

Gut Microbiota, Probiotics and Inflammatory Bowel Disease

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Abstract The colonization of humans with commensals is critical for our well-being. This tightly regulated symbiotic relationship depends on the flora and an intact mucosal immune system. A disturbance of either compound can cause intestinal inflammation. This review summarizes extrinsic and intrinsic factors contributing to intestinal dysbiosis and inflammatory bowel disease.

Keywords Commensals · Gut immunology · Probiotics · Dendritic cells · Macrophages

Abbreviations

IBD	Inflammatory bowel disease
CD	Crohn's disease
UC	Ulcerative colitis
GWAS	Genome-wide association studies
SNPs	Single-nucleotide polymorphisms
NOD	Nucleotide-binding oligomerization domain
IL-23R	Interleukin 23 receptor
GF	Germ-free
CV	Conventional
SCFA	Short-chain fatty acids
IECs	Intestinal epithelial cells
ITF	Intestinal trefoil factor
DSS	Dextran sodium sulfate
AMPs	Antimicrobial peptides
MyD88	Myeloid-differentiation factor 88
TLRs	Toll-like receptors
AIEC	Adherent-invasive <i>Escherichia coli</i>

MHC	Major histocompatibility complex
PRRs	Pathogen recognition receptors
PAMPs	Pathogen-associated molecular patterns
DAMPs	Danger-associated molecular patterns
LPS	Lipopolysaccharide
ss-RNA	Single-stranded ribonucleic acid
CEACAM6	Carcinoembryonic antigen-related cell adhesion molecule 6
Foxp	Forkhead-box-protein
IFN- γ	Interferon γ
GALT	Gut-associated lymphoid tissue
IELs	Intraepithelial lymphocytes
mLN	Mesenteric lymph nodes
iLF	Isolated lymphoid follicles
iLA	Intestinal lymph aggregates
PP	Peyer's patches
FAE	Follicle-associated epithelium
M-cell	Microfold cell
DC	Dendritic cell
pDCs	Plasmacytoid DCs
cDCs	Conventional DCs
PSA	Polysaccharide A
RA	Retinoic acid
CCR	Chemokine receptor
CLL	Chemokine ligand
TGF- β	Transforming growth factor β
ATP	Adenosine triphosphate
STAT	Signal transducer of activated T cells
IRF	Interferon regulatory factor
MDP	Muramyl dipeptide
T-bet	T-box transcription factor expressed in T cells
TNF	Tumor necrosis factor
TSLP	Thymic stromal lymphopoietin
CDAI	Crohn's Disease Activity Index

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Introduction

As the largest epithelial surface colonized with trillions of microbes the human intestine is permanently challenged by controversial tasks. At the same time, it has to tolerate symbionts, control facultative pathogens and fight obligate pathogens in order to maintain intestinal homeostasis. A disturbance of intestinal homeostasis results in intestinal dysbiosis which is a hallmark of inflammatory bowel diseases (IBD) including Crohn's disease (CD) and ulcerative colitis (UC) characterized by episodic, relapsing or continuous inflammatory processes affecting distinct layers and sections of the intestinal wall (Kaser et al. 2010).

Twin studies have shown a concordance rate among monozygotic twins of about 6% for UC and of about 58% for CD indicating pathogenic roles of both intrinsic and extrinsic factors (Tysk et al. 1988). On the one hand, genome-wide association studies (GWAS) have identified single-nucleotide polymorphisms (SNPs) in genes such as nucleotide-binding oligomerization domain containing 2 (NOD2) and interleukin 23 receptor (IL-23R) representing innate and adaptive immunity, respectively. On the other hand, molecular analysis of the gut microbiota has revealed a higher bacterial diversity in samples from healthy individuals compared to samples from Crohn's patients. In addition, monozygotic healthy twins display a more similar microbiota than monozygotic twins who are discordant for CD (Dicksved et al. 2008). Thus, IBD seems to result from inflammatory immune responses triggered by intestinal dysbiosis both of which are favoured by environmental factors and a genetic susceptibility of the host (Fig. 1).

The importance of the enteric flora for the development of IBD has hence been acknowledged. In this review we will discuss the role of the enteric flora in (1) maintaining the intestinal barrier, (2) interacting with distinct intestinal epithelial cells (IECs), (3) becoming recognized by intestinal antigen uptake pathways, (4) inducing tolerogenic immune responses, (5) mediating resistance towards pathogens (6) initiating destructive inflammatory immune responses and (7) being manipulated for the treatment of IBD.

Enteric Flora Maintains Intestinal Homeostasis

Comprising more than 400 m² the intestinal tract is colonized by the highest bacterial burden with approximately 100 trillion individual microorganisms (Macdonald and Monteleone 2005). The bacterial concentration increases along the intestinal tract with 10⁴ cells/g of luminal contents in stomach and duodenum up to a density of 10¹¹ to 10¹⁴ cells/g in the large intestine (Whitman et al. 1998). In total, the number of intestinal bacteria is approximately ten times the number of cells constituting the human body.

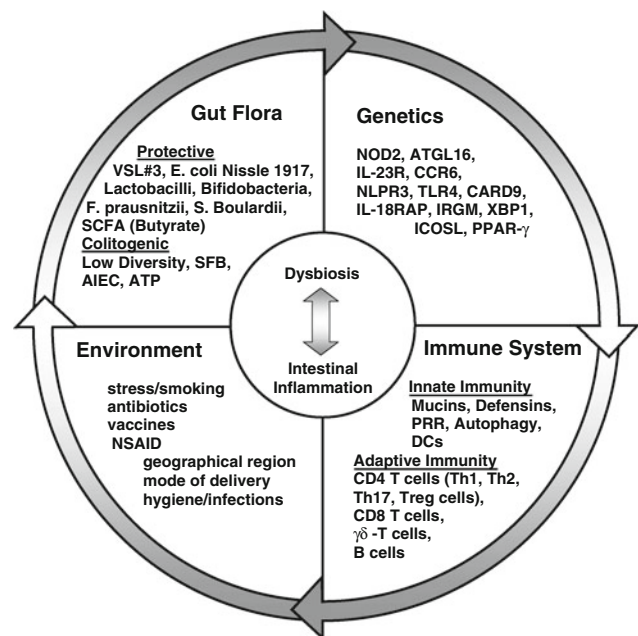


Fig. 1 Extrinsic and intrinsic factors trigger intestinal dysbiosis and inflammation. A crosstalk between environmental factors (e.g. stress, smoking, antibiotic treatment and mode of delivery), compounds of the gut flora with protective or colitogenic effects, genetic susceptibility and cellular as well as humoral compounds of the immune system determine the extent of intestinal dysbiosis and intestinal inflammation both of which enhance each other. *Escherichia coli* (*E. coli*), *Faecalibacterium prausnitzii* (*F. prausnitzii*), *Saccharomyces boulardii* (*S. boulardii*), small-chain-fatty-acids (SCFA), segmented filamentous bacteria (SFB), adenosine triphosphate (ATP), adherent-invasive *Escherichia coli* (AIEC), nucleotide-oligomerisation domain 2 (NOD2), adipose triglyceride lipase 16 (ATGL16), interleukin 23 receptor (IL-23R), chemokine receptor (CCR), NACHT, LRR and PYD domains-containing protein 3 (NLRP3), Toll-like receptor 4 (TLR4), caspase-recruitment domain 9 (CARD9), immunity-related GTPase family M (IRGM), x-box-binding protein 1 (XBP1), inducible co-stimulator ligand (ICOSL), peroxisome proliferator-activated receptor γ (PPAR- γ), pathogen recognition receptor (PRR), dendritic cells (DCs), non-steroidal anti-inflammatory drugs (NSAID)

Based on 16S rRNA sequencing, it was possible to identify up to 40,000 bacterial species in the intestine including non-culturable bacteria (Frank and Pace 2008). Phylotype census showed that 99% of intestinal bacteria are constituted by four phyla including Proteobacteria, actinobacteria and the two major phyla cytophaga-flavobacterium-bacteroides and Firmicutes (Manson et al. 2008). While *Bacteroidetes* species show a large variety between subjects, a high number of Firmicutes species belong to butyrate-producing clostridial clusters (Eckburg et al. 2005). The collective genome, also referred to as microbiome, contains 100-fold more genes than the entire human genome (Tsai and Coyle 2009). Accordingly, a tightly regulated relationship has evolved between the human intestine and its microbiota. If this relationship is of gain for both partners it is referred to as symbiosis whereas

a commensal relationship is characterized by a benefit for one and neither gain or loss for the other partner and a parasitic relationship is beneficial for one but harmful for the other partner. The human intestine aims for a symbiotic relationship which plays a fundamental role in human homeostasis including growth, metabolism and immunity. Experiments with germ-free (GF), gnotobiotic, conventional (CV) and conventionalized animals have opened new ways to analyse this interaction.

It has been demonstrated that 1–20% of the indispensable amino acids lysine and threonine in human plasma are produced by the gut flora and intestinal bacteria are an important source of essential vitamins, such as vitamin K and group B vitamins as well as minerals like iron and copper (Metges 2000; Reddy et al. 1965). Furthermore, GF animals need 30% more calories than CV animals to keep a stable weight approving an important role of bacterial enzymes especially in the digestion of complex polysaccharides (Wostmann et al. 1983). This finding explains a dramatic enlargement of the cecum in GF mice which is mainly caused by an accumulation of undegraded mucus (Gustafsson et al. 1970). The comparison of GF and CV rats has also revealed differences in intestinal motility. GF rats have a delayed gastric emptying and a prolonged intestinal transit caused by a slower spread of migrating motor complexes (Husebye et al. 1994). There is also accumulating evidence for immunomodulatory functions of microbial metabolites including short-chain fatty acids (SCFA) such as butyrate and products from the citric cycle

such as succinate. Upon binding to the G-protein coupled receptor GPR109A on IECs, butyrate dampens immune responses by suppressing NF κ B activation via neddylation of cullin-1 in IECs (Collier-Hyams et al. 2005). GPR43 is another receptor of SCFA. Similar to GF mice, GPR43 deficient animals suffer from exacerbated inflammatory responses in models of asthma, arthritis and colitis indicating a protective role of SCFA (Maslowski et al. 2009). Succinate binds to GPR91 on dendritic cells (DCs) and induces production of proinflammatory cytokines improving antigen-specific T cell responses (Rubic et al. 2008). Hence, antigen-specific T cell responses are impaired in GPR91 deficient mice.

The Mucosal Barrier Prevents the Translocation of the Flora

The intestinal epithelium consists of four different types of polarized IECs: absorptive enterocytes, mucus producing goblet cells, enteroendocrine cells and Paneth cells (Table 1). The renewal of IECs starts from multipotent stem cells in mucosal invaginations, called crypts. It has been estimated that the human intestine produces 50×10^6 cells/day which equates to approximately 250 g of cells (Croft and Cotton 1973). Accordingly, the self-renewal of the intestinal epithelium takes about 5 days. While enterocytes, goblet cells and enteroendocrine cells migrate upward from the crypt to the villus tip, Paneth cells migrate downward to

Table 1 Cellular compartments of the intestinal immune system

Compartment	Cells	Effector GALT	Inductive GALT	Function
Epithelium	Enterocytes	–	+	Digest and absorption of alimantal antigen, antigen presentation
	Paneth cells	–	–	Production of AMPs: lysozyme, RegIII γ , cathelicidin and α , β defensins
	Goblet cells	–	–	Production of mucins
	Enteroendocrine cells	–	–	Hormone production: motilin, secretin, serotonin, VIP, etc.
Lamina propria	Intraepithelial lymphocytes	+	–	Antigen-specific host defense
	T cells, B cells DCs, macrophages, granulocytes	+	–	Antigen transport to ILF/ILA, PP and mLN, homing of effector T and B cells, oxidative burst
ILF/ILA	T cells, B cells DCs, macrophages	–	+	Priming of antigen-specific T and B cells
Peyer's patches	T cells, B cells DCs, macrophages	–	+	Priming of antigen-specific T and B cells
Mesenteric lymph nodes	T cells, B cells DCs, macrophages	–	+	Priming of antigen-specific T and B cells

AMPs antimicrobial peptides, VIP vasoactive intestinal peptide, ILF intestinal lymphoid follicles, ILA intestinal lymphoid aggregates, DCs dendritic cells

+: frequent, -: not present

the base of the crypt. Moreover, Paneth cells predominantly exist in the terminal ileum and have a prolonged lifetime of about 20 days (Bjerknes and Cheng 1981a, b). The development of IECs depends on the presence of the enteric flora. GF mice show a delayed expression of lysozyme in Paneth cells and the induction of fucosyltransferase as well as fucosylated glycoconjugates are decreased in IECs from GF animals (Falk et al. 1998). The analysis of intestinal angiogenesis has shown an impaired development of intestinal capillary networks and Paneth cells in the absence of microbiota (Stappenbeck et al. 2002). The integrity of the intestinal tract is based on an intact epithelial layer which is often endangered by invading pathogens (Sakaguchi et al. 2002). Consequently, the intestine is challenged by fighting pathogenic and concurrently cooperating with symbiotic microbes in order to maintain homeostasis. To fulfil this complex task distinct strategies have evolved.

Globlet Cells and the Mucus Layer

Goblet cells produce large amounts of highly glycosylated proteins forming a two layered mucus that extends up to 150 μm (Johansson et al. 2008). While the inner layer contains antimicrobial peptides (AMPs) and is attached to the epithelium, the outer membrane is detachable, colonized by bacteria and its volume is enlarged by proteolytic cleavage of Muc2 mucin. Notably, Muc2 deficient animals suffer from intestinal inflammation and tumorigenesis underlining the protective function of the mucin layer which reduces microbial adherence to IECs. In addition, goblet cells secrete the protease-resistant intestinal trefoil factor (ITF) which is supposed to attenuate intestinal injuries by protecting IECs from apoptosis and promoting epithelial cell migration (Dignass et al. 1994; Taupin et al. 2000). Accordingly, ITF-deficient mice are characterized by impaired wound healing and accelerated colitis after challenge with dextran sodium sulfate (DSS) (Mashimo et al. 1996). Moreover, defects in goblet cell differentiation have been associated with Crohn's disease (CD) (Gersemann et al. 2009).

Paneth Cells and Autophagy

Paneth cells are critical for the maintenance of the intestinal barrier by producing zinc and AMPs such as lysozyme, RegIII γ , cathelicidin and defensins. The production of AMPs depends on the activation of myeloid-differentiation factor 88 (MyD88)-signalling pathways in Paneth cells (Vaishnava et al. 2008). In line, genetic ablation of Paneth cells which express high levels of Toll-like receptors (TLRs) results in an enhanced translocation of intestinal bacteria causing systemic infections. Moreover, Paneth cell function

depends on autophagy-related pathways. Autophagy displays a highly conserved catabolic process which is triggered by cell stress signals such as hypoxia, nutrient deprivation or growth factor depletion. The autophagosome is specialized for the recycling of amino acids by degrading defective proteins (Levine and Kroemer 2008). In addition, autophagosomal enzymes enhance immunity by destroying intracellular pathogens such as *Mycobacterium tuberculosis* and *Streptococcus pyogenes* (Gutierrez et al. 2004; Nakagawa et al. 2004). In this context, successful antigen presentation via major histocompatibility complex (MHC) class II molecules and concomitant induction of CD4⁺ T cell responses depend on detection of intracellular pathogens by intracellular receptors such as NOD2 and consecutive activation of the autophagosome (Cooney et al. 2010). Interestingly, not only NOD2 mutations but also mutations in the autophagy-related gene ATGL16 are significantly associated with CD and thereby provide strong evidence for a role of autophagy in the pathogenesis of IBD (Cadwell et al. 2008).

Sensing of the Microbiota by Epithelial Cells

IECs are equipped with pathogen recognition receptors (PRRs) such as TLRs, NLRs, c-type lectin receptors and retinoid acid inducible gene-I like receptors detecting pathogen-associated molecular patterns (PAMPs) and danger-associated molecular patterns (DAMPs). TLRs consist of highly conserved transmembrane receptors expressed on the cell membrane and on endosomal compartments (Takeda et al. 2003). TLRs 1, 2, 4, 5, 6 form homo- and heterodimers on the cell membrane and bind bacterial cell wall compounds such as lipoteichoic acid (TLR-2/6), lipopolysaccharide (LPS; TLR-4) and flagellin (TLR-5) whereas homodimers of TLRs 3, 7, 8, 9 are expressed on endosomal membranes and sense nucleic acids such as single-stranded ribonucleic acid (ss-RNA; TLR-3), double-stranded RNA (TLR-7,8) and CpG-rich deoxyribonucleic acid (double-stranded deoxyribonucleic acid; TLR-9). NLRs are cytoplasmic receptors including the NALP-, NAIP- and NOD-families which detect microbial compounds such as bacterial DNA as well as DAMPs like uric acid (Meylan et al. 2006). NOD2 binds peptidoglycan and subsequently induces secretion of proinflammatory cytokines via activation of the NF κ B pathway. About 15% of all CD patients carry homozygous or compound heterozygous mutations in the NOD2 gene causing an impaired NOD2 function and a reduced antimicrobial response as possible pathomechanism (Clayton et al. 2005; Hugot et al. 2001). Since symbiotic and pathogenic microbes express overlapping PAMPs, PRRs can hardly distinguish between pathogens and symbionts. In this context, compartmentalization and strength of PRR expression may help to

avoid excessive inflammatory responses to the commensals. IECs express high levels of Toll-inhibitor-protein (Tollip) but relative low levels of TLR-2 resulting in an unresponsiveness to corresponding ligands such as peptidoglycan or lipoteichoic acid (Melmed et al. 2003). In addition, results from IEC lines demonstrate a decreased expression of TLR-4 and its co-receptor CD14/MD2 (Abreu et al. 2001). By contrast, TLR-5 is highly but exclusively expressed on the basolateral membrane of IECs (Gewirtz et al. 2001). This expression profile suggests that only invasive pathogens induce inflammation by contacting the basolateral membrane whereas the interaction between symbiotic microbes and IECs induces a minor inflammatory response as it is restricted to the apical membrane. Nevertheless, MyD88, TLR-2 as well as TLR-4 deficient animals are highly susceptible towards DSS colitis and DSS colitis in antibiotic-treated mice can be ameliorated by oral application of TLR-2 or TLR-4 ligands (Rakoff-Nahoum et al. 2004). In addition to TLRs, IECs express the carcinoembryonic antigen-related cell adhesion molecule 6 (CEACAM6) which mediates adherence of adherent-invasive *Escherichia coli* (AIEC) on the apical membrane. Interestingly, CEACAM6 is upregulated on the inflamed epithelium of IBD patients indicating a pathomechanism which enhances intestinal inflammation (Barnich et al. 2007). These results point to the theory that symbiotic microbes induce a continuous production of AMPs by IECs during steady state which are essential to maintain intestinal homeostasis whereas changes in PRR expression or the presence of invasive enteropathogens favour intestinal inflammation.

Presentation of Luminal Antigens by Epithelial Cells

In addition to antigen recognition and antigen uptake, IECs are able to process and present antigen. IECs express molecules resembling the antigen presenting machinery including MHC class I and II molecules, HLA-DM, the Invariant chain, Lamp-1 as well as CD63 and CD68 molecules (Lin et al. 2005; Mayer et al. 1991). During steady state IECs induce CD4⁺ regulatory T cells (Tregs) expressing high levels of IL-10 and forkhead-box-protein 3 (Foxp3) whereas inflammatory conditions instruct IECs to prime interferon (IFN)- γ producing CD4⁺ T cells (Dotan et al. 2007; Westendorf et al. 2006).

Sensing of the Microflora by Intestinal Lymph Follicles

The gut-associated lymphoid tissue (GALT) contains about 70% of all immunocytes and thereby represents the largest secondary lymphoid organ (Corr et al. 2008). While intraepithelial lymphocytes (IELs) and lamina propria (lp)

lymphocytes including IpDCs are scattered cell populations which constitute the effector site of the GALT, mesenteric lymph nodes (mLN), isolated lymphoid follicles (iLF) and intestinal lymph aggregates (iLA) such as Peyer's patches (PP) represent the inductive site of the GALT (Niess 2008) (Table 1). In opposite to mLN residing at the mesenterium and receiving intestinal antigens through afferent lymph vessels, iLF and iLA develop in the intestinal wall and obtain antigens through the follicle-associated epithelium (FAE). Interestingly, GF and CV mice differ in the GALT architecture. The number of $\alpha\beta$ TCR-positive IELs increases after colonization of GF mice and GF mice possess underdeveloped PP, fewer CD4⁺ T cells and decreased numbers of IgA-producing plasma cells in the lamina propria (Macdonald and Monteleone 2005). Notably, development of iLF depends on the recognition of peptidoglycan from Gram-negative bacteria by the NOD1 receptor (Bouskra et al. 2008).

The co-operation between FAE and adjacent lymphoid tissue has been extensively studied in PP located at the antimesenteric side of the small intestine. Here, the FAE consists of absorptive enterocytes and specialized epithelial cells without microvilli but with microfolds on the luminal surface. Therefore, these cells were named microfold cells or M-cells (Owen and Jones 1974). M-cell progenitors have been detected in the early proliferative zone of the crypts indicating a common origin of M-cells and enterocytes (Gebert and Pabst 1999). In vitro experiments using adenocarcinoma cells (Caco-2) have suggested a relationship between M-like cell development and PP lymphocytes (Kerneis et al. 1997). However, other studies showed that M-like cells develop from Caco-2 cells even in the absence of lymphocytes (Blanco and DiRita 2006). Interestingly, M-cells do hardly secrete glycoproteins and thus have only a thin mucus layer which allows a close contact to luminal antigens of the intestinal tract. In addition, the basolateral membrane of M-cells forms a pocket-like invagination that is charged with DCs, macrophages, T and B lymphocytes. Based on these features, M-cells are specialized for trans-epithelial transport of particles, macromolecules and microorganisms, also referred to as transcytosis directed from the intestinal lumen to underlying immune cells. On the one hand, transcytosis allows a rapid induction of immune responses against intestinal pathogens but on the other hand, pathogens have evolved strategies to benefit from this entry site. For example, *Salmonella typhimurium* equipped with the *Salmonella* pathogenicity island 1 (SPI1) invades M-cells, destroys the FAE and causes large ulcers which pave the way to lymphoid follicles of PP (Jones et al. 1994). In turn, chemokine receptor 6 (CCR6⁺) DCs become activated, migrate to the subepithelial cell dome of PP and induce antigen-specific T cell responses. The impact of this response has been shown by infection of

CCR6-deficient animals with *S. typhimurium*. CCR6-deficient animals showed an enhanced susceptibility to *S. typhimurium* due to a decreased migratory capacity of CCR6-deficient DCs in PP (Salazar-Gonzalez et al. 2006). Interestingly, a SNP in the human CCR6 gene is associated with CD (Barrett et al. 2008).

Recognition of Intestinal Microbes by Myeloid Cells

Intestinal myeloid cells are a heterogeneous cell population that can be divided in CD11c⁺B220⁺ plasmacytoid DCs (pDCs) and CD11c⁺B220⁻ conventional DCs (cDCs) (Shortman and Liu 2002), macrophages and monocytes. cDCs can be further divided into CD4⁺, CD8⁺ and CD4⁻CD8⁻ DCs. In the lamina propria of the small and large intestine CD4⁻CD8⁻ cDCs are the predominant population. In addition, intestinal myeloid cells can be categorized according to the expression of CD103, the ligand of E-cadherin and CX₃CR1, the receptor for fractalkine/CX₃CL1. Moreover, recent work has identified monocyte-derived DCs (Mo-DCs) which are characterized by the expression of E-cadherin and drive intestinal inflammation by promoting Th17 responses (Siddiqui et al. 2010). Recently, Steinman and colleagues could show that microbial stimuli such as LPS drive differentiation of Mo-DCs marked by the c-type lectin receptor DC-SIGN/CD209 (Cheong et al. 2010).

CD103⁻CD11b⁺CD14⁺CX₃CR1⁺ mononuclear phagocytes develop from Ly6C^{high} monocytes in the presence of granulocyte-macrophage colony-stimulating factor (Varol et al. 2009). CX₃CR1⁺ myeloid cells do hardly migrate and seem to control local immune responses at the mucosal surface (Schulz et al. 2009). Further analysis revealed that lp CX₃CR1⁺CD11c⁺ cells express F4/80 and CD68 (Niess and Adler 2010). Because CX₃CR1 is expressed by pDCs, cDCs, monocytes and macrophages, CX₃CR1 cannot be considered as a classic lineage marker for DCs (Geissmann et al. 2010; Niess and Adler 2010). However, CX₃CR1⁺ mononuclear phagocytes stay in direct contact with intestinal microbes by forming transepithelial dendrites and expressing tight-junction proteins such as claudin and occludin which preserve integrity of the epithelial layer (Niess et al. 2005; Rescigno et al. 2001). In this way, CX₃CR1⁺ mononuclear phagocytes bypass IECs and gain access to luminal antigens. CX₃CR1 deficient mice lack this ability and show an enhanced susceptibility to enteroinvasive pathogens such as *Salmonella* species (Niess et al. 2005). Moreover, a reduction of intestinal microbes by antibiotic treatment as well as genetic ablation of the TLR adaptor molecule MyD88 in IECs decrease the number of transepithelial dendrites of CX₃CR1⁺ mononuclear phagocytes (Chieppa et al. 2006; Niess et al. 2005). In line,

colonization of the intestine guides the accumulation of CX₃CR1⁺ mononuclear phagocytes in the small and large intestinal lamina propria (Niess and Adler 2010). CX₃CR1⁺CD11c⁺F4/80⁻CD68⁻ mononuclear cells induce differentiation of Th1 and Th17 cells (Atarashi et al. 2008; Denning et al. 2007). In humans, a unique CX₃CR1⁺CCR9⁺ mononuclear cell that expresses DC (CD205, CD209) and macrophage markers (CD14, CD33, CD68) contributes to the pathogenesis of CD by inducing Th1 differentiation (Kamada et al. 2008).

In contrast to CX₃CR1⁺ mononuclear phagocytes, CD103⁺CX₃CR1⁻ lpDCs derive from macrophage-DC precursors (depending on fms-like tyrosine kinase 3) ligand signalling (Bogunovic et al. 2009; Varol et al. 2009). CD103⁺ lpDCs have an enhanced migratory potential which enables this subset to carry antigen to mLNs (Schulz et al. 2009). This process is critically influenced by expression of CCR7 on lpDCs and the presence of the corresponding ligands chemokine ligand (CCL) 21 and CCL19 (Jang et al. 2006). Homed to mLNs, antigen presenting lpDCs prime gut tropic T cells by secreting retinoic acid (RA) which induces expression of CCR9 and $\alpha 4\beta 7$ in T cells (Iwata et al. 2004; Johansson-Lindbom et al. 2003).

In addition, recent work has identified an innate lymphoid cell which is characterized by expression of Thy1, stem cell antigen 1, retinoic acid receptor-related orphan receptor γ t (ROR γ t) and IL-23R and produces IL-17 and IFN- γ upon stimulation with IL-23 (Buonocore et al. 2010). Accordingly, depletion of Thy1⁺ cells diminished acute and chronic intestinal inflammation.

The Enteric Flora is Tolerized by Intestinal Regulatory T Cells

Tregs are antigen specific T cells which prevent autoimmunity and preserve tolerance towards harmless non-self antigens. The latter function is of importance for the intestine since it stays in permanent contact with large amounts of foreign but essential antigen. Hence, the GALT has evolved a unique pathway to induce Tregs. Depending on the presence of transforming growth factor (TGF)- β and RA, CD103⁺ mesenteric lymph node DCs are capable to induce CD4⁺ Foxp3⁺ Tregs. (Coombes et al. 2007; Sun et al. 2007). Notably, TGF- β but not RA is sufficient to drive Treg development which becomes enhanced by a synergism of both cytokines (Chen et al. 2003). Bioactive RA is synthesized by CD103⁺ DCs through oxidation of the vitamin A derivative retinal. Thus, RA acts like a natural adjuvant improving oral tolerance. Functionally, RA operates even indirectly by inhibiting the release of pro-inflammatory cytokines such as IL-4, IFN- γ and IL-21 from CD44^{high} T cells (Hill et al. 2008). The source of

TGF- β has so far not been clearly defined. On the one hand, CD103⁺ DCs are assumed to produce TGF- β and on the other hand, in vitro experiments indicate that TGF- β secreted from IECs primes tolerogenic CD103⁺ DCs (Iliev et al. 2009).

Treg cells produce the effector cytokines TGF- β and IL-10. Treg cell-specific ablation of IL-10 results in spontaneous colitis and expression of TGF- β 1 by Treg cells is required to inhibit the development of colitogenic Th1 cells in a T cell transfer model (Li et al. 2007; Rubtsov et al. 2008). Moreover, genetic ablation of Foxp3⁺ Treg cells causes lethal multi-organ autoimmunity, similar to the phenotype of scurfy mice and the human X-linked syndrome (IPEX) (Bennett et al. 2001; Lahl et al. 2007). In line, Treg cells with decreased or without Foxp3 expression preferentially convert into Th2 cells that cause inflammation of the intestinal tract (Lahl et al. 2009; Wan and Flavell 2007). Therefore, functional Treg cells are indispensable for the maintenance of intestinal homeostasis. Regarding microbial factors that support Treg cell function, it has been observed that polysaccharide A (PSA) from *Bacteroides fragilis* inhibits Th17 cells and enhances IL-10 producing T cells conferring protection against *Helicobacter hepaticus*-induced colitis (Mazmanian et al. 2008). Moreover, distinctly phosphorylated products from the uracil, guanine and adenine metabolism influence the function of Treg cells. For example, adenosine inhibits proinflammatory T cells and induces Tregs upon binding to the A2A receptor on T cells (Huang et al. 1997; Zarek et al. 2008). Consequently, CD25⁺ T cells from A2A receptor deficient animals are not able to suppress colitis induced by CD45RB^{high} T cell transfer (Naganuma et al. 2006). Further, an increased frequency of the Firmicutes strain *Faecalibacterium prausnitzii* is associated with reduced recurrence rates in CD patients and increased frequencies of IL-10 producing T cells (Sokol et al. 2008).

Resistance to Pathogens is Mediated by the Enteric Flora

Accumulating evidence reveals that host tolerance controls not only host immunity but indirectly mediates host defense carried out by the enteric flora. For example, *Shigella flexneri*-induced enteritis in GF mice can be attenuated by prior colonization with specific commensal microbes and *S. typhimurium*—the most common cause of infectious diarrhea in humans world-wide—causes a more severe gastroenteritis in GF mice compared to CV mice (Maier and Hentges 1972; Nardi et al. 1989). Moreover, it has been demonstrated that *S. typhimurium* infection elicits a protective soluble (s)IgA response. However, sIgA deficiency does not impair pathogen clearance whereas mice

with a low complex enteric flora produce normal sIgA levels but are incapable to clear the pathogen (Endt et al. 2010). In this context, several defense mechanisms of the enteric flora have been described. One defense mechanism is mediated by the secretion of antibacterial proteins. *E. coli*, for example, produces antibacterial proteins such as colicins and microcins (Destoumieux-Garzon et al. 2002; Riley and Wertz 2002). Colicins are proteins with 25–80 kDa whereas microcins are much smaller with less than 10 kDa. Both groups of antibacterial proteins fight Gram-negative enteropathogens by damaging bacterial membranes or destabilizing membrane potentials, respectively. *E. coli* itself owns resistance towards its toxins. The fact that colonization of gnotobiotic rats with a strain of *Peptostreptococcus* confers protection against pathogenic bacteria such as *Clostridium (C.) perfringens* and *C. difficile* indicates the production of further, so far unknown toxins by this microbe (Ramare et al. 1993). Moreover, a strain of *Ruminococcus gnavus* has been isolated from human feces which secretes *ruminococcin A*, an antibacterial toxin that mediates resistance towards various pathogenic clostridia (Dabard et al. 2001). In addition, a protease from *S. boulardii* digests *C. difficile* toxin A and thereby inhibits intestinal ileal secretion and histologic damage in *C. difficile* colitis (Castagliuolo et al. 1996).

Apart from direct antibacterial effects, commensal microbes do also enhance host defense mechanisms. The analysis of *Toxoplasma gondii* infection has shown an impaired immune response in the absence of commensal microbes triggering innate and adaptive immune responses via TLRs and DCs (Benson et al. 2009). Accordingly, MyD88 deficient animals are even less protected towards gut injury (Rakoff-Nahoum et al. 2004). Furthermore, it has been observed that TLR9 deficient animals are more susceptible to oral infection with the microsporidium *Encephalitozoon cuniculi* (Hall et al. 2008). This effect was accompanied by decreased levels of IFN- γ in IELs but increased frequencies of Tregs in the epithelium, PP and Ip as well as increased systemic levels of IL-4 and IL-10 in *E. cuniculi*-infected TLR9 deficient mice. DNA extracted from gut flora inhibited induction of Tregs in vitro and oral application of CpG-rich DNA restored immune responses towards *E. cuniculi* in antibiotic-treated animals indicating that commensal microbes enhance immune responses towards enteropathogens via TLR9 signalling. *Lactobacilli* have been shown to induce secretion of intestinal mucins from IECs. In vitro experiments suggest that *lactobacilli* inhibit adhesion of enteropathogenic *E. coli* by upregulating expression and secretion of MUC2 and MUC3 from IECs (Mack et al. 1999). Moreover, the secretion of PSA from *Bacteroides fragilis* protects animals against *Helicobacter hepaticus* infection by dampening pro-inflammatory intestinal T cell responses (Mazmanian et al. 2008).

Together, these results demonstrate that only a symbiotic relationship between the enteric flora and the host organism provides a substantial defense towards enteropathogens.

Intestinal Th17 Responses: a Double-Edged Sword

The fact that enteric flora from IBD patients significantly differs from the one of healthy people indicates that intestinal dysbiosis triggers harmful T cell responses in IBD. Apart from Treg cells, intestinal CD4⁺ T cells can be subdivided into Th1, Th2 and Th17 cells. IL-17 producing Th17 cells are frequent cells in the lamina propria with highest frequency in the terminal ileum and cecum. In the absence of enteric flora, Th17 cells are reduced in the lamina propria (Ivanov et al. 2008; Niess and Adler 2010). A member of the non-pathogenic *Clostridium coccoides* species, the segmented filamentous bacterium (SFB), specifically attaches to the FAE of PP, recruits lymphocytes and induces differentiation of Th17 cells during steady state as shown in Fig. 2 (Gaboriau-Routhiau et al. 2009; Ivanov

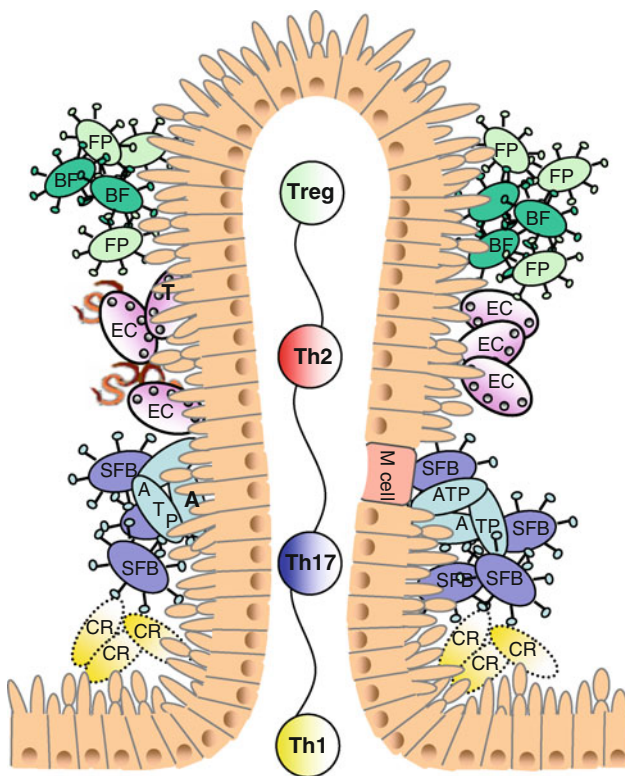


Fig. 2 Gut flora and fauna shape intestinal T cell responses. *Francisella prausnitzii* (FP), strains of *Bifidobacteria* (BF) such as *Bifidobacterium S17* and parasites such as *Encephalitozoon cuniculi* (EC) promote regulatory T cell (Treg) responses. Hence, worms such as *Trichuris muris* induce Th2 responses and segmented filamentous bacteria (SFB) as well as intestinal adenosine triphosphate (ATP) favour Th17 responses whereas Th1 responses become enhanced by *Citrobacter rodentium* (CR)

et al. 2009). Th17 cells are defined by transcription factors such as ROR γ t, interferon regulatory factor 4 (IRF4) and signal transducer of activated T cells 3 (STAT3) as well as the aryl hydrocarbon receptor. (Brustle et al. 2007; Harris et al. 2007; Ivanov et al. 2006; Veldhoen et al. 2008). The differentiation of naive T cells into Th17 cells occurs in the presence of IL-6 or IL-21 and TGF- β whereas IL-23 seems to be essential for maintenance and expansion of Th17 cells (Korn et al. 2007; Veldhoen et al. 2006; Zhou et al. 2007). However, recent work has shown that even a combination of IL-1 with IL-6 or IL-23 generates Th17 cells from naive T cells (Ghoreschi et al. 2010). At the same time, this cytokine pattern antagonizes Foxp3⁺ Treg cells (Bettelli et al. 2006). Moreover, it has been shown that adenosine triphosphate (ATP) promotes inflammatory intestinal Th17 responses (Atarashi et al. 2008). Th17 responses decrease upon degradation of intestinal flora by antibiotic treatment indicating that bacterial ATP production plays a critical role. Correspondingly, mice with genetic ablation of the CD39/ENTPD1 gene encoding an ATP-hydrolase suffer from exacerbated DSS colitis and the analysis of SNPs in a human case–control cohort revealed significant associations between SNPs in the human CD39 gene and an enhanced susceptibility to CD (Friedman et al. 2009). In a similar manner, the NOD2 ligand muramyl dipeptide (MDP) induces IL-17 production in human memory T cells by enhancing the release of IL-23 and IL-1 from monocyte-derived DCs primed by TLR agonists (van Beelen et al. 2007). However, TLR-primed Mo-DCs from patients with double-dose NOD2 mutations in the leucine-rich repeat domain fail to produce IL-23 upon stimulation with MDP. Moreover, the absence of IL-23 increases susceptibility to *Citrobacter rodentium*-driven colitis due to an impaired Th17 response (Mangan et al. 2006). In terms of fungal infections, the c-type lectin receptor Dectin-1 binds *Candida albicans* and subsequently induces IL-23 via Syk-CARD9 signalling (LeibundGut-Landmann et al. 2007). CARD9 deficient animals show a decreased Th17 response towards *C. albicans* and rapidly succumb to the fungus (Gross et al. 2006). IL-23 is constituted by IL-12p40 and p19, whereas IL-12 consists of p40 and p35 (Oppmann et al. 2000). Mice deficient for p19 or p35 show different phenotypes in a colitis model. (Uhlir et al. 2006). While the absence of p19 protects mice from intestinal pathology but not from wasting disease, p35 deficient animals show an increased intestinal inflammation but decreased weight loss. On the other hand, IL-23 is necessary to maintain chronic intestinal inflammation by inducing IL-17 and IL-6 producing T cells and IL-23 promotes extraintestinal disorders such as experimental allergic encephalomyelitis, joint inflammation and psoriasis (Chan et al. 2006; Cua et al. 2003; Murphy et al. 2003; Yen et al. 2006). Moreover, a large GWAS identified a highly significant

association between the human IL-23R subunit IL-23R located on chromosome 1p31 and CD (Duerr et al. 2006). In line, IRF4-deficient animals are protected from chemical-induced colitis by a decreased production of IL-6 in intestinal T cells and the blockade of IL-6 signalling ameliorates experimental colitis by induction of apoptosis in lamina propria T cells (Atreya et al. 2000; Mudter et al. 2008). Except IL-6, Th17 cells produce the effector cytokines IL-17A, IL-17F, IL-22 and IL-26 (Andoh et al. 2008). IL-26 has been detected in intestinal Th17 cells (Dambacher et al. 2009). Stimulation of IEC lines with IL-26 results in cell proliferation and enhanced expression of proinflammatory cytokines such as IL-8 and IL-22. Transfer of ROR γ -null, IL-17A^{-/-}, IL-17F^{-/-} as well as IL-22^{-/-} T cells into RAG1 deficient mice results in a more severe colitis compared to transfer of wildtype T cells. Moreover, colitis induced by transfer of IL-17F deficient T cells becomes attenuated by concomitant neutralization of IL-17A indicating redundant functions of IL-17A and IL-17F in IBD (Yang et al. 2008; Zenewicz et al. 2008). Correspondingly, GWAS have identified risk loci for UC in 7q22 and 22q13 (*IL17REL*) (McGovern et al. 2010). Taken together, these data demonstrate an important role of Th17 responses in host defense but concomitantly reveal that defects in genes regulating corresponding cytokine pathways predispose to develop harmful uncontrolled Th17 responses triggered by intestinal microbes. Thus, selected IBD patients might benefit from therapeutics which target Th17 associated pathways such IL-23 signalling or antagonize intestinal microbes triggering Th17 responses.

Enteric Flora Drives Inflammatory Th1 Responses

In the presence of IL-12, type I and type II IFNs naive T cells differentiate into Th1 cells. This process is characterized by activation of STAT1 and STAT4 inducing T-box transcription factor expressed in T cells (T-bet) and IFN- γ , both hallmarks of Th1 cells (Murphy et al. 1999). Elevated levels of IFN- γ were detected in sera of CD patients and increased frequencies of IFN- γ and T-bet expressing CD4⁺ T cells were found in intestinal biopsies of CD patients (Fuss et al. 1996). Moreover, lamina propria CD4⁺ T cells isolated from CD patients express elevated levels of IL-12R β 1, IL-12R β 2 and IL-18R representing typical features of Th1 cells (Okazawa et al. 2002). Accordingly, application of anti-IL-12- antibodies to mice with 2,4,6-trinitrobenzene sulfonic acid (TNBS)-induced colitis ameliorated disease and transfer of T-bet deficient CD45RB^{high} T cells into RAG-deficient mice did not cause colitis indicating a pivotal role of Th1 cells in IBD (Neurath et al. 1995; Neurath et al. 2002). Based on these results, it

has been hypothesized that CD patients benefit from therapies antagonizing Th1 responses. However, neither application of anti-IL-12 antibodies nor treatments with fontolizumab, an anti-IFN- γ antibody, could produce convincing results (Kaser et al. 2010). Interestingly, RAG2^{-/-}T-bet^{-/-} mice develop colitis despite the absence of adaptive immunity and wildtype mice develop colitis upon ingestion of intestinal flora from RAG2^{-/-}T-bet^{-/-} mice indicating that intestinal inflammation driven by innate immunity selects a bacterial flora with proinflammatory potential (Garrett et al. 2007). The influence of the microbiota on intestinal Th1 responses has been analysed in IL-2 and IL-10 deficient mice, respectively. Both genotypes spontaneously develop colitis caused by enhanced Th1 responses. However, only IL-10 deficient but not IL-2 deficient animals showed an ameliorated disease with decreased Th1 responses in the absence of TLR-MyD88 signalling (Rakoff-Nahoum et al. 2006). Furthermore, IL-10^{-/-}/TLR9^{-/-} animals showed an accelerated colitis progression compared to IL-10^{-/-}/TLR4^{-/-} mice indicating that bacterial DNA triggers Th1 responses via TLR-9 signalling (Gonzalez-Navajas et al. 2010).

Tumor necrosis factor (TNF)- α is another proinflammatory cytokine which is associated with Th1 responses and higher expressed by intestinal cells from IBD patients compared to healthy controls (MacDonald et al. 1990). Neutralization of TNF- α or genetic deletion of TNF- α reduced Th1 responses and intestinal inflammation in animal models (Kontoyiannis et al. 2002; Neurath et al. 1997). In line, intestinal inflammation is attenuated in Tnfr2^{-/-}Tnf^{ΔARE} mice, even absent in Tnfr1^{-/-}Tnf^{ΔARE} mutants and limited to superficial layers in RAG^{-/-}Tnf^{ΔARE} mice (Kontoyiannis et al. 1999). Accordingly, anti-TNF- α antibody treatment was tested in humans and has established a very efficacious therapy for human IBD (Baumgart and Sandborn 2007). However, the exact molecular mode of action of anti-TNF- α antibody therapy is only partially understood. Regarding the role of microbes, it has been demonstrated that intestinal flora drives TNF- α production by Ip CD4⁺ T cells (Niess et al. 2008). Moreover, *E. coli* strains isolated from feces of CD patients showed an enhanced mucosal adherence and invasiveness compared to *E. coli* strains isolated from healthy controls (Darfeuille-Michaud et al. 2004). Based on these features, AIEC enter the lamina propria and become phagocytosed by macrophages which subsequently produce large amounts of TNF- α (Barnich et al. 2007). *Citrobacter rodentium* infection elicits a Th1 response in mice which causes intestinal lesions similar to those in murine IBD models (Higgins et al. 1999).

Taken together, these results show that the enteric flora can induce colitogenic Th1 responses. However, the fact that IBD patients only benefit from anti-TNF- α , but not

from anti-IL-12 or anti-IFN- γ therapies indicates specific changes in the human genome and probably even in the microbiome that particularly enhance TNF- α production. In this way, NOD2 polymorphisms may favour bacterial dysbiosis triggering TNF- α production in IBD.

The Commensal Microflora Shape Intestinal Th2 Responses

Th2 cells are characterized by the transcription factor GATA-3 and become induced by antigen-presenting cells (APCs) secreting cytokines such as IL-4, IL-5 and IL-13 (Zheng and Flavell 1997). Not only classical APCs like macrophages and DCs but also basophils can promote differentiation of Th2 cells (Sokol et al. 2009). On the one hand, Th2 responses are essential to fight helminth and parasite infections but on the other hand, uncontrolled Th2 responses cause hyperinflammatory responses including excessive IgE production and mast cell activation which cause atopic diseases such as asthma. Interestingly, Th2 responses are even associated with IBD. IL-13 is produced in an oxazolone colitis model by nonclassical natural killer (NK) T cells that are restricted to the MHC molecule CD1d but do not respond to the invariant NKT ligand α -galactosylceramide (Fuss et al. 2004). In line, activation of IL-13R α 2 induces fibrogenic factors in TNBS colitis and IL-13R α 2 is upregulated in IECs from UC patients (Fichtner-Feigl et al. 2008; Mandal and Levine 2010). Neutralization of IL-13 as well as depletion of NKT cells prohibits colitis in animal models (Heller et al. 2002). Moreover, GWAS could detect highly significant associations between SNPs in the *ORMDL3* gene located on chromosome 17 and CD as well as childhood asthma indicating common pathomechanisms (Barrett et al. 2008; Moffatt et al. 2007). Regarding intestinal microflora and macrofauna, it has been shown that protective immunity against the worm *Trichuris muris* relies on Th2 responses driven by thymic stromal lymphopoietin (TSLP) from IECs. Being released, TSLP binds to its receptor on IpDCs and triggers release of Th2 cytokines via IKK β activation (Taylor et al. 2009; Zaph et al. 2007). TSLP-receptor deficient animals as well as DCs from *Ikkb*^{Villin-Cre} mice produce increased levels of Th1 associated cytokines such as IFN- γ and TNF- α which again decrease upon neutralization of IL-12/23p40. Surprisingly, antibiotic treatment of mice infected with *Trichuris muris* leads to a reduction of the microflora and the macrofauna accompanied by an increased Th2 response (Hayes et al. 2010). In this context, the infection of mice with the intestinal helminth *Heligmosomoides polygyrus* has shown a selective de novo induction of Treg cells but not Th2 cells through stimulation of the TGF- β receptor with a parasite-secreted protein

(Grainger et al. 2010). Thus, one can speculate that not only the microflora but also the macrofauna contributes to intestinal homeostasis. Accordingly, a small prospective study tested the safety and efficacy of live eggs from the porcine whipworm, *Trichuris suis* in IBD patients (Summers et al. 2003). The treatment could improve the Crohn's Disease Activity Index (CDAI) and the IBD Quality of Life Index without having side effects. Based on these results large randomized, double-blind studies have been planned.

Manipulating the Enteric Flora for the Benefit of the Host

The perception that not only host immunity controls intestinal microflora but vice versa intestinal microbes influence host immune responses resulted in the development of therapies manipulating the intestinal flora in order to dampen harmful immune responses in IBD by dissolving bacterial dysbiosis (Tables 2, 3).

In this context, the terms probiotics, prebiotics and synbiotics need to be mentioned. Probiotics have been defined as “a live microbial feed supplement which beneficially affects the host animal by improving its intestinal microbial balance” (Fuller 1991). The term prebiotic has been introduced to describe “a non-digestible food ingredient that beneficially affects the host by selectively stimulating the growth and/or activity of one or a limited number of bacteria in the colon” (Gibson and Roberfroid 1995). Thus, the therapeutic effect of prebiotics relies on the presence of probiotics. Finally, products which contain both pro- and prebiotics that act synergistically are referred to as synbiotics (Roberfroid 1998).

Lactobacillus (*L.*) species were one of the first bacteria whose probiotic potential has been evaluated in IBD. Animal studies showed that intracolonic application of *L. reuteri* R2LC to rats with acetic acid-induced colitis significantly ameliorated the disease and intragastric administration of *L. reuteri* R2LC to rats with methotrexate-induced enterocolitis resulted in decreased weight loss and reduced intestinal permeability (Fabia et al. 1993; Mao et al. 1996). Furthermore, *Lactobacillus* species attenuated colitis in IL-10 deficient mice (Madsen et al. 1999). Accordingly, IL-10 and TGF- β producing Treg cells became induced by co-culturing murine splenocytes with *L. paracasei* NCC2461 or by co-culturing human DC-SIGN⁺ Mo-DCs with *L. reuteri* or *L. casei* (Smits et al. 2005; von der Weid et al. 2001). Notably, anti-DC-SIGN antibodies blocked the induction of Tregs indicating a tolerogenic role of the c-type lectin receptor. Based on these promising results, *Lactobacillus* species were tested in IBD patients. However, except one open-label pediatric study, no randomized placebo-controlled study could so far

Table 2 Effects of probiotics on humans with IBD

Microbe	Disease	Design	Number	Outcome	References
Lactobacilli	CD	OL	4	CDAI ↓ Intest. perm. ↓	Gupta et al. (2000)
	UC	R	127	Pouchitis after surgery ↓	Gosselink et al. (2004)
Bifidobacteria	UC	R	21	Remission ↑ Relapse ↓	Ishikawa et al. (2003)
VSL#3	UC	R, DB	147, 144	Remission ↑ UCDAI ↓	Sood et al. (2009); Tursi et al. (2010)
<i>E. coli</i> Nissle 1917	UC	R, DB	327, 90	Remission ↑	Kruis et al. (2004); Matthes et al. (2010)
<i>F. prausnitzii</i>	CD	OL	13	Recurrence after surgery ↓	Sokol et al. (2008)
<i>S. boulardii</i>	CD	R	32	Recurrence ↓	Guslandi et al. (2000)
	UC	OL	24	Recurrence ↓	Guslandi et al. (2003)
<i>T. suis</i> ova	CD	OL	29	CDAI ↓	Summers et al. (2005a)
	UC	R, DB	54	UCDAI ↓	Summers et al. (2005b)

E. coli *Escherichia coli*, *F. prausnitzii* *Faecalibacterium prausnitzii*, *S. boulardii* *Saccharomyces boulardii*, *T. suis* ova *Trichuris suis* ova, CD Crohn's disease, UC ulcerative colitis; R randomized, OL open-label, DB double-blind, CDAI Crohn's Disease Activity Index, UCDAI Ulcerative Colitis Disease Activity Index, *intest. perm.* intestinal permeability

↑ up-regulated, ↓ down-regulated

Table 3 Effects of probiotics in animal studies

Microbe	Animal model	Effect	References
Lactobacillus	Acetic acid- and MTX-induced colitis in rats, IL-10 ^{-/-} mice	Colitis ↓	Fabia et al. (1993); Mao et al. (1996); Madsen et al. (1999)
Bifidobacteria	DSS-colitis in mice	NFκB activity ↓	Kim et al. (2010)
VSL#3	Murine IEC in vitro	IP-10 ↓	Hoermannsperger et al. (2009)
<i>E. coli</i> Nissle 1917	LPS-induced sepsis	TNF-α ↓	Arribas et al. (2009)
<i>S. boulardii</i>	TNBS-colitis	TNF-α signalling ↓	Lee et al. (2009)
IL-10 secreting <i>L. lactis</i>	DSS-colitis, IL-10 ^{-/-} mice	Colitis ↓	Steidler et al. (2000)
LcrV secreting <i>L. lactis</i>	DSS-colitis, TNBS-colitis	Colitis ↓	Foligne et al. (2007)

E. coli *Escherichia coli*, *S. boulardii* *Saccharomyces boulardii*, *L. lactis* *Lactobacillus lactis*, IL interleukin, MTX methotrexate, DSS dextran sodium sulfate, LPS lipopolysaccharide, NFκB nuclear factor 'κ-light-chain-enhancer' of activated B cells, IP10 interferon γ-induced protein 10, TNF-α tumor necrosis factor α, TNBS trinitrobenzene sulfonic acid

↑ up-regulated, ↓ down-regulated

show a significant benefit for treatments with *Lactobacillus* in CD (Gupta et al. 2000; Rolfe et al. 2006). Two randomized placebo-controlled trials tested the effect of *Lactobacillus johnsonii*, LA1 on the recurrence of CD after ileo-cecal resection and in both trials application of LA1 could not decrease recurrence rates (Marteau et al. 2006; Van Gossum et al. 2007). Regarding UC, a randomized-controlled trial could show that the onset of pouchitis after ileal pouch-anal anastomosis became delayed by a daily intake of *L. rhamnosus* GG (Gosselink et al. 2004). Promising data were also obtained from bifidobacteria. Here, a randomized-controlled trial could show that bifidobacteria-fermented milk supplement significantly reduced relapses and maintained remission in patients with UC (Ishikawa et al. 2003). In line, Cui et al. (2004) observed fewer relapses in UC patients treated with

bifidobacteria during remission. However, it needs to be considered that bifidobacteria strains differ in their anti-inflammatory potential which is particular strong in *Bifidobacterium bifidum* S17 (Preising et al. 2010).

VSL#3 is a mixture of eight bacteria including *L. acidophilus*, *L. casei*, *L. plantarum*, *L. bulgaricus*, *Bifidobacterium* (*B.*) *longum*, *B. breve*, *B. infantis* and *Streptococcus thermophilus*. The safety and efficacy of VSL#3 has been evaluated in an uncontrolled study that included 34 UC patients with mild or moderate disease activity. Here, no clinical or biochemical adverse effects occurred (Bibiloni et al. 2005). A double-blind, placebo-controlled study tested the probiotic potential of VSL#3 in 147 patients with mild or moderate UC. Randomized into two groups, the patients received either 3.6×10^{12} colony forming units (CFU) of VSL#3 or placebo twice daily for

12 weeks. After this time, significantly more patients treated with VSL#3 achieved remission and reported a decreased Ulcerative Colitis Disease Activity Index (Sood et al. 2009). Similar results were also obtained from a double-blind, placebo-controlled trial with UC patients treated about 8 weeks with VSL#3 (3,600 billion CFU/day) or placebo in addition to their immunosuppressive drugs (Tursi et al. 2010). Another prospective double-blind, placebo-controlled study analysed the efficacy of VSL#3 in children with newly diagnosed active UC. After 1 year, significant higher remission rates and significant less relapses were observed in children treated with VSL#3 (Miele et al. 2009). Regarding its biochemical mechanism, in vitro experiments suggest that compounds of VSL#3 downregulate secretion of TNF-induced IFN- γ -induced protein 10 (Hoermannsperger et al. 2009).

Similar results were obtained from the non-pathogenic strain *E. coli* Nissle 1917. Compared to a standard therapy with mesalazine, UC patients treated with *E. coli* Nissle 1917 achieved and maintained equal remission rates (Kruis et al. 2004; Kruis et al. 1997). In addition, application of *E. coli* Nissle 1917 enemas increased remission rates of left-sided UC in a dose dependent manner (Matthes et al. 2010). One study tested *E. coli* Nissle 1917 in patients with active CD treated with steroids. However, no beneficial effect of the probiotic was observed (Malchow 1997). Functionally, *E. coli* Nissle 1917 is able to inhibit adhesion and invasion of AIEC and in vitro experiments showed that *E. coli* Nissle 1917 induces production of human β -defensin-2 in IECs (Boudeau et al. 2003; Wehkamp et al. 2004). Moreover, colonization with *E. coli* Nissle 1917 decreased levels of TNF- α in a model of LPS-induced sepsis (Arribas et al. 2009). Thus, intestinal microflora as well as adaptive immunity are indispensable for the safety of *E. coli* Nissle 1917 (Gronbach et al. 2010).

The analysis of mucosa-associated microbiota in CD patients at the time of surgical resection and 6 months later revealed a significant association between reduced counts of the Firmicutes strain *Faecalibacterium (F.) prausnitzii* and a higher risk of ileal recurrence of CD (Sokol et al. 2008). Correspondingly, oral administration of *F. prausnitzii* or its supernatant to mice ameliorated TNBS-colitis. In vitro experiments suggest that these effects are mediated by a yet-to-be-defined secreted product(s) which inhibits NF κ B activity, reduces levels of IL-12 and IFN- γ and increases levels of IL-10.

Saccharomyces (S.) boulardii is a non-pathogenic yeast which interferes with multiple pro-inflammatory pathways such as NF κ B and mitogen-activated protein kinases and thereby inhibits production of inflammatory cytokines (Sougioultzis et al. 2006). In addition, a protease from *S. boulardii* cleaves *C. difficile* toxin A and its receptor, respectively, indicating a probiotic potential of this

microbe (Castagliuolo et al. 1996). Accordingly, a clinical trial has compared the efficacy of *S. boulardii* and mesalazine versus mesalazine alone in 32 CD patients. Notably, clinical relapses were less frequent in patients who received mesalazine plus *S. boulardii* (Guslandi et al. 2000). Results from a pilot trial with *S. boulardii* suggest that it also improves remission rates in UC patients treated with mesalazine (Guslandi et al. 2003).

As mentioned above, even the macrofauna represented by helminths plays an important role in gut homeostasis as it induces Tregs and balances Th1, Th2 and Th17 responses. Accordingly, Summers and colleagues performed a randomized, double-blind, placebo-controlled study wherein 54 patients with active UC received 2,500 *Trichuris suis* ova or placebo orally at 2-week intervals for 12 weeks (Summers et al. 2005b). Notably, 43.3% of the ova-treated patients but only 16.7% of the placebo group reached the primary efficacy variable which was defined as improvement of the Disease Activity Index to ≥ 4 . Analogue to this study, the effect of *Trichuris suis* ova was analysed in an open-label study which included 29 patients with active CD (Summers et al. 2005a). Here, 23 patients responded (decrease in CDAI >100 or CDAI <150) and 21 patients remitted (CDAI <150). In both studies, no adverse side effects were observed.

Apart from native microbes, the probiotic therapy has been extended to genetically manipulated bacteria expressing cytokines and/or delivering drugs and vaccines. For example, intragastric application of an IL-10 secreting *Lactococcus (L.) lactis* significantly decreased murine DSS-colitis and could even prevent colitis in IL-10 deficient mice (Steidler et al. 2000). Correspondingly, Foligne and colleagues could show that genetically engineered

L. lactis secreting the *Y. pseudotuberculosis* protein *LcrV* prevented TNBS- and DSS-colitis in mice (Foligne et al. 2007). Moreover, intranasal administration of tetanus toxin expressing *L. plantarum* elicited antigen specific humoral and cellular immune responses that protected mice from the toxin (Grangette et al. 2001). Nevertheless, it still needs pre-clinical trials to guarantee the safety of this new therapeutical approach.

Conclusions and Future Perspectives

The analysis of the human microbiome has revealed significant differences between the microbiota of IBD patients and healthy controls. Additional studies could show that not only genetic factors but also environmental factors influence each individual's microbiota. Therefore, strategies have been developed to treat IBD by manipulating the intestinal flora. Especially, probiotic bacteria seem to be capable of restoring intestinal symbiosis by unfolding

antiinflammatory effects. Selective colonization of GF mice with genetically manipulated bacteria will help to identify molecular mechanisms mediating antiinflammatory effects. These results are important to improve our knowledge about the interaction between the host and its microbiota in order to develop more specific therapies targeting intestinal dysbiosis in IBD.

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