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THE IMPACT OF CHIA FIBER ON A HEALTHY GUT MICROBIOTA

New findings about the gut microbiota and its interaction with the host's metabolic regulation have emerged during the last few decades. Metabolic diseases like type 2 diabetes (T2D) and cardiovascular diseases (CVD) are among the most important public health challenges in the world today [1]. Epidemiological studies have linked a high fiber intake to a reduced risk of T2D and CVD [2,3]. Inflammatory and metabolic changes induced by the gut microbiome are hypothesized to play a role in developing metabolic diseases such as T2D, CVD, and obesity [4,5,6,7].

In humans, the gut microbiota has evolved through a symbiotic relationship. It offers the host benefits thanks to the protection it provides against pathogens. It also maintains intestinal barrier integrity, contributes to nutrient production, and produces metabolites such as short-chain fatty acids (SCFA) [8,9]. A balanced bacterial composition is important for maintaining intestinal immunity and homeostasis [27]. Dietary components, including fiber, may influence bacterial composition, microbial-derived metabolites, and host metabolism [10,11].

Dietary fibers are either polysaccharides with a minimum of 10 monomeric units (MU)) or oligosaccharides containing between 3–9 MU. A further classification of dietary fiber is often based on its water solubility, viscosity, and fermentability [12,13,14]. Soluble fiber is typically fermented to SCFA, mainly acetate, propionate, and butyrate by the intestinal microbiota. Recent research has shown that SCFA has vital roles in regulating host metabolism [11]. SCFA are transported into the systemic circulation and may directly affect host metabolism via binding to G-protein coupled receptors (GPR) [15,16]. These receptors are expressed in several metabolically active tissues and are involved in responses to and regulation of many processes, including glucose homeostasis and lipid metabolism [17,18].

Evidence suggests that SCFA may act as histone deacetylase inhibitors, thereby modulating gene expression [11]. Furthermore, SCFA are an essential energy source for the intestinal epithelial cells and strengthen the gut barrier function [10,19]. Improved gut barrier function reduces the penetration of microbes and microbial molecules into the blood circulatory system, thereby reducing the immune responses that are associated with metabolic diseases [20]. There is also evidence that other microbial-produced metabolites may affect metabolic regulation. Indole and enterolactone are products of the microbial conversion of dietary tryptophan and lignan, respectively. Both are associated with increased fiber intake and a lower risk of T2D [21,22].

A recent study has reported the effect of soluble chia fiber on gut microbiota [28]. The good news is that 1) human digestive enzymes do not hydrolyze the chia soluble fiber, but gut microbes act upon it, producing metabolites like short-chain fatty acids. And 2), the study reports some "probiotic strains" have significantly increased after intake of chia fiber, including Enterococcus and Lactobacillus. This finding is in line with previous studies and indicates that certain types of soluble fibers, including inulin, beta-glucan, and GOS, can increase the number of "probiotic strains" [23,24,25,26].

Furthermore, after Chia fiber intake, there were evident increases in stool and plasma SCFA. SCFA derived from microbial fermentation of dietary fiber has recently been linked to beneficial effects on host metabolic regulation [11]. It is also important to consider the impact of functional redundancy in the gut; changes in the bacterial composition will not always translate into functional changes.

This is the first study that describes the prebiotic effect on the gut microbiota of chia fiber. There is a limited number on the relation between dietary fiber, production of SCFA, and metabolic regulation requires further investigation.

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