

## Review Article

# Interactions between Intestinal Microflora/Probiotics and the Immune System

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The digestive tract is home to millions of microorganisms and is the main and most important part of bacterial colonization. On one hand, the abundant bacterial community in intestinal tissues may pose potential health challenges such as inflammation and sepsis in cases of opportunistic invasion. Thus, the immune system has evolved and adapted to maintain the symbiotic relationship between host and microbiota. On the other hand, the intestinal microflora also exerts an immunoregulatory function to maintain host immune homeostasis, which cannot be neglected. In addition, the interaction of either microbiota or probiotics with immune system in regard to therapeutic applications is an area of great interest, and novel therapeutic strategies remain to be investigated. The review will elucidate interactions between intestinal microflora/probiotics and the immune system as well as novel therapeutic strategies.

## 1. Intestinal Immune System

Gut associated lymphoid tissue (GALT) is composed of the epithelium, lamina propria, and muscular layer [1]. Enterocytes constitute most of the intestinal epithelial cells and are able to absorb sugar, amino acid, and many other nutrients. Some enterocytes express Toll-like receptors (TLRs) and will secrete a series of proinflammatory chemokines (IL-8), cytokines (IL-1, IL-6, IL-7, IL-11, and TNF), and growth factors (SCF and G-CSF) when encountering with pathogens or toxins. These molecules will recruit peripheral neutrophils and mast cells to intestinal subepithelial regions and accelerate activation and differentiation of local lymphocytes. For instance, IL-7 and SCF secreted by intestinal epithelial cells can act synergistically to activate  $\gamma\delta$  intestinal intraepithelial lymphocytes (iIELs). Then, activated  $\gamma\delta$ -iIEL can also secrete cytokines and chemokines to

activate  $\alpha\beta$ -iIEL, thus initiating a more robust adaptive immune response [2–4]. Between intestinal epithelial cells are enteroendocrine cells, paneth cells, and goblet cells. When a pathogen invades the body, paneth cells release certain antibacterial molecules such as defensins into villi in the small intestine lumen while goblet cells secrete mucus to the intestinal surface, which is helpful for maintaining the intestinal barrier [5, 6]. Intraepithelial  $\alpha\beta$ T and  $\gamma\delta$ T lymphocytes, NK cells, and NKT cells can also be gathered among intestinal epithelial cells. Intestinal intraepithelial lymphocytes (iIELs) are a unique cluster of cells which reside in intestinal mucosal epithelium and have two different cell sources. Approximately 40 percent of iIELs are thymus-dependent  $\alpha\beta$  T cells and their phenotype is similar to peripheral T cells. About 60 percent of iIELs are thymus-independent  $\gamma\delta$  T cells.  $\gamma\delta$  T cells are innate immune cells with strong cytotoxicity as well as the capacity to secrete

various cytokines. Therefore, iIEL plays a vital role in immunosurveillance and cell-mediated mucosal immunity [7–9].

Lamina propria contains a large number of macrophages and neutrophils as well as a small number of NKT cells, mast cells, and immature dendritic cells. A certain number of mature  $\alpha\beta$  T cells and B cells as well as few  $\gamma\delta$  T cells also reside in the lamina propria [10, 11]. Lymphocytes in the lamina propria usually congregate together to form intestinal follicle, which contains germinal centers populated by B cells and follicular dendritic cells, topped by immature dendritic cells, macrophages, CD4<sup>+</sup>T cells, and mature B cells [12, 13]. Located in one side of intestinal follicle that is close to the intestinal luminal are specialized phagocytic cells named M cells, which can transport antigens across the epithelium to the side of basement membrane via transcytosis. Consequently, the antigens interact with the local immune cells and initiate mucosal immune responses where B cells differentiate into IgA secreting plasma cells [14–16]. The elements of intestinal mucosal immunity are summarized in Table 1.

The intestine is a unique organ which is in close contact with microorganisms. Most microbes are destroyed and killed by the harsh gastric acid environment, but a few can still make it through the intestine. The intestinal surface is covered with a large number of finger-like projections called microvilli (also named brush border), whose primary function is the absorption of nutrients. Brush border is wrapped up by a molecule called glycocalyx [17]. Since glycocalyx is a negatively charged and mucoid glycoprotein complex, microvilli could prevent the invasion of pathogenic bacteria. Besides, apical tight junctions of intestinal epithelial cells also ensure that pathogens do not pass through the intestine [18]. A vast population of immune cells reside within these and the underlying structures. As the most crucial intestinal sentinels, Peyer's patches are composed of B-cell follicles, interfollicular regions, macrophages, and dendritic cells [19]. A key function of Peyer's patch is sampling of particulate antigens, mostly bacteria and food through a specialized phagocytic cells called M cells, which can transport material from the lumen to subepithelial dome [20]. Then, local dendritic cells are able to sample antigens and present them to immune effector cells [21]. Nevertheless, intestinal tolerance is mainly mediated by CD4<sup>+</sup> Treg cells in the context of uptake of food antigens. These Treg cells secrete IL-10 and TGF- $\beta$  which exerts suppressive effects on immune cells within the lamina propria. However, a breakdown in the process of immune homeostasis will lead to gut pathology such as food allergy and inflammatory bowel disease [22, 23]. Intestinal barriers including mucin, antimicrobial peptides, and secretory IgA prevent the direct contact between the microorganisms and gut epithelial layer. Barrier destructions can contribute to bacteria influx, activation of epithelium, and inflammatory responses [24]. Proinflammatory antigen-presenting macrophages and dendritic cells are activated and release inflammatory cytokines such as IL-6, IL-12, and IL-23. Th1 and Th17 effector T-cell subsets are polarized and produce inflammatory cytokines such as TNF- $\alpha$ , IFN- $\gamma$ , and IL-17

[25]. In addition, neutrophils are recruited and undergo dramatic form of cell destruction called NETosis, with the production of neutrophil extracellular traps (NETs) and tissue injuries [26].

## 2. Intestinal Microflora and Probiotics

There are a large number of microorganisms in the intestine, which are mainly distributed in the colon. It is estimated that over 40 trillion bacteria (including Archaeobacteria) inhabit in the colon of adults, with a small proportion of fungus and Protista. In general, each individual carries an average of 600,000 intestinal microbial genes [27, 28]. In terms of bacterial strains, there is a distinct diversity among individuals. Each individual has his unique intestinal microflora, which is determined by host genotype, initial colonization through vertical transmission at birth, and dietary habits [29–32]. In healthy adults, the composition of bacterial flora in feces is stable regardless of time. Bacteroidetes and Firmicutes are two main bacteria in human intestinal ecosystem, accounting for over 90 percent of all microorganisms. The remains are Actinobacteria, Proteobacteria, Verrucomicrobia, and Fusobacteria [33, 34]. Probiotics are microorganisms that may be beneficial to health when consumed in adequate amounts [35]. Lactobacillus and Bifidobacteria are most commonly applied probiotics in clinical practice. Yeast *Saccharomyces boulardii* and *Bacillus* species are also widely used [36, 37]. The function of probiotics is closely related to the species of microorganisms that colonize within the intestine. The interaction between probiotics and host cells as well as intestinal flora is a key factor which influences the host health. Probiotics have an impact on intestinal ecosystem by regulating gut mucosal immunity, by having interactions with commensal microflora or potentially harmful pathogens, by producing metabolites (such as short-chain fatty acids and bile acids), and by acting on host cells through signaling pathways (Table 2). These mechanisms can contribute to the inhibition and elimination of potential pathogens, improvement of intestinal microenvironment, strengthening the intestinal barrier, attenuation of inflammation, and enhancement of antigen-specific immune response [38, 39].

Disturbed intestinal immune niche is a contributory cause for the digestive diseases such as inflammatory bowel disease (IBD), functional dyspepsia, gastroesophageal reflux disease, and nonalcoholic fatty liver disease. IBD patients are characterized by an increase in potentially aggressive gut microbial strains as well as decreased regulatory species [40–42]. Aggressive gut microbial strains activate inflammatory response by inducing Th1 and Th17 effector cells while decreased regulatory species inhibit the generation and function of regulatory cells including regulatory T cells (Treg), B cells (Breg), macrophages, dendritic cells (DCs), and innate lymphoid cells (ILCs). This has further resulted in elevated levels of TNF- $\alpha$  and inflammasome and reduced levels of IL-10, TGF- $\beta$ , and IL-35 [43]. Therefore, dysbiosis of the intestinal flora has contributed to dysfunctional immune system and the chronic inflammation in IBD.

TABLE 1: Elements of intestinal mucosal immunity.

| Structures       | Constitution  | Effect and mechanism  |
|------------------|---|---|
| Lumen            | Commensal bacteria                                  | Competitively inhibit pathogenic bacteria<br>Produce antimicrobial substances<br>Traps pathogens  |
|                  | Mucus   | Prevents access to epithelial layer<br>Contains secretory immunoglobulin A  |
|                  | Glycocalyx  | Provides physical barrier   |
| Epithelial layer | Enterocytes   | Connected by tight junctions<br>Surface TLRs induce secretion of proinflammatory chemokines, cytokines, and growth factors<br>Capture some antigens |
|                  | Goblet cells  | Secrete mucus   |
|                  | Paneth cells  | Produce defensins and antibiotic substances   |
|                  | Enteroendocrine cells                               | Produce neuroendocrine mediators<br>Promote $\alpha\beta$ IIEI activation through cytokine and chemokine secretion                                  |
|                  | $\gamma\delta$ IIEIs                                | Produce antimicrobial effectors and protect against pathogens   |
| Lamina propria   | M cells   | Prevent inflammation-induced epithelium damage<br>Capture and transport antigen   |
|                  | $\alpha\beta$ T cells, B cells, DCs, and other APCs | Initiate adaptive immune responses in lymphoid follicles  |
|                  | Treg cells  | Suppress activation and effector function of immune cells   |

TABLE 2: Mechanisms of probiotics and host interaction.

| Probiotics   |
|--|
| <i>Immunologic functions</i>   |
| Stimulate intestinal antigen-presenting cells such as macrophages or dendritic cells and increase immunoglobulin A (IgA) secretion |
| Regulate lymphocyte polarization and cytokine profiles   |
| Induce tolerance to food antigens  |
| <i>Nonimmunologic functions</i>  |
| Digest food and inhibitory compete with pathogens for nutrition and adhesion   |
| Alter local PH to create an unfavorable microenvironment for pathogens   |
| Generate bacteriocins to inhibit pathogens   |
| Scavenge superoxide radicals   |
| Promote epithelial antimicrobial peptides production and enhance intestinal barrier function                                       |

### 3. Immune Regulation by Microflora and Probiotics

3.1. *Promoting the Balance of Th1, Th2, Th17, and Treg Cells.* Actually, intestinal microorganism can elicit diverse signals and induce CD4+T-cell differentiation. Invasive bacteria such as ectopic colonization of *Klebsiella* species can induce DCs phagocytosis and release of proinflammatory cytokines (IL-6, IL-12, and TNF), which is closely associated with Th1 polarization. *Bacteroides fragilis* is a kind of symbiotic anaerobic bacteria which colonizes in human lower digestive tract. Polysaccharide A (PSA) in its outer membrane can be recognized by T-cell surface molecule TLR2, which induces differentiation of CD4+T cells into Treg cells. Here, the Treg cells secrete molecules such as IL-10 and TGF- $\beta$  which exert a suppressive action on immune cells. Actually, it has been demonstrated that administration of PSA or intestinal *Bacteroides fragilis* colonization can prevent intestinal inflammatory diseases in mice models [44–46]. In addition, segmented filamentous bacteria can be presented to T cells

by dendritic cells and contribute to the synthesis of Th17 cells in lamina propria of small intestine, thus playing a vital role in antibacterial immune response [47, 48]. Parasites, for instance, *Heligmosomoides polygyrus*, can contribute to a Th2 immune response. The parasite can bind to tuft cells and secrete high amounts of IL-25, which then acts upon dendritic cells. Dendritic cells produce IL-4 and TGF- $\beta$  and induce CD4+ T differentiation into Th2 subset, with upregulated levels of IL-4 and GATA3 transcription factor. The immunomodulatory effects of various probiotics are listed in Table 3.

3.2. *Regulation of Intestinal Related Gene Expression.* Previous reports have demonstrated that expression of multiple intestinal genes is regulated by probiotics. For instance, *Escherichia coli* and *Lactobacillus rhamnosus* can upregulate mucin expression in intestinal cells to enhance intestinal mucosal barrier. Probiotics can also regulate gene expression of enterocytes and dendritic cells. It has been

TABLE 3: The immunomodulatory effects of probiotics.

| Literature (PMID)  | Probiotic strains  | Mechanism and immunologic effects              |
|--------------------|--|--|
| 15940144, 11751960 | <i>Lactobacillus reuteri</i><br><i>Lactobacillus casei</i> | Promote IL-10 secretion by Treg cells          |
| 17521319, 16297146 | <i>Bifidobacterium bifidum</i>                             | Promote IL-10 secretion by mature DCs          |
| 15585777           | <i>Lactobacillus rhamnosus</i>                             | Inhibit T-cell proliferation                   |
| 15654823           | <i>Bifidobacterium longum</i>                              | Decrease IL-2 and IL-4 secretion by mature DCs |
| 21740462           | <i>E. coli</i> strain, Nissle 1917                         | Promote IL-10 secretion by DCs                 |
| 19300508, 18804867 | <i>Lactobacillus casei</i> , DN-114 001                    | Increase FoxP3+ Treg cells                     |
| 18670628           | <i>Bifidobacterium infantis</i> 35, 624                    | Promote IL-10 and TGF- $\beta$ secretion       |
| 19029003           | <i>Lactobacillus reuteri</i> (ATCC 23272)                  | Increase FoxP3+ Treg cells                     |
| 16522473           | <i>Bifidobacterium breve</i>                               | Inhibit TNF- $\alpha$ and IL-6 secretion       |
|                    |  | Increase FoxP3+ Treg cells                     |
|                    |  | Activate TLR2 and promote maturation of DCs    |
|                    |  | Increase IL-10 secretion                       |

demonstrated that probiotic VSL#3 in certain concentrations ( $10^7$  organisms/mL) could alter the DC phenotypes by the upregulation of costimulatory molecule (CD80, CD86, and CD40) expression [49].

**3.3. Regulation of Immune Response through Microbial Metabolites.** Probiotics can produce a series of metabolites by digesting different foods and impact the immune response within the body.

**3.3.1. Short-Chain Fatty Acids.** Short-chain fatty acid (SCFA) is fatty acid with carbon chain length of 1–6 carbon atoms. It is produced through fermentation of fibres by probiotics. Intestinal SCFA mainly includes acetate, propionate, and butyrate. SCFA can exert its immunoregulatory function as both extracellular and intracellular signaling molecules [50, 51]. Extracellularly, SCFA can act as ligands for cell surface G protein coupled receptors such as GPR41, GPR43, and GPR109a and regulate immune function indirectly. SCFA can bind to GPR43 in the surface of neutrophils and eosinophils to alleviate intestinal inflammation. GPR109a, which is expressed in colon epithelial cells and innate immune cells, can specifically bind to butyrate and induce differentiation of Treg cells [52, 53]. Intracellularly, SCFA can inhibit histone deacetylases (HDAC) and regulate gene transcription to exert immunoregulatory functions. For example, SCFA can promote acetylation of FoxP3 and synthesis of colon FoxP3+Treg cells to enhance their immunosuppressive function. Butyrate can suppress HDAC activity of macrophages in intestinal lamina propria and inhibit their secretion of inflammatory mediators such as nitric oxide, IL-6, and IL-12 [54, 55]. In addition, SCFA can also promote Tfh-cell production, B-cell differentiation, and antibody synthesis, as evidenced by latest reports [56].

SCFA also plays a crucial role in homing of T cells. Retinol, the main component of vitamin A, can be oxidized into retinaldehyde by retinol dehydrogenase. Retinal can be further oxidized to retinoic acid (RA) in vivo through an enzyme called Aldh1a. SCFA, the metabolites of probiotics, increases the activity of Aldh1a and promotes the conversion

of intestine absorbed vitamin A into RA. Dendritic cells in intestinal Peyer's patch (PP) and mesenteric lymph nodes (MLN) express Aldh1a1 and Aldh1a2, respectively, and therefore produce RA locally. When an antigen is presented to T cells by CD103+ dendritic cells in MLD, the local RA induces expression of  $\alpha 4$  in T-cell surfaces, which then binds with  $\beta 7$  to form  $\alpha 4\beta 7$  integrin. The  $\alpha 4\beta 7$  integrin can combine with MadCAM-1 molecule of high endothelial vein (HEV) surface. Meanwhile, RA also induces CCR9 expression in T-cell surface, which binds to CCL25 in intestinal epithelial cells [57, 58]. Therefore, probiotics can promote homing of T cells to intestinal mucosa.

**3.3.2. Amino Acid Metabolites.** Certain essential amino acids are produced as metabolites of probiotics. Particularly, tryptophan (Trp) is closely related to the immune system. Trp can be decomposed into various metabolites by microflora. In the gut, indolic acid derivatives, including indole-3-acetic acid (IAA), indole-3-aldehyde (IAld), indole acryloyl glycine (IAcrGly), indole lactic acid, and indole acrylic acid (IAcrA), originate from Trp catabolism. Specifically, intestinal bacteria, such as *Bacteroides*, Clostridia, and *E. coli*, can decompose Trp to tryptamine and indole pyruvic acid, which are then turned into IAA, indole propionic acid, and indole lactic acid. IAA can combine with glutamine to synthesize indolyl acetyl glutamine in the liver or converted to IAld through aerobic oxidation by peroxidase catalyzation. Indolyl propionic acid can also be further transformed to IAcrA and combine with glycine to produce IAcrGly in the liver or kidney [59]. Indole is the most effective product among various bacterial Trp metabolites. It can also attenuate TNF- $\alpha$ -induced activation of NF- $\kappa$ B and reduce expression of the proinflammatory chemokine IL-8 as well as the adhesive capacity of pathogenic *E. coli* to HCT-8 cells [60]. In addition, both indole and its derivatives (IAld, IAA, and tryptamine) can activate intestinal innate lymphoid cells (ILCs) and regulate local IL-22 synthesis by sensitizing AhR to maintain intestinal mucosal homeostasis [61–63]. Besides, indole has been confirmed to strengthen intestinal epithelial barrier by fortifying tight junctions between cells through the pregnane X receptor (PXR) [64].

Gut commensal *Ruminococcus gnavus* and Firmicutes *C. sporogenes* have the capacity to decarboxylate Trp to tryptamine [65]. Since tryptamine exerts inhibitory effect against IDO1, it is regarded as a potential target in immune escape [66]. Skatole has been reported to inhibit CYP11A1, leading to decreased synthesis of pregnenolone, glucocorticoids, and sex steroids [67]. In the intestine, formation of endogenous steroid hormones, for instance, the anti-inflammatory glucocorticoid cortisol, is essential for the maintenance of intestinal homeostasis [68]. Therefore, skatole has been reported to play a vital role in the pathogenesis of inflammatory bowel disease (IBD).

**3.3.3. Bile Acids.** Bile acids are mainly converted from cholesterol in hepatocytes and undergo a series of metabolic processes mediated by intestinal microflora in the intestine. With the help of probiotics, primary bile acids, namely, cholic acid and chenodeoxycholic acid, convert to deoxycholic acid and lithocholic acid, respectively [69, 70]. Since intestinal macrophages, dendritic cells, and natural killer T cells express bile acids receptors such as GPBAR1 and FXR, intestinal bile acids can bind to these receptors and suppress NLRP3 mediated inflammatory response to maintain immune homeostasis [71, 72]. In addition, bile acids also regulate chemokine CXCL16 expression on liver sinusoidal endothelial cells (LSECs) and the accumulation of CXCR6+ hepatic NKT cells, which exhibit activated phenotypes and inhibit liver tumor growth [73].

**3.3.4. Vitamins.** Intestinal microflora has the capacity to synthesize vitamins and is their important source, especially for vitamin B [74]. As is known to all, vitamins play a vital role in regulating the immune system. Vitamin B1 is a key cofactor of tricarboxylic acid cycle. A decrease in vitamin B1 levels results in reduction of naive B cells residing in intestinal Peyer's patch, thus influencing intestinal immune function [75]. As a cofactor of sphingosine-1-phosphate (S1P) lyase, vitamin B6 is involved in the degradation of S1P. Therefore, it plays a fundamental role in maintaining S1P concentration gradient and promoting intestinal lymphocytes migration to periphery [76–80]. Besides, vitamin B also acts as a ligand for immune cells. The interaction is mediated by major histocompatibility complex MHC class I related proteins, which bind to vitamin B2, leading to the activation of mucosal-associated invariant T cells (MAITs) as well as secretion of IL-17 and IFN- $\gamma$ . From this perspective, vitamin B2 has exerted the function of immune surveillance [81, 82].

At present, the immunoregulatory mechanism of probiotics is still not entirely clear regardless of its great variety and extensive clinical application. It requires further studies to investigate the in vivo process of probiotics through oral administration or enema therapy including the residence time, colonization, and reproduction, impact on original intestinal flora, and microbial interactions. And it is worthwhile to have a focus on the interaction of either microbiota or probiotics with immune system in regard to novel therapeutic applications. Apart from anti-TNF agents and immunomodulators, probiotics, prebiotics, and fecal

microbial transplantation have been applied empirically in IBD. In addition, multiple novel strategies have already done in preclinical and clinical trials through targeting certain microbial organisms and altering mucosal immune niches. These strategies include blocking fimH to inhibit AIEC mucosal attachment, introduction of bacteriophages to eliminate pathobionts, and applying CRISPER-CAS editing to generate specific bacteriocins [83–85]. Hopefully, these approaches will be more effective which can be applied in a personalized manner in the future.

## Conflicts of Interest

The authors declare that they have no conflicts of interest.

## Authors' Contributions

Chen-xing Zhang and Hui-yu Wang are co-first authors and contributed equally to the work.

## References

- [1] E. M. Brown, M. Sadarangani, and B. B. Finlay, "The role of the immune system in governing host-microbe interactions in the intestine," *Nature Immunology*, vol. 14, no. 7, pp. 660–667, 2013.
- [2] E. C. Lavelle, C. Murphy, L. A. O'Neill, and E. M. Creagh, "The role of TLRs, NLRs, and RLRs in mucosal innate immunity and homeostasis," *Mucosal Immunology*, vol. 3, no. 1, pp. 17–28, 2010.
- [3] D. P. Hoytema van Konijnenburg, B. S. Reis, V. A. Pedicord et al., "Cell crosstalk mediates a dynamic response to infection," *Cell*, vol. 171, no. 4, pp. 783–794, 2017.
- [4] A. Montalban-Arques, M. Chaparro, J. P. Gisbert, and D. Bernardo, "The innate immune system in the gastrointestinal tract: role of intraepithelial lymphocytes and lamina propria innate lymphoid cells in intestinal inflammation," *Inflammatory Bowel Diseases*, vol. 24, no. 8, pp. 1649–1659, 2018.
- [5] M. E. V. Johansson, M. Phillipson, J. Petersson, A. Velcich, L. Holm, and G. C. Hansson, "The inner of the two Muc2 mucin-dependent mucus layers in colon is devoid of bacteria," *Proceedings of the National Academy of Sciences*, vol. 105, no. 39, pp. 15064–15069, 2008.
- [6] C. L. Bevins and N. H. Salzman, "Paneth cells, antimicrobial peptides and maintenance of intestinal homeostasis," *Nature Reviews Microbiology*, vol. 9, no. 5, pp. 356–368, 2011.
- [7] N. Cerf-Bensussan and D. Guy-Grand, "Intestinal intraepithelial lymphocytes," *Gastroenterology Clinics of North America*, vol. 20, no. 3, pp. 549–576, 1991.
- [8] L. Van Kaer and D. Olivares-Villagómez, "Development, homeostasis, and functions of intestinal intraepithelial lymphocytes," *The Journal of Immunology*, vol. 200, no. 7, pp. 2235–2244, 2018.
- [9] Y. Qiu and H. Yang, "Effects of intraepithelial lymphocyte-derived cytokines on intestinal mucosal barrier function," *Journal of Interferon & Cytokine Research*, vol. 33, no. 10, pp. 551–562, 2013.
- [10] A. M. Mowat and W. W. Agace, "Regional specialization within the intestinal immune system," *Nature Reviews Immunology*, vol. 14, no. 10, pp. 667–685, 2014.

- [11] O. Pabst and G. Bernhardt, "The puzzle of intestinal lamina propria dendritic cells and macrophages," *European Journal of Immunology*, vol. 40, no. 8, pp. 2107–2111, 2010.
- [12] T. W. Spahn and T. Kucharzik, "Modulating the intestinal immune system: the role of lymphotoxin and GALT organs," *Gut*, vol. 53, no. 3, pp. 456–465, 2004.
- [13] M. Buettner and M. Lochner, "Development and function of secondary and tertiary lymphoid organs in the small intestine and the colon," *Frontiers in Immunology*, vol. 7, p. 342, 2016.
- [14] H. Ohno, "Intestinal M cells," *Journal of Biochemistry*, vol. 159, no. 2, pp. 151–160, 2016.
- [15] N. A. Mabbott, D. S. Donaldson, H. Ohno, I. R. Williams, and A. Mahajan, "Microfold (M) cells: important immunosurveillance posts in the intestinal epithelium," *Mucosal Immunology*, vol. 6, no. 4, pp. 666–677, 2013.
- [16] D. Rios, M. B. Wood, J. Li, B. Chassaing, A. T. Gewirtz, and I. R. Williams, "Antigen sampling by intestinal M cells is the principal pathway initiating mucosal IgA production to commensal enteric bacteria," *Mucosal Immunology*, vol. 9, no. 4, pp. 907–916, 2016.
- [17] S. W. Crawley, M. S. Mooseker, and M. J. Tyska, "Shaping the intestinal brush border," *The Journal of Cell Biology*, vol. 207, no. 4, pp. 441–451, 2014.
- [18] D. Delacour, J. Salomon, S. Robine, and D. Louvard, "Plasticity of the brush border—the yin and yang of intestinal homeostasis," *Nature Reviews Gastroenterology & Hepatology*, vol. 13, no. 3, pp. 161–174, 2016.
- [19] C. Jung, J.-P. Hugot, and F. Barreau, "Peyer's patches: the immune sensors of the intestine," *International Journal of Inflammation*, vol. 2010, Article ID 823710, 12 pages, 2010.
- [20] A. Reboldi and J. G. Cyster, "Peyer's patches: organizing B cell responses at the intestinal frontier," *Immunological Reviews*, vol. 271, no. 1, pp. 230–245, 2016.
- [21] C. Da Silva, C. Wagner, J. Bonnardel, J. P. Gorvel, and H. Lelouard, "The peyer's patch mononuclear phagocyte system at steady state and during infection," *Frontiers in Immunology*, vol. 8, p. 1254, 2017.
- [22] O. J. Harrison and F. M. Powrie, "Regulatory T cells and immune tolerance in the intestine," *Cold Spring Harbor Perspectives in Biology*, vol. 5, no. 8, Article ID a021022, 2013.
- [23] K. S. Kim, S. W. Hong, D. Han et al., "Dietary antigens limit mucosal immunity by inducing regulatory T cells in the small intestine," *Science*, vol. 351, no. 6275, pp. 858–863, 2016.
- [24] F. Haussner, S. Chakraborty, R. Halbgebauer, and M. Huber-Lang, "Challenge to the intestinal mucosa during sepsis," *Frontiers in Immunology*, vol. 10, p. 891, 2019.
- [25] K. R. Groschwitz and S. P. Hogan, "Intestinal barrier function: molecular regulation and disease pathogenesis," *Journal of Allergy and Clinical Immunology*, vol. 124, no. 1, pp. 3–20, 2009.
- [26] L. Vong, C. W. Yeung, L. J. Pinnell, and P. M. Sherman, "Adherent-invasive *Escherichia coli* exacerbates antibiotic-associated intestinal dysbiosis and neutrophil extracellular trap activation," *Inflammatory Bowel Diseases*, vol. 22, no. 1, pp. 42–54, 2016.
- [27] R. Sender, S. Fuchs, and R. Milo, "Revised estimates for the number of human and bacteria cells in the body," *PLoS Biology*, vol. 14, no. 8, Article ID e1002533, 2016.
- [28] C. A. Lozupone, J. I. Stombaugh, J. I. Gordon, J. K. Jansson, and R. Knight, "Diversity, stability and resilience of the human gut microbiota," *Nature*, vol. 489, pp. 220–230, 2012.
- [29] M. A. Conlon and A. Bird, "The impact of diet and lifestyle on gut microbiota and human health," *Nutrients*, vol. 7, no. 1, pp. 17–44, 2014.
- [30] A. Spor, O. Koren, and R. Ley, "Unravelling the effects of the environment and host genotype on the gut microbiome," *Nature Reviews Microbiology*, vol. 9, no. 4, pp. 279–290, 2011.
- [31] J. K. Goodrich, J. L. Waters, A. C. Poole et al., "Human genetics shape the gut microbiome," *Cell*, vol. 159, no. 4, pp. 789–799, 2014.
- [32] D. M. Chu, J. Ma, A. L. Prince, K. M. Antony, M. D. Seferovic, and K. M. Aagaard, "Maturation of the infant microbiome community structure and function across multiple body sites and in relation to mode of delivery," *Nature Medicine*, vol. 23, no. 3, pp. 314–326, 2017.
- [33] S. A. Shetty, F. Hugenholtz, L. Lahti, H. Smidt, and W. M. de Vos, "Intestinal microbiome landscaping: insight in community assemblage and implications for microbial modulation strategies," *FEMS Microbiology Reviews*, vol. 41, no. 2, pp. 182–199, 2017.
- [34] S. Kim, A. Covington, and E. G. Pamer, "The intestinal microbiota: antibiotics, colonization resistance, and enteric pathogens," *Immunological Reviews*, vol. 279, no. 1, pp. 90–105, 2017.
- [35] FAO/WHO, *Health and Nutritional Properties of Probiotics in Food including Powder Milk with Live Lactic Acid Bacteria*, World Health Organization, Basel, Switzerland, 2001.
- [36] O. Simon, "Micro-organisms as feed additives—probiotics," *Advances in Pork Production*, vol. 16, pp. 161–167, 2005.
- [37] European Food Safety Authority (EFSA), "Scientific Opinion on the update of the list of QPS-recommended biological agents intentionally added to food or feed as notified to EFSA (2017 update)," *EFSA Journal*, vol. 15, pp. 1–177, 2017.
- [38] P. Markowiak and K. Śliżewska, "Effects of probiotics, prebiotics, and synbiotics on human health," *Nutrients*, vol. 9, no. 9, p. 1021, 2017.
- [39] L. Lin and J. Zhang, "Role of intestinal microbiota and metabolites on gut homeostasis and human diseases," *BMC Immunology*, vol. 18, no. 1, p. 2, 2017.
- [40] H. Nagao-Kitamoto and N. Kamada, "Host-microbial cross-talk in inflammatory bowel disease," *Immune Network*, vol. 17, no. 1, p. 1, 2017.
- [41] R. B. Sartor and G. D. Wu, "Roles for intestinal bacteria, viruses, and fungi in pathogenesis of inflammatory bowel diseases and therapeutic approaches," *Gastroenterology*, vol. 152, no. 2, pp. 327–339.e4, 2017.
- [42] A. D. Kostic, R. J. Xavier, and D. Gevers, "The microbiome in inflammatory bowel disease: current status and the future ahead," *Gastroenterology*, vol. 146, no. 6, pp. 1489–1499, 2014.
- [43] Y. Mishima and R. B. Sartor, "Manipulating resident microbiota to enhance regulatory immune function to treat inflammatory bowel diseases," *Journal of Gastroenterology*, pp. 1–11, 2019.
- [44] N. K. Surana and D. L. Kasper, "The yin yang of bacterial polysaccharides: lessons learned from *B. fragilis* PSA," *Immunological Reviews*, vol. 245, no. 1, pp. 13–26, 2012.
- [45] E. B. Troy and D. L. Kasper, "Beneficial effects of *Bacteroides fragilis* polysaccharides on the immune system," *Frontiers in Bioscience*, vol. 15, no. 1, pp. 25–34, 2010.
- [46] S. K. Mazmanian, J. L. Round, and D. L. Kasper, "A microbial symbiosis factor prevents intestinal inflammatory disease," *Nature*, vol. 453, no. 7195, pp. 620–625, 2008.
- [47] I. I. Ivanov, K. Atarashi, N. Manel et al., "Induction of intestinal Th17 cells by segmented filamentous bacteria," *Cell*, vol. 139, no. 3, pp. 485–498, 2009.
- [48] Y. Goto, C. Panea, G. Nakato et al., "Segmented filamentous bacteria antigens presented by intestinal dendritic cells drive

- mucosal Th17 cell differentiation,” *Immunity*, vol. 40, no. 4, pp. 594–607, 2014.
- [49] J. Plaza-Diaz, C. Gomez-Llorente, L. Fontana, and A. Gil, “Modulation of immunity and inflammatory gene expression in the gut, in inflammatory diseases of the gut and in the liver by probiotics,” *World Journal of Gastroenterology*, vol. 20, no. 42, pp. 15632–15649, 2014.
- [50] S. Heinritz, E. Weiss, M. Eklund et al., “Impact of a high-fat or high-fiber diet on intestinal microbiota and metabolic markers in a pig model,” *Nutrients*, vol. 8, no. 5, p. 317, 2016.
- [51] W. J. Dahl, N. C. Agro, Å. M. Eliasson et al., “Health benefits of fiber fermentation,” *Journal of the American College of Nutrition*, vol. 36, no. 2, pp. 127–136, 2017.
- [52] M. A. Vinolo, H. G. Rodrigues, R. T. Nachbar, and R. Curi, “Regulation of inflammation by short chain fatty acids,” *Nutrients*, vol. 3, no. 10, pp. 858–876, 2011.
- [53] N. Arpaia, C. Campbell, X. Fan et al., “Metabolites produced by commensal bacteria promote peripheral regulatory T-cell generation,” *Nature*, vol. 504, no. 7480, pp. 451–455, 2013.
- [54] J. Park, M. Kim, S. G. Kang et al., “Short-chain fatty acids induce both effector and regulatory T cells by suppression of histone deacetylases and regulation of the mTOR-S6K pathway,” *Mucosal Immunology*, vol. 8, no. 1, pp. 80–93, 2015.
- [55] P. V. Chang, L. Hao, S. Offermanns, and R. Medzhitov, “The microbial metabolite butyrate regulates intestinal macrophage function via histone deacetylase inhibition,” *Proceedings of the National Academy of Sciences*, vol. 111, no. 6, pp. 2247–2252, 2014.
- [56] M. Kim, Y. Qie, J. Park, and C. H. Kim, “Gut microbial metabolites fuel host antibody responses,” *Cell Host & Microbe*, vol. 20, no. 2, pp. 202–214, 2016.
- [57] P. Czarnewski, S. Das, S. M. Parigi, and E. J. Villablanca, “Retinoic acid and its role in modulating intestinal innate immunity,” *Nutrients*, vol. 9, no. 1, p. 68, 2017.
- [58] M. Iwata, “Retinoic acid production by intestinal dendritic cells and its role in T-cell trafficking,” *Seminars in Immunology*, vol. 21, no. 1, pp. 8–13, 2009.
- [59] J. Gao, K. Xu, H. Liu et al., “Impact of the gut microbiota on intestinal immunity mediated by tryptophan metabolism,” *Frontiers in Cellular and Infection Microbiology*, vol. 8, p. 13, 2018.
- [60] T. Bansal, R. C. Alaniz, T. K. Wood, and A. Jayaraman, “The bacterial signal indole increases epithelial-cell tight-junction resistance and attenuates indicators of inflammation,” *Proceedings of the National Academy of Sciences*, vol. 107, no. 1, pp. 228–233, 2010.
- [61] A. Agus, J. Planchais, and H. Sokol, “Gut microbiota regulation of tryptophan metabolism in health and disease,” *Cell Host & Microbe*, vol. 23, no. 6, pp. 716–724, 2018.
- [62] J. Behnsen and M. Raffatellu, “Keeping the peace: aryl hydrocarbon receptor signaling modulates the mucosal microbiota,” *Immunity*, vol. 39, no. 2, pp. 206–207, 2013.
- [63] T. Zelante, R. G. Iannitti, C. Cunha et al., “Tryptophan catabolites from microbiota engage aryl hydrocarbon receptor and balance mucosal reactivity via interleukin-22,” *Immunity*, vol. 39, no. 2, pp. 372–385, 2013.
- [64] Y. Shimada, M. Kinoshita, K. Harada et al., “Commensal bacteria-dependent indole production enhances epithelial barrier function in the colon,” *PLoS One*, vol. 8, no. 11, Article ID e80604, 2013.
- [65] B. B. Williams, A. H. Van Benschoten, P. Cimermancic et al., “Discovery and characterization of gut microbiota decarboxylases that can produce the neurotransmitter tryptamine,” *Cell Host & Microbe*, vol. 16, no. 4, pp. 495–503, 2014.
- [66] T. Whiteside, “Immune suppression in cancer: effects on immune cells, mechanisms and future therapeutic intervention,” *Seminars in Cancer Biology*, vol. 16, no. 1, pp. 3–15, 2006.
- [67] A. Mosa, A. Gerber, J. Neunzig, and R. Bernhardt, “Products of gut-microbial tryptophan metabolism inhibit the steroid hormone-synthesizing cytochrome P450 11A1,” *Endocrine*, vol. 53, no. 2, pp. 610–614, 2016.
- [68] G. Bouguen, L. Dubuquoy, P. Desreumaux, T. Brunner, and B. Bertin, “Intestinal steroidogenesis,” *Steroids*, vol. 103, pp. 64–71, 2015.
- [69] M. J. Monte, J. J. Marin, A. Antelo, and J. Vazquez-Tato, “Bile acids: chemistry, physiology, and pathophysiology,” *World Journal of Gastroenterology*, vol. 15, no. 7, pp. 804–816, 2009.
- [70] J. R. Swann, E. J. Want, F. M. Geier et al., “Systemic gut microbial modulation of bile acid metabolism in host tissue compartments,” *Proceedings of the National Academy of Sciences*, vol. 108, no. Supplement\_1, pp. 4523–4530, 2011.
- [71] W. Jia, G. Xie, and W. Jia, “Bile acid-microbiota crosstalk in gastrointestinal inflammation and carcinogenesis,” *Nature Reviews Gastroenterology & Hepatology*, vol. 15, no. 2, pp. 111–128, 2018.
- [72] C. Guo, S. Xie, Z. Chi et al., “Bile acids control inflammation and metabolic disorder through inhibition of NLRP3 inflammasome,” *Immunity*, vol. 45, no. 4, pp. 802–816, 2016.
- [73] C. Ma, M. Han, B. Heinrich et al., “Gut microbiome-mediated bile acid metabolism regulates liver cancer via NKT cells,” *Science*, vol. 360, no. 6391, 2018.
- [74] J. G. LeBlanc, C. Milani, G. S. de Giori, F. Sesma, D. van Sinderen, and M. Ventura, “Bacteria as vitamin suppliers to their host: a gut microbiota perspective,” *Current Opinion in Biotechnology*, vol. 24, no. 2, pp. 160–168, 2013.
- [75] J. Kunisawa, Y. Sugiura, T. Wake et al., “Mode of bioenergetic metabolism during B cell differentiation in the intestine determines the distinct requirement for vitamin B1,” *Cell Reports*, vol. 13, no. 1, pp. 122–131, 2015.
- [76] J. G. Cyster and S. R. Schwab, “Sphingosine-1-phosphate and lymphocyte egress from lymphoid organs,” *Annual Review of Immunology*, vol. 30, no. 1, pp. 69–94, 2012.
- [77] J. Kunisawa and H. Kiyono, “Immunological function of sphingosine 1-phosphate in the intestine,” *Nutrients*, vol. 4, no. 3, pp. 154–166, 2012.
- [78] M. Ikeda, A. Kihara, and Y. Igarashi, “Sphingosine-1-phosphate lyase SPL is an endoplasmic reticulum-resident, integral membrane protein with the pyridoxal 5'-phosphate binding domain exposed to the cytosol,” *Biochemical and Biophysical Research Communications*, vol. 325, no. 1, pp. 338–343, 2004.
- [79] S. R. Schwab, J. P. Pereira, M. Matloubian, Y. Xu, Y. Huang, and J. G. Cyster, “Lymphocyte sequestration through S1P lyase inhibition and disruption of S1P gradients,” *Science*, vol. 309, no. 5741, pp. 1735–1739, 2005.
- [80] J. Kunisawa, Y. Kurashima, M. Higuchi et al., “Sphingosine 1-phosphate dependence in the regulation of lymphocyte trafficking to the gut epithelium,” *The Journal of Experimental Medicine*, vol. 204, no. 10, pp. 2335–2348, 2007.
- [81] L. Le Bourhis, L. Guerri, M. Dusseaux, E. Martin, C. Soudais, and O. Lantz, “Mucosal-associated invariant T cells: unconventional development and function,” *Trends in Immunology*, vol. 32, no. 5, pp. 212–218, 2011.
- [82] L. Kjer-Nielsen, O. Patel, A. J. Corbett et al., “MR1 presents microbial vitamin B metabolites to MAIT cells,” *Nature*, vol. 491, no. 7426, pp. 717–723, 2012.
- [83] A. Sivignon, J. Bouckaert, J. Bernard, S. G. Gouin, and N. Barnich, “The potential of FimH as a novel therapeutic

- target for the treatment of Crohn's disease," *Expert Opinion on Therapeutic Targets*, vol. 21, no. 9, pp. 837–847, 2017.
- [84] M. Galtier, L. De Sordi, A. Sivignon et al., "Bacteriophages targeting adherent invasive *Escherichia coli* strains as a promising new treatment for Crohn's disease," *Journal of Crohn's and Colitis*, vol. 11, pp. 840–847, 2017.
- [85] D. Bikard, C. W. Euler, W. Jiang et al., "Exploiting CRISPR-cas nucleases to produce sequence-specific antimicrobials," *Nature Biotechnology*, vol. 32, no. 11, pp. 1146–1150, 2014.