

Targeting the NF- κ B–Epigenetic axis using nutraceutical in chronic inflammatory disease management

Maya G. Pillai¹, S. Abhirami¹, D.S. Amrutha¹, Mani Sebastian¹, R. Haritha¹, D. Aashish², V.S. Salu¹, Yara Nader¹, Akhlaq A. Mehra¹, Helen Antony¹

¹Department of Biochemistry, University of Kerala, Kariavattom Campus, Thiruvananthapuram,

²Department of Zoology, Mahatma Gandhi College, Thiruvananthapuram, Kerala, India

Corresponding author: Helen Antony, Email: helenabios@keralauniversity.ac.in

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Abstract

Chronic inflammatory diseases, including cardiovascular disorders, metabolic syndrome, autoimmune diseases, cancer, and neurodegenerative conditions, are driven largely by continuous activation of nuclear factor kappa-B (NF- κ B) signalling. While NF- κ B is recognized as a transcription factor regulating immune and inflammatory gene expression, emerging evidence demonstrates that NF- κ B activity is tightly controlled through epigenetic mechanisms such as DNA methylation, histone modifications, chromatin remodelling, and non-coding RNA regulation. Dietary polyphenols have gained increasing attention as epigenetic modulators of this NF- κ B signalling pathway. This review focuses on current advances in understanding how dietary polyphenols including resveratrol, curcumin, epigallocatechin gallate (EGCG), quercetin, genistein, fisetin, luteolin, and epicatechin regulate inflammatory signalling through epigenetic reprogramming. These compounds influence DNA methyltransferases, histone acetyltransferases, histone deacetylases, Silent Information Regulator T1 (SIRT1) activation, and microRNA networks, ultimately reducing NF- κ B p65 acetylation, suppressing transcriptional activation of pro-inflammatory genes, and restoring immune homeostasis. Evidence from experimental studies reveal the potential of these polyphenols in managing chronic inflammatory disorders like atherosclerosis, type 2 diabetes, rheumatoid arthritis, cancer, and neuroinflammatory disorders. Despite promising insights, translational challenges remain, including limited bioavailability, variability in metabolism, optimal dosing strategies, and potential epigenome-wide effects. Future studies integrating nutrigenomics, epigenomics, systems biology, and clinical trials are required to validate polyphenol-based interventions. Targeting the NF- κ B–epigenetic axis is an innovative strategy for precision therapeutics and management of chronic inflammatory diseases through dietary and nutraceutical approaches.

Keywords: NF- κ B; Epigenetic regulation; Nutraceutical polyphenols; Chronic inflammation; DNA methylation; Histone modification.

Introduction

Inflammation is the immune system's response to harmful stimuli, such as pathogens, damaged cells, toxic compounds,

or irradiation,^[1] and acts by removing injurious stimuli and initiating the healing process.^[2] Inflammation is therefore a vital defence mechanism for health. Acute

inflammation has a rapid onset, typically resolves within a few days, exhibits typical signs and symptoms, and is characterised by a cellular infiltrate primarily consisting of neutrophils.^[3] The erythema observed in acute inflammation results from increased blood flow triggered by various mediators, like histamine acting on vascular smooth muscle cells. This process initially affects the arterioles and opens new capillary beds in the affected area.^[4] Lymphatic vessels are active in acute inflammation. During inflammation, lymph flow increases, facilitating the drainage of oedema fluid that accumulates as a result of increased vascular permeability.

Along with fluid, leukocytes, cell debris, and microbes may also enter the lymph.^[5] Similar to blood vessels, lymphatic vessels proliferate during inflammatory reactions to handle the increased load^[6]. Thus, the acute inflammation is a protective mechanism that removes the injurious stimuli and initiates a healing process, restoring the homeostasis of the organism.^[2] Uncontrolled acute inflammation, however, can become chronic, and may provide the basis of a variety of serious, chronic diseases.^[4-6]

Chronic inflammatory diseases constitute a major global health challenge, contributing significantly to morbidity and mortality worldwide. It is estimated that approximately 43 million individuals were affected by these diseases in 2021, accounting for more than 75% of non-pandemic deaths globally. In the same year, 18 million deaths occurred before the age of 70, of which 82% were reported in low- and middle-income countries. Cardiovascular diseases were the leading cause of mortality among non-communicable diseases (NCDs) causing 19 million deaths, followed by cancers (10 million), chronic respiratory diseases (4 million), and diabetes (over 2 million including kidney disease deaths caused by diabetes). Together, these

four groups of diseases accounted for 80% of all premature NCD deaths.^[7]

Despite advances in pharmacological therapy, existing treatments mainly focus on slowing disease progression, managing complications, and controlling risk factors rather than reversing by addressing upstream molecular regulators of inflammation.^[8] Persistent activation of inflammatory signalling pathways results in cytokine imbalance, oxidative stress, endothelial dysfunction, and progressive organ damage.^[9]

The transcription factor nuclear factor-κB (NF-κB) functions as a master regulator of inflammation by controlling genes involved in immune activation, cell survival, and stress responses.^[10] Dysregulated NF-κB signalling has been implicated in chronic inflammatory disorders like atherosclerosis, chronic obstructive pulmonary disease, chronic kidney disease, metabolic disorders, and neurodegenerative conditions.^[11]

Recent discoveries highlight that inflammatory signalling is not governed solely by genetic mechanisms but is profoundly influenced by epigenetic regulation. DNA methylation patterns, histone modifications, and microRNA networks determine chromatin accessibility and transcriptional activation of inflammatory genes. Importantly, epigenetic modifications are dynamic and responsive to environmental and dietary factors.^[12,13]

Nutraceutical polyphenols bioactive compounds abundant in fruits, vegetables, tea, spices, and medicinal plants—have attracted considerable interest for their ability to modulate epigenetic enzymes and signalling pathways. Rather than acting merely as antioxidants, these compounds influence transcriptional programming of inflammatory pathways, particularly the NF-κB axis.^[14,15]

Chronic inflammatory diseases are increasingly understood not merely as conditions of persistent immune activation but as disorders of maladaptive inflammatory memory. Repeated environmental, metabolic, and lifestyle stimuli induce stable epigenetic alterations that maintain inflammatory gene accessibility even after removal of the initial trigger.^[16,17] Within this framework, NF- κ B functions not only as an inducible transcription factor but as an epigenetic regulator that recruits chromatin-modifying enzymes, establishes transcriptional memory, and sustains inflammatory signalling programs.

Emerging evidence suggests that nutraceutical polyphenols do not simply suppress inflammation transiently; rather, they may reprogram inflammatory chromatin states, restoring regulatory balance through coordinated modulation of DNA methylation, histone acetylation, and non-coding RNA networks.^[14,18]

This review therefore examines chronic inflammatory diseases through the lens of the NF- κ B–epigenetic switch, positioning dietary polyphenols as potential agents in nutraceutical therapy capable of reversing pathological inflammatory memory.

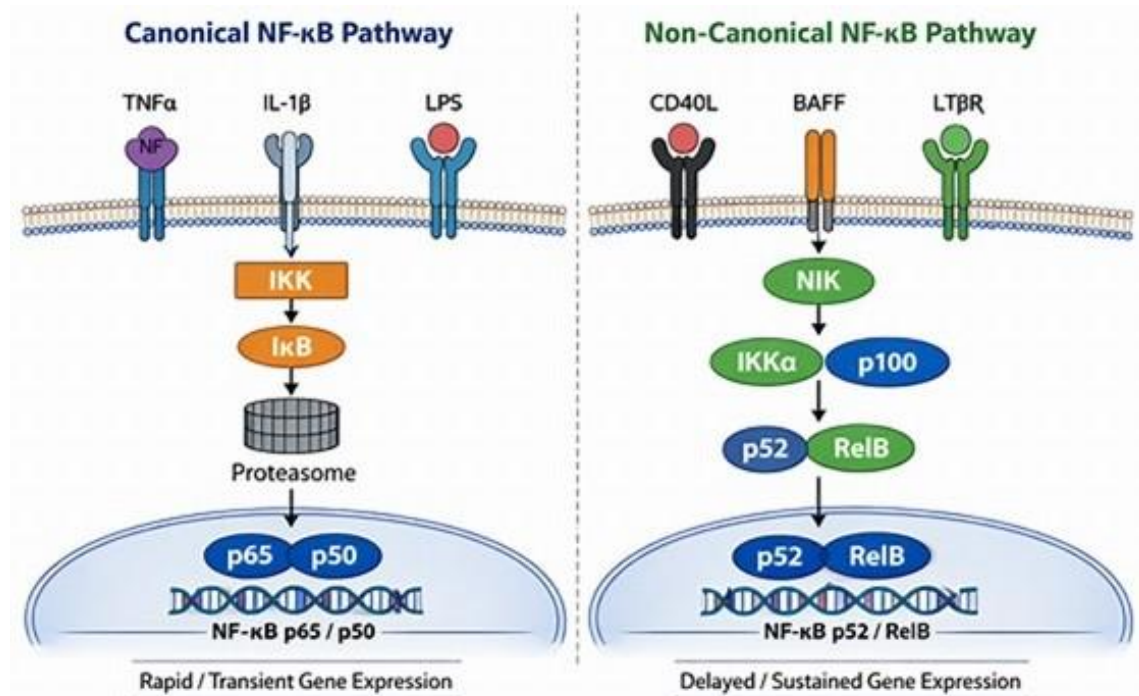
Nf- κ B signalling in inflammation

Nuclear factor κ B (NF- κ B) was first identified in B cells in 1986, where it bound to the enhancer element of the κ -IgG chain gene.^[19] Since then, NF- κ B has been recognized as a family of inducible transcription factors expressed in nearly all cell types, regulating apoptosis, cell cycle progression, immune responses, and inflammation.^[20,21] The NF- κ B family consists of five members—NF- κ B1 (p50), NF- κ B2 (p52), RelA (p65), RelB, and c-Rel—which form homo- or heterodimers that bind to κ B enhancer DNA elements to

regulate transcription.^[22,23] In resting cells, NF- κ B dimers are sequestered in the cytoplasm by inhibitory proteins of the I κ B family, of which I κ B α being the most studied. Precursor proteins p105 and p100 also act as I κ B-like inhibitors due to their C-terminal ankyrin repeat domains.^[24–26]

NF- κ B is activated in response to inflammatory stimuli such as cytokines, oxidative stress, microbial products, and metabolic imbalance. Activation commonly occurs through Toll-like receptor signalling and cytokine receptor engagement, leading to phosphorylation and degradation of inhibitory I κ B proteins. This process allows NF- κ B dimers to translocate into the nucleus and initiate transcription of pro-inflammatory genes.^[27,28] Key NF- κ B-regulated mediators include Tumour necrosis factor- α (TNF- α), Interleukin-6 (IL-6), Interleukin-1 β (IL-1 β), Cyclooxygenase-2 (COX-2), and Inducible nitric oxide synthase (iNOS).^[29]

Sustained NF- κ B activation promotes chronic inflammation, oxidative damage, fibrosis, and metabolic dysfunction; therefore, modulation of NF- κ B signalling represents a critical therapeutic target.^[30] The NF- κ B pathways that cells use to transmit signals to the nucleus include two primary mechanisms, known as the canonical and non-canonical NF- κ B pathways, which, are schematically outlined in Figure 1. These two pathways rely on completely different receptor systems, proteins, and timelines to control gene expression. In the *canonical pathway*, ligands (such as TNF- α , IL-1 β , and LPS) bind to their respective receptors, activating the IKK kinase complex. This complex phosphorylates I κ B, triggering its degradation by the proteasome and releasing the p65/p50 dimer. The dimer then rapidly translocate to the nucleus to activate pro-inflammatory genes. This response is eventually terminated by the resynthesis of



I κ B=Inhibitor of nuclear factor kappa B; IKK=*I κ B* kinase complex; IKK α =*I κ B* kinase alpha subunit; NIK=NF- κ B-inducing kinase; TNF α , IL-1 β , LPS, CD40L, BAFF, and Lt β are ligands.

Figure 1. Schematic illustration of the canonical (left) and non-canonical (right) NF- κ B pathways. Ligand binding to their respective receptors activates upstream kinases, leading to the degradation or processing of cytoplasmic inhibitors, followed by the release of the active nuclear factor dimers. The dimers then translocate to the nucleus and bind to specific DNA enhancer elements to regulate target gene transcription.

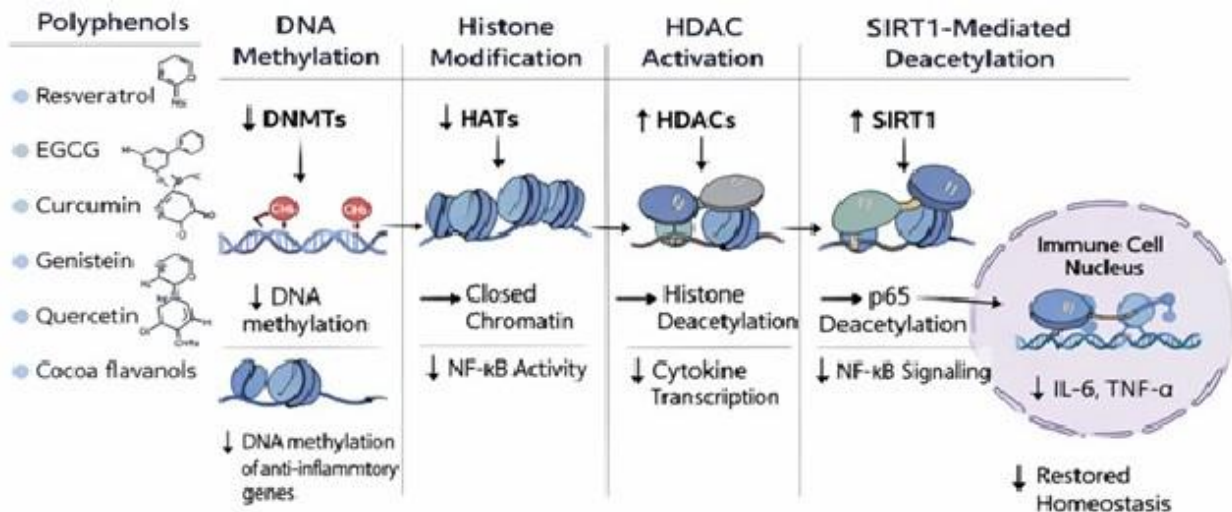
I κ B and its subsequent rebinding to nuclear factors, p65 and p50. In contrast, in the *non-canonical pathway*, ligands (such as CD40L, BAFF, and LT β) activate a distinct cascade mediated by NF- κ B-inducing kinase (NIK) and its subunit, IKK α . This induces partial proteasomal processing of the precursor p100 into p52, generating the active p52/RelB dimer to drive a delayed, sustained transcriptional response.

Epigenetic regulation of nf-kb activity

Epigenetic mechanisms determine the magnitude and duration of NF- κ B-mediated transcription. Immune tolerance is a highly regulated state and involves diverse mechanisms. Central to the induction of tolerance is the targeted modulation of T-cell

activities of both effector and regulatory T-cell activities, in which transcription factors play a significant role. Members of the NF- κ B family of transcription factors are critically involved in diverse T-cell responses and are regulated by multiple mechanisms that maintain immune tolerance and T-cell homeostasis.^[30,31]

NF- κ B, as a transcription factor, has been extensively studied in recent decades, and the molecular mechanisms that regulate NF- κ B activities have been well documented. However, recent studies have revealed exciting new roles for NF- κ B; in addition to its transcriptional activity, NF- κ B can also activate diverse epigenetic mechanisms that mediate extensive chromatin remodelling of target genes to regulate T-cell activities.^[32,33]



DNMT=DNA methyl transferase; EGCG=Epigallocatechin-3-gallate; HAT=Histone acetyltransferase; HDAC=Histone deacetylase; SIRT1=Sirtuin 1 (or Silent Information Regulator 1)

Figure 2: Modulation of DNMTs, HATs, and HDACs by polyphenols in immune regulation. Polyphenols suppress inflammation and help restore immune homeostasis through multiple epigenetic mechanisms by inhibiting DNMTs, thereby promoting the production of anti-inflammatory mediators through hypomethylation of genes involved; by inhibiting HATs, thereby influencing inflammatory signalling pathways through modulating chromatin structure; and by activating HDACs and SIRT1, thereby reducing the production of pro-inflammatory mediators through silencing specific genes.

Recent discoveries have expanded our understanding of NF κ B factor. Beyond its classical role in gene transcription, NF- κ B has now been shown to influence epigenetic processes (Figure 2). Through these mechanisms, NF- κ B exerts broad control over T-cell function, revealing new dimensions of its role in immune regulation.^[33,34]

DNA methylation

DNA methyltransferases (DNMTs) regulate the methylation of promoter regions of inflammatory genes. Hypomethylation enhances transcription of cytokine genes, whereas hypermethylation suppresses anti-inflammatory mediators.^[35]

DNA methylation involves the covalent addition of a methyl group to the 5' carbon of cytosine residues within CpG dinucleotides, catalysed by a family of DNA methyltransferases (DNMT1, DNMT3A, DNMT3B). This modification typically acts

as a transcriptional repressor, silencing gene expression by hindering transcription factor binding and recruiting methyl-CpG binding proteins.^[36,37] In chronic inflammatory diseases, promoter hypomethylation enhances transcription of cytokine genes (e.g., TNF, IL6, CXCL8), whereas hypermethylation suppresses anti-inflammatory mediators such as suppressors of cytokine signalling (SOCS) and PPAR- γ . Aberrant DNA methylation patterns have been identified as biomarkers and functional contributors in atherosclerosis, type 2 diabetes, chronic obstructive pulmonary disease (COPD), and rheumatoid arthritis.^[38,39]

Resveratrol has been shown to increase CpG methylation at the promoters of pro-inflammatory cytokine genes (IL-1, IL-6, TNF- α , IFN- γ) while decreasing methylation at the IL-10 gene promoter in the arterial intima of diabetic rats, correlating with reduced systemic inflammation and

endothelial protection.^[40–42] Epigallocatechin gallate, (EGCG) a natural antioxidant compound found mainly in green tea inhibits DNMT activity and has been shown to reactivate methylation-silenced genes in cancer cell lines, some of which are negative regulators of NF- κ B.^[43,44] Curcumin modulates DNMT function in models of diabetic retinopathy and colon cancer, contributing to epigenetic reprogramming of inflammatory and tumour suppressor gene networks. Consumption of cocoa flavanols has been shown to reduce global DNA methylation in peripheral leukocytes in a randomized trial, with implications for cardiovascular inflammatory risk.^[45–47]

Histone modifications

Histone acetylation promotes chromatin relaxation and transcriptional activation. Histone acetyltransferases enhance NF- κ B activity, whereas histone deacetylases (HDACs) suppress inflammatory gene expression.^[48]

HAT inhibition is the most widely reported epigenetic mechanism through which dietary polyphenols suppress NF- κ B. The HATs p300 and CBP function as transcriptional co-activators for the p65 subunit: when recruited to NF- κ B target gene promoters, they acetylate both histone H3/H4 tails and the p65 subunit itself at K310, amplifying transcriptional output. Several polyphenols directly inhibit p300/CBP acetyltransferase activity, thereby reducing p65 acetylation and chromatin remodelling at inflammatory gene promoters.^[14,49,50]

Curcumin is among the most potent dietary HAT inhibitors described to date. It inhibits p300 acetyltransferase activity *in vitro* with an IC₅₀ (half maximal inhibitory concentration) in the micromolar range and has been shown to reduce p65 acetylation and NF- κ B transcriptional activity in multiple cell models, including human monocytes and

synovial fibroblasts. In THP-1 monocytes under high-glucose conditions, curcumin significantly reduces HAT activity and p300 protein levels while simultaneously inducing HDAC2 expression, resulting in decreased production of IL-6 and TNF- α .^[51,52]

EGCG, the predominant catechin in green tea, likewise potently inhibits p300/CBP HAT activity. Choi and colleagues demonstrated that EGCG-mediated HAT inhibition led to p65 hypoacetylation and suppressed TNF- α -induced expression of IL-6, COX-2, and iNOS in multiple cell types. Similarly, quercetin has been shown to suppress p300 activity in breast cancer and endothelial cells, reducing p300-mediated acetylation of the p65 subunit and downstream angiogenic and inflammatory gene expression.^[53,54]

HDAC activation and SIRT1-mediated deacetylation

In parallel with HAT inhibition, many polyphenols promote the deacetylation of p65 and inflammatory gene histones by activating HDACs, particularly the NAD⁺-dependent deacetylase SIRT1. SIRT1 occupies a privileged position in NF- κ B regulation: it directly deacetylates p65 at K310, the key activating acetylation site, and has been shown to inhibit NF- κ B-mediated transcription and reduce inflammatory cytokine production in macrophages and other immune cells.^[55,56]

Resveratrol is the archetypal SIRT1-activating polyphenol. It directly activates SIRT1 through an allosteric mechanism, enhancing its catalytic activity towards p65 and other substrates. Pan and colleagues demonstrated that resveratrol-induced SIRT1 activation suppressed TNF- α -induced NF- κ B and p38 MAPK signalling in human umbilical vein endothelial cells (HUVECs), protecting against endothelial inflammation.^[57] In a randomized controlled trial in type 2 diabetes patients, resveratrol supplementation over six

months significantly increased SIRT1 expression in peripheral blood mononuclear cells, correlated with reduced H3K56 acetylation and decreased NF- κ B-dependent inflammatory gene expression.^[58–62]

Genistein, the soy isoflavone, similarly increases SIRT1 expression, leading to downstream inhibition of NF- κ B p65 and reduction of IL-1 β levels in experimental models of diabetes.^[63,64] Combined treatment with luteolin and fisetin has been shown to synergistically activate SIRT1 while suppressing HAT activity, providing additive anti-inflammatory effects in THP-1 monocytes. The convergence of HAT inhibition and HDAC/SIRT1 activation by polyphenols—operating in concert to reduce p65 acetylation and NF- κ B activity—represents a robust and potentially synergistic therapeutic strategy.^[65,66]

Non-coding RNA regulation

MicroRNAs such as miR-146a and miR-155 modulate NF- κ B signalling by targeting pathway components, thus providing an additional regulatory layer. Non-coding microRNAs (miRNAs) regulate NF- κ B signalling at multiple levels, by targeting upstream regulators (e.g., I κ B α , IKK subunits), the p65 subunit itself, and downstream effectors (Table 1). Several oncomiRs and inflammation-associated miRNAs are themselves NF- κ B transcriptional targets, creating regulatory feedback loops. Dietary polyphenols are emerging as significant modulators of these miRNA networks.^[67]

Genistein regulates miRNA-155, a key pro-inflammatory miRNA that normally suppresses Suppressor of Cytokine Signalling 1 (SOCS1), a negative regulator of the NF- κ B pathway. By upregulating SOCS1 through miRNA-155 suppression, genistein inhibits NF- κ B-mediated inflammation in

endothelial cells exposed to oxidized LDL.^[68,69] Curcumin has been shown to alter miRNA expression profiles in pancreatic cancer cells, affecting pathways that regulate NF- κ B activity. Resveratrol and its analogue pterostilbene modulate miRNA-mediated regulation of SIRT1 and DNMT expression in prostate cancer models, with anti-inflammatory consequences.^[70,71]

Disease-specific implications

Cardiovascular disease and atherosclerosis

NF- κ B-driven endothelial inflammation is a central event in atherogenesis, promoting expression of adhesion molecules, monocyte recruitment, and smooth muscle cell proliferation. Resveratrol, through SIRT1-mediated p65 deacetylation, has been shown to suppress TNF- α -induced NF- κ B activation in HUVECs, with protective effects on endothelial function.^[72–75] Genistein modulates the miRNA-155/SOCS1/NF- κ B axis to reduce oxidized LDL-induced endothelial inflammation.^[76,77] Cocoa epicatechin consumption reduces DNA methylation in leukocytes of individuals with cardiovascular risk factors in a clinical RCT. These findings collectively support a role for dietary polyphenols as epigenetic cardioprotective agents operating through NF- κ B inhibition.^[78,79]

Type 2 diabetes and metabolic syndrome

Chronic low-grade NF- κ B-driven inflammation in adipose tissue, liver, and immune cells contributes fundamentally to insulin resistance and the progression of type 2 diabetes. Curcumin, EGCG, fisetin, and luteolin have each been shown to suppress NF- κ B-dependent cytokine production in monocytes under high-glucose conditions by inhibiting HAT activity and activating HDACs. In a clinical randomized controlled trial resveratrol supplementation in type 2

Table 1. Dietary polyphenols: Epigenetic targets and effects on NF- κ B signaling

Polyphenol	Dietary source	Epigenetic mechanism	Effect on NF- κ B signalling
Resveratrol	Grapes, red wine	SIRT1 activation, DNMT modulation	Deacetylates p65; inhibits NF- κ B-mediated transcription; reduces IL-6, TNF- α
Curcumin	Turmeric	HAT inhibition, HDAC/DNMT modulation, miRNA regulation	Reduces p65 acetylation; inhibits I κ B α phosphorylation; downregulates COX-2, iNOS, TNF- α , IL-6
EGCG	Green tea	HAT inhibition, DNMT inhibition, HDAC activation	Hypoacetylates p65; suppresses NF- κ B-mediated IL-6, COX-2, iNOS
Quercetin	Onions, broccoli, blueberries	HAT inhibition (p300/CBP)	Suppresses p300-mediated NF- κ B acetylation; blocks NF- κ B binding to pro-inflammatory gene promoters
Genistein	Soy, legumes	DNMT inhibition, HAT activation, SIRT1 activation, miRNA	Increases SIRT1; reduces NF- κ B and IL-1 β ; modulates miRNA-155/SOCS1
Fisetin	Vegetables, strawberries	HDAC activation, HAT inhibition	Deacetylates p65; suppresses cytokine release via NF- κ B pathway
Luteolin	Parsley, celery	HDAC activation, HAT/p300 inhibition	Deacetylates p65; decreases IL-6 and TNF- α ; activates SIRT1 (combined with fisetin)
Epicatechin	Cocoa, red wine	HDAC modulation, HAT inhibition	Prevents H3K9 acetylation and H3K4 dimethylation; reduces NF- κ B expression and TNF- α
Gallic acid	Tea, berries, olive oil	HAT inhibition, HDAC activation	Decreases HAT activity in TNF- α -activated monocytes; attenuates inflammatory response
Ellagic acid	Berries, pomegranates	HAT inhibition, HDAC activation	Reduces HAT and increases HDAC activity in monocytic cells

diabetes patients increased SIRT1 expression and reduced NF- κ B-associated histone acetylation marks over six months, suggesting clinically relevant epigenetic anti-inflammatory effects. Genistein similarly increases SIRT1 and reduces NF- κ B activity in diabetic animal models.^[80,81]

Rheumatoid arthritis and inflammatory joint disease

Synovial NF- κ B hyperactivation drives the production of IL-6, TNF- α , matrix metalloproteinases, and RANKL, mediating

cartilage and bone destruction in rheumatoid arthritis (RA). Curcumin has been shown to reduce histone H3 acetylation at the IL-6 promoter in RA synovial fibroblasts by inhibiting HAT activity, thereby decreasing IL-6 expression. SIRT1 has been identified as a key epigenetic suppressor of NF- κ B in RA, and resveratrol's activation of SIRT1-mediated inhibition of the RANKL pathway represents a potential therapeutic approach. EGCG has shown similar epigenetic anti-NF- κ B effects in relevant cell models.^[82,83]

Cancer

Constitutive NF- κ B activation in tumour cells and the tumour microenvironment promotes survival, proliferation, invasion, and immune evasion. The epigenetic anti-NF- κ B activities of polyphenols are relevant to oncology in several ways. EGCG inhibits DNMT activity, potentially reactivating epigenetically silenced tumour suppressor genes that act as negative regulators of NF- κ B. Curcumin and resveratrol modulate HDAC and SIRT1 activity in cancer cell models, suppressing NF- κ B-driven survival signals. Genistein reverses hypermethylation of tumour suppressor genes and modulates miRNA networks that regulate NF- κ B in prostate and other cancers.^[84–86]

Neurodegenerative Diseases

Neuroinflammation driven by microglial NF- κ B activation is a key pathological feature of Alzheimer's disease, Parkinson's disease, and other neurodegenerative conditions. Curcumin, resveratrol, quercetin, and luteolin have all demonstrated anti-neuroinflammatory properties in cellular and animal models, at least in part through epigenetic suppression of NF- κ B. Curcumin modulates Nrf-2 signalling and antioxidant gene expression through epigenetic mechanisms, indirectly reducing oxidative-stress-driven NF- κ B activation in neural tissues.^[87–89]

Translational challenges as therapeutics

Bioavailability and metabolism

A fundamental challenge in translating the epigenetic NF- κ B-modulating effects of polyphenols into clinical benefit arises from their generally poor bioavailability. Most polyphenols undergo extensive metabolism, rapid conjugation (glucuronidation, sulfation, methylation), and microbial transformation in the gut, resulting in low systemic bioavailability of the parent compound. The

bioactive metabolites that reach target tissues may differ substantially in potency and mechanism from the parent polyphenol. For example, resveratrol undergoes rapid metabolism to piceid and other conjugates *in vivo*, which may retain some SIRT1-activating activity but at generally lower potency.^[90–94]

Strategies to enhance polyphenol bioavailability under investigation include nanoparticle encapsulation, liposomal formulations, co-administration with bioavailability enhancers (e.g., piperine with curcumin), and structural modifications to produce more bioavailable analogues (e.g., pterostilbene as a resveratrol analogue with greater lipophilicity and metabolic stability).

Dosing and clinical evidence

The concentrations of polyphenols required to produce epigenetic effects in cell culture models frequently exceed those achievable through dietary intake alone, raising questions about the clinical relevance of observed *in vitro* effects. Randomized controlled trials are limited in number and often confounded by issues of standardization, compliance, and variability in polyphenol metabolism between individuals. The two human trials reviewed here (resveratrol in type 2 diabetes and cocoa flavanols in cardiovascular risk) demonstrate proof-of-concept for clinically measurable epigenetic effects, but larger, more rigorously designed trials are needed.^[95,96]

Polyphenol interactions and dietary context

The human diet contains combinations of hundreds to thousands of polyphenols; however, the synergistic or antagonistic interactions between them remain poorly understood. The observed additive anti-inflammatory effects of fisetin-luteolin combination and the complementary mechanisms of resveratrol (SIRT1 activation)

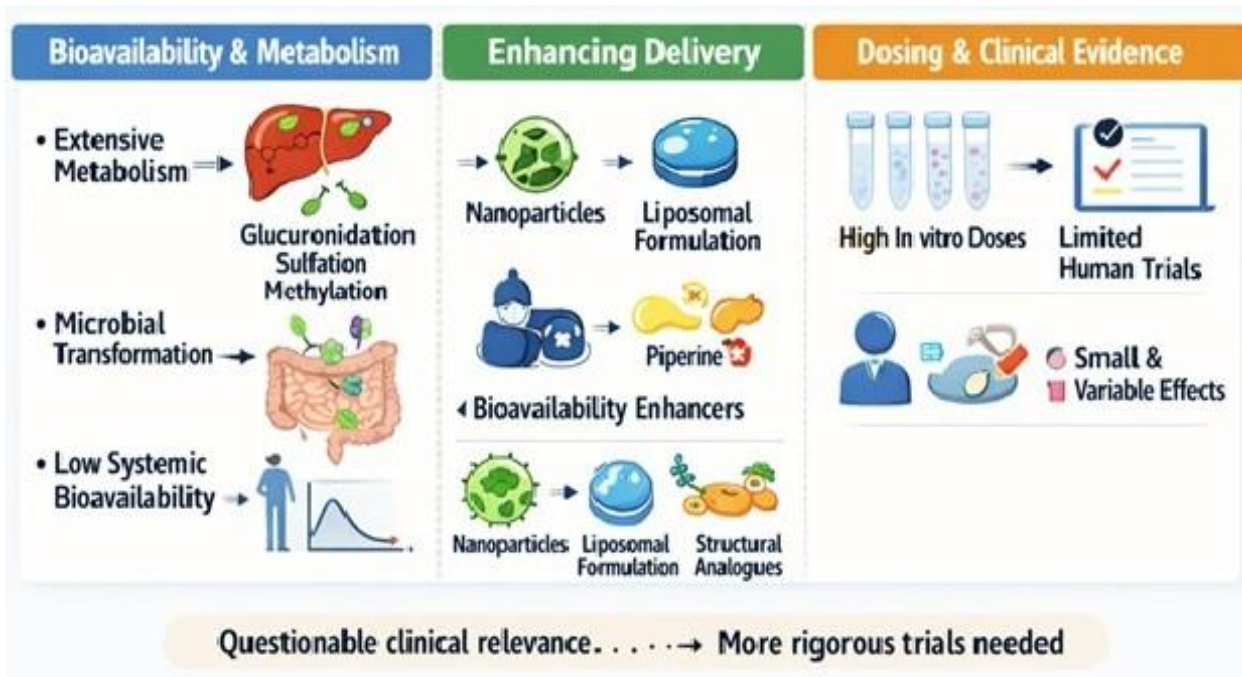


Figure 3. Clinical challenges of polyphenols. Polyphenols show limited clinical translation due to poor bioavailability, metabolic transformation, and rapid clearance. Delivery strategies (nanoparticles, liposomes, piperine) improve uptake, but high *in vitro* doses, few human trials, and variable effects highlight the need for more rigorous evidence.

and EGCG (HAT inhibition) suggest that co-administration or dietary patterns rich in diverse polyphenols may produce greater epigenetic NF-κB inhibition than individual compounds alone (Figure 3). Future research should examine polyphenol combinations and dietary pattern effects on NF-κB epigenetics.^[69,97]

Epigenome-wide effects and off-target risks

Epigenetic modifications are, by nature, pleiotropic: interventions that modulate HAT, HDAC, DNMT, or miRNA activity will affect the expression of thousands of genes, beyond those regulated by NF-κB. The long-term consequences of dietary epigenetic modulation by polyphenols, including potential effects on immune tolerance, cell differentiation, and genomic stability, are not well characterized. High-dose polyphenol supplementation has been associated with pro-oxidative effects and, in the case of isoflavones, potential hormonal effects,

underscoring the need for careful dose-response characterization and long-term safety monitoring in clinical trials.^[98,99]

Conclusion

Dietary polyphenols have been shown to exert anti-inflammatory effects through the epigenetic regulation of NF-κB activity. This review discusses how polyphenols such as resveratrol, curcumin, EGCG, quercetin, genistein, fisetin, luteolin, and epicatechin engage multiple epigenetic targets through HAT inhibition, HDAC/SIRT1 activation, DNA methylation modulation, and miRNA regulation, to reduce p65 acetylation, suppress NF-κB transcriptional activity, and decrease production of pro-inflammatory cytokines and mediators.

The interplay of HAT inhibition and SIRT1-mediated p65 deacetylation emerges as an epigenetic axis through which polyphenols modulate NF-κB. Different classes of

polyphenols can work together, suggesting that a variety of dietary sources may collectively provide epigenetic anti-inflammatory protection, supporting the use of diverse diets and polyphenol combinations in therapeutic strategies.

Despite promising preclinical evidence and emerging clinical data, significant challenges remain in translating polyphenol epigenetics into clinical practice. The issues of bioavailability, effective dosing, the complexity of polyphenol metabolism, interindividual variability, and the potential for off-target epigenomic effects must be addressed through rigorous clinical trial design and mechanistic research. However, the epigenetic modulation of NF-κB by dietary polyphenols is an emerging and rapidly advancing area of research that holds significant promise for the prevention and management of chronic inflammatory diseases.

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Conflict of interest

There are no conflicts of interest.

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