

Allyl isothiocyanate inhibits cell metastasis through suppression of the MAPK pathways in epidermal growth factor-stimulated HT29 human colorectal adenocarcinoma cells

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Abstract. Allyl isothiocyanate (AITC) has been found to present sources from consumed cruciferous vegetables. AITC is known to possess pharmacological and anticancer activities. The present study was designed to test the hypothesis that AITC suppressed the invasion and migration of epidermal growth factor (EGF)-stimulated HT29 cells and to elucidate the mechanisms for the antimetastatic abilities *in vitro*. The invasion and migration of EGF-stimulated HT29 cells were determined individually by Transwell cell invasion and wound-healing assays. Our results showed that AITC effectively inhibited both the invasive and migratory ability of HT29 cells. Furthermore, AITC downregulated the protein levels of matrix metalloproteinase-2 (MMP-2), MMP-9 and mitogen-activated protein kinases (MAPKs) (p-JNK, p-ERK and p-p38) by western blot analysis in HT29 cells following EGF induction. Thus, the metastatic responses in AITC-treated HT29 cells after EGF stimulation were mediated by the MMP-2/-9 and MAPK signaling pathways. We also used gene expression microarrays to investigate the gene levels related to cell growth, G-protein coupled receptor, angiogenesis, cell adhesion, cell cycle and mitosis, cell migration, cytoskeleton organization, DNA damage and repair, transcription and

translation, EGFR and PKB/mTOR signals. In summary, it is possible that AITC suppresses the invasion and migration of EGF-induced HT29 cells, resulting from MMP-2/-9 and MAPKs. Hence, AITC may be beneficial in the treatment of human colorectal adenocarcinoma in the future.

Introduction

Allyl isothiocyanate (AITC) is a cancer chemopreventive phytochemical agent found in naturally occurring dietary isothiocyanates (ITCs) (1-3). AITC was found to have a major glucosinolate in several commonly consumed cruciferous vegetables (cabbage, cauliflower and kale as well as Brussels sprouts) (4,5). Previous studies showed that AITC inhibited the growth of various human cancer cell lines, such as colorectal carcinoma (5,6), lung cancer (7), leukemia (4), breast adenocarcinoma (8), bladder cancer (5,9), brain malignant glioma (10), neuroblastoma (11), hepatoma (12,13) and prostate cancer cells (2,14,15). Of note, the half maximal inhibitory concentration (IC₅₀) values for the anticancer cell growth appear at the low micromolar ranges of AITC (9). On the other hand, AITC appears to be significantly less toxic to normal human bladder epithelial cells (5,9). AITC is likely to attenuate tumor cell growth by causing cell cycle arrest (8,10), induction of cell apoptosis (1,2) and to suppress metastasis via inhibition of invasion and migration in neoplastic cells (5,16). The earlier studies in our laboratory also demonstrated that AITC triggered G2/M phase arrest and provoked apoptosis in MDA-MB-468 human breast adenocarcinoma cells (8) and GBM 8401 human brain glioblastoma multiforme cells (10).

Matrix metalloproteinases (MMPs) play key roles during cancer cell metastasis (5,16). The levels of cell adhesion, invasion and migration were suppressed through the transcription of MMP-2/-9 by AITC at 0.1-5 μ M in SK-Hep-1 human liver cancer cells (16). However, few studies have addressed the AITC-inhibited cell metastasis in epidermal growth factor (EGF)-stimulated HT29 human colorectal cancer cells. The

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aim of the present research was to determine the decrease of cell metastasis in EGF-treated HT29 cells by AITC. The present study indicated that AITC suppressed the extracellular signal-regulated kinase (ERK), p38, c-Jun *N*-terminal kinase (JNK) mitogen-activated protein kinase (MAPK) pathways and, thus, reduced the MMP-2 and -9, leading to the inhibition of metastatic effects in EGF-stimulated HT29 cells *in vitro*. Furthermore, we examined the antimetastatic effects of AITC by altering the cell cycle response-related gene expression utilizing DNA microarray analysis. Our study is the first to report that MAPK signals are pivotal for the antimetastatic response of HT29 human colorectal adenocarcinoma cells induced by AITC.

Materials and methods

Materials and reagents. RPMI-1640 medium, fetal bovine serum (FBS), penicillin/streptomycin and trypsin-EDTA were bought from Gibco by Life Technologies (Carlsbad, CA, USA). Millicell Hanging Cell Culture Inserts (polyethylene terephthalate filters with 8 μ m pore size) were purchased from Merck Millipore Corp. (Billerica, MA, USA). All primary antibodies for immunoblotting and horseradish peroxidase (HRP)-conjugated secondary antibodies were purchased from Santa Cruz Biotechnology, Inc. (Santa Cruz, CA, USA). AITC and all other chemicals were purchased from Sigma-Aldrich Corp. (St. Louis, MO, USA) unless otherwise specified.

Cell culture. The human colorectal adenocarcinoma HT29 cell line was obtained from the Bioresource Collection and Research Center (BCRC) of Food Industry Research and Development Institute (Hsinchu, Taiwan). Cells were plated into 75-cm² tissue culture flasks and cultured in RPMI-1640 medium with 10% FBS, 100 U/ml penicillin and 100 μ g/ml streptomycin in a humidified atmosphere of 5% CO₂ and 95% air at 37°C as previously described (17,18). Cells were detached by 0.25% trypsin/0.02% EDTA to keep cell growth.

Transwell cell invasion assay. HT29 cells at a density of 1x10⁴ cells/0.4 ml serum-free RPMI-1640 medium were seeded with or without (basal) 10 ng/ml EGF into the upper chambers (Millicell Hanging Cell Culture Inserts; Merck Millipore Corp.) after pre-coating with Matrigel (BD Biosciences, San Jose, CA, USA) in the presence or absence of AITC at 5 and 10 μ M. Each lower chamber was filled with 600 μ l of 10% FBS medium. After incubation for 24 h, the chambers were removed from the wells to measure invasive ability and then fixed with methanol for 15 min before the non-invasive cells were wiped with a cotton swab. Consequently, cells were stained with 2% crystal violet for 10 min, and the invaded cells were then photographed under a phase-contrast microscope. The number of invasive cells was presented in the membrane/filter of three random fields as previously described (19,20). The invasion assay was performed with a 100% support value of basal cells, and invasive cells were quantified using NIH ImageJ 1.47 program.

Wound healing assay. HT29 cells in 6-well plates (~5x10⁵ cells/well) were grown to 80% confluence, and cell monolayer was scratched by a 200- μ l pipette tip to create a gap of constant

width. Subsequently, cells were washed with PBS twice to remove floating cells. Cells were exposed in the presence or absence of 10 ng/ml EGF and then treated with or without 5 and 10 μ M of AITC in serum-free RPMI-1640 medium for up to 24 h. The number of migrating cells in the gap was captured under a phase-contrast microscope as described elsewhere (21,22). Images for the scratch area of each well were counted in three random fields from each triplicate treatment. The number of migrated cells in EGF-untreated cells (basal) was expressed at 100% and these in treated cells showed related to the basal cells.

Total protein extraction and western blot analysis. HT29 cells were incubated with or without 10 ng/ml EGF and individually exposed to 5 and 10 μ M of AITC. After a 24-h treatment, each whole-cell protein extract was harvested and lysed in the PRO-PREP protein extraction solution (Intron Biotechnology, Seongnam-si, Gyeonggi-do, Korea). The protein concentration of the cell lysate was estimated with the Bio-Rad protein assay kit (Bio-Rad Laboratories, Hercules, CA, USA), and the total proteins (40 μ g) were electrophoresed by 10-12% SDS-PAGE before being transferred and blotted using iBlot dry blotting system with polyvinylidene difluoride (PVDF) membrane (Invitrogen by Life Technologies). The membranes were blocked and probed first with specific antibodies in blocking buffer at 4°C overnight as previously described (23,24), followed by incubation with the appropriate horseradish peroxidase (HRP)-linked secondary antibodies. Immobilon Western Chemiluminescent HRP substrate (Millipore) and X-ray film (GE Healthcare, Piscataway, NJ, USA) were applied to visualize, and the membranes were stripped and reprobed with β -actin to normalize to the protein expression as described elsewhere (25).

RNA extraction and expression microarray. HT29 cells (1x10⁶ cells/well) were maintained in RPMI-1640 medium with 10 ng/ml EGF and treated with or without 10 μ M AITC for 24 h. After exposure, cell pellets were subsequently harvested, and the total RNA from each treatment was purified using the Qiagen RNeasy Mini kit (Qiagen, Valencia, CA, USA) as previously described (23,26). The RNA purity was determined to check the quality at 260 nm and 280 nm using a NanoDrop 1000 Spectrophotometer (Thermo Fisher Scientific, Wilmington, DE, USA) (26,27). Each sample (300 ng) was amplified and labeled using the GeneChip WT Sense Target Labeling and Control Reagents kit (Affymetrix, Santa Clara, CA, USA) for expression analysis. The synthesized cDNA was labeled with fluorescence, and then hybridized for 17 h at 45°C and 60 rpm using Affymetrix GeneChip Human Gene 1.0 ST array (Affymetrix) to determine microarray hybridization following the manufacturer's recommendations.

The arrays were subsequently washed by Fluidics Station 450 (Affymetrix) and stained with streptavidin-phycoerythrin (GeneChip Hybridization, Wash and Stain kit, Affymetrix), and were scanned on a GeneChip Scanner 3000 (Affymetrix). The localized concentrations of fluorescent molecules were quantitated and analyzed using Expression Console software (Affymetrix) with default RMA parameters as previously described (28,29). The gene expression level of a 1.8-fold-change altered by AITC was considered a difference.

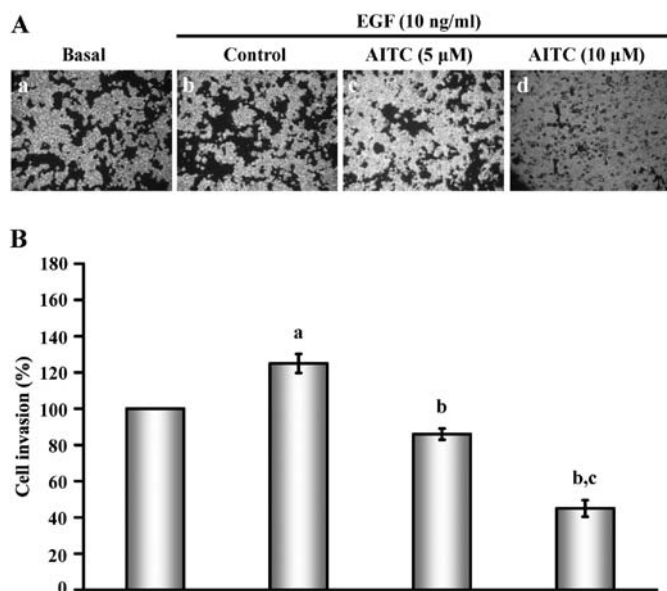


Figure 1. AITC suppresses cell invasion of EGF-induced HT29 cells. Cells in the presence or absence of 10 ng/ml EGF were treated with or without 5 and 10 μ M of AITC for 24 h. (A) Cell invasion was examined by Boyden chamber assay, and the polycarbonate membranes (pore size, 8 μ m) were precoated with Matrigel prior to use. (B) Invasive ability of HT29 cells was quantified by counting the number of cells under microscopy. The reported values are presented as the means \pm SD (n=3). ^aP<0.05, when compared with basal sample; ^bcP<0.05, significant difference compared with control and 5 μ M AITC treatment in HT29 cells after EGF challenge, respectively.

Statistical analysis. Each experiment was performed in triplicate and expressed as the means \pm standard deviation (SD) of analysis. The results were assessed by one-way ANOVA followed by Bonferroni's multiple comparison test, and the value of P<0.05 indicated statistically significant differences from other treatments.

Results

AITC suppresses EGF-stimulated invasion of HT29 cells. To investigate the effects of AITC on HT29 cell invasion *in vitro*, Transwell cell invasion assay was performed to determine the invasive ability of the HT29 cells with or without EGF stimulation. Results in Fig. 1A show that AITC at 5 and 10 μ M markedly decreased the invasion of HT29 cells induced by EGF relative to the control group. In addition, the invasive ability was reduced in a concentration-dependent manner (Fig. 1B). Our data demonstrated that AITC may effectively inhibit the invasion of HT29 cells *in vitro*.

AITC inhibits EGF-triggered HT29 cell migration. As shown in Fig. 2, using the wound healing assay, the concentrations of 5 and 10 μ M of AITC markedly inhibited HT29 cell migration (Fig. 2A) by ~48 and 81%, respectively, (Fig. 2B) after a 24-h incubation when compared with EGF-induced migration of HT29 cells. Based on these findings, we concluded that the migratory ability occurred in AITC-treated HT29 cells.

AITC alters the abundance of protein level with metastatic response in HT29 cells. Next, we clarified if AITC-suppressed migration and invasion is mediated through downregulation

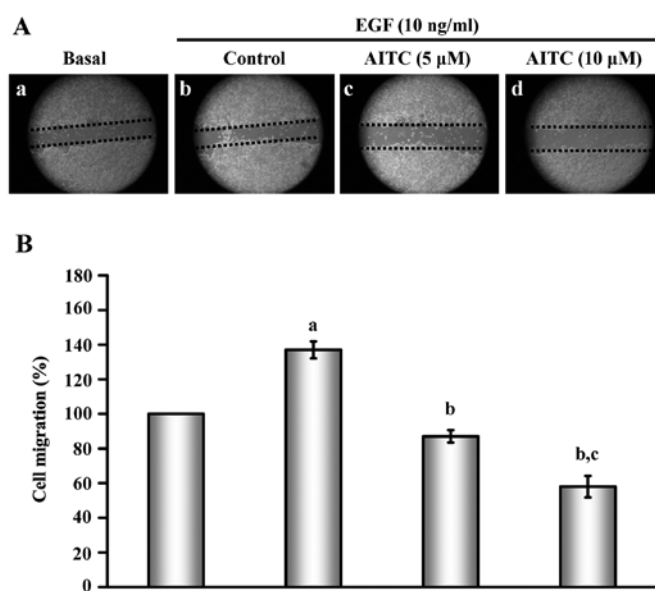


Figure 2. AITC reduces the migration of EGF-stimulated HT29 cells. Cells were exposed to 5 and 10 μ M of AITC for 24 h after 10 ng/ml EGF induction. (A) The wound healing assay was carried out to evaluate the inhibitory effects of AITC on HT29 cell migration. (B) The quantitation of the migrated cells in the gap of constant width was performed, and the HT-29 cells without EGF treatment (basal) were defined as 100%. Results shown as means \pm SD (n=3). ^aP<0.05, statistical comparison of the basal group; ^bcP<0.05 vs. control and 5 μ M AITC treatment of EGF-treated HT29 cells, respectively.

of associated protein signals. Treatment of EGF-treated HT29 cells with 5 and 10 μ M of AITC for 24 h, and data shown in Fig. 3 revealed that AITC decreased the protein expressions of MMP-2 and MMP-9 in EGF-treated HT29 cells. Alternatively, the level of the tissue inhibitor of metalloproteinase-1 (TIMP-1) was increased in examined HT29 cells (Fig. 3). We further determined the effect of AITC on the MAPK signaling pathways. Our results indicated that AITC inhibited the phosphorylation of JNK, ERK and p38 signaling in HT29 cells after EGF exposure (Fig. 3). Based on these results, we found that AITC affected MMP-9/-2, TIMP-1 and MAPKs signaling in EGF-treated HT29 cells *in vitro*.

Microarray analysis. Data were analyzed to examine the expressed genes in EGF-stimulated HT29 cells treated with or without AITC as can be seen in Table I. We showed that the transcripts of 58 genes were upregulated, while these of 24 genes were downregulated in HT29 cells exposed to AITC after EGF induction, respectively. Our results revealed that AITC regulated the expression of important genes that control cell growth (AKR1C2, AKR1C1, AKR1C1, ALDH3A1, TXNRD1 and ANKRD11), G-protein coupled receptor (AKR1C1 and AKR1C3), angiogenesis (HMOX1, MT1G and VEZF1), cell adhesion (TROAP, ITGB1 and EZR), cell cycle and mitosis (CSNK1A1, CDC20, BIRC5, KIF20A, CSNK1A1, ITGB1 and LIMA1), cell migration (HMOX1 and ITGB1), cytoskeleton organization (KIF20A and LIMA1), DNA damage and repair (SRXN1, G6PD, PTGR1, UNG, USP10 and PRKDC) and transcription and translation (EIF4A1, TRIM16 and ZKSCAN1) as listed in Table I. The Gene to GO BP test

Table I. The genes with more than 1.8-fold changes in mRNA levels in HT29 cells after AITC (5 μ M) 24-h treatment identified by DNA microarray.

| Fold-change | Representative public ID | Gene symbol | Gene Ontology biological process |
|-------------|--------------------------|---------------|--|
| 7.649 | NM_205845.1 | AKRIC2 | Positive regulation of cell proliferation; positive regulation of protein kinase B signaling cascade |
| 7.423 | NM_001353.5 | AKRIC1 | G-protein coupled receptor signaling pathway; positive regulation of protein kinase B signaling cascade |
| 6.365 | NM_001080538.1 | AKR1B10 | Cellular aldehyde metabolic process; steroid metabolic process |
| 5.879 | NM_020299.4 | AKR1B10 | Cellular aldehyde metabolic process; steroid metabolic process |
| 5.682 | NM_001080538.1 | AKR1B15 | Oxidation-reduction process; inferred from electronic annotation |
| 4.953 | NM_020299.4 | AKR1B10 | Cellular aldehyde metabolic process; steroid metabolic process |
| 3.708 | BM907551 | AKRIC1 | G-protein coupled receptor signaling pathway |
| 3.655 | NM_001135168.1 | ALDH3A1 | Positive regulation of cell proliferation |
| 2.585 | NM_002061.2 | GCLM | Response to oxidative stress; negative regulation of apoptotic process |
| 2.452 | AF121775.1 | ANKRD11 | Multicellular organism growth |
| 2.412 | NM_002133.1 | HMOX1 | Angiogenesis; negative regulation of cell migration; intracellular protein kinase cascade |
| 2.367 | BC022241.1 | AKT1S1 | Negative regulation of protein kinase activity; EGFR signaling pathway; negative regulation of TOR signaling |
| 2.285 | NM_012212.3 | PTGR1 | Oxidation-reduction process |
| 2.280 | NM_080725.1 | SRXN1 | Response to oxidative stress |
| 2.142 | AW003954 | TROAP | Cell adhesion |
| 2.140 | AK293322.1 | TXNRD1 | Signal transduction; cell proliferation |
| 2.138 | NM_003739.4 | AKRIC3 | G-protein coupled receptor signaling; cellular response to starvation; positive regulation of cell death |
| 2.114 | U79273.1 | EIF4A1 | Translational initiation |
| 2.044 | NM_003900.4 | SQSTM1 | Ubiquitin-dependent protein catabolic process; autophagy; apoptotic process; regulation of I- κ B kinase/NF- κ B cascade |
| 2.040 | NM_000187.2 | HGD | Oxidation-reduction process |
| 1.997 | NM_000402.3 | G6PD | Cellular response to oxidative stress |
| 1.969 | NM_006470.3 | TRIM16 | Positive regulation of transcription |
| 1.929 | AK304288.1 | GCLC | Negative regulation of neuron apoptotic process |
| 1.920 | AI377389 | CSNK1A1 | Protein phosphorylation; cell cycle; mitosis |
| 1.906 | BC053576.1 | UGT1A1 | Response to starvation; cellular response to glucocorticoid stimulus |
| 1.905 | DQ364250.1 | UGT1A1 | Metabolic process |
| 1.898 | NM_080489.3 | FKBP1A-SDCBP2 | Intracellular signal transduction |
| 1.888 | NM_001255.2 | CDC20 | Cell cycle checkpoint ; M phase of mitotic cell cycle |
| 1.876 | BC041809.1 | GCLM | Cysteine metabolic process; negative regulation of apoptotic process |
| 1.864 | AL519718 | BIRC5 | G2/M transition of mitotic cell cycle; M phase of mitotic cell cycle regulation of apoptotic process |

Table I. Continued.

| Fold-change | Representative public ID | Gene symbol | Gene Ontology biological process |
|-------------|--------------------------|-------------|---|
| 1.859 | M90656.1 | GCLC | Amino acid metabolic process; negative regulation of apoptotic process |
| 1.823 | AK316437.1 | ARHGAP11A | Small GTPase mediated signal transduction; positive regulation of GTPase activity |
| 1.823 | BC012999.2 | KIF20A | M phase of mitotic cell cycle; microtubule bundle formation |
| 1.819 | AK297737.1 | UGDH | UDP-glucuronate biosynthetic process |
| -1.897 | AK290883.1 | SAV1 | Positive regulation of apoptotic process; negative regulation of epithelial cell proliferation |
| -1.900 | NM_000492.3 | CFTR | ATP catabolic process; positive regulation of vasodilation |
| -1.938 | BC040361.1 | NR1P1 | Regulation of transcription; androgen receptor signaling pathway |
| -1.956 | BP319539 | MT1X | Cellular response to erythropoietin |
| -1.966 | NM_001003954.1 | ANXA13 | Cell differentiation |
| -2.007 | BC009894.2 | PAPSS2 | Small molecule metabolic process |
| -2.010 | NM_005100.3 | AKAP12 | Signal transduction; G-protein coupled receptor signaling pathway; positive regulation of PKA signaling |
| -2.010 | BC125158.1 | ANXA13 | Cell differentiation |
| -2.037 | AK299416.1 | UNG | DNA repair |
| -2.223 | NM_003439.1 | ZKSCAN1 | Regulation of transcription |
| -2.234 | AK298206.1 | LYPLA1 | Fatty acid metabolic process |
| -2.291 | AF291053.1 | LYPLA1 | Small molecule metabolic process |
| -2.305 | NM_005950.1 | MT1G | Cellular response to VEGF stimulus; negative regulation of growth |
| -2.424 | AK001650.1 | MOB1A | Hippo signaling cascade |
| -2.502 | BC009079.1 | JAK1 | Protein phosphorylation; intracellular signal transduction |
| -2.514 | CN349067 | ITGB1 | Mitotic cell cycle; cell-cell adhesion; cell-matrix adhesion; integrin-mediated signaling pathway; cell migration |
| -2.560 | A1479225 | CDC27 | Cell cycle; mitotic metaphase/anaphase transition; cell division |
| -2.642 | U81607.1 | AKAP12 | G-protein coupled receptor signaling pathway; positive regulation of PKA signaling |
| -2.762 | BG338144 | EZR | Cell-cell adhesion; regulation of cell shape |
| -2.780 | BG539466 | VEZF1 | Angiogenesis; regulation of transcription |
| -3.000 | BG390445 | USP10 | DNA repair; regulation of autophagy; DNA damage response |
| -3.005 | BF681396 | PRKDC | DNA repair; apoptotic process |
| -3.067 | NM_001134439.1 | PHLDB2 | Intracellular signal transduction |
| -3.631 | DA593848 | LJMA1 | Negative regulation of actin filament depolymerization; actin filament bundle assembly |

Table II. Gene to GO BP test for over-representation in HT29 cells after AITC (5 μ M) 24-h treatment identified by DNA microarray.

| Term | Count | Percentage | P-value |
|--|-------|------------|----------|
| GO:0007049-cell cycle | 114 | 10.73446 | 1.61E-18 |
| GO:0000278-mitotic cell cycle | 69 | 6.497175 | 2.74E-16 |
| GO:0022403-cell cycle phase | 73 | 6.873823 | 6.45E-16 |
| GO:0022402-cell cycle process | 87 | 8.19209 | 3.02E-15 |
| GO:0048285-organelle fission | 50 | 4.708098 | 9.32E-15 |
| GO:0000280-nuclear division | 48 | 4.519774 | 3.52E-14 |
| GO:0007067-mitosis | 48 | 4.519774 | 3.52E-14 |
| GO:0000087-M phase of mitotic cell cycle | 48 | 4.519774 | 7.18E-14 |
| GO:0000279-M phase | 60 | 5.649718 | 7.22E-14 |
| GO:0051301-cell division | 54 | 5.084746 | 1.30E-12 |

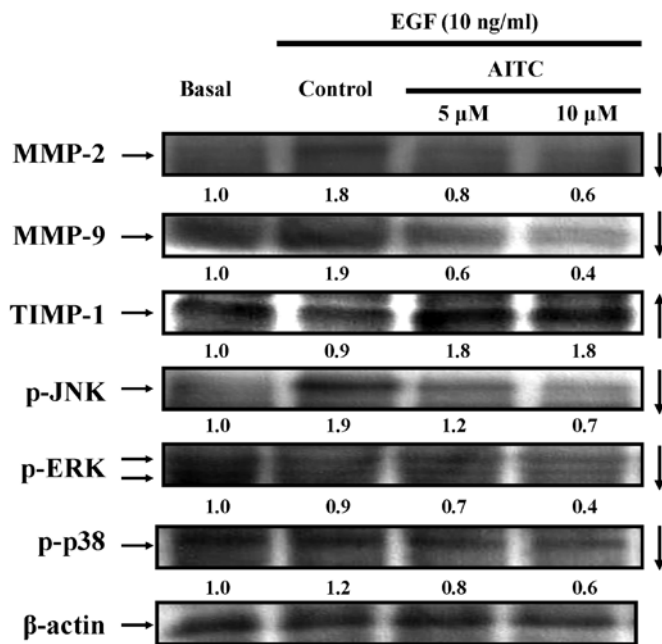


Figure 3. AITC alters the matrix metalloproteinases (MMPs) and mitogen-activated protein kinases (MAPKs) associated protein expression of EGF-treated HT29 cells. Cells were exposed to 10 ng/ml EGF and then incubated with or without 5 and 10 μ M of AITC for the indicated time (24 h). Whole-cell lysates were subjected to immunoblotting as described in Materials and methods. The protein expression of MMP-2, -9, tissue inhibitor of metalloproteinase 1 (TIMP-1), phosphorylated c-Jun N-terminal kinase (p-JNK), phosphorylated extracellular regulated protein kinase (p-ERK) and phosphorylation of p38 (p-p38) was probed using specific antibodies. β -actin protein level was adjusted for equivalent loading. Representative data are shown in three separate experiments with similar results.

for over-representation and pathways in HT29 cells after AITC 24 h-treatment identified by DNA microarray are listed in Table II. AITC altered the expression of negative regulation of protein kinase activity on EGFR and PKB/mTOR signaling genes (AKRIC2, AKRIC1, AKRIC1 and AKT1S1) in examined HT29 cells.

Discussion

It is well documented that cell metastasis is one of the major causes of colorectal cancer-related mortality (17,18,30). Interference with human epidermal growth factor receptor (EGFR) or downstream intracellular signaling provides a novel approach in cancer chemotherapeutic agents (31-33). Activation of the EGFR pathway promotes by EGF-stimulated responsible for colorectal cancer cell growth, invasion, metastasis and inhibition of cell death (34,35). Following EGF stimulation, EGFR is autophosphorylated, which turns on downstream intracellular signaling cascades such as MAPKs (ERK, p38 and JNK) signaling pathways (36,37). In the present study, we found that AITC was able to inhibit the invasion and migration in EGF-stimulated HT29 cells and could have a potential to treat colorectal cancer cell metastasis (Figs. 1 and 2). Cancer metastasis is a complicated progression that involves the increase in cell invasion, migration and degradation of extracellular matrix (ECM) then circulation in the vascular and lymphatic systems, finally the residence in distant organs (5,16,38). The matrix metalloproteinases (MMPs) are responsible for ECM degradation (39). The expression levels of MMP-2 and MMP-9 in colorectal cancer cells are highly related to the metastatic potential (40,41). Herein, we indicated that AITC was involved in MMP-2 and -9 by decreasing their protein level expression (Fig. 3). AITC also enhanced the expression of TIMP-1 level (Fig. 3), leading to the suppression of invasion and migration of EGF-stimulated HT29 cells. These findings also outlined the significance of MMP-2 and -9 in colorectal cancer cell metastasis.

MAPK (ERK, p38 and JNK) signals are known to be correlated with MMP-2 and -9 promoter induction through AP-1 and to regulate the activities of MMP-2/-9 in colorectal cancer cells (15,42). It was reported that inhibition of MAPK/AP-1-mediated transcription resulted in reduced migration, invasion, and metastasis in colorectal cancer cells (15). The present study indicated that AITC inhibited the metastasis of EGF-stimulated HT29 cells through reductions of the MAPK signaling pathways *in vitro* (Fig. 3).

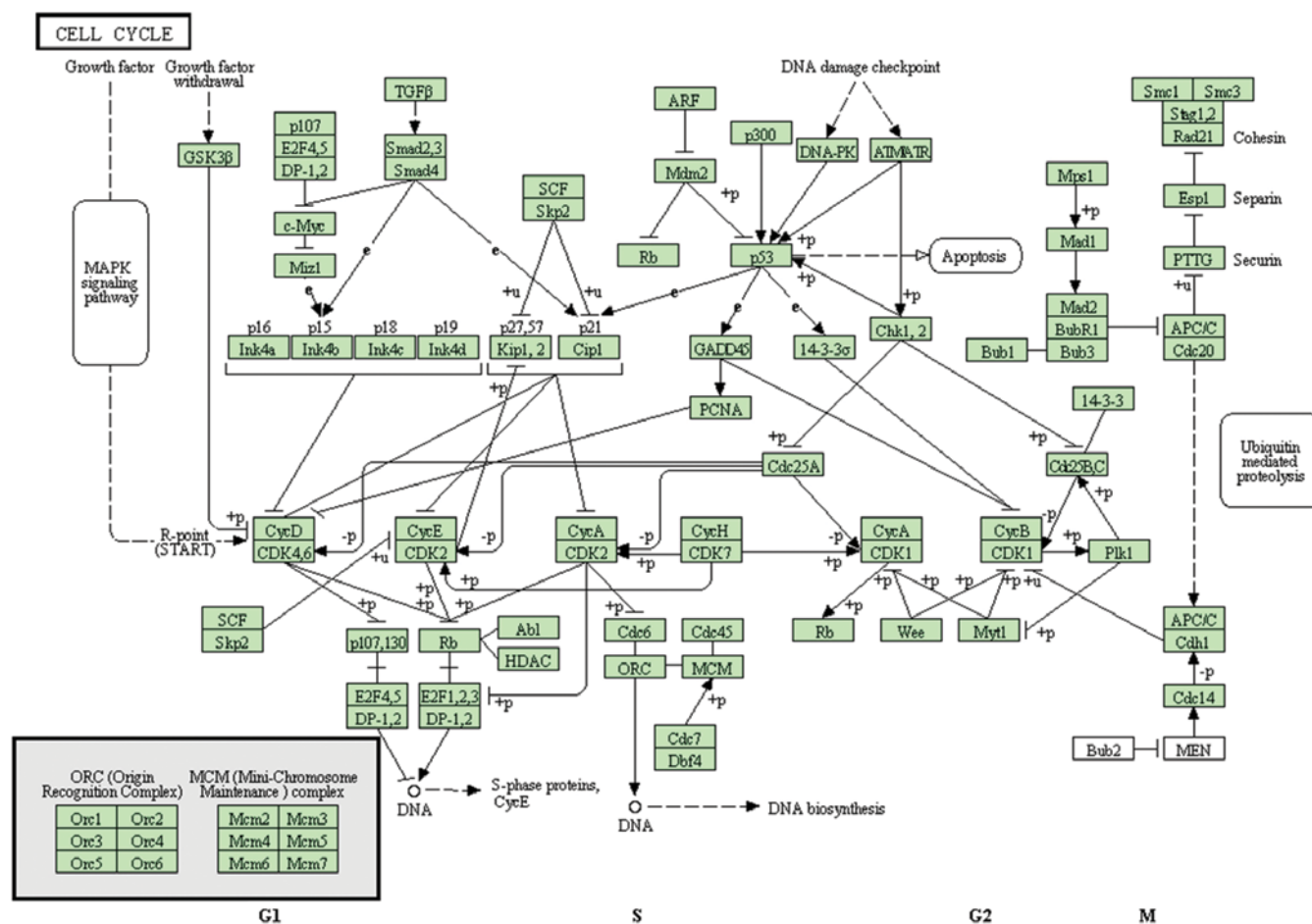


Figure 4. Proposed schematic diagram for the mechanisms of AITC-affected signaling pathways in EGF-stimulated HT29 human colorectal adenocarcinoma cells.

In our previous studies, we demonstrated that AITC induced cell cycle G2/M phase arrest in MDA-MB-468 cells and GBM 8401 cells (8,10). In addition, previous evidence reported that AITC also inhibited cell growth of SW620 human colorectal cancer cells (6), HL-60 leukemia cells (4) as well as prostate cancer PC-3 and LNCaP cells (2) through induction of G2/M phase arrest. In the current study, we examined the change of mRNA expression profile in AITC-treated EGF-stimulated HT29 cells by DNA microarray. Our data showed that cellular and molecular responses to AITC treatment were complicated and likely to be mediated through a variety of regulatory pathways (Fig. 4). AITC regulated the expression of important genes that control cell growth, G-protein coupled receptor, angiogenesis, cell adhesion, cell cycle and mitosis, cell migration, cytoskeleton organization, DNA damage and repair as well as transcription and translation (Table I). Regulation of these genes may be responsible for inhibiting the cell metastasis and cell proliferation of EGF-stimulated HT29 cells. However, we also found that AITC altered the expression of negative regulation of protein kinase activity on EGFR and PKB/mTOR signaling genes. We suggested that PKB/mTOR signaling genes are also the regulators of translation initiation in MMPs. Inhibition of the PKB/mTOR pathways might have the potential to prevent EGF-stimulated HT29 cell invasion and migration. The molecular signaling pathways involved in the effects of AITC on EGF-stimulated HT29 cells are summarized in Fig. 4.

In conclusion, this is the first study to demonstrate that AITC inhibits the metastatic potential actions, including invasion and migration of EGF-stimulated HT29 cells. AITC may be a promising agent in the therapy of colorectal cancer and metastasis of the disease.

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