

Tea–Gut Microbiota Interactions: Mechanisms, Health Benefits, and Future Perspectives

Teena Yadav, Shekhar Jain*

Faculty of Life Sciences, Mandsaur University, Mandsaur, Madhya Pradesh 458001, India

DOI: <https://dx.doi.org/10.51583/IJLTEMAS.2026.150700047>

Received: 29 July 2026; Accepted: 03 August 2026; Published: 08 August 2026

ABSTRACT

Tea, derived from *Camellia sinensis*, is one of the most widely consumed beverages worldwide and is rich in bioactive compounds, particularly polyphenols, that exhibit significant health-promoting properties. Growing evidence indicates that tea polyphenols interact extensively with the human gut microbiota, a complex microbial ecosystem essential for maintaining intestinal homeostasis, metabolic regulation, and immune function. Tea polyphenols, including catechins and theaflavins, are poorly absorbed in the small intestine and reach the colon, where they undergo microbial biotransformation into bioactive metabolites. These interactions are bidirectional, as gut microorganisms metabolize tea polyphenols while tea-derived compounds selectively modulate the gut microbial community by promoting beneficial bacteria such as *Bifidobacterium*, *Lactobacillus*, and *Akkermansia muciniphila* and suppressing pathogenic microorganisms. Such microbial modulation enhances short-chain fatty acid production, strengthens intestinal barrier function, and contributes to improved metabolic health, immune regulation, and a reduced risk of several chronic diseases. Emerging evidence further suggests that the microbiota-modulating effects of tea vary among green, black, oolong, and fermented teas because of differences in their polyphenolic composition and processing methods. However, most available evidence is derived from in vitro and animal studies, whereas robust human clinical trials remain limited. Variations in tea composition, dosage, and individual gut microbial profiles further complicate the interpretation of existing findings. Collectively, current evidence supports tea as a promising dietary modulator of the gut microbiota, although further mechanistic and clinical investigations are required to establish its therapeutic potential and facilitate microbiome-based nutritional interventions

Keywords: Tea polyphenols; *Camellia sinensis*; Gut microbiota; Catechins; Theaflavins; Microbial biotransformation; Short-chain fatty acids; Gut health

INTRODUCTION: GUT MICROBIOTA

Microbiota in the gut refers to the community of microbial cells which includes various bacteria archaea viruses and fungi, that inhabit the alimentary tract. The human gut can be home to an amazing number - literally trillions - of cells of microorganisms working together in a complex way and carrying out plenty of functions, including those related to health - such genes carried by microbiota greatly outnumber those in the human genome (Thursby & Juge 2017; Hasan & Yang 2019). These microorganisms form a symbiotic relationship with the host, contributing to various physiological functions essential for maintaining homeostasis. The composition of the gut microbiota varies among individuals and is influenced by multiple factors such as diet, age, genetics, environment, and lifestyle. The dominant bacterial phyla in the human gut include Firmicutes and Bacteroidetes, (Fujisaka & Tobe 2022; Khalil et al., 2024) along with smaller proportions of Actinobacteria and Proteobacteria (Rinninella et al., 2019). This microbial ecosystem is dynamic and can rapidly respond to dietary and environmental changes, making it a key target for nutritional and therapeutic interventions. This review synthesizes evidence from peer-reviewed experimental studies, clinical investigations, and recent review articles to provide a comprehensive overview of tea–gut microbiota interactions. Particular emphasis is placed on microbial modulation, polyphenol biotransformation, associated health outcomes, current research limitations,

inter-individual variability, and future research directions, while highlighting areas where robust evidence from well-designed human clinical studies remains limited.

IMPORTANCE OF GUT MICROBIOTA FOR HEALTH

The gut microbiota plays a fundamental role in maintaining human health through its involvement in several critical biological processes (Silva & Frozza 2020). One of its primary functions is the digestion of complex dietary components, particularly non-digestible carbohydrates such as dietary fibers, which are fermented by gut bacteria to produce short-chain fatty acids (SCFAs) like acetate, propionate, and butyrate (Portincasa et al., 2022; Zhang et al., 2023; Kasubuchi et al., 2015). These metabolites serve as energy sources for colonocytes, maintain intestinal barrier integrity, and exert anti-inflammatory effects.

In addition to its metabolic functions, the gut microbiota is essential for the proper development and regulation of the immune system (Yoo et al., 2020). It helps in the maturation of immune cells and the production of cytokines, thereby enabling the host to mount appropriate immune responses. The microbiota also provides protection against pathogenic microorganisms through mechanisms such as competitive exclusion, production of antimicrobial compounds, and maintenance of gut barrier function (Wang & Ai 2024; Khan et al., 2025).

Furthermore, the gut microbiota influences systemic physiological processes, including metabolism, endocrine signaling, and neurological function via the gut–brain axis. Emerging evidence suggests that alterations in gut microbiota composition, known as dysbiosis, are associated with a wide range of diseases, including obesity, type II diabetes, cardiovascular diseases, inflammatory bowel disease, and even neurodegenerative disorders (Facchin et al., 2015; Kasubuchi et al., 2015; Iațcu & Covașa 2021). Therefore, maintaining a balanced and diverse gut microbiota is critical for overall health and disease prevention.

TEA AS A WIDELY CONSUMED BEVERAGE

Tea, derived from the leaves of *Camellia sinensis*, is one of the most widely consumed beverages worldwide, second only to water (Bortolini et al., 2021). It holds significant cultural, economic, and nutritional importance across different regions. Tea is available in various forms, including green tea, black tea, oolong tea, and fermented teas, which differ primarily in their processing methods and degree of oxidation (Zhang et al., 2019; Mozumder & Hong 2025). These differences result in distinct chemical compositions and biological properties. Tea is particularly rich in bioactive compounds, especially polyphenols such as catechins, flavonoids, and theaflavins, which are known for their antioxidant, anti-inflammatory, and antimicrobial properties (Khan & Mukhtar 2018). Green tea is abundant in catechins like epigallocatechin gallate (EGCG), whereas black tea contains higher levels of theaflavins and thearubigins formed during fermentation (Wang et al., 2023). In addition to polyphenols, tea also contains caffeine, amino acids (such as L-theanine), vitamins, and minerals, all of which contribute to its health-promoting effects (Wnuk, E. 2025).

Recent research has increasingly focused on the role of tea as a functional beverage capable of modulating gut microbiota (Chen & Yang 2020). Due to their low bioavailability in the small intestine, a significant proportion of tea polyphenols reaches the colon, where they interact with gut microorganisms. These interactions can influence microbial composition by promoting beneficial bacteria and inhibiting harmful species, thereby contributing to improved gut health. Given its widespread consumption and rich phytochemical profile, tea represents an important dietary factor in the study of gut microbiota and its implications for human health (Huang & Chen 2026). While previous reviews have primarily focused on the general health benefits of tea or the individual roles of gut microbiota, this review provides an integrated perspective on the bidirectional interactions between tea polyphenols and the gut microbial ecosystem. It comprehensively examines the microbial biotransformation of tea polyphenols, the reciprocal modulation of gut microbial communities, and the resulting effects on intestinal homeostasis, metabolic regulation, and immune function. Furthermore, the review comparatively evaluates the microbiota-modulating properties of different tea varieties, including green, black, oolong, and fermented teas, and discusses current evidence, existing knowledge gaps, and future research opportunities. By integrating findings from nutrition, microbiology, and functional food research, this review

aims to provide a comprehensive framework for understanding the therapeutic potential of tea–gut microbiota interactions in promoting human health.

COMPOSITION OF TEA

Tea, derived from the leaves of *C. sinensis*, is a chemically complex beverage containing a wide range of bioactive compounds that contribute to its sensory properties and health benefits (Bond & Derbyshire 2019). The composition of tea varies depending on factors such as plant variety, processing method, and degree of oxidation (Liu et al., 2024; Yang et al., 2025). Among its constituents, polyphenols represent the most abundant and biologically significant group, followed by catechins and other compounds such as alkaloids, amino acids, vitamins, and minerals (Fig.1).

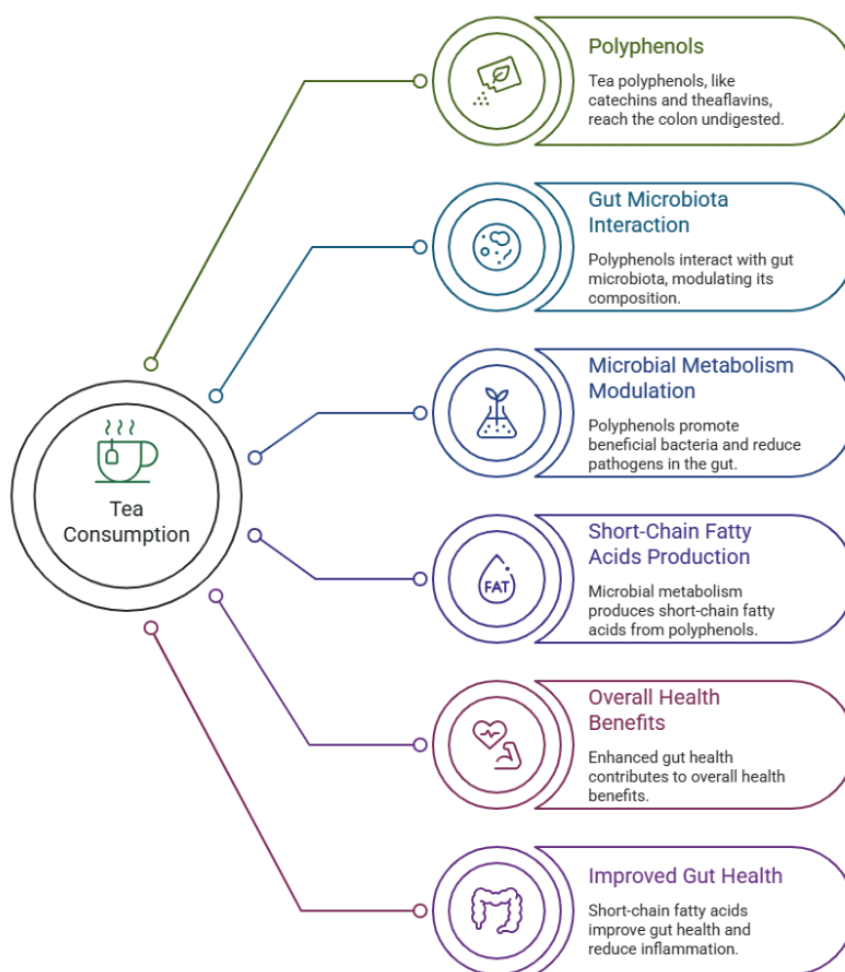


Figure: 1 Unveiling the Multifaceted Benefits of Tea Consumption

Polyphenols

Polyphenols are the major bioactive components of tea, accounting for nearly 30–40% of the dry weight of tea leaves. These compounds are responsible for many of the health-promoting properties of tea, including antioxidant, anti-inflammatory, and antimicrobial effects. Tea polyphenols primarily belong to the flavonoid group, which includes catechins, flavonols, and their derivatives (Zhang et al., 2019; Marina & Marc 2024; Wnuk, E. 2025).

The biological activity of polyphenols is largely attributed to their ability to neutralize free radicals and reduce oxidative stress. In addition, polyphenols interact with gut microbiota, where they undergo microbial metabolism to form smaller phenolic compounds that are more bioavailable and biologically active (Han et al., 2007;

Rudrapal et al., 2025). This interaction plays a key role in modulating gut microbial composition and function, making polyphenols central to the health effects of tea.

Catechins

Catechins are a subclass of flavonoids and represent the major type of polyphenols found in tea, particularly in green tea. The most important catechins include epigallocatechin gallate (EGCG), epigallocatechin (EGC), epicatechin gallate (ECG), and epicatechin (EC). Among these, EGCG is the most abundant and biologically active compound (Ferrari & Naponelli 2025; Capasso et al., 2025). Catechins are known for their strong antioxidant properties, which help in scavenging reactive oxygen species and protecting cells from oxidative damage (Farhan 2022). In addition to their antioxidant activity, catechins exhibit antimicrobial and anti-inflammatory effects (Yen & Chen 1995). They can inhibit the growth of pathogenic microorganisms by disrupting bacterial cell membranes and interfering with enzyme activity (De Rossi et al., 2025).

From a microbiological perspective, catechins are particularly important because they are poorly absorbed in the small intestine and reach the colon, where they are metabolized by gut microbiota. This process not only produces bioactive metabolites but also influences the composition of the microbial community by promoting beneficial bacteria such as *Lactobacillus* and *Bifidobacterium* (Musiał et al., 2020).

Other Bioactive Compounds

In addition to polyphenols and catechins, tea contains several other bioactive compounds that contribute to its overall health benefits.

Alkaloids

Tea contains alkaloids such as caffeine, theobromine, and theophylline. Caffeine is the most prominent and is responsible for the stimulant effect of tea. It also enhances alertness and cognitive function (Sahu et al., 2025; Payne et al., 2025).

Amino Acids

One of the most important amino acids in tea is L-theanine, which is known for its calming effects and its ability to improve cognitive performance. L-theanine may also influence gut–brain axis signaling (Williams et al., 2019).

Vitamins and Minerals

Tea contains small amounts of vitamins such as vitamin C and B-complex vitamins, as well as minerals like potassium, magnesium, and fluoride, which contribute to overall health (Mourya et al., 2019).

Other Compounds

Tea also includes pigments, carbohydrates, and volatile compounds that contribute to its flavor, aroma, and color. In fermented teas, additional microbial metabolites may be present due to fermentation processes (Chupeerach et al., 2021).

INTERACTION BETWEEN TEA AND GUT MICROBIOTA

The interaction between tea and gut microbiota is a complex and bidirectional process involving the metabolism of tea-derived compounds by intestinal microorganisms and the modulation of microbial composition by tea constituents (Liu et al., 2020). Polyphenolic compounds in tea, due to their limited absorption in the upper gastrointestinal tract, reach the colon in substantial amounts, where they interact extensively with gut microbiota (Khan & Mukhtar 2007; Khan & Mukhtar 2018). These interactions play a crucial role in shaping microbial ecology and influencing host health (Fig.2).

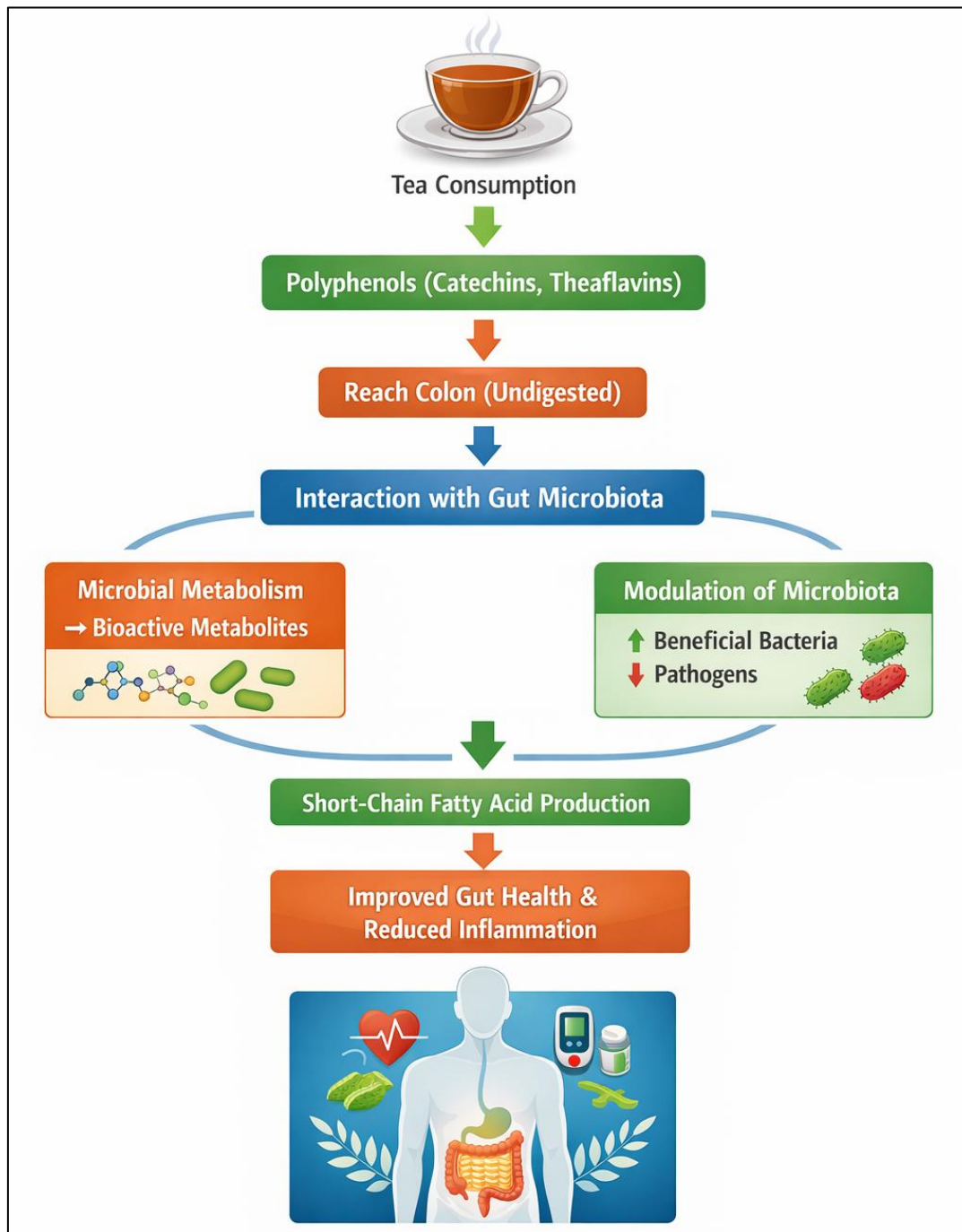


Figure: 2 Mechanism of Tea - Gut Microbiota Interaction

Prebiotic Effects of Tea

Tea bioactive compounds exhibit prebiotic-like properties by selectively promoting the growth and activity of beneficial gut microorganisms. Unlike traditional prebiotics such as dietary fibers, tea polyphenols are not carbohydrates; however, they can still influence microbial populations in a similar manner. Studies have demonstrated that regular tea consumption is associated with an increase in beneficial bacterial genera such as *Bifidobacterium* and *Lactobacillus*, which are known to contribute to gut health (Plamada & Vodnar 2021).

These beneficial bacteria play a key role in maintaining intestinal homeostasis by producing SCFAs, enhancing gut barrier integrity, and modulating immune responses (Khairudin et al., 2021). At the same time, tea polyphenols can inhibit the growth of pathogenic bacteria, including species such as *Clostridium perfringens* and certain strains of *Escherichia coli*. This selective antimicrobial activity helps maintain a balanced microbial environment, rather than causing broad-spectrum microbial suppression (Lee et al., 2006). The prebiotic effect

of tea is therefore characterized by its ability to promote beneficial microbes while suppressing harmful ones, contributing to improved gut health and reduced risk of disease.

Microbial Metabolism of Tea Compounds

A significant proportion of phenolic constituents of tea escapes digestion in the small intestine and reaches the colon, where they undergo extensive biotransformation by gut microbiota (Li et al., 2021). Microorganisms in the colon metabolize these complex polyphenols through enzymatic processes such as hydrolysis, dehydroxylation, and ring cleavage, resulting in the formation of smaller phenolic metabolites (Kawabata et al., 2019, Su et al., 2024). These metabolites, including phenolic acids and other low-molecular-weight compounds, are more easily absorbed into the bloodstream and often exhibit enhanced biological activity compared to their parent compounds (Sang et al., 2011). This metabolic transformation not only increases the bioavailability of tea-derived compounds but also contributes to their systemic health effects (Spencer, 2003).

Importantly, this process represents a bidirectional interaction: while gut microbiota transform tea polyphenols, the resulting metabolites can, in turn, influence microbial composition and function (Liu et al., 2020). This feedback loop highlights the dynamic relationship between dietary components and the gut microbiome. It is also known that microbial digestion of tea constituents results in greater generation of beneficial metabolites like, for example, short-chain fatty acids, these are substances indispensable for intestinal health maintenance, inflammation regulation, and metabolic processes support (Fraser et al. 2014).

EFFECTS ON MICROBIAL COMPOSITION

Tea consumption has been shown to significantly influence the composition and diversity of gut microbiota. The bioactive compounds present in tea, particularly polyphenols, exert selective effects on microbial populations, leading to an overall improvement in gut microbial balance. Rather than acting as broad-spectrum antimicrobial agents, tea components promote a favorable shift in microbiota by enhancing beneficial microorganisms and suppressing harmful species (Lee et al., 2006; Jin et al., 2012). This selective modulation plays a key role in maintaining intestinal homeostasis and supporting overall health.

Increase in Beneficial Bacteria

Numerous studies have reported that tea consumption is associated with an increase in beneficial bacterial genera such as *Bifidobacterium* and *Lactobacillus* (Zhao et al., 2024). These microorganisms are widely recognized for their positive effects on gut health. They contribute to the fermentation of dietary substrates and the production of SCFAs, including butyrate, acetate, and propionate, which are essential for maintaining intestinal barrier integrity and providing energy to colonocytes (Liu et al., 2020, Huang & Chen, 2026). In addition, beneficial bacteria play an important role in modulating the immune system by enhancing anti-inflammatory responses and reducing the risk of infections.

Tea polyphenols appear to promote a gut environment favorable for beneficial microbial taxa by acting as substrates for their growth and by inhibiting competing pathogenic organisms (Liu et al., 2019). This selective stimulation contributes to increased microbial diversity, which is often considered a hallmark of a healthy gut microbiota.

Reduction of Harmful Bacteria

In parallel with promoting beneficial microbes, tea polyphenols exhibit inhibitory effects on various pathogenic and opportunistic bacteria (Chen & Yang 2020). Studies have demonstrated that tea components can inhibit the growth of harmful microorganisms such as *C. perfringens*, certain strains of *E. coli*, and other toxin-producing bacteria. The antimicrobial activity of tea is primarily attributed to the ability of polyphenols to disrupt bacterial cell membranes, inhibit essential enzymes, and interfere with microbial metabolic processes (Almajano et al., 2008). Unlike conventional antibiotics, which may indiscriminately eliminate both beneficial and harmful bacteria, tea exerts a more selective effect, targeting pathogenic species while preserving or even enhancing

beneficial microbial populations. This dual action promotion of beneficial bacteria and suppression of harmful microbes helps restore microbial balance and may reduce the risk of gastrointestinal disorders, infections, and inflammation-related diseases (Chen & Yang 2020).

COMPARISON OF DIFFERENT TEAS

Different types of tea, all derived from *C. sinensis*, vary significantly in their chemical composition and biological effects due to differences in processing methods, particularly the degree of oxidation and fermentation. These variations influence the concentration and type of bioactive compounds present in tea, which in turn affect their interaction with gut microbiota and associated health outcomes (Zhao et al., 2024). The most commonly consumed types of tea include green tea, black tea, oolong tea, and fermented teas such as pu-erh tea.

Green Tea

Green tea is produced with minimal processing and no oxidation, allowing it to retain a high concentration of catechins, particularly epigallocatechin gallate (EGCG). Due to this rich catechin content, green tea has been extensively studied for its effects on gut microbiota (Mehrabi et al., 2024). Studies show that consuming green tea can result in the thriving of beneficial bacteria including *Bifidobacterium* and *Lactobacillus* while at the same time curbing the growth of pathogens (Chacko et al. 2010). What is more, its potent antioxidants and anti-inflammatory effects support a healthy gastrointestinal system as well as metabolic activity. Given these facts, it is not surprising that green tea is regarded as one of the top tea varieties when it comes to gut microbiota (Graham, 1992; Cabrera et al. 2006).

Black Tea

Black tea undergoes full oxidation during processing, which converts catechins into more complex compounds such as theaflavins and thearubigins. These compounds exhibit different biological properties compared to catechins (Rothenberg et al., 2018). Although black tea contains lower levels of catechins, its polyphenols still reach the colon and undergo microbial metabolism (Ruxton, 2008). Studies suggest that black tea also supports gut health by promoting beneficial microbial activity, though its effects may be less pronounced than those of green tea. The metabolites produced from black tea polyphenols may contribute to maintaining microbial balance and supporting metabolic health (Zhu et al., 2021).

Oolong Tea

Oolong tea is partially oxidized, representing an intermediate form between green and black tea. As a result, it contains a mixture of catechins and oxidized polyphenols (Zeng et al., 2020). Due to this unique composition, oolong tea exhibits combined properties of both green and black tea. It may contribute to gut microbiota modulation by promoting beneficial bacteria and supporting metabolic processes (Liu et al., 2019). However, compared to green and black tea, fewer studies are available on oolong tea, and its specific effects on gut microbiota remain less well understood.

Fermented Teas (e.g., Pu-erh Tea)

Fermented teas, such as pu-erh tea, undergo microbial fermentation during processing, which leads to the formation of unique bioactive compounds and the presence of microbial metabolites. This fermentation process introduces an additional dimension to the interaction between tea and gut microbiota (Zhao, et al., 2019). Fermented teas may have a more complex impact on gut microbiota due to the presence of both tea-derived compounds and fermentation-associated microorganisms or metabolites (Tong et al., 2020). Scientific research shows that consuming Pu-erh tea can significantly increase the abundance of *Akkermansia muciniphila* in gut. Some studies suggest that these teas can enhance microbial diversity and promote beneficial metabolic activities (Lin et al., 2008). However, their effects may vary depending on fermentation conditions and microbial composition (Fig.3).

Comparative Overview

Overall, while all types of tea have the potential to influence gut microbiota, their effects differ based on their chemical composition (Table-1):

- **Green tea:** Strongest microbiota modulation due to high catechin content
- **Black tea:** Moderate effects via theaflavins and microbial metabolites
- **Oolong tea:** Intermediate effects due to mixed composition
- **Fermented teas:** Complex effects influenced by microbial fermentation

These differences highlight the importance of considering tea type when evaluating its impact on gut microbiota and health.

Table 1: Comparison of Different Types of Tea and Their Effects on Gut Microbiota

Tea Type	Processing Method	Major Bioactive Compounds	Effect on Gut Microbiota	Key Health Implications
Green Tea	Unoxidized (minimal processing)	Catechins (EGCG, EGC, ECG, EC)	Increase <i>Bifidobacterium</i> and <i>Lactobacillus</i> ; inhibits pathogens	Strong antioxidant, improves metabolism
Black Tea	Fully oxidized	Theaflavins, Thearubigins	Moderate modulation via microbial metabolites	Supports gut balance, metabolic health
Oolong Tea	Partially oxidized	Mix of catechins & theaflavins	Intermediate effects on microbial composition	Aids digestion, moderate metabolic effects
Fermented Tea (Pu-erh)	Microbial fermentation	Microbial metabolites, polyphenols	Enhances microbial diversity; complex interactions	Improves digestion, supports gut health

HEALTH IMPLICATIONS OF TEA-INDUCED GUT MICROBIOTA MODULATION

Tea-induced modulation of the gut microbiota has broad implications for host metabolism, immune regulation, and disease prevention. With microbiota composition and activity, polyphenols from tea can influence a range of physiological processes, like metabolic control, immunity and, disease prevention (Wang et al, 2024). This, in essence, takes place mainly via the metabolite output by gut bacteria and the balance of the gut flora.

Metabolic Health

Tea-induced changes in gut microbiota have been closely associated with improvements in metabolic health (Yu et al., 2025). Beneficial bacteria stimulated by tea consumption enhance the fermentation of dietary components, leading to increased production of SCFAs such as butyrate, acetate, and propionate. These metabolites play a crucial role in regulating energy homeostasis, glucose metabolism, and lipid metabolism. SCFAs help improve insulin sensitivity, reduce fat accumulation, and regulate appetite by influencing hormonal signaling pathways (Khan & Mukhtar 2013). Additionally, tea polyphenols have been shown to reduce oxidative stress and inflammation, both of which are key contributors to metabolic disorders. Through these mechanisms, tea consumption may help lower the risk of conditions such as obesity, type II diabetes, and metabolic syndrome (Li et al., 2016; Xiao et al., 2024).

Immune Modulation

The gut microbiota is a key player in the development and control (modulation) of the immune system, while tea consumption, due to its effects on the microbiota's composition, may influence this mechanism. The ability of tea to encourage the growth of healthy microorganisms like *Lactobacillus* and *Bifidobacterium* not only boosts the generation of beneficial anti-inflammatory substances but also helps keep the immune system in good working condition through these effects (Wang et al., 2024). Short-chain fatty acids which are generated by gut microbes fermentation aid in regulating immunity by improving the intestinal wall integrity and hindering harmful bacteria translocation. Also, tea phenols have been seen to possess anti-inflammatory properties through cytokine inhibition and reduction of the release of molecules linked to inflammatory activities (Liu et al., 2020). This effects altogether lead to a proper immune balance, decreasing chronic inflammatory conditions as well as disorders related to the immune system.

Disease Prevention

The ability of tea to modulate gut microbiota has important implications for the prevention of various diseases (Zhao et al., 2024). A balanced and diverse gut microbiota is associated with reduced risk of gastrointestinal disorders, including inflammatory bowel disease and infections caused by pathogenic bacteria. In addition, tea-induced microbial changes may contribute to the prevention of metabolic diseases such as obesity and type II diabetes, as well as cardiovascular diseases, by improving lipid profiles and reducing systemic inflammation. Current evidence also suggests a potential role of gut microbiota in the gut–brain axis, indicating that tea consumption may have indirect effects on neurological health and mental well-being (Wang & Zheng 2022). However, while these findings are promising, most evidence is derived from experimental and observational studies, and further clinical research is needed to establish definitive cause and effect relationships.

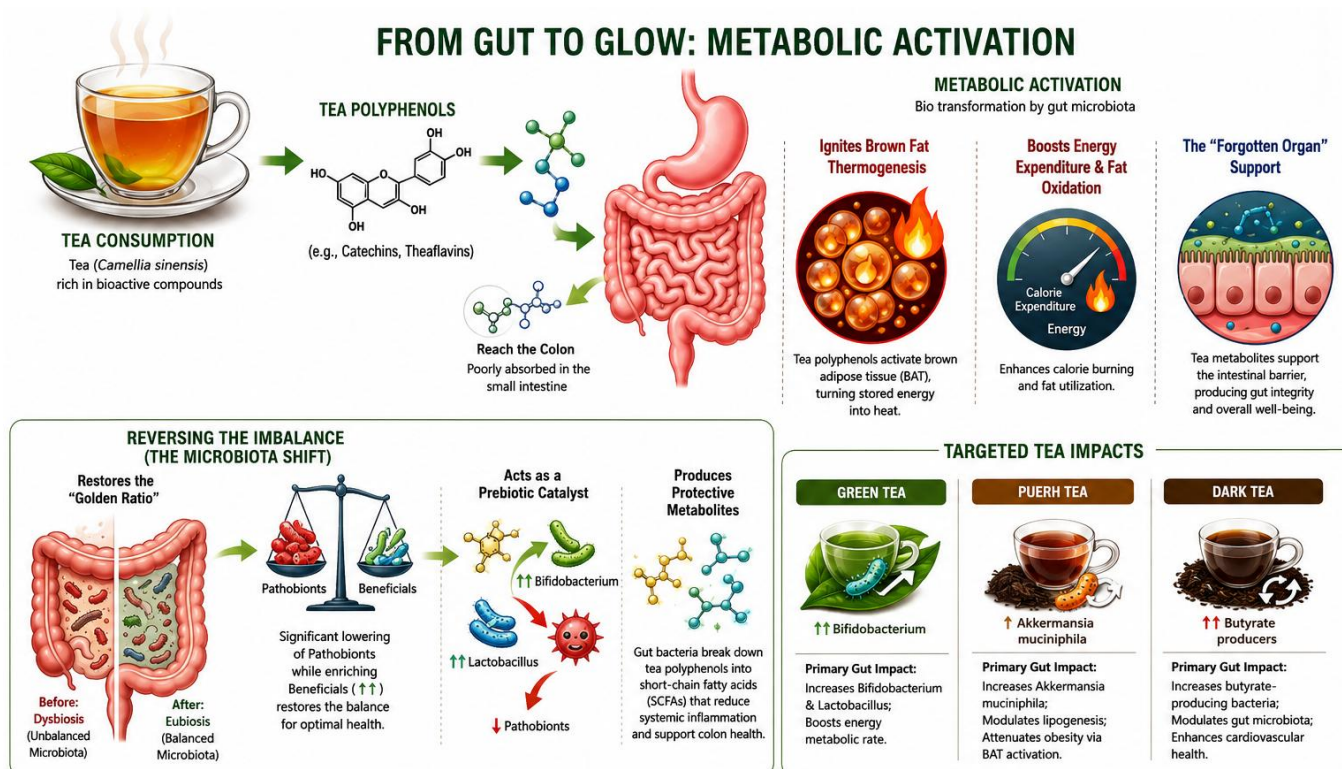


Figure: 3 Tea and the Gut: Brewing a Healthier Microbiome

In Figure-3 the interactions between tea polyphenols and the human gut microbiota and their associated health benefits have been showed. Tea polyphenols, including catechins and theaflavins, are poorly absorbed in the small intestine and reach the colon, where they are metabolized by gut microorganisms into bioactive metabolites

such as SCFAs. These compounds promote the growth of beneficial bacteria (e.g., *Bifidobacterium*, *Lactobacillus*, and *A. muciniphila*) while suppressing pathogenic microorganisms, thereby restoring microbial balance (eubiosis). The resulting modulation of gut microbiota enhances intestinal barrier integrity, stimulates brown adipose tissue thermogenesis, improves energy metabolism, and strengthens immune function. Different tea varieties, including green, Pu-erh, and dark tea, exert distinct microbiota-modulating effects, collectively contributing to improved gut health and reduced risk of metabolic and chronic diseases.

LIMITATIONS OF CURRENT STUDIES

Despite the growing body of evidence supporting the role of tea in modulating the gut microbiota, several limitations in the current literature must be carefully considered. These limitations restrict the ability to draw definitive conclusions regarding the extent and clinical relevance of tea-induced changes in the gut microbiome. One of the primary limitations is that a substantial proportion of the available evidence is derived from in vitro experiments and animal models (Liu et al., 2020). Although these studies provide valuable mechanistic insights into the interactions between tea polyphenols and gut microorganisms, they may not accurately reflect the complexity of the human gastrointestinal ecosystem. Differences in physiology, metabolism, immune responses, and microbial composition between humans and experimental models limit the direct translation of these findings to clinical settings (Wang et al., 2020).

Another important limitation is the scarcity of well-designed human clinical trials. Existing studies are relatively limited and frequently involve small sample sizes, short intervention periods, heterogeneous participant populations, and considerable variation in study design. Consequently, establishing clear cause-and-effect relationships between tea consumption and gut microbiota modulation remains challenging. Moreover, the composition of tea varies considerably depending on the tea variety, cultivation conditions, processing methods, geographical origin, and preparation techniques. Differences in brewing temperature, infusion time, concentration, and dosage further contribute to inconsistencies among published studies, making direct comparisons difficult and limiting the development of standardized dietary recommendations (Chen and Yang 2020; Zhang et al., 2023).

Furthermore, many investigations primarily focus on alterations in microbial composition while providing limited information on the functional consequences of these changes. Relatively few studies have comprehensively examined microbial metabolic activity, host–microbe interactions, or clinically relevant health outcomes. Consequently, understanding how tea-induced microbial alterations translate into measurable physiological and clinical benefits remains an important area for future investigation. In addition, the bioavailability, absorption, and microbial biotransformation of tea polyphenols are highly complex processes that are not yet fully understood. Variations in the metabolism of these compounds can substantially influence their biological activity and ultimately determine their health-promoting potential (Williams et al., 2019).

Another important challenge in interpreting the current evidence is the considerable inter-individual variability in responses to tea consumption. The metabolism of tea polyphenols and the resulting modulation of the gut microbiota are influenced by multiple host-related factors, including age, sex, genetic background, habitual dietary patterns, lifestyle, medication use (particularly antibiotics), and the baseline composition and diversity of the gut microbiome (Wang et al., 2022). Consequently, individuals may differ substantially in their capacity to metabolize tea polyphenols into bioactive microbial metabolites and in the magnitude of their physiological responses to tea intake. Furthermore, variations in tea preparation methods, including tea type, brewing temperature, infusion time, concentration, and frequency of consumption, may alter the availability of bioactive compounds, contributing to inconsistencies among published studies. Future research should systematically account for these variables through well-designed, standardized, and adequately powered human clinical trials. Integrating advanced microbiome profiling, metabolomics, and nutrigenomic approaches will further improve our understanding of personalized responses to tea consumption and facilitate the development of evidence-based dietary recommendations.

FUTURE RESEARCH DIRECTIONS

Although substantial progress has been made in understanding the interactions between tea consumption and the gut microbiota, several important questions remain unresolved. Future research should move beyond descriptive studies toward mechanistic and translational investigations that establish causal relationships between tea-induced microbial alterations and clinically relevant health outcomes. Addressing current knowledge gaps will require multidisciplinary approaches integrating microbiology, nutrition, metabolomics, systems biology, and clinical research. One of the highest priorities is the implementation of large-scale, randomized, placebo-controlled human clinical trials using standardized tea preparations, clearly defined intervention protocols, and extended follow-up periods. Such studies should include diverse populations differing in age, sex, ethnicity, dietary habits, and health status to improve the generalizability of findings. Establishing standardized methodologies for tea preparation, dosage, and microbiome analysis will further enhance the comparability and reproducibility of future investigations.

Advances in multi-omics technologies, including metagenomics, metatranscriptomics, metabolomics, and proteomics, offer unprecedented opportunities to better understand the functional interactions between tea polyphenols and the gut microbiota. Integrating these approaches with computational systems biology and artificial intelligence-based data analysis may facilitate the identification of key microbial species, metabolic pathways, and bioactive metabolites responsible for the health-promoting effects of tea. Such integrated analyses will provide a more comprehensive understanding of host-microbe interactions than microbial composition alone. Future investigations should also emphasize personalized nutrition by considering inter-individual variability arising from genetic background, baseline gut microbiota composition, habitual dietary patterns, lifestyle, age, medication use, and environmental factors. Understanding these determinants will enable the development of individualized dietary recommendations and improve the effectiveness of tea-based nutritional interventions. Furthermore, elucidating dose-response relationships, optimal intervention duration, and the comparative efficacy of different tea varieties will support evidence-based dietary guidelines.

Finally, increasing attention should be directed toward the development of tea-derived functional foods, nutraceuticals, and microbiota-targeted therapeutic strategies. Identification of specific microbial biomarkers associated with favorable responses to tea consumption may facilitate precision nutrition approaches and contribute to the prevention and management of metabolic, inflammatory, gastrointestinal, and neurodegenerative disorders. Collectively, these research directions will strengthen the scientific evidence supporting tea-gut microbiota interactions and accelerate the translation of laboratory findings into practical clinical and public health applications.

CONCLUSION

Tea-gut microbiota interactions represent an emerging area of research with important implications for human health and nutrition. Current evidence demonstrates that tea-derived polyphenols undergo extensive microbial biotransformation in the colon, generating bioactive metabolites that selectively influence the composition and functional activity of the gut microbiota. Through these bidirectional interactions, regular tea consumption has been associated with improved intestinal homeostasis, enhanced metabolic regulation, maintenance of intestinal barrier integrity, modulation of immune responses, and a reduced risk of several chronic diseases. Collectively, these findings highlight the potential of tea as a functional dietary component capable of supporting gut microbial balance and overall host health.

Despite these promising observations, important knowledge gaps remain. The predominance of *in vitro* and animal studies, limited availability of well-designed human clinical trials, heterogeneity in tea composition and intervention protocols, and substantial inter-individual variability continue to limit the translation of current findings into clinical practice. Addressing these challenges will require standardized clinical investigations supported by advanced multi-omics technologies and systems-level approaches to better understand the complex interactions among tea polyphenols, gut microorganisms, and host physiology. Overall, tea should be regarded as a promising dietary modulator of the gut microbiota rather than a standalone therapeutic intervention.

Continued interdisciplinary research integrating microbiology, nutrition, metabolomics, and clinical sciences will be essential for developing evidence-based dietary recommendations and realizing the potential of tea in precision nutrition and microbiota-targeted health strategies.

REFERENCES

1. Almajano, M. P., Carbo, R., Jiménez, J. A. L., & Gordon, M. H. (2008). Antioxidant and antimicrobial activities of tea infusions. *Food chemistry*, 108(1), 55-63.
2. Bond, T., & Derbyshire, E. (2019). Tea compounds and the gut microbiome: findings from trials and mechanistic studies. *Nutrients*, 11(10), 2364.
3. Bortolini, D., Haminiuk, C., Pedro, A., De Andrade Arruda Fernandes, I., & Maciel, G. (2021). Processing, chemical signature and food industry applications of *Camellia sinensis* teas: An overview. *Food Chemistry: X*, 12.
4. Cabrera, C., Artacho, R., & Giménez, R. (2006). Beneficial effects of green tea—a review. *Journal of the American College of Nutrition*, 25(2), 79-99.
5. Capasso, L., De Masi, L., Sirignano, C., Maresca, V., Basile, A., Nebbioso, A., Rigano, D., & Bontempo, P. (2025). Epigallocatechin Gallate (EGCG): Pharmacological Properties, Biological Activities and Therapeutic Potential. *Molecules*, 30.
6. Chacko, S. M., Thambi, P. T., Kuttan, R., & Nishigaki, I. (2010). Beneficial effects of green tea: a literature review. *Chinese medicine*, 5(1), 13.
7. Chen, T., & Yang, C. (2020). Biological fates of tea polyphenols and their interactions with microbiota in the gastrointestinal tract: implications on health effects. *Critical Reviews in Food Science and Nutrition*, 60, 2691 - 2709.
8. Chupeerach, C., Aursalung, A., Watcharachaisoponsiri, T., Whanmek, K., Thiyajai, P., Yosphan, K., Sritalahareuthai, V., Sahasakul, Y., Santivarangkna, C., & Suttisansanee, U. (2021). The Effect of Steaming and Fermentation on Nutritive Values, Antioxidant Activities, and Inhibitory Properties of Tea Leaves. *Foods*, 10.
9. De Rossi, L., Rocchetti, G., Lucini, L., & Rebecchi, A. (2025). Antimicrobial potential of polyphenols: Mechanisms of action and microbial responses—A narrative review. *Antioxidants*, 14(2), 200.
10. Facchin, S., Bertin, L., Bonazzi, E., Lorenzon, G., De Barba, C., Barberio, B., Zingone, F., Maniero, D., Scarpa, M., Ruffolo, C., Angriman, I., & Savarino, E. (2024). Short-Chain Fatty Acids and Human Health: From Metabolic Pathways to Current Therapeutic Implications. *Life*, 14.
11. Farhan, M. (2022). Green Tea Catechins: Nature's Way of Preventing and Treating Cancer. *International Journal of Molecular Sciences*, 23.
12. Ferrari, E., & Naponelli, V. (2025). Catechins and Human Health: Breakthroughs from Clinical Trials. *Molecules*, 30.
13. Fraser, K., Harrison, S. J., Lane, G. A., Otter, D. E., Hemar, Y., Quek, S. Y., & Rasmussen, S. (2014). Analysis of low molecular weight metabolites in tea using mass spectrometry-based analytical methods. *Critical reviews in food science and nutrition*, 54(7), 924-937.
14. Fujisaka, S., Watanabe, Y., & Tobe, K. (2022). The gut microbiome: a core regulator of metabolism. *The Journal of Endocrinology*, 256.
15. Graham, H. N. (1992). Green tea composition, consumption, and polyphenol chemistry. *Preventive medicine*, 21(3), 334-350.
16. Han, X., Shen, T., & Lou, H. (2007). Dietary polyphenols and their biological significance. *International journal of molecular sciences*, 8(9), 950-988.
17. Hasan, N., & Yang, H. (2019). Factors affecting the composition of the gut microbiota, and its modulation. *PeerJ*, 7.
18. Huang, J., & Chen, C. (2026). The influence of tea consumption on gut microbiota: evidence from a genome-wide association study. *Journal of the Science of Food and Agriculture*, 106(7), 4190-4198.
19. Iațcu, C., Steen, A., & Covașă, M. (2021). Gut Microbiota and Complications of Type-2 Diabetes. *Nutrients*, 14.

20. Jin, J. S., Touyama, M., Hisada, T., & Benno, Y. (2012). Effects of green tea consumption on human fecal microbiota with special reference to *Bifidobacterium* species. *Microbiology and immunology*, 56(11), 729-739.
21. Kasubuchi, M., Hasegawa, S., Hiramatsu, T., Ichimura, A., & Kimura, I. (2015). Dietary Gut Microbial Metabolites, Short-chain Fatty Acids, and Host Metabolic Regulation. *Nutrients*, 7, 2839 - 2849.
22. Kawabata, K., Yoshioka, Y., & Terao, J. (2019). Role of Intestinal Microbiota in the Bioavailability and Physiological Functions of Dietary Polyphenols. *Molecules*, 24.
23. Khairudin, M., Jalil, A., & Hussin, N. (2021). Effects of Polyphenols in Tea (*Camellia sinensis* sp.) on the Modulation of Gut Microbiota in Human Trials and Animal Studies. *Gastroenterology Insights*, 12, 202-216.
24. Khalil, M., Di Ciaula, A., Mahdi, L., Jaber, N., Di Palo, D., Graziani, A., Baffy, G., & Portincasa, P. (2024). Unraveling the Role of the Human Gut Microbiome in Health and Diseases. *Microorganisms*, 12.
25. Khan, M., Zohair, M., Khan, A., Kashif, A., Mumtaz, S., & Muskan, F. (2025). From Gut to Brain: The roles of intestinal microbiota, immune system, and hormones in intestinal physiology and gut-brain-axis. *Molecular and Cellular Endocrinology*, 607.
26. Khan, N., & Mukhtar, H. (2007). Tea polyphenols for health promotion. *Life sciences*, 81(7), 519-533.
27. Lee, H. C., Jenner, A. M., Low, C. S., & Lee, Y. K. (2006). Effect of tea phenolics and their aromatic fecal bacterial metabolites on intestinal microbiota. *Research in microbiology*, 157(9), 876-884.
28. Li, Q., & Van De Wiele, T. (2021). Gut microbiota as a driver of the interindividual variability of cardiometabolic effects from tea polyphenols. *Critical Reviews in Food Science and Nutrition*, 63, 1500 - 1526.
29. Li, Y., Wang, C., Huai, Q., Guo, F., Liu, L., Feng, R., & Sun, C. (2016). Effects of tea or tea extract on metabolic profiles in patients with type 2 diabetes mellitus: a meta-analysis of ten randomized controlled trials. *Diabetes/metabolism research and reviews*, 32(1), 2-10.
30. Lin, L. Z., Chen, P., & Harnly, J. M. (2008). New phenolic components and chromatographic profiles of green and fermented teas. *Journal of Agricultural and food chemistry*, 56(17), 8130-8140.
31. Liu, C., Gan, R. Y., Chen, D., Zheng, L., Ng, S. B., & Rietjens, I. M. (2024). Gut microbiota-mediated metabolism of green tea catechins and the biological consequences: An updated review. *Critical Reviews in Food Science and Nutrition*, 64(20), 7067-7084.
32. Liu, J., Hao, W., He, Z., Kwek, E., Zhao, Y., Zhu, H., & Chen, Z. Y. (2019). Beneficial effects of tea water extracts on the body weight and gut microbiota in C57BL/6J mice fed with a high-fat diet. *Food & function*, 10(5), 2847-2860.
33. Liu, Y. C., Li, X. Y., & Shen, L. (2020). Modulation effect of tea consumption on gut microbiota. *Applied Microbiology and Biotechnology*, 104(3), 981-987.
34. Marina, A., Filip, L., & Marc, R. (2024). *Camellia sinensis* L. (Green Tea): Bioactive Compounds and Pharmacological Properties – A Comprehensive Review. *Hop and Medicinal Plants*.
35. Mehrabi, M., Amiri, M., Razavi, R., Najafi, A., & Hajian-Tilaki, A. (2024). Influence of varied processing methods on the antioxidant capacity, antibacterial activity, and bioavailability of Iranian black, oolong, and green leafy teas. *Food chemistry*, 464 Pt 2, 141793.
36. Mourya, S., Bodla, R., Taurean, R., & Sharma, A. (2019). Simultaneous estimation of xanthine alkaloids (Theophylline, Theobromine and Caffeine) by High-Performance Liquid Chromatography. *International Journal of Drug Regulatory Affair*.
37. Mozumder, N., Lee, J., & Hong, Y. (2025). A Comprehensive Understanding of *Camellia sinensis* Tea Metabolome: From Tea Plants to Processed Teas. *Annual review of food science and technology*.
38. Musiał, C., Kuban-Jankowska, A., & Górska-Ponikowska, M. (2020). Beneficial Properties of Green Tea Catechins. *International Journal of Molecular Sciences*, 21.
39. Payne, E., Aceves-Martins, M., Dubost, J., Greyling, A., & De Roos, B. (2025). Effects of Tea (*Camellia sinensis*) or its Bioactive Compounds l-Theanine or l-Theanine plus Caffeine on Cognition, Sleep, and Mood in Healthy Participants: A Systematic Review and Meta-Analysis of Randomized Controlled Trials. *Nutrition Reviews*, 83, 1873 - 1891.
40. Plamada, D., & Vodnar, D. (2021). Polyphenols—Gut Microbiota Interrelationship: A Transition to a New Generation of Prebiotics. *Nutrients*, 14.

41. Portincasa, P., Bonfrate, L., Vacca, M., De Angelis, M., Farella, I., Lanza, E., Khalil, M., Wang, D., Sperandio, M., & Di Ciaula, A. (2022). Gut Microbiota and Short Chain Fatty Acids: Implications in Glucose Homeostasis. *International Journal of Molecular Sciences*, 23.
42. Rinninella, E., Raoul, P., Cintoni, M., Franceschi, F., Miggiano, G., Gasbarrini, A., & Mele, M. (2019). What is the Healthy Gut Microbiota Composition? A Changing Ecosystem across Age, Environment, Diet, and Diseases. *Microorganisms*, 7.
43. Rothenberg, D., Zhou, C., & Zhang, L. (2018). A Review on the Weight-Loss Effects of Oxidized Tea Polyphenols. *Molecules: A Journal of Synthetic Chemistry and Natural Product Chemistry*, 23.
44. Rudrapal, M., de Oliveira, A. M., & Singh, R. P. (2025). Dietary polyphenols maintain human health through modulation of gut microbiota. *Frontiers in Pharmacology*, 16, 1710088.
45. Ruxton, C. H. S. (2008). Black tea and health. *Nutrition Bulletin*, 33(2), 91-101.
46. Sahu, G., Ghosh, S., Kaur, S., Rawte, R., & Tyagi, M. (2025). Extraction and comparative analysis of caffeine and catechin present in tea and coffee sample. *International Journal For Multidisciplinary Research*.
47. Sang, S., Lambert, J. D., Ho, C. T., & Yang, C. S. (2011). The chemistry and biotransformation of tea constituents. *Pharmacological research*, 64(2), 87-99.
48. Silva, Y., Bernardi, A., & Frozza, R. (2020). The Role of Short-Chain Fatty Acids From Gut Microbiota in Gut-Brain Communication. *Frontiers in Endocrinology*, 11.
49. Spencer, J. P. (2003). Metabolism of tea flavonoids in the gastrointestinal tract. *The Journal of nutrition*, 133(10), 3255S-3261S.
50. Su, Y., Hu, K., Li, D., Guo, H., Sun, L., & Xie, Z. (2024). Microbial-Transferred Metabolites and Improvement of Biological Activities of Green Tea Catechins by Human Gut Microbiota. *Foods*, 13.
51. Thursby, E., & Juge, N. (2017). Introduction to the human gut microbiota. *Biochemical Journal*, 474, 1823 - 1836.
52. Tong, T., Liu, Y. J., Kang, J., Zhang, C. M., & Kang, S. G. (2019). Antioxidant activity and main chemical components of a novel fermented tea. *Molecules*, 24(16), 2917.
53. Wang, J., He, M., Yang, M., & Ai, X. (2024). Gut microbiota as a key regulator of intestinal mucosal immunity. *Life sciences*, 122612.
54. Wang, W., Le, T., Wang, W., Yu, L., Yang, L., & Jiang, H. (2023). Effects of Key Components on the Antioxidant Activity of Black Tea. *Foods*, 12.
55. Wang, X., Qi, Y., & Zheng, H. (2022). Dietary Polyphenol, Gut Microbiota, and Health Benefits. *Antioxidants*, 11.
56. Wang, Y., Zhou, J., Yang, M., Zhu, L., & Wang, F. (2024). Tea administration facilitates immune homeostasis by modulating host Microbiota. *Nutrients*, 16(21), 3675.
57. Williams, J., Everett, J., D'cunha, N., Sergi, D., Georgousopoulou, E., Keegan, R., Mckune, A., Mellor, D., Anstice, N., & Naumovski, N. (2019). The Effects of Green Tea Amino Acid L-Theanine Consumption on the Ability to Manage Stress and Anxiety Levels: a Systematic Review. *Plant Foods for Human Nutrition*, 75, 12-23.
58. Wnuk, E. (2025). The Antioxidant Potential of Black Tea Polyphenols in Heavy Metal Toxicity: An In Vitro Perspective. *International Journal of Molecular Sciences*, 26.
59. Xiao, T., Li, Y., Li, H., Wang, K., Huang, J., Liu, Z., & Zhu, M. (2024). Tea consumption in relation with metabolic syndrome and obesity: A systematic review and meta-analysis of randomized clinical trials. *Food Bioscience*, 61, 104322.
60. Yang, J., Chen, W., Chen, J., Xie, D., Wang, Y., & Zhou, J. (2025). Tea Polyphenol Epigallocatechin Gallate and the Gut–Health Axis: Unraveling Structural Characteristics, Metabolic Pathways, and Systemic Benefits. *Advances in Nutrition*, 16(12), 100545.
61. Yen, G. C., & Chen, H. Y. (1995). Antioxidant activity of various tea extracts in relation to their antimutagenicity. *Journal of agricultural and food chemistry*, 43(1), 27-32.
62. Yoo, J., Groer, M., Dutra, S., Sarkar, A., & McSkimming, D. (2020). Gut Microbiota and Immune System Interactions. *Microorganisms*, 8.
63. Yu, S., Zhu, X., Zhao, X., Li, Y., Niu, X., Chen, Y., & Ying, J. (2025). Improvement of chronic metabolic inflammation and regulation of gut homeostasis: Tea as a potential therapy. *Pharmacology & therapeutics*, 269, 108828.

64. Zeng, L., Zhou, X., Su, X., & Yang, Z. (2020). Chinese oolong tea: An aromatic beverage produced under multiple stresses. *Trends in food science & technology*, 106, 242-253.
65. Zhang, D., Jian, Y., Zhang, Y., Li, Y., Gu, L., Sun, H., Liu, M., Zhou, H., Wang, Y., & Xu, Z. (2023). Short-chain fatty acids in diseases. *Cell Communication and Signaling: CCS*, 21.
66. Zhang, L., Ho, C., Zhou, J., Santos, J., Armstrong, L., & Granato, D. (2019). Chemistry and Biological Activities of Processed *Camellia sinensis* Teas: A Comprehensive Review. *Comprehensive reviews in food science and food safety*, 18 5, 1474-1495.
67. Zhao, M., Su, X., Nian, B., Chen, L., Zhang, D., Duan, S., Wang, L., Shi, X., Jiang, B., Jiang, W., Lv, C., Wang, D., Shi, Y., Xiao, Y., Wu, J., Pan, Y. (2019). Integrated Meta-omics Approaches to Understand the Microbiome of Spontaneous Fermentation of Traditional Chinese Pu-erh Tea. *mSystems*, 4.
68. Zhao, Z., Chen, R., & Ng, K. (2024). Effects of differently processed tea on the gut microbiota. *Molecules*, 29(17), 4020.
69. Zhu, K., Ouyang, J., Huang, J., & Liu, Z. (2021). Research progress of black tea thearubigins: a review. *Critical Reviews in Food Science and Nutrition*, 61(9), 1556-1566.