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Gut Microbiota, Digestion, and Immunity Interaction: A Review

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ABSTRACT

The gut microbiome is a plentiful and a diversity of microbes community that live in the gut and play a critical role in the host's physiology, such as food metabolism, digestion, immunity, brain development, and behaviour. Their diversity is very important to the body; however it is always changed by the environmental factors. Any change in the variation and composition of the microbiome can have consequent impacts on the host's health. The interaction between gut microbiota, external factors, host physiology, development, and infectious diseases is really complicated. For example, food can modulate the gut microbiota at the same time the food is the main source of microbial metabolites that play an essential role in modulating immunity, and the regulation of immunity by the microbiome influences brain development and vice versa. In conclusion, the understanding of various pathways in which gut microbiome could affect and affected by digestion and immunity offers new approaches to treat various immune and infectious diseases. Therefore, this review sheds the light on various interaction mechanisms between gut microbiome, food digestion, and immunity.

Keywords: Gut Microbiota; microbiome; Digestion; Local immunity; Systemic immunity

INTRODUCTION

The microbiome is defined as several of microorganisms such as bacteria, fungi, and viruses, that live in or on our body, especially in the gut or on the skin. The first exposure to microbes happens even when the baby is inside the uterus. This community of microbiome is dynamically changed in response to the external environmental factors. High diversity of microbiome is beneficial to human health. The number of microbiomse roughly equal to the number of human body cells. The majority of these microorganisms inhabits our intestinal tract. Although some of these microorganisms can cause diseases, others could be benefitial. In fact, surviving without an intestinal microbiome will be very difficult [1]. It was mentioned that our body's physiology, such as digestion, immunity, metabolism, development and even our behaviour can be influenced by our own microbiome [2].

Digestively, in the previous paragraph it was mentioned that gut microbiomes are dynamically changed. Diversity and modification in the gut microbiota start from the moment of birth, depending on nutrition, genetic, and environmental factors. The diversity and modification can influence the intestinal permeability, digestion, and metabolism [3]. A mix of microorganisms in the

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gut regulating the digestion via processing and absorbing several nutrients and metabolites, such as bile acids, lipids, amino acids (AAs), vitamins, and short-chain fatty acids (SCFAs) [2]**.** It was mentioned that the important sugars in breast milk are digested by *Bifidobacteria* bacteria that live in the babies' intestines [4]. While other bacteria can break down fibers to a short chain of fatty acid that could be benefitial to the gut [5]. Involving the gut microbiome to nutrients metabolism can affect several mechanisms, such as body immunity, nervous system regulation and neurological behaviour, protection from infectious diseases, as well as maintaining cholesterol balance and lipid level reduction [2,6]. Also It was observed that the bacteria in the gut of people who suffer from obesity differ from those without obesity. Particularly microbiome number, it was found that there is a low diversity in the number of gut bacteria in obese compared to lean twins [7].

Immunologically, it was mentioned there is a complicated interaction not only between the gut microbiome and the first protective line in the intestine, such as epithelial layer and local immune system in the mucosa, but also with systemic immunity [8]. The essential role of the microbiome in human health and diseases has been well highlighted by researcher over the past ten years. Moreover using of advanced and new technologies, such as advanced analytic techniques play an important role in discovering the relationship between the microbiome and gastrointestinal diseases. It was found that dysregulation of gut microbiome is significantly associated with bowel irritation syndrome, inflammation of bowel disease (IBD), celiac disease and colorectal cancer and many immune mediates diseases and central nervous system diseases reviewed by [9]. Furthermore, recently it was mentioned that the gut microbiome plays an important role in the development and modulation of host immune responses [10].

To sum up microbiota are communities of microorganisms that live in and on the human body. They dynamically shaped and modified from the first birth moment. Some of the microbiome are harmful, while others are benefit. Most of them habit in the gut and involved in the body physiology through different ways. This review comes to highlight the important role of the microbiome in food digestion and immunity that could be helped in finding new ways for treating different complicated metabolic and immunological diseases.

INTERACTION BETWEEN GUT MICROBIOTA AND FOOD DIGESTION

Previously mentioned that gut microbiota are involved in fibers degradation, anaerobic protein and peptide break down, carbohydrate fermentation , biosynthesis of essential vitamins such as B and k, amino acid carboxylation, decreasing lipid level and cholesterol level reduction, foreign substance degradation for providing energy [11].

This section will summarize the interaction of gut microbiota in the processing and metabolism of various dietary molecules such as carbohydrates, fibers, vitamins, proteins and fats.

The Role of Gut Microbiota in Degradation of Carbohydrates, Fibers, Vitamins

Cellulose or wheat bran are dietary fibers that undigested by humans' enzymes [12]. However, gut microbiota plays an important role in the degradation of non-digestible carbohydrates anaerobically. This occurs via producing gas and short chain fatty acids (SCFAs) such as acetate, propionate, and butyrate by different pathways in the lumen. (SCFAs) play a critical role as antioxidants, anticancer, anti-inflammation and as an allergic protectors. In addition to degrading plant fiber polysaccharides, SCFAs producer cooperate with fructose and glucose specialized

fermenter bacteria called Bifidobacterium spp in generating SCFAs and gas. Produced SCFAs and gas are used as carbon and energy sources by bacteria that reduced sulphate and produced methane [13].

The main bacteria that involved in the SCFAs degradation are Eubacterium, Roseburia, Faecalibacterium, and Lactobacillus spp. and Bifidobacterium spp. [14]. Moreover Faecalibacterium prausnitzii, Eubacterium rectale, Eubacterium hallii, and Ruminococcus bromii bacteria that lived in colon play an important role in the metabolism of some fibers soluble in water to SCFAs and lactic acid . These metabolites serve as a protector against colon cancer [13].

Another evidence that gut microbiota involved in food digestion is that depending their diversity on the type of diet reviewed by [15]. The reshaping of the gut microbiome was studied in the obese for 2 years compared to non-obese. The study showed that Bacteroides; Prevotella; Roseburia, Ruminococcus, Parabacteroides distasonis, and Faecalibacterium prausnitziithere which characterized by their activity to digest carbohydrate producing (SCFAs) are increased in the obese compared to non-obese [6]. Moreover it was observed there is a decreasing in the gut microbiota Firmicutes and Bacteroidetes and increasing in the Proteobacteria in patients with inflammatory bowel diseases (IBD) which leads to decreasing the level of (butyrate) SCFAs. In addition, decreasing level of F. prausnitzii and butyrate in recurrent Crohn's disease patients may be indicated to the dysbacteriosis that make people susceptible to the IBD. Recently it was suggested that an increased in the F. prausnitzii level among the obese population could be a microbial indication of obesity. In fact, the modulation of *F. prausnitzii* in the gut and its usage as bio-indication for prediction and diagnosis intestinal disease has been discussed[13].

However, obesity could be correlated with a high consumption of high carbohydrate diet (HCD), that associated with decreasing of butyrate-producer bacteria and a remarkable changing in the ratio of Firmicutes/Bacteroidetes bacteria. Also as in type2 diabetes the disruption of gut microbiota has been represented in late pregnancy [16]. Fibers (indigestible carbohydrates) are very low in the HCD. Physiologically fibers are very beneficial to the body. For example they stimulate the production of incretin; provide energy for microbes in the colon that promote normal bowel movements; and produce SCFAs [17].

While food provides vitamins that are absorbed in the small intestine, some vitamins are produced in large intestine by a major microbe such as vitamin de novo, that are produced by Bacteroides spp as water-soluble B-vitamins. Microbial vitamins absorbed via special carrier system except vitamin cobalamin. They are played an important role as coenzymes in a wide range of biological reactions such as vitamin K2, as well as water-soluble B-vitamins such as folic acid, niacin, biotin, pantothenic acid, cobalamin, pyridoxine, riboflavin, and thiamine. Therefore gut microbiota synthesized them [18].interestingly it was observed there is an association between the high microbial diversity and abundance of bacteria produced lactic acid, Bifidobacterium and Lactobacillus with the consumption of plants for long period and calories restrictions. This could be due to polyphenols. In addition to abundance of polyphenols in plant produces by gut bacteria as derivative of food metabolism and converted into derivatives of aromatic SCFAs as phenylacetate or phenylbutyrate [19]. Polyphenols and SCFAs play a critical role in immunity and preventing and treating of several diseases reviewed by [15].

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The Role of Gut Microbiome in Degradation of Proteins and Fat

It was observed that consumption of high protein food makes shifting from carbohydrates to the protein fermentation by gut microbiota [20]. This causes a decreasing in the beneficial microbes such as butyrate producers, via inducing changes. There is sufficient energy and poor fibers in the animal diet. So the microbes that cannot digest fibers depend on full energy in the fat, protein and sugar for their growing [13].

On the other hand, although the ketogenic diet, which is rich with fat and proteins, causes a reduction in the gut microbes diversity but an increase in the SCFAs producer such as Akkermansia muciniphila, Parabacteroides, and Lactobacillus reviewed by [15].

One of the metabolites produced of protein catabolism by bacteria is branched-chain fatty acids (BCFAs), indoles, and phenols. Human enzymes are able to produce these metabolites. Therefore generation of them considered an indication to the protein fermentation in the colon [21].

Moreover, it was observed that some specific lineages of bacteria have disappeared due to the consumption of diet poor with carbohydrates that used by microbiota such as Western diet. This could lead to increasing the risk of wide range diseases [22].

A higher amount of choline and L-carnitine in the animal diet was converted to the trimethylamine (TMA) by several gut microbes. This increases the risk factor of cardiovascular diseases. Also it was found there is an association between consuming of saturated lipids and the occurrence of white adipose tissue growing (WAT) and inflammation, which happen due to inducing increasing macrophage and adverse consequences in this tissue by gut microbiome molecular mechanisms [23]. There are different types of saturated lipid such as lard rich in saturated lipids or fish oil, or rich in polyunsaturated lipids. Depending on the type of lipid the response of gut microbe varied. In a study on mice, it was observed that consuming of lard causes an increase in the Bacteroides, Turicibacter, and Bilophila in mice fed lard. Whereas consumption of fish oil cause an increase in other bacterial spp such as Actinobacteria, Lactobacillus, Streptococcus, Akkermansia muciniphila, Alphaproteobacteria, and Deltaproteobacteria [15,23]. Moreover mice fed high carbohydrate or obesity diet show an increase in A. muciniphila bacteria, which cause **i)** decreasing in gaining of fat mass and infiltrating of WAT macrophage, **(ii)** increasing gut barrier function, **(iii)** and increasing glucose metabolism [13]. Also it was reported that fermentation of amino acid by gut bacteria resulted in producing 4-ethylphenylsulfate (4EPS) and indolepyruvate, that inducing ASD in mice [6]. In addition there are several similar metabolites that used as marker of autism in the urine [13].

Also it was observed that using of Bacteroides fragilis orally in activating of maternal immune result in permeability improvement of the gut, modulation function and composition of gut microbes, improvement of communication deficiencies. This suggested the role of gut microbata and metabolismin formation behaviour [6].

Finally all low molecular weight metabolites such as s vitamins, polyamines, and SCFAs, as well as lipopolysaccharide (LPS) and peptidoglycan are generated by the gut microbiome. The interactions between these metabolites and microenvironment affect developing of normal behaviour and growth . Also these compounds can change the genome and their expression in the host cell , which alters the growth and cell function during human life [13].

INTERACTION BETWEEN GUT MICROBIOME AND HOST IMMUNITY

The immune system is an important for susceptibility, persistence, and clearance of infectious diseases, which lead to death in poor countries, infants and elderly. In addition to around 75% of immune cell in the intestine there is an interaction between intestinal microbiome and intestine. The interplay occurs via epithelial layer, and the local immune system in the mucosa. Moreover, gut microbiome interacts with the systemic immunity [8].

Interaction of the Gut Microbiota and Epithelial Barrier

There is a synergism interaction between multispecies of microbiomes and hosts [24,25]. Host provide the nutrition and home, while gut microbiome regulates several physiological host functions. Structure and function of intestinal microbial community can be disrupting by different factors that let opportunistic pathogens to colonize, growth and persist. However intestinal microbiota can overcome these pathogens through several mechanisms. Competition mechanism is one of them, in which there is a competition on resources, nutrition's and space between gut microbiota and infectious pathogens. Competition mechanism used to resist pathogens colonization. This mechanism occurs by continuous bacterial sensing to the environment, via employing the accumulation signalling molecules during microbial replication. This way called quorum sensing and by which commensal bacteria can monitor community density and adjust their gene expression [25]. Consequently, bacterial adherence, motility, intestinal density, and excretion of protective compounds are changed. As used quorum sensing by commensal bacteria to keep gut homeostasis, infectious pathogens use it to reduce immune responses and increase pathogenicity [24]. Diet, stress, and antibiotic and drug treatment can altered the community structure of gut microbiome or the composition of non-beneficial microbiota. Hence the overall dynamics between the microbiota and host are changed. Consequently, low-grade of inflammation, reduction of colonization resistance, and alteration infection susceptibility are resulted [8].

The gut epithelial layer is the next line in protection human from infectious pathogen after gut microbiota [26]. It acts as a barrier between the gut microbiome and the underlining tissue. It forms from one layer of cells, tightly that joined by protein complexes junction. Releasing toxins by certain bacteria can disrupt these protein junctions [25]. However, the epithelial barrier is lining with mucus that protect this layer from the invasion of bacteria, via preventing the direct interaction of the pathogens of mucosa and lumen with epithelia layer [24]. In addition, different antimicrobial molecules that produced by host such as IgA and defensins are stored in the mucus. Mucus produces and degrades via an intricate interaction between host and microbes, which regulated by recognizing of host to the molecular patterns of microbes and metabolites of bacteria. Therefore, mucus is susceptible to any change in the composition of gut microbiota. Any changes in the gut structure can alter the production and composition of the mucus, so that susceptibility to infection is increased [25].

Finally, constant immune signalling results from continuous interaction between the gut microbiota and intestinal epithelial layer [27]. In summary regulation of epithelial barrier integrity and permeability, as well as this immune signal, in the presence of beneficial and harmful microbiota, is an important for maintaining on the intestinal homeostasis. Therefore, any impairment occurred in this process inflammation and infection can be resulted.

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Interaction of Gut microbiota with Local Immune System

Immune system plays a critical role in the protection of human from diseases. Its involved two types of immunity these are innate and adaptive. Innate immunity includes several non-specific defence mechanisms such as skin, mucus membranes, enzymes, antimicrobial proteins, granulocytes cells, macrophages, and natural killer cells. Whereas adaptive immunity includes T- and B-lymphocytes, that provide specific protection against foreign antigens. Recognition of infectious agents inside the host cells occurs directly by T-cell, in addition to regulation of B-cells functions. This type of response called cellular immunity due to direct cell involvement, while recognition of specific antigens occurs by B-cells via secretion of specific antibodies and proteins. Due to the circulation of these proteins and antibodies in the fluid of the body this response is called humoral immunity [25].

Maintaining of the development and conformation of the gut microbiota means developing immune system and efficient immune response. This confirm by comparing free commensal microbiota mice with defined microflora mice and naturally growing animals, that all of them belongs to the same age, sex and strains. Using mice with defined microbiota provide a good an opportunity to study the effect of detected strains and microbial metabolites on intestinal homeostasis, local and systemic immunity [28]. This type of study highlights the essential role of innate immunity in the first recognizing of the gut microbiota and response to their metabolites. Single layer epithelial membrane is considered the first step of the innate immunity in the gut, which is directly exposed to the microbes and their product in the lumen. Recognition of microbes is critical to maintain the balance between host and microbes. This occurs via specific recognition receptors RRs. There are a large family of s these specific associated receptors that can recognize microbes extra and intra cellular such as Toll-like receptors (TLRs), C-type lectin receptors (CLRs), nucleotide binding oligomerization domain (NOD)-like receptors (NLRs), IL-1, and cytosolic sensors of DNA and RNA. Regulation of protective immune response occurs by chemokines and cytokines that are induced via RRs activation [29]. The inflammatory reactions and body immune response are regulated by proteins called nuclear factor-kappa-B proteins (NF-KBs). RRs, which are important in early immune response to bacterial invasion linked with NF-KBs via MYD88 molecules. These adapter molecules transport the signals from RRs to NF-KBs therefore any deficient in these molecules can affect the immunity and cause infectious diseases [30]. At the same time over activation of RRs can cause negative results, therefore responses of RRs are strictly controlled. Furthermore, one of the important innate immunity contributors is the antimicrobial peptides. Secretion of different bactericidal, anti-inflammatory, and anti-endotoxic peptides occurs by epithelial cells in the intestine [31]. These peptides play a crucial role in the limitation of pathogens interacted with the intestinal epithelium membrane. The secretion of these antimicrobial peptides can be inhibited by some microbes and elevated by other. Therefor the configuration of intestinal microbes is very important in the shaping of innate immunity.

Intestinal microbiota metabolites form another way for directing the immune response. A wide range of them shows a protective ability such as SCFAs that elevate the mucus production and secretion of antimicrobial peptides, in addition to stimulating the maturation and expansion of T-colonic cells that reduced the local inflammatory reactions against microbes. Also SCFAs can modulate colonic epithelial barrier and induced the proliferation and differentiation of intestinal cells consequently maintain on intestinal homeostasis in the colon. Moreover, SCFAs

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are essential for innate lymphoid cell (ILC3) proliferation and antimicrobial molecule production by epithelial cells [25].

Furthermore, essential receptor for maintaining intestinal homeostasis is aryl hydrocarbon receptor (AhR). This receptor is ligand by metabolites of SCFAs which is tryptophan and indoles. Therefore, if these metabolites lost inflammatory bowel disease can occurred [32].

Also, the derivatives of Bile acid activate farnesoid X receptor (FXR) and G protein-coupled bile acid receptor (TGR5) therefore they control on many host function and contribute to intestinal homeostasis. These derivatives are produced from the Bile acid due to the activity of bacterial enzymes called bile salt hydrolases (BSHs). Excessive loss of the genes expressed (BSHs) can be lead to f inflammatory bowel disease [33].

In summary the balance between microbiota, microbial metabolites, and host factors is an essential to mucosal homeostasis in the gut. And a tight physiological regulation of low-grade inflammation, optimal host defence results from the continuous between all these various aspects [34].

Interaction Between Gut Microbiota and Systemic Immunity.

Microbiome can condition systemic immunity via various stimuli these are metabolites, foreign molecular patterns, and antigens. Production of metabolites by microbiome in to circulation shows modulating ability to the innate and adaptive immune system functions [35]. In the mammalian host cells there are many systemic chemoreceptors that work as a network to sense microbial metabolites such as G protein-coupled receptors (GPCRs), nuclear receptors (NRs), and many other receptor systems, that can modulate systemic immune response [36]. The differentiation of T-cell to helper T-cell can be affects by metabolites of gut microbiota specifically SCFAs butyrate induce the modulation of T cells leading to inhibit of systemic inflammation development. In addition, this commensals product stimulates the differentiation of monocyte in the bone marrow to the tolerogenic phenotype. Furthermore, SCFAs pentanoate able to induce modulation of B cells and inhibit of Th17 cells generation. Moreover, microbial metabolites can regulate various immunological responses such as induction of Th17 cells expansion, elevation of intraepithelial CD4 + CD8αα + T cells, and major regulation of T cells by microbial ATP, products of breaking down tryptophan and polysaccharides from bacteria respectively. Consequently, the result of regulation ability of the microbiome is suppressor the inflammatory responses [25].

When commensal pathogens activate the memory T-cell and their transporting to the site of inflammation, play an essential role in the protection of the host from microbial infections [37]. Furthermore, commensals microbes have similar effect of specific toll-like receptor (TLR) in the protection of the host from bacterial infection, via active controlling on anti-inflammation mediator IL10. Also a variety of RRs, that sensitive to microbe-associated molecular patterns, are expressed by bone marrow [25]. For example, monocytes and macrophages, the form of trained immunity, are induced by the activation of CLR dectin-1 on stem cells [38].

In addition to all of the above, modulation of innate immunity also occurs by microflora signals via lymphoid stimulation in the spleen, regulation of migration and function of neutrophils, macrophage activation, and induction of the maturation of natural killer (NK) cells [25]. Also it was shown that inflammatory responses are regulated by specific bacterial species

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via reducing the levels of the specific anti-inflammatory steroid in the plasma membrane called corticosterone [39].

From the above, it's obvious that any an imbalance in the gut microflora can cause a reduction in the induction ability of local and systemic immune responses. Consequently, locally and distally inflammatory diseases are occurred specially via the airways infection. In fact, that an alteration in the commensal gut microbes due to antibiotics treatment can associate with developing of allergic airway disease, and increasing the risk of asthma development. Also the direct steering of innate and adaptive response by microbiota is important in the protection of the host from bacterial and viral respiratory infections. Migration of antigen-specific B cells from the mucosal gut to the site of infection via thoracic duct is another way by which gut situation influence respiratory disease. However, whether the changes in microbiota are a reason or result of lung diseases is undetermined, as in other field of microbiota research [25]. Finally, more researches are required to study the effects of gut microflora on lung diseases.

CONCLUSION

The research summarised first the responding mechanisms of the gut microbiome to the diet alteration, which facilitate the diversity of food. Diet is the most important factors that affect the gut microbiome shaping and diversity. Understanding dietary microbiome interaction provides a great promise for treating or prevention diseases –associated –microbiota. Second the interaction pathways between gut microbiome and local, innate and systemic immunity can be used to develop new strategies to prevent and treat infectious diseases. However, there are some challenges, such as personal variations in the microbiome and immunity between individuals as well as the ability of diet to induce changes in the microbiome.

Conflict of interests.

Non conflict of interest

References

[1] K. V. Johnson Gut microbiome composition and diversity are related to human personality traits." *Human microbiome journal* vol. 15, 2020: None. doi:10.1016/j.humic.2019.100069

[2] J. R. Brestoff, & D. Artis, "Commensal bacteria at the interface of host metabolism and the immune system." *Nature immunology,* vol. 14, no.7, pp. 676-684, 2013. doi:10.1038/ni.2640

[3] E.Z. Gomaa, "Human gut microbiota/microbiome in health and diseases: a review." *Antonie van Leeuwenhoek,* vol. 113, no. 12, pp. 2019-2040, 2020. doi:10.1007/s10482-020-01474-7

[4] S. Arboleya, C. Watkins, C. Stanton, & R. P. Ross, "Gut Bifidobacteria Populations in Human Health and Aging." *Frontiers in microbiology,* vol. 7, no. 1204, 19 Aug. 2016, doi:10.3389/fmicb.2016.01204

[5] J. Slavin, "Fiber and prebiotics: mechanisms and health benefits." *Nutrients,* vol. 5, no. 4, pp. 1417-1435, 22 Apr. 2013, doi:10.3390/nu5041417

[6] E. Y. Hsiao, S. W. McBride, S. Hsien, G. Sharon, & et al. "Microbiota modulate behavioral and physiological abnormalities associated with neurodevelopmental disorders." *Cell,* vol. 155, no. 7, pp. 1451-1463, 2013. doi:10.1016/j.cell.2013.11.024

[7] P. J. Turnbaugh, M. Hamady, T. Yatsunenko, B. L. Cantarel, & *et.al.*, "A core gut microbiome in obese and lean twins." *Nature,* vol. 457, no. 7228, pp. 480-484, 2009. doi:10.1038/nature07540

[8] Wiertsema, S. P., van Bergenhenegouwen, J., Garssen, J., & Knippels, L. M. J. "The Interplay between the Gut Microbiome and the Immune System in the Context of Infectious Diseases throughout Life

and the Role of Nutrition in Optimizing Treatment Strategies." *Nutrients* vol. 13,3 886. 9 Mar. 2021, doi:10.3390/nu13030886

[9] T. Choden, & N.A. Cohen, "The gut microbiome and the immune system". *Explor Med*., V.3, pp. 219–233, 2022. https://doi.org/10.37349/emed.2022.00087

[10] D. Zheng, T. Liwinski, & E. Elinav, "Interaction between microbiota and immunity in health and disease." *Cell research,* vol. 30, no. 6, pp. 492-506, 2020. doi:10.1038/s41422-020-0332-7

[11] M. Yadav, M. K. Verma, & N. S. Chauhan, "A review of metabolic potential of human gut microbiome in human nutrition." *Archives of microbiology,* vol. 200, no.2, pp. 203-217, 2018. doi:10.1007/s00203-017-1459-x

[12] J. M. Wong, R. de Souza, C. W. Kendall, A. Emam, & D. J. Jenkins, "Colonic health: fermentation and short chain fatty acids." *Journal of clinical gastroenterology* , vol. 40, no. 3, pp. 235-243, 2006. doi:10.1097/00004836-200603000-00015

[13] P. Vernocchi, F. Del Chierico, & L. Putignani, "Gut Microbiota Metabolism and Interaction with Food Components." *International journal of molecular sciences* vol. 21, no.10, pp. 3688. 23 May. 2020, doi:10.3390/ijms21103688

[14] J. Marchix, G. Goddard, & M. A. Helmrath, "Host-Gut Microbiota Crosstalk in Intestinal Adaptation." *Cellular and molecular gastroenterology and hepatology,* vol. 6, no. 2, pp. 149-162, 15 Feb. 2018, doi:10.1016/j.jcmgh.2018.01.024

[15] P. Vernocchi, F. Del Chierico, & L. Putignani, "Gut Microbiota Metabolism and Interaction with Food Components." *International journal of molecular sciences,* vol. 21, no. 10, pp. 3688, 23 May. 2020, doi:10.3390/ijms21103688

[16] M. K. W. Crusell, T. H. Hansen, T. Nielsen, K. H. Allin, & et al. "Gestational diabetes is associated with change in the gut microbiota composition in third trimester of pregnancy and postpartum." *Microbiome,* vol. 6, no. 1, pp. 89, 15 May. 2018, doi:10.1186/s40168-018-0472-x

[17] V. A. Mustad, D. T. T. Huynh, J. M. López-Pedrosa, C. Campoy, & Rueda, R. "The Role of Dietary Carbohydrates in Gestational Diabetes." *Nutrients,* vol. 12, no. 2, pp. 385, 31 Jan. 2020, doi:10.3390/nu12020385

[18] H. M. Said, & E. Nexo, "Gastrointestinal Handling of Water-Soluble Vitamins." *Comprehensive Physiology,* vol. 8, no. 4, pp. 1291-1311, 14 Sep. 2018, doi:10.1002/cphy.c170054

[19] A. Tomova, I. Bukovsky, E. Rembert, W. Yonas, & et al. "The Effects of Vegetarian and Vegan Diets on Gut Microbiota." *Frontiers in nutrition*, vol. 6, no. 47. 17 Apr. 2019, doi:10.3389/fnut.2019.00047

[20] K. Windey, V. De Preter, T. Louat, F. Schuit, & et al. "Modulation of protein fermentation does not affect fecal water toxicity: a randomized cross-over study in healthy subjects." *PloS one,* vol. 7, no. 12, e52387, 2012. doi:10.1371/journal.pone.0052387

[21] B. Geypens, D. Claus, P. Evenepoel, M. Hiele, & et al. "Influence of dietary protein supplements on the formation of bacterial metabolites in the colon." *Gut,* vol. 41, no. 1, pp. 70-76, 1997. doi:10.1136/gut.41.1.70

[22] E. D. onnenburg, S. A. Smits, M. Tikhonov, S. K. Higginbottom, & et al. "Diet-induced extinctions in the gut microbiota compound over generations." *Nature,* vol. 529, no. 7585, pp. 212-215, 2016. doi:10.1038/nature16504

[23] R. Caesar, V. Tremaroli, P. Kovatcheva-Datchary, & et al. "Crosstalk between Gut Microbiota and Dietary Lipids Aggravates WAT Inflammation through TLR Signaling." *Cell metabolism,* vol. 22, no. 4, pp. 658-668, 2015. doi:10.1016/j.cmet.2015.07.026

[24] S. Iacob, D.G. Iacob, L.M. Luminos, "Intestinal Microbiota as a Host Defense Mechanism to Infectious Threats." *Frontiers in microbiology,* vol. 9, pp. 3328, 23 Jan. 2019, doi:10.3389/fmicb.2018.03328

[25] S. P., Wiertsema, J. van Bergenhenegouwen, J. Garssen, & L. M. J. Knippels, "The Interplay between the Gut Microbiome and the Immune System in the Context of Infectious Diseases throughout Life and the Role of Nutrition in Optimizing Treatment Strategies." *Nutrients* vol. 13, No.3, pp. 886, 9 Mar. 2021, doi:10.3390/nu1303088

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[26] R. Okumura, & K. Takeda,"Roles of intestinal epithelial cells in the maintenance of gut homeostasis." *Experimental & molecular medicine,* vol. 49, no.5, e338, 26 May. 2017, doi:10.1038/emm.2017.20

[27] V. C. Harris, B. W. Haak, M. Boele van Hensbroek, & W. J. Wiersinga, "The Intestinal Microbiome in Infectious Diseases: The Clinical Relevance of a Rapidly Emerging Field." *Open forum infectious diseases,* vol. 4, no. 3 ofx144. 8 Jul. 2017, doi:10.1093/ofid/ofx144

[28] U. Fiebiger, S. Bereswill, & M. M. Heimesaat, "Dissecting the Interplay Between Intestinal Microbiota and Host Immunity in Health and Disease: Lessons Learned from Germfree and Gnotobiotic Animal Models." *European journal of microbiology & immunology,* vol. 6, no. 4, pp. 253-271. 1 Dec. 2016, doi:10.1556/1886.2016.00036

[29] M. Fukata, & M. Arditi, "The role of pattern recognition receptors in intestinal inflammation." *Mucosal immunology,* vol. 6, no. 3, pp. 451-463, 2013. doi:10.1038/mi.2013.13

[30] J. L. Kubinak, C. Petersen, W. Z. Stephens, R. Soto, & "MyD88 signaling in T cells directs IgA-mediated control of the microbiota to promote health." *Cell host & microbe,* vol. 17, no. 2, pp.153-163, 2015. doi:10.1016/j.chom.2014.12.009

[31] D. Vandamme, B. Landuyt, W. Luyten, & L. Schoofs, "A comprehensive summary of LL-37, the factotum human cathelicidin peptide." *Cellular immunology,* vol. 280, no. 1, pp. 22-35, 2012. doi:10.1016/j.cellimm.2012.11.009

[32] A. Rannug, "How the AHR Became Important in Intestinal Homeostasis-A Diurnal FICZ/AHR/CYP1A1 Feedback Controls Both Immunity and Immunopathology." *International journal of molecular science,s* vol. 21, no.16, pp. 5681. 8 Aug. 2020, doi:10.3390/ijms21165681

[33] A. Labbé, J. G. Ganopolsky, C. J. Martoni, S. Prakash, & M. L. Jones, "Bacterial bile metabolising gene abundance in Crohn's, ulcerative colitis and type 2 diabetes metagenomes." *PloS one,* vol. 9, no.12 e115175, 17 Dec. 2014, doi:10.1371/journal.pone.0115175

[34] S. Negi, D. K. Das, S. Pahari, S. Nadeem, & J. N. Agrewala, "Potential Role of Gut Microbiota in Induction and Regulation of Innate Immune Memory." *Frontiers in immunology,* vol. 10, pp. 2441. 25 Oct. 2019, doi:10.3389/fimmu.2019.02441

[35] M.A. Fischbach, "Microbiome: Focus on Causation and Mechanism." *Cell,* vol. 174, no. 4, pp. 785-790, 2018. doi:10.1016/j.cell.2018.07.038

[36] V. Marx "The chemistry of microbiome-host togetherness." *Nature methods,* vol. 19, no. 3, pp. 274-279, 2022. doi:10.1038/s41592-022-01413-6

[37] H. W. Mittrücker, D. Seidel, P. W. Bland, A. Zarzycka, & et al. "Lack of microbiota reduces innate responses and enhances adaptive immunity against Listeria monocytogenes infection." *European journal of immunology,* vol. 44, no. 6, pp. 1710-1715, 2014. doi:10.1002/eji.201343927

[38] M. Divangahi, P. Aaby, S. A. Khader, L. B. Barreiro, & et al. "Trained immunity, tolerance, priming and differentiation: distinct immunological processes." *Nature immunology,* vol. 22, no. 1, pp. 2-6, 2021. doi:10.1038/s41590-020-00845-6

[39] Z. Menezes-Garcia, R. D. Do Nascimento Arifa, L. Acúrcio, C. B. Brito, & et al. "Colonization by *Enterobacteriaceae* is crucial for acute inflammatory responses in murine small intestine via regulation of corticosterone production." *Gut microbes,* vol. 11, no. 6, pp. 1531-1546, 2020. doi:10.1080/19490976.2020.1765946 .

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الخلاصة

ميكروبيوم الأمعاء هو مجموعة كبيرة ومتنوعة من مجتمعات الميكروبات التي تعيش في الأمعاء وتلعب دورًا حاسمًا في فسلجة المضيف مثل التمثيل الغذائي للطعام والهضم والمناعة وتطور الدماغ والسلوك. تنوعها مهم جدًا للجسم، ولكنه دائما عرضة للتغيير بسبب العوامل البيئية. أي تغيير في التنوع وتكوين الميكروبيوم يمكن أن يكون له آثار لاحقة على صحة المضيف. إن التفاعل بين ميكروبات الأمعاء والعوامل الخارجية وفسيولوجيا المضيف والتطور والأمراض المعدية هو تفاعل معقد حقًا. على سبيل المثال، يمكن للطعام تعديل ميكروبات الأمعاء في نفس الوقت الذي يكون فيه الطعام المصدر الرئيسي للمركبات الأيضية التي تلعب دورًا أساسيًا في تعديل المناعة، وتنظيم المناعة بواسطة الميكروبيوم يؤثر على تطور الدماغ والعكس صحيح. في الختام, إن فهم المسارات المختلفة التي قد تؤثر وتتأثر بها ميكروبات الأمعاء على الهضم والمناعة يوفر نهجًا جديدًا لعلاج العديد من الأمراض المناعية والمعدية. لذلك، تأتي هذه المراجعة لتسليط الضوء على آليات التفاعل المختلفة بين ميكروبات الأمعاء وهضم الطعام والمناعة.

الكلمات المفتاحية: ميكروبات الأمعاء، الميكروبيوم، الهضم، المناعة المحلية، المناعة الجهازي

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