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EPIGENETIC REGULATION OF NRF2 AND URSOLIC ACID IN SKIN

CARCINOGENESIS

By

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ABSTRACT OF DISSERTATION

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Non-melanoma skin cancer (NMSC) is the most common cancer in the United States with over 4.0 million new cases diagnosed in 2012. An increase of exposure to environmental pollutants and sunlight are among the causative agents of the disease. Ursolic acid (UA), a well-known natural triterpenoid found in abundance in fruit peels, cranberries, and blueberries has been shown to possess beneficial health effects against a multitude of disorders including, cardiovascular, neurological, and oncological disorders. However, epigenetic modulation of UA in skin carcinogenesis is still poorly understood. Increasing evidence suggests epigenetics play an important role in the development and progression of cancer including NMSC. Among its many anti-cancer activities, UA has also been shown to have the ability to modulate epigenetic mechanisms *in vitro* and thus presents an attractive candidate to target the underlying epigenetic mechanisms of skin carcinogenesis. Preliminary data in our laboratory and that of others points to epigenetic regulation of key genes at the center of UA activities: 1) Skin carcinogenesis is enhanced in Nrf2 (-/-) mice; 2) The expression Nrf2 and its target gene HO-1 is reduced in skin tumors of Nrf2 (+/+)mice; 3) UA inhibits TPA-induced ear edema and tumor promotion; 4) Hypermethylation of the promoter region of Nrf2 resulting in reduced expression and its target genes is closely associated with prostate tumor progression; 5) Dietary phytochemicals epigenetically modify the hypermethylation of the Nrf2 promoter region and inhibit TPA-induced transformation. Based on the aforementioned observations, it was hypothesized UA can suppress skin carcinogenesis, in part, through the epigenetic regulation of Nrf2 signaling. We demonstrated for the first time that UA restores the expression of Nrf2 by demethylating CpG islands in the Nrf2 promoter in mouse epidermal cells resulting in an increase in the expression of cytoprotective detoxifying/antioxidant enzymes and suppression of tumor promoter-induced cell transformation. Furthermore, we demonstrate UA is able to suppress skin carcinogenesis *in vivo* using a relevant and novel B[a]P/TPA skin carcinogenesis model. The long-term goal of this research is to understand some of the underlying epigenetic mechanisms driving skin carcinogenesis and to develop safe and effective strategies to prevent/treat NMSC using phytochemicals such as UA who possess anti-cancer properties.

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Chapter I

Introduction^{1,2}

¹ A portion of this chapter has been published in *AAPSJ* as a review paper: <u>Ramirez CN</u> et al., (2017). *In vitro-in vivo* dose response of ursolic acid, sulforaphane, PEITC, and curcumin in cancer prevention. *AAPSJ*. Dec 20;20(1):19.

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1 Dietary Phytochemicals in cancer prevention

1.1 Introduction

Cancer is now the leading cause of death in 21 states in the US (1). Cancer is a chronic disease that could be prevented (2, 3). Cancer development can take about 10-30 years to develop, from initiation, promotion to progression (Figure 1) (4). Thus, the slow development of the disease potentially allows the intervention in the progression of cancer into advanced stages and metastases (Figure 2). Recent evidence suggests epigenetic alterations precede genetic mutations during cancer development. As such, naturally occurring phytochemicals have been shown to have the ability to activate the anti-oxidative stress, Nrf-2 mediated pathway, anti-inflammatory networks as well as others (5, 6), resulting in blocking cancer initiation, promotion and/or progression, in many *in vitro* and *in vivo* models (5). These pathways may be directly or indirectly regulated through epigenetic modulation by natural dietary phytochemicals. Among these, some of the most promising chemopreventive agents include ursolic acid (UA), sulforaphane (SFN), phenethylisothiocyanate (PEITC), and curcumin. The dose by which these phytochemicals produce their chemopreventive effects will be explored in this review

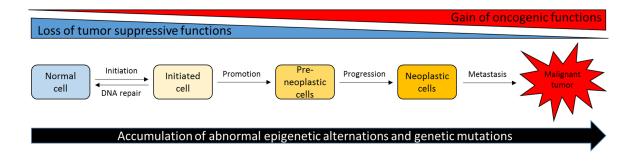


Figure 1. Development of carcinogenesis with aberrant epigenetics and genetics changes. The accumulation of genetic mutations and epigenetic alterations along with the loss of suppressive functions and the gain of oncogeneic functions permits the progression of normal cell initiation to metastasis.

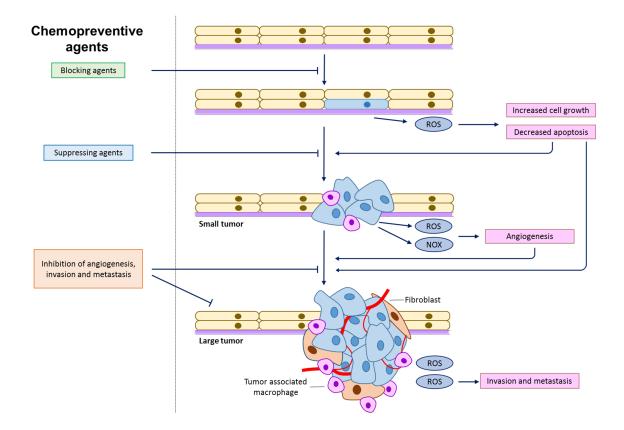


Figure 2. Illustration of chemopreventive agents on different carcinogenesis stages. Chemopreventive agents can intervene at the initiation stage, the promotion phase, and the progression phase of carcinogenesis.

1.2 The importance of dose in the *in vitro* and *in vivo* chemopreventive effects of phytochemicals

1.2.1 Triterpenoids

Triterpenoids are a natural class of compounds produced through the cyclization of squalene widely used in Asian medicine. Approximately 20,000 sources of triterpenoids exist in nature (7). This class of compounds has been shown to have antiinflammatory and anti-cancer properties. Specifically, the triterpenoids, oleanolic acid (OA, 3B-hydroxyolean-12-en-28oic acid) (8) and ursolic acid (UA, 3B-hydroxy-urs-12en-28-oic-acid), an isomer of OA, have shown great promise in these areas. The anticancer, anti-inflammatory, and chemopreventive effects of these compounds vary with dose and are explored here

UA is found in blackberries, blueberries, holy basil, thyme, lavender, catnip, peppermint leaves, olive oil, rosemary and apple peels (7). It has been shown to modulate a number of pathways implicated in the progression and the survival of cancer. The same can be said of OA, a triterpenoid found in ginseng root and the olive plant, bearberries, heather, three leaved caper, reishi, Chinese elder, and Sodom's apple (9). UA and OA are often found in combination and share many of their pharmacological properties (10). In addition to its anti-inflammatory and anti-cancer effects, OA possesses a wide range of pharmacological activities such as anti-viral, anti-microbial, anti-parasitic, anti-diabetic, and anti-analgesic (9) effects.

A multitude of experiments have shown UA is able inhibit proliferation and induce apoptosis of a variety of cell lines and in various animal models. Triterpenoids have been shown to exert their anti-inflammatory properties through the modulation of ROS and the attenuation of iNOS, COX-2 and NF- κ B, a key factor in controlling transcription of DNA, cytokine production and cell survival. In the T lymphoma Hut-78

cells, UA inhibited proliferation and induced early apoptosis at 10-80 μ M, with the highest effect achieved at 80 μ M. This was noted in the downregulation of NF- κ B p65, and p50 proteins and the upregulation of caspase-8, caspase-3, and caspase-9. In addition, COX-2 mRNA also decreased in the presence of UA (11). UA and OA have been shown to inhibit the proliferation of non-small cell lung cancer A549 cells in a nude mouse model at low and high doses of 50 and 100 mg/kg bw, respectively. At 100 mg/kg bw UA significantly inhibited the growth of the cells noted in tumor weight. Further investigations, noted UA and OA increased expression of Bid and decreased the protein levels of MMP-2, Ki-67, and CD34 (12). Additionally, UA has been shown to inhibit proliferation and induce apoptosis in MTC-SK cells, a medullary thyroid carcinoma cell line) at 10 μ M and 20 μ M *in vitro* (13). Additionally, UA and OA have been shown to induce apoptosis through a multitude of pathways in prostate cancer. These include the activation of JNK and inhibition of Akt pathways in PC-3 cells at 80 µM (14), and the down regulation of Bcl-2 in PC-3 and LNCaP prostate cancer cells at 55 µM and 45 µM respectively (15).

The anti-inflammatory capabilities of UA have been shown to be expansive in a number of experimental models. UA has been shown to inhibit tumor promotion by 12-O-tetradecanolphorbol-13-acetate (TPA) in a two-stage skin carcinogenesis ICR mouse model at 2 μ mol applied topically prior to application of TPA. UA reduced TPA-induced inflammation and decreased the gene expression of IL-1, IL-22, and Cox-2 inflammatory genes. In addition, UA reduced binding of NF-K β , Egr-1, and AP-1 (12). Furthermore UA has recently been shown to inhibit cell growth and proliferation of pancreatic cell lines AsPC-1, MIA, PaCa-2, and Panc-28 cells at 5-20 μ M *in vitro* (16). UA suppressed NF-K β activation and was able to suppress its target genes in Panc-28 cells *in vitro*. UA's anti-cancer effects were further confirmed in an orthotopically implanted pancreatic cancer model in which UA inhibited pancreatic cancer at a dose of 250 mg/kg bw given orally daily. Moreover, UA and OA have been shown to prevent ROS-induced hepatocellular carcinoma *in vivo* in a male Wistar rat model at an oral dosage of 20 mg/kg bw (17) and skin cancer through the attenuation of chemically induced ROS and protect against DNA damage induced hydrogen peroxide at concentrations 5 and 10 μ M in murine keratinocyte Ca3/7 cells (18). Furthermore, UA has been shown to induce anti-inflammatory activity at 5 μ M through the suppression of NF-K β in activated T cells, B cells and macrophages (19). UA's anti-inflammatory role was further solidified in a study demonstrating UA was able to reduce NF-KB activation and the release of cytokines at 10 μ M and 50 μ M in human colon cancer COLO 205 cells (20). The study extended their findings in a (DSS)-induced acute murine colitis treated model. When induced and treated with either UA 10 mg/kg or 20 mg/kg disease activity decreased (20).

UA has demonstrated anti-oxidative activity through the modulation of several pathways. When colorectal cancer Caco-2 cells were treated with UA it resulted in the normalization of antioxidant levels and protection against oxidative damage at 5 μ M and 10 μ M and (21). Furthermore, UA and OA have attenuated H₂O₂ and in neuroblastic PC12 cells at 20 μ M and 40 μ M (22).

A recent study demonstrates UA's role in epigenetic modulation in which UA increased phosphorylation of SAPK/JNK pathway in human non-small cell lung cancer H1299 and A549 cells *in vitro* at a concentration of 30 μ M. Further investigations demonstrated UA was able to decrease the expression of SP1 and in turn regulate

DNMT1 and EZH2 expression in H1299 and A549 cells (23). UA has also been reported to increase the acetylation of histone H3 and inhibit HDAC activity *in vitro* (24).

UA and OA have been shown to promote the differentiation of glioma, melanoma, and thyroid cancer cell lines, A375, U87, and ARO cell lines respectively, through the inhibition of endogenous reverse transcriptase (RT) at 10, 15, and 20 μ M (25). Furthermore, UA has been shown to induce the differentiation of HL60, U-937, and THP-1 leukemic cells at 10, 20 and 30 μ M via the activation of the ERK1/2 MAPK pathway (26). UA inhibits proliferation and induces apoptosis of ovarian epithelial cancer SKOV sphere cells at 12.5-50 μ g/mL. In addition, UA downregulates the expression of EMT markers including Snail, Slug, Twist, vimentin, N-cadherin and fibronectin. These effects translated *in vivo* in a SKOV3 sphere cell xenograft athymic nude BALB/c-nu mouse model at 60 mg/kg bw (27).

Triterpenoids demonstrate their anti-cancer activities at a concentration range of 5 μ M to 80 μ M *in vitro* and 10-250 mg/kg *in vivo*. The variations in concentrations can be attributed to pharmacological effects related to cell line, assay system, animal model and source of compounds. While there are less than a handful of clinical studies evaluating human. A clinical study evaluating the effect of 150 mg of UA given orally once a day for 12 weeks on metabolic syndrome, insulin sensitivity, and inflammation lead to a transient remission in 50% of patients (28). Another study evaluating UA at 50.94 mg for use in sarcopenia demonstrated a significant increase in the right-handgrip of female subjects in comparison to the control group (29). Overall, triterpenoids hold great promise in the area of chemoprevention and as such are being synthetically modified in order to increase potency *in vivo*.

1.2.2 Isothiocyanates (ITCs)

Numerous epidemiological and pharmacological studies suggest a correlation between the consumption of cruciferous vegetables and a reduced cancer risk in humans (30, 31). Over 200 naturally-occurring glucosinolates are found in cruciferous vegetables (32), which consist of a β -D-thioglucose group, a sulfonated oxime group, and a side chain derived from methionine, phenylalanie, tryptophan, or branch-chained amino acids (33). Interestingly, the chemopreventive effects are mostly attributed to the isothiocyanate (ITC)-containing compounds rather than their glucosinolate precursors. ITCs, converted by myrosinase mediated hydrolysis from glucosinolate, are characterized by the sulfur containing N=C=S functional group with a wide structural diversity. Ally isothiocyanate (AITC) from cabbage, mustard, and horseradish; benzyl isothiocyanate (BITC) and phenethyl isothiocyanate (PEITC) from watercress and garden cress; and sulforaphane (SFN) from broccoli, cauliflower, and brassicas have been mostly studied against a variety of human malignancies (34). In cell culture models, micromolar concentrations of ITCs have shown potent anti-cancer effects through different mechanisms in vitro (35, 36). Several pharmacokinetic studies have provided evidence that the concentration range is achievable *in vivo*. For example, in a pharmacokinetics study of PEITC in rats, it demonstrated that plasma concentration of PEITC could reach 9.2 and 42.1 µM after an oral dose of 10 and 100 µmol/kg body weight in rats (37). Interestingly, it was also found that PEITC was highly bound to serum protein in the rats with the protein-binding ratio around 98.1% and was not concentration-dependent. The high plasma concentration was due to the high oral bioavailability, which was 115 and 93% at doses of 10 and 100 μ mol/kg (37). Compared to PEITC, SFN is relative less

associated with protein binding and the binding ratio did not increase with time (38). In an in vitro study, the initial protein binding by PEITC was almost 3-fold higher than that of SFN. Four hours after incubation, cellular protein binding of PEITC became 6-fold higher than that of SFN (38). In an *in vitro* setting, PEITC also modified bovine serum albumin (BSA) covalently to a greater extent than SFN occurring exclusively at cysteine residue (38). Oral administration of 50 μ mol SFN in rats resulted in a peak plasma concentration of 20 μ M at 4 h (39). In a chemopreventive study using the ApcMin/+ mouse model, SFN inhibited adenoma formation with a steady-state concentration of 3-13 nmol/g (roughly equivalent to 3-10 μ M) in the gastrointestinal tract (40).

In clinical studies, there are several reports showing that the ITCs could potentially impact in the prevention of cancer. After receiving 1 week of PEITC treatment (10 mg in 1 mL of olive oil, 4 times per day), tobacco carcinogen 4-(methylnitrosamino)-1-(3-pyridyl)-1-butanone (NNK) metabolic activation ratio was reduced by 7.7% in a clinical trial containing 82 smokers, which suggests that PEITC could be a potent inhibitor of lung carcinogenesis in smokers (41). In a double-blinded, randomized, placebo-controlled clinical trial, 78 senior patients with increasing PSA levels after radical prostatectomy were given 60 mg sulforaphane 3 times daily for 6 months, a much lower plasma PSA level were found in the sulforaphane treated group, which potentially suggests a promising treatment in recurrence of prostate cancer after prostatectomy (42). A randomized controlled clinical study consisting of 54 women subjects revealed a mean 81.7 g/d intake of cruciferous vegetable, enriching of SFN, for over 4 years (August 2009 to December 2013) was associated with a lower level of Ki-67, a cellular marker for proliferation, in breast ductal carcinoma in situ tissue, which strengthen the correlation of cruciferous vegetable consumption and lowering breast cancer risk (43).

The chemopreventive effect of ITCs is considered to be associated with their ability to induce the expression of phase II drug metabolism/detoxifying enzymes. It has been extensively documented that SFN exerts potent activation of phase II/antioxidative gene expression in both in vitro and in vivo studies (44). In rats, 40 µmol/kg/day SFN treatments found increase glutathione-S-transferase (GST) were to and NAD(P)H:quinone oxidoreductase 1 (NQO1) activities in the duodenum, forestomach, and bladder tissues (45). In hepatocytes, SFN induced UGT1A1 and GSTA1 mRNA expression and protected cells against the 2-amino-1-methyl-6-phenylimidazo[4,5b]pyridine (PhIP, commonly found in cooked meat and considered as risk factors for cancer)-DNA adduct formation (46). Similarly, PEITC was found to induce hepatic phase II enzymes, resulting in decreased PhIP-DNA adduct levels in rat tissues (47). In mice, 12 h after an oral dose of PEITC, upregulation of several GST isozymes in the liver were identified using a microarray approach (48). Markedly, a number of studies on ITCs suggest that the induction of phase II/antioxidant enzymes is NF-E2-related factor-2 (Nrf2) dependent (48-50).

Mechanistic studies demonstrated that ITCs activate the Nrf2 pathway by modifying Nrf2-Keap1 interactions. Using a liquid-tandem mass spectrometry approach, Hong et al. provided evidence that SFN can directly react with the thiol groups of Keap1. The formation of SFN-Keap1 thionoacyl adducts releases Nrf2 from the Nrf2-Keap1-Cul3 degradation complex; this stabilization of cellular Nrf2 consequently results in Nrf2 nuclear translocation and activation (51). On the other hand, PEITC may induce the Nrf2/ARE signal through a different mechanism potentially mediated by mitogenactivated protein kinases (MAPKs). It has been reported that PEITC induces ARE activity through the attenuation of c-Jun N-terminal kinase-1 (JNK1) and extracellular signal-regulated kinase (ERK) inhibitors (50). In the same study, *in vitro* kinase assays showed that JNK1 and ERK2 directly phosphorylate Nrf2 protein. Collectively, PEITC increased the phosphorylation of ERK1/2 and JNK1/2 in cells, which, in turn, caused phosphorylation of Nrf2 and subsequent release from Keap1 binding, and resulted in translocation activation of the Nrf2/ARE pathway. To note, Nrf2-deficient mice have shown increased susceptibility in carcinogenesis models and less effective towards preventive treatment (52-54). Therefore, transcriptional induction of Nrf2/ARE mediated phase II enzymes would be considered as an important mechanism for the chemopreventive effects of ITCs.

Inactivation of the NF- κ B pathway by ITCs is another important mechanism that can contribute to their anti-cancer activities. Experimental evidence suggests that ITCs stabilize I κ B by inhibiting its phosphorylation and degradation, resulting in a reduction in nuclear translocation of p65 (a subunit of NF- κ B) and NF- κ B activation. In PC-3 cells, both SFN (20 and 30 μ M) and PEITC (5 and 7.5 μ M) strongly inhibited nuclear translocation of p65, with the concomitant decreased expression of NF- κ B regulated genes such as Bcl-XL, cyclin D1, and vascular endothelial growth factor (VEGF) (55). Correspondingly, PEITC and SFN were found to inhibit lipopolysaccharide (LPS)induced NF κ B luciferase activity in human colorectal cancer HT-29 cells, which was also mediated through the inhibition of I κ K β phosphorylation (56). In addition, SFN was proposed to interact with glutathione and other redox regulators like Ref-1 and thioredoxin, which in turn indirectly impairs the NF κ B-DNA binding ability (57). Another study by Heiss et al suggested SFN directly interacts with Cys residues of NF κ B subunits by forming dithiocarbamate, which results in decreased DNA binding abilities (58). Collectively, these findings indicate that redox modulation and thiol reactivity play certain roles in regulating NF κ B-dependent transcription by SFN. Interestingly, studies on the crosstalk between Nrf2 and NF κ B signaling have shown that Nrf2 downstream targets may inhibit of NF κ B nuclear translocation (59, 60). Accordingly, pre-treatment of SFN (25 mg/kg per day) mitigated dextran sodium sulphate (DSS)-induced acute colitis *in vivo*, while increased expression of Nrf2-dependent genes and reduced expression of inflammatory were observed in colon tissues (61). Similarly, SFN restored the number of sunburn cells to basal levels in Nrf2 WT but not Nrf2 knockout (KO) mice after UV irradiation. The inflammatory markers were lower in SFN treated Nrf2 WT tissues compared to Nrf2 KO tissues (62). These results suggest activation of Nrf2 by SFN can, in part, contribute to the suppression of proinflammatory signaling pathways.

Given that epigenetics lies on the molecular interface between genetics and environmental factors, there is a growing interest in evaluating the potential of dietary phytochemicals to block or reverse epigenetic abnormalities in cancer development. In a recent study, Wong et al. reported the effects of SFN on promoter DNA methylation profiles in prostate epithelial cells (PrEC), androgen-dependent (LNCaP) and androgenindependent (PC-3) prostate cancer cells (63). SFN treatment was found to decrease the DNMT levels in all the tested cell lines. Although SFN showed complex effects on genome-wide DNA methylation patterns among normal prostate epithelial and prostate cancer cells, the genes of altered methylation status were functionally similar within a single cell line (e.g. cell migration, cell adhesion etc.). In various *in vitro* and *in vivo* studies, SFN or PEITC treatments appeared to down-regulate DNMT activity, thereby resulting in promoter demethylation of epigenetically silenced genes, with the concomitant change of gene expressions (reviewed by (64, 65). Interestingly, DNA demethylation in a promoter region is often found to be associated with local relaxing of histone structure, although the precise mechanism remains to be elucidated. For example, in mouse prostate cancer TRAMP-C1 cells, SFN (1.0 and 2.5 μ M) restored the epigenetically suppressed Nrf2 levels by reversing the hypermethylation status of the Nrf2 promoter region via inhibition of DNMT activities, as well as HDACs (66). In mouse epidermal JB6 P+ cells, this change in methylation pattern by SFN is associated with increased Nrf2 level and a phenotype more resistant to TPA-induced neoplastic transformation (67).

On the other hand, HDACs are often upregulated in cancers therefore HDAC inhibition is considered as an important strategy in cancer prevention and therapy. Molecular docking experiments have shown the metabolite of SFN and several structural related ITCs directly interact with the HDAC catalytic core to inhibit the enzyme activity (68). In a clinical study, a single dose of 68 g of broccoli sprouts (containing ~105 mg of SFN) inhibited HDAC activity significantly in peripheral blood mononuclear cells (PBMC) 3 and 6 hours post consumption (69). Incubation of BPH-1, LNCaP, and PC3 prostate cancer cells with 15 μ M SFN significantly reduces HDAC expression by 30–40%, which is accompanied by a 50–100% increase in the acetylation of histones, as well as G2/M arrest of cell development and induction of apoptosis in a caspase-dependent manner (70).

Epigenetic upregulation of p21 gene expression by PEITC was found to be associated with chromatin remodeling, which compromises dynamic changes in both histone acetylation and methylation (71). To note, PEITC also exhibits the dual functions of CpG demethylation, HDAC inhibition and epigenetic regulation of various genes (72, 73). Last but not least, the anti-cancer effects of ITCs may be partially attributed to their ability to regulated miRNA. Using an oligonucleotide approach, we identified top altered miRNAs upon 2.5 µM PEITC treatment in prostate cancer cells. Among them, miR-194 was a primary target of PEITC which was able to suppress cell invasion (74).

ITCs have been shown to exert cytoprotection via the activation of Phase II enzymes within the Nrf2 pathway. Rat aortic smooth muscle cells treated with SFN at $0.25-5 \mu$ M, resulted in the increase of phase 2 antioxidant enzymes in a concentrationdependent manner. Furthermore, when pre-treated with SFN (0.5, 1, and 5 μ M), the cells were protected from oxidative and electrophilic cytotoxicity induced by xanthine oxidase (75). Incubation with SFN, BITC, and PEITC (0-10 μ M) protected against oxLDLinduced endothelial damage in a dose-dependent manner through the induction of Nrf2's target gene heme oxygenase-1 (HO-1). In addition, the expression of NF- κ B, ICAM-1, VCAM-1, and E-selectin were decreased (76). Human peripheral blood mononuclear cells (PBMC) treated with PEITC (1-10 μ M) for 24 h, increased the detoxification enzymes GPX1 (3.7-fold increase by 1 μ M PEITC treatment) and SOD2 (7.3-fold increase by 10 μ M PEITC treatment) (77).

Furthermore, SFN inhibited breast CSCs at concentrations 1-5 μ M *in vitro* which is much lower than the concentration needed to induce apoptosis (78). In an *in vivo* xenograft model, where 5-week-old female NOD/SCID mice with a xenograft of SUM159 cells received daily injections of 50 mg/kg SFN for 2 weeks, breast CSCs were found to be inhibited mainly due to the down-regulation of Wnt/ β -catenin self-renewal pathway (79). SFN is also effective in the treatment of leukemia by enhancing the differentiation of leukemic cells. When human promyelocytic leukemia cells were treated with 0.2-100 μ M SFN, SFN induced differentiation in the leukemic cells to granulocytic and macrophagic lineages. This process was mediated mainly through PKC (80).

GATA-3 is a marker for luminal progenitor cell differentiation and can actively promote the differentiation of cancer cells (81, 82). When PyMT transgenic mice were treated with PEITC (8 mmol/kg bw), the progression of tumor size was delayed and there were smaller tumors compared to the control. These findings were accompanied by a low expression of ER α , FOXA1 and GATA-3 (83). PEITC also inhibited CSC growth *in vitro* (84). PEITC transformed LNCaP floating spheres into prostate cancer stem cells (PCSC) due to the enhancement of H3K4 acetylation, the inhibition of DNMT1 and activation of GSTP1. After androgen deprivation, the PCSCs differentiate into neuroendocrine cells with decreased proliferation, expression of the androgen receptor, and PSA (85)

Extensive studies have shown ITCs are able to inhibit the growth of cancer cells via arresting the cell cycle through the regulation of cell cycle proteins, cyclin-dependent kinase activity, tubulin polymerization and histone acetylation, and the induction of apoptosis (86). PEITC induces extrinsic apoptosis pathway through stimulating death receptors and Fas (87, 88) and the intrinsic apoptosis pathway by regulating BCL2, BID and BAX (89-91). In addition, PEITC can induce G0/G1 arrest via p53 and G2/M cell arrest in a p53 independent manner (90, 92).

PEITC (0 to 10 μ M) significantly inhibited human laryngeal carcinoma Hep-2 cell growth and enhanced apoptosis with G2/M cell cycle arrest in a dose- and time-dependent manner while no effect was observed in the growth of normal human bronchial epithelial cells (93). Treating human non-small cell lung cancer L9981 cells with BITC (7.5 and 10 μ M) and PEITC (12.5 and 20 μ M) resulted in apoptosis through the stimulation of caspase-3 and cell cycle arrest at the G2/M phase via cyclin B1 regulation (94). BITC and PEITC also inhibited the growth of lung cancer L9981 cells with IC50 5.0 and 9.7 μ M respectively by suppressing Akt and NF-KB, enhancing ROS production, and reducing GSH (95).

SFN can inhibit the growth of cancer cells by causing cell cycle arrest and apoptosis induction. SFN can stimulate the intrinsic apoptosis pathway by activating BCL-2 and suppressing inhibitors of apoptotic proteins (IAPs) (96). Treating DU145 and PC-3 prostate cancer cells with SFN (10, 20, and 40 μ M) enhanced cytochrome c levels by producing more ROS leading to apoptosis (97). Additionally, in human bladder cancer T24 cells, SFN arrested the cell cycle in G0/G1 phase via the p27 pathway (98). It also induced G2/M cell cycle arrest by stimulating p21 pathway and suppressing Cdc2/Cyclin B1 (99, 100).

SFN can inhibit cell growth and induce apoptosis in a dose dependent manner. Incubation of A549 cells treated with 30 μ M SFN induced G2/M arrest via p21 pathway (101). Upon treating Caco-2 cells with various concentrations of SFN, 25 μ M SFN had the greatest effect on enhancing UGT1A expression via Nrf2 pathway, while 75 μ M SFN induced G1/G2 arrest and apoptosis via decreasing bcl-2 level and enhancing bax (102). When treating colorectal cancer (CRC), higher concentrations of SFN (12.5 and 25 μ M) produced apoptosis through decreasing caspase-3 and increasing caspase-2, -3, -8, and -9. The low dose SFN generated a mitotic delay (103). SFN inhibited the growth and induced apoptosis in a dose- and time-dependent manner in MDA-MB-231 human breast cancer cells, whereby 30 μ M SFN induced apoptosis by increasing caspase-3 and reducing BCL-2. Furthermore, it induced S and G2/M cell-cycle arrest by upregulating p21^{WAF1} and p27^{KIP1} expression and down-regulating cyclin A, cyclin B1 and CDC2 levels (104).

In summary, for ITCs, in the context of *in vitro* cell line dose response, it appears it is dependent on the cell line, biomarker measured, and the chemical structure of the ITC, among others. Nevertheless, there is a dose-dependency of dose response. For instance, in human hepatoma cell line HepG2-C8 expressing the ARE-luciferase reporter, SFN increases ARE activity at concentrations up to 35 μ M (105). Beyond 35 μ M, ARE activity decreases due to cellular toxicity. This higher dose-dependent cellular toxicity could be blocked by adding exogenous glutathione (GSH). Interestingly, at lower doses of SFN, GSH attenuated ARE activity, however, at higher dose level, GSH enhances ARE activity, due to blockade of caspase 3 activation and apoptosis. These dosedependency effects of SFN are quite similar to phenolic antioxidants butylated hydroxyanisole (BHA) and its metabolite *tert*-butylhydroquinone (tBHQ) (106, 107), although SFN in general is more potent by about one order of magnitude. From the above discussion, in our experience, it appears that SFN would activate epigenetic events in low micromolar concentrations, then it would activate Nrf2 signaling in low tenths micromolar and activation of caspases/apoptosis around fifty-one hundred micromolar concentrations. We have also reviewed this dose-dependency effects previously (108).

1.2.3 Curcumin

Polyphenols are a group of compounds that have at least one aromatic ring with one or more hydroxyl functional groups attached (109). Natural polyphenols, which are widely present in foods and beverages from plant origin (110), are another category of phytochemicals that have been extensively studied for their health beneficial effects in many diseases, including cancer. It is well accepted that their potent antioxidant and antiinflammatory activities largely contribute to their anticancer efficacy. In addition, experimental evidence suggests dietary polyphenols are able to modulate molecular targets and signaling pathways regulating detoxification enzymes, cell survival, proliferation, differentiation, migration, and angiogenesis. (111).

While flavonoids and phenolic acids account for over 90% of all the natural polyphenols, curcumin, the bright yellow colored polyphenol rich in rhizomes of *Curcuma longa* (turmeric) has a distinct chemical structure. Curcumin is considered a highly promising chemopreventive agent since it fulfills several ideal characteristics such as low toxicity, affordability, and easy accessibility. Numerous studies using cell lines and animal models have demonstrated curcumin is effective in inhibiting tumor growth, which warranted clinical trials to test its safety and efficacy. However, phase I/II clinical trials showed poor bioavailability of curcumin in humans. Oral administration at doses up to 8 g resulted in undetectable levels of curcumin in blood (112). It does not seem practically possible to reach the *in vitro* effective dose of curcumin in humans. Efforts have been made to circumvent the bioavailability challenge by chemical structure modifications (curcumin analogs) and diverse delivery systems (liposome, nanoparticles, and conjugates). However, 17 out of 49 curcumin double-blinded placebo-controlled

clinical trial showed efficacy. Another 27 clinical trials of curcumin pointed to the therapeutic benefits (113). Curcumin doses ranged from 180 mg/day to 3,000 mg/day have been used in human. Under the treatment with standard chemotherapy protocols, the bioavailable curcuminoid preparation (180 mg/day) for a period of 8 weeks as adjuvant therapy in cancer patients with solid tumors can significantly improve quality of life and suppress systemic inflammation (114). In addition, in curcumin (total 3 g/day) with external-beam radiation therapy of up to 74 Gy patients with prostate cancer group, plasma total antioxidant capacity significantly increased and the activity of superoxide dismutase decreased compared with those at baseline (115). The clinical results still support the use of curcumin as an effective cancer preventive agent, particularly, in several colorectal cancer trials (116, 117). The interactions between curcumin and the host body system are expected to be more complicated. The following sections will focus on the relationship between the exposure and the response of curcumin.

An important molecular switch through which curcumin may mediate its health benefits is the transcription factor nuclear factor 2-related factor (Nrf-2). Curcumin has been shown to induce reactive oxygen species (ROS) scavenging enzymes. ROS is a bifunctional cellular molecule in cancer cells. It can drive DNA mutations in carcinogenesis, and it can trigger mitochondrial apoptosis. In a study where astrocytes were treated with 5-15 μ M curcumin expression of NQO1 and GST, members of phase II detoxification enzymes, increased significantly. Moreover, HO-1 mRNA and protein expression were elevated after a 6 h incubation with 5–25 μ M curcumin. However, higher concentrations of curcumin (50–100 μ M) caused a substantial cytotoxic effect with no change in HO-1 protein expression (118). And in renal epithelial cells, curcumin stimulated the expression of Nrf-2 in a dose- and time-dependent manner (119). Conversely, curcumin is able to generate cellular ROS to drive mitochondrial apoptosis to treat malignancies (120). Despite paradoxical roles in regulating cellular ROS, the overall anticancer effect of curcumin has been clearly shown in a number of studies.

Curcumin is a traditional remedy for inflammatory diseases (121). The antiinflammatory effects of curcumin have been postulated on the basis of a number of *in vitro* and *in vivo* studies(122, 123). Curcumin dose-dependently increased the number of pre-apoptotic and apoptotic cells in phorbol myristate acetate (124) and stimulated human neutrophilic granulocytes (125). The application of curcumin significantly inhibited the activity of neutrophilic granulocytes in a rat model of arthritis (an inflammatory arthropathy), which confirmed the anti-inflammatory properties of curcumin *in vivo*. Moreover, a curcumin injection given to mice prior to an intraperitoneal LPS administration led to an inhibition of LPS-induced increased MCP-1 (monocyte chemoattractant protein 1) mRNA levels (126). LPS-induced mRNA and protein levels of MCP-1 and interleukin-8 (IL-8) were reduced by curcumin treatment in human renal epithelial cells HK-2. Furthermore, curcumin prevented LPS-induced NF-kB DNA binding (126).

The cytoprotective effect of curcumin has been well studied. 20 μ M curcumin has been reported to protect human proximal tubule HK-2 cells from apoptosis and necrosis induced by Shiga toxin (127). Interestingly, the protective effect of curcumin against stx1 and stx2-induced injury on HK-2 cells is not related to its anti-oxidative properties. Curcumin can attenuate palmitate-induced apoptosis in MIN6 pancreatic β -cells through PI3K/Akt/FoxO1 and mitochondrial survival pathways (128). In this study, 10 μ M

curcumin improved cell viability and enhanced glucose-induced insulin secretory function. Curcumin treatment neutralizes ROS generated by palmitate induction. The epithelial-to-mesenchymal transition (EMT) of mature tubular epithelial cells in kidney is considered to contribute to the renal accumulation of matrix proteins associated with diabetic nephropathy. Studies suggest 20 µM of curcumin protects renal tubular epithelial cells from high glucose-induced EMT through Nrf2-mediated upregulation of HO-1 (129). Alinejad et al. demonstrated a combination of safranal, thymoquinone and 50 µg/mL of curcumin can block glucose/serum deprivation (GSD)-induced cell death and has the potential to be used for management of cerebral ischemia and neurodegenerative diseases (130). Theracurcumin is a highly bioavailable curcumin analog. It has been found that 10 µM of both theracurcumin and curcumin may have potential protective effects against sodium nitroprusside-induced cytotoxicity by free radical-scavenging and iron-chelating activities (131). Curcumin modulates peroxisome proliferator-activated receptor- γ signaling, which is a key molecule in the etiology of bronchopulmonary dysplasia (BSD). In vivo studies showed curcumin, when given daily at 5 mg/kg bw intraperitoneally, effectively protected against short-term and long-term hyperoxiainduced lung injury. Curcumin prevented hyperoxia-induced increases in cleaved caspase-3 and the phosphorylation of Erk1/2. Molecular effects of curcumin, both structural and cytoprotective, suggest that its actions against hyperoxia-induced lung injury are mediated via Erk1/2 activation and that it is a potential intervention against bronchopulmonary dysplasia (BPD) (132).

Curcumin has been found to alter the differentiation of many different cells. *In vitro* studies have shown that 0.5 µM curcumin increases the differentiation rate of

neurons in neural stem cells via Wnt signaling pathway (133). It's also reported curcumin can enhance EB directed differentiation of H-9 human embryonic stem cells (hESCs). 10 uM of curcumin significantly increased gene expression of cardiac specific transcription factor NKx2.5, cardiac troponin I, myosin heavy chain, and endothelial nitric oxide synthase during ES cell differentiation through modulation of the nitric oxide-cyclic GMP pathway (134). Myeloid-derived suppressor cells (MDSC) accumulate in the spleen and contribute to tumor growth, angiogenesis, and progression. Curcumin treatment inhibited cell proliferation and colony formation of cancer cells and decreased the secretion of murine IL-6 by MDSCs in a co-culture system. In addition, polarized MDSCs toward a M1-like phenotype with an increased expression of CCR7 and decreased expression of dectin 1 (135). Also, 20 µM curcumin inhibited differentiation of adipocytes and cardiac fibroblasts. Adipocyte differentiation is a key process in determining the number of mature adipocytes in the development of obesity. Curcumin has been reported to have an anti-adipogenic function both in 3T3-L1 murine cells and in human primary preadipocytes (136). The differentiation of cardiac fibroblasts (CFs) into myofibroblasts and the subsequent deposition of the extracellular matrix is associated with myocardial fibrosis following various types of myocardial injury. Treatment with 20 μM curcumin effectively suppressed TGF-β1-induced CF differentiation via Smad-2 and p38 signaling pathways. These findings suggest curcumin may be a potential therapeutic agent for the treatment of cardiac fibrosis (137, 138).

Studies in our laboratory suggest that curcumin increases activity of activator protein (AP-1)-luciferase in a concentration-dependent manner at 1-25 μ M in HT-29 cells transfected with an AP-1- luciferase reporter gene. The protein expression of endogenous

cyclin D1, a gene that is in downstream of AP-1, increased with 10 μ M curcumin treatment (139). Additionally, we found 10 and 50 μ M curcumin inhibited LPS-induced NF- κ B-luciferase activity in HT-29 cells stably transfected with a NF- κ B-luciferase construct (127). We found 2.5 and 5 μ M curcumin inhibited colony formation of HT-29 cells, whereas, inhibition of colony formation failed in stable knockdown of deleted in lung and esophageal cancer 1 (DLEC1) cells. Furthermore, we observed 5 μ M curcumin up-regulated the mRNA expression of DLEC1 and decreased CpG methylation of the DLEC1 promoter in HT-29 cells. We further discovered 5 μ M curcumin down-regulated protein expression of DNA methyltransferases and subtypes of histone deacetylases, such as HDAC4, 5, 6 and 8 (140).

Furthermore, treatment with 50 μ M curcumin induced apoptosis in colon, leukemia, breast, hepatocellular and ovarian carcinoma cell lines. However, curcumin failed to display cytotoxicity in cell lines established from lung, kidney, cervix, prostate and CNS malignancies. The mechanism of curcumin-mediated apoptosis was determined to be related to the generation of ROS. The addition of N-acetyl cysteine (109), a ROS scavenger, during curcumin treatment resulted in the disappearance of apoptosis. Additionally, curcumin's failure to exhibit cell death in some cell lines is due to the overexpression of Hsp70 in the cells which protect cells from apoptosis (141). Several studies investigated the relationship of ROS level-effect and apoptosis-induction of curcumin. Different dosage effects of curcumin on cell death types in a human osteoblast cell line were explored. Curcumin at concentrations lower than 25 μ M caused apoptosis in human osteoblasts HFOb 1.19 cells, through the activation of JNK and cleavage of caspase-3, PARP and PAK2. However, 50-200 μ M curcumin induced necrotic cell death

instead of apoptosis in human osteoblasts. In addition, 12.5-25 µM curcumin directly increased oxidative stress demonstrated by the use of the cell permeable dye 2', 7'dichlorofluorescin diacetate (DCF-DA), an indicator for intracellular ROS, nevertheless, 50-200 μ M curcumin had much less activity. Moreover, NAC or α -tocopherol (ROS scavengers) pre-treatment significantly decreased intracellular ROS levels and 12.5-25 µM curcumin-induced apoptosis to necrosis. Pre-treatment with antimycin or 2deoxyglucose reverted apoptosis induced by 12.5-25 µM curcumin to necrosis which could induce ATP (a mediator of apoptosis versus necrotic cell death) depletion (142). Although curcumin caused cell death of HL-60 cells in a concentration- and timedependent manner, its effects on ROS production differed with fluctuations in concentration. Curcumin at less than 25 µM decreased ROS production, while 50-100 μ M enhanced ROS generation. Furthermore, the addition of antioxidant agents, ascorbic acid (ASA), NAC and glutathione (GSH), promoted the antioxidant and anti-cancer activities of curcumin at low concentrations (143). These studies were consistent with reports curcumin at low concentrations (<10M) prevents GSH depletion and higher concentrations decrease GSH levels (144). Proteasome inhibitors have been reported to cause apoptosis in cancer cells (18). Curcumin has been shown to demonstrate biphasic dose-response proteasome activity in human keratinocytes, specifically, 0.3 μ M and 1.0 µM curcumin increased proteasome activity by 34% and 46%, respectively. However, curcumin at higher concentrations of 3 and 10 µM decreased proteasome activity by 32% and 46%, respectively (145). It was suggested the biphasic dose-response is through a homeostasis mechanism, in which a low dose of agents stimulates signaling pathways to protect the organism, whereas a high dose displays an inhibitory effect (146) (147). A

similar phenomenon has been observed for many natural compounds, such as resveratrol (148) (22), berberine (149), clove and cinnamon essential oils (150).

In a study where dose-dependent differences on DNA-damage and the p53 response of quercetin and curcumin, whose chemical structures are similar, in HT1080 cells (a human cell line with wild-type p53), 8 μ M curcumin significantly increased the expression of phosphorylated H2AX, a biomarker of DNA damage, while as much as 20 μ M, quercetin could displayed similar activities. Curcumin (4 and 7 μ M, respectively) increased the protein expression of p53 and p-p53 (ser15) at lower concentrations than quercetin (30 and 20 μ M, respectively). It was suggested even with similar chemical structures, the two natural compounds displayed different effects on DNA-damage response patterns in terms of dose and cell fate (151)

Curcumin is recognized as an epigenetic modulator and plays a major role in the prevention of disease. Studies in our laboratory demonstrated that 10 μ M curcumin prevents prostate cancer progression via CpG demethylation in the promoter region of *Nrf2* in TRAMP-C1 cells (152). In HT-29 cells, curcumin inhibited anchorage-independent growth by decreasing CpG methylation of the promoter region of the tumor suppressor gene (153). After treatment with curcumin (2.5 and 5.0 μ M) for 5 days, protein levels of DNMT1, DNMT3b, HDAC4, HDAC5, HDAC6, and HDAC8 decreased (140). In human prostate LNCaP cells, curcumin treatment decreased the methylation of CpG islands of *Neurog1* as well as the binding ability of methyl-CpG binding protein 2 (MeCP2). The expression of HDAC1, 4, 5, and 8 increased whereas the expression of HDAC3 and the total HDAC activity decreased upon 2.5 μ M-curcumin treatment. ChIP analysis showed curcumin decreased the enrichment of H3K27Me3 in the *Neurog1*

promoter region (154). In breast cancer cell lines MCF7 and MDA MB 231, DNMT (i.e., DNMT1, DNMT3a, and DNMT3b) transcript levels and the protein levels of DNMT1, HDAC1, and MeCP2 decreased after treatment with 10 µM curcumin (155). In addition to curcumin, the curcumin analogue FN1 and liposomal-formulated curcumin (lipocurc) have been reported to have a protective effect on the development of disease (156, 157). Our previous work demonstrates FN1 is more potent than curcumin in activating the Nrf2-ARE pathway and inducing expression of Nrf2 and its downstream detoxifying enzymes. Not surprisingly, FN1 inhibited colony formation of prostate TRAMP C1 cells by decreasing the expression of Keap1 and CpG hypomethylation of the Nrf2 promoter (156). In a Park 7 (DJ-1)-knockout rat model of Parkinson's disease, lipocurc was found to improve the motor impairment and prevent neuronal apoptosis by targeting HDACs (157). Approximately 20-40% miRNAs are located close to CpGs and are suppressed by epigenetic mechanisms (158). Epigenetic compounds can induce upregulation of some miRNAs through reducing the percentage of CpG methylation of the promoters of miRNAs. An example is miR-203, a miRNA downregulated in bladder cancer. Restoration of miR-203 expression reduced cell viability, invasiveness and migration, and increased the number of cells in the G0–G1 phase of the cell cycle through Akt2 and Src signaling. Curcumin treatment (10 μ mol/L) induced demethylation of miR-203 promoter and subsequent augmentation of miR-203 expression (159).

1.3 Pathways targeted in cancer chemoprevention

As discussed, triterpenoids, ITCs and curcumin exude their chemopreventive properties through a variety of signaling pathways (Figure 3)c. These pathways are explored in greater details in this section.

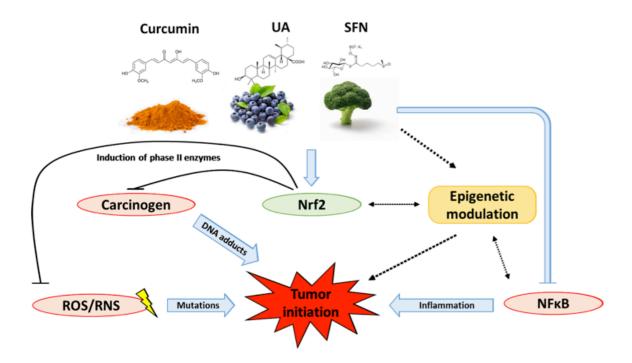


Figure 3. Schematic diagram on mechanisms of phytochemicals (curcumin, UA, SFN) inhibiting tumor initiation. Curcumin, UA, and SFN have the ability to epigenetically modulate Nrf2, which results in the inhibition of initiation and pro-inflammatory processes leading to the prevention of tumor initiation.

1.3.1 Nrf2-mediated ARE signaling

The anti-oxidant stress defense system is responsible for the direct inactivation or conjugation of reactive oxygen species (ROS) and reactive nitrogen species (RNS). ROS/RNS into less deleterious molecules. In response to reactive species the cell has implemented an antioxidant defense system encompassing both enzymatic and nonenzymatic mechanisms (160). The enzymatic system includes superoxide dismutases (SODs), catalase, and glutathione peroxidases (GPxs). These enzymes directly inactivate ROS/RNS. In addition to the direct inactivation of ROS/RNS, there are other antioxidant enzymes that facilitate the detoxification of ROS/RNS using reduction/conjugation

reactions and the recycling of thiols. The enzymatic soluble products of these reactions are easily excreted. These enzymes include phase II enzymes (e.g. NAD(P)H: quinone glutathione GST: oxidoreductase. NOO-1; S-transferases. UDP-glucuronosyl transferases, UGT; among others). These enzymes play an important role in this protective machinery as detoxifying enzymes that conjugate endogenous polar molecules to phase I metabolites, thereby facilitating xenobiotics (including carcinogens) elimination and excretion (127). Activation of these cytoprotective enzymes is important for maintaining cellular homeostasis towards environmental challenges. Activation of the genes encoding these enzymes and proteins are regulated in large part by the transcription factor nuclear factor erythroid 2-related factor 2 (Nrf2), a member of the NF-E2 family of nuclear basic leucine zipper (bZIP) transcription factors. Nuclear factor erythroid 2related factor 2 (Nrf2), a member of the NF-E2 family of nuclear basic leucine zipper (bZIP) transcription factors, is a master regulator controls the expression of phase II/antioxidant enzymes. Under normal conditions, Nrf2 is bound to Kelch-like erythroid cell-derived protein with CNC homology (82)-associated protein 1 (Keap1). Keap1, an adaptor protein for a Cullin 3 (Cul3)-based ubiquitin E3 ligase, sequesters Nrf2 in the cytosol and ensures its degradation by the proteasome. Upon oxidative stress, Nrf2 is released by Keap1 and translocates to the nucleus where it heterodimerizes with Maf and binds the ARE/EpRE of the antioxidant defense system genes. Unsurprisingly, Nrf2 has been shown to play an essential role in the protection of carcinogenic events and Nrf2 KO mice are susceptible to the initiation, promotion, and progression of cancer (161). As the master regulator of the antioxidant response, unsurprisingly, the induction of Nrf2 has become an attractive target in chemoprevention.

Oxidative stress occurs when there is an imbalance between the anti-oxidant defense system and the production of ROS/RNS (162, 163). The general terms ROS and RNS are given to the reactive species generated from the interaction of free radicals such as superoxide anion, hydroxyl radical, and nitric oxide with metals, oxidants, and reductants found in cells. ROS/RNS are important cellular messengers involved in a number of physiological processes: cellular respiration, immune response, ion transport, apoptosis, neuromodulation, and transcription (164). While important secondary messengers, the activities of ROS/RNS can exhibit a double-edged sword. In addition to endogenous production, exogenous production of ROS/RNS can be initiated through UV radiation, environmental pollutants, lipid peroxidation, and inflammatory cytokines (165). The anti-oxidant stress defense system is responsible for the direct inactivation or conjugation of ROS/RNS into less deleterious molecules. An excess of ROS/RNS can cause an imbalance in the system and induce oxidative stress; a hallmark of a number of neurodegenerative diseases and, of most importance here, cancer (166, 167). The excess oxidative stress results in the induction of the NFK-B signaling cascade and thus, activation of cytokines and the production of acute inflammation. Nuclear factor kappa B $(NF\kappa B)$ is a transcription factor lays on the molecular node linking inflammation, cell survival, and cancer progression signals (168). NF κ B is normally sequestrated by its cellular suppressor IkB in the cytosol. Upon activation, IkK phosphorylates IkB consequently leads to the degradation of $I\kappa B$, accompanied with release and nuclear translocation of NFkB. A considerable number of NF-kB target pro-inflammatory genes have been shown to be involved in cancer development, including various cytokines,

chemokines, cyclooxygenase-2 (COX-2), and inducible nitric oxide synthase (iNOS) among others. The inability of the cells to eliminate the exogenous culprits results in chronic inflammation. The immune cells involved in the inflammation cascade continuously use ROS/RNS as a means to recruit more immune cells. The excess production can lead to the mutagenesis of oncogenes and tumor suppressing genes and, ultimately, the initiation of cancer.

1.3.3 Epigenetic modulation

The term epigenetics is defined as heritable changes in gene expression without changes in the integrity of the DNA sequence (169). Recently, numerous evidences have shown that initiation and progression of carcinogenesis involves aberrant epigenetic alterations. Unlike genetic mutations, changes on the epigenetic level are considered reversible. Given that epigenetics lies on the molecular interface between genetics and environmental factors, there is a growing interest in evaluating the potential of dietary phytochemicals that blocks or reverses the epigenetic abnormity in cancer development. Epigenetic alterations encompass DNA methylation, histone modifications, and microRNA (mRNA) expression changes. Epigenetic alterations such as DNA methylation and histone modifications have been shown to contribute to the development and progression of cancer (170). DNA methylation is the mostly characterized epigenetic event in many cancers (139), which occurs at the 5' position of the cytosine residues within CG dinucleotides through addition of a methyl group by DNA methyltransferases (DNMTs). CpG dinucleotides tend to be grouped in regions known as CpG islands in the promoters of genes. In normal cells, the majority of CpG islands remain unmethylated leaving an open structure for the transcriptional machinery to bind and induce expression.

In cancer cells, certain areas of the promoter region of tumor suppressor genes are hypermethylated leading to the silencing of the tumor suppressor genes (171, 172). In addition, DNA methylation can also serve as a binding site for proteins such as methyl CpG binding domain proteins (MBDs) and methyl CpG binding protein 2 (MeCP2). These proteins can interact with a co-repressor complex to repress transcription. The corepressor complex includes proteins such as histone deacetylases (HDACs) involved in the modification of histones. Histone modification is tightly associated with DNA methylation. Histone modifications play an important role in chromatin structure. Chromatin is a densely packed macromolecular complex composed of histones, DNA, and non-histone proteins. Chromatin serves to package a large amount of material into the nucleus of a cell and to influence DNA replication. Histones play an essential role in chromatin structure and post-translational modifications of histories regulate gene expression. Some of these modifications include acetylation, methylation, phosphorylation, ubiquitination, and sumoylation (160). These modifications typically occur at serine, lysine, and arginine resides of N-terminal histone tails. The enzymes responsible for these modifications include histone acetyltransferases (41), histone methyltransferases (HMTs), histone demethylases (HMTs), and HDACs. The influence of these modifications on chromatin structure can either activate or suppress transcription.

The interplay of DNA methylation with histone modifications, transcription factors, transcriptional coactivators, and DNA binding proteins determines the status of gene transcription (127). Epigenetic modifications such as DNA methylation and histone modifications have been shown to be a hallmark of cancers (173-177). The promoter

region of human GSTP1 is hypermethylated in approximately 7-100% of prostate cancer specimens (178-180). Aberrant epigenetic modifications have also been associated with the development and progression of skin cancer (49, 181-183). Thus, targeting the reversal of DNA methylation and histone modifications presents a novel strategy for the prevention and treatment of cancer. The FDA has already approved chemotherapeutics targeting DNMTs and HDACs (184). However, their usage has been limited by adverse events. Targeting epigenetic modifications for the prevention or treatment of cancers using dietary phytochemicals has become increasingly more attractive. Dietary phytochemicals may prevent cancer through epigenetic modifications (185-187).

1.3.4 Cancer Stem Cells and Apoptosis

Stem cells are characterized by their ability to differentiate into a heterogenous population of specialized cells, their ability to self-renew, and their ability to balance self-renewal and differentiation based on environmental needs (188). Two of the pathways demonstrated to be involved in stem cell regulation and differentiation include Sonic hedge hog and Notch signaling pathways (189). Similarly, cancer stem cells (CSCs) are able to self-renew and differentiate using common pathways (186). However, CSCs are able to form tumors when implanted into animals (190). For this reason, CSCs are often referred to as tumorigenic cells or tumor initiating cells and are fundamental to the initiation and relapse of many tumor types (190-192) CSCs were first identified in 1997 (193) where CD34+CD38- cells derived from leukemic patients were able to initiate cancer in immunodeficient mice. Currently, cancer stem cells have been identified in a number of cancers including breast and colon (194). Pathways implicated in cancer stem cell renewal include Wnt (195), janus kinase (Jak), bone morphogeneic protein (BMP),

and octamer-binding transcription (Oct-4) signaling pathways (194). Natural dietary compounds have been shown to regulate CSCs by increasing their sensitivity to chemotherapeutic agents, enhancing their differentiation, and inhibiting their self-renewal signaling (196, 197).

One of the most important processes involved in regulating the proliferation of cells is apoptosis. The process of apoptosis can be divided into intrinsic and extrinsic pathways. The intrinsic pathway is in large part controlled by Bcl-2 family members, while the extrinsic pathway, is mediated by tumor necrosis factor (TNF) family members. The extrinsic pathway is initiated with the respective ligand binding to death receptors such as TNF-related apoptosis-inducing ligand receptor (TRAILR) and FAS. Oligomerization of the receptors leads to the activation of caspase-8 and caspase-10, which cleave caspase-3 and caspase-7 and ultimately leads to apoptosis (198). The intrinsic pathway is activated when stress stimuli induces BCL-2 homology domain 3 (BH3)-only protein activation which leads to BAX and BAK activity and consequently mitochondrial outer membrane permeabilization (MOMP). This results in the release of cytochrome c which interacts with apoptotic protease activating factor 1 (APAF1), which activates caspase-9. Caspase-9 then activates caspase-3 and caspase-7, which leads to apoptosis (198). Cancer cells have developed mechanisms by which apoptosis is evaded through the mutation of essential genes involved in regulation of the process. A number of phytochemicals have been shown to induce apoptosis in cancer cells/in vivo models (Table 1).

Table 1. The diverse anti-cancer properties of phytochemicals are driven by dose and model system.

Cancer/ Model Type	Cell Line/Animal Model	Concentration/ Dose	Phytochemical	Reference	Process/es Affected
Bladder	T24 cells	5-20μΜ	SFN	Shan, Sun (98)	A ¹
Breast	SUM159 xeonograph mouse model	50mg/kg	SFN	Li, Fu (96), (127)	CSCs ²
Breast	PyMT transgenic mice	8mmol/kg	PEITC	Singh and Singh (83)	CSCs ²
Breast	MDA-MB- 231	30µM	SFN	Kanematsu, Uehara (104)	A ¹
Colon	COLO 25	10μΜ, 50μΜ	UA	Chun, Kundu (199)	AI ³
Colon	DSS-induced acute murine colitis model	10mg/kg, 20mg/kg	UA	Chun, Lee (20)	AI ³
Colon	ApcMin/+ mouse model	3-13nmol/g	SFN	Hu, Khor (40)	A^1 , AI^3
Colon	(DSS)- induced acute colitis mouse model	25mg/kg/day	SFN	Wagner, Will (61)	NMAS ⁴
Colorectal	Caco-2 cells	5μΜ, 10μΜ	UA	Ramos, Pereira- Wilson (21)	NMAS ⁴
Colorectal	HT29 cells	25μΜ, 50μΜ	PEITC, SFN	Jeong, Kim (56)	A^1 , AI^3
Colorectal	Caco-2 cells	25μΜ, 75μΜ	SFN	Wang, Chen (102)	NMAS ⁴ , A ¹ (respectivel y)
Colorectal	CRC cells	12.5µM, 25µM	SFN	Chen, Tang (103)	A ¹
Gastro- intestinal related	Rat	40 μmol/kg/day	SFN	Munday and Munday (45)	NMAS ⁴
Glioma	A375 cells	10µM	UA, OA	Bonaccorsi, Altieri (25)	CSCs ²
Human study	РВМС	105mg	SFN	Myzak, Tong (69)	EM ⁵
Laryngeal carcinoma	Hep-2	10µM	PEITC	Dai, Wang (93)	A ¹
Leukemia	HL60, U-937, THP-1 cells	10μM, 20μM, 30μM	UA	Zhang, He (26)	CSCs ²
Leukemia	Promyelocytic leukemic cells	0.2-100µM	SFN	Fimognari, Lenzi (80)	CSCs ²

Liver	Male Wistar rat model	20mg/kg	UA, OA	Gayathri, Priya (17)	AI ³ , NMAS ⁴
Liver	HepG2 cells and Hepatocytes	1-10µM	SFN	Bacon, Williamson (46)	NMAS ⁴
Liver	HepG2 cells	2μΜ-20μΜ	SFN	Hong, Freeman (51)	NMAS ⁴
LPS- stimulated Inflammat ion	RAW 264.7 cells	25μΜ, 50μΜ	SFN	Heiss and Gerhauser (57)	AI ³
Melanoma	U87 cells	15µM	UA, OA	Bonaccorsi, Altieri (25)	CSCs ²
Neuronal related	PC12 cells	20μΜ, 40μΜ	UA, OA	Tsai and Yin (22)	CSCs ² , NMAS ⁴
Non-small cell lung	A549 Nude Mouse Model	50mg/kg, 100mg/kg	UA, OA	Cho, Rho (12)	A ¹
Non-small cell lung	H1299 and A549 cells	30µM	UA	Wu, Zhao (23)	EM ⁵
Non-small cell lung	L9981 cells	12.5µM, 20µM	PEITC	Yan, Zhu (94)	A ¹
Non-small cell lung	L9981 cells	5μΜ, 9.7μΜ	PEITC	Wu, Zhu (95)	AI ³
Non-small cell lung	A549 cells	30µM	SFN	Zuryn, Litwiniec (101)	A ¹
Ovarian	SKOV3 xenograft athymic BALB/c-nu mouse model	12.5-50μg/mL	UA	Zhang, Wang (27)	CSCs ²
Pancreatic	AsPC-1, MIA, PaCa-2, Panc- 28 cells	5-20µM	UA	Prasad, Yadav (16)	A^1 , AI^3
Pancreatic	Orthotopic Pancreatic Mouse Model	250mg/kg	UA	Prasad, Yadav (16)	A^1 , AI^3
Prostate	PC3 cells	80µM	UA	Zhang, Kong (200)	A^1 , AI^3
Prostate	PC3 cells, LNCaP cells	55μΜ, 45μΜ	OA	Kassi, Papoutsi (15)	A ¹
Prostate	PC3 cells	20μM & 30μM, 5μM & 7.5μM	SFN, PEITC	Xu, Shen (55)	AI ³
Prostate	LNCaP and PC3 cells	15µM	SFN	Wong, Hsu (63)	EM ⁵
Prostate	TRAMPC1	1μM, 2.5μM	SFN	Zhang, Su	EM ⁵

	cells			(66)	
Prostate	LNCaP	0.5-1µM	PEITC	Wang, Beklemishe va (201)	A^1 , EM^5
Prostate	LNCaP, PC3	2.5µM	PEITC	Zhang, Shu (74)	EM ⁵
Prostate	DU145 cells, PC3 cells	10μM, 20μM, 40μM	SFN	Singh, Srivastava (97)	A ¹
Prostate	BPH-1, LNCaP, PC3	15µM	SFN	Myzak, Hardin (70)	A^1 , EM^5
Skin	ICR Mouse Model	2µmol topical application	UA	Cho, Rho (12)	AI ³
Skin	Ca3/7 cells	5μΜ, 10μΜ	UA, OA	Kowalczyk, Walaszek (18)	NMAS ⁴ , AI ³
Skin	JB6 P+ mouse epidermal cells	5μΜ	UA	Kim, Ramirez (202)	EM ⁵
Skin	Nrf2 (+/+) and Nrf2 (-/-) mice	100nmol topical application	SFN	Saw, Huang (62)	NMAS ⁴ , AI ³
Skin	JB6 P+ mouse epidermal cells	2.5μΜ, 5μΜ	SFN	Su, Zhang (203)	EM ⁵
T-cell lymphoma	Hut-78 cells	10-80µM	UA	Yang, Shi (11)	\mathbf{A}^{1}
Thyroid	ARO cells	20µM	UA, OA	Bonaccorsi, Altieri (25)	CSCs ²
Thyroid	MTC-SK cells	10µM, 20µM	UA	Aguiriano- Moser, Svejda (13)	A ¹
Immune	Activated T cells, B cells, and macrophages	5μΜ	UA	Checker, Sandur (19)	AI ³
Anti- oxidative Stress	Nrf2 (+/+) and Nrf2 (-/-) mice	40mg/kg	PEITC	Hu, Xu (48)	NMAS ⁴
Neuronal	Astrocytes	5-15μM, 50- 100μM	Curcumin	Scapagnini, Colombrita (118)	NMAS ⁴ , A ¹ (respectivel y)
Differentia tion	Neuronal stem cells	0.5µM	Curcumin	Chen, Wang (133)	CSCs ²
Differentia tion	Embryonic stem cells	10µM	Curcumin	Mujoo, Nikonoff (134)	CSCs ²
Bone	HFOb 1.9	25µM	Curcumin	Chan, Wu	A^1

	cells			(142)	
Leukemia	HL60 cells	25μΜ	Curcumin	Chen, Wanming (143)	AI ³ , NMAS ⁴
Fibrosarco ma	HT1080 cells	8μΜ	Curcumin	Sun, Ross (151))	A^1
Colon	HT29 cells	2.5µM, 5µM	Curcumin	Guo, Shu (140)	EM ⁵
Prostate	LNCaP cells	2.5µM	Curcumin	Shu, Khor (154))	EM ⁵
Prostate	TRAMPC1 cells	10µM	Curcumin	Khor, Huang (152)	EM ⁵
Breast	MCF7 and MDA MB 231 cells	10µM	Curcumin	Mirza, Sharma (155)	EM ⁵

¹Apoptosis

² Cancer Stem Cells

³Anti-inflammation

⁴ Nrf2-mediated ARE Signaling

⁵Epigenetic Modulation

1.4 Perspective

Cancer is one of the leading causes of death in the United States and around the world. Modern diagnostics and treatment regimens have improved patient care, but advanced metastasized cancers remain a challenge to treat. Hence alternative strategies have to be integrated into regimens to reduce the burden of cancer using relatively non-toxic phytochemicals and or pharmaceutical agents such as non-steroidal anti-inflammatory drugs (NSAIDs), selective estrogen receptor modulators (SERMs), aromatase inhibitors, HMG-CoA reductase inhibitors (statins), among others.

The idea of cancer prevention by dietary and nutritional phytochemicals can be further refined to "NutriPrevention" versus "Chemoprevention". In 2013, the USDA

suggested "Myplate" replacing the previous "Food Pyramid", whereby half of the plate/meal includes fruits and vegetables for healthy living. This could be defined as "NutriPrevention", where low level phytochemicals would presumably effect and impact the epigenome of "healthy" cellular defense genetic pathways including the Nrf2regulated anti-oxidative stress/antioxidant pathways and anti-inflammatory pathways discussed above. However, if one were to be exposed to high environmental risk factors such as smoking, "bad/unhealthy diets", alcohol, environmental pollutants, occupational carcinogens, and/or other environmental factors/insults coupled with inherent genetics/epigenetics "stem cells" that could drive "initiated cells", then it would logically require higher pharmacological doses of certain dietary phytochemicals and/or non-toxic pharmaceutical agents and this may be classified as "PharmacoPrevention". During cancer remission, in order to prevent cancer from recurring, or high risk individuals with chronic inflammation diseases such as Inflammatory bowel disease (IBD), then one use "ChemoPrevention" with relatively higher but non-toxic doses would phytochemicals/botanicals alone and/or in combination with relatively nontoxic drugs such as NSAIDs, SERMs, HMG-CoA reductase inhibitors, among others. Analogously, these concepts could be applicable to other chronic diseases which are utilizing similar signaling pathways such as oxidative stress and inflammation.

1.5 Conclusions

In general, for many phytochemicals, it would appear much higher concentrations are required to elicit biological effects in *in vitro* cell culture models as compared to *in vivo* animal models. This phenomenon could be due to a variety of reasons. Most cell lines are tumor cell lines, thus, behave quite differently to their *in vivo* counterparts. They may possess efflux transporters that can exclude compounds from entering the cells, have very different cellular signaling response pathways as compared to normal cells, lack of active metabolism processes forming potential active metabolites and lack of endocrine-paracrine signaling as compared to *in vivo*. However, for many epigenetic effects, it appears that lower concentrations of phytochemicals are able to elicit an epigenetic response such as it relates to CpG methylation, DNMTs or HDACs in cell culture models. Further *in vitro-in vivo* animal and human studies would be warranted to ascertain these observations.

Chapter II

Triterpenoid ursolic acid enhances Nrf2 expression in mouse epidermal cells through

epigenetic modifications³

³A portion of this chapter has been published in *The Journal of Nutritional Biochemistry*: Kim H and <u>**Ramirez** C</u> *et al* (2016). Triterpenoid ursolic acid enhances Nrf2 expression in mouse epidermal cells through epigenetic modifications. J Nutr Biochem. 2016 Jul;33:54-62.

2.1 Introduction

UA is a lipophilic pentacyclic triterpenoid derived from apple peels, basil (Ocimum basilicum), blueberry (Vaccinium spp.), cranberry (Vaccinium macrocarpon), heather flower (*Calluna vulgaris*), labrador tea (*Ledum groenlandicum* Retzius), olive (Olea europaea), pear (Pyrus pyrifolia), and rosemary (Rosmarinus officinalis) (199, 200). UA exerts various biological effects, including anti-inflammatory, antiatherosclerosis, anti-diabetic, anti-viral, and anti-cancer activities. Additionally, UA has the ability to decrease reactive oxygen species (ROS) toxicity and increase the activity of antioxidant enzymes (199). In vivo and in vitro studies have shown that UA inhibits benzo[a]pyrene (B[a]P)- and 7,12-dimethylbenz[a]-anthracene (DMBA)-induced tumor initiating activity, suppresses TPA-induced skin inflammation and tumor promotion in CD-1 and ICR mice, and induces apoptosis in M4Beu human melanoma cells (201-203). Additionally, UA hinders UVA-induced ROS production, lipid peroxidation, MMP-2 expression, and DNA damage in human keratinocyte HaCaT cells (204). Recently, studies have revealed that UA protects the brain against cerebral ischemia and protects the liver against CCl₄-induced damage in mice via the nuclear factor E2-related factor 2 (Nrf2) pathway (205, 206). Notably, we have previously shown that dietary phytochemicals, such as apigenin, curcumin, 3,3'-diindolylmethane, γ -tocopherol-rich mixture of tocopherols, sulforaphane, tanshinone IIA, Z-ligustilide and radix angelica, regulate Nrf2 activation via epigenetic modifications (66, 67, 152, 207-211); however, the effect of UA on the epigenetic regulation of Nrf2 has not been previously examined.

Skin cancer is one of the most prevalent malignant tumors, contributing to the increasing mortality rate of cancer in the US (212). An imbalance between the production

and removal of ROS in the epidermis and dermis may lead to skin tumorigenesis. Exposure to ultraviolet (UV) radiation, ozone layer depletion, excessive time spent outdoors, indoor tanning, and noxious environmental insults induce ROS overproduction (213). Cells contain a self-defense mechanism that removes ROS through the synthesis of detoxifying/antioxidant enzymes, which include HO-1, NQO1, uridine 5'-diphospho-glucuronosyltransferase (UDP-glucuronosyltransferase, UGT), and GST (214). Unfortunately, these antioxidant defenses have limited capacity and can be impaired during certain conditions, thereby leading to a redox imbalance that promotes the development of skin cancer.

The genes encoding cytoprotective detoxifying/antioxidant enzymes are controlled by the transcription factor Nrf2. Under homeostatic conditions, Nrf2 is bound to Keap1 in the cytoplasm. Nrf2 is targeted for polyubiquitination and proteasomal degradation through the formation of a Keap1- and Cullin 3-based-E3/Rbx1 ligase complex. Under stress conditions, Nrf2 dissociates from Keap1 and translocates to the nucleus, where it binds to the AREs of target protective genes and activates transcription (215). Nrf2 has long been recognized as a pivotal player in the prevention of many diseases, including skin cancer. Nrf2 knockout mice are more susceptible to airway inflammation and asthma, striatal toxicity and behavioral dysfunction, colorectal carcinogenesis, gastric neoplasia, and skin carcinoma upon DMBA/TPA exposure compared with wild-type mice (52-54, 216, 217). Moreover, a recent study demonstrated that low Nrf2 expression is associated with the oncogenic transformation of mesenchymal stem cells and poor survival in patients with skin cutaneous melanoma, kidney clear cell carcinoma, and prostate cancers (218). Therefore, understanding the

molecular mechanisms by which Nrf2 expression can be altered to slow or prevent the progression of skin cancer is of great importance.

Frequent epigenetic changes during the early stages of tumorigenesis lead to genetic aberrations and promote cancer development (219). Epigenetics refers to changes in gene expression by DNA methylation and/or post-translational histone modification without alterations of the DNA sequence. The modifications to DNA and histories are driven by DNMTs and HDACs, respectively (220). DNA methylation occurs at the 5' position of cytosines within CpG dinucleotides found in CpG islands. The silencing of tumor suppressor genes by the hypermethylation of CpG islands within promoter regions is a hallmark of cancer. Such methylation in CpG islands impedes the binding of transcription factors and represses transcription. Moreover, protein complexes, such as the MBD family and HDACs, are recruited to specific loci where they alter the structure of the chromatin and facilitate gene silencing (220-222). As such, epigenetic modifications as preventive targets have been the focus of numerous studies in cancer, largely due to the notion that epigenetic changes are reversible and affect numerous cellular events in tumorigenesis. The FDA has approved four epigenetic agents for clinical use: the DNMT inhibitors 5-azacytidine (5-aza, azacytidine) and 5-aza-2'deoxycytidine (decitabine) and the HDAC inhibitors suberoylanilide hydroxamic acid (vorinostat) and depsipeptide (romidepsin) (184). However, off-target action, drug resistance and their selective applicability to selective cancers have mitigated their use in treating cancer (184, 223). As a way of circumventing this challenge, natural compounds found in fruits, vegetables, teas, and medicinal plants have attracted considerable interest due to their ability to overcome oxidative stress and regulate epigenetic events at nontoxic concentrations (5, 224-226). The aim of this study is to demonstrate the chemopreventive effect of UA and identify UA-induced epigenetic modifications in mouse epidermal cells. We demonstrated that UA activated the Nrf2 pathway by demethylating the Nrf2 promoter and reducing the expression of DNMTs and HDACs, resulting in the inhibition of TPA-induced cell transformation.

2.2 Materials and Methods

2.2.1 Reagents and Antibodies

Minimum essential medium (MEM), fetal bovine serum (FBS), penicillinstreptomycin (10,000 U/ml), versene, and Trypsin-EDTA were supplied by Gibco (Grand Island, NY). A Cell-Titer 96 Aqueous One Solution Cell Proliferation Assay Kit was obtained from Promega (Madison, WI). Platinum Taq DNA polymerase was purchased from Invitrogen (Grand Island, NY). Tris-HCl precast gels, turbo transfer buffer, and PVDF membranes were obtained from Bio-Rad (Hercules, CA). Tris-Glycine-SDS running buffer was from Boston BioProducts (Ashland, MA). Super Signal enhanced chemiluminescent substrate, NE-PER Nuclear and Cytoplasmic Extraction Reagents, and BCA Protein Assay Kit were purchased from Thermo (Rockford, IL). Antibodies against Nrf2 (C-20), HO-1 (C-20), NQO1 (H-90), UGT1A1 (V-19), and actin (I-19) were obtained from Santa Cruz Biotechnology (Santa Cruz, CA) and Abcam (Cambridge, MA). Anti-acetyl histone H3 was from Millipore (Billerica, MA). The protease inhibitor cocktail, radioimmunoprecipitation (RIPA) buffer, and antibodies against HDACs (HDAC1, HDAC2, HDAC3, HDAC4 and HDAC6) were supplied by Cell Signaling Technology (Beverly, MA). The anti-HDAC8 antibody was obtained from Proteintech Group (Chicago, IL), and the anti-HDAC5, -HDAC7, -DNMT3a and -DNMT3b

antibodies were from Abcam (Cambridge, MA). Anti-DNMT1 was supplied by Novus Biologicals (Littleton, CO). All other chemicals, unless otherwise noted, were obtained from Sigma (St. Louis, MO).

2.2.2. Cell culture

JB6 P+ mouse epidermal cells were obtained from the American Type Culture Collection (Manassas, VA). The cells were cultured in MEM supplemented with 5% FBS and penicillin-streptomycin (100 units/ml) at 37°C under a 5% CO₂ atmosphere. JB6 P+ cells stably transfected with shMock and shNrf2-knockdown (KD) were maintained in the same medium as JB6 P+ cells and 2 μ g/mL puromycin was added.

2.2.3. Cell viability assay

JB6 P+ cells were seeded at a density of 5×10^4 cells/well into 96-well plates in 5% FBS/MEM. After 24 h, the medium was removed, and the cells were treated with UA (1 and 2.5 μ M) in 1% FBS/MEM, where 0.1% DMSO was used as the vehicle control group. The medium containing UA was changed every 2 days for 3 and 5 days. On the day of the assay, 20 μ l of Cell Titer 96 Aqueous One Solution in 100 μ l of 1% FBS/MEM was added to each well, and the cells were then incubated for 1 h at 37°C in a 5% CO₂ incubator. The absorbance was measured at 490 nm.

2.2.4. Anchorage-independent cell transformation assay

JB6 P+ cells (8 × 10³/ml) were suspended in 1 ml of basal medium Eagle (BME) containing 0.33% agar and plated over 3 ml of a solidified BME consisting of 0.5% agar and 10% FBS in 6-well plates in the presence of TPA (20 ng/ml) alone or together with 1 or 2.5 μ M UA. The cells were maintained at 37°C in a 5% CO₂ incubator for 2 weeks.

The cell colonies were photographed using a Nikon ACT-1 microscope (Version 2.20; LEAD Technologies) and counted using Image J (NIH, Bethesda, MD).

2.2.5 RNA extraction and quantitative real-time PCR (qPCR)

Total RNA was extracted from JB6 P+ cells on days 3 and 5 after treatment using the RNeasy mini kit (Qiagen, Valencia, CA). For cDNA synthesis, 0.5 µg of total RNA was incubated with oligo $(dT)_{16}$ primers and MultiScribe reverse transcriptase (TaqMan reverse transcription reagents, Applied Biosystems, Grand Island, NY) with the following reaction conditions: 10 min at 25°C, 30 min at 48°C and 5 min at 95°C. The qPCR was performed with an ABI ViiA7 real-time PCR system (Applied Biosystems, Carlsbad, CA, USA) using synthesized cDNA, Power SYBR Green PCR Master Mix (Applied Biosystems, Carlsbad, CA), and a pair of gene-specific primers. β -actin was used as an internal control gene. Each sample was prepared in triplicate and normalized to β-actin. The primers for each **qPCR** reaction are as follows: Nrf2. 5'-AGCAGGACTGGAGAAGTT-3' (sense) and 5'-TTCTTTTTCCAGCGAGGAGA-3' 5'-CCTCACTGGCAGGAAATCATC-3' 5'-(antisense); HO-1. (sense) and 5'-CCTCGTGGAGACGCTTTACATA-3' (antisense); NQ01, AGCCCAGATATTGTGGCCG-3' (sense) and 5'-CCTTTCAGAATGGCTGGCAC-3' (antisense); UGT1A1, 5'-GAAATTGCTGAGGCTTTGGGGCAGA-3' (sense) and 5'-ATGGGAGCCAGAGTGTGTGATGAA-3' (antisense); β-actin. 5'-AGAGGGAAATCGTGCGTGAC-3' (sense) and 5'-CAATAGTGATGACCTGGCCGT-3' (antisense)

JB6 P+ cells were seeded at a density of 1×10^5 cells in 100-mm dishes with 5% FBS/MEM. After 24 h, the cells were treated with either 0.1% DMSO, 5-azacytidine (5aza, 250 nM), or each concentration of UA in 1% FBS/MEM. The medium containing each agent was changed every 2 days. The cells incubated with 5-azacytidine (5-aza) serving as a positive control were treated with trichostatin A (TSA, 50 nM) 24 h before harvest. On the day of the harvest, the cells were rinsed with cold PBS and resuspended in 100 µl of RIPA buffer containing a protease inhibitor cocktail and agitated on ice for 30 min. The cells were then centrifuged at 13,000 \times g for 15 min at 4°C, and only a clear supernatant was obtained. The total protein fraction (25 µg of protein) was separated by 4-15% Tris-HCl precast gels. The separated proteins were transferred onto PVDF membranes, which were blocked with PBS containing 0.05% Tween 20 (PBST) and 5% skim milk. After a sequential incubation of the membranes with the primary antibodies and the appropriate secondary antibodies, the immunoreactive bands were detected with the Super Signal enhanced chemiluminescent system and visualized using the Bio-Rad ChemiDoc imaging system (Bio-Rad, Hercules, CA). The band intensity was analyzed using Image J. The protein concentrations were determined using the bicinchoninic acid (BCA) assay.

2.2.7 DNA isolation and bisulfite genomic sequencing

Genomic DNA was isolated from each group of treated cells using the QIAamp DNA Mini Kit (Qiagen). Then, 500 ng of DNA was subjected to bisulfite treatment using the EZ DNA Methylation Gold Kit (Zymo Research, Irvine, CA). The converted DNA was amplified by touchdown PCR using bisulfite sequencing-specific primers for the first

2.2.8 HDAC activity assay

Nuclear extracts from the treated cells were isolated using NE-PER Nuclear and Cytoplasmic Extraction Reagents. HDAC activity was measured in nuclear extracts using Epigenase HDAC Activity/Inhibition Direct Assay Kit (Epigentek Inc, Farmingdale, NY) following the manufacturer's protocol.

2.2.9. Statistical analysis

All of the quantitative results are expressed as the mean values \pm SD of three independent experiments. Statistical significance was determined by one-way ANOVA and a *p* value of

<0.05 was considered statistically significant in all analysis.

2.3 Results

2.3.1 UA inhibits the growth of JB6 P+ cells

We first examined the dose and time-dependent cytotoxicity of UA using mouse epidermal JB6 P+ cells. The cells were treated with six different concentrations of UA (0, 2.5, 0.5, 1, 2.5, 5 or 10 μ M, final concentration) dissolved in DMSO (vehicle) for 3 and 5

days. Our previous studies and others have shown that it needs at least 3 days to have cells epigenetically altered (66, 67, 152, 207-211, 227, 228). UA was not cytotoxic up to 1 μ M (Figure 1); however, at 2.5 μ M the cell viability decreased approximately 23% in comparison with vehicle (0.1% DMSO). No difference was observed between 3 and 5 days of treatment, and concentrations greater than 2.5 μ M were found to be toxic. Because cell viability was greater than 70% at \leq 2.5 μ M and cytotoxicity was not time-dependent, the cells were treated with 1 and 2.5 μ M UA for 3 days to study the chemopreventive efficacy of UA in the subsequent experiments.

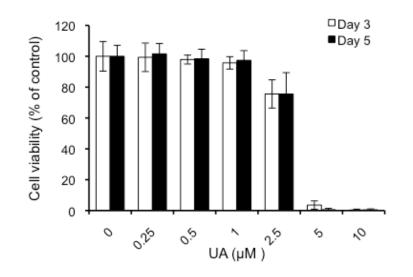


Figure 1. Effects of UA on the growth of JB6 P+ cells. Cells grown in a 96-well plate were treated with the indicated concentrations of UA, and cell viability was analyzed with an MTS assay after 3 and 5 days of treatment. The results are shown as the mean \pm SD of triplicate experiments. **p* < 0.05 compared with vehicle control (0.1% DMSO).

2.3.2 UA inhibits TPA-induced transformation of JB6 P+ cells

To determine whether UA exhibits anti-cancer and chemopreventive effects in skin, we studied the effects of UA on the tumor promotion of JB6 P+ cells induced by

TPA. The anchorage-independent cell transformation assay is an *in vitro* system that allows only cells transformed by tumor promoters such as TPA to grow and form colonies. As expected, the cells treated with TPA alone for 2 weeks developed a significant amount of colonies in the soft agar (Figure 2). The cells treated with TPA and 2.5 μ M UA inhibited TPA-induced transformation by 30% compared with the cells treated with TPA alone. Incubation with 1 μ M UA did not significantly inhibit transformation (16%). These results demonstrate the chemopreventive effects of UA against TPA-induced transformation in JB6 P+ cells.

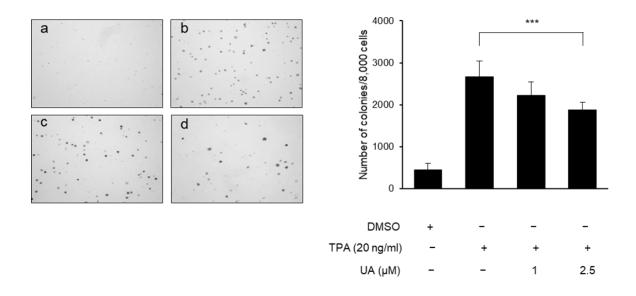


Figure 2. UA inhibits TPA-induced transformation in JB6P+ cells. Cells (8×10^3 /ml) in 1 ml of BME containing 0.33% agar were maintained in the presence of DMSO (control, a), TPA alone (b), UA 1 µM plus TPA (c) and UA 2.5 µM plus TPA. After 2 weeks, the cell colonies were counted. The data are presented as the mean ± S.D. ***p < 0.0001 compared with TPA alone

2.3.3 UA upregulates Nrf2 and its downstream detoxifying/antioxidant target gene

TPA-induced ROS production stimulates the neoplastic transformation of JB6 P+ cells (229). To test whether UA inhibits TPA-induced transformation through the induction of detoxifying/antioxidant enzymes, we investigated the expression levels of HO-1, NQO1 and UGT1A1 at the mRNA and protein levels using qPCR and Western blotting. The cells treated with 2.5 μ M UA showed an increase in HO-1, NQO1 and UGT1A1 mRNA expression, whereas 1 μ M UA did not (Figure 3A). Similarly, protein expression was elevated by 2.5 μ M UA treatment, but not by 1 μ M UA (Figure 3B). Nrf2 is regarded as an essential regulator of cytoprotective detoxifying/antioxidant enzymes. As such, we then determined whether UA increases Nrf2 expression in JB6 P+ cells. As expected, 2.5 μ M UA treatment increased Nrf2 expression; however, 1 μ M UA did not result in a significant increase in Nrf2 expression. These results demonstrate that UA inhibits TPA-induced transformation of JB6 P+ cells by, at least in part, augmenting detoxifying/antioxidant enzymes, which is mediated by enhanced Nrf2 expression.

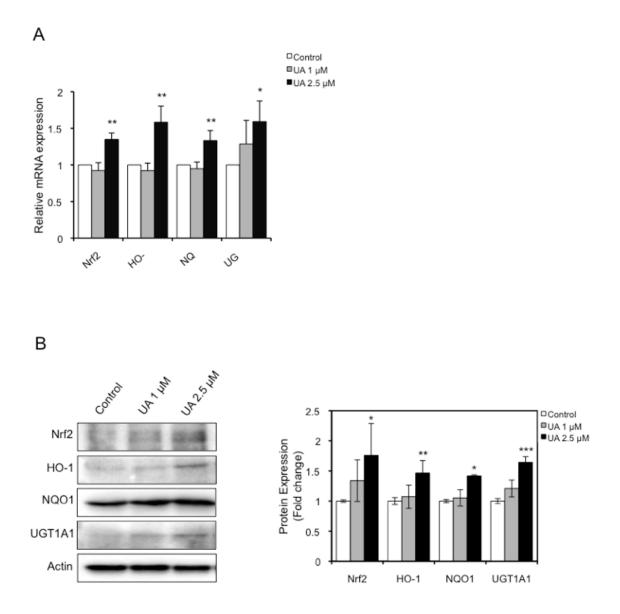


Figure 3. UA upregulates the expression of Nrf2 and its downstream target genes. Cells were treated with each concentration of UA for 3 days, and the total cells were divided for RNA and protein extraction. (A) Total 0.5 μ g of RNA was reverse transcribed for cDNA synthesis. The cDNAs were then used to perform qPCR by adding SYBR Green and a pair of gene-specific primers. (B) Western blots and quantification of protein levels. The data shown were normalized to β -actin and expressed as the relative fold change compared with the control. The values are the mean \pm SD of three independent

experiments. *p < 0.05, **p < 0.001, ***p < 0.0001 compared with vehicle control (0.1% DMSO).

2.3.4 Expression of Nrf2 downstream target genes by UA is Nrf2 dependent

Next, we clarified whether Nrf2 is required for induction of cytoprotective detoxifying/antioxidant genes by UA treatment. We used Nrf2-Mock and Nrf2-KD stable JB6 P+ cells established in our laboratory (67). The basal expression of Nrf2 was decreased by about 70% in Nrf2-KD JB6 P+ cells compared with control Nrf2-Mock (Figure 4). 2.5 μ M UA treatment significantly increased protein expression of Nrf2, HO-1, NQO1 and UGT1A1 in Nrf2-Mock JB6 P+ cells. Conversely, the inducing effects of 2.5 μ M UA on the expression of Nrf2 downstream target genes was much smaller in Nrf2-KD compared to those in Nrf2-Mock treated; 30%, 52%, and 51% decrease of HO-1, NQO1, and UGT1A1, respectively. The results indicate that Nrf2 is a direct regulator driving expression of cytoprotective detoxifying/antioxidant genes by UA in JB6 P+ cells.

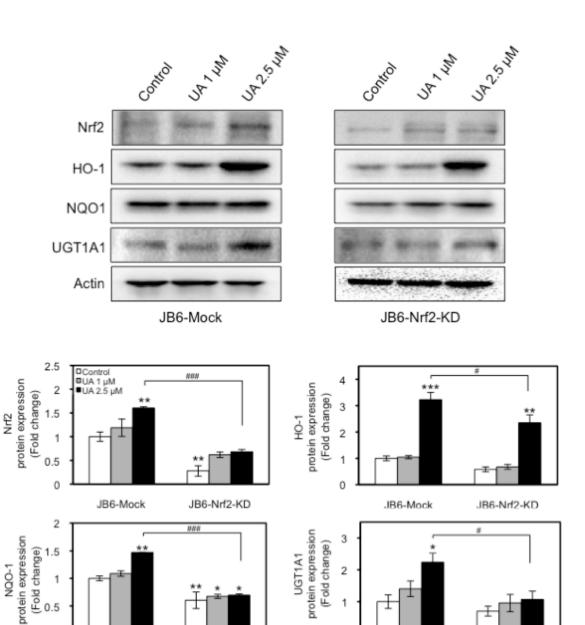


Figure 4. Nrf2 knockdown decreases expression of Nrf2 downstream target genes. Cells were treated with each concentration of UA for 3 days, and whole-cell extracts were prepared as described in Materials and Methods. Then, the proteins were subjected to Western blot to analyze the expression of Nrf2 and its downstream target genes indicated. The protein amounts were normalized to the levels of β -actin and expressed as the

JB6-Nrf2-KD

0

JB6-Mock

JB6-Nrf2-KD

0

JB6-Mock

relative fold change compared with JB6-Mock control. The values are the mean \pm SD of three independent experiments. *p < 0.05, **p < 0.001, and ***p < 0.0001 vs JB6-Mock control. #p < 0.05, ###p < 0.0001 vs JB6-Mock UA 2.5 μ M.

2.3.5 UA decreases Nrf2 promoter methylation

We previously showed that promoter demethylation of Nrf2 is an important epigenetic mechanism underlying Nrf2 activation in prostate cancer TRAMPC1 cells and JB6 P+ cells treated with phytochemicals (67, 152, 207, 209, 210). To determine whether Nrf2 was epigenetically regulated by UA, we determined the methylation status of the Nrf2 promoter using bisulfite genomic DNA sequencing. The first 15 CpG sites located between -1226 and -863 of the mouse Nrf2 gene promoter relative to the translation start site (+1) were analyzed (230). As previously reported, the Nrf2 promoter was hypermethylated in JB6 P+ cells (89.3%) (Figure 5). The cells treated with 5-aza and TSA, well-known inhibitors of DNA methylation and histone deacetylation, respectively, reduced methylation by 46.6%, which is similar to the results from previous studies (67). Treatment of JB6 P+ cells with 2.5 µM UA decreased methylation by 17% compared with JB6 P+ cells treated with vehicle. Treatment with 1 µM UA resulted in only a 7% decrease in methylation. These results are in accordance with (Figure 3), which shows that the levels of Nrf2 mRNA and protein were increased by 2.5 µM UA treatment, but they were unchanged by 1 µM UA treatment. These findings suggest that UA induces Nrf2 expression by altering the methylation status of the Nrf2 promoter.

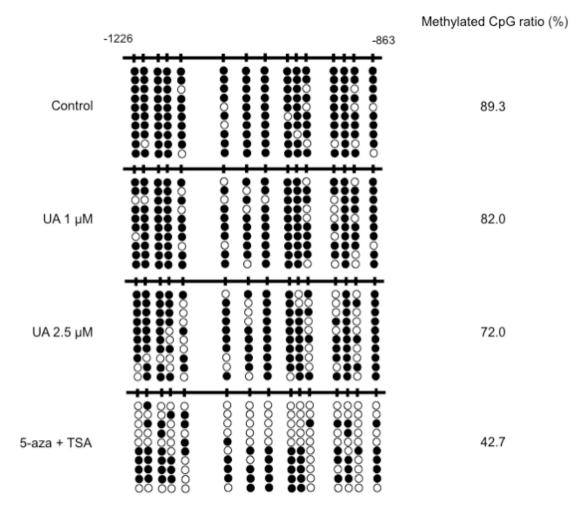
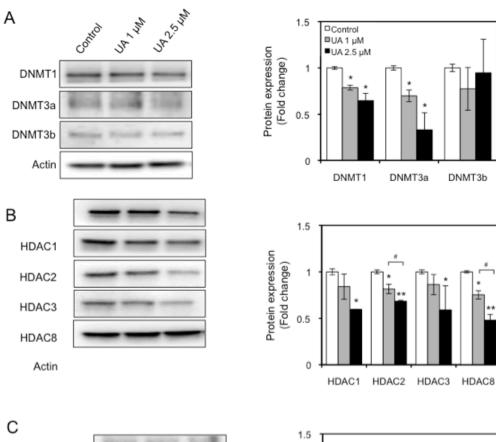


Figure 5. UA decreases Nrf2 promoter DNA methylation in JB6 P+ cells. The cells were treated with each concentration of UA for 3 days, and then the genomic DNA was isolated for bisulfite conversion. The methylation status of the first 15 CpG sites, the region between -1226 and -863 relative to the translational start site, within the promoter of Nrf2, was analyzed. Positive control cells were treated with 5-aza (250 nM) for 48 h and TSA (50 nM) for 24 h. Ten individual clones were analyzed. The filled and open dots indicate methylated and unmethylated CpG. The data are expressed as a percentage of the total number of methylated cytosines *vs.* total 15 CpGs of three independent experiments.

2.3.6 UA alters the levels of epigenetic modifying enzymes

To understand the mechanisms by which UA decreases Nrf2 promoter methylation in JB6 P+ cells, we determined an impact of UA on DNMTs and HDACs, which are involved in methylation-induced gene silencing (220). The family of DNMTs consists of three members, DNMT1, DNMT3a, and DNMT3b. Treatment with 2.5 µM UA resulted in a significant reduction in DNMT1 and DNMT3a protein levels (Fig. 6A). In addition, 1 µM UA treatment also slightly decreased both DNMT1 and DNMT3a. No significant difference was found between the effects of treatment with 2.5 and 1 µM UA. The DNMT3b protein levels were unaffected by UA treatment. HDACs are classified into four groups: Class I (HDAC1, 2, 3, and 8), Class II (HDAC4, 5, 6, 7, 9, and 10), Class III (SIRT1-7), and Class IV (HDAC 11). UA has previously been reported to increase histone acetylation by strongly inhibiting HDAC1, 3, 4, 5, and 6 (24). We examined the expression levels of HDAC 1, 2, 3 and 8 (Class I) and HDAC 4, 5, 6 and 7 (Class II). The protein expression levels of all HDACs were diminished in the JB6 P+ cells treated with 2.5 µM UA (Figure 6B and 6C). Among them, HDAC2 and 8 showed a dose-dependent reduction. The expression of HDAC4 was not affected by UA treatment and HDAC5 was not detected. The decrease of HDAC expression confirmed the inhibition of HDAC activity, whereas the levels of acetylated histone H3 (H3ac), an epigenetic marker for active genes, was increased by 2.5 µM UA treatment (Figure 6D). Taken together, these results indicate that UA-induced demethylation of the Nrf2 promoter is mediated by the negative regulation of epigenetic modification enzymes.



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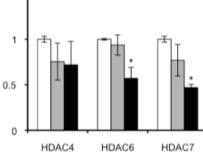
HDAC4

HDAC6

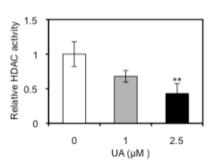
HDAC7

Actin





D



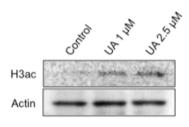


Figure 6. UA decreases the expression of DNMTs (A), Class I and II HDACs (B & C), inhibits HDAC activity, and increases H3ac levels (D) in JB6 P+ cells. The cells were treated with the indicated concentration of UA for 3 days, and the total cell lysates and nuclear proteins were harvested at the end of the treatment. Total protein (25 µg per lane) was separated by SDS-PAGE, and the levels of each protein of interest were determined by Western blot analysis. The isolated nuclear extracts from each group were used to determine total HDAC activity. The protein amounts in Western blot analysis were normalized to the levels of β -actin and data are expressed as the relative fold change compared with the control. The values are the mean \pm SD of three independent experiments. The figure H3ac is a representative of three individual experiments. **p* < 0.05 and ***p* < 0.001 *vs* control. #*p* < 0.05 *vs* UA 1 µM.

2.4 Discussion

A variety of external stimuli continuously make contact with the skin and accelerate the formation of ROS, impairing cellular metabolism, signal transduction, and genomic stability, and ultimately contributing to the development of skin cancer (231). Therefore, inhibiting and/or reducing oxidative stress by ROS is crucial in preventing skin cancer. Many dietary phytochemicals eliminate ROS toxicity by inducing detoxifying/antioxidant enzymes via Nrf2 activation, which has led to a decrease in cancer development (5). We have previously shown that curcumin, 3,3'-diindolylmethane, and a γ -tocopherol-rich mixture of tocopherols, sulforaphane, Z-ligustilide and radix angelica regulate Nrf2 activation through an epigenetic pathway in a prostate cancer model (66, 152, 208, 209, 211). Moreover, studies have shown that a variety of natural compounds interact with epigenetic regulators (222). These studies

suggest that natural dietary compounds that are able to epigenetically regulate gene expression are promising chemopreventive agents. Our findings demonstrate that UA, a naturally occurring triterpenoid in fruits and plants, restores the expression of the epigenetically silenced Nrf2 gene by demethylating CpG islands of the Nrf2 promoter, leading to upregulated Nrf2 expression. As a result, the expression of its target genes increases. Subsequently, this results in the inhibition of the TPA-induced neoplastic transformation in JB6 P+ cells.

JB6 P+ mouse epidermal cells, unlike P- cells, are susceptible to tumor promoterinduced transformation and are a suitable in vitro model to study progression in carcinogenesis and the molecular mechanisms of cancer chemoprevention (232). Previous studies have used JB6 P+ cells to investigate whether dietary agents have the capacity to suppress transformation induced by tumor promoters (67, 210, 233-235). Thus, we treated JB6 P+ cells with UA to test the chemopreventive potential of UA in TPA-induced transformation. The inhibitory effects of UA on tumor promotion by TPA and B[a]P or DMBA/TPA have been described in mouse skin (201, 202, 236). Consistent with these reports, we found that UA was effective in inhibiting the transformationinducing effects of TPA in JBP+ cells at a concentration in which the cytotoxicity was no more than 25% (Figure 1 and 2). The cumulative ROS production is detected in TPAinduced transformation (232). In addition, ROS inhibition by detoxifying/antioxidant enzymes attenuates TPA-induced transformation of JB6P+ cells (67, 237). Conversely, several reports indicate that UA remarkably reduces oxidative stress and increases the activity of antioxidant enzymes (238-240). We observed that the expression of HO-1 (antioxidant), NQO1, and UGT1A1 (detoxification) noticeably increased at both the

mRNA and protein levels in the JB6 P+ cells treated with UA; however, TPA activated AP-1, NF- κ B, and ERK 1/2 as well (232, 241). Moreover, UA targets AP-1, NF- κ B, and ERK 1/2 (200). Hence, our observations suggest that the inhibition of TPA-induced transformation of JB6 P+ cells by UA is partially reliant on ROS reduction through the accumulation of antioxidative/detoxifying enzymes. How UA alters the expression and activity of AP-1, NF- κ B, and ERK in TPA-induced transformation remains to be elucidated.

The production of phase II detoxifying/antioxidant enzymes is an innate cellular event that provides protection against deleterious endogenous and exogenous substances. In general, the genes encoding such cytoprotective enzymes are postulated to be regulated in an Nrf2-dependent manner. Thus, Nrf2 is central to the prevention of deleterious diseases, such as skin cancer. We have provided evidence that TPA-induced cell transformation is increased in Nrf2-KD JB6 P+ cells. Furthermore, the inhibitory effect of sulforaphane on TPA-induced cell transformation is blocked upon Nrf2-KD (67). Many cancer chemopreventive agents acting via Nrf2 activation are phytochemicals. Some examples include carnosol, curcumin, epigallocatechin-3-gallate (EGCG), phenethyl isothiocyanate (PEITC), sulforaphane, and resveratrol (242, 243). In our study, UA elevated the levels of Nrf2 mRNA and protein (Figure 3). Additionally, Nrf2 deficiency in Nrf2-KD JB6 P+ cells lowered the effects of UA on the protein expression of detoxifying/antioxidant genes (Figure 4). These results imply that UA is a chemopreventive dietary phytochemical that targets Nrf2. Our data are strongly supported by recent findings demonstrating that UA-driven activation of Nrf2 protects mice from neuronal defects induced by cerebral ischemia, and hepatotoxicity and

fibrosis caused by CCl₄ (205, 206). Furthermore, an isomer of UA, oleanolic acid, and the synthetic oleanane triterpenoid CDDO (2-cyano-3,12-dioxoolean-1,9-dien-28-oic acid), and its methyl (CDDO-Me) and imidazolide (CDDO-Im) derivatives have been shown to be potent Nrf2 inducers (244). Upregulated Nrf2 expression can in part be achieved by the increased half-life of Nrf2, which is mediated by the reduction of Keap1dependent ubiquitin/proteasome degradation of Nrf2 (245). Keap1 is a suppressor protein of Nrf2. Under normal circumstances, Keap1 binds to Nrf2 and causes rapid Nrf2 degradation via polyubiquitination. By contrast, upon high oxidative stress, a subset of cysteine residues in Keap1 are modified, which perturbs the Keap1/Nrf2 interaction and hinders Nrf2 ubiquitination. This enables the accumulation and translocation of Nrf2 into the nucleus where it triggers the transcription of various phase II cytoprotective genes (242). Sulforaphane modifies cysteine 151 within the BTB (Broad complex, Tramtrack, and Bric-a-brac) domain of Keap1, which results lowered Nrf2 in ubiquitination/degradation and increased stabilization (246). Moreover, a previous study revealed that Keap1 allows common inducers of phase II genes to alter its cysteine sulfhydryl groups regardless of the inducers' structures (247). As such, UA might modify cysteine residues in Keap1, resulting in an increase of Nrf2, which facilitates detoxifying/antioxidant expression by binding to the AREs in the promoters of its target genes.

DNA hypermethylation is the most common epigenetic modification in degenerative diseases such as cancer. This modification influences the depression of tumor suppressor genes. To date, many genes have been shown to be silenced by CpG hypermethylation within the promoter region during tumor progression. For example, in

skin cancer, 14-3-3sigma (cell cycle), MGMT (DNA repair), RASSF1 (signal transduction), PTEN (apoptosis), and others have been shown to be hypermethylated (221). Thus, discovering compounds that are able to reduce hypermethylation is an attractive strategy for the prevention of skin cancer. Studies by our group and others have revealed that Nrf2 expression is altered by methylation of CpG sites in the Nrf2 promoter region (66, 67, 152, 207-211, 248). These studies suggest that the epigenetic modulation of Nrf2 is likely to be a critical mechanism for Nrf2 activation. The present study demonstrates that UA decreased the methylation of the Nrf2 promoter in JB6 P+ cells. Although the effects were not comparable with those of the well-known epigenetic inhibitors 5-aza and TSA in combination, 2.5 µM UA treatment showed similar efficacy to that of 2.5 μ mol/L sulforaphane and 6.25 μ M apigenin in JB6 P+ cells (20% decrease compared with control in both). Notably, UA induces the expression of SHP-1, a tyrosine-specific protein phosphatase silenced by methylation in leukemias and lymphomas, in human multiple myeloma U266 cells (249). These results suggest that UA has the potential to modulate DNA methylation, which is implicated in carcinogenesis. Concomitantly, we found that UA decreased the protein levels of DNMT1 and DNMT3a. DNMT1 preserves DNA methylation patterns across generations, whereas DNMT3a and 3b act as de novo methyltransferases (220). The levels of DNMT1, DNMT3a, and DNMT3b are upregulated in UVB-induced murine skin tumors, and DNMT3a and DNMT3b are increased in stage III and IV cutaneous melanoma patients (250, 251). Hence, our observations indicate that UA functions as a natural DNMT inhibitor to reduce DNA methylation in the skin. In cancer cells, DNMT1 and DNMT3b collaborate to maintain hypermethylation in the CpG islands of promoters (252); however, UA did not have a significant effect on DNMT3b expression in JB6 P+ cells. This result may account for the weaker than expected inhibitory effect of UA on TPA-induced transformation and methylation of the Nrf2 promoter.

Hypermethylation in promoter regions provides binding sites for MeCP2, one of the MBD proteins, which subsequently recruits HDACs. HDACs remove acetyl groups from histones, mainly histone H3 and H4. This removal accelerates the formation of a compact chromatic structure, which drives the repression of transcription and causes gene silencing (220, 221). Because HDACs such as HADC1, HDAC2, HDAC3, HDAC6, and HDC8 are overexpressed in many cancers (253), the discovery of selective HDAC inhibitors has had significant implications for cancer therapy. As natural HDAC inhibitors for skin cancer, EGCG and grape seed proanthocyanidins have been reported to decrease the level of HDAC1 and HDAC activity, accompanied by reduced expression and activity of DNMTs in squamous cell carcinoma (221, 227). Recently, sulforaphane has been shown to reduce the protein levels of HDAC1-4 and 6 in human keratinocytes (254). Interestingly, UA from *Microtropis japonica* significantly decreases the protein levels of HDAC1, 3, 4, 5, and 6 in HL-60 myeloid leukemia cells (24). Similarly, in our experiments, UA downregulated all Class I HDACs, including HDAC1, 2, 3 and 8, and two from Class II HDACs, HDAC6 and 7 in JB6 P+ cells. Although HDAC4 expression did not decrease, similar results were found in JB6 P+ cells when treated with apigenin, sulforaphane, and tanshinone IIA (67, 207, 210). A decrease of HDAC expression was linked to a reduced HDAC activity and a dramatic increase of H3ac (Figure 6). Thus, UA-induced HDACs reduction results in a reduction of HDAC activity and, in turn, an enhanced acetylation of histone, which leads to epigenetic gene activation. Further, these

data, together with the DNMTs results, imply that UA prevents DNA hypermethylation through the regulation of DNMTs and HDACs, unlike 5-aza and TSA, which are only specific for the inhibition of DNA methylation and histone deacetylation.

2.5 Conclusion

In conclusion, this study demonstrated for the first time that UA restores the expression of Nrf2 by demethylating CpG islands in the Nrf2 promoter in mouse epidermal cells. The reduced expression of enzymes involved in DNA methylation and histone deacetylation and the increased level of histone acetylation mediated this alteration. The response to epigenetic alterations of Nrf2 by UA induced an increase in the expression of cytoprotective detoxifying/antioxidant enzymes, which resulted in the suppression of tumor promoter-induced cell transformation. Collectively, this data provided new insight into the function of UA as an epigenetic regulator for the prevention of skin cancer.

Chapter III

Ursolic acid suppresses skin carcinogenesis in a novel two-stage carcinogenesis model⁴

⁴A portion of this chapter is intended to be submitted as a research article.

3.1 Introduction

NMSC is the most common cancer in the United States and its incidence continues to rise (1, 255). Healthcare costs for the treatment and management of NMSC are approximately \$650 million per year (255). As such, effective preventative measures are needed. The most common skin cancers are subdivided into NMSC and melanoma skin cancer. NMSC is made up of basal cell carcinoma (BCC) and squamous cell carcinoma (SCC). BCC and SCC make up 98% of all skin cancer cases. The remainder is made up of the most severe form of skin cancer, melanoma. Causes for skin cancer include ultraviolet radiation and environmental pollutants. Occupational exposure to petroleum byproducts, organophosphate compounds, and arsenic are associated with the development of NMSC (256-259). Additional risk factors include family history or previous personal history, pigmentary characteristics (fair skin), immunosuppression (solid-organ transplant recipients), genetic disorders, therapeutic radiation exposure, and cigarette smoking (255, 259, 260). The most common treatment for NMSC is surgical management (261). Surgical treatment can be disfiguring and costly (262). The ideal preventative measure for skin cancer is to avoid exposure to the sun and environmental pollutants. In practice, it is nearly impossible to completely avoid these exposures. As such, secondary measures to prevent or suppress the promotion or progression of skin carcinogenesis using dietary phytochemicals is of great importance.

The process by which skin carcinogenesis occurs is a multi-faceted process that can be broken down into three distinct phases (263, 264). The first phase is the initiation phase. In this phase genetic mutations are acquired resulting in gene activation (v-Ha-ras oncogene) or gene inactivation (p53 tumor suppressor gene). The next stage is promotion. This stage is characterized by increased DNA synthesis and inflammation, the genetic alteration of gene expression and/or protein activities, and the clonal expansion of initiated cells (265). The clonal expansion of initiated cells containing genetic mutations is reversible and is an area of great interest in chemoprevention. The accumulation of clonally expanded initiated cells containing mutations with a dysregulation of apoptosis, epigenetic changes in DNA methylation, and infiltration of activated leukocytes is irreversible and leads to the development of pre-neoplastic papillomas (264). Simultaneously, vascularization occurs to nourish the pre-neoplastic lesion with oxygen and nutrients. The occurrence of additional mutations and accumulation of chromosomal abnormalities leads into the final phase, progression. In this phase pre-neoplastic lesions are converted into carcinoma. It can take up to 10 or more years for initiated cells to become a pre-neoplastic lesion while progression to carcinoma can occur in less than a year (4, 266). For this reason, many chemopreventive strategies are focused on the intervention of dietary phytochemicals in initiation and promotion phases. The most relevant model to study both phases operationally and mechanistically is the two-stage chemical carcinogenesis mouse model (265).

Chemical carcinogenesis was first reported in the 1770s Dr. Percival Pott noted there was a high incidence of scrotal cancer associated with chimney sweeps (267). This led to the hypothesis environmental pollutants can cause cancer and was further evaluated by scientists using a variety of models. The mouse model was first introduced in the 1920s when a mouse previously treated with tar was wounded and developed tumors (265). This finding led to the development of the two-stage chemical carcinogenesis mouse model to study multi-stage carcinogenesis.

The well-established two-stage chemical carcinogenesis model describes the initiation, promotion, and progression of mouse skin cancer due to its many similarities to the evolution of human non-melanoma SCC (268-270). The model is typically generated with a single dose chemical carcinogen followed by repeated topical applications of a tumor promoter. Commonly used initiating agents include the polycyclic aromatic hydrocarbons 7,12-dimethylbenz(a)anthracene (DMBA) and benzo{a]pyrene (B[a]P). B[a]P is a commonly found environmental pollutant implicated in the induction of skin cancer (124, 271-273) and induces mutations in Hras1 resembling human skin cancer etiology (266-268). The initiating event is irreversible and tumor formation will only appear after promotion with a promoting agent such as TPA. The combination of initiating agent and promoting agent causes sustained hyperplasia and inflammation, which in turn, leads to the selective clonal expansion of benign papillomas (263, 274-278). These papillomas can progress to SCC as early as 20 weeks after the start of promotion and is largely dictated by mouse strain and the dose of initiating and promoting agents (279-283).

As described previously, skin carcinogenesis is driven by inflammation and oxidative stress. As a key regulator of oxidative stress and inflammation responses in the cell, Nrf2 has been shown to protect against the development and progression of several skin cancers (214). Previous studies in our laboratory have shown Nrf2 (-/-) mice are more susceptible to DMBA-induced skin carcinogenesis (54). In addition, aberrant epigenetic changes have been observed in the development and progression of skin cancer (181-183). Our laboratory has recently identified extensive gene methylation profiles of skin carcinogenesis in a genome-wide epigenome analysis of DMBA/TPA-

treated CD1 mice (284) noting gene methylation as an attractive therapeutic target for skin carcinogenesis. The FDA has approved chemotherapeutic agents inhibiting epigenetic modifying enzymes but their use has been plagued by toxicity (285, 286). Therefore, dietary phytochemicals with the ability to modulate epigenetics involved in the promotion and progression of skin cancer are needed.

UA has been reported to possess many beneficial health effects. These effects include anti-cancer activity in various cancers, such as skin cancer. Skin cancer is the most common cancer in the world. Nrf2 is a master regulator of anti-oxidative stress response with anti-carcinogenic activity against UV- and chemical-induced tumor formation in the skin. Recent studies show that epigenetic modifications of Nrf2 play an important role in cancer prevention. In the previous chapter we demonstrated that the epigenetic effects of the triterpenoid UA could potentially contribute to its beneficial effects, including the prevention of skin cancer. Therefore, the ability of UA to modulate Nrf2 epigenetically *in vitro* warrants further investigation *in vivo*.

The efficacy of dietary phytochemicals including UA has been heavily explored in the two-stage chemical carcinogenesis model in our laboratory as well as others due to tumor response reproducibility (54, 287). The model generates a spectrum of different stages of carcinogenesis ranging from premalignant papilloma to metastatic tumors with H-Ras mutations resembling human cancer development (278, 288, 289) and thus is a suitable animal model to study the role of UA in skin carcinogenesis.

In this study, we evaluated the ability of UA to suppress skin carcinogenesis in a B[a]P/TPA SKH-1 mouse model. To our knowledge this is the first time the combination of B[a]P/TPA has been evaluated in an SKH-1 mouse model. This study will contribute

to the exploration of dietary phytochemicals in the prevention of skin cancer. Future work will evaluate epigenomic changes in the various phases of skin cancer and identify potential epigenomic biomarkers during skin carcinogenesis for the development of novel therapeutic strategies.

3.2 Materials and Methods

3.2.1 Animals

All animal experiments were performed in accordance with the Guide for the Care and Use of Laboratory Animals and were approved by the Animal Care and Use Committee of Rutgers, The State University of New Jersey (Protocol Number: 04-003).

3.2.1.1 Pilot Studies:

The SKH-1 mouse strain is homozygous WT for Nrf2 and was purchased from Charles River Laboratory (Bar Harbor, ME, USA). The SKH-1 Nrf2 (-/-) mice were generated by backcrossing SKH-1 Nrf2 (-/-) with SKH-1 WT mice as described previously ((290)). All animals were female. The genotype of each Nrf2 (-/-) animal was confirmed. DNA was extracted from the tail of each animal and was followed by polymerase chain reaction (PCR). Bands for Nrf2 (-/-) were visualized at 200bp by agarose gel electrophoresis, while WT mice display a band at 300bp as described previously (54). 7-8 week old female mice were used for the pilot studies. Mice were housed at the Rutgers Animal Facility, maintained under 12-h light/dark cycles, and provided *ad libitum* access to food and water.

3.2.1.2 Main Study:

5-6-week old female SKH-1 mice were purchased from Charles River Laboratory (Bar Harbor, ME, USA). Mice were housed as described in pilot studies. Upon their arrival, the 165 mice were weighed and randomized into experimental group cages to reduce any experimental bias. The mice were acclimatized for a period of 1 week. Enrichment was not provided in the animal cages to reduce any potential skin aggravation.

3.2.2 Chemicals

Acetone (HPLC grade), Ursolic Acid (UA) (U6753), Benzo[a]pyrene (B[a]P), and 12-O-tetradecanoylphorbol-13-acetate (TPA) were purchased from Sigma, Aldrich. (St. Louis, MO, USA). All solutions for the study were made in acetone.

3.2.3 Experimental design of pilot studies

The right ear of each mouse received 20μ L of the control group and the left ear of each mouse received 20μ L of the treatment group. For each application 10μ L was applied to the inner surface of the ear and 10μ L was applied to the outer surface of the ear. Six hours after TPA application, the mice were sacrificed and a 6 mm diameter disc from each ear was removed with an ear punch and weighed.

Pilot Study 1

Ear edema was induced on the left ear of 7-week old female SKH-1 mice with 2.6 nmol/20 μ L TPA, 1.3 nmol/20 μ L TPA, or 0.65 nmol/20 μ L TPA. The right ear of each mouse received 20 μ L of acetone.

Ear edema was induced on left and right ears of 7-week old female SKH-1 mice with 0.65 nmol/20 μ L TPA. 30 minutes prior to TPA application, acetone was applied to the right ear and 50nmol/20 μ L, 100 nmol/20 μ L, or 200 nmol/20 μ L UA was applied to the left ear.

Pilot Study 3

Ear edema was induced on the left and right ears of 7-week old female SKH-1 mice with 0.65 nmol/20µL TPA. 30 minutes or 15 minutes prior to TPA application, acetone was applied to the right ear and 200 nmol/20µL UA was applied to the left ear.

Pilot Study 4

Ear edema was induced on left and right ears of 7-week old female Nrf2 (+/+) or Nrf2 (-/-) SKH-1 mice with 0.65 nmol/20µL TPA. 30 minutes prior to TPA application, acetone was applied to the right ear and 200 nmol/20µL UA was applied to the left ear.

3.2.4 Experimental design of main study

165 mice were separated into four groups. The experimental study design is summarized in Table 1.

			Time of 2µM		
_	Group	No. of animals	UA Treatment	Initiation (nmol B[a]P)	Promotion
-	1	12	None	200µL acetone	200µL acetone
	2	51	None	200nmol + 100 nmol	6.8nmol TPA
	3	51	$Early^1$	200nmol + 100 nmol	6.8nmol TPA
	4	51	Late ²	200nmol + 100 nmol	6.8nmol TPA

Table 1 Experimental Design. ¹ UA applied one week prior and the day of B[a]P application. ² UA applied 30 minutes prior to each TPA application.

Chemicals were applied topically to the dorsal skin of approximately 8-week old female SKH-1 mice. Group 3 was treated with 2 μ mol/200 μ L UA twice a week prior to B[a]P application and prior to each application of B[a]P. Groups 2, 3, and 4 were given two applications of initiating doses of fresh B[a]P in 200 μ L of acetone. Once the first dose was completed, the second dose was given one week later. The initiating doses were followed by a week of rest to allow the B[a]P to have its effect and reduce exposure of personnel to the initiating agent. Following the week of rest, animals were treated with 2 μ mol/200 μ L UA (groups 3 and 4) or 200 μ L of acetone (group 2) 30 minutes prior to receiving 6.8 nmol/200 μ L TPA (groups 2, 3, 4) at the same site twice weekly for 31 weeks. Negative control animals were treated with 200 μ L acetone only at start of topical applications (early UA application) for 34 weeks. Animals were sacrificed at the time-points described in Figure 1 to capture all phases of the skin carcinogenesis model.

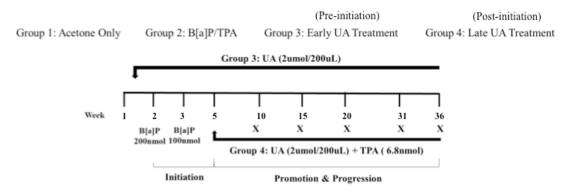


Figure 1. Study Design of B[a]P/TPA model in SKH-1 mice. B[a]P was applied twice at the age of 6 and 7 weeks. UA treatment started either 1 week before, prior to B[a]P initiation or after B[a]P initiation. TPA was applied twice a week starting 1 week after last B[a]P treatment for 31 weeks.

3.2.5 Preparation of skin specimens and histological examination

Skin samples (25 mm length and 5mm width) were obtained from the dorsal area of the mouse and were placed in 10% phosphate-buffered formalin at room temperature for 24-48 hours. The samples were then dehydrated in increasing concentrations (80, 95, and 100%) of ethanol, cleared in xylene, and embedded in Paraplast Plus (Fisher Scientific, Pittsburgh, PA, USA) using an automated platform (Leica). Paraffin blocks were submitted to Pathology Core Facility for further processing. The H&E sections were examined and imaged under a light microscope (Nikon Eclipse E600, Japan).

3.2.6 Data presentation and statistical analysis

The word tumor denotes papilloma, cyst, keratoacanthoma, carcinoma or sarcoma. The data are presented as the mean \pm standard error of the mean (63), except as otherwise stated. Student's t-test was used to determine statistically significant differences between control and treatment groups. A p value < 0.05 was considered statistically significant.

3.3 Results

3.3.1 SKH-1 mice are suitable for two-stage carcinogenesis investigation

To determine the optimal dose of TPA and UA to use in the main study three doses of TPA and three doses of UA were evaluated in an ear edema assay. Several two-stage carcinogenesis studies using TPA as the promoting agent have utilized concentrations between 5-15 nmol/200 μ L (265). As such, the following doses were evaluated in an ear edema assay: 0.65 nmol/20 μ L (1X), 1.3 nmol/20 μ L (2X), and 2.6 nmol/20 μ L (3X). All concentrations were found to result in a significant increase in ear edema in comparison to the acetone treated group (Figure 2A). Due to the possibility of

toxic effects resulting from the use of high doses, 0.65 nmol/20µL was selected for downstream ear edema assays. Preliminary studies in our laboratory demonstrated 2 µmol/200µL UA was the maximum tolerated dose for SKH-1 mice. For this reason the following doses of UA were evaluated in an ear edema assay: 50 nmol/20µL (1X), 100 nmol/20µL (2X) and 200 nmol/20µL (3X). While 100 nmol/20µL UA demonstrated only a 15% decrease in ear edema, a significant decrease of 37% was observed at 200 nmol/20µL UA (Figure 2B).

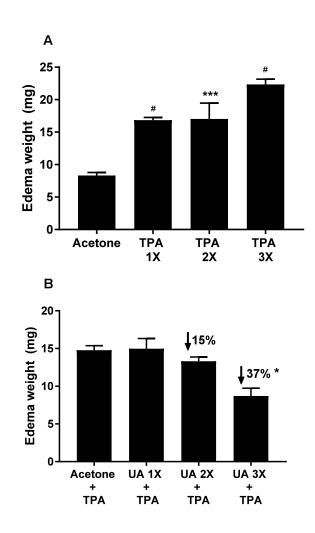


Figure 2. SKH-1 mice are suitable for use in two-stage carcinogenesis model. A) Nrf2 WT SKH-1 mice (n=3) were treated with or without three doses of TPA 0.65 nmol/20µL (1X), 1.3 nmol/20µL (2X), or 2.6 nmol/20µL (3X). Mice were sacrificed 6 hours after application. Ear punches were taken and average edema weight was determined. #p < 0.00001 and ***p < 0.0001 indicates significant differences compared to vehicle-treated group. B) Nrf2 WT SKH-1 mice (n=3) were treated with acetone or three doses of UA 50 nmol/20µL (1X), 100 nmol/20µL (2X), or 3X=200 nmol/20µL (3X) 30 minutes prior to 0.65 nmol/20µL TPA application. Mice were sacrificed 6 hours after application and ear punches were obtained. Average edema weight and the inhibition percentage of ear edema by UA were calculated. *p<0.05 indicates significant differences compared to untreated group.

3.3.2 Anti-inflammatory effects of UA may be time-dependent

Studies have reported pre-treatment prior to TPA application from 5 minutes to 1 hour (201, 291) For this reason a 30-minute prior to TPA application duration was chosen as a starting point in the UA dose response ear edema assay (3.3.1). To determine if it were possible to decrease this window to 15 minutes instead of 30 minutes for logistical reasons, an ear edema assay was run. 200 nmol/20µL UA was applied either 15 minutes or 30 minutes prior to TPA application. The data demonstrates little to no inhibitory effect by UA applied 15 minutes prior to TPA in comparison to the TPA control (Figure 3). Furthermore, UA applied 30 minutes prior had an inhibitory percentage comparable to the previous study (Figure 3 and Figure 2B).

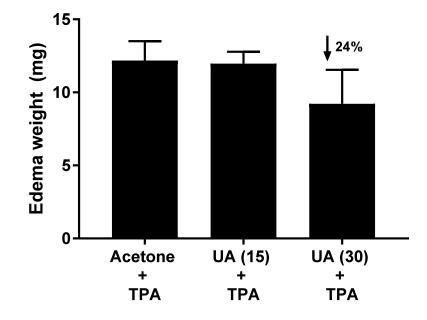


Figure 3. UA attenuates TPA-induced ear edema 30 minutes prior to TPA application but not 15 minutes prior to TPA application. Mice (n=4) were treated with acetone or 200 nmol/20 μ L of UA 30 minutes (30) or 15 minutes (15) prior to TPA application. Mice were sacrificed 6 hours after application and ear punches were obtained. Average edema weight and the inhibition percentage of ear edema by UA were calculated.

3.3.3 Nrf2 may be required for UA to inhibit TPA-induced inflammation

Because Nrf2 is central to the hypothesis of this research an ear edema assay was conducted evaluating UA's anti-inflammatory effect in Nrf2 (+/+) and Nrf2 (-/-) SKH-1 mice. The data demonstrated UA attenuates TPA-induced ear inflammation in Nrf2 (+/+) mice but not Nrf2 (-/-) mice (Figure 4). Furthermore, TPA-induced inflammation was enhanced in Nrf2 (-/-) mice (Figure 4). These results suggest UA inhibits TPA-induced inflammation and Nrf2 may be required.

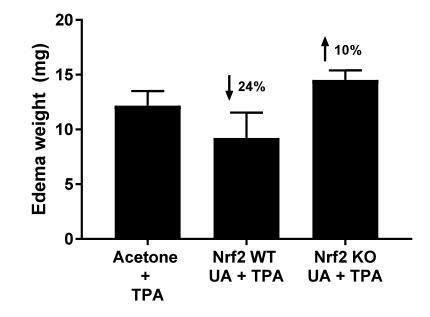


Figure 4. UA attenuates TPA-induced ear edema in Nrf2 (+/+) mice but not in Nrf2 (-/-) mice. Mice (n=4) were treated with acetone or 200 nmol/20µL of UA 30 minutes prior to TPA application. Mice were sacrificed 6 hours after application and ear punches were obtained. Average ear edema weight and the inhibition percentage of the ear edema by UA were calculated. The ratio of the ear punch weight in TPA versus acetone treated skin suggested that Nrf2 protected against TPA-induced increase in ear punch weight.

3.3.4 UA treatment suppresses skin carcinogenesis in a novel B[a]P/TPA model

Topical applications of acetone (vehicle), TPA, and UA (early or late) were applied to the dorsal region of SKH-1 mice twice a week as for 31 weeks post-TPA treatment. The body weight of mice was monitored every two weeks and it was found to increase steadily over the course of the study for all treatments (Figure 5A). The skin condition of the mice was monitored every three days for chemical-induced epidermal hyperplasia and actinic keratosis (265). Topical application of UA alone was not included in the study. Previous studies in our laboratory using a topical application of 2 μ mol/200 μ L UA in SKH-1 female mice did not demonstrate any toxic or carcinogenic effects. Late UA treatment reduced the percentage of tumor bearing mice, tumor multiplicity (tumor number per mouse), and tumor volume per mouse (Figure 5B, 5C, 5D). Of note, early UA treatment demonstrates comparable results to the B[a]P/TPA group (Figure 5B, 5C, 5D). Pharmacological effects of phytochemicals have been shown to be highly dependent on dose, timing, and duration of treatment (292). It is possible treatment with UA prior to B[a]P initiation resulted in UA acting as a co-carcinogen as previously seen with capsaicin (293). Further studies are needed to explore this observation.

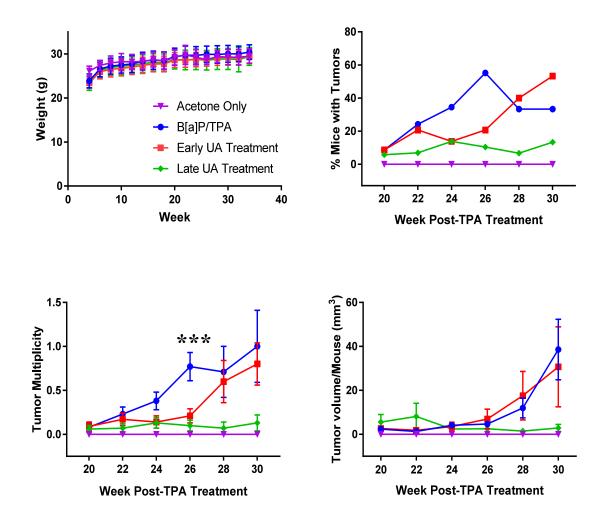
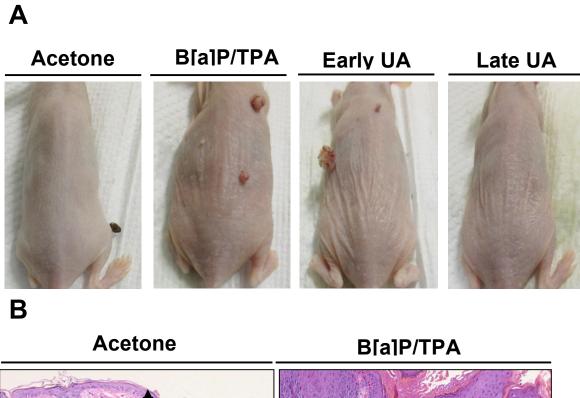
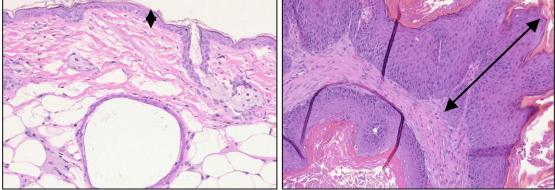


Figure 5. Late UA treatment prevents the progression of skin carcinogenesis. A) Treatment does not affect the body weight of animals. Mice were treated with topical applications of acetone (vehicle), TPA, and UA (early or late) twice a week for 31 weeks post-TPA treatment. Mice were weighed every two weeks and evaluated for any skin abnormalities. B) Percentage of mice with tumors. C) Number of tumors per mouse. P<0.001***B[a]P vs. Late UA. D) Volume of tumors per mouse.

3.3.5 B[a]P/TPA SKH-1 skin-carcinogenesis model generates squamous cell papillomas

SKH-1 hairless mice are widely used in dermatological research and are often used in UVB-induced skin carcinogenesis studies (294). However, early research in hairless mice reported a poor susceptibility to two-stage chemical carcinogenesis (295). We demonstrate here squamous papillomas can be generated in a B[a]P/TPA SKH-1 skin carcinogenesis model (Figure 6). Papillomas were present in B[a]P/TPA, early UA, and a small fraction of late UA treatment groups (Figure 6A and Figure 5B, 5C, 5D). Whole skin samples were obtained from all mice and processed for histopathological analysis as described in Materials and Methods. Two samples were randomly selected from each group. A representative image of the dorsal region of one of the two mice randomly selected demonstrates the presence of clonal-like growths (Figure 6A). Corresponding H&E images and pathologist consultation confirmed squamous papilloma formation in B[a]P/TPA and early UA groups while only a hyperplastic epidermis is seen in late UA treatment (Figure 6). In a two-stage skin carcinogenesis model a hyperplastic epidermis is expected early in the promotion phase without therapeutic intervention (265). As such, therapeutic intervention with UA (late) suppressed skin carcinogenesis as evidenced in tumor statistics and histopathological analysis (Figure 5 and Figure 6).





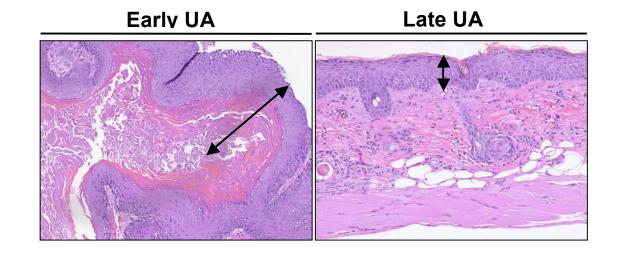


Figure 6. Representative images of each group at 31 weeks post-TPA treatment. A) Dorsal skin images of mice representative of each group. B) H&E images of whole skin samples and tumor samples of animals shown in A. B) Acetone: Normal skin from SKH-1 mice from surface to deep margin had several layers of desquamated keratin layer, 1-2 layers of epidermal cells, dermal extracellular matrix admixed with sebaceous glands, subcuticular adipose and pannicular fat. B) B[a]P/TPA:- Squamous cell papilloma. There was an exophytic neoplasm composed of focal to multifocal proliferation of squamous epithelium arranged in ridges and folds with irregular thickening of the overlying keratin layer. Neoplastic epithelium was well differentiated and uniform in appearance with no evidence of basement membrane invasion. There was orderly differentiation, maturation and keratinization near neoplasms' surface. Inflammation and erosion of the surface of the papilloma was sometimes present. B) Early UA: Squamous cell papilloma. There was an exophytic neoplasm composed of focal to multifocal proliferation of squamous epithelium arranged in ridges and folds with irregular thickening of the overlying keratin layer. Neoplastic epithelium was well differentiated and uniform in appearance with no evidence of basement membrane invasion. There was orderly differentiation, maturation and keratinization near neoplasms' surface. Inflammation and erosion of the surface of the papilloma was sometime present. B) Late UA: Skin with epithelial hyperplasia and slight increases in dermal mononuclear cells. Epithelium was composed of 5-15 layers of epithelial cells with scattered rare vacuolated degenerate cells or pyknotic necrotic cells. The dermal extracellular matrix containing increased numbers of lymphocytes, macrophages and to a lesser extent, neutrophils.

3.4 Discussion

In addition to UV, environmental pollutants such as B[a]P have been shown to promote skin cancer development (124, 271-273). B[a]P is one of the most common environmental carcinogens found as a byproduct from car exhaust and coal burning. The B[a]P/TPA two-stage skin carcinogenesis model has been used to study the potential involvement of epigenetic regulation including DNA methylation and histone modifications (49, 174, 296-300). Epigenetic regulation and global genomic hypermethylation are features associated with the enhancement of many cancers including prostate and colon cancers. Our laboratory has shown Nrf2 is epigenetically silenced during prostate carcinogenesis in TRAMP mice and has also been shown to occur in human prostate cancers (230). A number of studies in our laboratory have shown phytochemicals are able to restore the expression of Nrf2 by the demethylation of the Nrf2 promoter region (207, 301). In Chapter II we demonstrate UA is able to restore the expression of Nrf2 by the demethylation of the Nrf2 promoter region in vitro. In this study we've shown UA is able to reduce inflammation in an ear edema assay in and Nrf2 may be required (Figure 4) and late UA treatment is able to suppress skin carcinogenesis in a novel B[a]P/TPA in SKH-1 mice (Figure 6).

The two-stage carcinogenesis model has been explored extensively since the 1920s and a culmination of research has shown that the susceptibility of the model is dependent on mouse strain (302-305). Furred mice have been commonly used for two-stage carcinogenesis model investigation. However, hairless mouse models closely resemble the texture of human skin and have been shown to be more beneficial in skin cancer models (306). Using a hairless mouse model such as SKH-1 offers several

advantages over furred mouse models: 1) Saves time and avoids inflammatory reactions because hair depilation is not required. 2) The start of early carcinogenic response is easily spotted due to their non-pigmented skin. 3) The mice are immunocompetent (euthymic) and react to the development of SCC in a manner comparable to humans. Because the use of an SKH-1 mouse strain in a B[a]P/TPA model was novel, several pilot studies were conducted to determine the feasibility of model used. Firstly, we demonstrated TPA was able to induce inflammation in an ear edema assay using a range of doses that mimicked doses explored in previous two-stage carcinogenesis models. TPA-induced inflammation was demonstrated at all doses (Figure 2A). Taking into account potential toxic effects at the higher doses, 6.8nmol/200 μ L was selected for the main study. Secondly, we demonstrated UA was able to attenuate TPA-induced inflammation significantly at the highest dose (Figure 2B). Previous studies in our laboratory demonstrated the maximum tolerated dose for use in SKH-1 mice was 2 μ mol/200 μ L. With this in mind, 2 μ mol/200 μ L was selected for use in the main study.

In Chapter I we discuss the importance of dose, time, and model systems in the pharmacological response of phytochemicals. After determining the optimal doses for TPA and UA to use in the main study, we sought to determine the optimal time needed for UA to attenuate TPA-induced inflammation. We demonstrated UA is able to attenuate TPA-induced inflammation at 30-minutes but not at 15-minutes (Figure 3). This suggested, in addition to dose, timing is important in UA treatment. Noting this difference, UA application 30-minutes prior to TPA application was chosen to move forward.

A previous study in our laboratory demonstrated skin carcinogenesis induced in a DMBA/TPA model was enhanced in Nrf2 (-/-) mice in comparison to Nrf2 (+/+) mice and topical treatment of SFN was able to protect against skin carcinogenesis in Nrf2 (+/+) but not Nrf2 (-/-) (54). The same was observed for UA in the TPA-induced inflammation ear edema assay (Figure 4). In the absence of Nrf2 TPA-induced ear edema weight increased 10% despite treatment with UA suggesting Nrf2 is required.

Phytochemicals can prevent the initiation of carcinogenesis via the induction of the cellular defense detoxifying/antioxidant enzymes mediated by Nrf2 [Lee, 2013 #95]. Research has shown treatment with isothiocyanates (ITCs) pre-initiation inhibited cancer development in animal studies of chemically-induced carcinogenesis (307). With this in mind, UA treatment pre-initiation and post-initiation was assessed in the main study (Figure 1). As expected, animal weight increased over the course of the study suggesting treatment applications were not toxic (Figure 5A). UA treatment post-initiation (Late UA) was shown to dramatically suppress carcinogenesis (Figure 5B, 5C, 5D). Of note, UA treatment pre-initiation (Early UA) was comparable to the B[a]P/TPA positive control group suggesting early UA treatment had the opposite effect of what was expected (Figure 5B, 5C, 5D and Figure 6). A similar phenomenon has been observed for capsaicin. While a number of studies have shown capsaicin's chemoprevention potential (293). Other studies suggest it may act as a co-carcinogen or tumor promoter (293). These observations bring us back to the importance of dose, timing, and model systems used to evaluate the chemopreventive effects of dietary phytochemicals. It is possible UA added prior to B[a]P initiation had a co-carcinogenic effect. UA may be acting as a cocarcinogen by positively regulating the aryl hydrocarbon receptor (AHR) [Shin, 2007

#502]. B[a]P bind to AHR which stimulates the expression of CYP1 enzymes [Nebert, 2004 #503]. These enzymes metabolize B[a]P into toxic metabolites responsible for DNA adduct formation and ultimately genetic mutations. These observations warrant further investigation.

3.5 Conclusion

To our knowledge this is the first time a B[a]P/TPA skin carcinogenesis model has been explored in SKH-1 mice for chemopreventive studies. This study demonstrates the B[a]P/TPA SKH-1 model successfully generated squamous papillomas and can be used for future chemoprevention studies (Figure 6). Samples from this study will be further examined for global epigenomic changes through the different stages of skin carcinogenesis and in comparison the global epigenomic changes that arise during UA treatment using Next Generation Sequencing (NGS). This will allow us to determine the role, if any, of epigenetic modulation of Nrf2 in skin carcinogenesis. Ultimately, these studies will contribute to the identification of potential epigenomic biomarkers during skin carcinogenesis that can serve as novel therapeutic targets. Chapter IV

Significance and Future Prospects

4.1 Significance

4.1.1 Oxidative stress, inflammation, and the Nrf2 pathway in carcinogenesis

Oxidative stress occurs when there is an imbalance between the anti-oxidant defense system and the production of ROS. Although important secondary messengers, important secondary messengers, the activities of ROS can be detrimental to the cell if left unattended. In addition to endogenous production, ROS can be induced through UVradiation and environmental pollutants. The anti-oxidant stress defense system is responsible for relieving the deleterious effects of ROS. System enzymes such as SODs, catalase, and GPxs directly inactivate ROS. In addition, there are other antioxidant enzymes such as NQO1, UGTs, Txnd, and GSR that facilitate the detoxification of ROS using reduction/conjugation reactions, which facilitate excretion. Other proteins, which provide protection, include HO-1 and HO-2. Nrf2 regulates the genes encoding these enzymes and proteins. Under normal conditions, Nrf2 is sequestered by Keap1 in the cytosol and is degraded by the proteasome. Upon oxidative stress, Nrf2 is released by Keap1 and translocates to the nucleus where it binds the ARE of the antioxidant defense system genes. An excess of ROS can cause an imbalance in the system and induce oxidative stress; a hallmark of cancer (166, 167). The excess oxidative stress results in the activation of pro-inflammatory processes. If left unattended the excess oxidative stress will lead to chronic inflammation and in turn can lead to the initiation of cancer via genetic mutations and epigenetic aberrations. For this reason, the relationship between oxidative stress and inflammation as well as the role of Nrf2 in carcinogenesis is an active area of investigation in chemoprevention by phytochemicals.

4.1.2 Cancer epigenetics and regulation using phytochemicals

DNA methylation and histone modifications have been shown to contribute to the progression of cancer (170) and have been shown to be a hallmark of cancer (173-177). For example, the promoter region of human GSTP1 is hypermethylated in approximately 70%-100% of prostate cancer specimens (178-180). In addition, aberrant epigenetic changes have been associated with the development and progression of skin cancer (49, 181-183). As such, targeting the reversal of DNA methylation and histone modifications presents a novel target for the prevention and treatment of cancer. Chemotherapeutic targeting DNMTs and HDACs have already been approved by the FDA (184). However, they are plagued by adverse events. For this reason, targeting epigenetic modifications using dietary phytochemicals for the prevention or treatment of cancer has become an attractive area of investigation. Dietary phytochemicals have been shown to prevent cancer through epigenetic modulation (185-187).

4.1.3 Anti-cancer and Anti-oxidative effects of Ursolic Acid and the incidence of skin cancer

UA possesses the ability to modulate enzymes such as SOD and GST, regulated by Nrf2, and decrease (ROS) activity (311-313). In addition, a study in HaCaT cells, demonstrated UA's ability to hinder UVA-induced ROS production, lipid peroxidation, MMP-2 expression, and DNA damage (314). Furthermore, UA inhibits B[a]P-and 7,12-DMBA-induced tumor initiating activity *in vitro* and suppresses TPA-induced skin inflammation and tumor promotion in CD-1 and ICR mice (201, 202). UA has been shown to exhibit chemopreventive and anti-cancer effects against a number of cancers *in vitro* and *in vivo* including breast, hepatocellular, gastric, and colorectal (200). However, the chemopreventive effects of UA have not been extensively explored in skin cancer. As the protective layer of the body, the skin is in constant contact with environmental pollutants and UV-irradiation. Unsurprisingly, skin cancer incidence is rising steadily worldwide and NMSC is the most common cancer in the United States with over 4.0 million new cases diagnosed in 2012 (315). 700,000 were cutaneous SCC which metastasize at a rate of 2-6% (139). Over 5.4 million cases of NMSC are treated annually surmising an annual cost of approximately \$5 billion in the treatment of NMSC (316, 317). The development of strategies to reduce the occurrence of chemical induced skin cancer would have a major impact on reducing the economic burden of society.

4.2 Future Prospects

According to the National Center of Health Statistics, cancer was the culprit of nearly 600,000 deaths in 2016 in the United States. It is by far one of the most heterogeneous diseases to treat. Treatment for metastasized cancers remains a challenge despite modern diagnostics and treatment regimens. For this reason, alternative approaches are needed. Chemoprevention using dietary phytochemicals such as UA in the prevention of initiation and/or progression of cancer poses a promising alternative strategy. In this research we have showcased the potential use of UA as a promising chemopreventive agent against skin cancer. The epigenetic modulation of Nrf2 in skin carcinogenesis remains to be explored and will offer novel insight into the global epigenomic response of UA in skin carcinogenesis using NGS.

The epigenetic modulation of Nrf2 and the global epigenomic response of other dietary phytochemicals and synthetic compounds, such as CDDO-Im, have been explored

in our laboratory. Research conducted parallel to early UA studies demonstrated unlike UA, CDDO-Im may not posses the ability to epigenetically modulate Nrf2 (Figure 1).

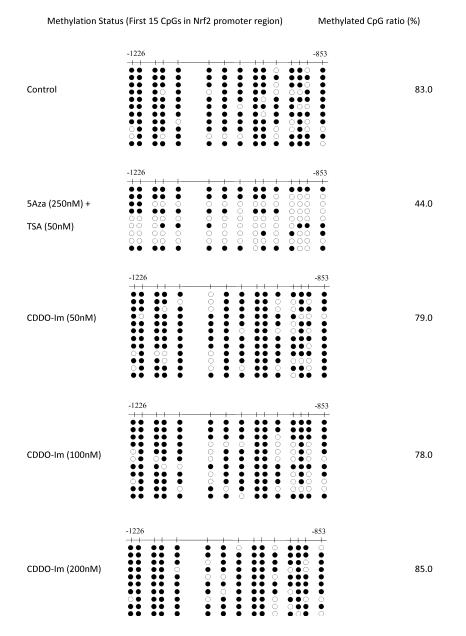


Figure 1. CDDO-Im may not decrease Nrf2 promoter DNA methylation in JB6 P+ cells. The cells were treated with each concentration of CDDO-Im for 5 days, and then the genomic DNA was isolated for bisulfite conversion as previously detailed for UA. The methylation status of the first 15 CpG sites, the region between -1226 and -863 relative to the translational start site, within the promoter of Nrf2, was analyzed. Positive control cells were treated with 5-aza (250 nM) for 48 h and TSA (50 nM) for 24 h. Ten individual clones were analyzed. The filled and open dots indicate methylated and unmethylated CpG. The data are expressed as a percentage of the total number of methylated cytosines *vs.* total 15 CpGs of three independent experiments

Although preliminary data suggests CDDO-Im does not posses this ability in the model system used, it may not be the case. We have seen with this research and that of others the *in vitro-in vivo* dose response of phytochemicals can vary due in part to the cell line/animal model used, the assay system of the biomarker used for the readout, chemical structure of the functional analog of the phytochemical, and the source of compounds used for the treatment study (292). While the response may vary across different experimental designs, the chemopreventive efficacy appears to remain and demonstrates the therapeutic potential of dietary phytochemicals in cancer prevention and in health in general.

Chapter V

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