REVIEW

Voices from within: gut microbes and the CNS

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Abstract Recent advances in research have greatly increased our understanding of the importance of the gut microbiota. Bacterial colonization of the intestine is critical to the normal development of many aspects of physiology such as the immune and endocrine systems. It is emerging that the influence of the gut microbiota also extends to modulation of host neural development. Furthermore, the overall balance in composition of the microbiota, together with the influence of pivotal species that induce specific responses, can modulate adult neural function, peripherally and centrally. Effects of commensal gut bacteria in adult animals include protection from the central effects of infection and inflammation as well as modulation of normal behavioral responses. There is now robust evidence that gut bacteria influence the enteric nervous system, an effect that may contribute to afferent signaling to the brain. The vagus nerve has also emerged as an important means of communicating signals from gut bacteria to the CNS. Further understanding of the mechanisms underlying

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microbiome-gut-brain communication will provide us with new insight into the symbiotic relationship between gut microbiota and their mammalian hosts and help us identify the potential for microbial-based therapeutic strategies to aid in the treatment of mood disorders.

Keywords Microbiota · Commensal bacteria · Probiotic · Brain · Behavior · Vagus

Microbiota-gut-brain axis

It is now well established that the brain and the gut are engaged in constant bi-directional communication. Most individuals are made aware of such communication when alteration in gastrointestinal function is communicated to the brain bringing about the perception of visceral events such as nausea, satiety, and pain or when, in turn, stressful experiences lead to altered gastrointestinal secretions and motility [1].

The mechanisms underlying gut-brain axis communication involve neural pathways as well as immune and endocrine mechanisms. The gastrointestinal tract is a point of interaction between the body's largest concentration of immune cells, a vast network of 500 million neurons and the gut microbiota. With an estimated mass of 1–2 kg, the approximately 100 trillion bacteria that constitute the human gut microbiota consist of at least 1,800 genera and up to 40,000 species of bacteria [2] and together possess 100 times the number of genes in the human genome [3]. Given the scale of the metabolic and genetic coding capacity of this "virtual organ", it is not surprising that the gut microbiota impacts various aspects of host physiology [4–7]. It is now clear that these influences include modulation of gut-brain communication. Indeed, it is emerging



that the gut microbiota can modulate host neural development and adult function, both peripherally, in the enteric nervous system, and centrally. Perhaps, most remarkably, evidence suggests a hitherto unrealised dimension to the integration of host and microbiome; that the overall balance in composition of the microbiota, together with the influence of pivotal species that induce specific responses, can influence the CNS leading to the modulation of brain function and consequently mood and behavior.

This review will highlight existing evidence that changes in the gut microbiota or intestinal exposure to specific commensal bacteria can modulate the peripheral and central nervous systems to consequently alter brain functions. There will also be a discussion of the potential mechanisms through which signals from gut bacteria are communicated to the brain.

The immunomodulatory effects of the gut microbiota and commensal bacteria have been extensively discussed elsewhere [8, 9], and it is clear that cytokine production and other immune changes can modulate the peripheral and central nervous system and are associated with altered mood and behavior [10, 11]. Thus, while acknowledging that the immune system may play an important role in many of the phenomena described below [12, 13], here we will focus specifically on non-immune aspects of communication between gut bacteria and the CNS.

Flies, pheromones, and neuropeptides

The study of insects has provided some clear examples of the potentially profound effect of the gut microbiota on behavior. The congregation of locusts into the vast swarms that result in crop devastation is dependent on pheromones, the major components of which are phenol and guaiacol [14]. Dillon et al. [14] identified that locust gut microbiota were critical in the production of aggregation pheromones. Specifically, it was determined that guaiacol was absent and phenol present at a reduced level in fecal pellets from germ-free insects [14]. Furthermore, the introduction and establishment of the bacterium Pantoea agglomerans in the gut of axenic locusts resulted in the re-appearance of the two phenolics in the feces. These investigators went on to determine that a number of bacterial species that commonly comprise the locust gut microbiota are capable of converting plant derived vanillic acid to guaiacol [15], indicating a closer degree of integration between the locust and its microbial community had previously been suspected.

In a recent study by Sharon et al. [16], a population of fruit flies was divided with one half fed on molasses medium and the other on a starch medium. When the isolated populations were mixed, molasses fed flies preferred to

mate with other molasses fed flies while starch-fed flies preferred to mate with other starch-fed flies. These differences in mating preference occurred after only one generation on different growth media and could be maintained for at least 37 generations [16]. Antibiotic treatment abolished mating preference, suggesting that the fly microbiota was responsible for the phenomenon. The mating preference could be re-established in antibiotic-treated flies by infecting them with microbiota obtained from fly media. Starch-fed flies had markedly higher levels of Lactobacillus species in the microbiota than malt-fed. Significantly, mating preferences of starch-fed antibiotic-treated flies could be reestablished by infecting with a mixed culture of Lactobacillus species and a pure culture of Lactobacillus plantarum. Importantly, parallel experiments using other bacterial species isolated from starch-bred flies had no effect on mating preference [16]. Thus, these experiments demonstrated that a single bacterial species could induce mating preferences in fruit flies. Again, this study served to identify a highly integrated relationship between microbiota and host. Indeed, it is proposed that these findings provide support for the hologenome theory of evolution [17]. The hologenome is defined as the sum of the genetic material of the host and its microbiota. It is posited that the holobiont (host plus its associated microorganisms) acts as a unit of selection in evolutionary change, and that variation, an important factor in evolution, can occur through modification in either the host or the microbiota genomes [17].

While Sharon et al. [16] did not identify a specific mechanism by which bacteria induce mating preference, they suggest that, as with aggregation pheromone in locusts [14], the bacterially-induced mating signal could be a volatile compound emitted by the fly or a detectable compound on its surface. In support of this, the study identified five cuticular hydrocarbon sex pheromones, which play a major role in fly mating [18], were produced at significantly different levels between starch- and malt-raised flies [16]. These differences were reduced with antibiotic treatment [18], suggesting that specific symbiotic bacteria can influence the levels of fly sex pheromones and, by doing so, modify fly behavior.

While gut bacteria producing mating and aggregation pheromones in insects may appear far removed from mammalian systems, there may be clear analogies in the underappreciated fact that bacteria can act as a source of various biologically active peptides and mediators normally associated with mammalian neurotransmission. Molecules such as GABA, serotonin, melatonin, histamine, and acetylcholine have been identified as being produced by bacteria [19].

Bacteria can also produce gaseous neurotransmitters. Lactobacilli have been demonstrated to convert nitrate to



nitric oxide (NO), a potent regulator of both the immune and nervous systems [20]. NO levels in the small intestine and the cecum were 3–8 fold higher in rats that had been fed live lactobacilli and nitrate compared to controls. In addition, H₂S that is produced by constituents of the gut microflora has been shown to modulate gut motility through action at the vanilloid receptor TRPV1 on capsaicin-sensitive nerve fibers [21].

It has been proposed that late horizontal gene transfer can explain the existence of genes encoding many of the enzymes involved in the synthetic and metabolic pathways of catecholamines, histamine, acetylcholine, and GABA from bacteria. This concept is concordant with increasing evidence that signaling molecules of quorum-sensing systems, used by bacteria to communicate and coordinate their actions [22], can also bind to mammalian receptors and directly influence the host [23, 24]. This concept of shared signaling pathways is further supported by evidence that neurotransmitters produced by the host can influence the function of components of the microbiota. For example, in Escherichia coli O157:H7, the QseC sensor kinase is bacterial receptor for host-derived epinephrine/ norepinephrine which activates transcription of virulence genes in the bacteria; a response that can be blocked specifically by adrenergic antagonists [25].

Visceral perception and interoception

While the concept that the brain can alter gut function is widely acknowledged, and the relationship between stress and disorders such as irritable bowel syndrome has been the focus of extensive research, it is less readily accepted that signals from the gut might influence the CNS with associated consequences for mood and behavior. Such gut-driven changes to brain function are more readily understood when considered within the context of interoception.

The term interoception refers to sensing the physiological condition of the body [26], as well as the representation of the internal state [27] within the context of ongoing activities. Interoception is closely associated with emotional awareness [28] and motivated actions to homeostatically regulate the internal state [27]. Interoceptive signals include sensations such as pain, temperature, itch, tickle, sensual touch, muscle tension, air hunger, stomach discomfort related to low pH, and intestinal tension [26]. These sensations are transmitted to the brain by vagal and glossopharyngeal afferents synapsing with the nucleus of the solitary tract (NTS) and via small diameter primary sympathetic afferent fibers to a specific thalamocortical relay nucleus, and are integrated to provide a sense of the body's physiological condition [26].

In the early 1970s, Cabanac [29] proposed that a given external stimulus can be perceived as either pleasant or unpleasant, depending upon interoceptive signals. However, the role of visceral sensory input in physiological or pathological modulation of perception was only recently recognized. While early studies concentrated on the modulation of responses directly relevant to a given sensory input (e.g., hunger to feeding, stomach movements to nausea), there is now experimental data to suggest that changes in visceral sensation can affect the perception and interpretation of external inputs [30]. This has led to the suggestion that altered interoceptive signals can influence our attitude to the outside world and that pathological changes in visceral sensory inputs may increase the risk of affective behavioral disorders [31]. If beneficial bacteria could alter interoceptive signaling in an appropriate way, they may have a future potential as adjuncts in the treatment of these disorders.

Microbiota and the enteric nervous system

Gut bacteria may modulate gut motility by action on the enteric nervous system (ENS), which consists of ganglionated plexuses in the gut wall and whose presence is essential to life. The myenteric plexus component of the ENS controls peristalsis. Hence, enteric aganglionosis due to Hirschsprung [32] or Chagas [33] diseases, or chemical ablation using benzalkonium chloride [34], severely reduces peristalsis and produces pseudo-obstruction in the affected region.

Myenteric Dogiel type II AH cells innervate the mucosa and are chemosensitive intrinsic primary afferent neurons (IPANs) in guinea pig [35], rat [36], and mouse [37]. IPANs project directly to motor- and interneurons (S cells), though which they modulate the intensity and timing of muscle motor complexes and co-ordinate peristalsis [38]. In fact, selective silencing of only AH cells causes aperistalsis similar to total aganglionosis [39].

By far the richest innervation of mucosal epithelial layer cells derives from the myenteric plexus, which provides more than 90 % of sensory neuropeptide-containing fibers to the mucosal layer [40, 41]. Each enteric IPAN innervates 80–120 villi [38], and there are about 500,000 neuropeptide (calcitonin gene-related peptide, CGRP)-containing IPANs in the mouse [42]. Thus, IPANs are ideally placed to respond to luminal commensal and probiotic microorganisms, and are plausible targets though which the microbes could influence gastrointestinal physiology, perhaps independent of commensal bacteria to immune system signaling (Fig. 1).

That IPANs are indeed a cellular target of neuroactive bacteria has been demonstrated by whole cell patch



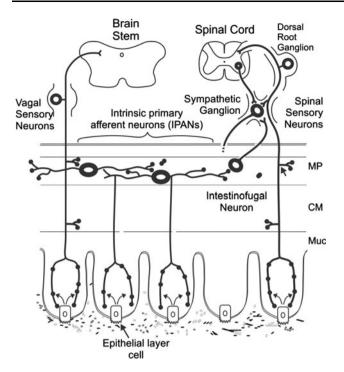


Fig. 1 Potential neural pathways from gut bacteria to the CNS. Sensory neurons include intrinsic primary afferent neurons (IPANs) in the myenteric plexus (MP) of the enteric nervous system, and vagal and spinal extrinsic primary afferent neurons. IPANs are multipolar with their somata and all neurites confined to the intestine. Vagal and spinal primary afferent neurons are pseudounipolar with somata extrinsic to the intestine; they have collaterals that enter enteric ganglia and form synapses with enteric neurons. Sympathetic and myenteric ganglia reciprocally innervate each other. Some 90 % of sensory neuropeptide containing axons that innervate the mucosal layers derive from intrinsic rather than extrinsic primary afferent neurons. Chemicals including hormones released from epithelial cells act on adjacent primary afferent neuron axons (curved arrows). Cell wall components or secreted products, including neurotransmitters, of microorganisms in the lumen or attached to epithelial cells may induce epithelial cells to release transmitter molecules that in turn modulate neural signaling, or act directly on primary afferent axons. MP myenteric plexus, CM circular muscle, Muc mucosa

clamp recording experiments using rats that were fed *L. rhamnosus* JB-1. Myenteric IPANs, but not motor- or interneurons, within colon segments taken from fed animals were more excitable than were those from controls. *JB-1* reduced the action potential firing threshold and discharge accommodation during injections of excitatory current pulses [36]. This increase in excitability was accompanied by a reduction in the post-action potential slow after hyperpolarization, which mediates discharge accommodation in IPANs [36]. It was proposed that the underlying molecular mechanism involved an intermediate conductance calcium-dependent potassium (IK_{Ca}) (Gardos type [43]) channel, because application of the IK_{Ca} channel blocker TRAM-34 mimicked the effects of JB-1, namely reducing the IPAN slow after hyperpolarization [36, 44].

Certain commensal or probiotic bacteria may have an analgesic action on the host. *L. rhamnosus* [45], *L. acidophilus* [46], or *L. paracasei* [47], as they have been shown to moderate pseudo-affective responses to nociceptive colorectal distension and to inhibit spinal neuron cellular memory of the distension.

The presence of anatomical synapses between extrinsic primary afferent (vagal [48] or spinal [49] axons and myenteric neurons suggest the possibility that the analgesia may have resulted from IPAN to extrinsic primary afferent transmission. However, while extrinsic fibres activate enteric neurons via slow excitatory postsynaptic potentials [50], intramural synaptic transmission does not appear to go in the opposite direction; that is, from enteric neurons to extrinsic primary afferent fibers [51]. Thus, the mechanisms underlying probiotic analgesia may involve alterations of the intensity of gut contractions [52] or modification of the excitability of extrinsic spinal primary afferent terminals within the mucosa.

Some of the anti-nociceptive effects accorded to a *Lactobacillus rhamnosus* were also seen with heat-killed or gamma-irradiated bacteria and even with conditioned medium obtained after culture of these bacteria [45]. Such experiments clearly suggest that components of bacteria and/or secreted products can mimic the effects of the live organisms. Ingestion by rats of a mutant bacterium, *L. plantarum*, in which p-alanine was markedly reduced within a cell wall constituent, lipoteichoic acid, was more effective than treatment with the parent wild strain in terms of immuno-regulatory effects [53] as well as inhibition of perception of visceral pain [54]. Thus, in this case, a bacterial cell wall component must, in part, have been a determinant of the immune as well as the neuronal effects.

In contrast to pain transmission, there are few chemical correlates of the functional effects that probiotics have on enteric neurons. Ingestion of Saccharomyces boulardii has been shown to decrease the number of pig myenteric AH cells that express the vitamin D-dependent cytosolic calcium binding protein calbindin-D28k [55]. A change in calcium intracellular buffering, as is suggested by this result, might be expected to alter the opening probability of IK_{Ca}. Yet, it is not clear, without further experiments, precisely how changes in calbindin correlate with the slow after hyperpolarization and neuronal excitability. The expression of μ -opioid and cannabinoid receptors in gut mucosal epithelial cells has been reported as being increased by feeding an analgesic stain of L. acidophilus [46]. Receptor tolerance that such receptors exhibit [56, 57] suggests that the increased expression may have resulted from a reduction in receptor activation by endogenous or microbial-produced agonists. However, it is not clear how epithelial opioid or cannabinoid receptors could gate



afferent signals in enteric nociceptive neurons. Clearly, further research is needed.

Evidence of gut microbiota influences on the CNS and behavior

Brain and behavior in the absence of gut microbiota

A number of important insights into the impact of the gut microbiota on host physiology have come from the study of germ-free animals. These key studies have indicated a role for gut bacteria in the normal development of behavior, and in particular in the stress response. Some of the earliest indications of a critical role of the gut microbiota in stress responses come from studies by Sudo and colleagues [7]. Germ-free animals were identified as having exaggerated hypothalamic–pituitary–adrenal (HPA) axis activation in response to stress. This hyperresponsiveness was reversed by reconstitution with feces from animals kept in a pathogen-free environment or with a single bacterial strain, *Bifidobacterium infantis* [7]. In contrast, mono-association with an enteropathogenic *E. coli* further enhanced the response to stress.

More recently, two studies have indicated that the absence of a microbiota results in decreased anxiety-like behavior compared to conventional animals [58, 59]. In one of these studies, Neufeld and colleagues [59] also demonstrated an increase in baseline plasma corticosterone of the germ-free mice. While seemingly incongruent with reduced anxiety, this finding is in keeping with the previous reports of an increased stress response in germ-free animals [7].

Interestingly, Heijtz et al. [58] demonstrated that early colonization of germ-free mice could normalize several germ-free behavioral patterns while conventionalization of adult mice failed to normalize the behavior. This indicates, as suggested by the earlier work of Sudo et al. [7], that the gut microbiota contributes to developmental programming; a process whereby an environmental factor acting during a developmental "window of vulnerability" can have a potentially life-long impact on physiological function [60].

Addressing neural correlates of reduced anxiety in germ-free animals, Heijtz et al. [58] demonstrated that NGFI-A mRNA expression was significantly lower in various subregions of the prefrontal cortex, including the orbital frontal cortex and the striatum, hippocampus dentate gyrus, and amygdala, compared with specific pathogen-free mice. Germ-free mice also had significantly lower BDNF mRNA expression in the hippocampus, amygdala, and cingulate cortex, which are important components of the neural circuitry underlying anxiety and fear [61, 62]. Such a reduction in BDNF expression levels

in the cortex and hippocampus relative to conventional mice was also noted by Sudo et al. [7]. Brain-derived neurotrophic factor is involved in the regulation of multiple aspects of cognitive and emotional behaviors, being a key promoter of neuronal survival and growth as well as differentiation of new neurons and synapses [63–65]. Serum levels of BDNF are significantly decreased in the plasma of depressed patients [66, 67], and in post-mortem hippocampal tissue from depressed suicide patients [68, 69]. The association between anxiety and BDNF is less clear, and studies have identified positive, negative, or no correlation between hippocampal levels and anxiety [70–73]. Perhaps reflecting this, Neufeld et al. [59] identified that reduced anxiety in germ-free mice was associated with an upregulation, rather than a decrease, in the expression of BDNF mRNA in the dentate gyrus of the hippocampus. The reasons underlying the conflicting findings regarding hippocampal BDNF in germ-free mice is unclear; however, both studies describing decreased BDNF expression were conducted in male mice [7] while Neufeld et al. [59] exclusively used female animals. This may be significant given existing evidence that the neurochemical and behavioral consequences of stress are sex-dependent [74]. Furthermore, the influence of BDNF on behavior appears to be sex-specific with increased anxiety-like behaviors observed in male but not female mice with joint serotonin transporter (SERT) and BDNF deficiency [75].

In addition to altered neurotrophin levels, changes have been reported in NMDA receptor subunit expression with decreased NR1 and NR2A in the hippocampus, decreased NR2A in the cortex, and decreased NR2B in the amygdala, but not in the hippocampus [7, 59]. Enhanced turnover rate of noradrenaline, dopamine, and 5-HT has also been demonstrated in the striatum of germ-free mice compared with specific pathogen-free mice [58].

It should be noted that at least one study has found no reduction in anxiety of germ-free mice when compared to controls, but instead identified impaired memory as assessed in the T maze [76]. The reasons for these distinct findings are unclear; however, taken together, existing data suggest that gut microbiota can influence a number of aspects of brain chemistry, stress responses, and behavior.

Modulation of the microbiota

In addition to the study of germ-free animals, the effects of changes in the composition of the conventional gut microbiota on behavior and brain chemistry have also been explored. Alterations in diet can lead to marked shifts in gut microbial populations [77, 78]. In a study by Li et al. [79], mice fed a diet containing 50 % lean ground beef were found to have a greater diversity of gut bacteria than those receiving standard rodent chow. The increase in



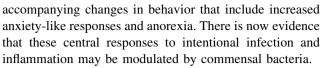
bacterial diversity was associated with an increase in working and reference memory as assessed in a hole-board open field test [79]. Furthermore, mice receiving the beef diet exhibited less anxiety-like behavior in response to the novelty of the testing environment. While no causal relationship was established, this study did provide early support for the suggestion that, in addition to any direct effects of dietary components, diet-induced changes in bacterial diversity may influence behavior.

More recent studies have involved the induction of experimental dysbiosis through the use of antimicrobial drugs. Bercik et al. [80] demonstrated that, in adult BALB/ c mice, oral administration of neomycin and bacitracin along with the antifungal agent primaricin led to a transient change in the composition of the gut microbiota. Interestingly, antibiotic treatment did not lead to quantitative changes in culturable bacteria but induced a significant change in composition; specifically, an increase in Actinobacteria and Lactobacilli species and decrease in γ-proteobacteria and bacteroidetes. The antibiotics also induced changes in behavior, with treated animals demonstrating evidence of increased exploratory drive and decreased apprehension in both the step-down and light/ dark preference tests. As was demonstrated in comparisons between germ-free and conventional animals, behavioral changes in antibiotic-treated animals were associated with altered BDNF levels in the brain, being decreased in the amygdala while increased in the hippocampus [80].

The effects of antibiotic treatment on the composition of the intestinal microbiota and on behavior were transient with treated mice resembling controls after a 2-week washout period. In these studies, a causal relationship between microbiota changes and behavioral effects is supported by the demonstration that, in contrast to oral antibiotic treatment, i.p. treatment did not influence behavior. Furthermore, antibiotic treatment had no effect on the behavior of germ-free animals [80]. Whether the behavioral changes can be attributed to specific alterations in the microbiota, e.g., increased lactobacilli and acintobacteria or decreased y-proteobacteria and bacteroidetes, was not investigated. However, this is an intriguing idea especially given subsequent studies demonstrating anxioeffects of feeding certain lactobacilli bifidobacterium strains [81, 82], and as such it would be interesting to assess the effects of agents that promote the growth of bifidobacteria and lactobacilli (often termed prebiotics [83]) on behavior.

Inflammatory models

Studies in animal models using chemical colitis or infection with pathogens have demonstrated that inflammation of the gastrointestinal tract can alter brain chemistry with



Citrobacter rodentium is being used increasingly as an infectious agent to investigate gut-brain axis function. In one such study of C. Rodentium-infected mice [76], no behavioral abnormalities were observed, either at the height of infection or following bacterial clearance. However when infected mice were exposed to acute stress, demonstrated to increase intestinal permeability [84, 85] as well as influence gut bacterial function[25], memory impairment was apparent both during infection and following clearance [76]. The dysfunction of non-spatial and working memory, assessed by the novel object and T maze tests, respectively, could be prevented by daily treatment of infected mice with a commercially available, mixed strain, probiotic preparation [76]. This probiotic pretreatment also ameliorated stress-induced serum corticosterone levels as well as preventing Citrobacter rodentium-induced reductions in hippocampal BDNF and c-fos expression [76].

In a recent series of studies, Bercik and colleagues [86], examined behavior and brain chemistry in mice following chronic mild gut inflammation induced by infection with Trichuris muris. They observed increased anxiety-like behavior as assessed by step-down and light/dark preference tests together with an associated decrease in mRNA message for hippocampal BDNF [86]. Feeding mice with a probiotic strain of B. longum normalized behavior and BDNF mRNA, and while many probiotic bacteria have been demonstrated to have anti-inflammatory actions [8], this particular B. longum strain did not alter intestinal levels of inflammatory cytokines TNF or IFN γ [86]. In the same model, treatment with the anti-inflammatory agents etanercept and budesonide, not surprisingly, did reduce TNF and IFNy in the intestine, but also normalized behavior. However this normalized behavior was not accompanied by a corresponding increase in central BDNF expression [86]. These results suggest different modes of action in normalizing behavior between B. longum and anti-inflammatory agents, but may also argue against a direct relationship between BDNF levels and anxiety-like behavior. While direct interaction between the probiotic and infectious agent may have contributed to the efficacy of B. longum in this model, it is important to note that the same strain of bacteria was demonstrated to normalize behavior in mice with non-infectious, chemically-induced colitis [82], again without altering markers of intestinal inflammation, in this case histological score and MPO levels.

These studies provide clear evidence for gut-brain communication being altered by changes in gut microbiota and more specifically following exposure to commensal or



probiotic strains. From a clinical perspective, they may be particularly relevant to certain inflammatory conditions, such as rheumatoid arthritis, chronic obstructive pulmonary disease, asthma, and inflammatory bowel disease, that are strongly associated with mood disorders or depression. However, there is also evidence that gut exposure to specific bacteria can alter constitutive brain chemistry and behavior in normal animals.

Conventional animals

Early evidence that bacteria in the gut can directly modulate central neural pathways even in the absence of an immune response came from the study of pathogen exposure [87]. Orally administered *Camphylobacter jejuni*, in subclinical doses, too low to elicit immune activation, can have anxiety-provoking effects in mice. In addition, at these same low doses, *C. jejuni* can activate visceral sensory nuclei in the brainstem. The areas of brainstem activation, the NTS and lateral parabrachial nucleus, participate in neural information processing that ultimately lead to autonomic neuroendocrine and behavioral responses [87].

It is also clear that non-pathogenic bacteria can activate central neural pathways. Tanida et al. [88] demonstrated that intraduodenal injection of the bacterial strain *Lactobacillus johnsonii* La1 reduced renal sympathetic nerve activity and blood pressure while enhancing gastric vagal nerve activity. All these effects could be abolished by pretreatment with a histaminergic H3-receptor antagonist. Similarly, the effects were absent in animals that had bilateral lesions of the hypothalamic suprachiasmatic nucleus, a major regulator of circadian rhythm. These findings suggest that the influence of the bacteria on autonomic neurotransmission and subsequently blood pressure is mediated centrally, likely through histaminergic nerves and the suprachiasmatic nucleus [88].

Early evidence that chronic treatment with a specific bacterial strain could affect, beneficially, neuronal systems and behaviors relevant to depression was obtained in a study using the rat maternal separation model [89]. This study compared the impact of chronic probiotic treatment with those of the antidepressant drug, citalopram, on behavior and biochemical changes in adult maternally separated offspring. Maternal separation induced a decrease in swim behavior and a concomitant increase in immobility in the forced swim test, features considered to indicate a state of behavioral despair [90]. The behavioral changes were associated with decreases in noradrenaline content in the brain, elevated CRF mRNA levels in the amygdaloid cortex, and enhanced release of the cytokine IL-6 following immune stimulation [89]. While the effects were not as marked as treatment with citalogram, treatment with the probiotic bacteria *B. infantis* resulted in reversal of behavioral deficits, restoration of basal noradrenaline concentrations in the brainstem, and normalization of the immune response [89]. Similarly, Gareau et al. [91] demonstrated that treatment of rat pups with a mixture of two lactobacillus strains attenuated the increase in serum corticosterone levels induced by maternal separation, suggesting an normalization of the HPA response in these animals.

More recently it was demonstrated that long-term (28-day) oral administration of a *L. rhamnosus* strain (JB1) could alter the normal behavior of adult balb/c mice [81]. Chronic treatment with the bacteria reduced anxiety-like behavior as assessed in an elevated plus maze and decreased the time spent immobile in a forced swim test. In addition, stress-induced plasma corticosterone levels were lower in treated mice, a similar effect to subchronic or chronic treatment with antidepressants that can prevent forced swim stress-induced increases in plasma corticosterone in both mice and rats. Overall, changes induced with *L. rhamnosus* were indicative of reduced anxiety and decreased depression-like behavior [81].

Experiments also indicated that the lactobacillus-treated mice had increased cue- and context-dependent freezing responses in the recall phase of a fear conditioning paradigm. While this may be suggestive of increased fear memory, this type of increased emotional learning may also be interpreted as enhanced anxiety behavior; under this interpretation, it may be that the bacteria have differential effects on conditioned compared with unconditioned aspects of anxiety [81].

Mice that received L. rhamnosus also demonstrated alterations in central GABA receptor subunit mRNA expression. Long-term L. rhamnosus administration decreased expression of GABA type B (GABAB) subunit 1 isoform b (GABAB1b) mRNA in the amygdala and hippocampus, while increased expression was detected in cortical areas. Furthermore, expression of GABAAa2 receptor mRNA was reduced in the amygdala and cortical areas, whereas levels were increased in the hippocampus [81]. As with many of the studies described here, it is difficult to attribute a causal relationship between behavioral effects observed and changes in brain chemistry. However, it is relevant to note that reduced expression of GABAB1b mRNA, in the amygdala, hippocampus, and locus coeruleus is consistent with the antidepressant-like effect of GABAB receptor antagonists [92]. The enhanced memory to an aversive cue and context is also suggestive of changes at the level of the amygdala and hippocampus [93, 94]. The changes in behavior and GABA receptor expression following L. rhamnousus treatment were also in keeping with studies of GABAB1b-deficient animals, indicating an important role for this subunit in the development of



cognitive processes, including those relevant to fear [95, 96]. However, no extensive investigation of the cognitive effects of bacteria treatment was pursed in this study. Indeed, with the exception of evidence of some memory dysfunction in germ-free mice [76], little is known of the potential for altered gut microbiota or exposure to specific gut bacteria to modulate cognitive functions.

Mechanisms underlying gut bacteria effects on the CNS

The vagus nerve

Information from the heart, lungs, pancreas, liver, stomach, and intestines are delivered tonically to the brain via sensory fibers in the vagus nerve [97]. Sensory vagal inputs arrive in the nucleus of the solitary tract (NTS), and are thence transmitted to widespread areas of the CNS, including the cerebral cortex and medulla oblongata. Neurones of the rostral ventrolateral medulla oblongata (RVLM) provide one of two major sources of afferent inputs to the locus coeruleus [98], which in turn projects to areas of the cortex that are associated with stress-related behavior and affective disorders. The locus coeruleus is also considered a major site for integrating stress responses [99]. Following repeated activations, a feed-forward system between noradrenergic locus coeruleus neurones and areas of the forebrain that produce corticotropin-releasing factor (CRF) can lead to altered behavioral responses [100]. Chronic activation of this system induces changes in neuronal activity that underlies anxiety, panic disorders, and depression [101].

The concept of interoception and experimental data suggesting that changes in visceral sensation can affect the perception and interpretation of external inputs [30] has led to the suggestion that altered sensory vagal inputs can influence our attitude to the outside world and that pathological changes in sensory vagal inputs may increase the risk of affective behavioral disorders. It has been proposed that chronic sensory vagal inputs could act as 'natural' breaks for augmentation of stress-related behavioral responses via tonic modulation of the neuronal activity in the locus coeruleus and in turn the forebrain [31]. In keeping with this, vagal stimulation is an FDA-accepted alternative treatment for intractable depression, and has also been used successfully in the treatment of refractory epilepsy, demonstrating clear behavioral effects of modulating vagal afferent signals [102].

Thus, given the key role of the vagus in communicating visceral signals to brain, and particularly to neural circuitry associated with mood and anxiety, it is perhaps not surprising that many investigations of communication between gut bacteria and the CNS have examined the role

of the vagus. There is now strong evidence from animal studies that gut microorganisms can activate the vagus nerve, and that such activation plays a critical role in mediating effects on the brain and, subsequently, behavior.

Such evidence came early from the study of animals infected with pathogens. Subdiaphragmatic vagotomy attenuated c-fos expression in the PVN of rats inoculated with Salmonella typhimurium [103]. Although S. typhimurium infection was accompanied by intestinal inflammation, subsequent studies have indicated that microorganisms in the gastrointestinal tract can directly activate neural pathways even in the absence of an identified immune response [87]. The anxiogenic effect of orally administered subclinical doses of Camphylobacter jejuni in mice was associated with a significant increase in c-fos expression in neurons bilaterally in the vagal ganglia and activated visceral sensory nuclei in the brainstem. The areas of brainstem activation, the NTS and lateral parabrachial nucleus, participate in neural information processing that ultimately lead to autonomic neuroendocrine and behavioral responses [87]. Similarly, the effect of a combination of C. rodentium infection and stress on the central nervous system of mice was accompanied by increased neuronal activation in vagal ganglia, leading the authors to propose that the gut to brain signaling in this instance was mediated through the vagus nerve [76].

Non-pathogenic bacteria also appear to activate vagal signaling from gut to brain. Intraduodenal injection of *L. lactis La1* was demonstrated to activate the gastric vagal nerve [88]. Consequently, infradiaphragmatic denervation of vagal nerve fibers surrounding the esophagus eliminated the ability of *L. lactis La1* to reduce renal sympathetic nerve activity and blood pressure, indicating that at least some of the effects of this bacteria on autonomic nerve responses were elicited by interaction with afferent vagal nerve fibers [88].

Subdiaphragmatic vagotomy blocked the anxiolytic and antidepressant effects of chronic L. rhamnosus ingestion in normal adult Balb/c mice, while also preventing the associated alterations in GABAA α 2 mRNA expression in the amygdala [81]. Similarly, the ability of B. longum to attenuate DSS colitis-induced anxiety was abolished by vagotomy [82].

Overall, studies indicate that vagal pathways mediate signals that can induce both anxiogenic and anxiolytic effects depending on the nature of the stimulus, and, interestingly, the vagus appears to differentiate between non-pathogenic and potentially pathogenic bacteria even in the absence of overt inflammation. Certainly, important advances in our understanding of the microbiome—gut—brain axis will come from studies of how distinct microbial stimuli activate the vagus and the nature of the signals transmitted to the brain that lead to differential changes in



the neurochemistry of the brain and behavior. However, while it appears that the vagus in critical to mediating gutbrain communication by specific bacteria in some model systems, it is by no means the only potential signaling method. Indeed, largely due to technical difficulties, few studies have investigated the role of spinal afferents in mediating bacteria-induced changes in behavior and brain chemistry. It is certainly possible that the observed changes in brain chemistry behavior induced by gut bacteria require parallel input from both the vagal and spinal afferents.

Furthermore, behavioral changes induced through disruption of the microbiota by antibiotic treatment have been demonstrated to be independent of vagal signaling [80], with some additional evidence that neither sympathetic afferents nor immune modulation is required. This clearly suggests that the bacteria in the gut can communicate to the brain through multiple pathways. A potential means of communication, that has been somewhat neglected in existing studies, involves hormonal signaling pathways.

The gut hormonal response

In addition to direct neural pathways, the gut also communicates to the brain utilizing hormonal signaling pathways that involve the release of gut peptides from enteroendocrine cells which can act directly on the brain at the area postrema (which lies outside the blood–brain barrier). These gut peptides include orexin, galanin, ghrelin, gastrin, and leptin. Primarily identified for their role in modulating feeding behavior and energy homeostasis, the gut hormonal response has also be linked with changes in sleep wake cycle, sexual behavior, arousal, and anxiety [104, 105].

Galanin stimulates the activity of the central branch of the HPA axis (i.e. the release of corticotropin-releasing hormone and ACTH), thereby enhancing glucocorticoid secretion from the adrenal cortex. This peptide can also directly stimulate glucocorticoid secretion from adrenocortical cells and norepinephrine release from adrenal medulla [106, 107]. Galanin appears to play a role in modulating the HPA axis response to stress and, given the established deleterious effects of galanin on cognitive function, the hormone may act as a link between stress, anxiety, and memory [108, 109]. In this regard, it has been suggested that galaninergic drugs could provide a novel therapeutic option for psychopathologies, such as posttraumatic stress syndrome [107]. Similarly, ghrelin possesses a marked ACTH/cortisol-releasing effect in humans, and is probably involved in the modulation of the HPA response to stress or changes in nutritional/metabolic status [110, 111]. Ghrelin acts in the brain to mediate anxiogenesis and increase memory retention [112]. Studies in gastrin-deficient mice indicate increased anxiety-like behavior compared to wild-type animals, suggesting normal circulating levels of gastrins may play a direct or indirect role in the regulation of locomotor activity and anxiety-like behavior [113, 114].

Neurotensin is an endogenous brain-gut peptide, with a close functional relationship with the mesocorticolimbic and neostriatal dopamine system. Dysregulation of neurotensin neurotransmission in this system has been hypothesized to be involved in the pathogenesis of schizophrenia. Additionally, neurotensin-containing circuits have been demonstrated to mediate some of the mechanisms of action of antipsychotic drugs, as well as the rewarding and/or sensitizing properties of addictive drugs [115].

The pancreatic polypeptide-fold (PP-fold) family includes pancreatic polypeptide (PP) and peptide YY (PYY), and neuropeptide Y (NPY). These peptides have broad peripheral actions on a number of organs. Both NPY and PYY have anxiolytic effects in rats, and NPY has been implicated in feeding and obesity, neuronal excitability, memory retention, anxiety, and depression [116]. Moreover, intracerebroventricular injection of NPY to rats has anti-depressive effects that are antagonized by NPY receptor blockers [117].

Leptin, a hormone secreted from adipose tissue, was originally discovered to regulate body weight. Leptin receptors can be found in limbic structures suggesting a potential role for this hormone in emotional processes. Indeed, Lu et al. [118] demonstrated that rats exposed to chronic unpredictable stress and chronic social defeat exhibit low leptin levels in plasma, and that systemic treatment with leptin reversed behavioral changes induced by chronic unpredictable stress. The behavioral effects of leptin were accompanied by neuronal activation in limbic structures, particularly in the hippocampus. Similar antidepressant-like effects of leptin have also been observed in diabetic mice [119].

While studies in germ-free animals suggest that the gut microflora influences the release of biologically active peptides and participates in the regulation of gastrointestinal endocrine cells [120], little is known about the effect of changes in gut microbiota or probiotic treatment on the expression and release of the hormonal components of gutbrain communication. However, given the ability of gut microbiota to alter nutrient availability [121], and the close relationship between nutrient sensing and peptide secretion by enteroendocrine cells [122], it seems plausible that probiotic treatment may modulate hormonal signaling by the gut. In support of this, piglets treated with the probiotic Pediococcus acidilactici were demonstrated to have a greater number of galanin- and calcitonin gene-related peptide (CGRP)-immunoreactive neurons than controls in the submucosal plexus ganglia of the ileum [123].



Furthermore, Lesniewska et al. [124] demonstrated that treatment with a mixture of *Lactobacillus rhamnosus* GG, *Bifidobacterium lactis*, and inulin, in addition to altering gut microflora, increased the portal plasma levels concentrations of NPY and PYY in adult rats, while, in elderly animals, the PYY concentration was unchanged and NPY levels were decreased by treatment. This study not only supports the idea that changes in composition of gut microflora can alter gut hormone release but it also suggests that the effects are dependant on the age and presumably the initial gut physiology and microbiome of the host.

A potentially novel means of gut bacterial influence over hormonal communication to the brain has been proposed by Fetissov and colleagues [125, 126]. These researchers detected IgG and IgA autoantibodies directed against leptin, ghrelin, peptide YY, neuropeptide Y, and other gut regulatory peptides are present in normal human and rat sera, suggesting that the immune system may interfere with peptidergic systems involved in appetite and emotional control [125]. This concept is supported by the demonstration of autoantibodies directed against two melanocortin peptides, α -MSH and adrenocorticotropic hormone (ACTH), in subjects with eating disorders, with correlation between autoantibody levels and the core psychopathologic traits in these patients [127, 128].

Decreased levels of IgA autoantibodies directed against several gut humoral peptides and increased levels of antighrelin IgG were found in germ-free rats compared with specific pathogen-free rats [125]. It was thus identified that, while the commensal microbiota is not required for the presence of IgA or IgG autoantibodies directed against regulatory peptides, it can selectively influence the levels of at least some of these autoantibodies [125].

The potential ability of the microbiota to selectively modulate regulatory peptide autoantibodies may be related to the concept of molecular mimicry. Fetissov et al. [125] identified numerous cases of sequence homology with these peptides among commensal and pathogenic microorganisms, including *Lactobacilli*, *bacteroides*, *Helicobacter pylori*, *Escherichia coli*, and *Candida* species.

The presence of fragments with identical sequences between microbial proteins and regulatory peptides suggests that such microbial proteins, presenting these sequences in the Peyer's patches or other lymphoid organs, may stimulate the production of immunoglobulins capable of binding to the identical region present in endogenous regulatory peptides, and thus modulate the corresponding hormonal signaling pathways.

The role of the gut hormonal response in mediating effects of gut microbiota changes on the CNS is clearly an area of research that demands more attention.



While the field is still in its infancy, study of the microbiome—gut—brain axis has already provided us with strong evidence to support the influence of gut bacteria on the nervous system and brain function. The emerging picture (Table 1) suggests that the gut microbiota plays a role in normal CNS development and, in particular, influences systems associated with stress response and anxiety [7, 58, 59], but may also affect memory function [76]. Exposure to certain key strains of bacteria can also mitigate the effects of early life stress on CNS development [89, 91].

It is also clear that disruption of the microbiota or exposure to specific gut bacteria can modulate brain chemistry and behavior in adult mammals. Effects of gut bacteria in adults include protection from the central effects of infection and inflammation [86, [82, 76], as well as modulation of normal behavioral responses of the animals [81]. While behavioral effects described by gut bacteria in adult animals are again largely related to stress responses and anxiety, these are the behaviors that investigators have focused on to date, and we await future studies that provide a more detailed analysis of gut microbiota influences on additional aspects of brain function, particularly memory and cognition.

An altered HPA axis response to stress is a common effect of gut bacteria in many model systems [7, 59, 81, 91, 89]. This may have important implications when considering the therapeutic potential of gut microbiota modulation. Psychological stress is a common risk factor for the development of major depression, and an identifiable stressor precedes most initial episodes of major depression [129]. Furthermore, hyperactivity of the HPA axis has been found in some psychiatric disorders, especially in older patients with severe depression [130]. Such studies suggest that the relationship between the state of the HPA axis and depression may at least in part be causal. There is therefore the potential that changes in gut microbiota or exposure to specific commensal bacteria may alter the HPA axis or other stress response systems, and in turn modulate stress related mood or behavioral disorders.

There is now robust evidence that gut bacteria influence the enteric nervous system, effects that may, in addition to regulating gut motility, contribute to afferent signaling to the brain [36, 44, 131]. The vagus nerve, which closely monitors gut contractions, has emerged as an important [81, 82], but clearly not exclusive [80], means of communicating signals from gut bacteria to the CNS. The central neural circuits influenced by the gut microbiota are reported to include the GABAergic [81], glutaminergic [7, 59] serotonergic [58], dopaminergic [58], histaminergic [88], and adrenergic [89] systems. Similarly, a number of studies have demonstrated that gut bacteria influence



Table 1 Studies of the microbiome-gut-brain axis

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Study	Model	Bacterial treatment	Behavior	HPA stress response	Hippocampal BDNF	Other neural correlates	Vagus
Sudo et al. [7]	Germ-free (mice)	na	1	†CORT	\rightarrow	NR1, NR2A	ı
Neufeld et al. [59]	Germ-free (mice)	na	Anxiety ↓ ^b	†CORT	←	(mppocampus) NR2B↓	I
				(baseline)		(amygdala) SHT1A	
						(hippocampus)	
Heijtz et al. [58]	Germ-free (mice)	na	Anxiety↓ ^b	I	\rightarrow	NA, DA, and 5-HT turnover↑	I
						(striatum)	
Gareau et al. [76]	Germ-free (mice)	na	Memory ↓	ı	1	I	I
Bercik et al. [80]	Antibiotic (mice)	na	Anxiety↑	I	\rightarrow	1	Vagus independent
Gareau et al. [76]	C. rodentium infection (mice)	L. rhamnosus/ L helveticus	Anxiety↓	↓CORT	←-	I	Vagus activated
Bercik et al. [86]	T.murius infection (mice)	B. longum	Anxiety↓	ı	← -	I	I
Bercik et al. [82]	DSS colitis (mice)	B. longum	Anxiety↓	ı	1	ı	Vagus dependent
Tanida et al. [88]	Mice	$L.\ johnsonif^c$	ı	ı	ı	Suprachiasmatic nucleus activation	Vagus dependent
Gareau et al. [91]	Maternal deprivation (rats)	L. rhamnosus/ L helveticus	I	↓CORT	I	I	I
Desbonnet et al. [89]	Maternal deprivation (rats)	B. infantis	Despair↓	I	I	↑5-HIAA (frontal cortex)	1
						↓DOPAC (amygdala)	
Bravo et al. [81]	Mice	L .rhannosus	Anxiety↓	↓ CORT	1	↓GABAR(Bb1)R (amygdala,hippocampus) ↓GABAR (Aα2) (amygdala) ↑GABAR (Aα2) hippocampus	Vagus dependent

\ Increase, \ decreased, \ unchanged

5-HT 5-hydroxytryptamine, 5HTIA 5-hydroxytryptamine receptor 1A, ACTH adrenocorticotropic hormone, CORT corticosterone, DA dopamine; DOPAC 3,4-dihydroxyphenylacetic acid, GABAR gamma-aminobutyric acid receptor, NA noradrenaline, NR N-methyl-D-aspartate receptor, – no data provided, na not applicable

^a Effects are mitigated by early colonization with SPF microbiota or B. infantis and exacerbated by pathogenic E. coli

^b Effects mitigated by early colonization

^c Intraduodenal injection



BDNF levels, particularly in the hippocampus [7, 59, 86]. How any of these alterations in brain chemistry are related to specific behavioral changes is unclear, but will likely be a focus of future research efforts.

Some of the major questions remaining concern what the relationship between gut bacteria and the brain means for human health. Is the composition of the gut microbiota associated with psychiatric conditions, as has been proposed for conditions such as obesity [132]? Can the hygiene [133] or microbiota [134] hypothesis for allergic disease also be applied to depression? And can we develop microbial-based therapeutic strategies for mood disorders? [135]. In this regard, human studies have been limited; however, there have been reports of reduced fatigue and anxiety in subjects with chronic fatigue syndrome [136, 137], and a study with a small number of subjects suggested beneficial psychological effects of treatment with a combination of *Lactobacillus helveticus* and *Bifidobacterium longum* in healthy adults [138].

We are at the very early stages of understanding the complex communication systems between gut bacteria and the brain. However, there is already strong supporting evidence for what was, only a few years ago, a largely hypothetical relationship between the gut microbiota, mood, and behavior [13, 135]. The rising interest in this area of research will no doubt lead to greater insights into the mechanisms underlying microbiome—gut—brain communication, and provide us with new understanding of the symbiotic relationship between the gut microbiota and their human host. Future studies will also help us identify the potential for microbial-based therapeutic strategies that may aid in the treatment of mood disorders.

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