



From bugs to brain: unravelling the GABA signalling networks in the brain–gut–microbiome axis

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Convergent data across species paint a compelling picture of the critical role of the gut and its resident microbiota in several brain functions and disorders. The chemicals mediating communication along these sophisticated highways of the brain–gut–microbiome (BGM) axis include both microbiota metabolites and classical neurotransmitters. Amongst the latter, GABA is fundamental to brain function, mediating most neuronal inhibition. Until recently, GABA's role and specific molecular targets in the periphery within the BGM axis had received limited attention. Yet, GABA is produced by neuronal and non-neuronal elements of the BGM, and recently, GABA-modulating bacteria have been identified as key players in GABAergic gut systems, indicating that GABA-mediated signalling is likely to transcend physiological boundaries and species.

We review the available evidence to better understand how GABA facilitates the integration of molecularly and functionally disparate systems to bring about overall homeostasis and how GABA perturbations within the BGM axis can give rise to multi-system medical disorders, thereby magnifying the disease burden and the challenges for patient care.

Analysis of transcriptomic databases revealed significant overlaps between GABA_AR subunits expressed in the human brain and gut. However, in the gut, there are notable expression profiles for a select number of subunits that have received limited attention to date but could be functionally relevant for BGM axis homeostasis.

GABAergic signalling, via different receptor subtypes, directly regulates BGM homeostasis by modulating the excitability of neurons within brain centres responsible for gastrointestinal (GI) function in a sex-dependent manner, potentially revealing mechanisms underlying the greater prevalence of GI disturbances in females. Apart from such top-down regulation of the BGM axis, a diverse group of cell types, including enteric neurons, glia, enteroendocrine cells, immune cells and bacteria, integrate peripheral GABA signals to influence brain functions and potentially contribute to brain disorders.

We propose several priorities for this field, including the exploitation of available technologies to functionally dissect components of these GABA pathways within the BGM, with a focus on GI and brain-behaviour-disease. Furthermore, *in silico* ligand–receptor docking analyses using relevant bacterial metabolomic datasets, coupled with advances in knowledge of GABA_AR 3D structures, could uncover new ligands with novel therapeutic potential. Finally, targeted design of dietary interventions is imperative to advancing their therapeutic potential to support GABA homeostasis across the BGM axis.

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Introduction: the long and winding road between gut, bacteria, the immune system and the brain

Just as greater use of common languages and technology has advanced communication across diverse communities, extraordinary evidence is emerging about how our individual organ systems have long employed common chemical messengers for effective internal communication across biological borders. A striking example is the appreciation of the roles of certain neurotransmitters beyond neural communication. Central to this pursuit has been the advancement in understanding the profound functional interconnectedness between the gut, its resident microbes, the local gut and systemic immune systems, and the brain, commonly termed the brain–gut–microbiome (BGM) axis.¹

An array of chemicals is emerging as mediators of this BGM interconnectedness. These chemicals include neurotransmitters, bacterial metabolites and immune mediators, which traditionally were thought to be produced predominantly by neurons, bacteria and immune cells, respectively. However, some chemical messengers and targets are common to all such systems, notably GABA and its receptors. Here, we review the evidence for GABA as an important common messenger that integrates the collective functions of these diverse systems and how these pathways may provide novel therapeutic targets for brain disorders, specifically in psychiatry.

GABA in the brain and beyond—more than a conventional inhibitory transmitter across the BGM axis

GABA signalling within and between neural circuits of the BGM axis

A detailed discussion of the complex organization of the BGM axis is beyond the scope of this review and is extensively described elsewhere.^{1–3} Here, we briefly outline the main elements of the BGM axis to provide the molecular, functional and theoretical context for a discussion of the role of GABA in the subsequent sections.

The term BGM axis has come to describe, in the animal kingdom, a bidirectional communication system between the brain and the gastrointestinal (GI) system, the latter often referred to as the gut. This complex highway utilizes specific neuronal pathways, most notably the vagus nerve,⁴ together with endocrine and immune signals and pathways, and a range of chemical messengers, many of which are of microbial origin. These include classical neurotransmitters such as serotonin (5-HT) and GABA, short-chain

fatty acids (SCFAs), bile acids and their metabolites,^{5–7} all of which act together with GI resident microbiota to provide optimal homeostatic regulation of the host's functions and physiology. Focusing on GABA, we begin by examining the neuronal roles of this molecule both in the brain and in GI functions and reviewing how GABA participates in reciprocal communication between the two ends of the BGM axis through tailored neuronal pathways.

GABA regulation of neuronal excitability in the central and enteric nervous systems

The quintessential notion of GABA's role in mammalian neural function is to provide the principal mechanism for neuronal inhibition. The canon of GABA-mediated neuronal inhibition in the CNS is founded on evidence, primarily in the brain, showing the exquisite organization of diverse sources of GABA, including both neuronal elements, notably interneurons,⁸ and glial cells.^{9,10} Furthermore, the release of GABA is spatially and temporally coordinated across distinct sub-cellular domains of target neurons and glia¹¹ in alignment with different GABA receptor subtypes in a cell-type- and brain-region-specific manner.^{12–14} The functional consequences are a myriad of pre- and postsynaptic inhibitory signatures. This signalling diversity, coupled with the burgeoning evidence of non-synaptic, persistent forms of tonic inhibition (see [Box 1](#)), serves to orchestrate neuronal activity within and across brain regions.¹⁵ However, the role of GABA extends beyond the brain since GABA appears to be a modulator of a variety of GI functions. Molecular analyses provide direct evidence for the expression of GABA, as well as its two main receptor types, the ionotropic GABA_A receptor (GABA_AR) and the G-protein coupled metabotropic GABA_B receptor (GABA_BR) within the enteric nervous system (ENS), also known as the second brain.¹⁶ However, functional roles for GABA in mediating fast synaptic transmission in the gut are largely indirect and based on the application of exogenous GABA or a combination of receptor ligands. Yet, recent evidence indicates that neurally-released GABA strongly modulates slow inhibitory potentials in the mouse ileum via ρ -containing GABA_ARs (previously known as GABA_CRs), which exhibit a distinct pharmacology, e.g. they are insensitive to bicuculline block (see also the 'Gastrointestinal GABA regulation of brain function' section).^{17,18}

Collectively, studies of GABA's physiological actions suggest a myriad of functions, including the modulation of motility, secretions and immune function. Providing unequivocal evidence for the contribution of endogenous GABA and/or other putative endogenous GABA agonists (e.g. taurine) to native GI function is a key priority for future research. Salient aspects of GABA-receptor signalling in the brain are summarized in [Box 1](#). An important

Box 1 Molecular, cellular and biophysical properties of GABA_AR and GABA_BR signalling in the brain

- GABA fulfils a canonical inhibitory role via two main distinct modalities: (i) the rapid, locally and temporally precise mode of inhibitory transmission mediated by the vesicular release of sub- to high-mM GABA concentrations acting mainly on synaptic GABA type A receptors (GABA_ARs); and (ii) a sustained, temporally diffused mode of tonic inhibition or a combination of both.¹⁹ The latter is mediated by both extrasynaptic GABA_ARs^{13,20,21} and GABA type B receptors (GABA_BRs),²² located beyond the synaptic domain, and activated by low micromolar GABA concentrations. Because of their conspicuous localization on presynaptic nerve terminals, the role of GABA_BRs in neuronal inhibition was initially viewed through the lens of the inhibition of transmitter release across neuronal networks. However, their participation in post-synaptic transmission, originally described in the hippocampus,²³ and tonic inhibition has received growing attention.¹⁵
- GABA_ARs and GABA_BRs exhibit distinct inhibitory mechanisms as members of ligand-gated and G-protein coupled receptor families, respectively. GABA_ARs are ligand-gated channels where GABA binding results in the rapid (on a sub-ms to ms time scale) opening of an associated channel, selectively conducting mainly negatively charged Cl[−] ions. In both the brain and spinal cord, Cl[−] ions mostly, but not always, flow into neurons because of an electrochemical gradient that drives Cl[−] influx, resulting in a membrane hyperpolarization that makes neurons less excitable.¹³ Importantly, this gradient is imposed by both the neuronal resting membrane potential and the relative expression of the two transport systems regulating the extrusion (KCC2) and influx (NKCC) of Cl[−].²⁴ Apart from being responsible for a hyperpolarizing response, GABA additionally produces an associated so-called shunting inhibitory action by decreasing the neuronal membrane resistance, as per Ohm's law ($V = IR$), making neurons less likely to reach the membrane potential threshold for action potential generation in response to excitatory signals, e.g. glutamate, the main excitatory transmitter in the CNS.²⁵
- GABA_BRs are G-protein receptors, coupled to either voltage-gated Ca²⁺ or K⁺ channels, and their activation results in a delayed net efflux of positively charged ions due to closure and opening of the G-protein linked Ca²⁺ and K⁺ channels. The net effect is hyperpolarizing but on a significantly longer time scale than GABA_ARs, i.e. hundreds of ms.²⁶
- Even within the brain, there are exceptions to this predominant inhibitory role for GABA. For example, during development, GABA_AR signalling in the brain, via chloride-permeable GABA_ARs, is depolarizing and excitatory,^{27–29} largely due to the delayed postnatal expression of the chloride-extruder KCC2, compared with NKCC,³⁰ in comparison to adult levels, when the former dominates the latter. Similarly, GABA can be hyperpolarizing and inhibitory or depolarizing and potentially excitatory on individual cells, depending on the GABA release sites across its surface and the associated electrochemical Cl[−] gradients. For example, GABAergic interneuron targeting of somatic and dendritic regions of cortical pyramidal neurons is hyperpolarizing but GABAergic axo-axonic cells, which selectively synapse on the pyramidal cell axon initial segments,³¹ have excitatory effects³² due to a reverse axo-somato-dendritic chloride gradient.³³ Nevertheless, depolarizing actions may still be inhibitory because of a prevailing shunting effect.^{34,35}

difference to GABA's predominantly hyperpolarizing and inhibitory effect in the adult brain is that in the gut and peripheral organs, it is generally, but not always (Box 1 and the 'Gastrointestinal GABA regulation of brain function' section), considered to be excitatory.³⁴ This excitatory action through GABA_ARs, is driven by an electrochemical gradient that leads to chloride (Cl[−]) efflux rather than influx, resulting in membrane depolarization.

A fundamental feature of GABA_AR-mediated inhibition, underpinning its widespread and complex influence in both brain and GI function, is the considerable receptor heterogeneity that supports a rich pharmacology. This diversity is provided by the molecular and structural organization of GABA_ARs, which are pentameric complexes derived from 19 different subunits (6α, 3β, 3γ, δ, ε, θ, π, 3ρ)³⁶ [Fig. 1A(i–iii)]. In principle, this heterogeneity allows for a potentially staggering number of receptor subtypes. However, the rules governing the specific subunit assembly *in vivo*, with initial estimates proposing 20–30 major subtypes, are yet to be fully understood.^{37,38} More recent studies strongly suggest an even greater degree of heterogeneity.^{39,40} The most commonly occurring receptor subtypes, at least in the brain, contain two α and two β subunits together with a γ, δ or ε subunit [Fig. 1A(ii)]. It should be noted that GABA_ARs are members of the Cys-loop family of membrane-spanning neurotransmitter-gated ion channels, which include most notably nicotinic acetylcholine, 5-HT₃ and glycine receptors,

and that there is a degree of cross-activity between some of the antagonists acting at these different receptors.

This GABA_AR diversity gives rise to an extensive pharmacology,^{36,38,42,43} with numerous therapeutically useful agents that enhance receptor function allosterically. These agents act via sites distinct from that of GABA itself, functioning as positive allosteric modulators (PAMs). Such ligands include benzodiazepines (BZs), a variety of general intravenous anaesthetics, including etomidate and propofol, and a class of brain-made steroids called neurosteroids (NSs)—notably the progesterone metabolite, 5α-pregnan-3α-ol-20-one, known as allopregnanolone (ALLO), and tetrahydrodeoxycorticosterone (THDOC), which are devoid of classical hormonal actions⁴⁴ [Fig. 1A(iv) and Box 3].

The receptor subunit composition impacts function, localization and pharmacology. For example, receptors incorporating the γ2 subunit together with either the α1,2,3 or 5 subunits are particularly sensitive to BZ ligands and localize, albeit not exclusively, to synaptic locations to mediate fast synaptic inhibition.¹³ Receptors without the γ2 subunit are not responsive to BZs,³⁸ whereas receptors incorporating the δ subunit are insensitive to classical BZ ligands but exquisitely sensitive to the agonist gaboxadol and exclusively localized to extrasynaptic neuronal domains.^{20,36,45} In each instance, the receptor subtypes display unique properties ideally suited to the form of inhibition they mediate. For example,

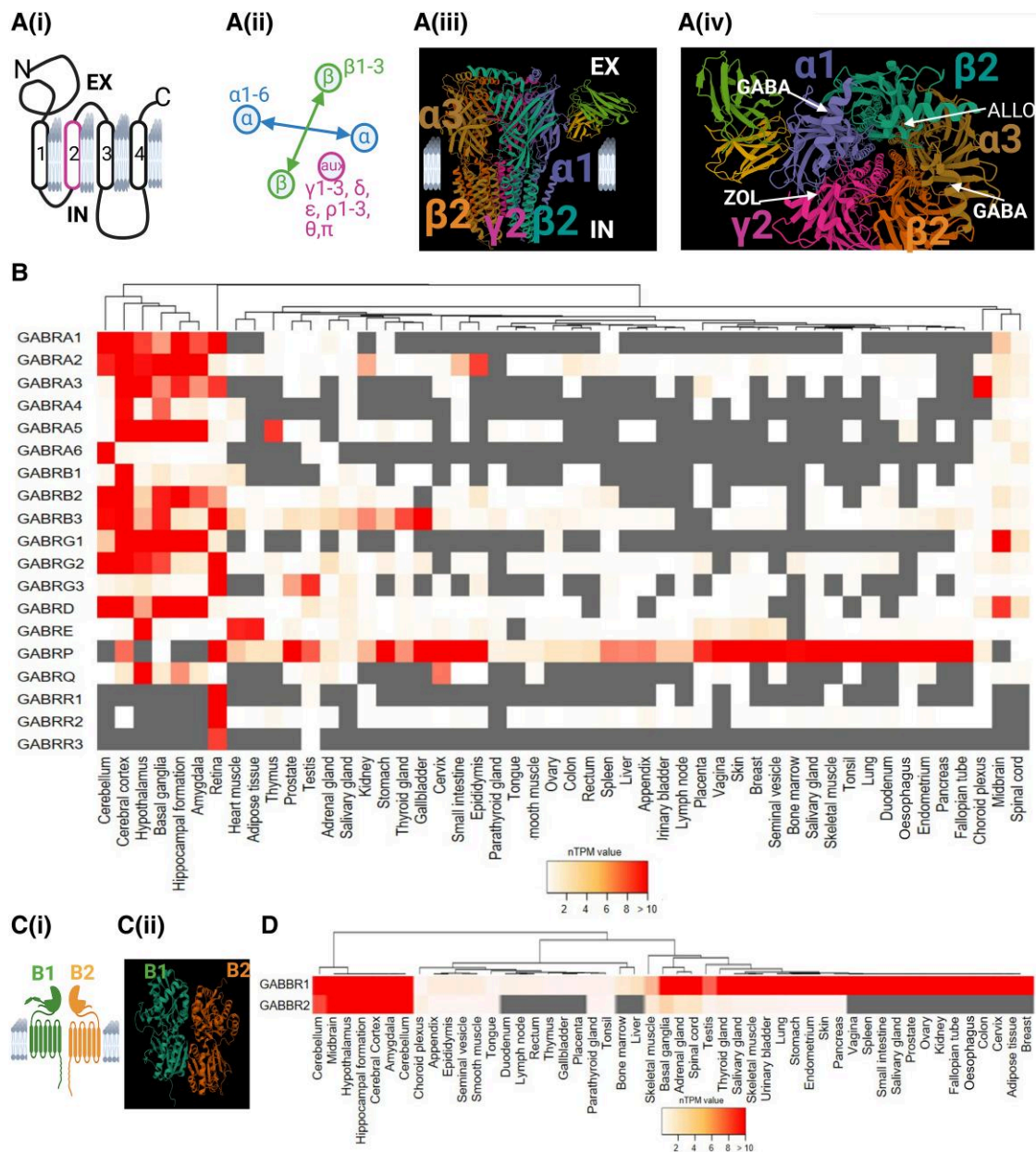


Figure 1 Molecular, pharmacological and expression diversity of mammalian GABA receptors throughout the body. [A(i)] The basic structure of an individual GABA type A receptor (GABA_AR) subunit (viewed from the side and flattened), when anchored in the plasma membrane. These proteins consist of four transmembrane domains (TM 1–4), two intracellular loops and one extracellular loop, an extracellular amino terminus (N) and carboxyl (C) termini. TM 2 is distinguished by putatively forming the lining of the ion channel. EX = extracellular; IN = intracellular. [A(ii)] The molecular diversity of individual GABA_AR subunits, as well as their general stoichiometry, assembling the pentameric GABA_AR complex, which contains two α - and two β -subunits and a single auxiliary (AUX) subunit. [A(iii)] Model of the 3D crystal structure of an assembled GABA_AR, viewed from the side. The image was generated by the Protein Data Bank in Europe, 8g5h, and is based on data originally published by Sun et al.⁴⁰ [A(iv)] provides a view from the top of the GABA_AR mentioned in iii, illustrating the diversity of receptor sites at which ligands have been shown to bind. These include separate sites for the endogenous ligand and neurotransmitter GABA, the exogenous, positive allosteric modulator zolpidem (ZOL) and the endogenous neurosteroid allopregnanolone (ALLO). The data indicate that the GABA binding site is located at the interface of the α - and β -subunits, zolpidem binds to the extracellular domain interface of the α 1- and 2-subunits, and the binding pockets for ALLO are located at the interface between TM 1 and 4 of the α -subunit and TM 3 of the adjacent β -subunit.⁴⁰ **B** illustrates the relative mRNA expression levels of 19 different human GABA_AR subunits across various tissues in the human body, based on consensus datasets from the Protein Atlas database (<https://www.proteinatlas.org/>). The heatmap was generated using Heatmapper (<http://www.heatmapper.ca/>). Expression levels are represented by colour intensity: grey indicates no expression, red indicates high expression levels and white indicates low expression levels. The values are presented in normalized transcripts per million (nTPM). [C(i)] The basic structure of an individual GABA type B receptor (GABA_BR). The receptor is composed of two subunits, GABAB1 and GABAB2, and belongs to the super-family of metabotropic G-protein coupled receptors. [C(ii)] Model of the 3D crystal structure of the extracellular regions of an assembled GABA_BR, viewed from the side. The image was generated by the Protein Data Bank in Europe, 4mr7, and is based on data originally published by Geng et al.⁴¹ **(D)** The relative mRNA expression levels of the two GABA_BR subunits across various tissues in the human body, based on consensus datasets from the Protein Atlas database, created in a similar manner to C. The figure was prepared using BioRender (www.biorender.com).

δ -subunit containing GABA_ARs (δ -GABA_ARs) have a high affinity for GABA and exhibit limited desensitization, both congruent for mediating sustained tonic inhibition. Indeed, some δ -GABA_ARs spontaneously open in the absence of GABA.^{46,47} We refer to comprehensive reviews for an in-depth discussion.^{20,48}

Although a relative consensus has been reached in terms of our understanding of the assembly,^{37–40} function and pharmacology of GABA_ARs in the brain,^{20,48} a similar knowledge base is a priority for other organ systems. This development is important because data indicate extensive and diverse GABA_AR subunit expression throughout most organs, at least at the transcriptomic level in humans (Fig. 1B). This diversity is also evident in other animals.^{49–52}

The molecular configuration of metabotropic GABA_BRs is much simpler since only two different subunits are required for their function, GABA_{B1} and GABA_{B2}. The GABA binding is on the GABA_{B1} subunit, while the GABA_{B2} subunit induces intracellular signalling⁵³ (Fig. 1C). As with GABA_ARs, GABA_BRs are widespread in the periphery (Fig. 1D), including the ENS,^{54–56} where they not only modulate presynaptic transmitter release⁵⁷ but may contribute to both synaptic and tonic inhibition, the latter via extrasynaptically located receptors, in a manner similar to that in the brain.⁵⁸

Organization of brain GABAergic pathways that regulate gut functions

The complex anatomical and physiological organization of brain GABAergic signalling in highly organized laminated regions such as the cortex has been widely described.^{12,59–63} However, we know comparatively less about the anatomically more diffuse cell groupings of subcortical brain regions that mediate gut function. Of particular importance is the full molecular, morphological and physiological characterization of individual GABAergic cell types. Furthermore, it is imperative to identify any distinctive GABA pharmacological and physiological signatures and their collective contribution to brain and gut functions. Specifically, GABA-mediated top-down CNS regulation of GI function is important in the context of BGM signalling in health and disease, as alterations to GI parameters commonly occur in a range of brain disorders, most notably those associated with maladaptive responses to psychosocial stress (see the ‘Gastrointestinal GABA regulation of brain function’ section). Here, we focus on three key nuclei, the medullary dorsal motor nucleus of the vagus (DMV), the pontine locus coeruleus (LC) nucleus and Barrington’s nucleus (BN), since they modulate motor pathways to the stomach/small intestinal (DMV) and large intestinal (LC and BN) segments of the GI tract (GIT), respectively.

The primary CNS motor output to the upper GIT is mediated by spontaneously firing DMV neurons,^{64,65} the majority of which are cholinergic.^{66,67} GABAergic regulation of DMV neuronal excitability significantly modulates the function of the GIT and other viscera (Fig. 2A). This DMV GABAergic tone arises from inputs of the neighbouring nucleus tractus solitarius (NTS)⁶⁸ and from a subpopulation of putative GABAergic local circuit interneurons.^{69,70} Immunolocalization analyses indicate that human DMV neurons express at least $\alpha 1$ – $\beta 2$ – $\gamma 2$ GABA_AR subunits.⁷¹ This is corroborated by pharmacological analyses of GABA_AR-mediated synaptic and tonic currents in rodent DMV neurons using the PAM zolpidem,^{72,73} which exhibits preferable affinity and efficacy at $\alpha 1$ - versus $\alpha 2/3$ -, and none for $\alpha 5$ -, subunit-containing GABA_ARs^{74,75} [Fig. 2A(i)] and the δ -preferring GABA_AR agonist gaboxadol,³⁶ respectively.⁷³ Indeed, a recent single-cell RNA

sequencing (scRNA-seq) transcriptomic analysis revealed two populations of DMV cholinergic cell types co-expressing either cholecystokinin or prodynorphin and projecting selectively to either ENS cholinergic or nitrergic neurons of the stomach⁷⁶ [Fig. 2A(ii)]. Our analysis of their deposited data for GABA_AR subunit mRNA expression levels revealed significant differences between these two populations of DMV neurons [Fig. 2A(iii)]. Irrespectively, the net effect of activating DMV GABA_ARs is decreased GI function. This is evidenced by the *in vivo* application of the GABA_AR antagonist bicuculline to the DMV, which increases gastric motor function, intragastric pressure, gastric motility and gastric secretion.^{77,78}

Intriguingly, this GABA_AR-mediated inhibition of DMV neurons is sexually dimorphic. Indeed, the application of the GABA_AR antagonist bicuculline to DMV neurons induced a more significant increase in the firing rate of DMV neurons, as well as gastric tone and motility, in female rats that were in the high-oestrogen/low-progesterone stage of their cycle, compared to those in the low-oestrogen/high-progesterone stage and male rats.⁸⁹ This difference in GABAergic tone could contribute to the documented sex differences in native GI functions⁹⁰ and GI disorders.⁹¹ In contrast to the inhibitory effect of DMV GABA_AR activation on GI function, the activation of DMV GABA_BRs enhances its output.⁹² GABA_BRs are often located at axon terminals, such as those of GABAergic interneurons, where they might reduce their output, suggesting that pre- and postsynaptic GABAergic tone on DMV neurons dynamically contributes to GI homeostasis.

The direct influence of DMV neurons on GI function arises, in part, because most of these neurons project to ENS neurons in the myenteric plexus (see the ‘Gut neuronal GABAergic pathways’ section; Fig. 2) as well as to the pacemaker interstitial cells of Cajal (ICC) in the upper GI tract.^{93–95} BN is another pontine centre⁹⁶ important for regulating visceral organ function. Its preeminent role is in the neural modulation of micturition,⁹⁷ but it also regulates the voiding behaviour of the gut.⁹⁸ Whilst the DMV primarily modulates upper GI functions related to the oesophagus, stomach and small intestine, the BN-LC circuitry has been shown to regulate distal colonic functions and those of other pelvic viscera. Indeed, distension of the urinary bladder, distal colon, rectum or stomach induces significant activation of the principal noradrenergic neurons of the LC^{99,100} (Fig. 2B). This regulation appears to be bi-directional since the activation of a key input to the LC, namely BN, increases colonic intraluminal pressure.⁹⁸ Convergent data indicate a trans-neuronal circuit¹⁰¹ linking LC and BN activities¹⁰² to the regulation of pelvic organ voiding behaviours.¹⁰³ Similar to the DMV, both GABA_ARs and GABA_BRs are expressed within the LC^{71,85,104} and regulate the spontaneous firing rate of the principal neurons.^{105–107} The sources of GABA input are diverse and include putative inhibitory neurons in the LC pericoerulear dendritic region⁸⁴ and the LC nuclear core.^{81–83} However, contrary to the DMV, where both centres contain $\alpha 1/2/3$ -containing GABA_AR subtypes, within the LC, these subunits are expressed selectively on either principal cells or local circuit interneurons. Indeed, LC noradrenergic neurons express only $\alpha 2/3$ -containing GABA_AR subtypes and not the $\alpha 1$ subtype.^{85,86} The deletion of the $\alpha 3$ subunit increases LC noradrenergic neuron excitability.⁸⁶ In contrast, local GABAergic interneurons, which mediate the inhibitory regulation of LC noradrenergic neurons, express the $\alpha 1$ subunit. Activation of these receptors is likely to decrease the activity of such local inhibitory inputs to LC noradrenergic neurons. This increases noradrenergic tone, mirroring other brain regions with similar GABA_AR expression patterns, such as the ventral tegmental area.¹⁰⁸ Importantly, pontine GABAergic somatostatin-expressing neurons,

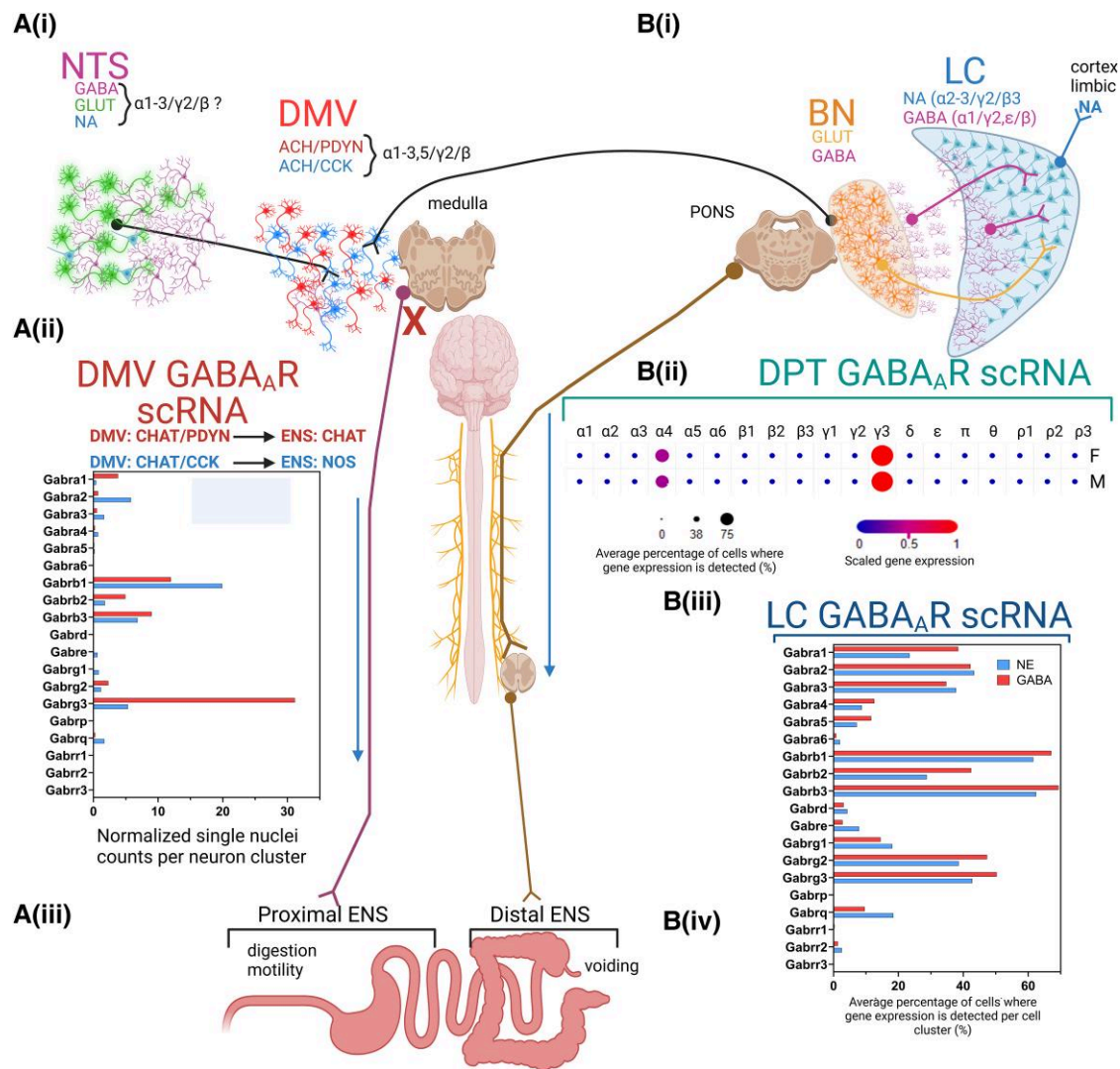


Figure 2 Roles of GABAergic signalling in brain-to-gut neuronal pathways. (A) Key brain centres located within the medulla that are involved in providing motor output to the gastrointestinal tract (GIT). [A(i)] Organization between neurochemically diverse neurons of the nucleus of the solitary tract (NTS) and one of its major projection targets, the dorsal motor nucleus of the vagus (DMV). GABAergic inputs from the NTS onto DMV neurons are mediated by a range of GABA type A receptor (GABA_AR) subtypes.^{71–73} Whilst the majority of DMV neurons express acetylcholine (ACh), they can also be divided into two subpopulations based on their co-expression of either cholecystikinin (CCK) or prodynorphin (PDYN).⁷⁶ DMV axons project via the 10th cranial nerve (X) to make direct synaptic connections with their enteric nervous system targets in the myenteric plexus. [A(ii)] The two distinct types of DMV cholinergic neurons, CCK (blue) and PDYN (red), contact different enteric neuronal types (Chat+ and NOS1+) to induce gastric contraction and relaxation, respectively. A single-nucleus RNA sequence (snRNA-seq) analysis performed on data retrieved from a report by Tao et al.,⁷⁶ revealed the differential expression of GABA_AR subunits between the two types of DMV cholinergic neurons, CCK and PDYN, in mouse models. A(iii) shows that this NTS–DMV pathway, as well as the associated GABA_AR subtypes, preferentially regulates the proximal regions of the GIT. (B) Key brain centres located within the pons that are involved in providing motor output to the distal GIT (B4). [B(i)] Barrington's nucleus (BN) interacts with the locus coeruleus (LC) in regulating voiding behaviour of the gut viscera through their modulation of the distal colon. The principal noradrenergic (NA) neurons of the LC receive excitatory input from BN neurons.⁷⁹ They also receive inhibitory inputs from GABAergic interneurons located near BN⁸⁰ as well as within the LC.^{81–84} Whilst LC NA neurons have been shown to express α2/3-β-γ-GABA_AR subunits, non-NA, GABAergic LC neurons express α1-β-γ-GABA_AR subunits.^{71,85,86} [B(ii)] Single-nucleus RNA sequencing (RNA-seq) data reported by Nardone et al.⁸⁷ were inspected in the Broad Institute Single Cell portal (https://singlecell.broadinstitute.org/single_cell), reference 'pons_exc_neurons_snrnaseq' to compare the gene expression of GABA_AR subunits between female (F) and male (M) mice in the dorsal pontine tegmentum (DPT) region. The sizes of the dots in the dot plot indicate the percentage of cells in which gene expression was detected, and the colour scale indicates the magnitude of gene expression (scaled gene expression defines the expression maximum value as 1 and the minimum as 0). The DPT includes the pre-LC, LC, BRN and mesencephalic trigeminal nucleus (MTN) centres. [B(iii)] An analysis of mouse LC single-cell RNA-seq data reported by Luskin et al.⁸⁸ shows the average percentage of GABA_AR subunit gene expression per cell cluster. Noradrenergic (NE) neurons are shown in blue and GABA neurons in red. [B(iv)] The selective innervation of distal colon by this pathway and its involvement primarily in voiding behaviour. The figure was prepared using BioRender (www.biorender.com).

putatively linked to LC–BRN circuits that regulate visceral organs, provide GABAergic modulation of LC neurons⁸⁰ [Fig. 2B(i)]. Our detailed analysis of data from recent scRNA-seq studies of dorsal pons⁸⁷ and LC cells⁸⁸ is shown in Fig. 2(ii and iii) and offers a

more comprehensive picture of GABA_AR subunit expression. In summary, GABA_AR ligands, depending on their pharmacological profiles, potentially either increase or decrease BN–LC neuron activity and thus influence downstream targets, such as pelvic viscera,

in comparison with DMV neurons, which are invariably inhibited. Collectively, the impact of these central GABA pathways in both the DMV and BN-LC extends to vast swathes of GI homeostatic mechanisms.

Organization of gut neuronal GABAergic pathways and how they modulate brain function

Whilst the DMV provides top-down brain modulation of GI function, its activity is strongly mediated by GABAergic neurons from the NTS, which in turn are strongly modulated by GI afferents via the vago-vagal reflex.¹⁰⁹ These afferent signals represent integrated information from a constellation of different cell types within the ENS of the stomach, duodenum and upper jejunum. These signals are conveyed by sensory axons arising from the inferior ganglion neurons of the vagus nerve, the nodose ganglia. Nodose ganglionic centrally projecting axons innervate the NTS¹¹⁰ [Fig. 3A(i)]. Similarly, sensory information about the physiological status of the distal colon is conveyed via sensory axons of lumbosacral dorsal root ganglion neurons (LSDRG). Centrally projecting axons from LSDRG innervate sacral spinal projecting neurons to activate brain centres, including BN and the LC [Fig. 3A(ii)].

A number of GI neuronal and non-neuronal cell types have been documented to express different GABA_AR subunits, including intrinsic primary afferents, enteric glia, enterocytes, tuft cells and enteroendocrine cells (EECs) [Fig. 3A(iii)]. Several EEC subtypes have been identified based on location and the peptides and hormones they secrete, and they are particularly important in integrating GI, endocrine and brain signalling.¹³¹ An important subtype of EECs, the enterochromaffin cells (ECs), utilize 5-HT to signal, but there is a sub-population that is immunoreactive for GABA.¹²⁰ Furthermore, 5-HT-containing ECs also express GABA_ARs,^{121,122} and their activation has been shown to induce 5-HT release.^{132,133} Here, 5-HT is thought to act in a paracrine manner to stimulate nodose sensory neurons.¹³⁴ GABA_ARs are also likely to be present on other EEC subtypes, where they may modulate the release of a variety of hormones and peptides, e.g. cholecystokinin.¹³⁵

GABA also plays an important role in the intrinsic nervous system of the gut (ENS). The ENS regulates all facets of GI function, including motility, secretions and immune response¹³⁶ using a plethora of functionally and neurochemically diverse neurons distributed throughout the two neural networks of the myenteric and submucosal plexuses.¹³⁶ Remarkably, ENS neuronal activation has also been shown to modulate the gut microbiome, metagenome, transcriptome, metabolome and proteome directly.¹³⁷ A range of corroborative methods indicate the expression of GABA-containing neurons in the mammalian ENS, including humans.^{138,139} Most of the GABA-containing neurons have been detected in the myenteric plexus and are estimated to comprise 5%–8% of total ENS neurons.¹⁴⁰ However, the extent and diversity of GABA_ARs throughout the intestine provide a more informative appraisal of the likely importance of GABAergic signalling to overall GI function. Functionally and pharmacologically distinct GABA_AR subtypes are expressed on neurochemically and functionally diverse ENS neurons^{50,115,141} [Fig. 3B(i)], and their activation has contrasting effects on GI parameters including contractility⁵¹ [Fig. 3B(ii)] and immune status^{127,128} [Fig. 3B(iii)].

GABA signalling within the ENS has also been shown to include enteric glia [Fig. 3A(iii)], which have established roles in the BGM axis in health and disease.^{142,143} Enteric glia produce GABA¹⁴⁶ and thus can directly modulate GI functions such as motility.¹¹⁷ The result is an ENS-GABA-mediated modulation of a range of GI

functions, including receptor subtype-specific relaxation and enhancement of intestinal contractility, secretions, mucosal function and blood flow.¹⁴⁴ Our analysis of previously published ENS scRNA-seq data¹²⁹ revealed expression for a range of GABA_AR subunits within these cell types (Fig. 3C). The consequences of GABA signalling at the local GI level can extend to the brain via tailored anatomical connections as illustrated in Fig. 3 or via diffuse systemic messengers (discussed in the ‘Gastrointestinal GABA regulation of brain function’ section).

BGM GABA signalling beyond neurons and glia: bacterial GABA in brain health and disease

A traditional neuroscience tenet is that the neurotransmitters that modulate neural function are of neural origin. This view broadly holds true for central neural pathways within the blood–brain barrier (BBB), where the communities of cell types are largely homogeneous—that is, only neurons and glia. However, in peripheral pathways, neurons co-exist with a range of non-neuronal cells, glia and tissues, without the parcellation that comes with the BBB. This renders PNS neurons susceptible to modulation by neurotransmitters produced by such non-neuronal elements. Given the influence of PNS pathways on brain function discussed earlier, such diverse peripheral neurotransmitters will impinge on brain function, albeit indirectly. There is no greater demonstration of this constellation of non-neuronal producers of neurotransmitters than the GI tract. In this organ, non-neuronal neurotransmitter sources include immune cells¹⁴⁵ (see the ‘Gastrointestinal GABA regulation of brain function’ section) and endocrine cells. Moreover, it has recently become apparent that resident gut microbes, most notably bacteria, can produce and utilize a variety of chemical messengers, including neurotransmitters, to mediate homeostasis within the microbiome, the gut and putatively beyond, i.e. the brain. This is important because a disrupted equilibrium in the gut microbiome, known as dysbiosis, is implicated in various medical conditions, including various brain disorders.^{146,147} We summarize the growing evidence that resident gut microbiota, specifically bacteria, are a significant source of GABA and how this may contribute to health and disease.

Microbial GABA synthesis: a focus on bacteria

A bacterial source of GABA in the mammalian GI was initially inferred from the finding of reduced GABA content in both the stool and blood of germ-free mice.¹⁴⁸ This finding was corroborated by (i) the observation that faecal GABA levels are decreased by antibiotic use¹⁴⁹ and (ii) genetic analysis of the bacterial community in mammalian gut isolates.¹⁵⁰ While most evidence discussed here is derived from studies on colon-resident bacteria, emerging evidence suggests an important role for the less-investigated, although documented, bacteria that reside in the small intestine,¹⁵¹ some of which (e.g. *Lactobacilli*) produce GABA.¹⁵²

Microbes synthesize GABA via several routes, but the glutamic acid decarboxylase (GAD) and (to a minor extent) putrescine pathways predominate (Fig. 4A). GABA biosynthesis was first reported in strains from the genera *Lactobacillus*, *Lactococcus*, *Streptococcus* and *Bifidobacterium*,¹⁵³ with additional genera and species subsequently added.^{154,155} Using GAD gene expression as a proxy for the ability to synthesize GABA, a variety of bacterial genera/species from the human gut microbiome have been identified, with the

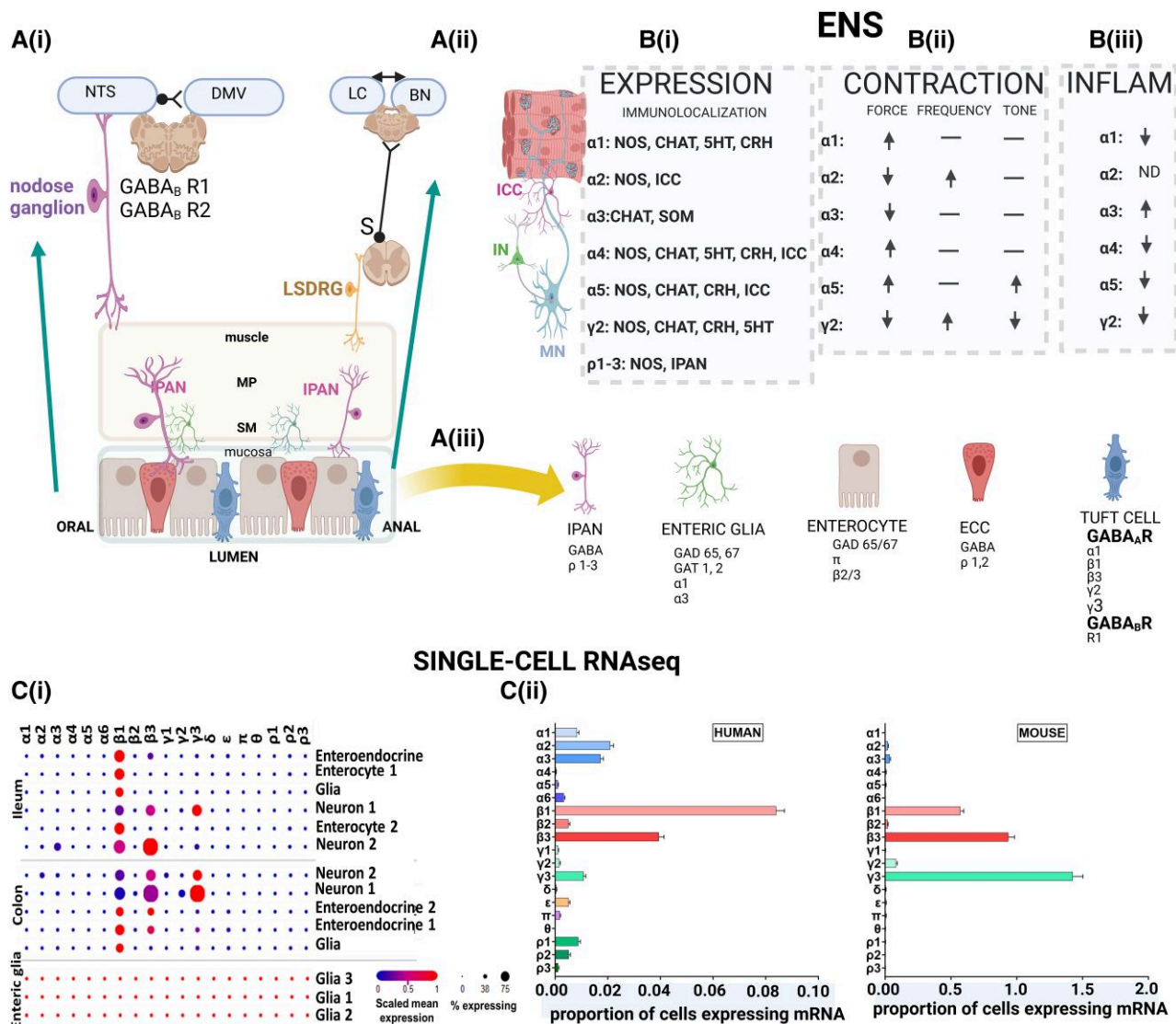
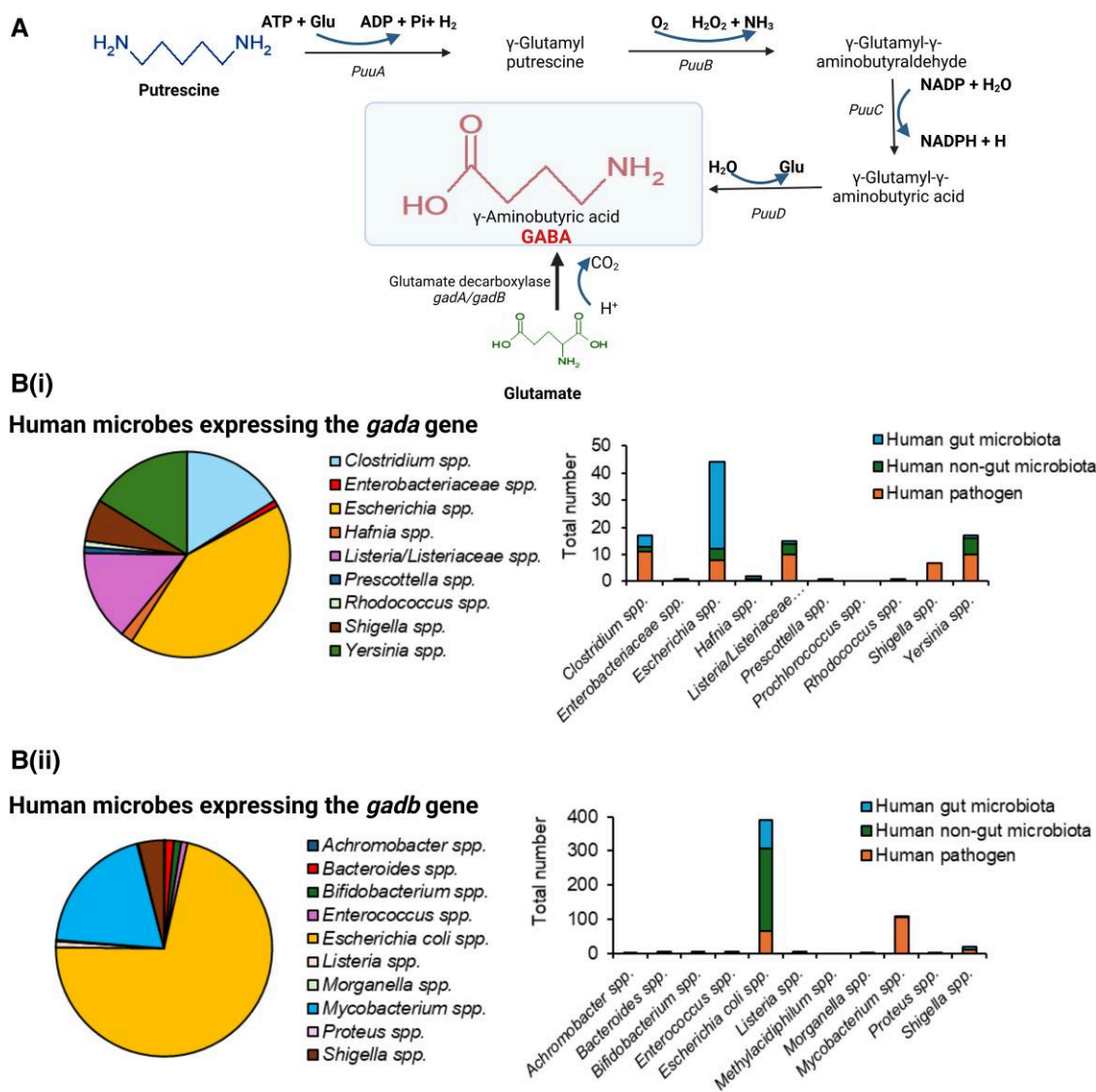


Figure 3 The roles of GABAergic signalling in neuronal and non-neuronal gut-to-brain pathways. (A) Schematic summary of the circuitry relaying gastrointestinal (GI) signals to the brain. [A(i)] In proximal (ORAL) regions, nodose ganglion (NG) sensory axons innervate the wall of the GI tract (GIT), with their centrally projecting axons innervating the nucleus tractus solitarius (NTS). The NTS in turn projects to neurons within the dorsal nucleus of the vagus (DMV). The NG is immunopositive for GABA type B receptors (GABA_BRs) but not type A receptors (GABA_ARs).¹¹¹ While NG cells are devoid of synaptic inputs, GABA may act here as diffusible transmitter released non-synaptically, for example, from local satellite glial cells.^{112,113} [A(ii)] In distal (ANAL) regions of the GIT, sensory axons of lumbosacral dorsal root ganglion (LSDRG) neurons make a variety of contacts throughout the GIT, including the muscle, enteric nervous system (ENS) and submucosa.¹¹⁴ LSDRG centrally projecting axons innervate sacral (S) spinal neurons that project to Barrington's nucleus (BN), which in turn activates neurons in the locus coeruleus (LC). [A(iii)] An overview of different cell types located in the mucosa and the associated GABAergic molecular machinery they have been demonstrated to express, including IPANs,¹¹⁵ enteric glia,^{116–118} enterocytes,¹¹⁹ enteroendocrine cells (EEC)^{120–122} and tuft cells.^{123–126} MP = myenteric plexus; SP = submucosal plexus. The green arrows indicate the direction of efferent information flow from the gut to the brain. B summarizes the expression and function of different GABA_A receptor subtypes within the mouse ENS. ICC = interstitial cells of Cajal; IN = interneuron; MN = motor neuron. [B(i)] The neurochemical identity of ENS neurons that have been shown immunohistochemically to express specific GABA_A receptor subunits.^{50,51,115,127} [B(ii)] The effects of the pharmacological activation of different GABA_A receptor subtypes on various parameters underlying spontaneous contractions of the mouse colon.⁵¹ [B(iii)] The effects of the pharmacological activation of different GABA_A receptor subtypes on intrinsic colonic inflammation.¹²⁸ N.D. = not determined. (C) An analysis of previously published single-cell RNA sequencing datasets of ENS GABA_A receptor subunit mRNA expression. [C(i)] An analysis of data published by Drokhlyansky et al.¹²⁹ The sizes of the dots in the dot plot indicate the percentage of cells in which gene expression was detected, and the colour scale indicates the magnitude of gene expression (scaled gene expression defines the expression maximum value as 1 and the minimum as 0). [C(ii)] An analysis of data published by Wright et al.¹³⁰ depicting the proportion of cells expressing subunits. The figure was prepared using BioRender (www.biorender.com).

genus *Bacteroides* the most abundantly represented^{150,154} (Fig. 4B). Conversely, some strains that require GABA for growth have also been isolated from the human microbiome.¹⁵⁶ Further indirect support for a physiological role for bacterial GABA came from a recent in-depth screening of intestinal *Bacteroides*,¹⁵⁷ which demonstrated

a high prevalence of GABA producers in human gut isolates. Crucially, 16/17 strains tested produced GABA at concentrations ranging from 0.09 to 60.84 mM, comparable with levels observed in high GABA-producing *Lactobacillus* and *Bifidobacterium* strains.¹⁵³ These levels fall within a physiological bioactive concentration



From the Integrated Microbial Genomes & Microbiomes Database 2024

Figure 4 Bacterial GABA synthesis. (A) Pathways utilized by bacteria to synthesize GABA. The main synthetic route occurs via glutamic acid decarboxylase (GAD), encoded by *gadA/B* genes, while the putrescine pathways represent a minor route used by certain species such as *Escherichia coli*. These pathways are absent from *Lactobacillus* and *Bifidobacterium* strains, which instead utilize the GAD pathway.¹⁵⁸ In addition to the *gadA/B* genes, the bacterial GAD operon also includes a *gadC* gene, which encodes an antiporter, allowing GABA to be exported from the cell, as reviewed by Sarasa *et al.*,¹⁵⁵ Diez-Gutierrez *et al.*¹⁵⁸ and Yogeswara *et al.*¹⁵⁹ Note that the measured concentrations (sub to low mM) of GABA produced by human gut bacteria fall within a physiological bioactive range.¹⁵⁷ (B) An overview of human microbes expressing (i) *gadA* and (ii) *gadB* gene. Human microbes expressing either gene were identified from the Integrated Microbial Genomes & Microbiomes database (accessed on 30 June 2024). These microbes were categorized into gut microbiota, non-gut microbiota and pathogens. Pie charts illustrate the distribution, including types and relative contributions of all human microbial species from the database. Histograms depict the distribution of gut microbiota, non-gut microbiota and pathogens. The total number and percentages of human microbial species obtained from the database are described in the [Supplementary material](#). The figure was prepared using BioRender (www.biorender.com).

range (Box 1). Dysbiosis of GABA-producing bacteria is increasingly associated with medical disorders, notably GI and psychiatric conditions, suggesting an important role for microbial GABA in the optimal functioning of the entire BGM axis.

A role for bacterially derived GABA in brain disorders? A focus on psychopathology

The importance of GABAergic signalling within the CNS for homeostasis and some brain disorders is well documented.^{43,160} However, emerging evidence associates perturbations of bacterially-derived GABA from BGM dysregulation as a putative contributory factor to

certain brain disorders, although the evidence is currently correlative rather than unequivocally causative. However, it is noteworthy that alterations in bacterially-derived GABA and/or the expression of GAD-system genes have been reported for a number of psychiatric and neurological disorders, including autism,^{161,162} depression,^{156,163,164} schizophrenia,¹⁶⁵ alcohol use disorder,^{166,167} and Alzheimer's disease.^{168,169} Next, we focus specifically on the emerging evidence regarding mood disorders.

Bacteria from the genus *Bacteroides* are some of the main GABA producers implicated in altered mood. However, available evidence paints a complex and, in places, contradictory picture of how bacterial abundance is linked to health and disease. Several

reports suggest that deficits in *Bacteroides* numbers may negatively impact mood. In a recent functional MRI study, the abundance of *Bacteroides* was inversely correlated with both connectivity within the default mode network and the clinical depressive profile of a population with major depressive disorder (MDD). This finding is important because the default mode network, a group of brain regions showing coherent activity, is involved in negative rumination and self-referential thinking and shows elevated connectivity in the depressive state, which is normalized in response to antidepressant treatment.¹⁷⁰ Further corroborating evidence is provided by the reduced abundance of *Bacteroides* in faecal samples of MDD subjects.^{171–173} Human faecal metagenomic analyses indicate a potential role of altered microbial GABA production in depression.¹⁶⁴ Conversely, in healthy subjects, *Bacteroides* levels associate positively with grey matter volume in cortical regions, coupled with diminished anxiety/distress in healthy women exposed to images with emotional content.¹⁷⁴ Finally, the abundance of GABA-producing bacteria (*Bacteroides* and *Parabacteroides*) appears inversely related to fear behaviour in red fowls,¹⁷⁵ which could indicate that the BGM mechanisms linking emotional regulation with particular gut bacteria are conserved across species.

Although the *Bacteroides* genus is most consistently associated with brain connectivity studies,¹⁷⁶ the association between their abundance and psychopathology is inconsistent across publications, with some studies documenting an increase rather than a decrease in depressive clinical cohorts.¹⁷⁷ These results, coupled with findings from previous studies of MDD clinical populations, which uncovered additional significant changes in other microbiota genera and species (e.g. decreased *Faecalibacterium*¹⁷⁸ and increased *Prevotella* and *Klebsiella*^{179,180}), strongly suggest that, while playing an important role, the *Bacteroides* genus alone cannot fully account for the depressive phenotype in human MDD. Instead, a balance amongst different microbiota species is likely a crucial driver of health or pathology. This complexity suggests that a more granular analysis at the species or strain level is necessary, as supported by a recent study that individually phenotyped mice colonized with one of the four most represented individual *Bacteroides* species identified in the microbiome of a 40-strong medicine-free MDD patient versus control cohort. This analysis revealed that only colonization with *Bacteroides fragilis*, *B. uniformis* or to a lesser extent *B. caccae* but not *B. ovatus* (see later) recapitulated both the behavioural and molecular indices of the stress-induced ‘depressive’ phenotype observed following transplantation with the whole microbiome from the MDD cohort.¹⁸¹ Similar mechanistic approaches using mixed human-animal models are a major priority for establishing definitive causal relationships between gut bacteria and human mental states.¹⁸²

The immunomodulatory profile of bacterial species may be particularly relevant in health and disease. A case-control study in school-aged children with depression revealed that a significant decrease in the *Bacteroides* genus correlated positively with a variety of inflammatory markers. Conversely, a negative association was evident for anti-inflammatory indicators.¹⁸³ This is consistent with growing evidence indicating that gut-associated systemic inflammation is a driver of mood disorders, e.g. depression.^{184–189} Furthermore, as microbiota can generate a diverse signalling system, including but not limited to GABA, it is likely that the type and abundance of additional microbial products, e.g. SCFAs such as butyrate or acetate or other neurotransmitters, e.g. 5-HT^{190,191} (see the ‘Gastrointestinal GABA interaction with SCFA and 5-HT’ section), participate in the observed clinical phenotypes.

In terms of the role of microbial GABA, specifically GABA derived from *Bacteroides*, in regulating mood, certain but not all *Bacteroides* species may contribute to the functional GABAergic deficits in the CNS that have been implicated consistently in clinical studies of depressive illness.^{192–194} Of specific interest is a recent investigation revealing that colonization by *B. ovatus* influences the abundance of intestinal GABA and SCFA but not dopamine or noradrenaline.¹⁹⁵ Furthermore, *B. ovatus* is the most effective stimulator of IgA production¹⁹⁶ (Fig. 5), which is essential to gut homeostasis.¹⁹⁷ This finding is significant in view of the study discussed earlier,¹⁸¹ where only mice transplanted with *B. ovatus* but not *B. fragilis*, *B. uniformis* or *B. caccae* appeared resistant to the stress-induced depressive phenotype and showed a selective increase in hippocampal BDNF, a putative biomarker of antidepressant action.¹⁸¹ Finally, many of these findings are also relevant to substance use disorders since a disrupted microbiome, inflammation and psychiatric disturbances such as anxiety and depression have been implicated in the development and maintenance of chronic drug consumption,^{198,199} notably alcohol use disorder.^{166,189,200–204}

Mechanisms of gastrointestinal-derived GABA regulation of brain function

The mechanisms by which brain-derived GABA contributes to brain function in health and disease are widely reported.^{43,225,226} In contrast, precisely how peripheral GABA systems modulate brain function via their influence on the GI system is less well understood. Since GABA is unlikely to cross the BBB,^{227–229} peripherally produced GABA almost certainly influences brain function indirectly. Here, we focus on three key mechanisms: (i) the activation of GABA_ARs in the ENS; (ii) GABA_AR activation in the immune system; and (iii) GABA stimulation of exosome-mediated signalling (Fig. 5). Additionally, GI-derived GABA may influence brain function as a modulator of gut microbiota by acting as a nutrient, fine-tuning microbial communities or targeting bacterial GABA_ARs (Fig. 5 and Box 2).

Gastrointestinal GABA modulates brain function by activating GABA receptors on ENS neurons

GABA_AR subtypes expressed on neurochemically diverse ENS neurons modulate various GI functions, including motility, local immune function and barrier integrity.^{51,128} These observations are important because, as discussed later, alterations to these GI parameters commonly occur in a range of brain disorders, especially those associated with maladaptation to psychosocial stress. For example, exposing rodents to stress that induces anxiogenic- and depressive-like behaviour increased colonic contractility, induced GI inflammation and impaired barrier function.¹²⁸ This overlap of GI and brain symptoms is commonly present in patients with stress-associated conditions such as dysmotility and inflammation in irritable bowel syndrome (IBS)²⁴⁴ as well as mental illnesses such as anxiety.²⁴⁵ Importantly, some GABA_AR PAMs ameliorate both GI and brain symptoms, further evidencing the interconnectedness of GABA pathways throughout the BGM axis in health and disease. For example, the widely used anxiolytic alprazolam, a known PAM of GABA_ARs, induces a robust relaxation of GI tone in animals.⁵¹ This may represent the amelioration of dysmotility, a core somatic component of anxiety. Moreover, a novel role has emerged for $\alpha 3$ -GABA_ARs, since in a rodent model of early-life stress (ELS), $\alpha 3$ -GABA_ARs appear necessary and sufficient for the ELS-evoked

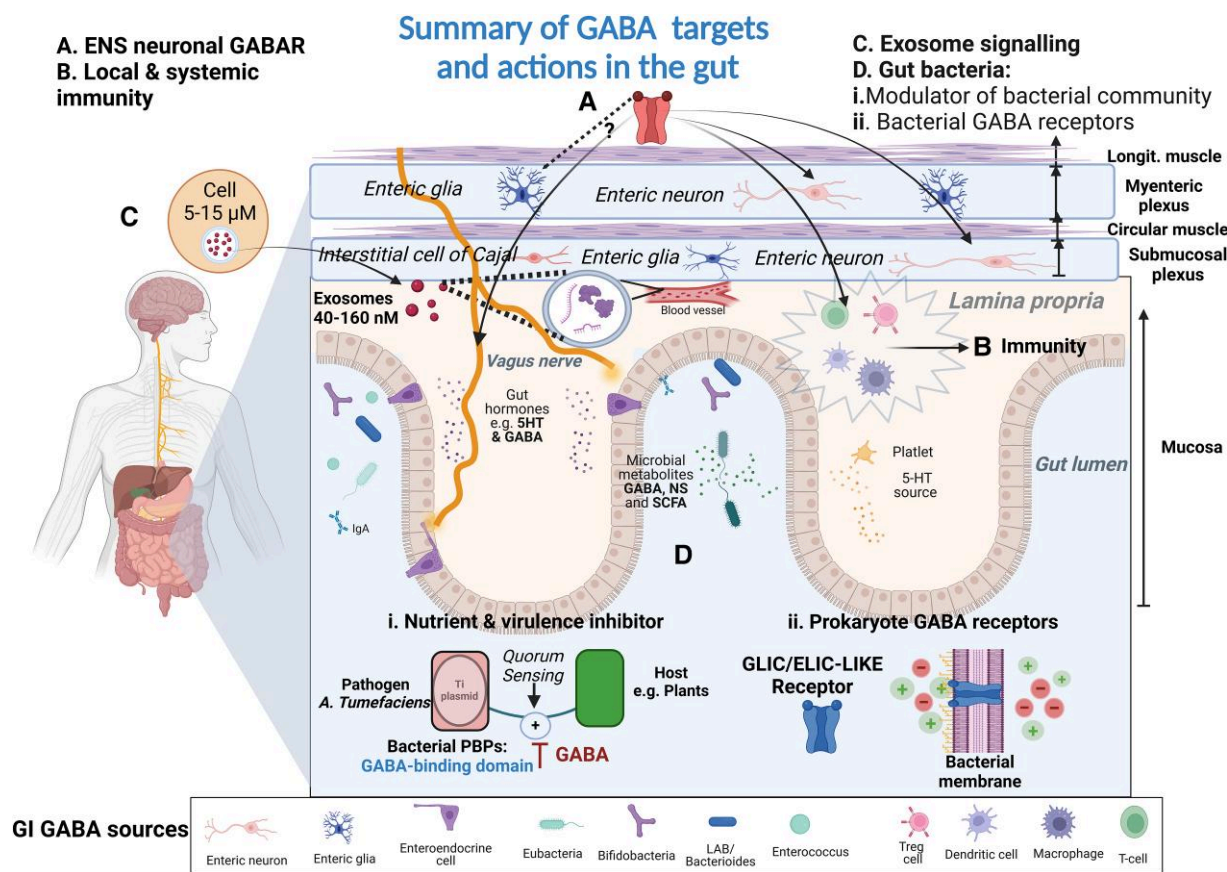


Figure 5 Versatile sources, actions and targets of GABA in the gastrointestinal tract. GABA and putatively neurosteroids (NSs)²⁰⁵ exhibit pleiotropic actions and targets in the gastrointestinal (GI) tract. (A) GABA targets neuronal and potentially glial GABA receptors in the submucosal and myenteric plexuses of the enteric nervous system and modulates vagal transmission.^{110,206–209} GABA can act on local and systemic immune cells^{145,210} (B), which express both GABA type A and B receptors (GABA_ARs and GABA_BRs).²¹¹ As the gut-associated lymphoid system accounts for ~70% of the body's immune cells,²¹² the GI GABA system is ideally placed to influence immunity. Although the specific mechanisms are yet to be fully elucidated, gut GABA can also induce blood-detected exosome signalling associated with brain plasticity, e.g. in the hippocampus^{213–215} (C). Finally, GABA can act on bacterial communities to modulate their relative abundance [D(i)], either by acting as an essential nutrient¹⁵⁶ or by affecting the expression or transfer of crucial genes, e.g. as a virulence inhibitor of invading plasmids from pathogenic species such as *Agrobacterium tumefaciens*.^{216,217} GABA specifically promotes the degradation of quorum sensing signals that control plasmid transfer.²¹⁸ Interestingly, unique GABA binding motifs have been identified in the periplasmic bacterial protein (PBP) Atu4243 of *A. tumefaciens*, which functions as a selective GABA-sensor and transporter to satisfy nutritional requirements.²¹⁷ These opposite roles of GABA suggest that GABA participates in and fine-tunes the complex relationship between hosts and biotrophic pathogens. Albeit speculative at present, GABA may also target bacterial receptors [D(ii)], akin to the identified GLIC (Gleobacter ligand-gated ion channel)²¹⁹ and ELIC (Erwinia ligand-gated ion channel)^{220,221} prokaryotic GABA receptors of the *Cyanobacteria* phylum, closely related to some recently identified human gut bacteria.²²² In indirect support, recent evidence has revealed that GABA modifies the bioelectrical properties of a known commensal bacterial strain *Lactobacillus reuteri* to impact their growth,²²³ congruent with the known bacterial use of change in membrane potential to convey and process key information.²²⁴ The figure was prepared using BioRender (www.biorender.com).

inflammatory and anxious phenotype, which is characterized by disruption of gut barrier function along with a concomitant significant increase in a range of inflammatory markers.¹²⁸

Here, we surmise that the following GABA_AR subtypes are relevant in terms of modulating connected BGM axis functions. Convergent genetic and pharmacological studies strongly implicate $\alpha 2/3$ -GABA_AR subtypes in anxiolysis produced by benzodiazepines²⁴⁶ and neurosteroids.²⁴⁷ It is notable from the expression data in Fig. 1B that these α -subunits are abundantly expressed in both brain and gut. As mentioned earlier, $\alpha 3$ -GABA_ARs are implicated in stress-induced GI inflammation.¹²⁸ Given the prevalence of GI symptoms and systemic inflammation in comorbid mental illness such as anxiety and depression (see the 'GABA's role in immunity' section), assessing the efficacy of $\alpha 2/3$ -GABA_AR-selective ligands that do or do not have brain penetrance in such patient populations would improve our understanding of which GABA_AR subtypes

within specific segments of the BGM axis contribute to such complex medical conditions. Based on human expression data (Fig. 1B), ϵ -GABA_AR subtypes could also be integral to BGM axis regulation. The highest brain expression of ϵ -GABA_AR is in the hypothalamus, with considerable expression across several peripheral organs (Fig. 1B). Given the preeminent role of the hypothalamus in coordinating body homeostasis, the expression of the same GABA_AR subtypes throughout these brain-body pathways is likely to enhance coordination across functionally diverse organ systems. Thus, the development of appropriate ϵ -GABA_AR research tools (verifiably specific antibodies; selective ligands; gene-deleted mice) could be instrumental in advancing science and medicine across diverse disciplines. Interestingly, ρ -subunit-containing GABA_ARs, originally described in the retina²⁴⁸ and previously called GABA_CRs, but apparently expressed more widely (Fig. 1B), including in the ENS,¹¹⁵ have been implicated in modulating rodent intestinal

Box 2 GABA actions on gut bacteria

Modulation of gut bacteria

- GABA may affect brain function by modulating key bacterial communities either as a nutrient or a fine tuner/modulator. The former, i.e. as a source of carbon and nitrogen, is well documented in plants,^{230–233} where GABA was first identified in potato tubers over 70 years ago²³⁴ before being recognized as the main inhibitory neurotransmitter in the vertebrate brain. Therefore, it is no surprise that GABA is a vital nutrient within the human microbiome.¹⁵⁶ This raises the prospect that GABA-dependent microbes may be beneficial for human health and GABA may be an intermediate inter-kingdom messenger able to confer directly and/or indirectly, a range of health advantages for animals and humans.
- GABA may additionally modulate the presence and abundance of specific microbial communities via more tailored strategies as described for plant-microbial interactions. For example, there is ample evidence that plants utilize GABA to overcome biotic stress brought about by pathogenic microbes.^{235–237} The GABA-mediated defence approach by plants embraces a variety of mechanisms including support for key energetic pathways.²³⁷ In addition, GABA can reduce the virulence of some pathogens such as *Agrobacterium tumefaciens* and *Pseudomonas syringae* by interfering with the production of molecules by quorum sensing, a complex signalling system utilized by bacteria to control several processes including survival and colonization of specific ecosystems.^{218,238} The protective role of GABA against pathogenic colonization by inhibiting specific quorum signalling molecules appears important to preventing the conjugation and amplification of the Ti plasmid, used by *A. tumefaciens* to transfer DNA and transform the plants it invades.²³⁹ Intriguingly, *A. tumefaciens* possesses a selective GABA-binding protein where highly conserved amino acid residues have been proven critical for the inactivation of the quorum signal implicated in Ti plasmid actions.^{216,217} Thus, a specific and primordial mechanism exists to enable GABA protective actions against microbial pathogens, suggesting a similar approach may also be operative in mammalian gastrointestinal systems.

GABA as an agonist of bacterial GABA receptors

- GABA may also regulate the microbial ecosystem by modifying their bioelectrical properties, which are dynamic and can be utilized to serve a variety of functions and communication strategies.²²⁴ In support, two recent pioneering studies employing population measurements of bacterial membrane potential with fluorescent voltage-sensitive dyes revealed that bacterial membrane depolarization is associated with bacterial growth. Furthermore, sub-micromolar concentrations of GABA can reduce the degree of depolarization of known microbiome bacterial strains *Lactobacillus reuteri*²²³ and *Enterococcus faecalis*.²⁴⁰ The impact of GABA on bacterial growth remains to be established since the ultimate effect of depolarization appears dependent on the activated or inhibited state of the bacteria.²⁴¹ Potential molecular targets of this GABA effect include bacterial homologues of pentameric ligand-gated channels, including GABA_ARs, previously identified, e.g. *Erwinia* ligand-gated ion channels (ELICs)^{220,221} and *Gleobacter* ligand-gated ion channels (GLICs)²¹⁹ from *Erwinia chrysanthemi* and *Gleobacter violaceus* of the *Cyanobacteria* phylum, respectively. These prokaryotic receptor homologues are sensitive to GABA (i.e. ELIC)^{220,221,242} and/or GABA-active ligands including neurosteroids.²⁴³ Interestingly, bacteria closely related to *Cyanobacteria* have been identified in both the human and animal gastrointestinal tracts,²²² with tantalizing implications for human health.

contractility.^{17,249} Specifically, receptors with a ρ -type pharmacology were implicated in the contractility of the mouse duodenum²⁴⁹ and increased cholecystokinin release in a neuroendocrine tumour intestinal cell line (STC-1),¹³⁵ which shares many properties with native intestinal enteroendocrine cells.²⁵⁰ Importantly, ρ -GABA_ARs are distinct amongst other subtypes. This is due to their relatively high affinity for GABA, insensitivity to the classical GABA_AR antagonist bicuculline and lack of desensitization.¹⁸ These features make them ideally tailored to mediating sustained GABA inhibition via a shunting action (Box 1). It is important to determine precisely how ρ -GABA_ARs differ from other subtypes in terms of regulating GI function, e.g. by inducing ENS neuronal inhibition, despite the reported local GABA depolarizing actions.²⁵¹

Gastrointestinal GABA modulates local and systemic immunity by activating immune-cell GABA receptors

A compelling body of evidence implicates immune system dysregulation in psychopathology.¹⁸⁹ However, there are many crucial unanswered questions about whether associated systemic inflammation drives brain pathology or primary alterations to brain function result in changes to immune function in the rest of the body.

This has stimulated the assessment of neurochemical involvement, most notably GABA, in immune processes.^{145,210} What has emerged is convincing evidence that the GABA molecular apparatus is expressed in both arms of the immune system—in the innate, e.g. mononuclear phagocytes, and adaptive response factors, e.g. T and B cells. The components of the molecular apparatus include molecules underpinning GABA metabolism, GABA transport and secretion, both GABA_A and GABA_BRs, GABA signal regulation by cation chloride co-transporters (CCCs) and effector Ca²⁺ signalling via voltage-dependent channels.^{145,210} Furthermore, functional studies confirm that GABA signalling via both A and B receptor subtypes regulates inflammatory and anti-inflammatory responses in both arms of the immune system.^{211,252} These findings suggest that the GI GABA system is ideally placed to influence immune function since the gut-associated lymphoid system accounts for ~70% of the body's immune cells²¹² (Fig. 5). In support, the activation of specific GABA_AR subtypes induces or suppresses colonic inflammation in addition to impacting barrier permeability.¹²⁸ Thus, there is the potential for such GABA-mediated production of local GI immune mediators to distribute more widely throughout the body, allowing systemic inflammation to impair BBB integrity. This would result in a variety of molecules obtaining access to the brain, such as inflammatory

cytokines, which negatively impact brain function, thereby contributing to psychological symptoms.

Key questions remain in terms of which specific GABA_AR subtypes drive changes in immune function, as well as their cellular location, with evidence indicating that specific subtypes are important for brain and systemic immune pathways.²¹¹ There is also heterogeneity in the expression of GABA_AR subtypes across distinct immune cells,¹⁴⁵ a feature shared with both the CNS^{37,253,254} and ENS.^{50,51} However, a full mechanistic appreciation of the role of GABA_A/B_AR_S in modulating local and systemic immunity will require novel knowledge of the specific receptor subtypes and associated roles within specific immune cell populations, along with a better understanding of the specific biological context driving the expression of the identified receptor subtypes. Moreover, given that immune cells can additionally synthesize GABA, e.g. in phagocytes, via cytosolic GAD67²⁵⁵ or T cells,²⁵⁶ via a vesicle-independent process, elucidation of the specific GABA secretory pathway(s) will aid the understanding of GABA's role in the regulation of immune tone and whether GABA may function as an autocrine or paracrine messenger.^{256,257} Intriguingly, studies have revealed that sub-micromolar concentrations of GABA affect specific functions, e.g. cytokine release.²⁵⁵ These observations raise the prospect that these effects are mediated by receptor subtypes associated with extra-synaptic function in neuronal populations, which are also activated by low GABA concentrations and show limited desensitization^{21,45,258} (see the 'GABA signalling within the BGM axis' section). This suggestion is supported by the abundant expression in immune cells of subunits typically associated with neuronal extrasynaptic subtypes, e.g. $\alpha 4$, $\alpha 5$, $\alpha 6$ and δ , and $\rho 1/2$ receptor isoforms, also known to exhibit high affinity for GABA and limited desensitization.^{145,248,255,256,259,260} Nevertheless, the additional expression of receptor subunits that are typically linked with synaptic activation in neuronal networks e.g. $\alpha 1$ and/or $\alpha 2/3$ - $\gamma 2$ -containing subtypes coupled with expression of proteins, e.g. GABARAP,²⁵⁶ long known to support synapse stability,²⁶¹ suggests that GABA concentration gradients may also be required for modulation of specific immune functions.

Gastrointestinal GABA modulates brain function via exosome-mediated signalling

Exosomes are a subtype of extracellular vesicles (~40–160 nm in diameter) with a lipid-enveloping structure. They are released extracellularly by different cell types and function like carriages, shuttling basic cell biomolecules, including DNA, mRNA, miRNA, lipids and proteins (Fig. 5), to mediate short- as well as long-distance communications^{262–264} in both physiological and pathological processes.²¹³ A role for GABA-induced exosomes from intestinal tissue has recently emerged. Exosomes isolated from the blood of mice orally administered with GABA but not those derived from vehicle-treated mice produced neuronal activity in SH-SY5A cell lines via a unique complement of genes associated with neuronal function.^{214,215} Moreover, their presence in the blood of GABA-treated mice was associated with hippocampal changes in the expression profile of genes governing neuronal function.²¹⁵ The exact mechanisms of exosome-mediated gut-to-brain GABA-evoked communication are yet to be uncovered. GABA could either target the brain directly via exosomes or indirectly by activating GABARs in the intestinal tissue to modulate exosome content. Future studies will provide clarity and uncover potential new mechanisms that may be exploited to therapeutic advantage.

Gastrointestinal GABA modulation of brain function: other microbiota metabolites and neurotransmitters

Evidence suggests that peripheral GABA has the potential to influence the production of, or interact with, other important mediators of the BGM axis with neuroactive properties and, thus, has brain-modulating potential. Here, we focus on two such classes of BGM axis messengers, namely SCFA and 5-HT, because of their relevance to mental health.

GABA and short-chain fatty acids

SCFAs are the main metabolites produced in the colon by bacterial fermentation of dietary fibres and resistant starch.²⁶⁵ Apart from being a necessary waste product for resident bacteria to balance redox equivalent production in the anaerobic environment of the gut,²⁶⁶ compelling evidence points to microbiome-derived SCFAs playing a beneficial role in brain function and behaviour.²⁶⁷ Thus, mechanisms that stimulate SCFA production could, in theory, positively influence brain processes. Whilst the evidence is still in its infancy, GABA has been shown to increase caecal SCFA content in mice,²⁶⁸ suggesting a potential therapeutic target. One particular SCFA, acetate, not only crosses the BBB^{269,270} but also participates in neuronal GABA synthesis (approximately 30%).²⁷¹ Furthermore, studies in rodents demonstrate that direct acetate supplementation improves depressive-like behaviours.²⁷² Additionally, acetate and GABA are implicated in reducing depressive- and anxious-like behaviours in mice supplemented with the probiotic *B. licheniformis*, with a positive correlation reported between the increased levels of acetic acid and GABA.²⁷³ Collectively, these findings support further investigations regarding the underlying signalling mechanisms.

GABA and 5-HT

Another well-documented chemical messenger and regulator of the BGM axis is 5-HT.²⁷⁴ Significant evidence implicates dysregulation of the 5-HT system (including metabolism of its key precursor, tryptophan) at both ends of the BGM axis in psychopathology.^{1,274–277} While an extensive discussion of the roles and targets of the 5-HT signalling system in the working of the BGM axis²⁷⁶ is beyond the scope of this review, we focus on its potential interaction with GABA in the context of BGM signalling, specifically in the homeostatic regulation of emotional states.

Different lines of evidence support directly or indirectly a GABA-5-HT interaction not only in the brain²⁷⁸ but also potentially in the periphery and gut. Dysregulation of both GABAergic and serotonergic systems has been documented in clinical cohorts^{279–284} and animal models of psychopathology.^{193,285–287} Intriguingly, emerging evidence also implicates, directly or indirectly, both GABA (see the 'Future research priorities' section) and 5-HT^{288–291} in the beneficial effects of certain dietary interventions. For example, *Bifidobacteria*-based probiotic interventions, which are amongst the most widely used and effective for the prevention and treatment of psychological disturbances,^{292–294} have been reported to involve modulation of both the serotonergic²⁹⁵ and GABAergic^{296,297} systems. In further indirect support, most utilized pharmacological treatments for anxiety and depressive disturbances target GABAergic (e.g. benzodiazepines) and/or serotonergic transmission (i.e. selective serotonin reuptake inhibitors). Collectively, these observations suggest a possible synergy between these neurotransmitters to optimize emotional regulation.

This proposal is consistent with the role of 5-HT as a neuromodulator, and that dysregulation of the 5-HT system in depression and anxiety represents a biological risk factor rather than being the primary cause of psychopathology.²⁹⁸ Similarly, CNS functional GABAergic deficits, while apparent in many clinical cohorts, do not appear sufficient to be the sole cause of depression.^{43,299}

How could GABAergic and serotonergic systems interact in the context of BGM signalling? In the brain, various mechanisms have been proposed to underpin physiologically and pathologically important interactions between GABA and 5-HT,²⁹⁹ including modulation of transmitter release. For example, GABA release can be influenced by the activation of 5-HT targets, i.e. increased by excitatory 5-HT₃ receptors (5HT₃R) expressed in GABAergic interneurons, particularly in the amygdala³⁰⁰ and hippocampus.³⁰¹ Conversely, 5-HT release is modulated by GABAergic transmission, e.g. in the dorsal raphe via GABA_A³⁰² and GABA_B receptors,^{303,304} which mediate a decrease and increase, respectively. Although functional evidence is currently lacking, similar mechanisms may also occur in the gut where 5HT₃Rs are abundantly expressed, for example, on inhibitory motor neurons in the ENS,³⁰⁵ which comprise the majority of GABAergic neurons.³⁰⁶

When considering the regulation of 5-HT levels both in the brain and the GIT, it is important to emphasize that approximately 95% of 5-HT in the body is produced in the gut, and of this 80% is produced by ECs in the GI epithelium (Fig. 5), whereas ENS neurons are a minor, albeit important, source.^{277,307,308} Interestingly, both GABA_ARs and GABA_BRs are expressed in ECs,¹³² providing a means for GABA-mediated regulation of 5-HT levels at its main source.

Gut microbiota also modulate 5-HT levels directly or indirectly.^{274,288,309} Conversely, 5-HT can modulate bacterial colonization in the gut.³¹⁰ For example, the synthesis of 5-HT is modulated by microbiota products such as SCFA, which can upregulate the expression of the key enzyme involved in 5-HT synthesis in ECs, namely tryptophan hydroxylase 1 (TPH1).³¹¹ As discussed earlier, GABA may regulate SCFAs levels^{268,312} and so may also indirectly modulate 5-HT levels. Intriguingly, *Clostridium perfringens*, an anaerobic gram-positive spore-forming bacillus associated with dangerous gastrointestinal infections and long known to modulate the production of gut 5-HT also displays high amounts of GAD, the key GABA synthesizing enzyme.³¹³ Neurosteroids (Box 3) may also be implicated in the regulation of gut 5-HT levels, probably via GABA_ARs. Thus, withdrawal from chronic inhibition of neurosteroid synthesis with finasteride, a selective inhibitor of a key neurosteroid synthetic enzyme, 5 α -reductase, produces profound changes in rat colon neurosteroid levels, while concomitantly increasing 5-HT levels and altering local GABA_AR expression.³¹⁴ Importantly, both changes are reversed by treatment with ALLO.³¹⁴

Immunomodulation is a key element of BGM signalling³³⁷ and another potential converging platform for 5-HT and GABAergic interactions. As noted earlier, evidence implicates inflammation and immune dysregulation in psychopathology.^{185,187,189,338} Notably, both are key features of irritable bowel syndrome.³³⁹ This condition is also known to be co-morbid with both anxiety and depressive disorders^{340–342} and accompanied by dysregulated GABAergic³⁴³ and serotonergic signalling.^{270,344,345} Some elements of the alterations in GABAergic and 5-HT systems may be mediated via the immune system. Thus, the role of 5-HT as a key regulator of the local and systemic immune responses (e.g. via 5-HT-enriched platelets; Fig. 5) is well established.³⁴⁶ However, some immune dysregulation may also implicate and/or modulate GABA. For example, GABA may modulate 5-HT receptor expression in immune cells both locally and systemically, thus affecting their function and vice versa.

When exploring potential mechanisms underpinning GABA–5-HT interaction, the depolarizing actions of GABA in the periphery compared to its traditional hyperpolarizing role in the majority of CNS neurons are likely important. Indeed, depolarizing action by GABA could be followed by the activation of specific voltage-gated channels, for example, Ca²⁺-mediated conductances. This would, in turn, trigger various signalling cascades, possibly leading to changes in the genetic expression of receptors and other cellular components. If and how GABA and 5-HT interact to regulate immunity locally in the gut and systemically remains to be established and could offer a new understanding of some molecular underpinnings of BGM homeostasis and dysfunction.

Finally, the vagal afferent system (see the 'GABA signalling within the BGM axis' section and Fig. 5) offers another pathway whereby GABAergic and serotonergic signalling may interact.⁴ From an anatomical perspective, vagal innervation of the small intestine is well documented,³⁴⁷ while recent reports provide further compelling evidence^{348,349} to support earlier studies on vagal innervation and regulation of the colon where, common to the entire GIT, intraganglionic lamellar endings and related structures in the myenteric ganglia mediate the interaction between ENS and vagal afferents.^{347,350,351} Both GABA and 5-HT receptors are present on vagal terminals^{110,206,207,352} where 5HT₃Rs are abundantly expressed³⁵³ and implicated in gut-derived GABA-²⁰⁸ and 5-HT-mediated³⁵⁴ effects. Moreover, vagotomy prevents both GABAergic²⁰⁹ and serotonergic³⁵⁵ effects on behavioural and molecular end points of gut-targeted interventions. Conversely, stimulation of the vagus nerve, which can reduce anxiety and depressive-like behaviour in rodents^{356,357} and is a US Food and Drug Administration-approved treatment for resistant depression (since 2005),³⁵⁸ increases levels of 5-HT in anatomically relevant brain centres, i.e. dorsal raphe.^{359,360} The vagally mediated behavioural effects implicating GABA and 5-HT may also involve modulation of the immune system.³⁶¹ In summary, a GABA–5-HT interaction is well documented in the brain and highly likely to occur in the GI tract, supporting the bidirectional conversation between the two ends of the gut-brain axis.

Key priorities for future research

Identifying direct evidence for neuronally-released GABA regulation of gastrointestinal function

As discussed in Box 1, within the CNS, there is compelling evidence for the variety mechanisms by which the release of endogenous GABA alters the excitability of target neurons, including fast phasic or persistent tonic currents. In stark contrast, such direct evidence for GABA-mediated postsynaptic potentials in the ENS is lacking.³⁶² This is despite the array of studies, using exogenously applied GABA or GABA receptor ligands, providing compelling evidence for the roles of GABA receptors in a variety of GI functions, most notably smooth muscle contractility. There is evidence for GABA expression in excitatory motor neurons, descending interneurons and inhibitory motor neurons³⁰⁶ and of neurally released GABA to modulate slow inhibitory potential in the mouse ileum via ρ -containing GABA_ARs.¹⁷ Yet, clear evidence of GABA acting directly on GI muscle is lacking. However, GABA_ARs have been detected by immunohistochemistry in non-neuronal ICCs,⁵¹ which lie at the interface between the ENS and intestinal smooth muscle. Given that the activity of ICC is believed to underlie spontaneous intestinal contractions,³⁶³ ICC GABA_ARs may represent a key molecular link through which GABA modulates GI muscle contractility.

Box 3 A role for neurosteroids in the regulation of the brain-gut-microbiota axis?

- A class of endogenously occurring steroids synthesized in the CNS, neurosteroids, are documented potent efficacious positive allosteric modulators (PAMs) of GABA type A receptor (GABA_AR) function at physiologically and pathologically relevant levels.^{44,315–319} Most research investigating the GABA_AR-active properties of neurosteroids has focused on CNS excitability. However, converging evidence indicates that local production of GABA_AR-active neurosteroids within the gastrointestinal tract is also relevant to CNS function and behaviour.
- Such local production may be regulated dynamically by the resident microbiota. Specifically, an abundant expression of the steroidogenic machinery that regulates levels of neurosteroids and their precursors is apparent in the adult rat colon, suggesting local synthesis.³²⁰ Importantly, enzymes (e.g. 3 α -hydroxysteroid-oxido reductase) critical to the synthesis of the GABA_AR-active neurosteroid allopregnanolone (ALLO) are more densely expressed in the colon than in brain steroidogenic tissue, e.g. the cerebral cortex.³²⁰ In agreement, the levels of ALLO are markedly higher in the colon than the cortex/plasma.³²⁰ Indirect support for microbiota influencing neurosteroid levels comes from studies of germ-free mice, where both the brain and peripheral abundance of GABA_AR-active steroids are altered, albeit differentially in the brain compared to the periphery.³²¹ Neurosteroids may also originate from gut microbiota, as a significant population of the human gastrointestinal flora express the necessary enzymes to convert progesterone and testosterone.^{322,323} Moreover, certain human gut bacteria, namely *Gordonibacter pamelaeae* and *Eggerthella lenta*, convert abundant, micromolar, biliary corticoids into GABA_AR-active neurosteroids, particularly during pregnancy.²⁰⁵ The microbiota contribution to neurosteroid modulation of neuronal homeostasis is further emphasized by the inhibition of neurosteroid synthesis by finasteride. This inhibitor of the 5 α -reductase enzyme is associated in male rats with a depressive-like phenotype, neuroinflammation and concomitantly an alteration of the gut microbiota composition.³²⁴ Importantly, in rodents, ALLO provides protection against gut inflammation induced by withdrawal from chronic finasteride treatment. Thus, ALLO decreases the raised expression levels of some inflammatory cytokines, namely IL-1 β and TNF α and reverses the concomitant mRNA changes in β 2-, β 3- (decrease) and δ - (increase) GABA_AR subunits,³¹⁴ thus implicating GABA_ARs in ALLO's protective actions. These findings may be clinically relevant to post-finasteride syndrome, a condition affecting vulnerable male patients treated with finasteride for benign prostatic hyperplasia or alopecia, who develop mood and cognitive impairments amongst other side effects which persist even after finasteride discontinuation.^{320,325–328} In this patient population, the documented abnormal plasma and CSF neurosteroid levels^{329,330} and gut dysbiosis³³¹ may result in peripheral and brain neuroinflammation. Similarly, the protective effect of neurosteroids against CNS neuroinflammation that features both in psychopathology¹⁸⁹ and neurodegenerative conditions³³² may arise from their peripheral effects in the gut, reducing systemic inflammation via the brain–gut–microbiome (BGM) axis.
- Overall, these findings suggest a putative role for neurosteroids in regulating the function of the enteric nervous system (ENS), microbiota composition and BGM axis, impacting the modulation of brain function.
- A role for neurosteroids is also emerging in the regulation of neuroendocrine pathways of the BGM, implicated in brain homeostasis. A variety of putative targets and mechanisms are likely to mediate neurosteroid actions within the gastrointestinal tract. In common with GABA, GABA_AR-acting neurosteroids modulate the function of GABA_ARs located in the gastrointestinal tract, thus including those expressed both in the ENS and immune cells. Growing evidence also supports an important role for the peroxisome proliferator-activated receptor (PPAR)- α receptor as a key molecular link between neurosteroids, gut bacteria, inflammation and physiologically relevant behavioural and molecular phenotypes. This nuclear receptor is ubiquitously expressed throughout the gastrointestinal tract, including epithelial and immune cells, and its absence associates with significant dysbiosis and an inflammatory phenotype.^{333,334} Importantly, PPAR α activation both stimulates neuro-steroidogenesis, e.g. of ALLO, and anti-inflammatory responses, while also preventing both stress-induced depressive phenotypes in animal models and the concomitant brain decrease in GABA_AR-acting neurosteroids.^{334,335} These findings are significant for GABAergic signalling, as evidence of a causal relationship between neurosteroid metabolism and expression of GABA_AR subtypes already exists in animals.³³⁶

Future targeted investigations should explore this possibility. A major confound derives from the co-expression of GABA with other neurotransmitters known to modulate smooth muscle contractility, such as acetylcholine. The exploitation of transgenic models allowing for the selective activation of subsets of GABAergic cell types whilst recording physiological responses with neighbouring cells could be instructive in terms of defining connected cell circuits.

Characterizing individual segments of the BGM with relevance to gut physiology and brain diseases

Compelling evidence links the integration of different cell groups and circuits of the brain-gut axis in mediating homeostasis and their involvement in medical disorders. Going forward, it will be important to disentangle the functional contributions of individual

elements and how these change in disease. This progression is imperative if we are to address associated medical conditions by targeting and modifying the underlying mechanisms, rather than providing purely symptomatic relief. Whilst technical challenges have in the past prevented the selective manipulation of individual cell types or cell circuits during different behavioural or physiological states, the latest technologies allow for such direct interrogation of brain-body mechanisms. For example, using a combination of cutting-edge genetic, physiological and behavioural technologies, the cardiogenic control of affective behavioural states has recently been elegantly demonstrated in mice.³⁶⁴ This study showed that the activation of heart rate can induce anxiogenic-like behavioural states, depending on the context of the environment, thereby illustrating the profound influence of peripheral physiological states in driving brain function and behaviour. It would be

intriguing to determine whether certain GI physiological states have such profound impacts on brain function and behaviour or whether the influence is predominantly unidirectional in a top-down manner. Recent reports demonstrate the feasibility of assessing the GI molecular and functional consequences of selectively activating specific ENS neurons.¹³⁷ It would be instructive to determine how such specific GI manipulations impact brain function and behaviour related to psychopathology. Furthermore, GABA_AR subunit-specific genetically modified mice (gene-deleted or rendered insensitive to specific ligands) have advanced our understanding of their contributions to native brain function, behaviour and disorders, as well as the pharmacological profiles of GABAergic ligands.^{43,365–368} However, the next generation of animal models should target the manipulation of individual subunit expression discretely in selected peripheral organs to gain a more granular understanding of their roles throughout the body and to realize the therapeutic potential of targeting these peripheral receptors in associated inflammatory conditions of other organs as in inflammatory bowel disease.

Allied to this, and given the mutual interactions between the brain and gut, it will be important to unequivocally identify the primary site/s of action of GABA-based compounds in mediating their therapeutic efficacy. For example, are the effects of anxiolytics solely driven by changes in brain function, or do they work in combination with changes in peripheral organs? A further key question is in which GABA_AR subtypes to target. Given the plethora of subunits expressed throughout the body (Fig. 1B), it is essential to identify the contribution of specific receptor subtypes to specific GI functions if we are to minimize unwanted effects. This is exemplified by *in vitro* studies demonstrating that compounds with different GABA_AR subtype profiles exert contrasting effects on basic GI functions, such as the force and frequency of colonic contractions,⁵¹ as well as immune functions (Fig. 3B).^{127,128}

Targeting the gut and microbiome: psychoactive GABA modulators and GABA-based dietary interventions

Identifying endogenous allosteric modulators of GABA receptors: relevance to psychopathology

Whilst GABA is understandably responsible for the majority of GABA_AR tone, there are some important exceptions. For example, certain endogenous neurosteroids act as potent efficacious enhancers of GABA_ARs at a specific site,^{369,370} thereby influencing neuronal activity and consequently behaviour (see the 'GABA signalling within the BGM axis' section and Boxes 1 and 3).^{44,315,316} Indeed, perturbations of neurosteroid levels are implicated in a variety of neurological and psychiatric disorders such as certain types of epilepsy and postpartum and major depression.^{36,371–375}

Although neurosteroid research has primarily focused on their role in the CNS, high levels of these powerful GABA_AR PAMs are found in the GI tract, and their peripheral abundance influences brain function (Box 3). Therefore, if such significant endogenous PAMs of GABA_ARs are found in the periphery, it begs the question of whether other such chemicals exist. These could be bacterial metabolites, including neurosteroids (Box 3) that then impart the microbiome's functional influence on the brain. The discovery of such ligand-receptor interactions has traditionally relied on serendipity. However, the combination of public databases hosting bacterial metabolomic arrays, alongside structural and biophysical models of individual GABA_ARs, using high-throughput *in silico* ligand-receptor

docking techniques provide unique opportunities for the targeted identification of novel, endogenous compounds potentially able to influence GABA_AR function. The potential outcome could be to identify a variety of novel potentially druggable compounds.

GABA-based dietary interventions to therapeutically target microbial GABA pathways in the gut microbiome

There is increasing evidence identifying bacterial metabolites, including but not limited to GABA, that affect GABA_ARs and impart beneficial effects (see the 'Gastrointestinal GABA interaction with SCFA and 5-HT' section). A potential strategy to naturally exploit such signalling pathways could be to stimulate their production indirectly with agents that influence the microbiome. Such an approach could be in the form of dietary interventions based on the use of prebiotics, probiotics or a combination of both (synbiotics).³⁷⁶ Such preparations have become increasingly popular worldwide because of their putative positive effect on human health via actions beneficial to GI homeostasis.³⁷⁷ Amongst the biotic-type of dietary interventions, a considerable pre-clinical (in animal models) and clinical literature over the past 20 years has developed around those based on GABA, which is offered either in fermented food/beverages or via supplements containing GABA-producing bacteria (see Braga et al.¹⁵⁴ for a recent excellent review). Next, we will briefly discuss GABA-based probiotic and prebiotic approaches.

Probiotic interventions

Amongst the GABA-producing microorganisms utilized in dietary interventions, those most used in the food and drink industry belong to the genera *Lactobacillus* and *Bifidobacterium*. Several beneficial health claims for such GABA-based dietary products (both food and beverages) have been reported, including improvements in psychiatric conditions such as anxiety,^{166,209,378,379} depression,^{380–383} schizophrenia³⁸⁴ and cognition,³⁸⁵ neurological disorders such as epilepsy³⁸⁶ and pain,¹⁵⁰ and cardiovascular disorders such as hypertension^{387,388} and cancer.³⁸⁹ Here, we focus on the evidence concerning the putative mental health benefits of GABA-based dietary interventions and discuss what advances are necessary to realize their translational potential.

Studies in animal models offer generally compelling evidence for the beneficial profile of GABA-based diets in many of the disorders mentioned. Recent systematic reviews of the clinical literature also offer a promising outlook. Specifically, reviews of randomized control trials (RCTs) for the treatment of anxiety and/or depressive disorders have concluded that probiotics—especially those known to produce, albeit not exclusively, GABA; that is, the *Lactobacilli* and *Bifidobacteria* strains—may be effective in improving psychological symptoms associated with depression^{390,391} and possibly anxiety.²⁹⁴ Moreover, overall, psychological symptom reduction is more consistently evident in clinical rather than healthy cohorts.^{392–394}

Yet, while these studies are promising, a consensus is still to be reached in the clinical arena for probiotic dietary interventions in psychopathology.²⁹⁴ Confounding factors include the limited scale and heterogeneity of the clinical studies, which have complicated the interpretation of the data. Clearly, these limitations need to be addressed, together with Mendelian randomization,^{395,396} to draw firm conclusions on the causal relationship between the intervention and the measured clinical outcome.

Prebiotic interventions

GABA appears also to play a role in the health-promoting actions of certain prebiotics, taken alone or in combination with probiotic

strains such as *L. plantarum*.^{397,398} The prebiotics most utilized belong to the polysaccharide group and include fructo-oligosaccharides (FOS), inulin, abundant in fruits and vegetables,³⁹⁹ galacto-oligosaccharides (GOS) and human milk oligosaccharides (HMOs), which have recently received significant attention,⁴⁰⁰ within the context of dietary approaches for ameliorating IBS.^{401–403}

The beneficial effects of the prebiotics on gut health in humans appear to be mediated by enhancing the abundance of specific microbiota strains and, thus, the levels of their metabolic products. These chemicals include but are not limited to GABA and SCFAs (see the ‘Gastrointestinal GABA interaction with SCFA and 5-HT’ section). Specifically, these prebiotics enrich classical probiotics of the genera *Lactobacillus* and *Bifidobacterium*. Many prebiotic-supported species also reside in the human gut and produce SCFAs and GABA amongst their main metabolic products.^{153,296} While the genera *Lactobacillus* and *Bifidobacterium* are some of the most widely characterized and used GABA-producers in the food industry, individual prebiotics or combinations of prebiotics may also promote the abundance of other human gut GABA-producing probiotic strains. These include the *Bacteroides* and *Eubacterium* genera.¹⁵⁶ Indeed, inulin-degrading species are widely distributed across *Bacteroides* and *Eubacterium*,⁴⁰⁴ and these strains may play an indirect role in a healthy gut (see later). Moreover, recently, in an *in vitro* gut model, treatment of humans with certain HMOs alone or in various combination blends was shown to increase GABA in faeces in children and, especially, in adults.⁴⁰⁵ Notably, HMOs boosted GABA production, likely mediated by an increase in various microbial species and especially *Bifidobacterium adolescentis*, consistent with previous studies.^{153,296} On the other hand, in the same study, a marked correlation was also evident between GABA and *Bacteroides* species when fructans were used as prebiotics, thus indicating a prebiotic-selective effect on the gut microbiota profile.⁴⁰⁶ This finding suggests specific prebiotic combinations may achieve optimal health benefits at least partially by increasing GABA synthesis via specific microbial species. Furthermore, evidence from a recent report⁴⁰⁷ using an *in vitro* human model demonstrated a significant physiological increase in GABA production with a combined 2'-fucosyllactose and oligofructose supplementation.

Another class of prebiotics of considerable interest includes non-carbohydrate molecules or polyphenols. They are abundant in plants and linked with a variety of health benefits including mental health.^{408,409} Such ligands could also be utilized in the development of targeted GABA-based dietary interventions directly by supporting GABA-producing species or indirectly by supporting their enzymatic capabilities, e.g. bacterial vitamin B6 for GABA production.^{406,410–413} Emerging evidence indicates that GABA-consuming bacteria in the human gut^{156,190} may indirectly promote other bacteria, indicating mutualistic interactions amongst gut bacteria that are essential for a healthy and adaptable gut ecosystem.^{402,407,414–416} Thus, the impact of GABA in the context of a healthy BGM axis could be far-reaching and on present evidence, probably both directly and indirectly mediated.

In summary, whilst there is evidence supporting GABA-based dietary interventions to modulate brain function, larger and better-designed RCTs for both probiotic- and prebiotic-type interventions are needed to strengthen these observations. Specifically, there is a lack of studies with rigorous controls for: concomitant pharmacological treatment; the pre-existence of dysbiosis; and both the duration and role of diet before, during and after the intervention. Furthermore, more homogenous methods of analysis are required to improve consensus amongst different studies. Such advances,

coupled with a more targeted identification of beneficial prebiotic and/or probiotic interventions, e.g. based on newly acquired knowledge on the beneficial profile of specific species and their key nutritional requirements, will open a new chapter in the design of effective and advantageous brain modulating dietary interventions.

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Supplementary material

[Supplementary material](#) is available at *Brain* online.

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