Targeting the gut to treat multiple sclerosis

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The gut-brain axis (GBA) refers to the complex interactions between the gut microbiota and the nervous, immune, and endocrine systems, together linking brain and gut functions. Perturbations of the GBA have been reported in people with multiple sclerosis (pwMS), suggesting a possible role in disease pathogenesis and making it a potential therapeutic target. While research in the area is still in its infancy, a number of studies revealed that pwMS are more likely to exhibit altered microbiota, altered levels of short chain fatty acids and secondary bile products, and increased intestinal permeability. However, specific microbes and metabolites identified across studies and cohorts vary greatly. Small clinical and preclinical trials in pwMS and mouse models, in which microbial composition was manipulated through the use of antibiotics, fecal microbiota transplantation, and probiotic supplements, have provided promising outcomes in preventing CNS inflammation. However, results are not always consistent, and large-scale randomized controlled trials are lacking. Herein, we give an overview of how the GBA could contribute to MS pathogenesis, examine the different approaches tested to modulate the GBA, and discuss how they may impact neuroinflammation and demyelination in the CNS.
Targeting the gut to treat multiple sclerosis

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Introduction

The gut-brain axis (GBA) is the bidirectional communication between the CNS and the gastrointestinal system, linking brain and gut functions. It involves a complex network of interactions between the endocrine, immune, autonomic, and enteric nervous systems. The gut microbiota and the intestinal barrier, key players in the GBA, have recently attracted much interest due to their emerging role in mediating health and disease and potential use as therapeutic targets. The gut microbiota affects many aspects of brain development and function, including microglia and astrocyte maturation and polarization, blood-brain barrier (BBB) formation and permeability, neurogenesis, and myelination (1–7). GBA disruption may participate in the pathophysiology of several brain disorders, including multiple sclerosis (MS) (6, 8–10). Numerous reports in the last decade have focused on the role of the gut microbiota and intestinal barrier in MS and its main animal model, experimental autoimmune encephalomyelitis (EAE). However, a great deal of controversy exists surrounding the extent and the exact mechanisms through which altered GBA may influence the development of CNS inflammation, demyelination, and axonal loss. In this Review, we summarize current literature exploring the GBA’s role in MS and relevant animal models, focusing on current and potential therapeutic strategies targeting the GBA to improve disease in people with MS (pwMS).

The GBA in MS and its animal models

MS is a multifactorial disease arising from a complex interplay between genetic and environmental factors (11, 12). Alterations in gut microbiota composition (13–18), gut-derived products (19–21), intestinal permeability (22–24), and endocrine (25) and enteric nervous system functions (26) have been described in pwMS. The consequences of these disruptions are linked directly or indirectly to activation of the immune system against CNS self-components and development of CNS autoimmunity. These pathophysiological aspects have started to be characterized in MS animal models, whereas mechanistic studies in pwMS are still scarce. Below, we will consider the role of the different GBA components (gut microbiota, intestinal barrier, and immune, autonomic, and endocrine systems) in CNS autoimmunity and evidence of their alterations in pwMS and in MS animal models.

The gut microbiota and products of bacterial metabolism

Previous studies have described perturbations in both gut microbiota composition and gut-related metabolic pathways in pwMS (13–21, 27). Differences in single taxonomic units are more widely reported than large-scale gut microbiota differences when comparing pwMS with healthy controls (HCs) (13, 14, 16, 28). Unfortunately, results across studies lack consistency. Sample size, subject heterogeneity, study design, type of controls, geographical location, sequencing platforms, and regions of 16S rRNA gene sequencing may all contribute to lack of reproducibility (29). Despite this limitation, certain taxa are consistently noted as differentially represented in pwMS compared with HCs. In a study involving 34 monozygotic twins discordant for MS, the genus Akkermansia was overrepresented in the untreated MS twin compared with the healthy twin (16). Two other studies confirmed these results, also demonstrating an increase in Acinetobacter and Methanobrevibacter and a decrease in Parabacteroides and Butyricimonas genera (13, 17). Other consistent changes observed across
multiple studies included a reduced abundance of Bacteroidaceae family, Faecalibacterium, Clostridium species, and Prevotella strains (15, 27, 30, 31). Clostridium species were shown to promote Treg accumulation in the colon, with a consequent immunomodulatory effect (32). Polysaccharide A, from the capsule of the human commensal Bacteroides fragilis, has been described as a powerful immune cell activator that induced clonal CD4+ T cell expansion (33) and IL-10 secretion in T and B cells (34, 35). Whether these gut microbiota alterations in MS could contribute to disease pathogenesis or are just a consequence remains unknown. Supporting a real pathogenic role is the finding that gut microbiota or gut-derived molecules obtained from pwMS could modulate EAE when transferred into mice (16, 17, 36).

Microbial metabolites are altered in pwMS. Pathways most commonly found modulated in the gut microbiota of pwMS include carbohydrate and lipid metabolism and short chain fatty acid (SCFA) and bile acid synthesis (14, 37). SCFAs, including acetate, propionate, and butyrate, are produced by microbial fermentation of dietary fiber in the colon, where they maintain intestinal barrier integrity and dampen intestinal inflammation (38). They are then absorbed by the host and exert systemic immunomodulatory effects (20, 38, 39). Emerging evidence indicates that SCFAs can cross the BBB and control neuroimmune homeostasis (40). SCFAs were significantly decreased in people with secondary progressive MS with long disease duration compared with HCs (20). Propionate levels were reduced in serum and stool samples of two different cohorts of pwMS across different disease subtypes compared with HCs. This alteration was concomitant to a reduction in the abundance of SCFA-producing gut bacteria, decreased Tregs, and increased IL-17–producing T cell proportions in blood (21).

In contrast, plasma levels of acetate were reported to be higher in a cohort of pwMS compared with HCs and correlated with both Expanded Disability Status Scale (EDSS) score and proportions of IL-17–producing CD8+ cells (41).

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untreated mice, indicating this bacterial product’s protective role. Mice supplemented with the secondary bile acid tauroursodeoxy-
cholic acid (TUDCA) had lower EAE disease burden compared with untreated mice, indicating this bacterial product’s protective role.

The intestinal barrier
The intestinal barrier’s critical role in absorbing nutrients and metabolites, while preventing the permeation of intestinal microbes, toxins, and other antigens (44), is achieved through the actions of key components: the intestinal immune system; the epithelial layer, which regulates paracellular permeability or “gut leakiness”; and secretory products, including the mucus lining, which creates physical separation between the epithelium and luminal contents, and IgA, which is carried along the mucus lining (24, 45) (Figure 1).

The intestinal epithelium consists of a single layer of highly specialized cells held together by more than 50 transmembrane tight junction (TJ) proteins (45, 46). TJ proteins form a physical barrier between the apical and basolateral epithelial compartments and selectively regulate passive diffusion of ions and water-soluble molecules through the paracellular pathway (47).

The three major TJ proteins are occludin, claudins, and junctional adhesion molecule proteins (48). TJ barriers are dynamic, and TJ protein expression is influenced by many factors, including age, microbial antigens, and certain cytokines such as TNF-α (49–52). In human small intestine, the secreted protein zonulin or haptoglobin 2 precursor (HP2) is a master regulator of TJ protein expression, and its presence triggers TJ disassembly (47). Heightened intestinal permeability or “leaky gut” can cause unregulated passage of luminal contents into the host (47) and subsequent activation of immune cells by otherwise nonimmunogenic commensal microbes. Indeed, a leaky gut is a common hallmark of inflammatory disease, and HP2 overexpression has been observed in multiple autoimmune diseases, including MS (23, 47, 53).

A recent pilot study demonstrated that people with relapsing-remitting MS (RRMS) are more likely to have compromised intestinal permeability (54). Plasma from pwMS displays higher biomarkers of intestinal barrier integrity, particularly HP2 (55). These changes correlate with BBB disruption, as measured by MRI (55). Interestingly, HP2 is thought to pass into the bloodstream to reach the BBB, providing a possible mechanistic explanation for how intestinal barrier integrity may influence BBB permeability and subsequently CNS inflammation (24, 55). However, increased BBB permeability by HP2 was demonstrated only in vitro (24).

Consistent with altered gut barrier integrity, pwMS have increased low-grade bacterial translocation as measured by detectable plasma levels of LPS (23, 47) and increased LPS-binding protein, which was also reported in EAE (55, 56). More recently, peptidoglycan, an abundant bacterial cell wall component, was detected in brain tissue lesions of pwMS (57, 58). However, whether its presence in blood is indicative of inflammatory disease is not understood since peptidoglycan was previously detected in the serum of healthy patients (57).

As in pwMS, EAE mice develop increased intestinal barrier permeability accompanied by morphological changes in the small intestine (22, 59). These intestinal alterations were observed after adoptive transfer of myelin oligodendrocyte glycoprotein–reactive (MOG-reactive) CD4+ T cells, suggesting that circulating autoreactive T cells are critical to induce gut barrier alterations (22). Further, loss of intestinal barrier integrity worsened at EAE day 15 versus day 7, suggesting that EAE progression promotes gut permeability (22).

The intestinal tract’s mucus lining is a critical physical barrier between the host and microbes (60), composed of glycosylated proteins, collectively termed mucins, and electrolytes, lipids, and IgA (60). Mucin loss or excessive mucin degradation has been demonstrated to increase gut permeability and thereby create an inflammatory state. Certain microbes, such as A. muciniphila, are known to degrade the mucus layer and thereby alter the local immune milieu (61). As outlined above, A. muciniphila is increased in both pwMS and EAE mice (13, 62). While a strong correlation exists between the presence of mucus-degrading bacteria and MS, its contribution to disease pathogenesis remains unknown. Mucus-degrading bacteria may facilitate the inflammatory effects of other microbes and therefore only wreak havoc when combined with certain immunogenic bacteria (63). In contrast, a study in which miR-30d transfer promoted Akkermansia abundance found that EAE symptoms were suppressed via Treg promotion (36). Consistent with this, a recent study associated Akkermansia with lower disability in pwMS, and
when transferred in mice, Akkermansia ameliorated EAE via reduction of RORγt+ and IL-17–producing γδ T cells (64), suggesting an overall beneficial role similar to that observed in obesity, diabetes, and aging (65). Therefore, it is possible that Akkermansia's effects on health and diseases are context dependent and should be considered within the specific disease setting and parallel changes of other bacteria and gut microbiome structure.

The intestinal immune system

The mammalian gastrointestinal tract (GIT) harbors the body's greatest proportion of immune cells (66). These cells are in close contact with local microbiota and have the difficult task of protecting against pathogens while remaining tolerant toward food antigen and nonpathogenic commensals. The intestinal immune system comprises innate and adaptive immune cells, detailed extensively elsewhere (66, 67) (Figure 1). The microbial environment critically shapes the local immune system, as revealed by the vastly diminished immune compartment observed in the GIT of germ-free (GF) mice (67–69). In normal conditions, the intestinal lamina propria (LP) harbors a high proportion of Th17 cells (70), which protect against pathogens, while Tregs attenuate inflammatory responses and initiate immune tolerance (71, 72). It is thought that an imbalance between Tregs and Th17 cells may contribute to the breakdown of immune tolerance, driving a number of autoimmune diseases, including MS and EAE (73–75).

The microbiota can influence activation and proliferation of Tregs and Th17 cells, and both GF and antibiotic-treated mice develop attenuated EAE (76, 77). In one study, recolonization of GF mice with commensal bacteria restored EAE susceptibility by promoting differentiation of Th17 cells in the gut, and recolonization with segmented filamentous bacteria alone was enough to promote EAE development via stimulation of IL-17 production (75). People with active RRMS had significantly higher percentages of Th17 cells in the small intestinal mucosa compared with HCs (31). In EAE, MOG-specific Th17 cells migrate to the colonic LP before disease onset and induce dysbiosis; in this study, blocking intestinal homing of Th17 cells attenuated disease severity (78). New research has revealed that IL-17−/− mice have a distinct microbiota, which protects from EAE development. However, this protection was lost following transfer of microbiota from WT mice, indicating that intestinal IL-17 production might directly influence gut microbiome composition and be necessary for disease development (75). In contrast, another study found that blocking MOG-specific Th17 cells’ migration to the gut worsened disease severity in a mouse model of spontaneous EAE. This study's authors concluded that these cells were no longer sequestered in the intestine and so continued to contribute to disease progression within the CNS (79).

Humoral immunity also plays a paramount role in the gut. Gut microbiota influence differentiation of IgA+ plasma cells (PCs), and IgA binding of specific bacteria was shown to influence gut colonization and niche formation in the human colon (80). Accordingly, GF mice have very low IgA levels (81). In a recent paper, pwMS exhibited a reduction in fecal IgA during MS relapses, and IgA+ B cells were able to gain access to the inflamed CNS (82). IgA+ B cell removal exacerbated EAE, an outcome rescued by PC transfer, demonstrating their protective role (82). Moreover, gut microbiota–specific IgA+ B cells showed a different specificity in pwMS compared with HCs in another recent paper: the most prominent operational taxonomic units bound by IgA in pwMS, but not in HCs, were A. muciniphila, Eggerthella lenta, Bifidobacterium adolescentis, and Ruminococcus (83).

The autonomic and enteric nervous systems

The autonomic nervous system comprises the sympathetic, parasympathetic, and enteric divisions, which together connect the gut and the CNS (84, 85). The ENS consists of neurons and glial cells located in the gut smooth muscle and submucosal layers. These cells can regulate intestinal motility and permeability independently of CNS inputs. Gut microbiota influence both CNS and ENS development, as evident in GF mice, whose myenteric plexus is structurally abnormal, exhibiting decreased nerve density and number of neurons per ganglion (86). Some neurotransmitters are common between the CNS and ENS, and perturbations of the ENS have been described in neuroinflammatory and neurodegenerative diseases (8, 26, 85). In a B cell/antibody-dependent EAE model, ENS degeneration in the myenteric plexus was described before disease onset and was mediated by autoantibodies (26), which were also detected in a small cohort of pwMS, along with ENS gliosis (26).
The vagus nerve is the principal component of the parasympathetic nervous system. Its afferent and efferent fibers innervate the GIT and communicate directly and indirectly with the gut microbiota and the immune system. Vagal afferent fibers can sense bacterial products such as LPS and hormones (e.g., cholecystokinin, glucagon-like peptide-1, peptide YY) produced by enteroendocrine cells in response to food intake or microbial metabolites (87, 88). Acetylcholine (ACh), the neurotransmitter released by vagus efferent fibers, was shown in vitro to inhibit proinflammatory cytokine production in macrophages, leading to the “cholinergic antiinflammatory hypothesis” (89). Interestingly, people with RRMS have reduced ACh both in serum and cerebrospinal fluid (CSF), along with increased inflammatory cytokines (87, 88). Acetylcholine (ACh), the neurotransmitter released by vagus efferent fibers, was shown in vitro to inhibit proinflammatory cytokine production in macrophages, leading to the “cholinergic antiinflammatory hypothesis” (89). Interestingly, people with RRMS have reduced ACh both in serum and cerebrospinal fluid (CSF), along with increased inflammatory cytokines (87, 88). Acetylcholine (ACh), the neurotransmitter released by vagus efferent fibers, was shown in vitro to inhibit proinflammatory cytokine production in macrophages, leading to the “cholinergic antiinflammatory hypothesis” (89). Interestingly, people with RRMS have reduced ACh both in serum and cerebrospinal fluid (CSF), along with increased inflammatory cytokines (87, 88). Acetylcholine (ACh), the neurotransmitter released by vagus efferent fibers, was shown in vitro to inhibit proinflammatory cytokine production in macrophages, leading to the “cholinergic antiinflammatory hypothesis” (89). Interestingly, people with RRMS have reduced ACh both in serum and cerebrospinal fluid (CSF), along with increased inflammatory cytokines (87, 88). Acetylcholine (ACh), the neurotransmitter released by vagus efferent fibers, was shown in vitro to inhibit proinflammatory cytokine production in macrophages, leading to the “cholinergic antiinflammatory hypothesis” (89). Interestingly, people with RRMS have reduced ACh both in serum and cerebrospinal fluid (CSF), along with increased inflammatory cytokines (87, 88).

### The endocrine system

The endocrine system is another pathway of communication between the gut and the CNS (Figure 2). The HPA axis is considered a major neuroendocrine organ, regulating a multitude of body functions. In situations of stress, CRH, produced by the hypothalamus, induces the release of ACTH by the pituitary gland, which determines the release of corticosteroids by the adrenal gland (94). CRH and related hormones urocortin 1–3 influence intestinal motility, permeability, and immune responses (95–97). Evidence of a link between the GBA and HPA axes is derived, again, from experiments using GF mice. GF mice exhibited exaggerated HPA axis activation in response to stress that was not reverted upon recolonization in adult mice (8). Emerging evidence indicates the existence of bidirectional communication between the neuroendocrine system and gut microbiota (98). The presence of gut microbiota influenced not only the physiology of the HPA axis but also its response to stress, possibly through the modulation of vagal responses (99, 100). Altered levels of brain-derived neurotrophic factor (BDNF), NMDA, and 5-HT expression in the cerebral cortex, amygdala, and hippocampus have been described in GF mice (101). Several lines of evidence implicate the HPA axis in MS pathogenesis, MS disease progression, and occurrence of comorbid mood disorders (102–104). Clinical and postmortem studies in pwMS demonstrated elevated basal cortisol plasma levels, enlarged adrenal glands, higher cortisol levels in CSF, and increased CRH-producing hypothalamic neurons (104–106). Notably, low HPA axis activity was correlated with increased disease severity in pwMS (25).

### Targeting the gut to modulate CNS autoimmunity

Animal studies clearly support the involvement of gut microbiota in regulating CNS inflammation, microglia functions, myelination, and BBB integrity (1, 2, 107). Since these processes have proven relevant in the pathophysiology of CNS autoimmunity, perturbations of the gut microbiota and/or gut permeability are expected to impact the pathology and clinical course of disease in mice and possibly in humans. Accordingly, various interventions targeting gut microbiota composition and/or intestinal integrity have been implemented to treat CNS autoimmunity in preclinical and clinical studies (Figure 3). Most studies evaluating the effects of gut manipulation on CNS inflammation have been performed in the EAE model; however, a handful of studies have used other experimental MS models, such as the Thiefer’s murine encephalomyelitis virus

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**Table 1. Preclinical studies testing antibiotic therapy to modulate CNS autoimmunity**

<table>
<thead>
<tr>
<th>Animal model</th>
<th>Intervention</th>
<th>Results</th>
<th>Proposed mechanisms</th>
<th>Ref.</th>
</tr>
</thead>
<tbody>
<tr>
<td>EAE SJL mice</td>
<td>Oral ampicillin, vancomycin, neomycin, and metronidazole for 7 days before EAE induction</td>
<td>Disease amelioration</td>
<td>Accumulation of Tregs in peripheral lymph nodes</td>
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<tr>
<td>EAE C57BL/6 mice</td>
<td>Intraperitoneal ampicillin treatment in late-stage EAE</td>
<td>Disease worsening</td>
<td>↓ commensal bacteria capable of transforming tryptophan into AHR agonists</td>
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<tr>
<td>EAE NOD/ShIlt mice</td>
<td>Oral antibiotic mix before EAE induction</td>
<td>Disease amelioration</td>
<td>Altered gut microbiome and increased Tregs in Peyer patches</td>
<td>110</td>
</tr>
<tr>
<td>TMEV SJL/J mice</td>
<td>Oral ampicillin, vancomycin, neomycin sulfate, and metronidazole starting after TMEV infection</td>
<td>Prevented motor disfunction, limited axon damage and CNS immune cell infiltration</td>
<td>↑ CD4+ CD39+ T cells and CD5+CD16+ B cell populations in the CNS and decreased IL-17 production in the periphery</td>
<td>112</td>
</tr>
<tr>
<td>EAE C57BL/6 mice</td>
<td>Oral norfloxacin and Clostridium butyricum (C. butyricum) for 7 days before EAE induction</td>
<td>Disease amelioration</td>
<td>↓ Firmicutes/Bacteroidetes ratio and Th17, while increasing Treg responses in the GIT</td>
<td>30</td>
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<tr>
<td>Lyssolecithin-induced CNS demyelination C57BL/6 mice</td>
<td>Oral treatment with antibiotic mix for 12 weeks before lyssolecithin</td>
<td>↑ inflammatory activation of infiltrating macrophages and resident microglia; impaired myelin debris clearance and OPC differentiation</td>
<td>Altered gut microbiota composition</td>
<td>114</td>
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<tr>
<td>EAE C57BL/6 mice</td>
<td>Oral ampicillin, vancomycin, neomycin, or metronidazole or a combination of these before immunization</td>
<td>Prevented demyelination in the spinal cord</td>
<td>Depleted gut microbiome and decreased number of MOG-specific T cells</td>
<td>109</td>
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AHR, aryl hydrocarbon receptor; OPC, oligodendrocyte precursor cell.

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(TMEV) model and toxin-induced models of CNS demyelination. Tables 1, 2, 3, and 4 summarize preclinical and clinical studies targeting the gut to modulate CNS autoimmunity.

**Antibiotic treatment.** Antibiotic treatment has been shown to ameliorate EAE through effects mediated via the gut microbiota (30, 77, 108–110). Seminal work demonstrated that oral treatment with broad-spectrum antibiotics significantly altered the gut flora (30, 77, 108–110). Seminal work demonstrated that oral treatment getting the gut to modulate CNS autoimmunity.

### Table 2. Preclinical studies testing probiotic supplementation to modulate CNS autoimmunity

<table>
<thead>
<tr>
<th>Animal model</th>
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<th>Proposed mechanisms</th>
<th>Ref.</th>
</tr>
</thead>
<tbody>
<tr>
<td>EAE C57BL/6 mice</td>
<td>Oral administration of a Lactobacilli mix 12 days before immunization</td>
<td>Disease amelioration</td>
<td>↓ CNS infiltration by CD4+ T cells and production of IFN-γ and TNF-α. ↑ Tregs and IL-10 in the periphery</td>
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<td>EAE C57BL/6 mice</td>
<td>Monocolonization with SFB in GF mice</td>
<td>Restored EAE susceptibility</td>
<td>Restored the capacity of gut DCs to stimulate T cell responses</td>
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<td>EAE C57BL/6 mice</td>
<td>Treatment with Lactobacillus (L. plantarum) and Bifidobacterium animalis (B. animalis) starting at EAE induction</td>
<td>Disease amelioration</td>
<td>↓ CNS infiltration and increased the number of Tregs in lymph nodes and spleen.</td>
<td>124</td>
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<tr>
<td>EAE C57BL/6 mice</td>
<td>Oral administration of E. coli Nissle 1917 after EAE induction</td>
<td>Disease amelioration</td>
<td>↓ migration of MOG-reactive T cells into the CNS. Prevented intestinal barrier perturbation</td>
<td>59</td>
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<tr>
<td>EAE C57BL/6 mice</td>
<td>Monocolonization of GF mice with Prevotella histicola (P. histicola)</td>
<td>N/A</td>
<td>↑ IL-10*CD4+ T cell differentiation in peripheral lymphoid tissues</td>
<td>17</td>
</tr>
<tr>
<td>EAE HLA-DR3.008 double-transgenic mice</td>
<td>Oral treatment with Prevotella histicola (P. histicola)</td>
<td>Suppressed EAE development</td>
<td>↑ levels of IL-10 and TGF-β. ↓ production of IL-17 and IFN-γ by splenocytes after in vitro stimulation with proteolipid protein</td>
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<tr>
<td>EAE C57BL/6 mice</td>
<td>Intraperitoneal treatment with Lactobacillus helveticus starting 3 weeks before immunization</td>
<td>Disease amelioration</td>
<td>↓ Th17 in the peripheral lymph nodes and their infiltration into the CNS.</td>
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<tr>
<td>EAE C57BL/6 mice</td>
<td>Oral Lactobacillus reuteri (L. reuteri) starting at immunization</td>
<td>Disease amelioration</td>
<td>↓ CNS infiltration and Th1/Th17 cells and their cytokine production</td>
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<tr>
<td>EAE C57BL/6 mice</td>
<td>Cocolonization of GF mice with L. reuteri with a novel strain of Erysipelotrichaceae</td>
<td>Worsened disease: amplified MOG response</td>
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</tbody>
</table>

In summary, EAE studies suggest that antibiotic treatment has beneficial effects when administered preventatively but not once disease is established. Mechanisms mediating antibiotics’ effects are not understood but likely are due to microbial modulation, which may in turn alter immune activation (111, 118). Long-term antibiotic therapy in pwMS shows promising results but carries risks, such as promoting the growth of opportunistic pathogens, including Clostridium difficile (C. difficile), fungi, and antibiotic-resistant infections (119). Furthermore, the possibility of direct side effects, such as dental discoloration, rash, and photosensitivity with minocycline treatment (117), must also be considered.

**Probiotic supplementation.** Probiotics have gained much interest recently as potential therapeutic agents in MS. These live microorganisms are believed to exert their effects by modulating the gut flora to one that promotes intestinal barrier integrity and differentiation and activation of immunoregulatory over inflammatory cell subsets (120, 121). Probiotic administration in rodents with EAE has focused mainly on the effects of Lactobacillus strains, either alone or in combination with other strains (122–128). Most studies report an attenuation of EAE clinical course, but results are inconsistent and often contradictory. Herein we...
discuss some of the main published studies, mindful that this is not a comprehensive review of the literature on this topic (121). Daily oral administration of a mixture of *Lactobacillus* strains in EAE was effective both at preventing disease development and reversing established disease, an outcome that was IL-10 dependent and correlated with Treg induction in mesenteric lymph nodes and the CNS (125). Similarly, treatment with a mixture of *L. plantarum* of human origin and *B. animalis* attenuated EAE clinically and induced Tregs in lymph nodes and spleen (124). Oral administration of human-derived *L. reuteri* after immunization ameliorated EAE with a decrease in Th1/Th17 subsets and related cytokines (122). In contrast, a recent study showed that *L. reuteri* administration amplified MOG-specific responses in GF mice monoclonized with a novel strain of the Erysipelotrichaceae family (109). The molecular similarity observed between MOG and the *uvrA* gene product of *L. reuteri* was advocated as the possible mechanism mediating EAE exacerbation (109). Similarly, another study found that *L. reuteri* exacerbated EAE in genetically susceptible mice (129). Such conflicting findings may result from *L. reuteri’s* interaction with other commensal microbes present and their combined impact. Besides *Lactobacillus* strains, other gut bacteria given orally have been associated with probiotic effects and EAE amelioration, such as *C. butyricum* (30), *E. coli* strain Nissle 1917 (59), and *P. histicola* (130). Administration of a mixture of probiotics (Streptococcus, Bifidobacterium, and Lactobacillus strains) was also tested in the TMEV infection model, with beneficial effects of decreased CNS inflammation and increased motor activity during the disease (131).

Human studies are scarce, and treatment with a probiotic mix has only been tested in three studies involving pwMS (132–134). In two small double-blinded randomized controlled trials (RCTs), pwMS who received a mix of *Lactobacillus* and *Bifidobacterium* daily for 12 weeks showed significant improvements in disability score, depression, anxiety, and inflammatory markers, including reduced IL-8 and TNF-α expression in PBMCs (132, 133). Similarly, Tankou and collaborators administered a probiotic mix containing *Lactobacillus*, *Bifidobacterium*, and *Streptococcus* to pwMS and HCs twice daily for 2 months and found reduced CD80 expression on peripheral monocytes. The described changes in gut microbiota composition and the immune system were not maintained after probiotic discontinuation, thus suggesting the necessity of continuous supplementation (134).

In summary, research into probiotic supplementation in EAE and MS remains inconclusive and rigorous clinical trials are lacking. Results may be affected by dosage, duration, and type of bacterial strains; host genotype; immune status; and endogenous microbiota. Nevertheless, probiotic supplements are currently widely used by pwMS (121). A clinical study evaluating the effect of probiotic mix on patients with MS and CIS is ongoing (NCT04038541).

*Products derived from the gut microbiota.* Preclinical and clinical investigations into the therapeutic potential of microbial products, particularly SCFAs, are currently ongoing. Increase in SCFA levels is commonly achieved through either high-fiber diet or direct SCFA supplementation (135). While SCFA supplementation has shown efficacy particularly SCFAs, are currently ongoing. Increase in SCFA levels is commonly achieved through either high-fiber diet or direct SCFA supplementation (135). While SCFA supplementation has shown efficacy.

### Table 3. Preclinical studies testing SCFA supplementation, FMT, and diet modifications to modulate CNS autoimmunity

<table>
<thead>
<tr>
<th>Intervention</th>
<th>Animal model</th>
<th>Intervention</th>
<th>Results</th>
<th>Proposed mechanisms</th>
<th>Ref.</th>
</tr>
</thead>
<tbody>
<tr>
<td>SCFA</td>
<td>EAE</td>
<td>Supplementation with LCFAs or SCFAs at immunization or at disease onset</td>
<td>Treatment with LCFAs exacerbated and treatment with SCFAs ameliorated EAE</td>
<td>LCFAs induced mainly Th1/Th17 cells SCFAs induced Tregs</td>
<td>136</td>
</tr>
<tr>
<td></td>
<td>EAE</td>
<td>Oral administration of SCFAs for 3 weeks before immunization</td>
<td>Disease amelioration</td>
<td>↑ proportion of Tregs in the spleen and peripheral lymph nodes</td>
<td>137</td>
</tr>
<tr>
<td></td>
<td>EAE</td>
<td>Oral administration of SCFAs for 2–4 weeks before immunization</td>
<td>Disease amelioration</td>
<td>↓ expression of proinflammatory cytokines ↑ expression of IL-10 in the spinal cord</td>
<td>20</td>
</tr>
<tr>
<td>FMT</td>
<td>SJL mice (spontaneous RR model)</td>
<td>Colonization with microbiota obtained from twins discordant for MS</td>
<td>Disease worsening (microbiota from MS patients)</td>
<td>↓ IL-10 production by T cells after in vitro stimulation</td>
<td>16</td>
</tr>
<tr>
<td></td>
<td>EAE</td>
<td>Colonization with microbiota from pwMS 6 weeks before immunization</td>
<td>Disease worsening</td>
<td>Lack of IL-10 Treg induction in mesenteric lymph nodes</td>
<td>17</td>
</tr>
<tr>
<td></td>
<td>EAE</td>
<td>Oral treatment with mirt-30d after EAE onset</td>
<td>Disease amelioration</td>
<td>↑ CD4 Treg and MOG-specific Tregs in the spleen</td>
<td>36</td>
</tr>
<tr>
<td>Diet modification</td>
<td>EAE</td>
<td>IF started before or on the day of immunization</td>
<td>Prevented or ameliorated EAE</td>
<td>N/A</td>
<td>150</td>
</tr>
<tr>
<td></td>
<td>EAE</td>
<td>IF regimen started 4 weeks before immunization</td>
<td>Disease amelioration</td>
<td>Altered microbiome composition ↓ serum leptin and ↑ adiponectin ↓ IL-17 CD4+ T cells in the gut</td>
<td>144</td>
</tr>
<tr>
<td></td>
<td>EAE</td>
<td>Tryptophan-free diet started at the day of immunization</td>
<td>Prevented EAE</td>
<td>↓ MOG-reactive CD4+ T cells and IL-17A; altered microbiome composition</td>
<td>153</td>
</tr>
<tr>
<td></td>
<td>EAE</td>
<td>Methionine restriction started 2 weeks prior to immunization</td>
<td>Disease amelioration</td>
<td>↓ the expansion of Th17 cells</td>
<td>154</td>
</tr>
</tbody>
</table>

IF, intermittent fasting; LCFAs, long-chain fatty acid; RR, relapsing-remitting.
unveiled a possible dual role of SCFAs during CNS inflammation, whereby supplementation with a mix of propionate, butyrate, and acetate dampened EAE by increasing IL-10-producing T cells, but also induced inflammatory T cells through the GPCRs GPR41 and -43 (20). Additionally, propionate supplementation before EAE induction, but not at disease onset, ameliorated disease and increased Tregs in the intestinal LP (136). In the cuprizone model of CNS demyelination, butyrate treatment for 1 week before commencing toxin administration decreased demyelination and enhanced remyelination (138). Administration of an SCFA mix via drinking water in GF mice in steady-state conditions rescued microglia defects associated with the absence of gut microbiota and gut-derived metabolites similarly to that observed in GF mice reconstituted with live gut bacteria (139).

A recent clinical trial tested the effects of propionate supplementation for 2 weeks, as an add-on therapy in 91 pwMS and 24 HCs. Propionate lowered Th17 cells and increased Tregs and their in vitro suppressive capacity in an IL-10-dependent manner, and the effects were more pronounced in pwMS (21). Longitudinal data in 97 pwMS who underwent propionate supplementation for at least 1 year showed similar immunological changes, with a decrease in annualized relapse rate, disability stabilization, and a decrease in brain atrophy (21).

Besides SCFAs, other gut-derived metabolites have been studied as possible modulators of neuroinflammation. Bhargava and collaborators recently demonstrated that TUDCA administration reduced EAE clinical severity and could modulate astrocyte and

### Table 4. Clinical trials testing gut-based therapies in pwMS

<table>
<thead>
<tr>
<th>Intervention</th>
<th>Ref.</th>
<th>Study details</th>
<th>Results</th>
</tr>
</thead>
<tbody>
<tr>
<td>Antibiotics</td>
<td>115</td>
<td>Open-label trial: <em>n</em> = 15 pwMS with breakthrough disease activity were treated with IFN-β1a and 100 mg of doxycline daily for 4 months</td>
<td>Improved EDSS score and reduced gadolinium-enhancing lesions at MRI</td>
</tr>
<tr>
<td>Double-blind clinical trial: <em>n</em> = 60 pwMS with breakthrough disease were treated with 44 μg subcutaneous IFN-β1a 3 times a week or 30 μg intramuscular IFN-β1a once a week plus 100 mg of doxycline daily for 6 months</td>
<td>↓ relapse rate and improved EDSS score</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Randomized placebo-controlled clinical trial: <em>n</em> = 142 subjects diagnosed with CIS assigned to receive either minocycline or placebo for 24 months</td>
<td>↓ risk of conversion to MS at 6 months</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Probiotics</td>
<td>132</td>
<td>Randomized double-blind, placebo-controlled study: <em>n</em> = 60 (30/group) pwMS (18–55 years of age) with EDSS ≤ 4.5 receiving a probiotic mixture containing <em>Lactobacillus acidophilus</em> (L. acidophilus), <em>Lactobacillus casei</em> (L. casei), <em>Bifidobacterium bifidum</em> (B. bifidum), and <em>Lactobacillus fermentum</em> (L. fermentum) (each 2 × 10⁷ CFU/g) for 12 weeks</td>
<td>Improved plasma levels of CRP, nitric oxide metabolites, and MDA ↓ serum insulin and ameliorated insulin resistance parameters Improved EDSK, Beck depression inventory, general health questionnaire, and depression anxiety and stress scale</td>
</tr>
<tr>
<td>Gut-derived bacterial products</td>
<td>21</td>
<td><em>n</em> = 179 pwMS and 68 HCs received oral propionic acid for 14 days</td>
<td>↑ Treg induction and enhancement of Treg function Imbalance between Treg and Th17 cells in pwMS was restored</td>
</tr>
<tr>
<td>FMT</td>
<td>142</td>
<td>Case report on 1 SPMS (EDSS 6) patient receiving an FMT. Ten-year follow-up</td>
<td>EDSS score stabilized</td>
</tr>
<tr>
<td>Dietary restriction</td>
<td>143</td>
<td>Randomized, double-blind, placebo-controlled clinical trial: <em>n</em> = 60 participants assigned to ketogenic diet (<em>n</em> = 20), fasting mimicking diet for 7 days followed by Mediterranean diet (<em>n</em> = 20), or control (<em>n</em> = 20) for 6 months</td>
<td>Well tolerated ↑ in MS-related quality of life ↓ disability</td>
</tr>
<tr>
<td>Prospective cross-sectional study: <em>n</em> = 218 RRMS patients who were able to fast during Ramadan</td>
<td>↑ cognitive domain score at the MFIS and physical and mental health composites at the QOL scales</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Randomized, double-blind, placebo-controlled clinical trial: <em>n</em> = 36 RRMS randomly assigned to daily caloric restriction, intermittent caloric restriction, or control for 8 weeks</td>
<td>Weight loss ↑ emotional well-being</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Randomized, double-blind, placebo-controlled clinical trial: <em>n</em> = 17 RRMS, enrolled during a relapse, randomly assigned to IF or control for 15 days</td>
<td>Weight loss ↓ leptin and modulated gut microbiome composition</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

CIS, clinically isolated syndrome; CRP, C-reactive protein; KEGG, Kyoto Encyclopedia of Genes and Genomes; MDA, malondialdehyde; MFIS, Modified Fatigue Impact Scale; QOL, quality of life; SPMS, secondary progressive MS.
microglia polarization in vitro (19). To the best of our knowledge, studies testing bile acids in humans have not been published yet, but an ongoing RCT is evaluating safety and tolerability of TUDCA in people with progressive MS (ClinicalTrials.gov NCT03423121).

To conclude, initial studies on SCFA supplementation are promising. While there are no known side effects, adherence to supplementation is impaired by butyrate’s poor palatability. However, more randomized studies testing SCFAs or other gut bacterial products in pwMS are necessary to draw any conclusion.

Fecal microbiota transplantation. Given the condition of dysbiosis observed in pwMS, FMT has been proposed as a possible approach to reestablish a balanced gut microbiota. In EAE, FMT from naive into immunized mice resulted in reduced microglia and astrocyte activation, lower BBB leakage, and reduced demyelination and axonal loss (140). In a case study, a patient with MS who received daily FMTs from five donors displayed increased relative abundance of *F. prunetizii* and levels of propionate, butyrate, and BDNF and decreased proinflammatory cytokines in the weeks following the transplant. Clinically, the patient demonstrated an improvement in balance and walking capacity (141). Another report described clinical stability during a 10-year follow-up in a patient with secondary progressive MS who underwent an FMT procedure to treat recurrent *C. difficile* infections (142).

In summary, there is insufficient evidence to suggest a clinical benefit of FMT in pwMS, and several clinical trials are ongoing (ClinicalTrials.gov NCT04096443, NCT03594487, NCT04150549). Difficulties in implementing this approach arise from lack of consensus on variables such as donor selection, fecal matter processing, route of administration, recipient premedication, and frequency of transplant. Such variables also create challenges when comparing outcomes from different studies.

**Diet.** Manipulating calorie intake and diet composition is another way to modulate CNS autoimmunity through changing gut microbial ecology and possibly other GBA components. Dietary interventions such as dietary restriction (DR), ketogenic diet, high-fiber and high-fat diets (143–146), and Paleolithic diet constitute a large proportion of phospholipids in the mucus layer of the intestine. Small studies on ulcerative colitis showed how phosphatidylcholine supplementation was more effective than placebo in reaching clinical remission through enhancing barrier integrity (155). While this remains untested in patients with MS, it provides a potential area to be explored.

**Effects of current MS treatments on the GBA**

Disease-modifying treatments (DMTs) and immunosuppressive drugs currently used to treat MS can have some effects on the GBA (Figure 1). Therapy-induced changes in the gut microbiota (e.g., favoring microbes with antiinflammatory properties) could possibly contribute to their clinical efficacy, even though these aspects have not been well investigated. A recent cross-sectional study analyzed the effects of glatiramer acetate (GA) and DMF in 168 pwMS; while they did not change the overall microbial community structure compared with untreated pwMS, both impacted the abundance of several genera, with the most significant effect of DMF being on the order of Clostridiales (156). In contrast, a pilot study using delayed-release DMF found no statistically significant effects on the gut microbiota (157). Other studies also reported changes in gut microbiota composition after GA or IFN-β treatment, such as increased abundance of the genera *Prevotella* and *Sutterella*, with overall effects that tended to normalize some of the alterations observed in pwMS compared with...
HCs (13, 15). In EAE, the immunomodulatory effect of type I IFNs on CNS autoimmunity was linked to the induction of the transcription factor AHR, which was subsequently activated by microbiologically derived metabolites of tryptophan and resulted in antiinflammatory effects within the CNS. However, this study did not demonstrate a direct effect of treatment with type I IFNs on gut microbiota composition (113). Notably, both fingolimod and IFN-β have gut barrier-stabilizing properties by promoting intestinal barrier integrity, partly by regulating TJ proteins (55, 158). Natalizumab, an anti-α4 integrin mAb, modulates lymphocyte trafficking and inflammation across both the BBB and gut epithelia and has been shown to reduce the severity of inflammatory bowel disease (159).

Immunosuppressive drugs could affect the gut microbiota’s function and composition. In nonhuman primates, alterations in gut microbiota composition and the immune system were described after treatment with alemtuzumab. Alemtuzumab induces profound systemic lymphocyte depletion that is also observed at the intestinal level (160). Lymphocyte depletion is associated with decreased abundance of Lactobacillus species and Weisella cibaria, decreased fungal diversity, and expansion of specific phylotypes, including Candida albicans (161, 162).

Steroids are commonly used to treat MS symptoms during a relapse, but little is known about the effect of steroid treatment on gut microbiota in pwMS. In mice, short- and long-term treatment with dexamethasone increased the abundance of Actinobacteria, Bifidobacterium, and Lactobacillus (163). As underlined above, pwMS show an overactivation of the HPA axis with higher levels of cortisol in the CSF compared with HCs (25). The activation of the HPA axis, associated with increased cortisol levels, can alter gut permeability, increasing circulating levels of immunostimulatory molecules (164).

Symptomatic treatments, such as drugs used for motor and/or psychiatric symptoms in pwMS, may also influence gut microbiota composition and could contribute to clinical efficacy. For example, antidepressant use can alter gut microbiota composition both directly and indirectly through modulation of neurotransmitter levels. The potential antimicrobial activity has been demonstrated for various classes of antidepressant drugs, such as tricyclics and selective serotonin reuptake inhibitors (165, 166), although the exact effect on gut flora composition is not clear. Similarly, a drug combining delta-9-tetrahydrocannabinol and cannabidiol, which is commonly used to treat muscle spasticity in pwMS, has been shown to reduce the levels of proinflammatory cytokines and the relative abundance of A. muciniphila in EAE (167).

Conclusions
Rapidly growing evidence supports the GBA’s role in MS pathogenesis, with the gut microbiome as a critical player. However, more research is needed to better clarify molecular pathways connecting gut and brain functions and how they impact CNS autoimmunity. Interventions including FMT, probiotics, antibiotics, and diet that modulate the GBA have been actively investigated in preclinical models and to some extent also in clinical settings. Despite promising immunomodulatory effects of these therapies, only limited data exist on their impacts on neurodegenerative disease mechanisms. Nevertheless, we believe that in the future, therapies targeting the gut microbiota may be beneficial as an add-on treatment to already approved DMTs because they could potentially act synergistically. Some of these gut-based approaches (e.g., probiotic supplements) are already often implemented by pwMS because they are easily accessible as over-the-counter medications. While they do not have major side effects, the lack of appropriate regulatory organizations to control different preparations underlines the necessity for more controlled studies.

Looking ahead, microbiome-associated therapeutics will likely serve as an important component for precision medicine in MS. This will require a comprehensive understanding of patients’ distinct gut microbial composition and function and thorough characterization of microbial interaction with the host immune system and other GBA components. This novel approach could also assist in monitoring response to treatments and may greatly benefit people suffering from this debilitating disease.

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