Aim of the study: Genistein, an isoflavonoid, plays roles in the inhibition of protein tyrosine kinase phosphorylation, induction of apoptosis, and cell differentiation in breast cancer. This study aims to induce cellular stress by exposing genistein to determine alterations of miRNA expression profiles in MCF-7 cells.

Material and methods: XTT assay and trypan blue dye exclusion assays were performed to examine the cytotoxic effects of genistein treatment. Expressions of miRNAs were quantified using Real-Time Online RT-PCR.

Results: The IC_{50} dose of genistein was 175 μ M in MCF-7 cell, line and the cytotoxic effect of genistein was detected after 48 hours. miR-23b was found to be up-regulated 56.69 fold following the treatment of genistein. It was found that miR-23b was up-regulated for MCF-7 breast cancer cells after genistein treatment.

Conclusions: Up-regulated ex-expression of miR-23b might be a putative biomarker for use in the therapy of breast cancer patients. miR-23b up-regulation might be important in terms of response to genistein.

Key words: breast cancer, genistein, miRNA, MCF-7.

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Genistein-induced mir-23b expression inhibits the growth of breast cancer cells

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Introduction

Breast cancer is the most common cancer type among women. After respiratory cancers, including lung and respiratory tract cancers, breast cancer is the second leading cause of death among women [1]. Incidence and mortality rates of breast cancer may differ depending on the age, ethnicity, and socioeconomic status of patients [2]. The presence or absence of oestrogen receptor (ER), progesterone receptor (PR), and HER2/Neu receptor determine the sub-molecular classification and progression of breast cancer [3]. miRNAs are non-coding small RNA molecules (17-24 nucleotide) that repress mRNA transcription when they bind to their target region (3' untranslated region). Reregulation of expression profiles of miRNAs has a putative role in cancer development [4]. Decreasing expression of miRNA that suppress mRNA of oncogene, or increasing of expression of miRNA that suppress mRNA of tumour suppressor gene, can trigger the cancer process [4, 5]. It has been demonstrated that oncomirs such as miR-21, miR-27a, miR-155, and miR-145 exhibit different expression patterns between breast cancer cells and non-cancerous breast cells [6-8]. In addition to this difference, altered miRNA expression profile is detected differently among molecular sub-types of breast cancer [9]. Abnormal miRNA expression pattern can induce angiogenesis and metastasis in breast cancer tumours [10]. miRNA dysregulation in breast cancer is also associated with poor survival and poor therapeutic outcome [11, 12].

Genistein, an isoflavonoid, is a prime anti-cancer component of soybean, and it plays roles in the inhibition of protein tyrosine kinase phosphorylation, induction of apoptosis, and cell differentiation in breast cancer [13]. The interaction between genistein and oestrogen receptor signalling pathway in breast cancer has been well characterised. Genistein induces oestrogen-dependent cell growth and up-regulation of ER expression, thus it has a potential impact for hormone therapy [14, 15]. Genistein-mediated ER α expression is associated with histone modification changes and genistein re-sensitises ER α -negative breast cancer cells to tamoxifen [16]. Although it has been known that genistein affects chemotherapy agent efficiency and apoptosis, the effect of genistein on miRNA profiles is still unknown for breast cancer. This study aims to induce cellular stress by exposing genistein to determine the IC $_{50}$ doses of treatment conditions in MCF-7 cells. This study also aims to evaluate the single effect in terms of miRNA expression levels.

Material and methods

Tumour cell line

Breast cancer cell line (MCF-7), which was purchased from ATCC, was used as a breast cancer model.

Cell culture

Breast cancer cell line (MCF-7) was cultured in RPMI-1640 medium supplemented with 100 IU/ml penicillin, 10 mg/ml streptomycin, 1% L-glutamine, and 10% heat-in-activated foetal bovine serum, at 37°C in a humidified 95% air 5% CO₂ atmosphere.

Treatment of genistein and cytotoxicity assay

MCF-7 cells were incubated at a density of 2 × 10 5 cells/ml of medium using 96-well plates for 24, 48, and 72 hours. Studied concentrations of genistein were 75 μ M, 100 μ M, 125 μ M, 150 μ M, 175 μ M, and 200 μ M. XTT assay and trypan blue dye exclusion assays were performed to examine the cytotoxic effect of IC $_{50}$ dose of genistein in the MCF-7 cell line. Formazan formation was quantified spectrophotometrically at 450 nM (reference wavelength 620 nM) with a microplate reader. Viability was calculated using the background-corrected absorbance. Cells without any treatment were taken as a control group.

Isolation of miRNA

miRNA was isolated from cells exposed to IC_{50} dose of genistein and the control group. Isolation of miRNA and cDNA synthesis was performed using RT² qPCR-Grade miRNA Isolation Kit and RT² first Strand Kit, respectively, according to the manufacturers' instructions.

Relative quantification of miRNAs

Relative quantitation of 88 microRNAs (Table 1) was measured by using real-time online RT-PCR (LightCycler 480). SNORD48, SNORD47, SNORD44, U6 were used as human endogenous controls. Alterations in the miRNAs expressions of genistein were compared to the control group. Data analysis was evaluated by $\Delta\Delta$ CT method, "Light Cycler® 480 Quantification Software" program, and statistical analysis was evaluated with web-based RT² Profiler PCR Array Data Analysis.

Results

Cytotoxic effect of genistein on MCF-7 cells

Cells were incubated at a density of 2 \times 10⁵ cells/ml of medium using 96-well plates for 24, 48, and 72 hours. Studied concentrations of genistein were 75 μ M, 100 μ M, 125 μ M, 150 μ M, 175 μ M, and 200 μ M (Fig. 1). Untreated MCF-7 cells were considered as a control group. The IC₅₀ dose of genistein was 175 μ M and the cytotoxic effect of genistein was detected after 48 hours.

miR-23b is up-regulated miRNA by genistein in MCF-7 cell line

Alterations in the expressions of miRNAs were compared with genistein untreated MCF-7 cells. miRNA expression was detected 48 hours after genistein treatment. SNORD44, SNORD47, SNORD48, and U6 genes were

Table 1. Target and housekeeping miRNAs that were analysed for the genistein group. Expression analyses for 88 target miRNAs were performed by real-time PCR. Table 1 describes the sequences of miRNAs

niRNA	Sequence	miRNA	Sequence	miRNA	Sequence
nsa-miR-142-5p	CAUAAAGUAGAAAGCACUACU	hsa-miR-191	CAACGGAAUCCCAAAAGCAGCUG	hsa-miR-320	AAAAGCUGGGUUGAGAGGGCGA
nsa-miR-16	UAGCAGCACGUAAAUAUUGGCG	hsa-miR-17	CAAAGUGCUUACAGUGCAGGUAG	hsa-miR-374a	UUAUAAUACAACCUGAUAAGUG
nsa-miR-142-3p	UGUAGUGUUUCCUACUUUAUGGA	hsa-miR-130a	CAGUGCAAUGUUAAAAGGGCAU	hsa-let-7e	UGAGGUAGGAGGUUGUAUAGUU
nsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	hsa-miR-20a	UAAAGUGCUUAUAGUGCAGGUAG	hsa-miR-151-5p	UCGAGGAGCUCACAGUCUAGU
ısa-miR-15a	UAGCAGCACAUAAUGGUUUGUG	hsa-miR-27b	UUCACAGUGGCUAAGUUCUGC	hsa-miR-374b	AUAUAAUACAACCUGCUAAGUG
nsa-miR-29b	UAGCACCAUUUGAAAUCAGUGUU	hsa-miR-26b	UUCAAGUAAUUCAGGAUAGGU	hsa-miR-196b	UAGGUAGUUUCCUGUUGUUGGG
nsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	hsa-miR-146a	UGAGAACUGAAUUCCAUGGGUU	hsa-miR-140-3p	UACCACAGGGUAGAACCACGG
sa-miR-126	UCGUACCGUGAGUAAUAAUGCG	hsa-miR-200c	UAAUACUGCCGGGUAAUGAUGGA	hsa-miR-100	AACCCGUAGAUCCGAACUUGUG
sa-miR-143	UGAGAUGAAGCACUGUAGCUC	hsa-miR-99a	AACCCGUAGAUCCGAUCUUGUG	hsa-miR-103	AGCAGCAUUGUACAGGGCUAUGA
ısa-let-7b	UGAGGUAGUAGGUUGUGGUU	hsa-miR-19a	UGUGCAAAUCUAUGCAAAACUGA	hsa-miR-96	UUUGGCACUAGCACAUUUUUGCU
ısa-miR-27a	UUCACAGUGGCUAAGUUCCGC	hsa-miR-23a	AUCACAUUGCCAGGGAUUUCC	hsa-miR-302b	UAAGUGCUUCCAUGUUUUAGUAG
sa-let-7f	UGAGGUAGUAGAUUGUAUAGUU	hsa-miR-30a	UGUAAACAUCCUCGACUGGAAG	hsa-miR-194	UGUAACAGCAACUCCAUGUGGA
ısa-miR-9	UCUUUGGUUAUCUAGCUGUAUGA	hsa-let-7i	UGAGGUAGUAGUUUGUGCUGUU	hsa-miR-125a-5p	UCCCUGAGACCCUUUAACCUGUGA
sa-miR-26a	UUCAAGUAAUCCAGGAUAGGCU	hsa-miR-93	CAAAGUGCUGUUCGUGCAGGUAG	hsa-miR-423-5p	UGAGGGCAGAGAGCGAGACUUU
sa-miR-24	UGGCUCAGUUCAGCAGGAACAG	hsa-let-7c	UGAGGUAGUAGGUUGUAUGGUU	hsa-miR-376c	AACAUAGAGGAAAUUCCACGU
sa-miR-30e	UGUAAACAUCCUUGACUGGAAG	hsa-miR-106b	UAAAGUGCUGACAGUGCAGAU	hsa-miR-195	UAGCAGCACAGAAAUAUUGGC
sa-miR-181a	AACAUUCAACGCUGUCGGUGAGU	hsa-miR-101	UACAGUACUGUGAUAACUGAA	hsa-miR-222	AGCUACAUCUGGCUACUGGGU
sa-miR-29a	UAGCACCAUCUGAAAUCGGUUA	hsa-let-7g	UGAGGUAGUAGUUUGUACAGUU	hsa-miR-28-3p	CACUAGAUUGUGAGCUCCUGGA
sa-miR-124	UAAGGCACGCGGUGAAUGCC	hsa-miR-425	AAUGACACGAUCACUCCCGUUGA	hsa-miR-128a	UCACAGUGAACCGGUCUCUUU
sa-miR-144	UACAGUAUAGAUGAUGUACU	hsa-miR-15b	UAGCAGCACAUCAUGGUUUACA	hsa-miR-302c	UAAGUGCUUCCAUGUUUCAGUGG
sa-miR-30d	UGUAAACAUCCCCGACUGGAAG	hsa-miR-28-5p	AAGGAGCUCACAGUCUAUUGAG	hsa-miR-423-3p	AGCUCGGUCUGAGGCCCCUCAGU
sa-miR-19b	UGUGCAAAUCCAUGCAAAACUGA	hsa-miR-18a	UAAGGUGCAUCUAGUGCAGAUAG	hsa-miR-185	UGGAGAAAAGGCAGUUCCUGA
sa-miR-22	AAGCUGCCAGUUGAAGAACUGU	hsa-miR-25	CAUUGCACUUGUCUCGGUCUGA	hsa-miR-30b	UGUAAACAUCCUACACUCAGCU
sa-miR-122	UGGAGUGUGACAAUGGUGUUUG	hsa-miR-23b	AUCACAUUGCCAGGGAUUACC	hsa-miR-210	CUGUGCGUGUGACAGCGGCUGA
sa-miR-150	UCUCCCAACCCUUGUACCAGUG	hsa-miR-302a	UAAGUGCUUCCAUGUUUUGGUGA	SNORD48	TAACTCTGAGTGTGTCGCTGA
sa-miR-32	UAUUGCACAUUACUAAGUUGCA	hsa-miR-186	CAAAGAAUUCUCCUUUUGGGCU	SNORD47	CCGTTCCATTTTGATTCTGAG
sa-miR-155	UUAAUGCUAAUCGUGAUAGGGGU	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	SNORD44	GGTCTTAATTAGCTCTAACTGAC
sa-miR-140-5p	CAGUGGUUUUACCCUAUGGUAG	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	U6	ATTGGAACGATACAGAGAAGATTAG
sa-miR-125b	UCCCUGAGACCCUAACUUGUGA	hsa-let-7d	AGAGGUAGUAGGUUGCAUAGUU	miRTC	ACACTAAGTACGTCGTATTAC
sa-miR-141	UAACACUGUCUGGUAAAGAUGG	hsa-miR-30c	UGUAAACAUCCUACACUCUCAGC	miRTC	ACACTAAGTACGTCGTATTAC
	113 1111003 011110110000000011011	1 15 4541	3 3 C 3 IIII C 3 IIII C CII C CII C CCII		
ısa-miR-92a	UAUUGCACUUGUCCCGGCCUGU	hsa-miR-181b	AACAUUCAUUGCUGUCGGUGGGU		

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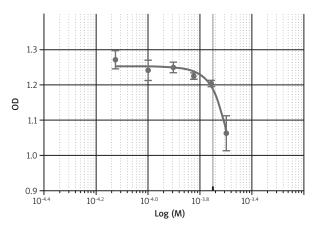
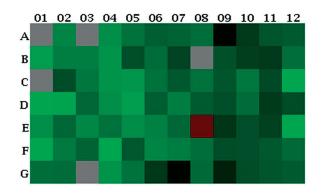


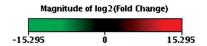
Fig. 1. Dose-dependent cytotoxicity of genistein. MCF-7 cells were treated with various concentrations of genistein. The studied concentrations of genistein were 75 μM , 100 μM , 125 μM , 150 μM , 175 μM , and 200 μM . The IC50 dose of genistein was 175 μM

used for housekeeping miRNAs as the endogenous normalisation factor to define miRNA expression profiles of 88 miRNAs. miR-23b was found to be up-regulated 56.69 fold in the treatment of genistein compared to the control group of genistein untreated cells (Fig. 2).

Discussion

Several studies have reported that genistein, which is an isoflavonoid and is a prime anti-cancer component





of soybean, can affect miRNA expression levels [17-20]. miR-151, which has an oncogenic effect, is up-regulated in prostate cancer cell lines (PCa), and genistein treatment down-regulates the relative expression of miR-151 in PCa [21]. It is known that genistein induces expression of miR-574-3p, which has a tumour suppressor role, and this induction inhibits cell proliferation, migration, and invasion in vitro and in vivo for prostate cancers [22]. Zaman et al. showed that genistein decreases the expression of miR-23b-3p in A-498 renal cancer cell line [23]. Furthermore, suppression of miR-23b-3p increases the number of total apoptotic cells and decreases cell invasion [23]. Although it is known that genistein affects chemotherapy agent efficiency and apoptosis, the effect of genistein on miRNA profiles is still unknown for breast cancer. In this study, it was found that treatment condition, which was genistein, affected miRNA expressions in MCF-7 breast cancer cell line. The cytotoxic effects of the defined group were examined independently. Cells in the genistein group were treated with an IC_{so} dose of genistein for three days. The cytotoxic effect of treatment group was observed after 48 hours. After the IC₅₀ dose of genistein was determined, miRNA qPCR array method was performed to detect regulation of miRNAs expressions in MCF-7 cell line. In this study, it was found that expression of miR-23b was up-regulated in the genistein treatment group. Majid et al. clearly showed that miR-23b is a methylation-silenced tumour suppressor in prostate cancer, and a high expression level of miR-23b is associated with higher survival rates in prostate cancer patients [24]. Stabile ectopic expression of miR-23b in HCT-116 colon carcinoma cell line reduces migration, invasion, and resistance to anoikis [25]. In vivo tumour models, which are generated from miR-23b-expressing HCT 116 cells, show that miR-23b-expressing tumours are encapsulated, non-invasive, and have low growth rate [25]. miR-23b regulates colony morphology and increases epithelial characteristics in MCF-7 cells. It is observed that miR-23b enhances focal adhesion connections and provides less lamellipodia structure after transfection in MDA-MB-231 breast cancer cells [26]. miR-23b regulates cytoskeletal reorganization and reduces cell motility and invasion via the PAK2 gene, which is a target for miR-23b in MCF-7 and MDA-MB-231 cells [26]. Furthermore, inhibition of miR-23b increases cell migration and metastasis for in vivo breast cancer models [26]. Because it is known that miR-23b has

	1	2	3	4		6	7	8	9	10	11	12
A	miR-142-5p	miR-16	miR-142-3p	miR-21	miR-15a	miR-29b	let-7a	miR-126	miR-143	let-7b	miR-27a	let-7f
	-62,47	-160,34	-62,47	-228,33	-88,95	-49,69	-58,28	-82,42	-4,13	-16,39	-40,09	-47,34
В	miR-9	miR-26a	miR-24	miR-30e	miR-181a	miR-29a	miR-124	miR-144	miR-30d	miR-19b	miR-22	miR-122
	-360,79	-132,06	-131,14	-267,8	-33,47	-76,37	-24,17	-62,47	-34,9	-19,49	-17,57	-83
С	miR-150	miR-32	miR-155	miR-140-5p	miR-125b	miR-141	miR-92a	miR-424	miR-191	miR-17	miR-130a	miR-20a
	-62,47	-30,38	-105,05	-273,42	-279,17	-92,73	-41,5	-86,52	-40,36	-106,52	-28,74	-40202,57
D	miR-27b	miR-26b	miR-146a	miR-200c	miR-99a	miR-19a	miR-23a	miR-30a	let-7i	miR-93	let-7c	miR-106b
	-1108,97	-489,44	-65,57	-217,52	-373,51	-50,39	-137,66	-47,34	-33,94	-73,26	-17,81	-31,23
E	miR-101	let-7g	miR-425	miR-15b	miR-28-5p	miR-18a	miR-25	miR-23b	miR-302a	miR-186	miR-29c	miR-7
	-217,52	-62,03	-168,31	-92,73	-197,4	-150,64	-65,12	56,69	-14,07	-31,89	-21,63	-6912,54
F	let-7d	miR-30c	miR-181b	miR-223	miR-320a	miR-374a	let-7e	miR-151-5p	miR-374b	miR-196b	miR-140-3p	miR-100
	-590,18	-118,19	-59,1	-716,59	-42,67	-153,81	-123,21	-85,33	-29,96	-32,56	-42,08	-69,31
G	miR-103	miR-96	miR-302b	miR-194	miR-125a-5p	miR-423-5p	miR-376c	miR-195	miR-222	miR-28-3p	miR-128	miR-302c
	-80,17	-75,85	-62,47	-264,11	-92,09	-15,94	-4,18	-71,26	-7,75	-30,38	-38,72	-47,34

Fig. 2. miRNA expression profiles after treatment. For the genistein group, miR-23b was up-regulated 56.69 fold after treatment. miRNA expression visualization about log2 (Fold Change) associated with genistein, compared with control

a tumour suppressor role for metastasis of breast cancer cells, miR-23b up-regulation might be important in terms of response to genistein.

In conclusion, up-regulated expression of miR-23b might be a putative biomarker for use in the therapy of breast cancer patients.

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