Proceedings of ICMMGH 2027 Symposium: Clinical OMICS for Drug Discovery and Personalized Medicine
DOI: 10.54254/2753-8818/2027.MB38698

# *Recent Advances in the Interaction Mechanisms and Health Effects of Tea Polyphenols with Gut Microbiota*

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***Abstract.*** Tea polyphenols, such as catechins from green tea and theabrownins from dark tea, are able to produce multiple beneficial influences on human bodies, for instance antioxidant, anti-inflammatory and metabolic-regulating functions, but human bodies can barely take in these compounds after oral consumption. Most polyphenol compounds will arrive at the colon, where they carry out mutual interactions with gut microbes. Gut microbes can decompose tea polyphenols and convertthem into small-moleculemetabolites including phenyl-γ-valerolactone, phenolic acids and short-chain fatty acids (SCFAs), so human bodies can absorb and utilise these transformed substances more readily, and these metabolites also show relatively higher biological activity.At the same time, tea polyphenols can modulate gut microbiota homeostas,which promote the reproduction of beneficial bacteria, boost the production of short-chain fatty acids, repair impaired intestinal barrier structures and regulate local intestinal immune responses. Different tea processing procedures will alter polyphenol compositions, which leads to varied modulatory effects on gut microbes.Even though plenty of findings have been obtained from animal and in-vitro experiments, researchers still meet many obstacles when translating these findings into human clinical use, such as the absence of unified dosage-effect standards, ambiguous mechanisms behind individual differences and unclear detailed molecular interaction patterns. This review summarises the intestinal metabolic process of tea polyphenols as well as their major ways to regulate gut microbiota, and it can provide certain references for subsequent research on precise nutrition and metabolic disease intervention.

***Keywords:*** Tea polyphenols, gut microbiota, catechins, short-chain fatty acids

## 1. Introduction

### 1.1. Overview of polyphenolic natural drugs

Tea polyphenols are a general name for phenolic compounds contained in tea leaves. Catechins are the most abundant substances among them, and catechins also show relatively strong biological activity. The main catechin substances in green tea contain epicatechin (EC), epigallocatechin (EGC), epicatechin gallate (ECG), and epigallocatechin gallate (EGCG); EGCG accounts for the largest proportion, and it has the strongest biological activity among all green-tea catechins. But human bodies can only absorb very small amounts of tea polyphenols after oral administration. One

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DOI: 10.54254/2753-8818/2027.MB38698

research work mixed green tea catechins (GTCs) with human fecal microbes to carry out anaerobic fermentation in laboratory conditions; researchers used ultra-high-performance liquid chromatography coupled with quadrupole-Orbitrap tandem mass spectrometry (UHPLC-Q-Orbitrap-MS/MS) to test metabolite components, and researchers adopted 16S ribosomal RNA (rRNA) gene sequencing technology to observe changes in microbial communities. The research results show that only a small share of green tea catechins will be absorbed by the small intestine, most of these substances will flow into the colon, and gut microbes will decompose these substances into low-molecular-weight compounds such as phenyl-γ-valerolactone, phenolic acids, and short-chain fatty acids (SCFAs) [1]. This process can improve the absorption efficiency of these metabolite products, and it can also make green tea catechins show richer biological functions. EGCG also has low absorption efficiency inside human bodies; the mutual reactions between EGCG and gut microbes play an important role in its transformation and its health-promoting effects. It should be noted that the experimental results obtained from this kind of in-vitro anaerobic fermentation cannot fully simulate the complex intestinal physiological environment inside real human bodies.

### 1.2. Significance of studying gut microbiota homeostasis and polyphenols

Gut microbiota can complete many important tasks for human hosts. These tasks include keeping host metabolism stable, maintaining normal immune function, and keeping the intestinal barrier intact. One systematic review paper points out that the close connection between gut microbiota and human health represents one important path for tea to exert its beneficial effects on human bodies [2]. When gut microbiota loses its balanced state, this situation will connect with many kinds of chronic illnesses, such as obesity, non-alcoholic fatty liver disease (NAFLD), inflammatory bowel disease, and type 2 diabetes [3]. Polyphenols come from plants. They can resist inflammation and clear oxidative substances, and researchers think these substances can improve non-alcoholic fatty liver disease by changing the composition of gut microbiota. Tea polyphenols can bring health benefits by changing the composition of gut microbes; at the same time, gut microbes will also change the absorption and metabolic process of tea polyphenols. Researchers built obese mouse models through high-fat diet (HFD) feeding, and they combined 16S rRNA sequencing detection, biochemical testing, and tissue morphological observation in their experiments; the experimental results confirm that tea polyphenols can produce anti-obesity effects, because these substances can raise the quantity of beneficial bacteria and adjust energy consumption conditions inside animal bodies [4]. Tea catechins can change the composition of gut microbial communities, and these changes will further improve the physical condition of hosts [5]. This two-way interactive relationship makes the regulatory axis formed by tea polyphenols and gut microbiota a potential research direction for dietary intervention which can improve chronic metabolic disorders.

## 2. Composition characteristics and intestinal metabolism patterns of tea polyphenols

### 2.1. Core active components and functional differentiation of tea polyphenols

Tea polyphenols refer to the total polyphenolic substances in tea. Their composition varies significantly depending on the tea variety, origin, and processing method. Green tea mainly contains catechin-type compounds, including epicatechin, epigallocatechin, epicatechin gallate, and epigallocatechin gallate (EGCG). In vitro anaerobic fermentation experiments co-culturing green tea catechins (GTCs) with human fecal microorganisms, followed by UHPLC-Q-Orbitrap-MS/MS

DOI: 10.54254/2753-8818/2027.MB38698

metabolomics and 16S rRNA gene sequencing, showed that human intestinal microorganisms exhibit a strong metabolic effect on GTCs, yielding a total of 35 microbial transformation metabolites—far exceeding previous reports. Among them, five metabolites (EGCG quinone, EGC quinone, ECG quinone, EC quinone, and mono-oxygenated EGCG) were identified for the first time in GTCs fermented by human gut microbiota. Notably, the antioxidant activity, α-amylase, and α-glucosidase inhibitory activities of fermented GTCs were higher than those of unfermented samples. 16S rRNA analysis indicated that GTCs significantly altered microbial diversity and enriched genera such as Eubacterium and Flavonifractor. Black tea forms key bioactive components represented by tea brown pigments through fermentation. The formation pathways, structural complexity, and diverse biological functions of the brownins have been systematically reviewed [6]. Theabrownins are the main polyphenol-derived pigments and key bioactive components formed via microbial fermentation or enzymatic oxidation in dark tea. They exhibit multiple activities, including anti-obesity, anti-diabetic, anti-inflammatory, antioxidant, anti-tumor, anti-photodamage, and gut microbiota-regulating effects. These effects are mediated through regulation of bile acid metabolism, gut microbial composition, circadian rhythm genes, and multiple signaling pathways such as AMP-activated protein kinase/peroxisome proliferator-activated receptor gamma coactivator 1-alpha, phosphoinositide 3-kinase/protein kinase B, forkhead box O/peroxisome proliferator-activated receptor, farnesoid X receptor/fibroblast growth factor 15, nuclear factor erythroid 2-related factor 2, and nuclear factor kappa-light-chain-enhancer of activated B cells (NF-κB), as well as effects on cell apoptosis, autophagy, and epigenetic modifications [6]. Black tea and its main active components (tea polyphenols, theabrownins, and tea polysaccharides) affect the intestinal microbiota through promoting metabolism, providing nutrition, protection, and immune regulation [7].

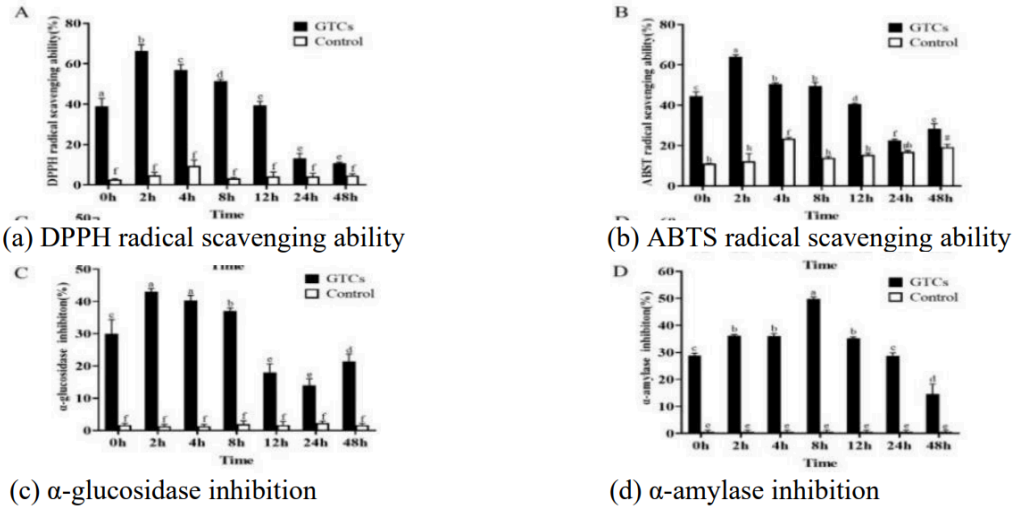
### 2.2. The regulatory influence of processing techniques on the activity of tea polyphenols

People can divide tea products into six major categories in accordance with processing approaches. These categories include green tea, white tea, yellow tea, oolong tea, black tea, and dark tea. Different fermentation degrees and different processing operating conditions will change the polyphenol composition of finished tea products, so different tea products will bring different influences on gut microbiota. Researchers collected and organized experimental data published from 2004 to 2024; these collected data cover in-vivo animal feeding tests, in-vitro human fecal fermentation experiments, and human feeding trials, and the analysis results show that teas made by different processing methods will produce quite different effects on gut microbes. The processing technology will change the types and quantities of bioactive substances inside tea raw materials, and this factor will determine how tea polyphenols get metabolized inside the intestines and what health effects these substances can produce. Tea processing procedures can change the material composition of tea, and such changes will further alter the intestinal protective capacity of tea products; bioactive substances from tea can play an important role in keeping the intestinal barrier intact [8]. Different processing techniques will bring different protective effects for intestinal barriers; active components extracted from tea can lower the damage to the physical barrier and chemical barrier, and they achieve this effect by adjusting the expression of barrier-related proteins; these substances can also keep the immune barrier and biological barrier in stable conditions through changing inflammatory factor levels and regulating gut microbial metabolism.

DOI: 10.54254/2753-8818/2027.MB38698

## 2.3. Metabolic transformation of tea polyphenols in the gut and bidirectional interactions with microbiota

Green tea catechins will go through absorption, distribution, metabolism, and excretion after entering human bodies, but human bodies cannot absorb large amounts of these substances after oral intake. In-vitro anaerobic fermentation experiments show that only a small fraction of green tea catechins will be absorbed by the small intestine; most of these substances will move into the large intestine, and gut microbes will decompose these substances into low-molecular-weight metabolites in this position. Researchers used UHPLC-Q-Orbitrap-MS/MS technology to find 35 metabolites generated from microbial transformation, and researchers also put forward corresponding metabolic pathways based on experimental data. Differences in gut microbiota among different individuals, together with the types and contents of microbial metabolites, will change the final physiological effects brought by green tea catechins. The 16S rRNA sequencing results indicate that green tea catechins can greatly change gut microbial diversity, and these substances can enrich bacteria from Eubacterium and Flavonifractor. Researchers sorted out published pre-clinical and clinical research literature, and the sorting results clearly illustrate that green tea catechins can bring metabolic health benefits, and these benefits are mainly produced inside intestinal tissues [9]. The specific working mechanisms include improving the unbalanced state of flora, reducing mucosal inflammation and oxidative stress injury, strengthening intestinal barrier functions, cutting down lipid absorption and lipid metabolism inside intestines, adjusting nuclear-receptor-related signal responses on mucous membranes, and changing the overall metabolite composition of the intestinal lumen. Some recent clinical experimental data can support the conclusions obtained from pre-clinical experiments. The interaction process between catechins and gut microbiota is one key factor which decides the metabolic benefits of catechins. Even though many research papers have discussed how tea catechins improve gut microecology, researchers still do not understand the two-way interaction rules between phenolic substances and gut microbes very well. As Figure 1 shows, compared with the control group samples, green tea catechin samples treated by human gut microbiota fermentation have stronger 2,2-diphenyl-1-picrylhydrazyl (DPPH) radical scavenging capacity, stronger 2,2'-azino-bis (ABTS) radical scavenging capacity, and higher inhibitory activity for α-glucosidase and α-amylase; these improving effects will also change with fermentation time.




(a) DPPH radical scavenging ability

(b) ABTS radical scavenging ability

(c) α-glucosidase inhibition

(d) α-amylase inhibition

Figure 1. Antioxidant activities and α-glucosidase inhibitory activity of green tea catechins before and after fermentation by human gut microbiota [1]

DOI: 10.54254/2753-8818/2027.MB38698

## 3. The core mechanism by which tea polyphenols regulate the gut microbiota

### 3.1. Selective antibacterial effect, correcting dysbiosis of the microbial community

Tea polyphenols can change the component structure of intestinal microbiota. These substances can restrain harmful bacteria selectively and offer favorable growth conditions for useful bacteria, and this represents one core working mechanism for tea polyphenols to maintain the balanced state of intestinal microecology. Tea catechins can adjust gut microbial communities, and these adjustments can improve host health conditions [5]. In the obese mouse models induced by high-fat-diet feeding, adding tea polyphenols into animal feed can increase the abundance of beneficial bacteria such as Blautia and Faecalibaculum, and these substances can also stop conditional pathogenic bacteria from reproducing in large quantities [4]. This selective bacteriostatic effect can change the competitive relationship among different intestinal microbes, and beneficial bacteria can get more chances to settle and multiply in intestinal tracts under such conditions.

### 3.2. Promote the proliferation of beneficial bacteria and enhance microbial diversity

Drinking black-tea products can help useful microbial communities form inside the intestines, it can raise microbial diversity, and it can keep the overall structure of gut microbiota in balanced conditions [7]. Tea polyphenols can increase the quantity of certain bacterial groups which can produce short-chain fatty acids (SCFAs), and these changes will improve the overall diversity and functional performance of gut microbiota. Higher microbial diversity means the intestinal microecosystem has stronger stability and anti-interference capacity, and this condition acts as an important guarantee for tea polyphenols to play long-term health-promoting roles. Adjusting gut microbiota composition can ease non-alcoholic fatty liver disease (NAFLD), because such adjustments can reduce inflammatory reactions, cut down fat accumulation in liver tissues, and lower liver enzyme contents [3]. Polyphenols are natural micronutrient substances derived from plants. They can produce anti-inflammatory effects and antioxidant effects.

### 3.3. Regulate the metabolic profile of the microbial community and promote the synthesis of short-chain fatty acids

Short-chain fatty acids are important metabolite products generated from gut microbial fermentation reactions, and these substances play very meaningful roles in keeping intestinal health and adjusting host metabolic states. In the high-fat-diet-induced obese mouse models, supplementing tea polyphenols can raise the abundance of Blautia and Faecalibaculum, it can obviously activate G-protein-coupled receptors (GPCRs), and it can restrain histone deacetylases (HDACs), so more short-chain fatty acids can be generated in animal intestines [4]. The changed microbial conditions will increase short-chain fatty acid content, and they will reduce lipopolysaccharide (LPS) levels at the same time, so the endotoxemia symptom can be relieved. Most existing research projects about tea-polyphenol-mediated gut-microbiota regulation and anti-obesity effects are completed on animal models; even though most experimental results confirm these beneficial effects, researchers still cannot confirm the effective dosage range, and relevant toxicology research data are not sufficient [10]. Short-chain fatty acids serve as key signaling molecules between gut microbiota and host metabolism. They can exert important influences on energy metabolism, insulin sensitivity, and inflammatory response regulation. Polyphenols can improve gut microbiota composition; these substances can support the growth of useful bacteria (such as Lactobacillus and Bifidobacterium),

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and they can reduce the number of harmful bacteria which are related to non-alcoholic fatty liver disease [3].

### 3.4. Repair the intestinal barrier and block the vicious cycle of inflammation and microbiome dysbiosis

The intact state of intestinal barrier is very essential for maintaining stable intestinal environments. Tea polyphenols can raise the expression level of intestinal tight-junction proteins, they can reduce intestinal permeability, and the intestinal barrier can keep intact under these effects; these substances can also obviously lower the expression quantity of inflammatory cytokines, and they can block the activation process of Toll-like receptor 4 (TLR4) signal pathways [4]. Tea polyphenols can change intestinal barrier functions. These changes are realized through adjusting the expression state of intestinal epithelial cells, changing the secretion situation of mucus layers, and altering the composition of gut microbes [11]. These multiple effects together can stop the vicious cycle formed by inflammation and unbalanced flora, and these changes can offer structural support for the reconstruction of gut microecology. Bioactive substances extracted from tea can produce protective effects for intestinal barrier functions [8]. Human intestines can protect human bodies against harmful substances and pathogenic microbes, and physical barrier, chemical barrier, microbial barrier, and immune barrier will work together to realize this intestinal protective function. Tea polyphenols can improve non-alcoholic fatty liver disease, because these substances can reduce intestinal permeability and weaken liver inflammatory responses induced by endotoxin [3].

### 3.5. Mediate the balance of the gut-immune axis and regulate local intestinal immunity

Tea polyphenols can also take part in the adjustment process of local intestinal immune responses. These substances can obviously reduce the expression of inflammatory cytokines, and they can restrain the activation of TLR4 signaling pathways, so the inflammatory degree of the intestinal mucosa will decrease [4]. Active ingredients from tea can keep the immune barrier and biological barrier stable. These ingredients achieve this goal by adjusting inflammatory factor levels and changing gut microbial metabolic conditions [8]. The intestinal mucosal immune system and gut microbiota interact closely with each other; tea polyphenols can adjust this interactive network between immunity and microbes, and these adjustments can help human bodies maintain stable intestinal immune states, so the occurrence risk of chronic inflammatory diseases can be reduced.

## 4. Different characteristics of intestinal flora regulation by various tea polyphenols

### 4.1. Green tea polyphenols: highly effective in inhibiting bacteria and reducing inflammation

EGCG is the most abundant catechin substance in green tea. It can promote the growth of beneficial bacteria, restrain pathogenic bacteria, strengthen intestinal barrier performance, and boost short-chain fatty acid production, and these multiple effects are quite remarkable. One systematic review which sorts out pre-clinical and clinical research data clearly points out that green tea catechins can bring metabolic health benefits; these benefits come from improving unbalanced flora conditions, easing mucosal inflammation and oxidative injury, and strengthening intestinal barrier functions [9]. Metabolite products transformed from green tea catechins by microbes can play key roles in adjusting intestinal microecology and producing anti-inflammatory effects [1]. In the obese mouse models built with high-fat-diet feeding, green tea polyphenols can obviously slow down

DOI: 10.54254/2753-8818/2027.MB38698

weight-gain speed and shrink the volume of fat cells [4]. The interaction events between tea catechins and intestinal microbes will generate great influences on human physical health.

### 4.2. Oolong tea polyphenols: mild and long-lasting, maintaining microbiota homeostasis

Oolong tea belongs to the semi-fermented tea category; the polyphenol composition of oolong tea sits between green tea and black tea. Researchers summarized experimental data from animal tests, in-vitro fermentation tests, and human trials published from 2004 to 2024. These data record the different influences of tea products processed by different methods on gut microbiota, and oolong-tea-related results are also included in these records [2]. Tea products processed in different ways will produce different protective effects for intestinal barriers [8]. Oolong-tea-derived polyphenols can bring health-related effects. These substances can change microbial structure, increase short-chain fatty acid output, and repair the intestinal barrierrier tissues, and their acting intensity is relatively gentle while their effect duration is long. This feature makes oolong tea have unique advantages in long-term dietary intervention aimed at chronic metabolic diseases.

### 4.3. Fermented tea polyphenols: targeted regulation of metabolism, improving metabolically imbalanced microbiota

Fermented-tea products contain rich polyphenols and catechin derivative substances, and these tea products may become one feasible auxiliary means for obesity management. Fermented-tea-related substances can slow down weight gain and fat accumulation; these substances can support beneficial bacteria to grow and inhibit the reproduction of harmful bacteria [12]. Increased short-chain fatty-acid yield and recovered intestinal-barrier integrity will connect with improved insulin sensitivity and reduced inflammatory-marker levels. But researchers still face many obstacles to clinical application. For example, people need to set unified standards for fermentation technologies, and researchers need to complete accurate dosage evaluation work. Black tea and its main active components can exert influences on intestinal microbiota; these influences are realized through promoting metabolic reactions, offering nutrient sources, playing protective roles, and adjusting immune responses [7]. As we can observe in Figure 2, catechin substances from tea will go through complex oxidation and polymerization reactions to generate theabrownins. At the initial stage, tea catechins (including epicatechin, epigallocatechin, epicatechin gallate, and epigallocatechin gallate) are oxidized by polyphenol oxidase (PPO) and oxygen ($O_2$), and catechin quinones and gallocatechin quinones are generated from this oxidation reaction; these quinone substances carry out further oxidation and polymerization reactions, and theaflavins (TFs) are produced afterwards. Next, theaflavins will interact with microbes, polysaccharides, caffeine, protein substances, and lipid substances, and thearubigins (TRs) will form in this process. Finally, the rubigins will combine with these substances mentioned above, or quinone substances will directly react with microbes, polysaccharides, caffeine, protein substances, and lipid substances, and TBs will be obtained in the end [6]. The brown adipose tissue can greatly improve the obesity state induced by high-fat-diet feeding, and gut-microbiota adjustment may partly account for these beneficial effects. Even though the brownins have many kinds of biological activities, researchers still have difficulties in confirming their accurate molecular structure, optimizing large-scale production processes, and translating experimental results obtained from cell tests and animal tests into human clinical trials. The targeted adjustment features of fermented-tea-derived substances show good application prospects in the intervention work of obesity and related metabolic syndromes.

DOI: 10.54254/2753-8818/2027.MB38698

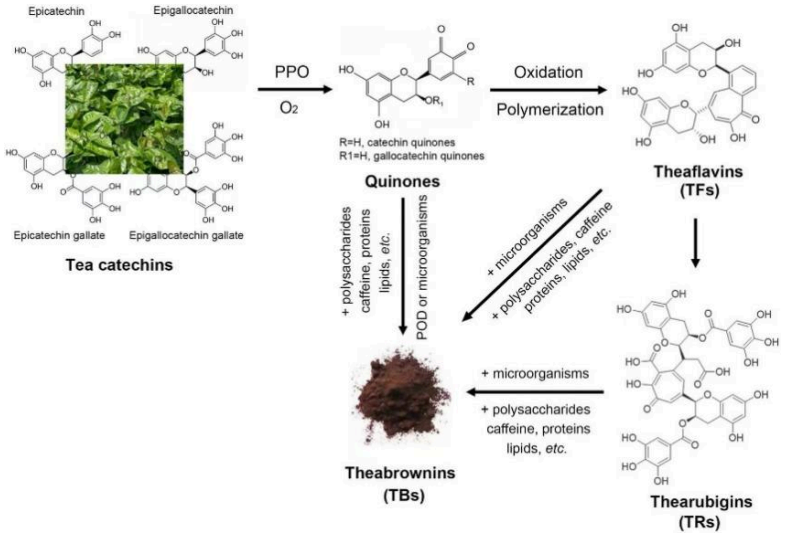



Figure 2. Formation pathway of theabrownins from tea catechins [3]

## 5. Future perspective

### 5.1. Limited study models and incomplete clinical evidence

Most research projects which explore the interaction relationships between tea polyphenols and gut microbiota adopt animal experiments or in-vitro fermentation models, and human clinical trial data are relatively scarce. One systematic review sorts out tea-and-gut-microbiota-related studies published from 2004 to 2024; these collected research works contain in-vivo animal feeding experiments, in-vitro human fecal fermentation experiments and human feeding trials. This review points out different experimental models will yield inconsistent research results, and researchers should discuss experimental results of each tea type under the three model categories separately [2]. Researchers have found many problems when they study the biological activity of catechin substances; recent clinical research can support the conclusions from pre-clinical experiments, but many obstacles still exist when people try to extend animal-model research conclusions to human trials, and some feasible research directions for follow-up intervention experiments have been put forward [9]. Fermented-tea products still have barriers to clinical application, people need to formulate standardized fermentation technical specifications, and researchers need to finish accurate dosage assessment work. These points restrict fermented-tea-related substances from being used as intervention tools for obesity treatment [12].

### 5.2. Unclear dose-response relationships and safety thresholds

Different research papers have adopted quite different dosage values for tea polyphenols; there is no unified dosage standard and complete safety evaluation system yet. Experimental data obtained from animal tests and human trials about different processed-tea products and gut microbiota can offer basic references for people to compare dose-effect relationships [2]. However, researchers still cannot confirm the optimal effective dosage and potential toxicity threshold, and this situation hinders the transformation toward clinical application. Most existing research works are finished on animal models; even though most experimental results confirm that tea polyphenols can adjust gut microbiota and resist obesity, the exact effective dosage is still not clear, and the toxicology research materials are not sufficient [10].

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### 5.3. Individual differences mechanisms unclarified

Host gut-microbiota composition will show differences among different people, and individual inner-self differences also exist; green tea catechins can greatly change intestinal microbial diversity, but gut-microbiota differences among individuals will change metabolite composition, and these changes will influence the final physiological effects brought by green tea catechins [1]. Follow-up research work should pay more attention to core functional microbial groups, instead of only analyzing microbial community composition; this research idea can help researchers predict individual microbial metabolic characteristics more accurately, and researchers can divide experimental subjects into specific "enterotypes" or "metabolic phenotypes." The metabolic capacity of colon microbes for catechin substances represents one key factor which leads to different health outcomes among different individuals [9].

### 5.4. Microscopic molecular interaction mechanisms need further exploration

Even though the brownins own multiple biological activities, researchers still have difficulties in confirming their accurate molecular structures, optimizing large-scale production processes, and translating experimental results obtained from cell experiments and animal experiments to human clinical trials. The complicated chemical structure of theabrownins makes it hard for researchers to find out their exact molecular constitution, and this condition prevents people from understanding the connection rule between their structure and function deeply [6]. Researchers still have not fully found out the exact molecular network, key metabolic enzymes, and signaling pathways which take part in the interaction process between EGCG and gut microbes. Researchers have identified 35 metabolite products from microbial transformation and put forward corresponding metabolic pathways with the help of in-vitro fermentation models, but the key enzyme systems and their coding genes which are responsible for green tea catechin microbial transformation need further exploration. People still do not understand the detailed molecular mechanisms for the interaction between catechin substances and gut microbiota very well [9]. Besides that, researchers need to carry out more in-depth research work to clarify how polyphenols improve non-alcoholic fatty liver disease with the help of gut-microbiota mediation [3].

## 6. Conclusion

This review sorts out the compositional features, intestinal metabolic pathways, and gut-microbiota-regulating mechanisms of tea polyphenols, and this paper mainly focuses on the two-way interaction situations between tea polyphenols and gut microbes. Gut microbes can break down tea catechins and turn them into low-molecular-weight metabolites such as phenyl-γ-valerolactone, phenolic acids, and short-chain fatty acids, and these metabolite products can greatly improve the absorption efficiency and biological activity of raw tea polyphenol substances. On the other hand, tea polyphenols can maintain the stable state of gut microbiota through five main approaches. These approaches include restraining pathogenic bacteria selectively, supporting beneficial-bacteria reproduction, promoting short-chain fatty-acid synthesis, repairing intestinal barrier structures, and adjusting local intestinal immune responses. Different tea-processing operations will change polyphenol composition, so different tea products will bring different adjustment effects on gut microbiota; green-tea-derived polyphenols show strong bacteriostatic performance and anti-inflammatory performance, oolong-tea-derived polyphenols exert gentle and long-lasting effects, and fermented-tea-derived polyphenols can target the unbalanced flora state caused by obesity.

DOI: 10.54254/2753-8818/2027.MB38698

Even though pre-clinical research has accumulated a large amount of experimental evidence, many defects still exist in current research work; human clinical trial data are still insufficient, dose-effect relationships and safety thresholds are not clearly defined, the causes of individual differences have not been fully explained, and the detailed molecular interaction networks between tea polyphenols and gut microbes need more exploration. Follow-up research projects should focus on building standardized clinical evaluation systems, confirming optimal effective dosage and safe dosage range, finding out the microbial basis which causes individual differences, and identifying key enzymes and signal pathways involved in tea-polyphenol-gut-microbiota interaction processes, so researchers can promote the application of tea polyphenols in precise-nutrition fields and metabolic-disease-intervention fields.

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