

REVIEW

The effects of green tea and curcumin on COMT and MAO pathways in nutrigenetics-based epigenetic approaches: Clinical benefits and the balanced management of psycho-oncological risks

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Abstract

The worldwide prevalence of all cancer types continues to rise. In this context, the psychological burden of cancer—particularly anxiety and depression—has emerged as a critical yet frequently overlooked component of comprehensive oncological care. In addition to clinical and psychosocial factors, growing evidence suggests that epigenetic mechanisms significantly influence both cancer biology and mental health, indicating that gene-environment interactions may affect psychological vulnerability in oncology contexts. Nutrigenetics-based epigenetic approaches enable personalized dietary and nutraceutical interventions based on individual genetic variability. Green tea catechins and curcumin are widely used bioactive compounds due to their epigenetic and anticancer potential. However, by altering the activity of catechol-O-methyltransferase (COMT) and monoamine oxidase (MAO), important enzymes that degrade dopamine, norepinephrine, and serotonin, these substances have an impact on monoaminergic neurotransmission. Functional polymorphisms in the COMT and MAO genes may lead to substantial interindividual differences in mood regulation, stress responsiveness, and anxiety susceptibility. This review addresses molecular, clinical, and psycho-oncological aspects of the effects of green tea and curcumin on COMT and MAO pathways within a nutrigenetics-based epigenetic nutrition framework. The findings emphasize that the potential clinical benefits of epigenetically active



nutraceuticals should be evaluated through a genotype-guided, individualized, and balanced approach.

Keywords: COMT, curcumin, epigenetic nutrition, green tea, MAO, nutrigenetics

Introduction

It is estimated that about 50.5 million people around the world have had cancer in the past five years. Even though the number of cancer survivors is rising, comprehensive care often ignores the psychological toll that cancer takes. Individuals with cancer frequently do not receive the necessary treatment for their psychological symptoms. These symptoms are often seen as a “normal” reaction to a cancer diagnosis or blamed on the physical symptoms that come with it (Carlson et al., 2023). Depression and anxiety are the most common mental health issues seen in cancer patients, no matter what stage of the disease, where the primary tumor is, or what phase of treatment they are in. These problems can range from mild emotional states like sadness, worry, concern, and heightened feelings of hopelessness to more serious mental illnesses like anxiety disorders and depressive disorders (Grassi et al., 2023).

Epigenetics is a big part of how cancer starts and grows. Our genes can also be affected by our current mental state, epigenetic processes, and environmental factors. Epigenetics can modify gene activity without altering the DNA sequence, presenting novel opportunities for cancer prevention and treatment. DNA methylation, histone modifications, non-coding RNA action, and nucleosome remodeling are all important epigenetic processes that are necessary for cells to grow and change properly. Nonetheless, their disruption is associated with the initiation of cancer. Epigenetics is a hot area for anti-cancer therapy because it targets epigenetic regulators whose activities are controlled by DNA methyltransferases (DNMTs) and histone deacetylases (HDACs), which stop cancer cells from growing. Phytochemicals, which are bioactive compounds found in fruits, vegetables, and seeds, are another way to deal with this besides traditional treatments. Researchers are looking into substances like curcumin, epigallocatechin-3-gallate (EGCG), genistein, resveratrol, quercetin, and sulforaphane more and more to see how they can gently change the epigenome through nutrition-based epigenetic modulation, which can make cells work better. Mechanisms have been documented (Bakrim et al., 2025; Meeran et al., 2010; Vrânceanu et al., 2022).

Green tea catechins, particularly EGCG and curcumin, defined as polyphenolic “epi-nutrients,” are capable of inhibiting DNA methyltransferases and histone deacetylases, modulating microRNA expression, and supporting the reactivation of tumor suppressor genes, thereby reducing cellular proliferation, angiogenesis, and metastasis (Bakrim et al., 2025; Carlos-Reyes et al., 2019; Henning et al., 2013; Reuter et al., 2011; Teiten et al., 2013; Vrânceanu et al., 2022). However, when these epigenetic mechanisms are considered in clinical practice, it should be recognized that the use of epigenetic interventions without accounting for individual nutrigenetic background may pose risks, particularly for mood regulation. Dopamine (DA), serotonin (5-HT), and norepinephrine (NE) are important monoamine neurotransmitters that control mood, behavior, and thought processes. In patients with cancer, mood disturbances are common due to environmental stressors, the psychological burden of the disease, and treatment-related factors. In this context, the effects of phytochemicals such as green tea and curcumin when used without knowledge of the underlying genetic background may intersect with monoaminergic neurotransmission via *COMT* and *MAO*,

potentially exacerbating anxiety, restlessness, or mood instability in certain oncology cases (Aronica et al., 2022; Carlson et al., 2023; Chen et al., 2005; Naoi et al., 2025).

Polyphenols in green tea work as both substrates and inhibitors of *COMT*, which is an important enzyme that breaks down catecholamines and EGCG. In addition, these polyphenols may inhibit *MAO*, which plays a critical role in the degradation of dopamine, serotonin, and norepinephrine. Functional *COMT* polymorphisms, particularly rs4680 (Val158Met), significantly influence catecholamine levels and anxiety susceptibility; individuals carrying low-activity *COMT* alleles may exhibit heightened sensitivity to catecholamine-modulating supplements, including green tea extracts (Aronica et al., 2022; Chen et al., 2005; Naoi et al., 2025). Curcumin also affects monoaminergic systems by acting as an antioxidant, anti-inflammatory, and epigenetic agent. These effects impact neuroprotective signaling pathways and are crucial in shaping monoamine-related psychiatric traits (Hassan et al., 2019; Ramaholimihaso et al., 2020). An expanding body of nutrigenetic evidence indicates that curcumin, green tea polyphenols, sulforaphane, and related phytochemicals may trigger restlessness, anxiety, or subjective discomfort in a genetically susceptible subgroup of individuals. Collectively, these findings strongly underscore the necessity of genotype-guided epigenetic nutrition strategies, particularly in clinical populations where neuropsychiatric vulnerability and environmental stressors coexist (Meral et al., 2024).

Methodology

This study was conducted as a narrative review aiming to synthesize current evidence on the interactions between nutrigenetics-based epigenetic approaches and *COMT*/*MAO* pathways, with a particular focus on green tea catechins and curcumin. A literature search was performed using major electronic databases, including PubMed, Scopus, and Web of Science. The search primarily included studies published between 2000 and 2025, with additional earlier landmark studies incorporated where necessary for conceptual background.

Relevant peer-reviewed articles were identified using combinations of keywords such as “nutrigenetics,” “epigenetics,” “*COMT*,” “*MAO*,” “green tea,” “curcumin,” “polyphenols,” “monoamine neurotransmitters,” and “cancer-related psychological outcomes.” Studies were included if they addressed molecular mechanisms, genetic polymorphisms, epigenetic regulation, or clinical/psychological effects related to the *COMT* and *MAO* pathways.

Given the narrative nature of this review, a formal systematic review protocol (e.g., PRISMA) was not followed. This represents a limitation of the study, as the selection process may be subject to potential bias. However, efforts were made to include high-quality, up-to-date, and conceptually relevant literature to provide a comprehensive and balanced overview of the topic.

Nutrigenetics-based epigenetic approach

Precision medicine

Precision medicine aims to ascertain how an individual's genetic composition, along with phenotypical and environmental influences, affects health risks. The concept of 4P medicine (predictive, preventive, personalized, and participatory) emerged from the recognition of health risks, which is crucial for the diagnosis and management of chronic diseases. Instead of using a one-size-fits-all strategy, this strategy emphasizes customized medical care (Çamlica & Eti Aslan, 2022; Tekpinar & Erdem, 2019). Individuals differ in their susceptibility to specific diseases and

in their responses to particular treatments. As a result, precision medicine promotes adjusting medical treatments to the particular needs of each patient. This method lowers the need for needless diagnostic procedures and treatments while simultaneously improving the quality of care provided by directing healthcare decisions toward the best course of action for a particular patient (Ginsburg & Phillips, 2018). A person's phenotype is directly impacted by the nutrigenomic effects of their diet. The nutrigenomic effects of nutrition directly influence an individual's phenotype. Dietary strategies and supplement selections planned according to an individual's genotype may enhance clinical outcomes and, importantly, contribute to improvements in patients' psychosocial well-being (Meral et al., 2024).

Responses to foods and nutrients are influenced not only by genetic background but also by dietary habits, which can affect gene expression via epigenetic mechanisms. Nutrigenetics and nutrigenomics focus on understanding how genetic and epigenetic differences determine individual reactions to diet, aiming to develop personalized nutrition strategies that account for variability in dietary preferences, needs, and responses (Bordoni & Gabbianelli, 2019).

Dietary epigenetic modulators: Curcumin and green tea

The importance of specific nutrients in activating epigenetic enzymes is a growing research focus that highlights the intricate link between diet and gene regulation. Certain dietary components can directly influence epigenetic enzymes, altering their activity and affecting epigenetic modifications (Abdul et al., 2017; Bakrim et al., 2025). For instance, curcumin, a bioactive compound in turmeric, is known to control histone-modifying enzymes, which shows how diet can affect epigenetic processes. Curcumin modulates the activity of histone acetyltransferases (HATs) and histone deacetylases (HDACs), thereby influencing genes associated with inflammation, cancer, and neurodegenerative disorders (Hassan et al., 2019).

The primary polyphenol in green tea, epigallocatechin-3-gallate (EGCG), has been shown to inhibit DNA methyltransferases (DNMTs). EGCG can change DNA methylation patterns and gene expression by stopping DNMT activity. Because of these qualities, EGCG has become very popular as a natural epigenetic regulator that could be used to prevent and treat cancer (Singh et al., 2011). However, the effects of these dietary components, commonly used in oncology, on enzymes like *COMT* and *MAO* go beyond their epigenetic and anticancer roles. They may also impact the psychological well-being and mood of cancer patients. This underscores the need to consider both genetic and psychosocial factors when integrating epigenetically active dietary elements into clinical practice.

COMT polymorphisms, phenotypic responses, and interaction with green tea

COMT polymorphisms

Individual variations in *COMT* activity, among the genetic differences that influence psychosocial traits, have been linked to a wide range of neuropsychiatric and neurodegenerative conditions that rely on dopamine and norepinephrine signaling. In this context, *COMT* polymorphisms have been associated with various cognitive phenotypes, psychiatric disorders, as well as changes in brain activation patterns and structural features (Antypa et al., 2013; Bastos et al., 2017; Witte & Flöel, 2012).

Catecholamines such as epinephrine, norepinephrine, and dopamine, along with catechol estrogens, certain pharmaceuticals (e.g., L-DOPA), and xenobiotics are influenced by the enzyme *COMT*. The main job of the *COMT* enzyme, which is made by the *COMT* gene, is to move a methyl group from S-adenosylmethionine (SAM) to catechol substrates. This O-methylation process is one of the main ways that dopamine, epinephrine, and norepinephrine break down, and it is very important for keeping their levels in check (Aronica et al., 2022; Bastos et al., 2017; Chen et al., 2004). Polymorphisms in the *COMT* gene can significantly influence both the expression level and enzymatic activity of *COMT*. One of the most well-characterized functional variants is the rs4680 polymorphism (Val158Met, G>A), located in exon 4 of the gene, which results in the substitution of valine with methionine. This single-nucleotide polymorphism causes significant differences in *COMT* enzyme activity, resulting in three main phenotypes: the A/A genotype is linked to low *COMT* activity, the A/G genotype to intermediate activity, and the G/G genotype to high activity. Notably, the rs4680 A allele is connected to a *COMT* enzyme with about 40% lower activity compared to the G allele. Reduced *COMT* activity has been linked to elevated anxiety levels, increased neuropsychiatric vulnerability, and heightened sensitivity to environmental toxins (Aronica et al., 2022; Chen et al., 2004; Mir et al., 2018).

Phenotypic responses

Genetic links between the *COMT* gene and various psychiatric traits often differ between women and men. Although some of these differences remain unconfirmed or show small effect sizes, several findings display reasonable consistency and strength. The functional Val(158)Met polymorphism in the *COMT* gene has been associated with obsessive–compulsive disorder (OCD) in males and anxiety traits in females; furthermore, its impact on cognitive function is more pronounced in boys than in girls (Harrison & Tunbridge, 2008). Another meta-analysis supports the Val158Met polymorphisms as a risk factor for OCD, particularly in men, consistent with these findings. Overall, these data imply that *COMT* might influence OCD development through dopaminergic pathways and that genetic risk could vary depending on sex (Kumar & Rai, 2020).

Although few studies have directly examined *COMT* genotypes in cancer patients, a study involving women with breast cancer found that those with the Met/Met genotype of the *COMT* Val158Met polymorphisms had higher anxiety scores compared to those with at least one Val allele (Val/Val or Val/Met). These findings suggest that lower *COMT* enzyme activity may increase catecholamine levels, which could contribute to stress-related conditions like anxiety disorders in this group (Hajj et al., 2021).

Interaction with green tea

This genetic background is important for explaining why the effects of dietary bioactive compounds may vary substantially among individuals. Catechin polyphenols found in green tea, particularly EGCG, have the capacity to inhibit the *COMT* enzyme (Chen et al., 2005; Lu et al., 2003). However, in individuals with low *COMT* activity, slower catechin metabolism may disrupt neurotransmitter balance, thereby increasing the risk of anxiety and neuropsychiatric symptoms. Conversely, *COMT* inhibition may confer therapeutic advantages in certain clinical contexts. A notable instance is the clinical application of *COMT* inhibitors in Parkinson's disease to augment the bioavailability of levodopa in the brain. Experimental studies have demonstrated that both EGCG and green tea extract can exert neuroprotective effects in patients with Parkinson's disease (Afzal et al., 2015; Rivest et al., 1999). Overall, these results indicate that catechin-based nutraceuticals might be more effective for genotypes with higher *COMT* activity and emphasize the need for nutrigenetics-based, personalized dietary and supplement strategies.

MAO polymorphisms, phenotypic responses, and interactions with green tea and curcumin

MAO polymorphisms

Monoamine oxidases (MAOs) are genes frequently studied in behavioral genetics, located on the X chromosome. These mitochondrial enzymes help break down neurotransmitters like dopamine, norepinephrine, and serotonin by oxidative deamination in the brain and other tissues. Consequently, MAOs are crucial for maintaining neurotransmitter balance. Levels of the *MAOA* enzyme have been linked to the regulation of human behavior and personality traits (Edmondson et al., 2005; Sarwar et al., 2021; Shih et al., 1999). Reduced *MAO* activity causes a slower breakdown of monoamines, leading to higher levels of these neurotransmitters, especially dopamine a biochemical state linked to the development of schizophrenia. In fact, it has been reported that the presence of the *MAO* rs6323 T allele, associated with low *MAO* activity, along with increased dopamine levels, may contribute to the emergence of positive symptoms of schizophrenia (Tanifuji et al., 2021). When combined, these results show that genetic differences in *MAO* offer a crucial key to comprehending behavioral characteristics, neurotransmitter metabolism, and the biological causes of neuropsychiatric disorders.

Phenotypic responses

Some studies have shown that individuals carrying genetic polymorphisms associated with low *MAO* activity may exhibit atypical or exaggerated emotional responses to environmental and social stimuli (Print. Specifically, studies examining the link between the *MAO-A* rs6323 (T941G) polymorphism and aggression have shown a positive association between the G allele and a higher risk of aggressive and violent behavior. Conversely, the T allele has been linked to reduced aggressive tendencies and is thought to have a protective effect (Sarwar et al., 2021). These findings indicate that *MAOA* activity may represent a key biological mechanism underlying emotional regulation and behavioral responses. According to a recent study, major depressive disorder symptom severity is substantially correlated with *MAO-A* polymorphisms. This association was particularly pronounced in individuals with adverse childhood experiences, in whom higher depression severity was observed, with the effect being more evident in women. When considered in conjunction with environmental stressors, this effect appeared to be further amplified (Toledo-Lozano et al., 2023). A significant class of medications used to treat depression and other neurological conditions are monoamine oxidase inhibitors (*MAOIs*) (Chaurasiya et al., 2022). *MAO* inhibitors may be clinically appropriate in people with high *MAO* enzymatic activity.

Interactions with green tea and curcumin

Curcumin is thought to be an antioxidant that helps with different metabolic diseases. It may also have potential *MAO* inhibitory activity by downregulating the enzymes that breakdown the monoamine neurotransmitters which are important for neural growth and functioning. Khatri and Juvekar (2016) have proposed curcumin as a potential *MAO* inhibitor for the management of Parkinson's disease and other neuromuscular disorders. EGCG can also inhibit monoamine oxidase (*MAO*) activity. Research on varying tea types and their effects on *MAO* discovered that green tea has the highest levels of inhibition of all the *MAO* isoforms when compared to other teas (Topaz et al., 2019; Yüce-Dursun, 2017). A study on cancer patients found that the regression coefficient of *MAO* with depression was positive. *MAO* activity is likely a marker of psychological adjustment (IA) problems in those suffering

from cancer, and it may be a risk factor for survival. Additional research involving larger patient cohorts may corroborate this assertion (Giraldi et al., 2007).

Nutrigenetics-based personalized nutrition

The primary objective of nutrigenetics-based nutrition is to develop individualized dietary and supplement plans tailored to an individual's genetic profile, rather than applying standardized approaches in which the same diets and supplements are recommended for everyone. This strategy not only enhances clinical effectiveness but also helps prevent unnecessary and uncontrolled supplement use (Koç, 2018). Nutrition represents one of the most powerful yet modifiable environmental factors influencing epigenetic regulation. Accordingly, nutrigenetic and nutri-epigenetic approaches aim to personalize food and supplement selection based on genetic variants. However, particularly in individuals diagnosed with cancer, such interventions may influence not only biological processes but also psychological well-being. This underscores the importance of addressing nutrigenetics-based approaches within a holistic framework that considers both biological and psychosocial dimensions.

Conclusion

In patients with cancer, anxiety, restlessness, and mood disturbances are shaped not only by the disease itself, treatment-related biological stress, inflammation, and environmental factors, but also by individual genetic susceptibilities. Despite this, psychological outcomes are frequently treated as secondary or are often overlooked altogether in many nutrition-based or phytochemical support studies conducted in oncology. Due to their anticancer and anti-inflammatory qualities, curcumin and green tea catechins are frequently advised as supplements to cancer treatment; however, their effects on the central nervous system and their interactions with individual genetic variability have not been thoroughly studied. Current research shows that *MAO* biology interacts with both psychological adaptation and cancer progression, and it also points to a possible link between *COMT* genotype and anxiety levels in cancer patients. Nevertheless, no clinical research has yet directly compared how common phytochemicals, like curcumin or green tea, affect mood differently depending on *COMT* and *MAO* genotypes in cancer populations. This draws attention to a significant gap in the body of current research. Future research in this area should focus on measuring anxiety and depression levels using validated scales, thoroughly documenting the use of phytochemicals, and evaluating *COMT* and *MAO* variants in cancer patients. Such an approach is critical for the development of personalized supportive strategies. Importantly, it may reveal that certain natural compounds widely regarded as “safe for everyone” can induce adverse psychological effects in genetically susceptible subgroups of patients, thereby contributing to the advancement of a more holistic and individualized model of supportive care in oncology.

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Conflict of interest

The authors declare that they have no conflict of interest related to this study.

Data availability statement

The data and materials included in this review are based on previously published scientific studies and are publicly accessible through the relevant journals or academic databases in which they were originally reported. All references to the studies reviewed are provided in detail in the reference list of this article. No original data were generated as part of this review; therefore, no study-specific datasets or data repositories are associated with this publication. Readers who wish to access the full texts of the cited studies are encouraged to consult the appropriate academic databases or to contact the authors of the original publications directly. Care has been taken to ensure that all sources are accurately cited and that the information presented in this review reflects the current state of the literature.

Ethics committee approval

Not applicable.

Authors' contribution statement

Conceptualization: G.M.; Writing – original draft: G.M., E.S.A., N.B.; Writing – review & editing: G.M., E.S.A., N.B., M.O., E.G.A.A.; Supervision: G.M., E.S.A.

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