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The Gut Micro Biome and Mucosal Immune System Interaction

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The gut micro biota, the largest symbiotic ecosystem with the host, has been shown to play important roles in maintaining intestinal homeostasis. Symbiosis of the gut micro biome is caused by the imbalance between the commensal and pathogenic micro biomes. The commensal micro biome regulates the maturation of the mucosal immune system, while the pathogenic micro biome causes immunity dysfunction, resulting in disease development. The gut mucosal system, which consists of lymph nodes, lamina propria and epithelial cells, constitutes a protective barrier for the integrity of the intestinal tract. The composition of the gut micro biota is under the surveillance of the normal mucosal immune system. Inflammation, which is caused by abnormal immune responses, influences the balance of the gut micro biome, resulting in intestinal diseases. In this review, we briefly outlined the interaction between the gut micro biota and the immune system and provided a reference for future studies [1].

The mammalian gut contains a microbial community, defined as the micro biome, which includes bacteria, viruses, fungi, etc. Microbial genome sequences contain 3 × 106 genes, which is approximately 150-fold the length of the human genome. In recent decades, next generation sequencing technology has contributed to understanding the intricate relationship between the micro biome and related diseases. 16S rRNA sequencing results showed that Formicates and Bacteroidetes make up approximately 92% of the human micro biome. Gut micro biota include 1,000 to 1,500 bacterial species; however, an individual contains only approximately 160 bacterial species, indicating that the composition of the micro biome is substantially different between individuals and is said to environmental changes and genetic inheritance. Environmental factors play a very important role in the gut micro biome. Even mice with an equivalent genotype housed in separate cages within an equivalent facility show different micro biota compositions. The composition of the mouse gut micro biome is especially influenced by variations in diet, age and inflammation. A review of studies also showed that the composition of the gut micro biome in an eczema population is influenced by environmental factors, including pregnancy duration, delivery method, feeding type, rearing style, number of siblings, lifestyle, etc. The intestinal micro biome, a microbial organ that is shaped in combination with the host's genotype, responds to the growth process and environmental exposure. The coordinated interactions between intestinal microbial populations contribute to maintaining intestinal homeostasis and play a crucial role within the immune process [2].

The immune system is regulated by immune organs, immune cells, and soluble cytokines and cell receptors. The intestine mucosal system consists of three different mucosal lymphoid structures: Peyer's patches, the lamina propria and therefore the epithelia.

The mucus layer on the surface of epithelial cells is that the first line of defense within the organism's physiological barrier. In the intestine epithelia, Paneth cells located at the bottom of crypts are capable of secreting antimicrobial peptides (AMPs) in response to bacteria or pathogens within the gut lumen and contribute to intestinal innate host defense. The AMPs include α-defensins (HD5 and HD6 in humans and cryptdins in mice), Reg III and lysozymes, etc. The mucus layer and AMPs constitute the mucosal barrier to stop the invasion of symbiotic bacteria. Pioneering studies have discovered an important role for AMPs in the host mucosal defense, indicating that they directly affect the micro biome in the intestinal lumen. AMPs can exert antimicrobial activities to kill microorganisms in vitro. Reg III specifically targets Gram-positive bacteria. Additionally, bacteria and bacterial antigens increased the expression of Reg III γ, crypt din, and human β-defensin 2. Moreover, Reg III β was significantly increased, and it was released into the gut lumen in response to infection. Reg III γ played a vital role in segregating the bacteria from the intestinal epithelium, and the absence of Reg III γ led to increased bacteria colonization on the epithelium and the activation of adaptive immunity [3].

Over the course of evolution, the micro biome maintains symbiosis with the gut environment. The human gut provides nutrients and a breeding environment for intestinal micro flora; in turn, intestinal microflora assists in carbohydrate fermentation and synthesizes vitamins by reducing intestinal permeability and increasing the epithelial defense reaction to make a mucosal barrier. The intestinal mucosal immune system constitutes the largest immune component in vertebrates, functioning closely with the intestinal micro biome. The balance of the intestinal mucosa system plays a key role in host homeostasis and defense. Studies on GF mice suggested that the intestinal micro biome plays a vital role in the formation of mucosal immunity. Compared with specific pathogen free (SPF) animals, GF animals produce fewer IELs and have significantly reduced IgA-secreting plasma cells in the lamina propria, as well as fewer Trigs. Angiogenin-4 (Ang4) may be a class of microbicidal proteins in Paneth cells and may be secreted into the gut lumen against microbes. Real-time quantitative RT-PCR suggested that the mRNA expression level of Ang4 markedly decreased in GF mice compared with conventional mice. This result indicates that gut micro biota is required for mucosal immunity. Additionally, Peyer's patches in GF mice contain a smaller germinal center than in conventional mice. The intestinal mucosa is that the main site for micro biome-host interactions [4].

In summary, intestinal micro biota coordinates to shape host immunity and contribute to maintaining intestinal homeostasis and inhibiting inflammation. Recent data have shown the pivotal role of intestinal micro biota in mucosal immunity. An impaired interaction between intestinal micro biota and mucosal immune system is associated with the pathogenesis of inflammatory diseases, such as IBD,

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RA, SLE, AS, etc., and it highlights the importance of exploring the function of micro biota in such diseases. Thus, intestinal micro biota has become effective targets for the development of new diagnostic methods. Balancing the gut micro biome will likely represent an efficient treatment for chronic inflammatory diseases [5].

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Conflict of interest

None

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