

ATM expression is attenuated by promoter hypermethylation in human ovarian endometriotic stromal cells

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ABSTRACT: A number of genes involved in the pathogenesis of endometriosis are silenced by the hypermethylation of their promoter regions. We assessed the effect and mechanism of the DNA demethylating agent 5-aza-2'-deoxycytidine (5-aza-dC) (10 μM) on the cell cycle in human endometriotic cyst stromal cells (ECSCs) and normal endometrial stromal cells (NESC)s by flow cytometry. The DNA methylation status of G2/M checkpoint regulators were investigated by methylation-specific PCR. The expression of ataxia telangiectasia mutated (ATM) and the effect of 5-aza-dC on its expression were also evaluated by quantitative RT-PCR and western blotting analysis. 5-aza-dC treatment resulted in the cell cycle arrest of ECSCs at the G2/M phase. In contrast, 5-aza-dC did not affect the cell cycle of NESC)s. The promoter region of the ATM gene was hypermethylated in ECSCs, but not in NESC)s. ATM mRNA expression was attenuated in ECSCs compared to that in NESC)s. Further, 5-aza-dC was found to restore ATM expression in ECSCs by its promoter demethylation. Our findings indicate that ATM promoter hypermethylation occurs in endometriosis, and that ATM silencing is involved in tumorigenesis during this disease; moreover, selective DNA demethylating agents and molecular target drugs against ATM silencing are promising for the treatment of endometriosis.

Key words: endometriosis / DNA methylation / ataxia telangiectasia mutated (ATM) / DNA demethylating agent / cell cycle arrest

Introduction

Endometriosis is an estrogen-dependent neoplasm that is frequently observed in women of reproductive age (Giudice and Kao, 2004). Histologic features of endometriosis resemble normal endometrium in the proliferative phase (Giudice and Kao, 2004); however, there are many molecular differences at the epigenetic, genetic, mRNA, and protein levels (Nasu et al., 2011a, 2011b; Abe et al., 2013). In 2014, endometriosis was classified as a benign tumor (Kurman et al., 2014) and, although rare, this disease is recognized as the origin of secondary malignant ovarian neoplasm.

DNA methylation of CpG islands in gene promoter regions is the best understood epigenetic modification. CpG islands of gene promoters are usually unmethylated and participate in active gene transcription (De Smet et al., 2004). When promoter CpG islands are methylated, expression of the associated gene is typically silenced by the suppression of transcriptional activity (Jones and Baylin, 2002). Aberrant DNA methylation in promoter regions has been reported

in endometriosis, and involves genes such as progesterone receptor (PR)-B (Wu et al., 2006), HOXA10 (Wu et al., 2005), estrogen receptor (ER)-β (Xue et al., 2007a), steroidogenic factor-1 (SF-1) (Xue et al., 2007b), aromatase (Izawa et al., 2008), miR-196b (Abe et al., 2013), and miR-503 (Hirakawa et al., 2016).

DNA methylation of CpG islands is relatively stable and reversible. The maintenance by DNA methyltransferases (DNMTs) such as DNMT1, DNMT3A, and DNMT3B promote epigenetic inheritance during DNA replication (Wu et al., 2007; Nasu et al., 2011a). DNMT inhibitors are currently tested in clinical trials or already used in clinics, especially for cancer treatment. 5-aza-2'-deoxycytidine (5-aza-dC) is one of the most studied DNMT inhibitors; this compound inhibits DNA methylation and reactivates gene expression, which involves the incorporation of these molecules at cytosine positions during DNA replication (Esteller, 2008; Nasu et al., 2011a).

In the present study, we investigated the effect of 5-aza-dC on the cell proliferation, apoptosis and cell cycle progression of ovarian endometriotic cyst stromal cells (ECSCs) and normal endometrial

stroma cells (NESCs). We found that 5-aza-dC treatment resulted in the cell cycle arrest of ECSCs at G2/M phase. Then, we evaluated the promoter methylation status of genes associated with G2 checkpoint control and discussed the epigenetic mechanisms of cell cycle control in endometriosis.

Materials and Methods

ECSC and NESC isolation procedure and cell culture conditions

Ovarian endometriotic tissues were obtained from patients during salpingo-oophorectomy or ovisceration for ovarian endometriotic cysts ($n = 19$, aged 26–47 years). NESCs were obtained from premenopausal patients during hysterectomies for subserosal leiomyoma with no evidence of endometriosis ($n = 18$, aged 38–50 years). Patients who had not received any hormonal treatments for at least 2 years were chosen for the tissue collection. All specimens were diagnosed as mid- to late-proliferative phase. This study was conducted under the approval by the institutional review board of the Faculty of Medicine, Oita University, and with written informed consent of the patients.

ECSCs and NESCs were isolated from ovarian endometriotic cyst and eutopic endometrium, respectively, through enzymatic digestion as previously described (Nishida et al., 2004). Isolated ECSCs and NESCs were cultured in DMEM supplemented with 100 IU/ml of penicillin, 50 mg/ml of streptomycin, and 10% heat-inactivated fetal bovine serum (all obtained from Gibco-BRL, Gaithersburg, MD, USA), at 37°C with 5% CO₂ in air.

ECSCs and NESCs in monolayer culture after the third passage were >99% pure as determined by immunocytochemical staining with antibodies specific for vimentin, CD10, cytokeratin, factor VIII, and leukocyte common antigen, and were used for the following experiments (Nishida et al., 2004). CD10 was used as a marker of Müllerian origin. Each experiment was performed in triplicate and repeated at least three times.

Assessment of the effects of 5-aza-dC on ECSC cell viability

The effects of 5-aza-dC on the cell viability of NESCs and ECSCs were analyzed by modified methylthiazolotetrazolium (MTT) assay using the Cell Proliferation Kit I (Roche Diagnostics, Basel, Switzerland), as previously described (Abe et al., 2013; Hirakawa et al., 2016). Briefly, 5×10^3 NESCs and ECSCs placed in 96-well flat-bottomed microplates (Corning Inc., Corning, New York, NY, USA) were incubated for 96 h with or without 5-aza-dC (10 μ M). Thereafter, cell viability was measured according to the manufacturer's instructions. Data were calculated from triplicate samples and are presented as the percent viability relative to those of untreated NESCs.

Assessment of the effects of 5-aza-dC on ECSC apoptosis

The effects of 5-aza-dC on apoptosis in NESCs and ECSCs were analyzed by the direct determination of nucleosomal DNA fragmentation using the Cell Death Detection ELISA (Roche Diagnostics),

as previously described (Abe et al., 2013; Okamoto et al., 2015; Hirakawa et al., 2016). Briefly, 5×10^3 NESCs and ECSCs placed in 96-well flat-bottomed microplates (Corning Inc.) were incubated for 96 h with or without 5-aza-dC (10 μ M). Thereafter, nucleosomal DNA fragmentation was measured according to the manufacturer's instructions. Data were calculated from triplicate samples and are presented as the percent viability relative to those of untreated NESCs.

The effects of 5-aza-dC on the activities of caspase-3 and caspase-7 of NESCs and ECSCs were analyzed by the Caspase-Glo 3/7 Assay (Promega, Madison, WI, USA), as described (Abe et al., 2013; Okamoto et al., 2015; Hirakawa et al., 2016). Briefly, 5×10^3 NESCs and ECSCs placed in 96-well flat-bottomed microplates (Promega) were incubated for 96 h with or without 5-aza-dC (10 μ M). Thereafter, caspase-3 and caspase-7 activities were measured according to the manufacturer's instructions. Data were calculated from triplicate samples and are presented as the percent viability relative to those of untreated NESCs.

Assessment of the effects of 5-aza-dC on ECSC cell cycle by flow cytometry

The effects of 5-aza-dC on the cell cycle of NESCs and ECSCs were analyzed by flow cytometry after 96 h of culture with or without 5-aza-dC (10 μ M), as previously described (Abe et al., 2013; Hirakawa et al., 2016). Briefly, ECSCs were cultured at <60% confluence for 4 days with or without 5-aza-dC (10 μ M). Flow cytometric analysis of the cell cycle was performed after propidium iodide staining using the CellFIT program (Becton-Dickinson, Sunnyvale, CA, U.S.A), in which the S-phase was calculated using a ModFit model. Data were calculated as the percentage of values obtained for 5-aza-dC-treated cells relative to those of untreated controls.

Methylation-specific PCR

Based on a database search using the UCSC Genome Browser on Human, December 2013 (GRCh/hg38) Assembly (<http://genome.ucsc.edu/cgi-bin/hgGateway>), we detected the presence of dense CpG islands surrounding the genes listed in Fig. 1, except for *cdc25A*. Considering the functions of proteins encoded by these genes as the negative regulators of the G2/M checkpoint (Fig. 1), methylation status of ataxia telangiectasia mutated (*ATM*), ataxia telangiectasia and Rad3-related (*ATR*), p53, p21^{Waf1/Cip1}, checkpoint kinase (*Chk1*), and *Chk2* were evaluated by Methylation-specific PCR (MSP), as described (Abe et al., 2013). Genomic DNA was extracted from cultured NESCs ($n = 8$) and ECSCs ($n = 8$) with a QIAamp[®] DNA Mini kit (Qiagen, Tokyo, Japan). Then, genomic DNA (1 μ g) was subjected to bisulfate conversion using the EpiTect Bisulfite Kit (Qiagen) and further processed for the PCR amplification of specific CpG island regions of candidate genes. MSP for candidate genes and the predicted size of PCR products are listed in Table I and the PCR was performed as previously described (Fruhwald et al., 2001; Brakensiek et al., 2005; Roy et al., 2006; Wang et al., 2010; Mazumder Indra et al., 2011). PCR products were analyzed by 2% agarose/ethidium bromide gel electrophoresis.

Quantitative RT-PCR

The expression of ATM mRNA in NESCs and ECSCs was evaluated by quantitative RT-PCR, as described (Abe et al., 2013;

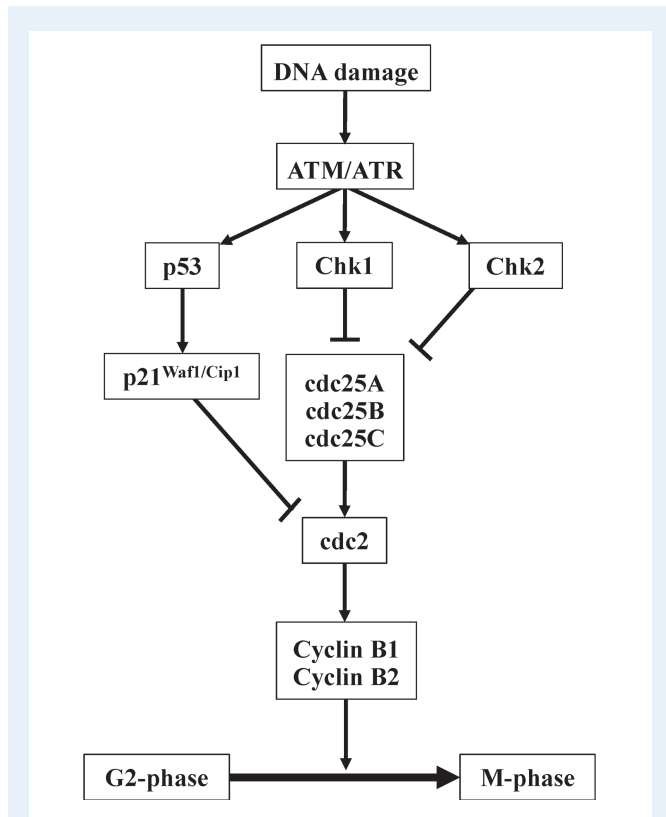


Figure 1 Regulatory mechanism of G2/M checkpoint. Representative regulators of G2/M checkpoint and their signal pathways are shown. Except for *cdc25A*, all of these molecules possess dense CpG islands in the promoter region of their genes.

Hirakawa *et al.*, 2016). Briefly, total RNA was extracted from NESC (n = 10) and ECSC (n = 10), cDNA was synthesized, and quantitative RT-PCR was performed as described (Abe *et al.*, 2013; Hirakawa *et al.*, 2016). Primers specific to *ATM* (Assay ID: Hs01112355, Applied Biosystems, Carlsbad, CA, USA) and *GAPDH* (Assay ID: Hs02758991_g1) were used. The candidate mRNA expression levels relative to *GAPDH* mRNA expression were calculated by using calibration curve. The data were calculated from 10 samples and are presented as the percentage of values compared to those of NESC.

The effect of 5-aza-dC on *ATM* mRNA expression in ECSCs was also evaluated by quantitative RT-PCR. Briefly, 96 h after 5-aza-dC (10 μ M) treatment, total RNA was extracted from ECSCs and subjected to quantitative RT-PCR, as described. The data were calculated from triplicate samples and are presented as the percentage of the values compared to those of untreated controls.

Protein expression

The expression of ATM protein in NESC (n = 5) and ECSC (n = 5) was evaluated by western blotting analysis, as described (Nishida *et al.*, 2004; Abe *et al.*, 2013; Hirakawa *et al.*, 2016). Antibodies against ATM (ab82512, Abcam, Cambridge, UK) and *GAPDH* (mAbcam 9484, Abcam) were used as primary antibodies. The expression of ATM protein relative to that of *GAPDH* in NESC was analyzed using Image LabTM software (Bio-Rad Laboratories, Hercules, CA, USA) and the data are presented as the percent values.

The effect of 5-aza-dC on ATM and phosphorylated p53 protein expression in ECSCs was also evaluated by western blotting analysis. An antibody against phosphorylated p53 (#9284, Cell Signaling Technology, Danvers, MA, USA) was used as the primary antibody.

Statistical analysis

All data were obtained from triplicate samples and are presented as percentages relative to the corresponding controls as mean \pm SD; these values were appropriately analyzed using the Bonferroni test, Student's *t*-test, or Mann-Whitney *U*-test with Statistical Package for Social Science software (IBM SPSS statistics 24; IBM, Armonk, NY, USA). *P*-values <0.05 were considered statistically significant.

Results

Marginal effects of 5-aza-dC on cell viability and apoptosis of ECSCs

The effects of 5-aza-dC on the cell viability of NESC and ECSC were determined by modified MTT assay. Although there was no significance, 5-aza-dC tends to attenuate the cell viability of NESC and ECSC (Fig. 2A).

The effects of 5-aza-dC on apoptosis of NESC and ECSC were determined by the Cell Death Detection ELISA. As shown in Fig. 2B, 5-aza-dC significantly induced the apoptosis of NESC. However, 5-aza-dC showed a marginal effect on the apoptosis of ECSC.

The effects of 5-aza-dC on the caspase 3/7 activities in NESC and ECSC were determined by the Caspase-Glo 3/7 Assay. As shown in Fig. 2C, 5-aza-dC significantly activated caspase 3/7 in NESC and ECSC.

5-aza-dC induces G2/M phase cell cycle arrest in ECSCs

The effects of 5-aza-dC on the cell cycle of NESC and ECSC were determined by flow cytometry. As shown in Fig. 3, compared to that in control cells, culture of ECSC for 96 h in the presence of 5-aza-dC (10 μ M) resulted in an accumulation of cells in the G2/M phase of the cell cycle (12.6 \pm 0.4% vs. 21.3 \pm 0.7%, respectively; *P* < 0.0001), with a concomitant decrease in the proportion of these cells in the G0/G1 phase (83.7 \pm 0.5 vs. 73.5 \pm 0.6, respectively; *P* < 0.0001). In contrast, 5-aza-dC (10 μ M) did not affect the cell cycle of NESC.

Hypermethylation of ATM in ECSCs

The methylation status of genes known as negative regulators of the G2/M checkpoint including *ATM*, *ATR*, *p53*, *p21^{Waf1/Cip1}*, *Chk1*, and *Chk2* was evaluated by MSP. As shown in Fig. 4A, CpG islands in the promoter region of *ATM* (Table II) were hypermethylated in ECSCs, but not in NESC. In contrast, CpG islands in the promoter region of *Chk2* were hypermethylated in both NESC and ECSC. CpG islands in the promoter regions of *ATR*, *p53*, *p21^{Waf1/Cip1}*, and *Chk1* were hypomethylated in NESC or ECSC.

Table 1 Primers for MSP and size of their PCR products.

Gene name	Methylation status	Primer sequence	PCR product	References
ATM	Methylated	Forward: GGAGTTCGAGTCTGAAGGGC Reverse: CTACCTACTCCCGTTCCGA	239 bp	Roy et al. (2006)
	Unmethylated	Forward: GTTTTGGAGTTTGAAGGGT Reverse: AACTACCTACTCCACTTCCAA	246 bp	
p21 ^{Waf1/Cip1}	Methylated	Forward: TACGCGAGGTTTCGGGATC Reverse: CCCTAATATACAACCGCCCCG	171 bp	Brakensiek et al. (2005)
	Unmethylated	Forward: GGATTGGTTGGTTTGTGGAATTT Reverse: ACAACCCTAATATACAACCACCCCA	161 bp	
p53	Methylated	Forward: TTCGGTAGCGGATTATTTG Reverse: AAATATCCCCGAAACCCAAC	139bp	Fruhwald et al. (2001)
	Unmethylated	Forward: TTGGTAGGTGGATTATTTGTTT Reverse: CCAATCCAAAAAACATATCAC	247bp	
Chk1	Methylated	Forward: GGGGGTAGGAGGGATTAATTC Reverse: AAAAACGATATAAAAACAAAAACGC	194bp	Mazumder Indra et al. (2011)
	Unmethylated	Forward: GGGGTAGGAGGGATTAATTT Reverse: AAAAAACAATATAAAAACAAAAAACC	195bp	
Chk2	Methylated	Forward: TTACGTTTGTGTTTTAGATTTTCGT Reverse: AAATCTTCTACCCACAATACCG	213bp	Wang et al. (2010)
	Unmethylated	Forward: TTATGTTTGTGTTTTAGATTTTGT Reverse: CAAATCTTCTACCCACAATACCA	213bp	

ATM mRNA and protein expression in ECSCs

Next we evaluated ATM mRNA levels in NESCs and ECSCs using quantitative RT-PCR. As shown in Fig. 4B, ATM mRNA expression was significantly attenuated in ECSCs, compared to that in NESCs (45.9 ± 25.6 vs. 100.0 ± 42.2 , respectively; $P < 0.01$).

However, ATM protein expression in ECSCs ($n = 5$) was similar to that in NESCs ($n = 5$; 88.9 ± 45.3 vs. 100.0 ± 47.5 , respectively). (Fig. 4C).

Demethylation of ATM promoter, restoration of ATM mRNA and protein expression, and phosphorylation of p53 in ECSCs by 5-aza-dC

Finally, we confirmed that 5-aza-dC (10 μ M) treatment induced the demethylation of ATM promoter (Fig. 5A). Simultaneously, 5-aza-dC (10 μ M) treatment significantly induced the mRNA expression of ATM ($P < 0.0001$) (Fig. 5B). The protein levels of ATM and phosphorylated p53 were also increased by 5-aza-dC (10 μ M) treatment (Fig. 5C).

Discussion

In the present study, we investigated the effects of a DNA demethylating agent, namely 5-aza-dC, on cell viability, apoptosis, and the cell cycle of NESCs and ECSCs. We demonstrated for the first time that 5-aza-dC treatment results in the cell cycle arrest of ECSCs at the

G2/M phase. In contrast, 5-aza-dC did not affect the cell cycle of NESCs. However, 5-aza-dC treatment revealed stronger effects on apoptosis in NESCs compared to that of ECSCs. It is suggested that the mechanism of apoptosis is different from that of cell cycle arrest in these cells. Thereafter, we focused on the mechanisms of cell cycle arrest induced by 5-aza-dC. We evaluated the promoter methylation status of genes that negatively regulate the G2/M checkpoint and found that the promoter of ATM was hypermethylated in ECSCs. ATM mRNA expression was also found to be attenuated in ECSCs compared to that in NESCs. Finally, 5-aza-dC was found to restore the mRNA expression of ATM. These findings suggest that promoter hypermethylation of ATM occurs in endometriosis. Further, silencing of this gene could be involved in the tumorigenesis of this benign disease by mediating the escape from cell cycle arrest at the G2/M phase. Moreover, with the development of novel DNA demethylating agents selective for hypermethylated DNA, these drugs would become promising options for the treatment of endometriosis. Alternatively, molecular target drugs against ATM silencing are also promising.

Cell cycle checkpoints including G1/S, intra-S, and G2/M are involved in DNA damage response reactions. When DNA is damaged, the G2/M checkpoint functions to prevent damaged DNA from being segregated into daughter cells, and defects in this checkpoint pathway can result in genomic instability, cell death, and tumorigenesis (Molinari, 2000; Abraham, 2001). As shown in Fig. 1, a G2/M checkpoint is initiated by the activation of ATM and ATR kinases in response to DNA damage (Shiloh, 2003). Activated ATM and ATR mediate subsequent signal transduction cascades that include Chk1, Chk2, and p53/p21^{Waf1/Cip1} (Bartek and Lukas, 2003;

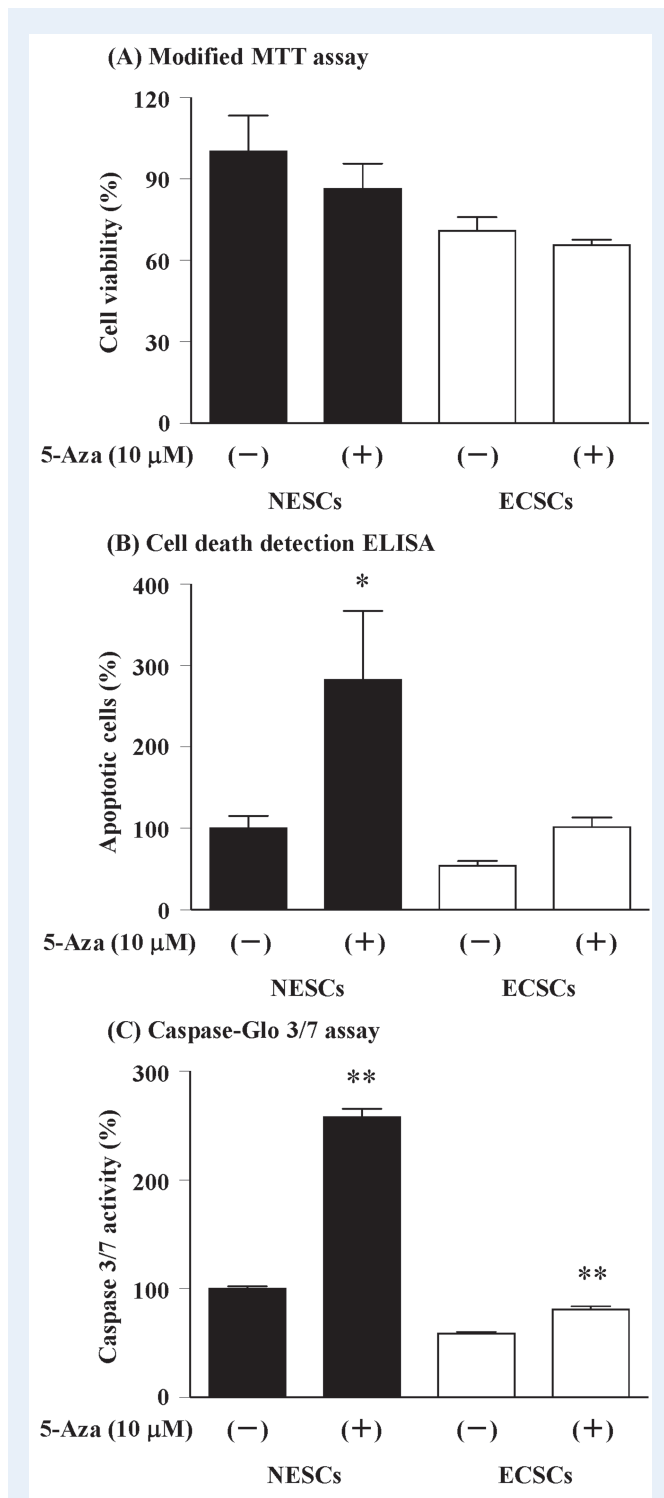


Figure 2 Effects of 5-aza-dC on cell viability and apoptosis of NESCs and ECSCs. **(A)** Modified MTT assay. 5-aza-dC treatment had marginal effects on the cell viability of NESCs and ECSCs. **(B)** Cell death detection ELISA. 5-aza-dC significantly induced the apoptosis of NESCs, but had a marginal effect on the apoptosis of ECSCs. **(C)** Caspase-Glo 3/7 assay. 5-aza-dC significantly activated caspase 3/7 in NESCs and ECSCs. Data were presented as mean \pm SD. * $P < 0.01$, ** $P < 0.005$ vs. controls (Bonferroni test).

Lobrich and Jeggo, 2007). Chk1 and Chk2 inhibit the activity of their shared downstream substrates, cell division cycle 25A (*cdc25A*), *cdc25B*, and *cdc25C*. Inhibition of *cdc25A/B/C* activity results in the induction of G2/M cell cycle arrest through inhibition of *cdc2* and its effectors, cyclin B1 and cyclin B2 (Liu et al., 2000; Niida and Nakanishi, 2006; Lobrich and Jeggo, 2007). ATM and ATR also activate tumor suppressors p53 and p21^{Waf1/Cip1} (Bartek and Lukas, 2003). Activation of p21^{Waf1/Cip1} negatively regulates *cdc2* and induces G2/M cell cycle arrest (Zhan et al., 1999).

Of these negative regulators of the G2/M checkpoint, we found that only ATM expression was attenuated by methylation in ECSCs. Disruption of the tumor suppressor function of this protein can allow the cell to bypass the G2/M checkpoint. Accordingly, loss of functional ATM is associated with both decreased genomic integrity and increased cancer risk. Repression of ATM expression by DNA hypermethylation has been reported in head and neck carcinomas (Ai et al., 2004), oral squamous cell carcinoma (Rigi-Ladiz et al., 2011), colorectal cancers (Bai et al., 2004), non-small cell lung cancer (Safar et al., 2007), breast cancers (Vo et al., 2004), and malignant lymphomas (Huang et al., 2007). It has also been suggested that epigenetically repressed ATM might be responsible for resistance to DNA damage signals and the acquisition of the proliferative characteristics of endometriosis. ATM is a pleiotropic nuclear protein that is activated by endogenous DNA breaks or DNA-damaging agents (Kastan and Lim, 2000; Khanna and Jackson, 2001; Shiloh, 2003; Lavin et al., 2005; Shiloh and Ziv, 2013). ATM promotes cell cycle arrest to prevent the processing of damaged DNA, activate DNA-repair pathways, and induce apoptosis after severe DNA damage (Kastan and Lim, 2000; Lavin et al., 2005). Regarding the mechanism associated with the G2/M checkpoint, ATM further activates negative regulators of the cell-cycle checkpoint including p53, Chk1, and Chk2 after DNA damage, as summarized in Fig. 1.

We demonstrated that 5-aza-dC treatment results in G2/M cell cycle arrest by restoring ATM expression in ECSCs. It has been reported that DNMT1, DNMT3A, and DNMT3B, the enzymes responsible for DNA methylation, are overexpressed in endometriosis (Wu et al., 2007), suggesting the presence of rampant hypermethylation in corresponding genes associated with endometriosis pathogenesis (Nasu et al., 2011a). The mechanism of action of the DNA demethylating agent 5-aza-dC is associated with its incorporation into DNA by inhibiting DNA methyltransferase activity (Haaf, 1995). Consequently, genes silenced by hypermethylation are demethylated and re-expressed. 5-aza-dC is one of the most studied nucleoside analogs of cytosine and the mechanism through which it inhibits DNA methylation involves its incorporation at cytosine positions during DNA replication (Esteller, 2008; Nasu et al., 2011a). It is widely recognized that nucleoside analogs of cytosine, such as 5-aza-dC, exert their anti-tumor effects by reactivating aberrantly hypermethylated growth regulatory genes. Further studies on DNA demethylating agents in endometriosis and the selective reactivation of genes repressed by DNA hypermethylation might lead to promising epigenetic treatment strategies for endometriosis. Otherwise, molecular target drugs against ATM silencing are also hopeful for the treatment of endometriosis.

Hypermethylation of gene promoters and silencing of the corresponding genes have been reported in endometriosis, for as *PR-B* (Wu et al., 2006), *HOXA10* (Wu et al., 2005), *ER- β* (Xue et al., 2007a),

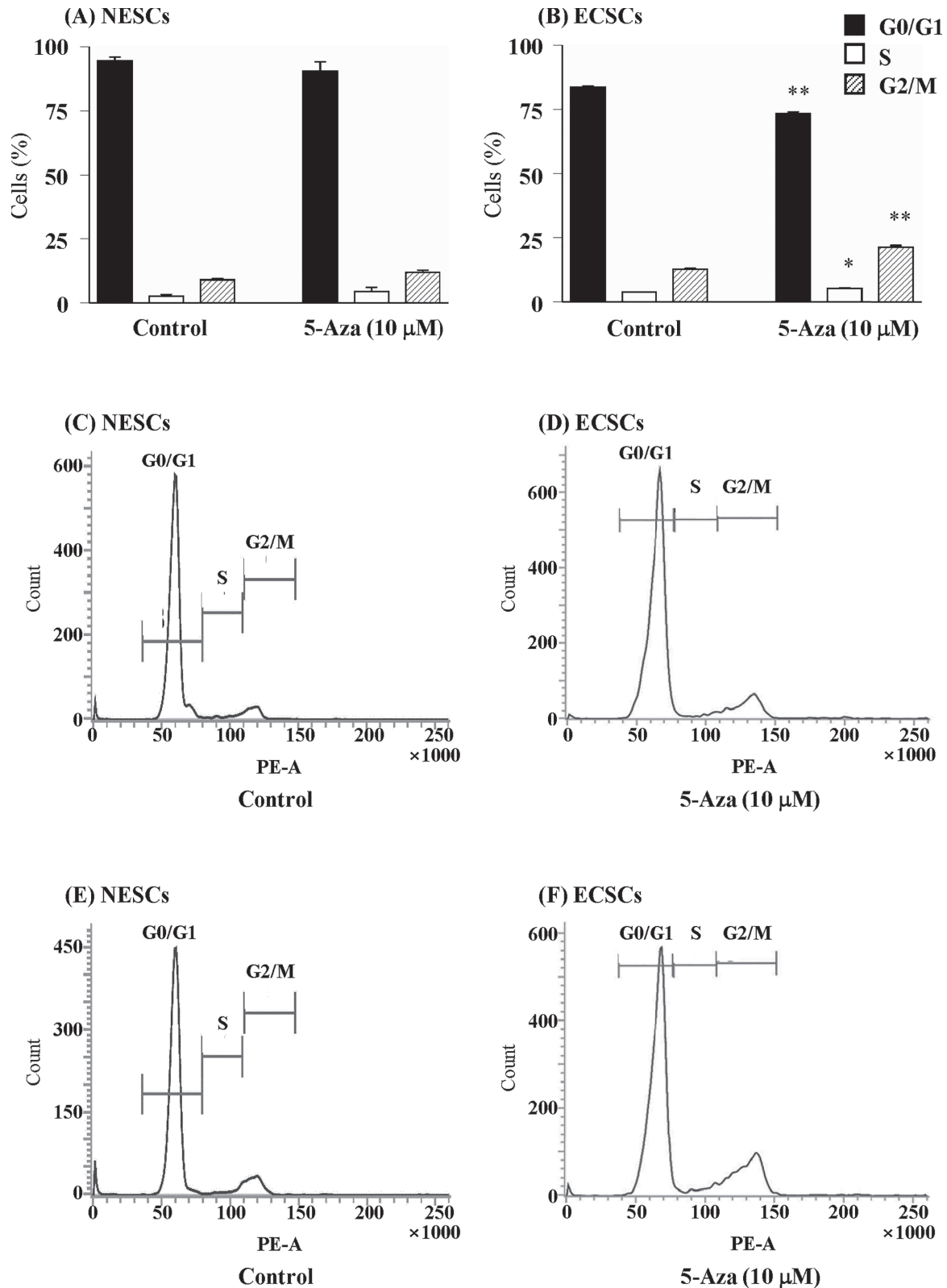


Figure 3 Effects of 5-aza-dC on the cell cycle of NESC (A, C, E) and ECSC (B, D, F). Treatment with 5-aza-dC (10 μ M) for 96 h did not affect the cell cycle of NESC ($n=3$), whereas, 5-aza-dC treatment induced the cell cycle arrest of ECSC ($n=3$) at G2/M phase. Error bars show the mean \pm SD. * $P < 0.05$, ** $P < 0.0001$ vs. controls (Bonferroni test).

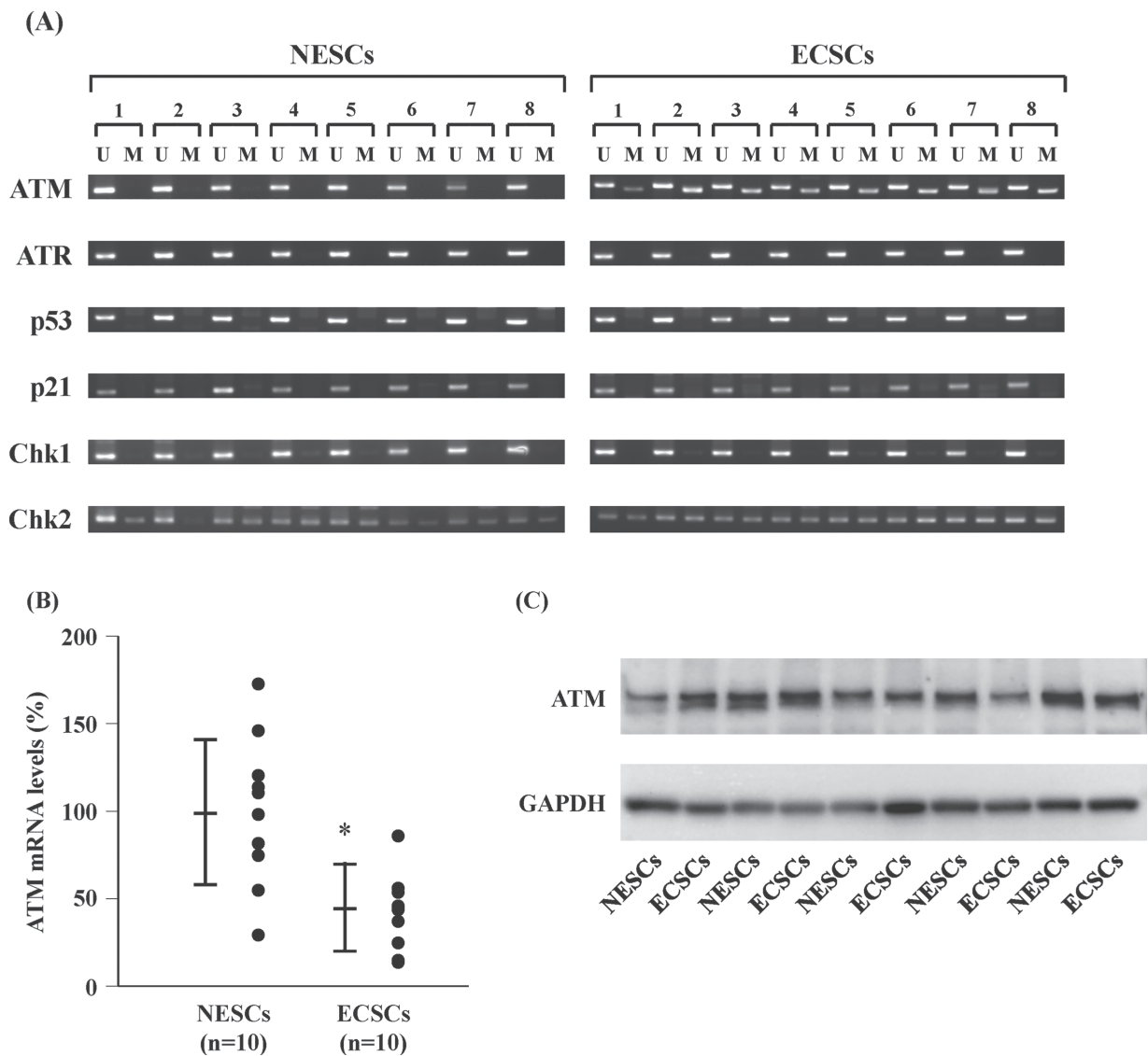


Figure 4 Results of MSP, RT-PCR, and western blotting analysis. (A) Methylation status of the gene promoters of the negative regulators of G2/M checkpoint in NESC ($n = 8$) and ECSC ($n = 8$). CpG islands in the promoter region of *ATM* were hypermethylated in ECSCs, but not in NESC. In contrast, CpG islands in the promoter region of *Chk2* were hypermethylated in both NESC and ECSC. CpG islands in the promoter regions of *ATR*, *p53*, *p21*, and *Chk1* were hypomethylated in NESC or ECSC. U, unmethylated alleles; M, methylated alleles. (B) *ATM* mRNA expression in ECSC ($n = 10$) and NESC ($n = 10$). *ATM* mRNA expression is significantly attenuated in ECSC compared to that in NESC. Error bars show the mean \pm SD. * $P < 0.01$ vs. NESC (Mann-Whitney *U*-test). (C) *ATM* protein expression in ECSC ($n = 5$) and NESC ($n = 5$). *ATM* protein expression in ECSC was similar to that in NESC (88.9 ± 45.3 vs. 100.0 ± 47.5 , respectively).

aromatase (Izawa *et al.*, 2008), *STRA6* (Yamagata *et al.*, 2014), *HSD17 β 2* (Yamagata *et al.*, 2014), *miR-196b* (Abe *et al.*, 2013), and *miR-503* (Hirakawa *et al.*, 2016). However, the promoter regions of *GATA6*, *SF-1*, and *STAR* genes are hypomethylated in endometriosis (Xue *et al.*, 2007b; Dyson *et al.*, 2014; Yamagata *et al.*, 2014; Izawa *et al.*, 2018). It is suggested that the alteration of these gene expressions are favorable for the progression of endometriosis. Recently, DNA methylation microarray techniques have demonstrated the aberrant methylation status in endometriosis (Dyson *et al.*, 2014; Yamagata *et al.*, 2014; Yotova *et al.*, 2017; Izawa *et al.*, 2018). Yamagata *et al.* (2014) compared the methylation status of eutopic endometrial stro-

mal cells from women with endometriosis and to those from women without endometriosis and found that the methylation status of some genes were different between these cell types. It is considered that the changes of methylation status might be associated with pathogenesis of endometriosis. The methylation status of *ATM* was not described in these reports. However raw data of DNA methylation microarrays were available in public databases in two of the reports (Yamagata *et al.*, 2014; Yotova *et al.*, 2017), and these showed a tendency toward hypermethylation of *ATM*. Interestingly, *ATM* promoter methylation status had marginal effect on the *ATM* protein expression. It is considered that the post-transcriptional regulatory mechanisms of *ATM* is complicated.

Table 2 A map of the CpG islands in the *ATM* promoter.

ATAGCCGGGTCCAATAACCCTCCATCCCCTCCGCTCCGCGCTTACCCAATAACAAGCCGGGCTACGTCCGAGGGTAACAACATGATCAAACCACAG
 CAGGAACCACAATAAGGAACAAGACTCAGGTTAAAGCAAACACAGCGACGCTCCTGCGCCGCATCTCCTGGTTCCAGTGGCGGCACTGAAC
 TCGCGGCAATTTGTCCCGCTCTTTCGCTTACGGCAGCCAATCGCTTCCGCCAGAGAAAGAAAGGCGCCGAAATGAAACCCGCTCCGTTT
 GCCTTCGGAAGTGTCTCACTTCCGCTCAGACTTGGAGGGGCGGGGATGAGGAGGGCGGGGAGGACGACGAGGGCGAAGAGGGTGGGT
 GAGA GCCCCGGAGCCCGAGCCGAAGGGC GAGCCGCAAACGCTAAGTCGCTGGCCATTGGTGGACATGGCGCAGGCGGTTTGTCTCCGA
 CGGGCCGAATGTTTTGGGGCAGTGTTTGAGCGCGGAGACCCGCTGATACTGGATGCGCATGGGCATACCGTGCTCTGCGGCTGCTTGGCGT
 TGCTTCTTCTCCAGAAGTGGGCGCTGGGCAGTCACGCAGGGTTTGA CCGGAAGCGGGAGTAGGTAGCT GCGTGGCTAACGGAGAAAA
 GAAGCCGTGGCCGCGGGAGGAGGCGAGAGGAGTCCGGATCTGCGTTCAGCCACC GCCGCGTTGATACTACTTTGACCTTCCGAGTGCAG
 TGGTAGGGGCGCGGAGGCAACGCAGCGCTTCTGCGCTGGGAAATTCAGTCGTGTGCGACCCAGTCTGTCTCTCCCAGACCGCCAATCTC
 ATGCACCCCTCCAGAG.

Underline indicates the CpG islands. Primer binding sites for unmethylated DNA are indicated by a box. Primer binding sites for methylated DNA are indicated by half-tone meshing.

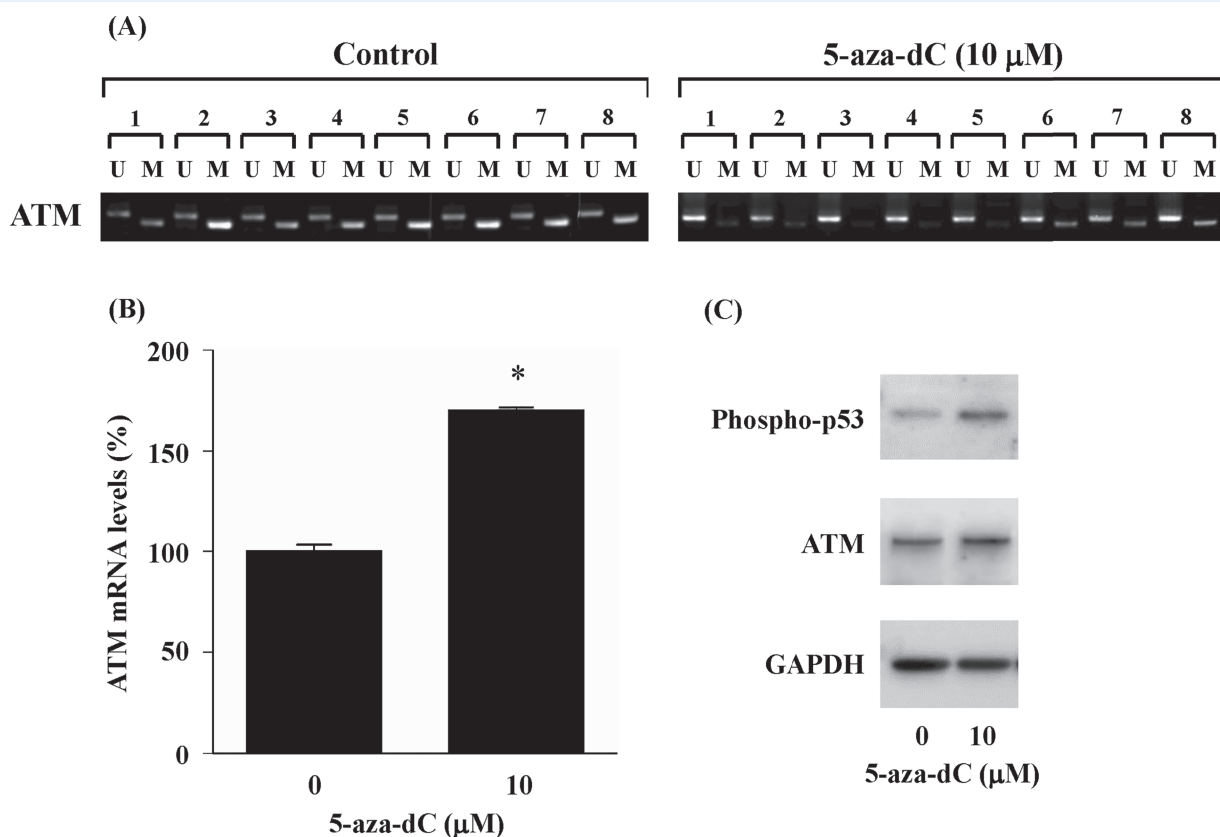


Figure 5 Effects of 5-aza-dC on the methylation status of *ATM* promoter, *ATM* expression, and phosphorylation of p53. **(A)** Treatment with 5-aza-dC (10 μ M) for 96 h induced demethylation of *ATM* promoter in ECSCs ($n=8$). **(B)** Treatment with 5-aza-dC (10 μ M) for 96 h induced *ATM* mRNA expression in ECSCs ($n=3$). Error bars show the mean \pm SD. * $P < 0.0001$ vs. controls (Student's t -test). **(C)** Treatment with 5-aza-dC (10 μ M) for 96 h upregulated the *ATM* protein levels and induced the phosphorylation of p53 in ECSCs. Representative results of three repeated experiments are shown.

The limitation of the present study is that we only used *in-vitro* culture model of stromal cells to evaluate the mechanism associated with 5-aza-dC. Since endometriotic tissues consist of a variety of cell types, further studies with endometriotic epithelial cells as well as the whole tissues are necessary to fully understand the epigenetic changes in this disease. In addition, similar experiments with

eutopic endometrial stromal cells from women with endometriosis are necessary to strengthen the findings of the present study. Moreover, considering the malignant transformation that can accompany endometriosis, the methylation status of *ATM* and its related genes in secondary malignant neoplasms should be examined.

In conclusion, we observed that *ATM* expression was repressed in ECSCs via the hypermethylation of its promoter. Further, 5-azadC induced the cell cycle arrest of ECSCs at the G2/M phase by restoring *ATM* expression. These findings provide important evidence that endometriosis is ultimately an epigenetic and neoplastic disease. These results and further studies on the methylation status of other genes associated with the development of endometriosis might lead to novel treatment strategies for this disease.

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Authors' roles

KN and HN participated in the study design, data analysis and manuscript drafting. TH, YA, KT, and RZ executed the study.

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Conflict of interest

None declared.

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