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## Epigenetics/epigenomics and prevention by curcumin of early stages of inflammatory-driven colon cancer

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### Abstract

Colorectal cancer (CRC) is associated with significant morbidity and mortality in the US and worldwide. CRC is the second most common cancer related death in both men and women globally. Chronic inflammation has been identified as one of the major risk factors of CRC. It may drive genetic and epigenetic/epigenomic alterations such as DNA methylation, histone modification, and noncoding RNA regulation. Current prevention modalities for CRC are limited and some treatment regimens such as use the NSAID aspirin may have severe side effects, namely gastrointestinal ulceration and bleeding. Therefore, there is an urgent need of developing alternative strategies. Recently, increasing evidence suggests that several dietary cancer chemopreventive phytochemicals possess anti-inflammation and anti-oxidative stress activities, and may prevent cancers including CRC. Curcumin is the yellow pigment that is found in the rhizomes of turmeric (*Curcuma longa*). Many studies have demonstrated that curcumin exhibits strong anticancer, anti-oxidative stress and anti-inflammatory activities by regulating signaling pathways such as Nrf2, NF- $\kappa$ B, and epigenetics/epigenomics pathways of histones modifications, and DNA methylation. In this review, we will discuss the latest evidence in epigenetics/epigenomics alterations by curcumin in CRC and their potential contribution in the prevention of CRC.

### Keywords

colon cancer; inflammation; epigenetics; curcumin

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Conflict of Interest

The authors declare no conflicts of interest.

## 1. Introduction

Curcumin is a polyphenolic derivative produced from turmeric (*Curcuma longa*) (1). It is the main active ingredient in turmeric and gives turmeric its yellow color. The IUPAC name for curcumin is (1*E*, 6*E*)-1,7-bis(4-hydroxy-3-methoxyphenyl)-1,6-heptadiene-3,5-dione, and its molecule structure contains a symmetric structure of two aromatic *o*-methoxy phenolic groups, linked by a diketone unsaturated carbon bridge (2). Previous reports have demonstrated that the curcumin content in turmeric are significantly different and affected by geology and environment, among other factors (3). For example, curcumin content reaches as high as 3.14% by weight in both turmeric and curry powders purchased from South California (4), while in Japan, fertilizing the plant with nitrogen, phosphorus and potassium in greenhouses, the content of curcumin in turmeric yields in the range of 0.12% to 0.21 % by weight (5). Regional similarity also found that the curcumin content grown in Japan, Indonesia and Vietnam is around 0.18% to 0.44%, 2.3%, and 3.2% by weight, respectively (6). Due to curcumin's hydrophobic structure, rapid metabolism and systemic elimination occurs upon entering the human body and the bioavailability of curcumin is considered very poor (7). In vivo studies in rats show that oral administration of curcumin (500 mg/kg body weight) leads to a maximum serum concentration of  $0.06 \pm 0.01 \mu\text{g/mL}$  at  $41.7 \pm 5.4$  min. In addition, the elimination half-life for curcumin oral administration (500 mg/kg) and IV injection (10 mg/kg) are  $28.1 \pm 5.6$  and  $44.5 \pm 7.5$  min, respectively (8). To improve the bioavailability of curcumin, piperine has been used in combination with curcumin, and the bioavailability could be increased by 20-fold in human clinical trials (9). Curcumin-loaded nanoparticles have also been developed to improve curcumin's bioavailability (10). Lipidated curcumin was shown to increase the bioavailability and promote human health by decreasing the plasma triglyceride and increasing the free radical scavenging ability (11). While multiple delivery systems are designed to reach superior curcumin bioavailability, the mechanisms of curcumin metabolism and bioactivity are not fully understood.

Chronic inflammation is highly related to human digestive tract disorders including ulcerative colitis, Crohn's disease and colon cancer. Risk factors such as oxidative stress, cytokines, duration of colon inflammation and family history are all associated with colon cancer incidence (12). The possible genetic mechanisms of colon cancer induced by inflammation include loss of function of tumor suppressor genes such as adenomatous polyposis coli (*Apc*) and *p53*, and elevated expression of the inflammatory genes such as cyclooxygenase-2 (*COX-2*) and nitric oxide synthase-2 (*NOS-2*) (13, 14). In addition, accumulating evidence has revealed that epigenetic mechanisms, heritable alterations that are not caused by changes to the DNA sequence, could play an important role in colon carcinogenesis (15). DNA methylation, with the addition of a methyl group to 5-cytosine in the CpG dinucleotide, is one of the common epigenetic mechanisms associated with aberrant gene expression in cancer. Specifically, CpG hypermethylation in promoter regions is believed to play a crucial role in suppressing gene expression, perhaps by blocking transcription factor binding (16). Grimm et al. and our group identified aberrant methylation in a well-established *Apc*(min/+) intestinal tumorigenesis model using methylated DNA immunoprecipitation (MeDIP) and next-generation sequencing approaches (17, 18).

Katsurano et al. observed that aberrant DNA methylation accumulates in epithelial cells during DSS-induced inflammation (19). More recently, Abu-Remaileh et al. used whole-genome bisulfite sequencing to demonstrate that inflammatory signals establish a novel epigenetic landscape that silences gene sets important for cellular transformation in an AOM/DSS-induced CRC model (20). Current studies suggest that gut microbiota also plays important roles during the development of colon cancer (21, 22). To reduce colon cancer rate by anti-inflammatory intervention, therapeutic treatments including utilizing bioactive phytochemicals appears to be logical. Curcumin has been demonstrated to reduce colitis-accelerated colon cancer in both in vitro and in vivo models (23-25). More details regarding colon cancer carcinogenesis and its prevention by curcumin will be discussed subsequently.

## 2. Epigenetics/epigenomics of colon cancer carcinogenesis

Alterations in epigenetics have been reported for several age-related diseases, including CRC (26). The estimated loss of epigenetic control may be one to two fold higher than that of somatic DNA mutations in colon cancer (27). The NF- $\kappa$ B and STAT3 signaling pathways play particularly important roles in the transformation of inflammation into cancer, and both are critical in cellular signal transduction and appears to be constitutively activated in cancer by abnormal changes including epigenetics. The NF- $\kappa$ B and STAT3 signaling pathways contribute to the microenvironment for tumorigenesis through secretion of a large number of pro-inflammatory cytokines and their crosstalk in the nucleus makes it even more difficult to treat colon cancer (28).

In CRC, three molecular carcinogenesis pathways have been identified; (1) chromosomal instability (CIN), (2) microsatellite instability (MSI), and (3) CpG island methylator phenotype (CIMP), each account for ~85%, 15%, and 17%, respectively (29, 30). Around 30–40% of proximal site colon tumors and 3–12% of distal colon and rectal tumors are characterized by high CIMP, in which numerous CpG islands are methylated and several tumor suppressor genes or ncRNA are inactivated (31). Based on CIMP profiles, primary CRC may be clustered into three distinct but relatively homogeneous subclasses: CIMP1, characterized by intense methylation of multiple genes, MSI and BRAF mutations; CIMP2, including methylation of a limited group of genes, increased methylation level for age-related genes, and mutation in KRAS; and CIMP negative, characterized by rare methylation with p53 mutation (29). CIMP1 and CIMP2 phenotypes are more often expressed in the proximal colon; CIMP1 has a good prognosis, whereas CIMP2 has a poor prognosis (32). Lind and colleagues found frequent promoter hypermethylation of CNRIP1, FBN1, INA, MAL, SNCA, and SPG20 in both CRCs (65–94%) and adenomas (35–91%), whereas normal mucosa samples were rarely (0–5%) methylated (33).

Chromatin remodeling together with DNA CpG methylation, are two of the key mechanisms of regulating gene expression (34, 35). Chromatin remodeling consists of modifications at conserved lysine residues on the tails of histone proteins. Lysine acetylation generally enhances transcription by weakening the association of the histones with DNA and permitting the accessibility of transcription factors to bind to promoter/enhancer regions and subsequent transcriptional activation. SOCSs and SHP1 genes play an important role as tumor suppressors in CRC cells (36-38). Xiong and colleagues reported that trichostatin A

(TSA), a histone deacetylase inhibitor (HDACi), increased the mRNA levels of SOCS1 and SOCS3. The induction of SOCS1 and SOCS3 expression by TSA in human CRC cells was due to increased acetylation of histone H3 and H4 in their promoter regions (39).

Chromosomal anomalies (deletions, translocations, copy number alterations), DNA mutations and epigenetic dysregulation of the miRNAs or genes involved in their biogenesis have been found during tumor progression (40-43). The best-characterized miRNAs dysregulated by DNA hypermethylation in tumors including CRC, and the functional consequences in tumor cells have been reviewed recently (44). Loss of miR-133a and gain of miR-224 are associated with CRC tumorigenesis. Reduced expression of miR-143 and miR-145 were found in CRC and adenomatous polyps (45). The level of miR92 and miR173p has been reported to be significantly higher in the plasma of colon cancer patients compared with healthy controls, and is implicated as potential markers for CRC (46). The expression of the miR-17-92 cluster, which encodes for a total of fifteen miRNAs, and miR135 are also significantly increased in CRC patients (47).

### 3. Colon cancer prevention by curcumin via non-epigenetic and epigenetic mechanisms

Curcumin has many biological anti-cancer activities in colon cancer, including induction of apoptosis, anti-oxidation and anti-inflammation. In this section, we will highlight the potential mechanisms of CRC prevention by curcumin, focusing on apoptosis, antioxidative, anti-inflammatory and epigenetic regulation in *in vitro* studies.

#### 3.1 Cancer prevention through non-epigenetic pathways

A number of studies have demonstrated that curcumin can induce apoptosis and cell cycle arrest in many colon cancer cell lines, including human colon cancer HT-29 (48, 49), SW480 (50, 51), CT26 (52), HCT-116 (53-56), HCT-15 (57), COLO 205 (58, 59), LoVo (60) and DLD-1 cells (61). The molecular mechanisms by which curcumin induces apoptosis or cell cycle arrest vary, depending on the cell type and the doses of curcumin. Generally, curcumin-induced apoptosis or suppressed proliferation involves inhibition of Wnt/ $\beta$ -Catenin pathways (50, 62), mitochondria-mediated apoptotic pathway (60, 63), oxidative stress (53), accumulation in G2/M phase (64, 65), targeting CDK2 (54), modulating EGFR and IGF-1R (66) and activation of Caspase-3, -7 and -9 (55, 59, 67).

High expression of NADPH oxidase 1 (NOX1) promotes proliferation of colon cancer cells by regulating ROS-dependent signal transduction (68). Curcumin possesses antioxidant and radical scavenging properties (69, 70). Curcumin may protect colon cells from oxidative stress by free radical scavenging and colon repair mechanism (52). Curcumin also is a fairly strong Nrf2 activator, resulting in induction of Nrf2-mediated antioxidant and detoxifying enzymes (71-75). Many studies have also shown that curcumin and its derivatives possess great anticancer effects in colon cancer, due to induction of ROS production, ROS-dependent mitochondrial dysfunction, and ER stress-dependent apoptosis accompanied with cell cycle arrest (56, 76-78). This latter phenomenon is probably due to much higher doses as compared to the lower doses needed to activate the Nrf2 mediated anti-oxidative stress

pathway (79). In addition, curcumin as a well-known anti-inflammatory agent, possesses very strong anti-inflammatory activities (80, 81). Curcumin regulates its anti-inflammatory effects by downregulating inflammatory transcription factors, cytokines and redox states (82), as well as interrupting the NF- $\kappa$ B signaling pathway, a major transcription factor in inflammation (83-85). Curcumin could also exhibit its anti-inflammatory activities through Nrf2-mediated pathways, since in LPS-stimulated Nrf2<sup>-/-</sup> macrophages curcumin's inhibition of cyclooxygenase-2 (COX-2), interleukin-6 (IL-6) and inducible nitric oxide (iNOS) mRNA was dampened as compared to the LPS-stimulated Nrf2<sup>+/+</sup> macrophages (86).

### 3.2 Cancer prevention through epigenetic regulations

We have previously reported that curcumin reduced the CpG methylation in the promoter of DLEC1 (Deleted in lung and esophageal cancer 1), a tumor-suppressor gene, with corresponding increase in mRNA expression in human colon HT29 cells (87). The demethylation was associated with reduced protein expression of DNMTs and HDACs and this was similarly observed in another study using in DNMT1 and DNMT3B knockout HCT116 cells (88). Microsatellite instability, a hypermutable phenotype, is observed in 15% of CRCs, out of which 12% are resulted from hypermethylation of the promoter of MLH1 (mutL homolog 1) (89). Clinical tissues with sporadic deficient mismatch repair in colorectal cancer have hypermethylation in MLH1 promoter, which may cause microsatellite instability, leading to BRAF mutations and double-hit somatic mutations of MSH2 and MSH6 (90). Curcumin abrogates G2/M arrest and enhances apoptosis in MLH1- or MSH2-knockdown HCT116 cells and RKO cells (91). In this context, the apoptosis inductive mechanism of curcumin may be associated with hypomethylation of MLH1 promoter and disruption of microsatellite instability (89-91). Combination of curcumin with UCN-01, an inhibitor of the cell cycle check point kinase Chk1, increases apoptosis even in MLH1<sup>+</sup> and MSH2<sup>+</sup> cells, potentially via epigenetic mechanism, which could be a promising treatment modality for CRC (91).

Decreased expression of miR-491 and increased expression of PEG10 (paternally expressed gene),  $\beta$ -catenin, and Wnt have been identified in colon cancer tissues (92). In HCT116 cells, it has been reported that curcumin increases miR-491 expression, suppressed PEG10 expression and consequently silences the Wnt/ $\beta$ -catenin signaling pathway as a mechanism of inducing apoptosis and inhibiting cells proliferation (92). Curcumin can also inhibit the AP-1 transcription factor components c-Jun and c-Fos, and bind to the promoter of pri-miR-21 which arrests cells in the G2/M phase, inhibits cell migration/invasion in vitro (HCT116 and RKO cells), and suppresses tumor growth and metastasis in vivo (93). Through inhibition of miR-21, curcumin could increase the protein expression of Pcd4 (colorectal tumor suppressor programmed cell death protein 4) (93).

Study by Roy et al. showed that difluorinated curcumin (CDF), a synthetic analog of curcumin, demethylated miR-34a and miR-34c promoter, restoring the expression of miR-34a and miR-34c that were down-regulated in colon cancer cell lines (HCT116 and SW620) and colon cancer tissues (94). The up-regulation of miR-34 by CDF resulted in decreased expression of its target gene Notch-1. Elevated Notch-1 expression in CRCs

inhibits apoptosis (95, 96) while promoting epithelial to mesenchymal transition and stemness (97, 98). Another study showed that CDF could inhibit miR-21 and restore expression of PTEN (phosphatase, and tensin homolog), normalizing the dysregulated miR-21-PTEN-Akt axis in chemo-resistant HCT116 and HT29 cells (99). In RKO and SW480 cells, curcumin and curcumin analog, RL197, have been shown to inhibit cell growth and induce apoptosis through suppressing miR-27a and miR-20a/miR-17-5p and downregulating the specificity protein transcription factors (Sp1, Sp3, and Sp4) (100). The proposed mechanisms include induction of reactive oxygen species (ROS) (100).

#### 4. Colon cancer prevention by curcumin in *in vivo* animal studies: epigenetics/epigenomics

Curcumin's preventive effects against inflammation-associated colorectal carcinogenesis have been widely studied in various animal models, among which azoxymethane (AOM) and/or dextran sulfate sodium (DSS) induced mouse model is one of most commonly used animal model to recapitulate the pathogenesis of CRC in patients (101-103). This multistep carcinogenesis process usually involves a single AOM injection (an initiation factor that induces aberrant crypt foci (ACF) by causing DNA damage) and DSS in the drinking water (a promotion factor that induces colitis by imposing inflammatory damage in the epithelial lining of the colon). We have recently reported using this model the molecular mechanisms of inflammation-associated colon carcinogenesis utilizing next generation RNA sequencing (RNA-seq) and its prevention by combination of curcumin and aspirin in C57BL/6 mice (104). In the study, diets supplemented with 0.02% aspirin (ASA), 2% curcumin (CUR) or 0.01% ASA+1% CUR were given to mice from 1 week prior to AOM initiation through the end at 22 weeks post AOM initiation. The results showed that CUR had a superior inhibitory effect in colon carcinogenesis compared to that of ASA. Additionally, the combination of CUR and ASA at a lower dose level exhibited similar efficacy to that of a higher dose of CUR at 2%. RNA-seq analysis revealed that the low-dose combination of ASA and CUR modulated a larger set of genes than the single treatment of ASA or CUR. Pathway analysis showed these differentially expressed genes were found in several cellular functions which are specifically in the inflammatory networks and liver metastasis in CRC. We also identified a small subset of genes as potential molecular targets involved in the preventive action of the combination of ASA and CUR. This study provides the first evidence in support of the chemopreventive effect of a low-dose combination of ASA and CUR in CRC, and a framework for identifying the mechanisms underlying the carcinogenesis process from normal colonic tissue to tumor development. Surprisingly, when we conducted a second study of CUR and ASA in CF-1 mice, the results show that only aspirin but not curcumin inhibited DSS-induced inflammation and AOM+DSS induced carcinogenesis (unpublished results). The different results between CF1 versus C57BL/6 mice are not clear, however, could be due to differences in genetic background and or obesity (CF-1 mice are generally inactive and obese as compared to C57BL/6) or other factors, and further study would be needed.

In a similar follow-up study, we focused on the epigenetic/epigenomic mechanisms of colon cancer prevention by curcumin in AOM-DSS-induced CRC in C57BL/6 mice (23). We



performed RNA-seq and DNA CpG methyl-seq and identified lists of differentially expressed and differentially methylated genes in pairwise comparisons and several pathways involved in the potential cancer prevention effects of curcumin were uncovered. These pathways include LPS/IL-1-mediated inhibition of RXR function, Nrf2-mediated oxidative stress response, production of NO and ROS in macrophages and IL-6 signaling. Among the differentially expressed and methylated genes, Tnf (also known as Tnf- $\alpha$ ) stood out with decreased DNA CpG methylation of Tnf in the AOM-DSS group and reversal of the AOM-DSS-induced Tnf demethylation by curcumin. These observations of Tnf methylation correlated with increased and decreased Tnf expression in RNA-seq. In addition, the DNA methylation level of a group of inflammatory genes was decreased in the AOM+DSS group but restored by curcumin and the results were validated by pyrosequencing. Our study shows for the first time that global epigenomic changes in DNA CpG methylation particularly in the inflammatory response from colitis-associated colon cancer and the reversal of their CpG methylation alterations by curcumin, which could potentially contribute to the overall cancer chemopreventive effect of curcumin in this CRC mouse model.

Other investigators in the past decades also performed several *in vivo* studies of cancer prevention effects of curcumin with the AOM/DSS model. As early as in 1994, a study by Huang et al. showed that administration of 0.5-4% curcumin in the diet decreased the number of AOM-induced colon tumors by 51-66% when fed during the initiation period (105). Other forms of curcumin such as tetrahydrocurcumin and phytosomal curcumin also have the ability of preventing AOM/DSS induced colon carcinogenesis (106, 107). As for the mechanisms of action, it has been reported that curcumin prevents colon carcinogenesis through decreasing the expression of Tnf- $\alpha$ , NF- $\kappa$ B, IL-6, COX-2, NOS, and IFN- $\gamma$  (102, 106, 108, 109). Other studies suggest that curcumin, in combination with turmeric oils, have superior cancer preventive effects than curcumin alone (110, 111). MaFadden et al. reported that curcumin reduced colonic tumor burden, in association with increased colon bacteria richness and relative abundance of *Lactobacillales*, and decreased *Coriobacterales* order (112).

## 5. Colon cancer prevention by curcumin: clinical studies

Curcumin as the treasure of the dietary supplement world has been studied for its potential health benefits primarily in cell culture and animal models. Although the therapeutic use of curcumin was studied as early as 1748 (113), the first study referring to the use of curcumin for human disease was published in 1937 (114). Over the past quarter century, many scientists performed clinical studies with curcumin in both healthy humans and in patients, in the management of oxidative and inflammatory conditions, anxiety, metabolic syndrome, hyperlipidemia, ulcerative colitis and some other digestive disorders, as well as arthritis (115). As discussed above, curcumin's pleiotropic activities emanate from its capability of modulating many signaling molecules such as pro-inflammatory cytokines, adhesion molecules, apoptotic proteins, C-reactive protein, NF- $\kappa$ B, 5-LOX, prostate-specific antigen, phosphorylase kinase, Tgf- $\beta$ , triglyceride, ET-1, creatinine, HO-1, AST, and ALT in human participants (116). However, the poor bioavailability of curcumin appears to be the most challenging barrier for advancing to human studies due to its poor absorption, rapid metabolism, and fast systemic elimination (7).

Most recently, we performed a simple pharmacokinetics (PK)-pharmacodynamics (PD) acute study with health human subjects (117). We found that the plasma levels of curcumin were below our LCMS detection limit (0.1 ng/ml) and only curcumin glucuronide, a metabolite of curcumin, was detected (117). Similar observations were reported in other studies (118). However, we also found that curcumin administration increased the mRNA expression of antioxidant genes NRF2, HO-1 and NQO1 while suppressing the expression of epigenetic gene histone deacetylases including HDAC1, HDAC2, HDAC3 and HDAC4 in leucocytes. HDACs are a class of epigenetic enzymes that remove the acetyl groups from an  $\epsilon$ -*N*-acetyl lysine amino acid on a histone protein. And histone modifications are among the most important epigenetic changes, because it can alter gene expression and modify cancer risks (119). This result suggests that curcumin can elicit the *in vivo* biological responses like antioxidant and epigenetic effects which could contribute to the overall beneficial effects of curcumin in normal healthy population, despite the very low blood levels of curcumin (117). Bora-Tatar et al. reported that among 33 carboxylic acid derivatives, curcumin was the most effective HDAC inhibitor, and that it was even more potent than valproic acid and sodium butyrate, which are well-known HDAC inhibitors (120). In another study, it was reported that the protein levels HDACs 1, 3, and 8 were significantly decreased by curcumin, resulting in increased levels of histone H4 acetylation (121). Similarly, Chen et al. reported significant decrease in the expression of HDAC1 and HDAC3 were also detected after treatment with curcumin (122).

To date, majority of curcumin studies in humans have been in populations with existing health problems, especially some inflammatory related diseases such as Crohn's disease, ulcerative colitis, ulcerative proctitis, and colon cancer. Perhaps this is because studies with healthy people can be challenging where the benefits may not be as immediate and measurable if biomarkers are normal at baseline. Some promising effects have been observed in patients with various pro-inflammatory diseases including ulcerative colitis, ulcerative proctitis, irritable bowel syndrome, Crohn's disease, gastric inflammation and even colorectal cancer (116, 123-126). The biological effects of curcumin in healthy volunteers, CRC patients, Crohn's disease, ulcerative proctitis, ulcerative colitis, inflammatory bowel disease, irritable bowel syndrome and the potential molecular targets are summarized in Table 1. As shown in Table 1, the clinical trials conducted thus far indicate the potential therapeutic benefits of curcumin against a wide range of human inflammatory-driven diseases including colon cancer. Moreover, these human studies indicate curcumin's ability to modulate multiple biomarkers such as tumor necrosis factor (TNF- $\alpha$ ), interleukin [IL]-1 $\beta$ , IL-6, IL-10, among others. Some of the potential pitfalls of performing the anti-cancer treatment studies of CRC patients with curcumin could be due to the advanced stages of CRC with many genetic mutations, epigenetics changes and chromosomal instability, the doses selected, the curcumin products used with varied curcumin content, and the etiology/genetic background of the patients, among others. Nevertheless, in summary, curcumin has shown promising beneficial effects from clinical trials and most of these effects can be attributed to its anti-oxidative, anti-inflammatory, epigenetic/epigenomic and other signaling modulating properties, which would contribute to the overall cancer chemopreventive effects of curcumin in early stages of inflammatory-mediated CRC (115, 116).



## 6. Conclusion

Colon cancer continues to be a major public health burden. Several factors from genetics to diets contribute to the incidence of this malignancy. Although there have been significant advances in the development of targeted therapies, the 5-year prognosis for distant CRC is about 15% (135). With our increased understanding of the molecular and epigenetic/epigenomic changes during CRC development, we will be able to develop new and more precise therapies, including relatively non-toxic dietary cancer chemopreventive regimens including curcumin either with individual therapy or in combination with other relatively non-toxic drugs such as NSAIDs (aspirin with lower doses), to prevent early stages, and or treat newly diagnosed inflammatory-mediated colon cancers in humans.

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**Table 1.**

Pharmacological effects of curcumin in clinical studies.

Diseases	Dosage; duration	Outcome (reference)	Molecular targets
Healthy volunteer	4 g/person; 1 single dose	Upregulated Nrf2/ARE genes; Downregulated HDACs (117)	NRF2 ↑, HO1 ↑, NQO1 ↑, HDAC 1, 2 & 3 ↓
	0.036–0.18 g/day; 4 mo	Reduced glutathione S-transferase activity (127)	GST ↓(127)
	0.45–3.6 g/day; 4 mo	Reduced PGE2 production (128)	PGE2 ↓ (128)
	0.45–3.6 g/day; 7 d	Reduced the levels of MIG (129)	MIG ↓ (129)
Colorectal cancer	1.44 g/day; 6 mo	Reduced the number and size of polyps without any appreciable toxicity (130)	
	2 or 4 g/day; 1 mo	Reduced ACF formation in smokers (131)	
	1.08 g/day; 10–30 d	Improved body weight, reduced serum TNF- $\alpha$ , and induced p53 expression (132)	TNF- $\alpha$ ↓, Bcl-2 ↓ p53 ↑, Bax ↑(132)
Crohn's disease	1.08 g/day, 1 mo	Significant reductions in CDAI and inflammatory indices in patients (125)	
	1.44 g/day, 2 mo		
Ulcerative proctitis	1.1 g/day; 1 mo	Significant reduction in symptoms as well as inflammatory indices in patients (125)	
	1.65 g/day; 1 mo		
Ulcerative colitis	2 g/day; 6 mo	Prevented relapse of disease (124)	
	0.5 g/day; 2-10 mo		
Inflammatory bowel disease	5-20 $\mu$ M; 0.5-24 h	Suppressed p38 MAPK activation, reduced IL-1 $\beta$ , and enhanced IL-10 levels in mucosal biopsies; suppressed MMP-3 in colonic myofibroblasts (133)	CRP ↓, ESR ↓, CDAI ↓ (125) p38 MAPK ↓, IL-1 $\beta$ ↓, MMP-3 ↓, IL-10 ↑(133)
	0.072 or 0.144 g STE/d; 8 wk		
Irritable bowel syndrome	0.5 g in food	Increased bowel motility and activated hydrogen producing bacterial flora in the colon (126)	

↓, Downregulation; ↑, upregulation; mo, month; d, day; wk, week; h, hour.