively stable throughout the lifetime of an individual [5, 6]. However, recent papers demonstrated that the composition of gut microbiota is changing, and the fluctuations of the gut microbiota might occur as a result of its interactions with the surrounding environment [7]. Considering the environmental factors shaping the gut microbiota composition through the human lifetime, diet represents one of the most powerful factors to consider.

2. DIET AS AN IMPORTANT MODULATOR OF THE GUT MICROBIOTA THROUGHOUT LIFE

The gut microbial community develops rapidly at birth and fluctuates widely. The evolution of this maturation process of gut microbiota is strongly affected by diet in each life stage. At the beginning of life, the first food introduced to babies mainly modulates the gut microbial establishment. While lactose rich and oligosaccharides components of human breast milk orients microbiota composition directly by encouraging the colonization of human milk oligosaccharide-utilizing bacteria such as *Bifidobacterium* [8]: the formula milk with an abundance of long-chained fatty acids increases *Enterobacteriaceae, Coriobacteriaceae*, and *Enterococcaceae* within the first day of life [9]. Once the solid foods are initiated, the gut microbial community changes towards becoming more adult-like, that is an immensely diverse ecosystem. Diet has profound impacts on shaping the microbiota community in adults over other possible variables such as geography [10], climate [11], and physiological states, etc. It is clear that the long-term consumption of different dietary patterns such as the plant-based diet or animal based diet shapes different microbiota at various levels in the taxonomic hierarchy of gut microbiota structure [12]. Individuals consuming a high-fiber diet have higher Bacteroidetes/Firmicutes ratio in their gut microbiota than did groups consuming a high-fat, high-protein diet.

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Furthermore, food constituents which are known as materials for gut microbial metabolism are an important determinant of promoting or inhibiting for specific enterotypes. The main enterotypes of gut microbiota include *Bacteroides, Prebotella*, and *Ruminococcus*. They have been associated with some partial aspects of nutrients intake, like as Prevotella with carbohydrates and simple sugars, Bacteroides with saturated fats, amino acids and proteins [12]. It has been proved that one enterotype dominated depending on the diet, the alteration of diet resulted in a significant change in the numbers of bacterial species [13]. Numerous studies have shown that the differences in the relative proportions of the dietary patterns, as well as the differences in food components, affects the human gut microbiome. Dietary carbohydrates, mainly plant origins such as fruits, vegetables, and grain, containing the rich of polysaccharides and oligosaccharides that normally provide the materials to microbial fermentation activities in the large intestine [14]. Because each gut microbial species contains a range of genomes involved in specific enzymes in lipid, protein, and carbohydrate metabolism [15], increased consumption of fermentable dietary carbohydrate might be expected to influence on both the activity and the abundance of the bacterial groups, especially the carbohydrate-degrading bacteria. Clearly, the plant-based diet is very rich in dietary fiber including resistant starch, non-starch polysaccharides, and inulin that would promote the increasing proportion of carbohydrate-degrading microbiota. These bacteria such as *Prevotella, Roseburia, Eubacterium rectale*, and *Ruminococus bromii* possess numerous enzymes involved in the hydrolysis of carbohydrate including cellulose, glycosidase, amylase, glycosidase, or beta-galactosidase [16]. On the other hand, the animal-based diet that is high in protein and fat stimulates the growth of bile-tolerant bacteria (*Alistipes, Bilophila*, and *Bacteroides*) due to increased chylomicron and bile acids, the rich in saturated fats trigger the growth of *Bacteroides* enterotypes and the high protein constituents correlated to the decrease in *Roseburia/ Eubacterium* population [17]. Thus, this could partly explain why geography is also associated with the different structure of the microbial community because the population will consume consistently different dietary regimens due to different geographic areas. Additionally, the alteration of food structure, which is mostly affected by the reduced chewing and swallowing ability tends to modify Firmicutes to Bacteroidetes ratio in gut microbiota with the higher proportion of phylum Bacteroidetes in the elderly in comparison with the abundance of phylum Firmicutes in adults [18].

3. THE INDIV IDUAL DIFFERENCES RESPONDING TO DIETS WOULD ROOT ON THE FLUCTUATIONS OF GUT MICROBIOTA

The composition and diversity of gut microbiota have the different aspects of limited or sufficient effectiveness in impacting human health and the individual diversity of gut microbiota provides the different effects in digesting and absorbing the energy and nutrients, which results in individual differences responding to diets [7]. Therefore, the clustering structure began to shift within individuals, with some genera becoming more common and others less common. Previous studies showed that individuals whose diet found more in plant origins such as fruits, vegetables, grain tended to have more Prevotella cluster in their flora, whereas Bacteroides became more prevalent in others who consumed more the foods of animal origins [12]. Indeed, the dietary impact could partly explain the tendency in structuring the microbial community. Interestingly, the rapid responses of gut microbiota to diet were revealed in recent studies in which microbiota composition is promptly affected by the dietary fluctuations within a day, even by cyclical shifts in daily feeding or fasting [17]. Thus, the microbial community in the gut is well adapted to increase specific genus in the presence of food constituents in various dietary.

4. CONCLUSION AND FUTURE PERSPECTIVE

Alterations in the relative abundance of the gut microbial structure with dietary intervention demonstrated that the dietary habits changed extensively human gut microbiota. Therefore, the sensitivity of the gut microbiota to different dietary regimens could inform that diet is an important modulator of human gut microbiota. Having suggested that the gut microbiota is a highly dynamic ecology, more integrative studies are needed to understand why it varies, so that this knowledge can support interpreting clinical results. Therefore, dietary interventions are probably controlled factors that potentially modify abnormal gut microbiota, known as gut dysbiosis, in numerous microbiota-related gastrointestinal diseases such as diarrhea condition, inflammatory bowel diseases. The sensitivity of the gut microbiota to environmental factors, especially diet, will develop microbiota-based therapeutic strategies for preventing or treating human diseases. On the other hand, this study supports the possibility that the gut habitat itself may select for specific ratios of divisions. Taken together, our review strongly argues for that there changes that take place constantly in the gut environment as well as suggests a potential application of dietary interventions for modifying the composition of gut microbiota that is related to numerous diseases.

CONFLICT OF INTEREST

The authors declare no conflicts of interest.

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