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Research Article

Dietary Fiber's Effect on the Micro Biota in the Gut in Host Health and Disease

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Abstract

Food is a fundamental requirement for our survival and health. However, the symbiotic microbial communities that populate the digestive tract the gut micro biota are also modulated and supported by diet, which is essential for human growth, reproduction, and health. Our food's type, quality, and origin influence our gut microbes' composition and function, influencing interactions between hosts and microbes. We will focus on dietary fibers in this review because they directly interact with microbes in gut and cause production of important metabolites like short chain fatty acids. We will also talk about how dietary fiber affects the ecology of microbes in gut and how it affects health of host.

Keywords: Microbial communities, Symbiotic, Microbes, Dietary fibers, Short chain fatty acids, Microbial ecology

INTRODUCTION

There are trillions of microbes in our gut that are necessary for the development and physiology of host. These microbes come from all kingdoms of life. This "gut microbiota" is a complex community that works with host and each other to control biological processes that are important to health. Our comprehension of the biological functions that gut micro biome plays, such as influencing juvenile growth, immune system maturation, and glucose and lipid metabolism modulation, has significantly increased over past ten years. Microbiome plays a role in the homeostatic regulation of various body tissues. Nevertheless, despite the fact that the overall relationship between humans and their micro biota can be described as a mutualistic symbiosis, eubiosis, which refers to a healthy balance of the microbes in gut, can be disrupted, causing a variety of chronic diseases with an underlying inflammation condition (Andersen CJ, 2016).

As needs be, the low admission of dietary filaments and expanded measures of fat and sugar in our food, regular for a Westernized way of life and sustenance, may to a limited extent contribute to exhaustion of explicit bacterial taxa. These changes may cause dysfunctions, which may increase the risk of developing chronic inflammatory diseases like IBD (Intestinal Bowel Disease), Colorectal Cancer (CRC), allergies, autoimmune diseases, and obesity. By specifically focusing on the mechanisms by which a low fiber diet disrupts the microbial ecosystem and leads to a predisposition to chronic inflammatory diseases, we will discuss how dietary fiber impacts the gut microbial ecology, host physiology, and health in this section (Aune D, 2016).

DISCUSSION

Effects of dietary fiber on the gut micro biome

Gut micro biota composition, diversity, and richness are significantly influenced by diet. Various parts of the eating regimen will shape the stomach. Bacterial networks in a period subordinate way. So called entero types are associated with long term dietary patterns, particularly the consumption of protein and animal fat (Bacteroides) rather than carbohydrates or plant based foods (Prevotella).This disparity in the ratio of Prevotella to Bacteroides also existed between industrialized and non industrialized human populations. This suggests that these bacterial populations are influenced by long term diet differences, such as meat (which drives Bacteroides in the West) and dietary fiber (which drives Prevotella in non Western populations).

Contrasting stomach micro biota of youngster's from provincial versus metropolitan (Italy) people group mirrored the effect of diet on the micro biome. I was found the composition of the gut micro biota was significantly different in the two groups after weaning. In BF children, the ability of these individuals to degrade complex carbohydrates was reflected by a significant increase in the abundance of bacteria from the genera Prevotella and Xylanibacter associated with higher levels of fecal SCFAs (B€ackhed F et al., 2014) (Baye K, 2017).

As the gut bacterial communities of BF children living in urban, as opposed to rural, areas of BF became more similar to those of Italian children; these differences are independent of ethnicity. At the point when individuals move to metropolitan regions, they are presented to a Westernized way of life, remembering admittance to food rich for fat and straight forward sugars. Children in rural areas have a bacterial reservoir (enriched in Prevotella, Treponema, and Succinivibrio) adapted for fiber and carbohydrate fermentation from vegetables, whereas children in urbanized areas of BF have bacteria that are better suited to metabolizing animal protein, fat, and sugar rich foods. Intriguingly, the microbial communities of BF children living in urban areas were comparable to those of Italian children, demonstrating the importance of the diet regardless of the host's genetic makeup. A research done by a group of scientists lends credence to these findings that demonstrated hunter gatherers have higher levels of microbial biodiversity and richness than Italian urban controls. Unexpectedly, these individuals lacked the Actino bacteria phylum, including low levels of Bifid bacterium, and their gut microbiota contained more Bacteroidetes than Firmicutes. Interestingly, while the Italian cohort had more butyrate, SCFA production in Hadza was characterized by higher propionate concentrations (Beaugerie L, 2015) (Belcheva A, 2014).

Bacteria's food webs are made of fiber

There are a few consistent features in the way that dietary fiber affects the composition of the microbiota. First, nondigestible carbohydrates only affect a small number of taxa in humans, regardless of whether they are considered prebiotics. Second, specific species account for more than 30% of the total sequences obtained by amplicon sequencing of the fecal microbiota, indicating that the induced changes can be significant. But these changes only last as long as the substrate is used. Thirdly the microbial response to dietary fiber is highly individual. It is still unclear why this individuality exists. Keystone species may be absent from individuals or lack strains that can utilize a particular substrate through enzymatic means (Bergman CJ, 1997).

The local advantage of fiber consumption for IBD and CRC

Westernization of diet and decreased gut bacterial diversity, particularly in terms of butyrate producing bacteria, have been linked to an increase in IBD prevalence in western nations. The effects of 40 distinct diets on mice and found that demonstrated that the development of colitis was affected in different ways by fiber and protein in the diet. In a similar vein, found that the proportion of fiber in the diet that contributed to the development of DSS-induced colitis in mice. Fibers may increase SCFA levels in the feces, particularly butyrate, which is known to have anti-inflammatory properties and may work through GPR43 .CRC, the third most common cancer, can result from IBD. Genetic and environmental factors, such as eating habits, smoking, and physical activity, are linked to CRC, and butyrate creating microbes are diminished in CRC patients contrasted with sound workers (Bernstein H, 2015).

Consuming less fiber in one's diet is linked to an increased risk of CRC. As a result, it should not come as a surprise that the Food and Drug Administration (FDA) has approved health claims that low-fat, high-fiber diets high in vegetables, fruits, and grains may lower the risk of developing certain types of cancer. A diet that increased dietary fibers in African Americans also altered the micro biome and increased butyrogenesis, lowering biomarkers of cancer risk (Berthon BS, 2013).

Dietary fibers have an independent effect on SCFA

The fermentation of fibers into SCFAs has been the primary focus of this review thus far. However, it is essential to note that microbial metabolism of fibers also has additional effects. Ferulic Acid (FA) is a phenolic compound that contributes to the rigidity and strength of plant cell walls. Bacteria like L. fermentum NCIMB 5221 with the FA esterase gene release FA through microbial metabolism of dietary fibers, such as cereal bran. FA can either act locally in the digestive tract to change the physiology of the gut or move freely into the bloodstream to change the health of the whole body. FA has antioxidant and anti-inflammatory properties, so it could be used as a treatment for cancer, obesity, diabetes, neuro degeneration, and other chronic diseases. In Alzheimer's disease models, FA administration was found to prevent antibiotic related toxicity and stimulates neurogenesis in corticosterone-treated mice. FA treatment reduced pro inflammatory cytokines and increased IL-10 in a model of ulcerative colitis, demonstrating its anti inflammatory properties. Additionally, diet induced obesity can be avoided with FA, and it works to prevent diabetes: Diabetic rats treated with this compound had their blood sugar and insulin levels returned to normal (Bindels LB, 2015).

CONCLUSION

In conclusion, dietary fibers are important ancestral compounds that keep gut ecology alive by controlling host physiology and macronutrients. The next challenge to significantly impact gut micro biota associated human diseases will be screening novel fibers, both those extracted and purified from food and those selectively modified or synthesized, for their potential as next generation prebiotics and defining effective strategies to reintroduce a high amount of fibers with the goal of replenishing the gut micro biome with essential missing microbes. Finally, a personalized nutrition strategy that targets and reduces the incidence of chronic inflammation diseases will benefit from a better understanding of the interactions between diet and micro biota.

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CONFLICT OF INTEREST

None

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