



Probiotics in inflammatory bowel disease: Pathophysiological background and clinical applications

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Abstract

Ulcerative colitis and Crohn's disease, collectively termed the inflammatory bowel diseases (IBD), are chronic inflammatory disorders of the gastrointestinal tract. A "dysbiotic" relationship between the commensal gut flora and the intestinal mucosa-associated immune system has been at the core of the pathogenesis of these conditions. Probiotics are "good bacteria" with the ability to benefit the health of the host and their therapeutic application has been studied in IBD. The theoretical basis for such utilization relies upon the ability of probiotic microorganisms to interfere with the dysregulated homeostasis that takes place in IBD and restore the immune-bacterial interaction at the intestinal mucosa. Proposed mechanisms of action include the reconstitution of altered flora composition, enhancement of the integrity of the epithelial barrier, promotion of tolerogenic action by dendritic cells, strengthening of the defensive mechanisms of the innate immunity, and the suppression of pro-inflammatory adaptive immune responses. Despite this abundance of supporting experimental evidence, clinical application of probiotics in IBD has been disappointing. Possible expla-

nations for such discrepancy include the great diversity of microorganisms that fall under the definition of probiotics, the lack of standardization of dosages and administration schemes, the heterogeneity between clinical trials, and the inclusion in the treatment arms of patients with a large variety of clinical phenotypes. Addressing these important issues will be critical for the optimal usage of probiotic-based therapies for patients with IBD.

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Key words: Probiotics; Commensal flora; Mucosa-associated immune system; Inflammatory bowel disease; Clinical trials; Pouchitis; Ulcerative colitis; Crohn's disease

Core tip: Inflammatory bowel diseases are chronic debilitating diseases of the gastrointestinal tract. Current therapies are not effective in a great proportion of patients and are associated with serious adverse effects. The use of probiotics has been tried as an alternative and safe treatment. Herein, we review the pathophysiological basis for such an application and summarize the data from the major clinical trials.

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INTRODUCTION

In recent years, great progress has been made regarding our understanding of the structure and function of intestinal microbiota, leading to attractive novel perspectives for different pathologic conditions. An increasing number of investigational studies have shed light to the

pivotal role of the physiologic host-bacterial mutualistic relationship for health maintenance, as well as the pathophysiological relevance of the disturbance of such balance for the occurrence of several human diseases^[1]. Research in this field has been directed towards the two main actors of this interplay: the gut microflora and the intestinal mucosal immune system.

The great advancement that has been achieved regarding laboratory techniques for the quantitative and qualitative evaluation of commensal flora has led to the evolution from a culture-based approach to the metagenomic (molecular profile) and metabolomic (metabolic activity) investigation of bacterial species hosted inside the human gut^[2]. Modern analytical methodologies provided a large body of information which, on the one hand, has expanded our comprehension of genera- and species-composition of intestinal microbiota; furthermore, the effects of internal (aging, pathology) and external (drugs, diet) factors on the stability and variation of the flora can be accurately determined^[1]. On the other hand, paradoxically, data interpretation has become a difficult task, in the face of the growing diversity of flora composition and its temporal and spatial distribution and the need to correctly balance similarity with inter- and intra-individual variability. In an attempt to simplify this complexity, a stable core microbiome has been described for healthy individuals and people affected by some pathologic conditions (enterotype)^[3]. Surprisingly, complexity decreases when considering gene expression profile rather than bacterial species definition^[4], indicating that functional analysis of microbiota may provide a more solid framework for future studies.

A comprehensive study of the microbiota is inseparable from the parallel investigation of the host counterpart of the intestinal ecosystem, *i.e.*, the innate and adaptive immunity of the intestinal mucosa. Evidence that the host immune system can shape intestinal gut flora relies on data from animal models. Mice with deficiency of T-bet, a T-box transcription factor family member with important roles in adaptive and innate immunological responses, develop spontaneous colitis that is transmissible to immunological intact mice by fecal transplantation^[5]. To date, molecular insight into the mechanism of bacterial recognition points to a binomial pathway, which originates from pathogen-associated molecular pattern/pattern recognition receptor (PAMP/PRR) interaction and, through the activation of transduction proteins (*i.e.*, MYD88, IRAK), leads in turn to the activation of specific genes and production of proteins (*i.e.*, mucins, defensins) that are able to modulate intestinal microflora^[6]. To further complicate the picture, many external and internal factors may activate molecular modulators with the potential to induce different pathways^[7]. Perturbations affecting microflora and/or innate mucosal immunity are likely to alter the physiological balance between the two compartments. The real impact of such alteration on the development of specific diseases represents a challenge for scientists involved in this field of research.

One major application of research in this field is the opportunity to interfere with the host-bacterial cross-talk. One such way of reinforcing the communication to the benefit of the host, is by means of specific bacterial supplements, namely probiotic bacteria. Although the concept of “good bacteria”, capable of benefiting individual health is about 100-year-old, it is only in the last decades that the implementation of probiotics for therapeutic purposes has become widely tested. This was driven on the one side by the impulse of microbiota research, and on the other by market suggestions. To date, rigorous scientific evidence for probiotic utilization has been accomplished for few clinical conditions, such as treatment of acute diarrhea in children and post-antibiotic diarrhea prevention^[8,9], prevention of *Clostridium difficile* infection^[10], and prevention of atopic eczema associated with cow milk allergy^[11].

When considering probiotic administration for the treatment of a specific condition several confounding factors need to be taken into account. First, a variety of different bacterial species and compounds fall under the “probiotic” label. As such microbial diversity is inevitably translated into functional variability, individual strain properties may render one product applicable to a specific clinical setting but not in a different one. At the same time, not every probiotic microorganism may be suitable for a particular condition. Second, the majority of evidence is being generated in experimental models, including animal mimics of human diseases. Although the important contribution of such methods to the elucidation pathogenetic mechanisms cannot be overemphasized, data are not directly translatable in clinical scenarios. Finally, therapeutic doses and schemes are far from being characterized, even for the same probiotic species.

Investigation of the role of probiotic bacteria in inflammatory bowel diseases (IBD) is a valid exemplification of the skepticism presented above. IBD represents a heterogeneous group of disorders that are characterized by persistent intestinal inflammation of unknown etiology. The major forms of IBD are ulcerative colitis (UC) and Crohn’s disease (CD), which share many clinical, pathological and immunological characteristics, but are also distinguished by unique phenotypic signatures^[12]. Despite a large number of studies that has been published in recent years, solid evidence for the efficacy of probiotics in IBD remains scarce. On the other hand, current research has led to clarification of different molecular pathways that are involved in the action of such bacteria, both during the active phase of inflammation (induction of remission) and as prevention of disease flares (maintenance of remission). Such progress should ideally lead to a critical revision of previous clinical experience with probiotic compounds in IBD and will hopefully lead to the design of translational clinical studies.

In the present review, we critically address the influence of commensal flora in IBD, and the current concept of IBD pathogenesis, in order to evaluate the rational of probiotic use and their putative mechanisms of action

in inflammatory conditions. Moreover, we present and discuss current clinical data of probiotic supplementation in IBD, and we try to delineate the indications for future investigation.

PATHOPHYSIOLOGICAL BACKGROUND

The “dysbiotic” microbiota in IBD

Evidence for a “microbiota influence” in IBD originates from observations in both experimental models and patients. Early studies have outlined a “negative” role of commensal bacteria on IBD onset. First, the majority of animal models of IBD do not develop inflammation when raised on “germ free” conditions; furthermore, re-introduction of bacteria in the gut induces the development of colitis^[13,14]. Second, antibiotic therapy has been associated with amelioration of the severity of clinical and experimental intestinal inflammation^[5,15]. Third, fecal diversion has been proven efficient in ameliorating inflammation in CD patients and reinfusion of fecal content into a previously excluded ileum resulted in reappearance of the disease^[16,17]. Nevertheless, more recent studies have questioned the previous data, putting forward the hypothesis that some commensal species may have protective roles against the development of inflammation. In fact, spontaneous ileitis in SAMP1/YitFc mice develops in a germ-free environment, even though with attenuated severity in comparison to their specific-pathogen-free (SPF) counterparts^[18]. In addition, DSS-colitis is more severe in germ free than in SPF mice^[19].

The development of novel techniques for microbiota evaluation has opened the way for the identification and characterization of a “dysbiotic state” between commensal flora and gut-associated mucosal immune system in IBD patients compared with normal individuals. Although studies so far failed to identify a single etiologic microorganism for the pathogenesis of disease, many studies reported a reduced diversity of intraluminal and mucosa-adherent microbiota in IBD patients^[20]. In general, a reduction of *Firmicutes* have been observed in patients with IBD, with consequent relative increase of *Enterobacteriaceae*^[21,22]. Controversial data are available regarding differences between UC and CD patients, as well as between inflamed and uninfamed areas from individual patients^[20,23-25]. Alteration of the interspecies balance may have detrimental effects on the homeostasis and development of inflammatory disease by two different reasons. First, the reduction of bacterial diversity may favor the overgrowth of “enteropathogens” with pro-inflammatory properties. Along that line, several studies have reported increased concentration of mucosa-adherent-invasive *E. coli* (AIEC) strains with specific virulence factors in IBD patients^[26-28]. Such bacteria were isolated in 36% of ileal specimens of CD patients, compared with 6% of normal control^[28], and have the ability to stimulate the production of pro-inflammatory cytokines from macrophages both *in vitro* and *in vivo*^[29,30]. Conflicting data are also available for the pro-inflammatory role

of *Mycobacterium avium sub. paratuberculosis*^[31], pathogenic *Yersinia*^[32,33] and *Listeria monocytogenes*^[34,35]. Alternatively, dysbiosis may be signified by the reduction of “protective” bacterial species. Several members of *Firmicutes* are strong producers of short chain fatty acids metabolites (acetate and butyrate) with anti-inflammatory properties and important trophic function for colonic mucosa^[36]. In this regard, of particular relevance are *Clostridial* cluster IV and XIV, which are relatively less abundant in IBD patients compared with normal controls^[23]. Moreover, *Bacteroides fragilis* and *Faecalibacterium prausnitzii* are bacteria with anti-inflammatory properties that are reduced in IBD patients^[37,38].

Several probiotic bacteria supplements have been shown to affect microbiota composition and, in particular, to increase diversity. *Lactobacillus casei* and *L. plantarum* have been shown to increase *Lactobacillus* diversity in mouse colon^[39]. *L. rhamnosus subsp. GG* (LGG) administered to mothers increases Bifidobacterial diversity in 5-day-old newborns^[40]. Several studies indicate that the administration of the multiple probiotic compound VSL#3, a high dose (450 billions/g) supplement of 8 different bacterial species (4 *Lactobacilli*, 3 *Bifidobacteria* and *S. thermophilus*), affects human and mouse gut flora composition, incrementing diversity^[41-43]. Still a matter of debate is the question of the real role of the dysbiosis in the IBD pathogenesis. Recent support to the hypothesis that microflora alteration is not just a consequence but may have a causative role in the development of inflammatory disease in wild type mice by fecal content transplantation from T-bet-deficient mice^[5], and by the promising results of microbiota fecal transplantation in humans^[44]. Thus, both gut flora composition and mucosal immune response appears to be equally involved and interconnected in homeostasis maintenance and in the onset of inflammation.

Restoring the barrier defect: Stimulating innate immunity and IEC activity

In the last years, the general conception of IBD pathogenesis has been drastically changed. Indeed, focus has been shifted from an over-reactive immune response, mainly driven by activated T cells^[45], to a primarily immunodeficient condition whereby the chronic inflammatory reaction is a paradoxical consequence of a defective immune response, in particular of the innate compartment^[46]. This leads to an insufficient handling of the bacterial burden at the intestinal mucosa and, eventually, to the onset of pathological chronic inflammation^[47]. In this scheme of events, a compromise of the barrier function of intestinal epithelial cells may be the initiating event. Defective barrier function at the mucosal level can be identified at two separate levels: intestinal permeability and anti-bacterial molecule production^[48,49]. Several studies have outlined increased intestinal permeability as an early event in IBD^[50]. Older studies have reported increased permeability in patients with CD and their first

degree relatives, suggesting a possible primary etiological role of this alteration for disease occurrence^[51]. Derangement of tight junctions, with up-regulation of claudin 2 and down-regulation and redistribution of claudins 5 and 8, has been described in patients with mild to moderate CD^[52]. In the spontaneous ileitic SAMP/YitFc murine strain, the primary defect leading to the onset of chronic intestinal inflammation appears to be related to an epithelial permeability increment^[53].

Additional levels of homeostatic control include the active secretion of mucins and defensins by epithelial cells. Pathologic mucin production and assembly has been described in human IBD^[54], and such alterations has been demonstrated to be associated with colitis in experimental models^[55,56]. Alterations in α - and β -defensins production, by Paneth cells and enterocytes, has been reported in IBD^[57,58]. The possible role of flawed defensin production in the pathogenesis of CD has been further confirmed by the detection of such defects in patients with polymorphisms of the CD-associated genes nucleotide oligomerization domain 2 (NOD2) and autophagy related protein 16-like 1 (ATG16L1)^[59,60]. Moreover, importance of epithelial production of NF- κ B mediated production of cytokines (IL-1b, IL-8, TNF) for mucosal homeostasis maintenance has been demonstrated^[61,62].

Probiotics have been shown to positively stimulate IEC activity and intestinal permeability. LGG effectively improved intestinal permeability in rats with ethanol-induced colitis, by increased gastric production of Muc6 and PGE2^[63]. *L. acidophilus* upregulated muc2 and IL-8, IL-1b and TNF α in IEC, thus inhibiting the attachment of *E. coli* O157:H7^[64]. VSL#3 increased mucins genes expression and secretion in IEC^[65], and improved intestinal permeability in IL-10 deficient mice^[66]. VSL#3 and *L. fermentum* improved intestinal permeability by upregulation of human beta defensin 2 by NF- κ B and MAPKs related pathways^[67]. VSL#3 effectively prevented ileal inflammation in SAMP1/YitFc mice by NF- κ B activation in epithelial cells and consequent production of TNF α and restoring of intestinal permeability; notably, the beneficial effect of probiotics was completely abrogated by the concomitant administration of anti-TNF antibodies^[68]. In a further study, the direct effect of epithelial TNF α on amelioration of epithelial barrier permeability in this experimental model, via the modulation of tight junctions proteins, occludin and claudin, was confirmed^[69].

Dendritic cells

Intestinal dendritic cells (DC) in the lamina propria of the mucosal layer represent a unique population of innate immune cells whose characteristics are shaped by cell-cell and host-bacteria interactions^[70]. Among the specific function of those cells are luminal antigen sampling, T-cell stimulation and differentiation, microbial uptake, pathogen defense, and, notably, the modulation of tolerance toward non pathologic stimuli, such as commensal bacteria, by means of IL10/IL12 balance at mucosal side^[71]. The possible relevance of DCs alterations in IBD

is supported by experimental data in which mice with deregulated DC-related pathways (*i.e.*, A20, β -catenin and phosphatidylinositol-3-kinase) develop either spontaneous colitis or increased susceptibility to experimental colitis^[72,73]. Furthermore, in IBD patients, lamina propria DCs and macrophages produce higher amount of pro-inflammatory cytokines compared with normal controls^[74].

For their relevance in the mucosal homeostasis maintenance, and for their crucial “bridging” role between innate and adaptive immunity activation, DCs has been indicated as potential targets of probiotic bacteria in IBD. In fact, *L. salivarius* Ls33 and *L. rhamnosus* Lr32 promoted tolerogenic action of DC *in vitro*, and administration of probiotic-incubated DC ameliorated trinitro-benzene-sulfonic acid induced colitis in mice^[75]. A fermentation product of *B. breve* has been shown the potential to modulate DC function *in vitro* by selective activation of MAPK, GSK3 and PI3K^[76]. Five commensal/probiotic bacteria incubated with immature DC induced a distinct cytokines profile and a tolerogenic phenotype through the selection of hyporesponsive T cells^[77]. The probiotic mixture VSL#3 increased IL-10 in intestinal and blood DC's from healthy volunteers, and inhibited Th-1 cells and IL-12 production^[78].

Immunomodulation of the acquired immune response

IBD has been considered for a long time as a disease primarily caused by dysregulation of acquired immune responses, with over-reactive effector pathways of the Th1 (CD) or Th2 (UC) type. This view was sustained by the observed increase of cytokines of the Th1 pathways (TNF, IFN γ) in CD patients and overexpression of IL-5 and IL-13 in colonic specimens of UC patients^[79]. Furthermore, the importance of activated lymphocytes has been confirmed by the development of animal models of IBD with specific up-regulation of Th1 derived cytokines (IL-10 KO, TNF Δ ARE mice)^[80,81], and by the observation that inflammatory disease in experimental models can be induced to SCID mice by the adoptive transfer of specific subpopulations of lymphocytes^[82]. The immune imbalance may be due either to defective regulatory pathways (T-regs, IL-10 and TGF β) and/or the increment of pro-inflammatory Th1 and/or Th2 derived cytokines. In recent years, this schematic paradigm has been consistently disputed: cytokines of both Th1 and Th2 derivation has been observed both in CD and UC patients^[46] and efficacy of anti-TNF antibodies in UC confirmed that Th1 cytokines has an important role for inflammation even in UC and not only in CD^[83]. At present the classical pathogenic scheme has been replaced by a model in which different mediators (cytokines) interplay in the induction, development and maintenance of inflammatory disease (in CD and UC)^[46], thus overcoming the schematic division of the past. Despite the overwhelming recent evidence supporting a primary role of innate immunity in the pathogenic cascade leading to IBD development, the dramatic efficacy of anti-TNF antibodies, the fact that blockage of adaptive immune responses

remains the main target of therapy (*i.e.*, corticosteroids, immunosuppressants), the promising data from leukocytopheresis^[84], bone marrow and mesenchymal stem cells transplantation^[85], testify that acquired immune response over-activation is an important factor for inflammation onset and maintenance in IBD. In addition, the recent discovery of the relevance of IL23/IL17 pathways, supported by the observation of increased concentration of Th17 lymphocytes (producing IL17 upon stimulation of IL23) in the inflamed mucosa of CD patients^[86,87], and the effective amelioration of experimental inflammation by selective blocking of IL23/IL17 pathways^[88,89], has given new impulse to the investigation of the role of the adaptive compartment in IBD pathogenesis. Accordingly, monoclonal antibody targeting of the p40 subunit of IL12/IL23 (Ustekinumab) is currently under investigation as potential therapy in CD^[90]. Commensal bacteria have an important role in the physiologic maturation of the adaptive compartment of the immune system, since germ-free mice have low number of CD4 T cells producing IL17, IFN γ , TNF α and IL-10^[91].

Several probiotic bacteria have a direct inhibitory effect on the pro-inflammatory cytokines production and a concomitant stimulatory function on T-reg cells and modulatory cytokines. The probiotic mixture VSL#3 was shown to induce IL-10 dependent T-reg cells in an animal model of recurrent chemical-induced colitis^[92], and to increase tissue levels of IL-10 and reduce pro-inflammatory cytokines, nitric oxide synthesis and metalloproteinase activity in the inflamed pouch^[93]. In a microarray analysis, LGG altered the expression of several genes related to immune response and inflammation in human duodenal mucosa^[94]. In the IL-10 KO model of colitis, the probiotic bacteria *L. plantarum*, *B. infantis* and *L. salivarius* prevented and/or ameliorated inflammation by down-regulation of pro-inflammatory Th1 derived cytokines^[95,96]. Three strains of Lactobacilli reduced Th2 response and activated T-reg frequency in health mice in a strain dependent way^[97]. In a pediatric study, rectal enemas with *L. reuteri* ameliorated inflammation by augmenting mucosal expression of IL-10 and reducing of IL1 β , TNF α and IL8^[98]. *Bifidobacteria* and *S. thermophilus* stimulated the production of TGF β and the development of T-reg cells in PBMC from humans^[99]. Finally, in a mouse model of allergic asthma, *L. gasseri* suppressed the Th-17 pro-inflammatory response^[100].

CLINICAL APPLICATION

Despite the large amount of experimental data and the pathophysiological rationale for their use in IBD, solid clinical evidence for the applicability of probiotic supplementation in these conditions is still lacking. Existing data are convincing for maintenance of remission in pouchitis, promising for maintenance of remission in UC, but disappointing for CD (Table 1). In fact, a recent workshop of an expert committee expressed a grade A (supported by strong positive studies) recommendation for probi-

otic use for prevention and maintenance of remission of pouchitis (VSL#3) and for remission maintenance in UC (VSL#3 and *E. coli* Nissle 1917), a grade B (positive-controlled studies but some negative studies) for inducing remission in UC (VSL#3 and *E. coli* Nissle 1917), and a grade C (some positive studies but clearly inadequate amount of work to support the outcome) for induction of remission of pouchitis (VSL #3) and in CD (*E. coli* Nissle 1917, *S. boulardii*, LGG)^[101]. Interestingly, in the same expert workshop held three years before, all IBD indications scored a C grade of recommendation, with the sole exception of pouchitis prevention and maintenance of remission (A grade)^[102].

One of the major limitations for probiotic utilization is that considerable variability exists between studies in regards to probiotic species used, dosage and duration of therapy, as well as variability of the underlying inflammatory disease and concomitant medication usage. Indeed, IBD comprises a continuum spectrum of disease, which far exceeds the simplistic subdivision in the two main clinical entities of UC and CD. In the two far ends of the spectrum are patients with very mild and limited rectal disease and patients with extended and devastating complications such as perianal and systemic involvement. Thus, it is not surprising that the best results for probiotics have been accomplished in experimental models of IBD, where the inflammatory condition is the consequence of alteration of single specific pathways. Besides the appropriate design of clinical trials which should include clear end-points, satisfactory statistical power, well-selected probiotic formulations given in adequate dose and scheme^[103,104], the key for the future clinical investigation of probiotics application in IBD is the comprehension of the complexity of the single conditions and the appropriate selection of patients with similar characteristics in terms of disease activity, extension, phenotype and molecular features.

Pouchitis

Acute and chronic pouchitis are relatively frequent events in patients with Ileal Pouch Anal Anastomosis (IPAA) following colectomy for UC. The application of probiotics for the maintenance of remission after pouchitis represented the earliest and most established clinical indication of probiotics in IBD. The therapeutic administration of probiotics in patients with pouch has been proven effective in the remission maintenance and prevention of pouchitis, and for this indication the probiotic mixture VSL#3 has been included in the European Crohn and Colitis Organization (ECCO) guidelines^[105]. In fact, a recent Cochrane systematic review included two studies of VSL#3 *vs* placebo for remission maintenance of pouchitis after remission induced by antibiotics, and probiotic treated patients had significant lower rate of recurrence after 9 mo^[106] and 1 year^[107]. Accordingly, LGG administration significantly increased the duration time of remission in a three-year follow-up^[108]. The same meta-analysis included two studies analyzing the VSL#3 administration

Table 1 Main published randomized control trial on probiotics administration in patients with inflammatory bowel diseases

Author, year	Disease	Indication	Probiotic	n	Outcome
Gionchetti <i>et al</i> ^[106] 2000	IPAA	Remission maintenance	VSL#3	20 treated 20 placebo	Superior to placebo
Mimura <i>et al</i> ^[107] 2004	IPAA	Remission maintenance	VSL#3	20 treated 16 placebo	Superior to placebo
Gionchetti <i>et al</i> ^[109] 2003	IPAA	Prevention	VSL#3	20 treated 20 placebo	Superior to placebo
Gosselink <i>et al</i> ^[108] 2004	IPAA	Prevention	LGG	38 treated 35 no treatment	Superior to no treatment
Pronio <i>et al</i> ^[110] 2008	IPAA	Prevention	VSL#3	16 treated 15 no treatment	Superior to no treatment
Kuisma <i>et al</i> ^[111] 2003	IPAA	Pouchitis	LGG	10 treated 10 placebo	No difference
Rembacken <i>et al</i> ^[117] 1999	UC	Inducing and maintenance remission	<i>E. coli</i> Nissle 1917	57 treated 59 mesalamine	Not inferior
Kato <i>et al</i> ^[116] 2009	UC	Inducing remission	Fermented milk (<i>B. breve</i> + <i>B. bifidum</i>)	10 treated 10 placebo	No difference
Tursi <i>et al</i> ^[118] 2004	UC	Inducing remission	VSL#3	30 VSL#3 + balsalazide 30 balsalazide 28 mesalamine	VSL#3 + balsalazide better
Furrie <i>et al</i> ^[115] 2005	UC	Inducing remission	Synbiotic (<i>B. longum</i>)	9 treated 9 placebo	No difference
Matthes <i>et al</i> ^[124] 2006	UC	Inducing remission	<i>E. coli</i> Nissle 1917 (enemas)	20 treated (3 groups different doses) 20 placebo	Superior to placebo
Sood <i>et al</i> ^[126] 2009	UC	Inducing remission	VSL#3	77 treated 70 placebo	Superior to placebo
Miele <i>et al</i> ^[125] 2009	UC (pediatric)	Inducing and maintenance remission	VSL#3	14 treated 15 placebo	Superior to placebo (corticosteroids)
Tursi <i>et al</i> ^[118] 2004	UC	Inducing remission	VSL#3	71 treated 73 placebo	No difference
Kruis <i>et al</i> ^[119] 1997	UC	Remission maintenance	<i>E. coli</i> Nissle 1917	58 treated 60 mesalamine	Not inferior
Ishikawa <i>et al</i> ^[127] 2003	UC	Remission maintenance	Bifidobacteria-fermented milk	11 treated 10 placebo	Superior to placebo
Cui <i>et al</i> ^[128] 2004	UC	Remission maintenance	Bifidobacteria	15 treated 15 placebo	Superior to placebo
Kruis <i>et al</i> ^[120] 2004	UC	Remission maintenance	<i>E. coli</i> Nissle 1917	162 treated 165 mesalamine	Not inferior
Zocco <i>et al</i> ^[121] 2006	UC	Remission maintenance	LGG	65 LGG 62 LGG + mesalamine 60 mesalamine	No difference remission rate LGG longer relapse-free time
Wildt <i>et al</i> ^[122] 2011	UC	Remission maintenance	<i>L. acidophilus</i> LA-5 and <i>B. animalis</i> subsp. <i>Lactis</i> BB-12	20 treated 12 placebo	No difference
Malchow <i>et al</i> ^[136] 1997	CD	Remission maintenance	<i>E. coli</i> Nissle 1917	10 treated 10 placebo	No difference
Guslandi <i>et al</i> ^[135] 2000	CD	Remission maintenance	<i>S. boulardii</i>	16 mesalamine + probiotic 16 mesalamine	No difference
Prantera <i>et al</i> ^[131] 2002	CD	Remission maintenance (post-surgery)	LGG	18 treated 19 placebo	No difference
Schultz <i>et al</i> ^[134] 2004	CD	Inducing and maintenance remission	LGG	4 treated 5 placebo	No difference
Bousvaros <i>et al</i> ^[133] 2005	CD (pediatric)	Remission maintenance	LGG	39 treated 36 placebo	No difference
Marteau <i>et al</i> ^[139] 2006	CD	Remission maintenance	<i>L. johnsonii</i> (LA1)	48 treated 50 placebo	No difference
Van Gossum <i>et al</i> ^[140] 2007	CD	Remission maintenance	<i>L. johnsonii</i> (LA1)	34 treated 36 placebo	No difference
Chermesh <i>et al</i> ^[142] 2007	CD	Remission maintenance	Symbiotic 2000	15 treated 15 placebo	No difference

RCT: Randomized control trial; IPAA: Ileal pouch anal anastomosis; UC: Ulcerative colitis; CD: Crohn's disease; LGG: *L. rhamnosus* subsp. GG; *E. coli*: *Escherichia coli*.

in the prevention of pouchitis onset, finding the probiotic mixture superior to placebo^[109] and to no treatment^[110].

For acute pouchitis data are still sparse and conflicting. LGG was not superior to placebo in a randomized con-

trol trial (RCT)^[111], while in an open-label study VSL#3 was effective in patients with mild pouchitis^[112].

UC

Probiotic applications in UC are encouraging, although solid evidence for their use is still unproven. Two Cochrane systematic reviews analyzed the utilization of probiotics in induction of remission and in remission maintenance, respectively^[113,114]. The first included four studies: two small trials compared a symbiotic preparation with *B. longum* ($n = 9$ patients in treatment group *vs* $n = 9$ controls)^[115] and fermented milk supplemented with *B. breve* and *B. bifidum* ($n = 10$ treated *vs* $n = 10$ controls) to placebo in addition to standard therapy^[116]; in one trial supplementation of *E. coli* Nissle 1917 was equal to mesalamine ($n = 57$ probiotics *vs* $n = 59$ mesalamine group)^[117], and in one study patients treated with balsalazide plus VSL#3 ($n = 30$) had increased remission compared with patients receiving only balsalazide ($n = 30$) or mesalamine ($n = 28$)^[118]. The authors concluded that there is no evidence that probiotics are superior to placebo or mesalamine in inducing remission in UC^[113]. In the meta-analysis for remission maintenance, four studies were included. Two multicenter studies compared the administration of *E. coli* Nissle 1917 to mesalamine for 3 ($n = 58$ probiotic and $n = 60$ mesalamine) and 12 mo ($n = 162$ probiotic and $n = 165$ mesalamine), finding no difference in recurrence rate^[119,120], and one study compared LGG ($n = 65$), LGG+ mesalamine ($n = 62$) and mesalamine alone ($n = 60$) at 12 mo, finding no difference in remission rate but a longer disease free time in LGG treated group^[121]. One small trial compared administration of a probiotic mixture of *L. acidophilus* strain LA-5 and *B. animalis* subsp. *Lactis* strain BB-12 ($n = 20$) to placebo ($n = 12$), finding no difference^[122]. The authors of the meta-analysis conclude that there is no evidence that probiotics are superior to mesalamine or placebo for maintenance of remission in UC patients^[114]. Another recent meta-analysis analyzed 13 RCT of probiotics utilization in UC, both in induction of remission ($n = 7$) and in remission maintenance ($n = 8$, two studies analyzed both the outcomes)^[123]. For induction of remission, three supplemental studies were analyzed in addition to the ones already included in Cochrane's review, in which *E. coli* Nissle (only in abstract form^[124]) and VSL#3, in a pediatric^[125] and adult group of UC patients^[126], were tested. Overall, in a total of 399 patients (219 probiotics *vs* 180 standard therapy/placebo) the authors did not report significant difference in inducing remission between probiotic treated and placebo/standard therapy treated patients. In the maintenance of remission, eight clinical trials were included, five of which were previously excluded by the Cochrane meta-analysis due to lack of remission of the patients at the beginning of the trial^[117,125,127], short follow-up^[128], or because it was not a RCT^[129]. A total of 709 patients were globally analyzed (390 probiotics *vs* 319 standard therapy/placebo), and there was a statistically significant difference in favor of probiotic group for re-

mission rate (recurrence rate = 0.69, 95%CI: 0.47-1.01, $P < 0.05$). It is of note that the results of this meta-analysis should be interpreted with caution for the presence of significant heterogeneity across the studies.

CD

A Cochrane meta-analysis analyzed seven RCT (five full papers and two abstracts) for application of probiotic for maintenance of remission in CD patients, with a total of 160 patients^[130]. In two studies the remission was surgically-induced^[131,132], and in five medically-induced^[133-137]. Probiotics tested were LGG^[131,133,134,137], VSL#3^[132], *E. coli* Nissle 1917^[136], and *S. Boulardii*^[135]. Authors conclude that probiotics were not superior to placebo or aminosalicylates. Another recent meta-analysis examined probiotics in the post-operative prophylaxis, including five studies, none of which showed effectiveness of probiotics *vs.* placebo for the prevention of recurrence^[138]. Probiotics tested were *L. johnsonii*^[139,140], LGG^[131], VSL#3 in a study available only in abstract form^[141], and the preparation Symbiotic 2000^[142]. Only one small RCT tested the efficacy of probiotic in inducing remission in CD^[134], with no difference *vs* placebo. The disappointing results of human studies are confirmed in experimental models: in SAMP/YitFc spontaneous model of CD, administration of VSL#3 was effective only for prevention of disease, and not in established disease, and the preventive effect was obtained only with a 50-times higher dose comparing to the one effective in experimental colitis^[68]. Those data underscore that probably the application of probiotics in CD needs to be further improved in terms of dose and timing of administration.

CONCLUSION

The recent expansion of research on gut microbiota opened the way to the application of probiotic therapy for IBD. Probiotic bacteria may be of value in IBD, since consistent experimental work has unraveled potential molecular targets in the pathogenesis of intestinal inflammation. In IBD patients, altered bacterial composition, defects in the barrier function, impairment in innate and adaptive immune response, may lead to a deregulated chronic inflammatory condition. Probiotics are likely to act through different mechanism affecting all the aforementioned defects and restore alterations at several levels, thus promoting gut health and homeostasis. Nonetheless, clinical data are still inconclusive, in particular in CD. It is desirable that the progress in the research in IBD pathogenesis and in host-bacteria interaction will drive to a tailored approach, including appropriate selection of patients with specific features of disease, utilization of bacterial species with proven efficacy, and with the characterization of effective therapeutic schemes.

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