



HERBAL MODULATORS OF GUT DYSBIOSIS: PREBIOTIC, PROBIOTIC, AND SYNBIOTIC PERSPECTIVES

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ABSTRACT

Gut dysbiosis is defined as a state of disturbed homeostasis in the microbiota-host relationship producing deleterious effects on human health, and it has been associated with a variety of diseases, such as metabolic, gastrointestinal, neurological, and autoimmune diseases. This review delineates the therapeutic potential of herbal drugs in ameliorating gut-microbiota dysbiosis through prebiotic, probiotic, and synbiotic action. Plant-derived secondary metabolites, including polyphenols, flavonoids, saponins, and polysaccharides from substances such as *Curcuma longa*, *Panax ginseng*, *Camellia sinensis*, and *Allium sativum*, selectively ferment beneficial species of microbiota, increase the production of short-chain fatty acids (SCFA), and inhibit pathogens. These phytochemicals also modulate host metabolism via the control of bile acid conversion, integrity of the gut barrier, and systemic inflammation. In addition, fermented herbal formulas contain live microbial strains that resemble probiotics and promote microbiome diversity. The review raises the opposite nature of herbal drugs as substrates and modulators for microbial activity, which enables them to be candidates for microbiome-targeted interventions. Herbal therapeutics might provide an effective treatment modality for gut homeostasis restoration and dysbiosis-induced diseases via dietary, microbial, as well as lifestyle manipulations.

KEYWORDS: Gut dysbiosis, Microbiome, Probiotics, Systemic inflammation, Phytochemicals.

1. INTRODUCTION

Both prebiotics and probiotics are important for the homeostasis of the gut and influence in alleviating gut dysbiosis, a more-than-normal change in the composition or function of gut microbiota. Probiotics, which are “live micro-organisms that provide a health benefit to the host when administered in adequate quantities,”^[1] exert their effects mainly through restoration of microbial diversity, improvement of colonization resistance, and immunomodulation. Several studies indicate that the probiotic strains *Lactobacillus* or *Bifidobacterium* might compete with the pathogenic bacteria, strengthen the intestinal barrier, and generate short-chain fatty acids (SCFAs) for maintaining the mucosal edge.^[2] Prebiotics, such as nondigestible carbohydrates like inulin and fructooligosaccharides, stimulate the growth of specific beneficial microbes and are also expected to strengthen

the resistance of gut microbiota against dysbiosis.^[3] These compounds act as fermentation substrates, resulting in the formation of SCFAs, which regulate pH, limit pathogen colonisation, and influence host systemic metabolic and inflammatory pathways.^[4] It has been reported that prebiotics and probiotics could synergize in their efforts to rectify dysbiosis and regulate immunity, a phenomenon also called synbiotics, which has many applications in terms of ameliorating host immunity, especially in metabolic disorders, gastroenteritis, or inflammatory bowel disease.^[5] As a result, the intervention in dysbiosis to become the new, healthier self can be viewed as a possible tool to be used in modulating the gut microbiota with diet using prebiotics and probiotics to achieve a healthier and balanced situation.

Table 1: Body Site–Specific Microbiota Metabolic Roles and Dysbiosis Effects.

Microbiota Site	Dominant Metabolic Contributions	Dysbiosis Effects on Metabolism
Gut	SCFA production; bile acid transformation; amino acid & xenobiotic metabolism; modulation of host energy extraction & lipid profiles	Obesity, insulin resistance, NAFLD; elevated LPS; dyslipidaemia; increased BCAA & imidazole propionate; disrupted gut barrier
Oral	Metabolites in saliva (amino acids, volatile compounds); contributions to systemic inflammatory load; oral microbiota as a source of gut colonization/translocation	Increased risk of MAFLD, type 2 diabetes, dyslipidemia, systemic inflammation, and modulation of insulin sensitivity
Skin	Lipid and sebum metabolism; microbial breakdown of skin components; generation of metabolites that enter systemic circulation; immune signalling molecules	Inflammatory skin disease; altered systemic metabolite profiles; exacerbation of metabolic disease via inflammation; impaired barrier, increased infections

The human body harbors diverse microbial communities, collectively referred to as the microbiota, which play essential roles in maintaining host physiology and metabolic balance. *Streptococcus*, *Actinomyces*, *Veillonella*, and *Fusobacterium* species are the main constitutive components of the oral commensal microbiota, which normalize the pH of the mouth and provide resistance to pathogenic colonisation (Lamont et al., 2018). The oropharyngeal microbiota has been suggested to have a role in periodontal disease, as well as in systemic disease, including cardiovascular and metabolic dysfunction.^[6]

The cutaneous microbiota, predominantly of species: **Staphylococcus*, *Corynebacterium*, and *Cutibacterium*, plays a role in maintaining the integrity of the barrier effect and immune response regulation.^[7] Disruptions to a normal cutaneous microflora are linked to pathologies of the skin, such as acne vulgaris, atopic dermatitis, and wound infections.

The phyla Firmicutes and Bacteroidetes constitute the most complex and functionally beneficial microbial ecosystem of the human gut microbiota, with minor contributions made by Actinobacteria and Proteobacteria. These bacteria contribute to digestion, vitamin production, and bile acid metabolism, as well as host immune modulation.^[8] Disturbance of gut microbiota, lower diversity, and a change in the Firmicutes/Bacteroidetes ratio can be linked to inflammatory bowel disease (IBD), obesity, diabetes, or even neurodegenerative diseases. Recently, herbal medicines have attracted more attention for their property to modulate gut microbiota as natural prebiotics and probiotics, and play a therapeutic role in gut dysbiosis. Polyphenol-rich plants such as green tea (*Camellia sinensis*) and turmeric (*Curcuma longa*) are metabolized by GM into bioactive compounds that can modulate microbial composition while simultaneously exerting antioxidant and anti-inflammatory properties.^[10] Also, ginsenosides and saponins from ginseng (*Panax*

ginseng) are fermentable substrates that lead to increased diversity of the microbial community and contribute to metabolic resistance.^[11]

The human microbiota is involved in the control of host metabolism in complex interactions such as nutrient absorption and energy harvesting, and signaling pathways. Notably, the gut microbiome is of paramount importance since it breaks down non-digestible dietary fibers, which are fermented to form short-chain fatty acids (SCFA), including acetate, propionate, and butyrate, which are key regulators of glucose metabolism, lipid homeostasis, and energy balance.^[12]

Examples of such include butyrate, which provides energy to colonic epithelial cells and maintains gut barrier integrity, propionate, which regulates hepatic gluconeogenesis, and acetate, which mediates lipogenesis.^[13]

Obesity and metabolic syndrome are associated with changes in the gut microbiota, including an increased ratio of Firmicutes/Bacteroidetes, which presumably increases dietary caloric extraction.^[14] In addition, gut microbial metabolites themselves are signaling molecules, which bind host receptors and affect global metabolism. SCFAs act on G-protein coupled receptors (GPR41, GPR43) to regulate insulin sensitivity, appetite, and inflammatory responses.^[15] Gut microbiota (GM) also modulates bile acid metabolism by secondary conversion of primary bile acids to secondary signaling molecules (secondary bile acids) that activate receptors such as FXR and TGR5, which control lipid/glucose metabolism. Moreover, microbial gut metabolites of tryptophan — such as indole derivatives - are involved in the control of intestinal hormone secretion and insulin responses.^[16] In obesity, type 2 diabetes, and non-alcoholic fatty liver disease, a loss of microbial diversity and changes in metabolite generation (dysbiosis) are indeed very likely related to each other.

Table 2: Microbiome and Systemic Health.

Niche (Site)	Dominant Phyla / Genera	Dysbiosis Indicators	Impact on Gut / Systemic Health
Saliva, plaque	<i>Firmicutes</i> , <i>Bacteroidetes</i> , <i>Actinobacteria</i> ; <i>Streptococcus</i> , <i>Veillonella</i> , <i>Prevotella</i>	Increased cariogenic <i>Streptococcaceae</i> ; reduced diversity	Shifts in gut flora; association with IBD, metabolic effects.
Subgingival / plaque	<i>Firmicutes</i> , <i>Synergistota</i> , <i>Spirochaetota</i> in disease states	Elevated pathogenic complexes (red/orange), sex-based differences in composition	Cancer risk; promotes inflammation; possible gut colonization

So, the microbiota is a metabolic organ that incorporates nutritional cues and host physiology; dysbiosis in this system could trigger metabolic diseases. A change in the composition of the microbiome by dietary interventions, probiotics, prebiotics, or fecal microbial transplantation represents an exciting therapeutic approach to restore metabolic balance.

Communication between the body pH and microbial flora is an important modulator of microbial colonisation, survival, and activity in a variety of body

niches. The human body has region-specific pH levels that affect the resident flora. As an example, the skin's acidic surface range of pH 4.0 to 6.0 favors the growth of *Staphylococcus epidermidis* and *Cutibacterium acnes*, promoting the formation of an acid mantle and preventing pathogens⁷. On the other hand, a rise in skin pH has been linked to dysbiosis and disease predisposition, with the example being an enhanced colonisation of the previously mentioned, the disease-causing species, *Staphylococcus aureus*, in the skin in atopic dermatitis.^[17]

Table 3: Oral Microbiota and Metabolic Dysregulation Mechanisms.

Mechanism	Description	Recent Findings
Oral-Gut Axis & Microbial Translocation	Oral microbes may be swallowed or translocated via the bloodstream; they can colonize the gut or influence gut flora composition.	In metabolic syndrome, oral microbiome dysbiosis (increased <i>Porphyromonas</i>) correlates with insulin resistance and dyslipidemia.
Inflammation & Systemic Immune Activation	Periodontitis and oral dysbiosis lead to local inflammation, the release of inflammatory mediators (e.g., IL-6, TNF- α) that spill over systemically, contributing to insulin resistance.	“Oral microbiota-induced periodontitis: a new risk factor of metabolic diseases” review shows ~27–53% increased risk of diabetes in periodontitis patients.
Salivary Metabolome Alterations	Disease stages (e.g., periodontitis) show varying metabolites in saliva (e.g., changes in amino acids, volatile compounds) that may reflect or contribute to metabolic disruptions.	A recent 2025 study, “Salivary metabolomics analyses reveal variable metabolites in distinct staging of periodontitis,” showed differential metabolite profiles across periodontitis stages.
Association with MAFLD (Metabolism-Associated Fatty Liver Disease)	Oral dysbiotic signatures correlate with MAFLD; diversity and abundance of oral microbes relate to liver fat content, liver function tests.	Systematic review (to mid-2024) of 13 studies shows significant associations between oral microbiota diversity/composition and MAFLD progression.

Similarly, the oral cavity also maintains a relatively neutral pH (close to 6.5–7.5), which is conducive to the growth of complex microbial populations, such as *Streptococcus* and *Actinomyces*. Whereas a decrease in salivary pH as a result of sugar fermentation supports the growth of cariogenic (acidogenic) bacteria, including *Streptococcus mutans*, that cause dental decay and periodontal disease.^[19]

In the gut, microbial survival is restricted to acid-tolerant species such as *H. pylori* by the highly acidic condition of the stomach (pH 1.5–3.5).^[20] Conversely, the small and large intestines are slightly neutral to acidic (pH 5.5–7.0), which supports high microbial density. Yet dense microbial populations consisting of *Firmicutes* and

Bacteroidetes predominate in this niche.^[21] Also typical of dysbiosis are shifts in luminal pH; an example of such shifts is the lowering of short-chain fatty acid (SCFA) production under dysbiotic conditions, which will raise colonic pH and thereby confer an advantage to pathogenic bacteria, such as *C. difficile*.^[22] Another example of the significance of pH in microbiota control is the urogenital tract: an acidic vaginal pH (<4.5), supported by *Lactobacillus* spp., prevents the colonization of BV-related bacteria; a more neutral vaginal pH (which is highly correlated with dysbiosis and susceptibility to infection) promotes colonization by BV-related bacteria.^[23]

Gut dysbiosis, characterized by an imbalance in microbial diversity, composition, and metabolic activity, has been increasingly recognized as a key contributor to both gastrointestinal and systemic diseases. In the gastrointestinal tract, dysbiosis disrupts mucosal integrity and immune tolerance, leading to inflammatory bowel disease (IBD) and irritable bowel syndrome (IBS).

Patients with IBD show reduced levels of *Firmicutes* and *Bacteroidetes*, accompanied by an overgrowth of pro-inflammatory *Proteobacteria*.^[24] Dysbiosis also increases susceptibility to *Clostridioides difficile* infection, as depletion of commensal species diminishes colonization resistance.^[25]

Table 4: Gut Flora Regulate Host Metabolism: Gut (and more generally body) flora influence metabolism via multiple interlocking pathways.

Mechanism	Description	Recent Findings
Short-Chain Fatty Acids (SCFAs)	Produced by microbial fermentation of dietary fibers; act via G-protein-coupled receptors (e.g. GPR41, GPR43), influence gut barrier, immunity, glucose & lipid metabolism.	A recent synbiotic supplementation (probiotic + prebiotic) increased butyrate and propionate levels, improved metabolic markers (reduced p-cresol), and enhanced bile acid deconjugation.
Bile Acid Metabolism	Microbes convert primary bile acids into secondary bile acids; these interact with host receptors (FXR, TGR5) to regulate lipid and glucose metabolism.	Review “The gut microbiome: a core regulator of metabolism” outlines how dysbiosis alters the bile acid pool, impacting FXR signalling and contributing to metabolic disease.
Gut Barrier Function & Endotoxemia	Integrity of intestinal epithelium prevents translocation of lipopolysaccharide (LPS); dysbiosis can increase gut permeability → low-grade inflammation → insulin resistance.	Many animal and human studies, “Impact of gut microbiota on inflammation, obesity, and metabolic disease,” delineate how low-grade endotoxin (LPS) leakage provokes metabolic syndrome.
Regulation of Lipid and Energy Metabolism	Microbes influence the expression of host genes in the liver, adipose, regulation of triglycerides, phospholipids, fatty acid oxidation vs lipogenesis.	Comparative studies between germ-free (GF) and colonized mice show that GF mice have increased fatty acid oxidation and decreased lipogenesis; the presence of microbiota alters lipid species in serum, adipose tissue, and liver.
Modulation of Hormones / Metabolites	Microbiota influence secretion of gut hormones (e.g., GLP-1, PYY), levels of branched-chain amino acids, tryptophan metabolites (e.g., indole derivatives), and imidazole propionate; these affect insulin sensitivity, appetite, and energy balance.	Review “Gut Microbiome: Core Regulator” details how decreased SCFAs and increased BCAA & imidazole propionate correlate with insulin resistance. Also, a study showed that carbohydrate metabolism by microbiota is associated with insulin resistance via inflammation and host metabolite changes.

Beyond local effects, gut dysbiosis has systemic metabolic consequences. Altered microbial fermentation and a reduced production of short-chain fatty acids (SCFAs) are strongly linked to obesity and type 2 diabetes, with an increased *Firmicutes/Bacteroidetes* ratio enhancing dietary energy harvest and promoting insulin resistance.^[9] Dysbiosis-induced modulation of bile acid metabolism further contributes to non-alcoholic fatty liver disease (NAFLD) progression by promoting hepatic lipid accumulation and inflammation.^[26] In addition, alteration in the composition of gut microbiota has been associated with CVD, especially by microbial metabolism of dietary choline and carnitine into trimethylamine N-oxide (TMAO), which promotes atherosclerosis progression.^[27]

It has been suggested that dysbiosis of the gut is also involved in neuropsychiatric abnormalities via a “gut-brain axis”. Changes in microbial metabolites, including tryptophan metabolites and SCFAs, have been linked to depression, anxiety, and neurodegenerative diseases such as Parkinson’s disease.^[28] Dysbiosis-induced immune

dysregulation can also make individuals more susceptible to autoreactive diseases such as rheumatoid arthritis, multiple sclerosis by affecting peripheral immune activation.^[29]

In fact, gut dysbiosis is associated with a diverse range of disorders involving both local GI diseases and general metabolic, cardiovascular, and neurologic abnormalities, not to mention autoimmune diseases. These observations highlight the importance of maintaining microbial homeostasis and establishing microbiota-guided methods to prevent and treat diseases caused by dysbiosis.

Gut dysbiosis cannot be addressed with a single solution, but multi-pronged approaches may be beneficial to restore microbial diversity and functions and host-microbe relationships. Dietary intervention is the lowest hanging fruit and may provide IBD patients with various bioactive ions, such as SCFAs, nutrients (amino acids and vitamins), and signaling suppressing factors that have been found as environmental modulators of host-microbial responsiveness.^[30] High fiber diets rich in

prebiotic fibers like inulin, fructo-oligosaccharides, and resistant starch selectively encourage the growth of desirable bacterial species like *Bifidobacterium* and *Lactobacillus*, concomitantly contributing to short-chain fatty acid production along with gut side wall activity. Conversely, Western diets, rich in fats and sugars, only increase dysbiosis by favoring pro-inflammatory bacteria, including *Proteobacteria*.^[31] Plant-based, fiber- and polyphenolic-rich dietary patterns have also been demonstrated to increase microbial diversity and lead to metabolic homeostasis.^[32]

Probiotic supplementation is also an exciting option. Some strains, such as *Lactobacillus rhamnosus* GG and *Bifidobacterium longum*, are effective in restoring the balance between bacteria, improving intestinal barrier function, and reducing inflammation.^[33] Synbiotics become part of the larger benefits when added to the prebiotic effect, by allowing the presence of substrates and colonization to be accomplished.^[5] In the same line, fecal microbiota transplantation (FMT) has appeared as a very powerful therapy, especially for relapsing *C. difficile* infection, where the goal is to transfer a diverse microbial consortium from a healthy donor and re-establish homeostasis (ecological balance).^[34]

Apart from microbial interventions, lifestyle changes, including regular exercise and stress relief, have a supportive effect on the preservation of microbial stability because stress-induced dysbiosis is correlated with systemic inflammation and metabolic diseases.^[35] Also, it is important to use antibiotics wisely because of the long-lasting effects that broad-spectrum antibiotics cause alterations in microbial communities; narrow-spectrum options and adjunct probiotic therapeutics may mitigate these side effects.^[36]

As a whole, the re-establishment of gut microbial homeostasis includes dietary and microbial interventions implementation supported by lifestyle and clinical approaches. In addition to reducing dysbiosis-related phenotypes, these strategies also improve host immunity and metabolic status, thus placing the microbiome as a candidate therapeutic target in precision medicine.

Herbal drugs

Herbal medicines have traditionally contributed to the idea that they can regulate the gut microbiome and serve as natural prebiotics/probiotics with potential therapeutic effects (e.g., in the treatment of gut dysbiosis). The long-term use of these botanicals has resulted in a popular consensus that these preparations are effective, even though there is a dearth of hard evidence correlating their usage with clinically significant consequences.

Specifically, polyphenol-containing herbs, including green tea (*Camellia sinensis*) and turmeric (*Curcuma longa*), are broken down into bioactive metabolites by intestinal microbiota, which not only affect the make-up of the gut microbiome but have anti-oxidant and anti-inflammatory effects.^[37] It is believed that these metabolites can interplay with microbial taxa and host signaling pathways, and thus result in a healthier microbial ecosystem.

Another example would be the ginsenosides and saponins found in ginseng (*Panax ginseng*), which could serve as fermentable substrates that stimulate the richness of the microbiome and thus metabolic stability.^[38] This implies these compounds may be prebiotic, enhancing a healthier and more robust gut microbiota. Some herbal formulations not only have a prebiotic role, but they also mimic the activity of probiotics as they contain them in vivo, carrying naturally occurring live microbiota-Ostroumova et al. For instance, Ayurvedic and TCM herbal fermentations contain *Lactobacillus* and *Saccharomyces* species that also directly colonize the gut, contributing to restoration of the microbiota.^[39] Moreover, herbal compounds can enhance probiotic activity by creating a favorable intestinal environment; polyphenols from grape seed extract, for example, synergize with probiotics to suppress pathogenic bacteria and reduce intestinal inflammation.^[40] Importantly, several herbs exhibit synbiotic potential, wherein their phytochemicals not only serve as substrates for probiotic growth but also act synergistically when combined with probiotic strains in therapeutic formulations.^[41]

Table 5: List of herbs that can regulate the gut microbiome and their mechanism.

Herb	Key Phytochemicals	Mechanisms of Action	Microbiota Effects	Therapeutic Benefits
<i>Curcuma longa</i> (Turmeric)	Curcumin	Anti-inflammatory, antimicrobial, bile acid modulation, prebiotic effect on beneficial microbes	Increases <i>Bifidobacterium</i> , <i>Lactobacillus</i> ; suppresses <i>Enterobacteriaceae</i>	Anti-inflammatory, anti-obesity, antidiabetic, improves metabolic health by enhancing SCFA production and reducing inflammation
<i>Panax ginseng</i> (Ginseng)	Ginsenosides, polysaccharides	Microbial biotransformation into bioactive metabolites, enhancing microbial diversity and	Promotes <i>Akkermansia muciniphila</i> , <i>Bifidobacterium</i>	Improves glucose metabolism, insulin sensitivity, intestinal barrier integrity, and metabolic health

		metabolic resilience		
Camellia sinensis (Green Tea)	Polyphenols (catechins)	Fermented by gut microbes into bioactive phenolic acids, prebiotic effects, and antimicrobial properties	Increases Bifidobacterium, inhibits Clostridium and E. coli	Reduces risk of metabolic syndrome, promotes gut health, aids in lipid metabolism, and maintains energy balance
Allium sativum (Garlic)	Fructooligosaccharides, sulfur compounds (allicin)	Prebiotic effect on Lactobacillus and Bifidobacterium, antimicrobial action against pathogenic bacteria	Enhances growth of Lactobacillus, Bifidobacterium; reduces intestinal pathogens	Prebiotic, antimicrobial, improves gut health, reduces inflammation, modulates satiety hormones, and lipid accumulation
Aloe vera	Polysaccharides	Supports SCFA production, creates a favorable environment for probiotics	Increases Bifidobacterium, enhances SCFA production	Modulates colonic health, supports gut microbial balance, is anti-inflammatory, and improves gut barrier function
Glycyrrhiza glabra (Licorice)	Flavonoids, saponins	Prebiotic effects on Lactobacillus spp., suppression of pro-inflammatory microbes	Stimulates Lactobacillus, suppresses pro-inflammatory microbes	Reduces intestinal inflammation, supports gut barrier integrity, promotes beneficial microbiota growth
Nigella sativa (Black Seed)	Thymoquinone	Suppresses pathogenic bacteria, promotes microbial diversity, and enhances microbial balance	Inhibits pathogenic species, enhances microbial diversity	Restores microbial balance, supports symbiotic microbes, has anti-inflammatory effects, and improves gut homeostasis
Chicory root	Inulin	Prebiotic effect, increases SCFA production, supports Lactobacillus growth.	Promotes growth of Lactobacillus, Bifidobacterium	Improves gut microbiota diversity, reduces lipid accumulation, supports satiety hormone production (GLP-1)
Fructooligosaccharides (FOS)	Fructooligosaccharides	Prebiotic fibers for beneficial microbes like Lactobacillus and Bifidobacterium	Enhances the growth of Lactobacillus, Bifidobacterium	Supports metabolic health, improves gut barrier function, enhances immune function, and reduces inflammation

Thus, herbal drugs influence the gut microbiome through dual mechanisms: acting as prebiotics by selectively stimulating beneficial microbes, and functioning as probiotics by delivering or supporting live microbial strains. These interactions enhance microbial diversity, SCFA production, and host immunity, making herbal therapeutics promising candidates for microbiome-targeted interventions in gut dysbiosis.

Several medicinal herbs have been reported to exert significant modulatory effects on the gut microbiota, functioning as natural prebiotics and microbiota regulators. Curcuma longa, rich in curcumin, has demonstrated anti-inflammatory and microbiota-modulating properties by increasing *Bifidobacterium* and *Lactobacillus* while suppressing pro-inflammatory *Enterobacteriaceae*.^[42] Panax ginseng, containing

ginsenosides and polysaccharides, undergoes microbial biotransformation to bioactive metabolites that enhance the abundance of *Akkermansia muciniphila* and *Bifidobacterium*, thereby improving metabolic health.^[43] Similarly, Camellia sinensis polyphenols are metabolized by gut microbes into bioactive phenolic acids that promote *Bifidobacterium* growth and inhibit pathogenic *Clostridium* species.^[44]

Other herbs, such as Glycyrrhiza glabra (licorice), have been reported to stimulate *Lactobacillus* spp. Through their flavonoid and saponin content, contributing to improved gut barrier function and anti-inflammatory effects.^[45] Allium sativum (garlic), due to its fructooligosaccharide content and sulfur compounds, exhibits strong prebiotic activity, selectively enhancing beneficial bacteria and reducing intestinal pathogens. In

addition, Aloe vera polysaccharides have been shown to support the proliferation of *Bifidobacterium* and modulate short-chain fatty acid (SCFA) production, which plays a crucial role in colonic health.^[46] Crucially, black seed (*Nigella sativa*) has also been associated with the modulation of microbial equilibrium through inhibiting pathogenic bacteria and promoting symbiotic microorganisms due to the presence of thymoquinone in it.^[47]

Together, these herbs (such as polyphenols, polysaccharides, flavonoids, and saponins), which exert a substrate property for beneficial bacteria, increase SCFA production from gut flora, and inhibit pathogens with the active phytochemicals in them, can correct dysbiosis. There is new evidence that herbal drugs appear to be modulators of the gut microbiome, thus affecting the prevention and treatment of gastrointestinal conditions.

Several such medicinal herbs have been studied for their probiotic and prebiotic-like activities, exerted through the action of phytochemicals in selectively stimulating commensal microbes, metabolites from microbial entities, and inhibiting pathogens. Curcuma longa has been suggested to have prebiotic effects via its bioactive curcumin, through increasing the growth of *Bifidobacterium* and *Lactobacillus*, and decreasing Enterobacteriaceae. This modulation is, in part, dictated by curcumin's antimicrobial activity and ability to change the bile acid metabolism and consequently recover gut microbiota balance.^[48] Being a source of ginsenosides, Panax ginseng is utilized as the substrate for gut microbes that metabolize these saponins into potent active substances. TMAO, through this biotransformation process, selectively promotes the growth of *Akkermansia muciniphila* and *Bifidobacterium* to enhance glucose metabolism and intestinal barrier integrity.^[49]

Polyphenols from the *Camellia sinensis* (catechins) resist host digestion and arrive in the colon, where they are metabolized by commensal bacteria. This fermentation promoted the growth of *Bifidobacterium* and suppressed pathogenic *Clostridium perfringens* and *Escherichia coli*, the mechanism for which is associated with microbial metabolism of polyphenols to phenolic acids possessing antimicrobial effects.^[50] *Allium sativum* is a prebiotic and antimicrobial; its fructooligosaccharides provide fermentable substrates for *Lactobacillus* and *Bifidobacterium*, while sulfur-containing compounds like allicin inhibit pathogen bacteria, which contribute to the self-regulating mechanism of eubiosis.^[51] Aloe vera polysaccharides are also fermentable substrates that subsequently increase the formation of short-chain fatty acids (SCFA), reduce colonic pH, and shift microbial communities in a direction unfavorable to pathogens and favorable to symbiotic bacteria colonization.^[52]

Glycyrrhiza glabra flavonoids and saponins also exert a prebiotic activity by increasing *Lactobacillus* spp. and

repelling pro-inflammatory organisms, which ultimately results in a lower intestinal inflammation.^[53] Furthermore, due to its bioactive thymoquinone, *Nigella sativa* has microbiota-modulatory properties in that it can inhibit pathogenic microbes and stimulate the diversity of microbial species by doing so, having an indirect probiotic-like effect.^[54] In the majority of cases, these herbs also have synbiotic potential since their phytochemicals function as substrates and increase the capability of colonization by probiotic strains while also playing a synergistic role on gut homeostasis.^[2]

Taken together, such accounts collectively indicate the role of herbs as natural microbiome modulators involving SCFA production, modulation of bile acids, and antimicrobial activities, among others, via the provision of fermentable substrates to the microbial community and bio-transformation of phytochemical metabolites. These dual prebiotic-probiotic functions suggest potential therapeutic applications of herbal interventions for the prevention and treatment of gut dysbiosis.

Herbal-based prebiotics and probiotics have been gaining attention as promising candidates for the treatment of metabolic diseases such as obesity, type 2 diabetes, dyslipidemia, and metabolic syndrome via the gut microbiota modulation. There are secondary metabolites, including polyphenols, saponins, and flavonoids in high content of the herb, which can be the substrates for beneficial bacteria and induce SCFA production (modulating glucose lipid metabolism through G-protein coupled receptors (GPR41/43) activation and insulin sensitivity improvement).^[55] For example, ginsenosides derived from Panax ginseng are metabolized by microbes to active metabolites that improve glucose tolerance and insulin sensitivity via alterations in the abundance of *Akkermansia muciniphila* and *Bifidobacterium* spp.^[56] Likewise, curcumin derived from Curcuma longa mediates anti-obesity and antidiabetic effects through bile acid changes in bile acid metabolism, reducing pro-inflammatory cytokines and elevating the proportion of SCFA-producing bacteria.^[57]

Some plant fibers, such as inulin from chicory root and fructooligosaccharides present in garlic, have also shown potential benefits, exerting a prebiotic effect, characterized by inhibition of lipid accumulation and the modulation effects on satiety hormones (GLP-1), thus regulating appetite and body weight.^[58] Additionally, polyphenols of *Camellia sinensis* modulate energy metabolism by lowering lipid absorption and enhancing fatty acid oxidation mediated by gut microbiota metabolites, thus reducing susceptibility to metabolic syndrome.^[10] The synbiotic opportunity through the combination of herbs with probiotic strains increases their effectiveness, such as the herbal polysaccharides mediated colonization of *Lactobacillus* and *Bifidobacterium*, in which glycemic control, systemic inflammation are better managed.^[2]

Overall, our results indicate that nature-based prebiotic-probiotic herbal drugs can be a natural and sustainable solution for synthetic drugs in the management of metabolic disorders. These herbs may offer a combination of benefits linked to modulating gut microbiota, decreasing endotoxemia, and increasing insulin sensitivity on top of lipid metabolism, making them potentially useful supplements or substitutes in managing metabolic diseases.^[59]

CONCLUSION

Herbal therapeutics are also a promising target to reduce gut dysbiosis through prebiotic, probiotic, and synbiotic strategies. Showcasing both positive and negative effects, phytochemicals of botanicals like *Curcuma longa*, *Panax ginseng*, *Camellia sinensis*, and *Allium sativum* alter microbial balance by selectively stimulating beneficial microbiota and increasing short-chain fatty acid production, and by inhibiting putative pathogenic taxa. In addition to acting as fermentable substrates, these compounds are converted by microbes to produce bioactive metabolites. Bile acid regulation, gut barrier maintenance, and inhibition of inflammatory signaling make them promising agents in the treatment of various dysbiosis-related maladies, such as metabolic syndrome, gastrointestinal pathology, and neuro-immune dysfunctions. As our understanding of the gut microbiome continues to grow, herbal therapeutics, when implemented in personalized medicine schemes, could provide safer and more sustainable options in an integrative paradigm. To realize the full therapeutic potential of these botanicals as microbiome-centric interventions, their mechanistic actions and clinical efficacy still need to be elucidated.

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