

In consequence, whatever process of tumor shrinkage works, the key to achieving local control of tumors associated with residual tumor masses is to increase the target dose. The use of chemoradiotherapy in place of RT treatment alone likely enhances the RR during EBRT.<sup>22</sup> The effect of chemotherapy on RR was, however, not analyzed in this study because of the small number of patients and the heterogeneity of their backgrounds, such as age. In addition to routine use of chemoradiotherapy, we currently further intensify treatment by performing more than three ICRTs with shortening of the ICRT interval or the addition of interstitial RT for those patients in whom post-EBRT MR imaging reveals a residual mass of substantial size.

Post-ICRT volume correlated significantly with the post-EBRT volume, whereas the pre-RT volume did not predict the post-EBRT volume. This result shows that RR during EBRT represents the RR during both EBRT and ICRT. Therefore, the appropriate timing of MR imaging from the standpoint of clinical practice is immediately before the start of ICRT (post-EBRT), as was done in the present study. This finding supports the results of Mayr et al.<sup>23</sup> Post-EBRT MR imaging is also useful for specifying the target volume in ICRT, whereas post-ICRT imaging is beneficial only in patients with a substantial residual mass observed on post-EBRT MR images.

Recent advances in target volume specification using MR imaging, as well as in dose distribution optimization using a computerized high-dose-rate ICRT unit, have allowed the introduction of image-guided ICRT for cervical cancer.<sup>24–26</sup> Regardless of tumor radioreponse, this and other innovations in ICRT technique can facilitate personalized treatment by increasing the minimum target dose in accordance with the individual target volume and contribute to improvements in local tumor control without an increase in the incidence of complications.

## Conclusion

The difference in the impact of physical treatment was not directly shown as a difference in RR of cervical cancer during EBRT and ICRT. This inconsistency probably is due not only to error-causing factors such as approximate tumor-volume estimation but also to biological factors such as tumor clearance mechanisms. Whatever mechanisms work in regard to tumor shrinkage, post-EBRT MR imaging is useful not only for assessing the tumor volume before ICRT (used to estimate the minimum target doses via ICRT) but also for predicting the residual tumor mass after ICRT because

a strong correlation was seen between the post-ICRT and post-EBRT tumor volumes.

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## Aneuploidy Predicts Outcome in Patients with Endometrial Carcinoma and Is Related to Lack of *CDH13* Hypermethylation

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**Abstract** **Purpose:** Many investigators have reported that aneuploidy detected by flow cytometry is a useful prognostic marker in patients with endometrial cancer. Laser scanning cytometry (LSC) is a technology similar to flow cytometry but is more feasible for clinical laboratory use. We evaluated the usefulness of DNA ploidy detected by LSC as a prognostic marker in patients with endometrial cancer and investigated genetic and epigenetic factors related to aneuploidy. **Experimental Design:** Endometrial cancer specimens from 106 patients were evaluated. The methylation status of *CDH13*, *Rassf1*, *SFRP1*, *SFRP2*, *SFRP4*, *SFRP5*, *p16*, *hMLH1*, *MGMT*, *APC*, *ATM*, and *WIF1* and mutations in the *p53* and *CDC4* genes were investigated. LSC was carried out to determine DNA ploidy. Fluorescence *in situ* hybridization was done with chromosome-specific centromeric probes to assess chromosomal instability. **Results:** Univariate and multivariate analyses revealed that *p53* mutation and lack of *CDH13* hypermethylation associated positively with aneuploidy. Univariate analysis showed that aneuploidy, chromosomal instability, and lack of *CDH13* hypermethylation as well as surgical stage were significantly predictive of death from endometrial cancer. Furthermore, multivariate analysis revealed that stage in combination with either DNA aneuploidy or lack of *CDH13* hypermethylation was an independent prognostic factor. **Conclusion:** These results suggest that analysis of DNA ploidy and methylation status of *CDH13* may help predict clinical outcome in patients with endometrial cancer. Prospective randomized trials are needed to confirm the validity of an individualized approach, including determination of tumor ploidy and methylation status of *CDH13*, to management of endometrial cancer patients.

Endometrial cancer is one of the most common genital cancers in women worldwide. The highest incidences are observed in western Europe and North America (1), whereas the incidence is lower but rapidly rising in Japan (1, 2). The number of endometrial cancer patients in Japan was estimated as 1.5 to 1.7 per 100,000 women in the 1970s; however, it has been steadily increasing and is now estimated as 6 to 7 cases per 100,000 women in the 2000s (2). Changes in diet and lifestyle related to obesity, a risk factor for endometrial cancer (3), may account for the drastic increase in endometrial cancer in Japan.

Surgical stage is used routinely to guide patient treatment. Histologic grade is also used because the prognosis for low-grade endometrial cancers is better than for high-grade endometrial cancers (4). Improved tumor classification is needed, however, because patients with tumors that are identical in grade and stage often have significantly different clinical outcomes or responses to therapy. In previous studies, flow cytometric analysis of DNA ploidy has been shown to provide stronger, independent prognostic information (5–10). Laser scanning cytometry (LSC) is a technology similar to flow cytometry, but LSC generates data from analysis of successive microscopic fields and is advantageous for certain clinical and research applications (11). In general, the advantages of LSC include reduced specimen size requirements, simplified methodologies, the ability to examine individual cells, microscopically allowing for direct comparison between cytologic morphology and objective fluorescence measurements, and the ability to scan the same cells within an individual specimen repeatedly (11). Although LSC seems more suitable for clinical application, the relation between DNA ploidy detected by LSC and the clinicopathologic features in patients with endometrial cancer has not been studied.

Tumor cells can become aneuploid as a result of aberrant mitotic divisions that are caused by errors in centrosome duplication, chromosome cohesion, spindle attachment, or

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cytokinesis (12). Mitotic checkpoint defects lead to aneuploidy in cultured cells (13) and mouse models (14). However, mutations of such mitotic checkpoint genes have been detected in only a fraction of human cancers (15). This prompted us to speculate that multiple factors, such as DNA methylation and chromatin modification, are key players in tumor cell aneuploidization.

In the present study, we evaluated the efficacy of DNA ploidy determined by LSC as a prognostic marker in patients with endometrial cancer and investigated clinicopathologic, genetic, and epigenetic factors related to aneuploidy and patient outcomes. We found that aneuploidy and lack of *CDH13* hypermethylation as well as surgical stage were predictive of death from endometrial cancer and that age, *p53* mutation, and lack of *CDH13* hypermethylation were related to aneuploidy.

## Materials and Methods

**Specimens.** We evaluated endometrial cancer specimens from 106 patients who underwent surgical resection of the uterus. Mean age of the patients was 58.0 y (range, 32–81 y). Mean follow-up time was 34.8 mo (range, 3.2–89.4 mo). Stage, grade, and histologic type were determined with the surgical staging system of the International Federation of Gynecology and Obstetrics (1988) and WHO (1994). All tumors were diagnosed histologically as endometrioid carcinomas of the uterine corpus and included 94 endometrioid adenocarcinomas, 10 adenoacanthomas, and 2 adenosquamous carcinomas. No patient received preoperative neoadjuvant therapy. Normal endometrium was obtained from 27 patients with leiomyoma who underwent hysterectomy. The study was approved by the review board of Yamaguchi University.

**Microdissection and DNA extraction.** Routine frozen resection specimens were fixed in 99.5% ethanol followed by H&E staining. DNA was prepared from 5- $\mu$ m microdissected histopathologic sections as described previously (16).

**Hypermethylation of genes.** Hypermethylation of *CDH13* and *Rassf1* is frequent in endometrial cancer (17). However, association of methylation of *CDH13* and *Rassf1* with clinicopathologic and cytogenetic features in endometrial cancer has not been clarified. This challenged us to investigate the relations. Furthermore, some of endometrial cancers and colon cancers have a common molecular feature such as microsatellite instability via *hMLH1* methylation (18–20). This promoted us to study *hMLH1* methylation status in endometrial cancer followed by methylation of other genes, including *p16*, *SFRP1*, *SFRP2*, *SFRP4*, *SFRP5*, *WIF1*, *APC*, *ATM*, and *MGMT*, which are methylated frequently in colon cancer (21–26).

The methylation status of *Rassf1*, *SFRP1*, *SFRP2*, *SFRP4*, *SFRP5*, *p16*, *hMLH1*, *MGMT*, *ATM*, and *APC* was determined by bisulfite treatment of DNA followed by methylation-specific PCR or combined bisulfite restriction analysis as described previously (21–25, 27).

*WIF1* methylation-specific PCR primers for the methylation reaction were 5'-CGTTTATTGGGCGTATC-3' (forward) and 5'-CGAAACCAACAATCAACG-3' (reverse) and for the unmethylation reaction were 5'-CGGTGTTTATTGGGCGTATT-3' (forward) and 5'-CTAACAAAACCAACAATCAACA-3' (reverse; Supplementary Fig. S1).

Methylation status of *CDH13* was assessed by combined bisulfite restriction analysis assay. Primer sequences were 5'-TTAAAGAAG-TAAATGGGATGTT-3' and 5'-CCAAAACCAATAACITTAACAAA-3'. The PCR product was digested with *NruI* (TaKaRa). The digested PCR products were separated by electrophoresis on 3% agarose gels. The digested fragments, which represent methylated DNA, were quantitated by densitometry.

DNA from normal lymphocytes was used as the control for unmethylated genes and placental DNA treated with *SssI* (CpG) methylase (New England Biolabs) was used as the positive control

for methylated genes. Each sample was analyzed in duplicate. The criterion for the presence of hypermethylation was detection of a methylated band in both independent methylation-specific PCR assays. In combined bisulfite restriction analysis assay, hypermethylation was defined as  $\geq 14\%$  of methylation for *CDH13* and  $\geq 9\%$  of methylation for *Rassf1* on the bases of upper 95% of mean methylation level of each gene in normal endometrium.

**Assay for *p53* and *CDC4* mutations.** DNA sequencing was used to screen for mutations in the *p53* and *CDC4* genes. For *p53*, four sets of oligonucleotide primers were used to amplify exons 5 to 8 as described previously (Supplementary Table S1; ref. 28).

For *CDC4*, 10 sets of oligonucleotide primers were used to amplify exons 2 to 11 (Supplementary Table S1). PCR products were purified with shrimp alkaline phosphatase and exonuclease I (GE Healthcare) per the manufacturer's instructions. Purified PCR products were sequenced on an ABI Prism 3100 DNA Analyzer with the ABI Prism BigDye Terminator Cycle Sequencing kit version 3.1 (Applied Biosystems). Primers used for amplification were also used for sequencing. Sequencing results were analyzed with DNA Sequencing Analysis Software version 5.1 (Applied Biosystems) and Mutation Surveyor (SoftGenetics).

**Fluorescence in situ hybridization analysis.** Fluorescence *in situ* hybridization was carried out on touch smear specimens on cell array glass slides with chromosome-specific centromeric probes for chromosomes 7, 8, 10, 11, and 17 (Abbott Molecular) as described previously (29). Briefly, the DNA probe mixture and 10  $\mu$ g of Cot-1 DNA (Abbott Molecular) were dissolved in hybridization buffer (Abbott Molecular). The probe mixture was denatured at 73°C for 5 min, applied to the denatured touch smears, and incubated in a moist chamber at 37°C overnight. After the slide was rinsed, nuclei were counterstained with 4',6'-diamidino-2-phenylindole II (Abbott Molecular). The number of nuclear hybridization signals was determined for 100 nuclei from each sample. The variant fraction was defined as the fraction of cells for which the chromosome number differed from the modal chromosome number (30). Unstable chromosomes were tentatively defined as  $>20\%$  of the average variant fractions of chromosomes 7, 8, 10, 11, and 17, with reference to Lengauer et al. (31) and Yamamoto et al. (32). A tumor was considered to have chromosomal instability (CIN) if the tumor was unstable for more than three chromosomes as described previously (29).

**Laser scanning cytometry.** LSC was carried out to determine DNA ploidy as described previously (29). Briefly, touch smears fixed with 95% ethanol were stained in 25  $\mu$ g/mL propidium iodide solution containing 0.1% RNase. A coverslip was put on the slide and sealed with nail polish. DNA content was measured with a laser scanning cytometer (LSC101, Olympus). A DNA histogram was generated, and DNA ploidy was determined. The DNA index was calculated according to published principles (33). Tumors with a DNA index  $\leq 1.2$  were categorized as diploid tumors, and those with a DNA index  $>1.2$  were classified as aneuploid tumors (29).

**Statistical analysis.** Statistical analysis was done with StatView statistical software (SAS). To compare variables, Fisher's exact test, Student's *t* test, and logistic regression method were used. A *P* value of  $<0.05$  was considered statistically significant. To identify potential distinct subgroups among endometrial cancer patients, we applied an unsupervised hierarchical cluster analysis based on methylation profiling of *CDH13* and *Rassf1*, aneuploidy, and CIN using Euclidean distances and average linkage algorithm (Clustered Image Map program package, CIMminer; ref. 34).

## Results

**Methylation and mutation profile.** Clinicopathologic features, gene hypermethylation, gene mutation, aneuploidy, and CIN profiles in 106 endometrial cancers are shown in Fig. 1. The frequencies of gene hypermethylation in normal

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Fig. 1. Diagram of clinicopathologic, epigenetic, and genetic alterations in 106 endometrial cancers. Shading indicates the presence of a molecular alteration, x indicates unavailable data, and an open cell indicates absence of the alteration.

**Table 1.** Frequency of hypermethylation of genes in normal endometrium and endometrial cancer

Gene	Hypermethylation	
	Endometrium Frequency (%)	Cancer Frequency (%)
<i>hMLH1</i>	1/27 (3.7)	34/106 (32.1)
<i>CHFR</i>	2/25 (8.0)	9/106 (8.5)
<i>MGMT</i>	1/27 (3.7)	9/105 (8.6)
<i>p16</i>	2/27 (7.4)	4/103 (3.9)
<i>APC</i>	2/26 (7.7)	43/104 (41.3)
<i>WIF1</i>	3/25 (12.0)	43/99 (43.4)
<i>CDH13</i>	4/27 (14.8)	75/106 (70.8)
<i>Rassf1</i>	6/25 (24.0)	80/97 (82.5)
<i>SFRP1</i>	2/27 (7.4)	16/101 (15.8)
<i>SFRP2</i>	4/25 (16.0)	54/105 (51.4)
<i>SFRP4</i>	0/27 (0.0)	5/103 (4.9)
<i>SFRP5</i>	4/22 (18.2)	50/105 (47.6)
<i>ATM</i>	7/20 (35.0)	11/103 (10.7)

endometrium and endometrial cancer are shown in Table 1. Hypermethylation of *CDH13* and *Rassf1* was observed frequently in endometrial cancer (70.8% and 82.5%, respectively) as described previously (17). The quantitative analysis of *CDH13* methylation showed that endometrial cancer had higher levels of *CDH13* methylation than normal endometrium (Fig. 2A). The mean methylation level was 40.3% for endometrial cancer and 7.1% for the normal endometrium

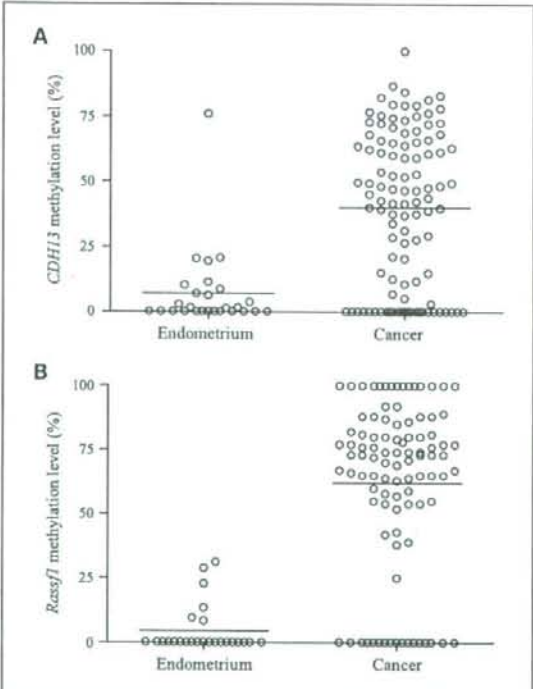


Fig. 2. Distribution of *CDH13* and *Rassf1* methylation (%) in normal endometrium and endometrial cancer. The horizontal lines represent the mean methylation level in each group.

( $P < 0.0001$ ). Mean methylation level of *Rassf1* was also greater in endometrial cancer than in normal endometrium (62.3% versus 4.6%;  $P < 0.0001$ ; Fig. 2B). These data suggest that detection of *CDH13* and *Rassf1* methylation using cytologic materials may be useful as a screening test for endometrial cancer as reported previously (17).

*p53* and *CDC4* mutation were observed in 21 of 104 (20.2%) and 5 of 60 (8.3%) endometrial cancers, respectively. Aneuploidy and CIN were found in 19 of 106 (17.9%) and 16 of 106 (15.1%) endometrial cancers, respectively.

**Comparison of gene methylation, *p53* mutations, and *CDC4* mutations with aneuploidy and CIN.** Aneuploidy and CIN were highly concordant with an expected relation in 91.4% of the carcinomas ( $P < 0.0001$ ) as reported previously (29). Thirteen of 19 (68.4%) cases with aneuploidy had CIN, whereas 84 of 87 (96.6%) cases without aneuploidy did not have CIN [odds ratio (OR), 60.7; 95% confidence interval (95% CI), 13.5-273.1;  $P < 0.0001$ ].

Association between various factors, including clinicopathologic variables, gene hypermethylation, and gene mutation,

and the presence of aneuploidy is shown in Table 2. In addition, these factors were also compared with CIN for validation (Table 2). Hypermethylation of *CDH13* was shown to have an inverse association with aneuploidy and CIN. In other words, lack of *CDH13* hypermethylation associated positively with aneuploidy and CIN. Only 7 of 75 (9.3%) tumors with *CDH13* hypermethylation had aneuploidy, whereas 12 of 31 (38.7%) tumors without *CDH13* hypermethylation had aneuploidy ( $P = 0.0007$ ). Similarly, 7 of 75 (9.3%) tumors with *CDH13* hypermethylation had CIN, whereas 9 of 31 (29.0%) tumors without *CDH13* hypermethylation showed CIN ( $P = 0.0160$ ). *p53* mutation related positively with aneuploidy and CIN. Eleven of 21 (52.4%) tumors with *p53* mutations had aneuploidy, whereas 8 of 83 (9.6%) cases without *p53* mutations had aneuploidy ( $P < 0.0001$ ). In addition, 9 of 21 (42.9%) tumors with *p53* mutations had CIN, whereas only 6 of 83 (7.2%) cases without *p53* mutations had CIN ( $P = 0.0003$ ). Mean age was significantly higher in cases with aneuploidy and CIN than in those without. Mean age was 62.0 years for cases with

**Table 2.** Aneuploidy and CIN in relation to clinicopathologic features, hypermethylation of genes, and mutation of genes

Variable		Aneuploidy			CIN		
		Frequency (%)	OR (95% CI)	P	Frequency (%)	OR (95% CI)	P
Grade	1	4/27 (14.8)	1.0 (Reference)		2/27 (7.4)	1.0 (Reference)	
	2	11/59 (18.6)	1.3 (0.4-4.6)	0.7672	11/59 (18.6)	2.9 (0.6-13.9)	0.2138
	3	4/20 (20.0)	1.4 (0.3-6.6)	0.7073	3/20 (15.0)	2.2 (0.3-14.6)	0.6377
Stage	I	6/60 (10.0)	1.0 (Reference)		6/60 (10.0)	1.0 (Reference)	
	II	3/8 (37.5)	5.4 (1.0-28.5)	0.0652	1/8 (12.5)	1.3 (0.1-12.3)	1.0000
	III	9/33 (27.3)	3.4 (1.1-10.6)	0.0406	8/33 (24.2)	2.9 (0.9-9.2)	0.0773
	IV	1/5 (20.0)	2.3 (0.2-23.6)	0.4453	1/5 (20.0)	2.3 (0.2-23.6)	0.4453
<i>hMLH1</i>	H	4/34 (11.8)	0.5 (0.2-1.7)	0.2931	3/34 (8.8)	0.4 (0.1-1.7)	0.2590
	U	15/72 (20.8)			13/72 (21.1)		
<i>CHFR</i>	H	1/9 (11.1)	0.5 (0.1-4.7)	1.0000	0/9 (0.0)	0.3 (0.0-4.7)	0.3493
	U	18/97 (18.6)			16/97 (16.5)		
<i>MGMT</i>	H	3/9 (33.3)	2.7 (0.6-12.0)	0.1818	1/9 (11.1)	0.7 (0.1-6.3)	1.0000
	U	15/96 (15.6)			14/96 (14.6)		
<i>p16</i>	H	0/4 (0.0)	0.5 (0.0-9.5)	1.0000	0/4 (0.0)	0.6 (0.0-11.8)	1.0000
	U	18/99 (18.2)			15/99 (15.2)		
<i>APC</i>	H	6/43 (14.0)	0.6 (0.2-1.7)	0.4423	5/43 (11.6)	0.6 (0.2-1.9)	0.4000
	U	13/61 (21.3)			11/61 (18.0)		
<i>WIF1</i>	H	8/43 (18.6)	1.1 (0.4-2.9)	1.0000	5/43 (11.6)	0.5 (0.2-1.7)	0.4098
	U	10/56 (17.9)			11/56 (19.6)		
<i>CDH13</i>	H	7/75 (9.3)	0.2 (0.1-0.5)	0.0007	7/75 (9.3)	0.3 (0.1-0.8)	0.0160
	U	12/31 (38.7)			9/31 (29.0)		
<i>Rassf1</i>	H	16/80 (20.0)	1.2 (0.3-4.6)	1.0000	13/80 (16.3)	0.9 (0.2-3.6)	1.0000
	U	3/17 (17.6)			3/17 (17.6)		
<i>SFRP1</i>	H	2/16 (12.5)	0.6 (0.1-2.8)	0.7297	2/16 (12.5)	0.7 (0.1-3.5)	1.0000
	U	17/85 (20.0)			14/85 (16.5)		
<i>SFRP2</i>	H	9/54 (16.7)	0.8 (0.3-2.2)	0.8016	7/54 (13.0)	0.7 (0.2-2.0)	0.5917
	U	10/51 (19.6)			9/51 (17.6)		
<i>SFRP4</i>	H	0/5 (0.0)	0.4 (0.0-7.0)	0.5812	0/5 (0.0)	0.5 (0.0-8.6)	1.0000
	U	19/98 (19.4)			16/98 (16.3)		
<i>SFRP5</i>	H	6/50 (12.0)	0.4 (0.2-1.3)	0.1367	6/50 (12.0)	0.6 (0.2-1.8)	0.4260
	U	13/55 (23.6)			10/55 (18.2)		
<i>ATM</i>	H	2/11 (18.2)	1.0 (0.2-5.0)	1.0000	1/11 (9.1)	0.5 (0.1-4.3)	1.0000
	U	17/92 (18.5)			15/92 (16.3)		
<i>p53</i>	M	11/21 (52.4)	10.3 (3.4-31.8)	<0.0001	9/21 (42.9)	9.6 (2.9-32.0)	0.0003
	W	8/83 (9.6)			6/83 (7.2)		
<i>CDC4</i>	M	2/5 (40.0)	2.4 (0.4-16.0)	0.5817	1/5 (20.0)	1.5 (0.1-14.9)	0.5699
	W	12/55 (21.8)			8/55 (14.5)		

Abbreviations: H, hypermethylated; U, unmethylated or lack of hypermethylation; M, mutated; W, wild-type.

aneuploidy and 57.1 years for cases without aneuploidy ( $P = 0.0448$ ) and 63.8 years for cases with CIN and 56.9 years for cases without CIN ( $P = 0.0074$ ). According to multivariate analysis, lack of *CDH13* hypermethylation and *p53* mutation related positively to aneuploidy (Table 3). Similarly, age, lack of *CDH13* hypermethylation, and *p53* mutation were associated significantly with CIN (Table 3).

We also studied correlations between methylated genes in endometrial cancer (Supplementary Table S2). Five markers, including *hMLH1*, and four genes (*CHFR*, *WIF1*, *Rassf1*, and *SFRP4*), which were methylated concurrently with *hMLH1* methylation, were used to determine methylation phenotype. Endometrial cancer was classified as having methylator phenotype if 50% or more of the evaluated markers were methylated. Relation of the methylator phenotype with aneuploidy, CIN, and *p53* mutation was shown in Supplementary Table S3. Interestingly, the methylator phenotype correlated negatively with CIN in endometrial cancer, as shown for colon cancer (35). None of 16 (0.0%) cancers with CIN has methylator phenotype, whereas 26 of 90 (28.9%) cancers without CIN have methylator phenotype ( $P = 0.0105$ ).

**Risk factors for nonsurvival.** Results of univariate analysis of risk factors for nonsurvival are shown in Table 4. Regardless of differences in follow-up time, variables including stages III and IV, CIN, and aneuploidy related significantly to death from the disease ( $P = 0.0451$ ,  $0.0296$ ,  $0.0280$ , and  $0.0120$ , respectively). In addition, *CDH13* hypermethylation associated negatively with unfavorable outcome ( $P = 0.0143$ ). In other words, lack of *CDH13* hypermethylation was associated with negative prognosis. Age of the patients did not correlate with death from endometrial cancer. Mean age of the patients who died was 61.6 years; mean age of patients who survived was 57.2 years ( $P = 0.1851$ ).

Multivariate analysis showed that the stage in combination with either DNA aneuploid type or lack of *CDH13* hypermethylation was significantly predictive of death from the disease (Table 5A and B). However, CIN and *Rassf1* methylation were not independent prognostic markers (data not shown).

Based on the hierarchical clustering result, we estimated the number of clusters at 2 (Supplementary Fig. S2). The cluster 2 related significantly to death from the disease. Frequency of nonsurviving patients was 4 of 75 (5.3%) for the cluster 1,

whereas it was 5 of 17 (29.4%) for the cluster 2 (OR, 7.4; 95% CI, 1.7-31.5;  $P = 0.0097$ ).

## Discussion

In the current study, we found that aneuploidy was a useful prognostic marker in patients with endometrial cancer, which is consistent with the results of previous studies (5-10). Interestingly, DNA aneuploidy was associated with increased mortality even for stage I endometrial cancer (5, 10). Furthermore, Susini et al. (9) have reported results of a 10-year prospective study in which the presence of aneuploidy in endometrial cancer identified high-risk cases among patients considered to be at 'low risk' based on stage and grade of differentiation. Thus, DNA aneuploidy can be a useful prognostic marker in patients with endometrial cancer. Although our finding is not new, this is the first study that evaluated the usefulness of laser scanning cytometric DNA analysis for predicting patient outcomes. The utility of flow cytometric measurements of DNA ploidy in various carcinomas remains controversial (36). Retrospective studies of large numbers of patients and the exchange of samples among laboratories are hampered by the relative scarcity of archival frozen material and difficulties in transporting frozen specimens (37). However, LSC can resolve these problems. Touch preparations for LSC require only small amounts of fresh material (11) and can be stored and transported at 4°C or even at room temperature. Furthermore, another advantage of LSC is that cells selected visually can be quantified. Conversely, cells selected by LSC measurement can be relocated and examined visually. This is important for analyzing cellular properties of malignant tumors because contamination with normal cells is inevitable. Thus, LSC seems more feasible for clinical laboratory use than flow cytometry. Further studies with larger sample sizes and multiple laboratory groups are needed to confirm the feasibility of laser scanning cytometric DNA analysis as a clinical laboratory test.

We found that lack of *CDH13* hypermethylation is positively associated with aneuploidy, CIN, and an unfavorable outcome. Evaluation of methylation level of *CDH13* may assist in therapeutic decision for patients with endometrial cancer. To our knowledge, ours is the first report on the relation of lack of *CDH13* hypermethylation to aneuploidy, CIN, and death from endometrial cancer. *CDH13* (also known as H-cadherin or T-cadherin) is an atypical glycosylphosphatidylinositol-anchored member of the cadherin superfamily (38). Down-regulation of *CDH13* gene expression related to promoter hypermethylation has been reported frequently for breast, lung, and colon carcinomas (39, 40). In contrast, in primary hepatocellular carcinomas, *CDH13* is globally overexpressed in approximately half of all tumor specimens (38). Although *CDH13* can mediate weak homophilic cell-cell aggregation (41), accumulating evidence suggests that *CDH13* might not function as a true intercellular adhesion molecule (42, 43). Because the function of *CDH13* is not yet known, further studies are needed.

Aneuploidy, a state of abnormal chromosome number and content, is characteristic of many human cancers, and it plays an important role in tumor formation and development (44). Genetic change leading to aneuploidy is termed CIN, which is defined by continuous and conspicuous changes in

**Table 3.** Results of multivariate analysis of risk factors for aneuploidy and CIN in patients with endometrial cancer

Factor	OR (95% CI)	P
A. Risk factors for aneuploidy		
Age	1.1* (1.0-1.1)	0.0546
Lack of <i>CDH13</i> hypermethylation	11.8 (2.8-49.9)	0.0007
<i>p53</i> mutation	18.7 (4.1-84.2)	0.0001
B. Risk factors for CIN		
Age	1.1* (1.0-1.2)	0.0164
Lack of <i>CDH13</i> hypermethylation	4.0 (1.0-15.6)	0.0434
<i>p53</i> mutation	12.4 (3.1-50.5)	0.0004

NOTE: Variables were considered for the multivariable models if their univariable  $P$  value was  $<0.05$ .

\*OR for an age interval for 1 y.

**Table 4.** Univariate analysis of risk factors for nonsurvival

Factor		Frequency of nonsurviving patients (%)	OR (95% CI)	P
Grade	1	1/26 (3.8)	1.0 (Reference)	
	2	4/53 (7.5)	2.0 (0.2-19.3)	1.0000
	3	4/20 (20.0)	6.3 (0.6-61.1)	0.1512
Stage	I	2/57 (3.5)	1.0 (Reference)	
	II	0/7 (0.0)	1.5 (0.1-33.9)	1.0000
	III	5/30 (16.7)	5.5 (1.0-30.3)	0.0451
	IV	2/5 (40.0)	18.3 (1.9-179.1)	0.0296
hMLH1	H	4/34 (11.8)	1.6 (0.4-6.4)	0.4888
	U	5/65 (7.7)		
CHFR	H	1/9 (11.1)	1.3 (0.1-11.6)	0.5920
	U	8/90 (8.9)		
MGMT	H	1/9 (11.1)	1.5 (0.2-13.5)	0.5512
	U	7/89 (7.9)		
p16	H	0/4 (0.0)	1.1 (0.1-22.6)	1.0000
	U	8/93 (8.6)		
APC	H	3/43 (7.0)	0.6 (0.1-2.6)	0.7269
	U	6/54 (11.1)		
WIF1	H	5/42 (11.9)	1.6 (0.4-6.5)	0.5068
	U	4/52 (9.5)		
CDH13	H	3/71 (4.2)	0.2 (0.0-0.7)	0.0143
	U	6/28 (21.4)		
Rassf1	H	9/77 (11.7)	4.3 (0.2-77.9)	0.3460
	U	0/15 (0.0)		
SFRP1	H	3/16 (18.8)	3.4 (0.7-16.1)	0.1294
	U	5/79 (6.3)		
SFRP2	H	5/52 (9.6)	1.1 (0.3-4.4)	1.0000
	U	4/46 (8.7)		
SFRP4	H	0/5 (0.0)	0.9 (0.0-17.8)	1.0000
	U	8/92 (8.7)		
SFRP5	H	3/47 (6.4)	0.5 (0.1-2.2)	0.4902
	U	6/51 (11.8)		
ATM	H	1/11 (9.1)	1.0 (0.1-8.6)	1.0000
	U	8/86 (9.3)		
p53	M	3/21 (14.3)	2.0 (0.4-8.7)	0.3983
	W	6/77 (7.8)		
CDC4	M	0/5 (0.0)	0.7 (0.0-13.5)	1.0000
	W	6/53 (11.3)		
CIN	+	4/15 (26.7)	5.8 (1.3-24.7)	0.0280
	-	5/84 (6.0)		
Aneuploidy	+	5/19 (26.3)	6.8 (1.6-28.5)	0.0120
	-	4/80 (5.0)		

Abbreviations: +, present; -, absent.

chromosome structure and number (45). It is well known that CIN is associated with aneuploidy (29, 30, 46). It is also widely accepted that tumor cells become aneuploid as a result of aberrant mitotic divisions that are caused by errors in centrosome duplication, chromosome cohesion, spindle attachment, or cytokinesis (12). Indeed, mitotic checkpoint defects lead to aneuploidy in cultured cells (13) and mouse models (14). However, mutations of such mitotic checkpoint genes have been detected in only a fraction of human cancers (15). This prompted us to speculate that multiple factors, such as DNA methylation and chromatin modification, are key players in tumor cell aneuploidization. Several studies have shown a possible association between DNA methylation status and CIN in cancer cells. For example, hypomethylation of pericentromeric satellite sequences predisposes to chromosomal breakage and recombination, leading CIN in tumor cells (47, 48). Interestingly, *CDH13* hypomethylation is associated with satellite DNA hypomethylation in ovarian and breast cancers (49, 50). Thus, lack of *CDH13* hypermethylation

may be a predictive marker for aneuploidy via satellite DNA hypomethylation.

We found that mutation of *p53* is related to aneuploidy and CIN as found in previous studies (9). Normal *p53* function imposes a barrier to genomically unstable cells by stimulating G<sub>1</sub>-S or G<sub>2</sub>-M checkpoint responses, mitotic catastrophe, and apoptotic cell death (51). In contrast, cells with inactivated *p53* may overcome these barriers and maintain proliferative activity despite CIN (52). The most frequent form of genomic instability in human cancer, aneuploidy, often coincides with loss of *p53*. However, there is mounting evidence that a defect in *p53* does not have a direct role in CIN but instead promotes CIN indirectly (52-54). In addition, the present finding that *p53* mutation correlates with aneuploidy and CIN but not patient outcomes suggests that *p53* mutation alone may be only an early event in the CIN pathway and have little effect on the malignant behavior of tumor cells.

In the current study, *CDC4* mutations were not associated with aneuploidy or CIN. Rajagopalan et al. (55) reported that



**Table 5.** Results of multivariate analysis of risk factors for nonsurvival in patients with endometrial cancer

Variable	OR (95% CI)	P
A. Risk factors for nonsurvival		
Aneuploidy	7.2 (1.4-36.4)	0.0167
Stage		
II	0.0 (NA)	0.9787
III	3.6 (0.6-21.9)	0.1601
IV	19.5 (1.7-221.5)	0.0167
B. Risk factors for nonsurvival		
Lack of <i>CDH13</i> hypermethylation	7.0 (1.5-33.8)	0.0153
Stage		
II	0.0 (NA)	0.9792
III	5.3 (0.9-31.2)	0.0645
IV	17.9 (1.5-212.8)	0.0225

NOTE: Logistic regression was used to test multivariate associations of stage and aneuploidy (A) or lack of *CDH13* hypermethylation (B) with cancer death. Variables were considered for the multivariable models if their univariable *P* value was <0.05. Abbreviation: NA, not applicable.

*CDC4* (F-box and WD40 domain protein 7, *FBW7*, *FBXW7*) is a CIN gene for human cancer. However, the association between *CDC4* mutation and CIN is controversial. Hubalek et al. (56) screened for *CDC4* mutations in endometrial

cancers. When they excluded isoform-specific changes, they found mutations in 6 of 12 aneuploid and/or polyploid cancers and in none of 3 diploid lesions. Although these data were suggestive of a link between *CDC4* mutations and CIN, the association was not statistically significant (*P* = 0.19, Fisher's exact test). Furthermore, Kemp et al. (57) screened 244 colorectal tumors and 40 cell lines for *CDC4* mutations and CIN. They found that 18 of 284 (6%) tumors, including near-diploid (CIN<sup>-</sup>) lesions, harbored *CDC4* mutations and that there was no association between *CDC4* mutations and CIN. These results suggest that *CDC4* mutations are not associated with CIN.

In conclusion, we found a significant relation between DNA aneuploidy and lack of *CDH13* hypermethylation in endometrial cancer. Furthermore, we observed a significant association of DNA aneuploidy and lack of *CDH13* hypermethylation with negative prognosis. The validity of an individualized approach to management of endometrial cancer patients, including determination of tumor ploidy and *CDH13* methylation status, should be properly evaluated in prospective randomized trials.

#### Disclosure of Potential Conflicts of Interest

The authors declare that there is no conflict of interest.

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## Phase I Study of Irinotecan Combined with Mitomycin-C and 5-Fluorouracil for Gynecological Malignancies: The JGOG Study

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**Abstract.** Background: A phase I study to evaluate combined therapy with irinotecan (CPT-11), mitomycin-C (MMC), and 5-fluorouracil (5-FU) was performed in patients with gynecological malignancy, especially non-squamous cell carcinoma of the uterine cervix. Materials and Methods: Eligibility for the study included patients with previously untreated, chemotherapy-naïve cervical and ovarian carcinoma. CPT-11 and MMC were administered on days 1 and 15 by intravenous infusion, while 5-FU was given on days 3 to 7. This regimen was repeated after 5 weeks. Four escalating dose levels were carried out (CPT-11/MMC: 120/5, 120/6, 150/6, and 150/7 mg/m<sup>2</sup>; 5-FU 600 mg/m<sup>2</sup> fixed). Results: Fourteen patients were enrolled in the study. Although all the patients had no previous chemotherapy, three patients had undergone a simple hysterectomy and nine had a radical hysterectomy performed before this chemotherapy. The maximum tolerated dose was not reached by using CPT-11 150 mg/m<sup>2</sup>, MMC 7 mg/m<sup>2</sup>, and 5-FU 600 mg/m<sup>2</sup> because none of the patients experienced any hematological or non-hematological toxicities of grade 4 during the first cycle. Conclusion: The recommended doses of this new regimen are CPT-11 150 mg/m<sup>2</sup>, MMC 7 mg/m<sup>2</sup>, and 5-FU 600 mg/m<sup>2</sup> which can be well tolerated for gynecological malignancies.

The major treatments for gynecological malignancies consist of surgery, radiotherapy, and chemotherapy. In patients with epithelial ovarian carcinomas, the histological subtype is one

of the most important prognostic factors. It is widely acknowledged that the prognosis of clear cell carcinoma and mucinous adenocarcinoma of the ovary is poorer than that of serous and endometrioid adenocarcinoma (1, 2). The platinum-based regimens such as paclitaxel (PTX) plus carboplatin (CBDCA) therapy (TC), which has been introduced broadly as a standard regimen for ovarian cancer (3, 4), may not be the optimal chemotherapy in patients with mucinous and clear cell carcinoma (1, 2). Thus new combined chemotherapies including irinotecan hydrochloride (CPT-11) have been examined (5) and a randomized phase III trial of TC compared with CPT-11 plus cisplatin (CDDP) for clear cell carcinoma is an ongoing study (international collaborative study: GCIG/JGOG3017).

Although the number of patients with cervical cancer has decreased recently, the incidence of adenocarcinoma of the cervix has increased. A recent report of SEER data demonstrated that the rate of non-squamous cell carcinoma has increased by 29.1% over the last 20 years (6). Most patients with locally advanced squamous cell carcinoma of the uterine cervix are commonly treated with radiotherapy or chemoradiotherapy (7-9), but other types of cervical carcinomas are less sensitive to radiotherapy (10, 11) and have a poorer prognosis (12-15). However, there have been few studies of the efficacy of adjuvant chemotherapy for cervical adenocarcinoma (16, 17). CDDP has commonly been used in patients with gynecological malignancies and the response rate of CDDP alone was 20% and for combined chemotherapy with CDDP plus PTX was 60% in non-squamous carcinoma of the cervix (18, 19). However, patients with advanced and recurrent cervical carcinoma often have complications such as ureteral stenosis and renal dysfunction and since it is known that CDDP can cause renal disorders, a new combined regimen to achieve clinical benefits needs to be developed.

CPT-11 is a semisynthetic derivative of camptothecin, a plant alkaloid obtained from *Camptotheca acuminata* (20),

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The antitumor effects of CPT-11 are related to the inhibition of DNA topoisomerase I (21). CPT-11 has shown strong activity against various experimental tumors with little renal toxicity because CPT-11 is excreted into the gastrointestinal tract (22). In patients with gynecological malignancies, monotherapy and combined chemotherapy using CPT-11 have been performed (23-28). 5-Fluorouracil (5-FU) is a key drug for colorectal adenocarcinoma, which is histologically like cervical adenocarcinoma and mucinous ovarian carcinoma. Combined therapy with CPT-11 plus 5-FU/leucovorin (LV) is one of the most standard regimens for primary and metastatic colon cancer (29-31). 5-FU had an effect on cervical adenocarcinoma, with a response rate of 14% (32). In our preliminary study (JGOG 1057, unpublished data), the response rate was 2 out of 17 (11.8%) patients with CPT-11 (150 mg/m<sup>2</sup>, days 1 and 15) plus 5-FU (600 mg/m<sup>2</sup>, days 3 to 7). Grade 4 leukopenia, thrombocytopenia, and diarrhea using this combined chemotherapy was present in 21.2%, 5.3%, and 5.3% patients, respectively. This combination chemotherapy was well tolerated and there appears to be the possibility of adding another antitumor agent. In *in vitro* experiments using cervical adenocarcinoma cell lines, mitomycin-C (MMC) is one of the most effective antitumor agents (33). It has been reported that MMC is a modulator of CPT-11 activity because it increases topoisomerase I expression (34).

Non-squamous cell carcinoma of the uterine cervix and mucinous or clear cell adenocarcinoma of the ovary are diseases with poor prognosis, and are not effectively treated with the present chemotherapy. Therefore, the cervical cancer committee members of the Japanese Gynecologic Oncology Group (JGOG) performed a phase I trial of CPT-11, MMC and 5-FU for gynecological malignancies, especially non-squamous cell carcinoma of the cervix, in order to determine the maximum tolerated dose (MTD) and the dose-limiting toxicity (DLT).

## Patients and Methods

**Patient selection.** Patients enrolled in this study were required to fulfil the following eligibility criteria: histologically proven non-squamous cell carcinoma of the cervix or clear cell or mucinous adenocarcinoma of the ovary; no prior chemotherapy or radiotherapy; age  $\leq 75$  years; performance status (WHO)  $\leq 2$  and life expectancy  $\geq 3$  months. The patients were also required to meet all of the following laboratory criteria: an adequate bone marrow reserve (leukocyte count of  $4.0\text{--}12.0 \times 10^3/\mu\text{l}$ , platelet count  $\geq 100 \times 10^3/\mu\text{l}$ , and hemoglobin  $\geq 9.5$  g/dl), and adequate renal and hepatic function (24-hour creatinine clearance  $\geq 60$  ml/min, serum creatinine  $\leq 1.5 \times$  the upper limit of normal, serum total bilirubin  $\leq 1.5$  mg/dl, and AST/ALT  $\leq 2 \times$  the upper limit of normal). All the participants gave written informed consent for the study. Patients were excluded for any of the following reasons: metachronous or synchronous other carcinomas, concurrent infection, pre-existing diarrhea, ileus, or bowel obstruction, interstitial pneumonia or

Table I. Dose escalation scheme.

Dose level	Irinotecan mg/m <sup>2</sup>	Mitomycin-C mg/m <sup>2</sup>	5-Fluorouracil mg/m <sup>2</sup>	No. of patients	No. of cycles
1	120	5	600	4	7
2	120	6	600	4	4
3	150	6	600	3	5
4	150	7	600	3	3

pulmonary fibrosis, massive ascites, pleural effusion, uncontrolled diabetes, or a history of severe drug hypersensitivity. This trial was approved by the Review Board of the Japanese Gynecologic Oncology Group and by the Institutional Review Board of each participating hospital.

**Regimen.** On day 1, MMC dissolved in 20 ml physiological saline was administered as a bolus infusion, after which CPT-11 (in 500 ml of normal saline or 5% glucose solution) was also administered intravenously over 90 min. On days 3 to 7, 5-FU (600 mg/m<sup>2</sup>) was given intravenously over 12 hours. On day 15, MMC dissolved in 20 ml physiological saline was administered as a bolus infusion, after which CPT-11 (in 500 ml of normal saline or 5% glucose solution) was also administered intravenously over 90 min. Granulocyte colony-stimulating factor (G-CSF) was administered if grade 3 neutropenia occurred with a fever  $\geq 38.5^\circ\text{C}$  or if grade 4 neutropenia developed with or without fever. This treatment schedule was repeated every 5 weeks.

The doses and the treatment schedule were modified to avoid severe side-effects. CPT-11 and MMC were not given on day 15 if the leukocyte count was  $< 3.0 \times 10^3/\mu\text{l}$  or the platelet count was  $< 100 \times 10^3/\mu\text{l}$ . The treatment was also withheld if the patient developed diarrhea  $\geq$  grade 2 according to the Eastern Cooperative Oncology Group scale (35). Before the next course was started, the patient condition was evaluated and the starting criteria included a leukocyte count of  $\geq 4.0 \times 10^3/\mu\text{l}$  and a platelet count  $\geq 100 \times 10^3/\mu\text{l}$ . In addition, there had to be no diarrhea and the renal function of eligibility criteria had to be within acceptable limits. Dose modification was not carried out for low blood cell counts or diarrhea during the same course.

**Dose escalation plan and toxicity evaluation.** The starting dose of CPT-11 was 120 mg/m<sup>2</sup> and MMC was 5 mg/m<sup>2</sup> and the dose of 5-FU was fixed at 600 mg/m<sup>2</sup>. Four escalating dose levels of CPT-11/MMC (120/5, 120/6, 150/6, and 150/7 mg/m<sup>2</sup>) were studied (Table I). Intra-patient dose modification was not permitted. Toxicity was evaluated by the Japan Clinical Oncology Group (JCOG) Criteria (36), except for diarrhea which was assessed by the Eastern Cooperative Oncology Group scale (35). The DLT was defined as any grade 3 or higher nonhematological toxicity (except alopecia, nausea or vomiting, appetite loss and general fatigue) and hematological toxicity of leukopenia grade 4 ( $> 5$  days), leukopenia grade 3 with a fever  $\geq 38.5^\circ\text{C}$ , thrombocytopenia grade 4 or thrombocytopenia grade 3 with severe bleeding. Three patients were initially enrolled at each dose level, however, the number of patients at levels 1 and 2 was 4 because the last 2 patients were registered on the same day. If none of the patients experienced DLT during the first treatment cycle, the next cohort of three patients was tested at the next higher dose level. If any DLT was observed in one of the

patients, an additional three patients were enrolled at the same dose level. If two patients in the first cohort or three or more of all the patients at each dose level experienced any DLT, the MTD had been reached and the dose level below the MTD was considered to be the recommended dose for further study. The determination of MTD was based on the toxicity observed in the first cycle of each patient. Toxicity in the patients was evaluated if the patients received at least one full course of the protocol therapy, except for an omission of therapy on day 15.

## Results

**Patient demographics.** Between 2001 and 2006, 14 patients with carcinomas of the cervix or ovary who had no prior chemotherapy entered this trial in four cooperative institutions in Japan. The characteristics of the patients are listed in Table II. Among the 14 eligible patients, 8 were diagnosed with adenocarcinoma of the cervix, 3 with adenosquamous carcinoma of the cervix, 2 with clear cell carcinoma of the ovary, and 1 with mucinous adenocarcinoma of the ovary. The median age was 57 (39-70) years and all the patients had a performance status of 0 to 1. In the patients with cervical carcinoma, the following clinical stages based on the International Federation of Gynecology and Obstetrics (FIGO) were found; five patients had stage Ib, two patients had stage IIa, and four patients had stage IIb. The patient with mucinous ovarian carcinoma was diagnosed as stage Ic and the two patients with clear cell carcinoma had stage IIIb and IIIc disease. All three patients with ovarian carcinoma received simple hysterectomy and bilateral adnexectomy before this protocol chemotherapy. Nine out of the 11 patients with cervical carcinoma had radical hysterectomy performed before this chemotherapy. Only two patients received this chemotherapy in a neoadjuvant setting. Thus, 12 out of the 14 patients did not have any measurable disease.

**Treatment under study.** Out of a total of 19 cycles of this protocol therapy, 4 dose levels were administered in 14 patients (Table I). Ten patients (71%) received one cycle of protocol therapy and the other patients received 2 or 3 cycles (Table II). All the patients were assessable for toxicity. Ten out of the 14 patients received at least one complete cycle of protocol therapy, whereas four patients (dose level 1, one patient; dose level 2, one patient; dose level 4, two patients) were not administered CPT-11 and MMC on day 15. Only the two patients with cervical adenocarcinoma who received this chemotherapy in a neoadjuvant setting had a tumor >4 cm in diameter in the uterine cervix at the time of treatment. After cycle 1, one patient showed no change (NC) and the other was a partial response (PR) and these patients underwent radical hysterectomy after this protocol therapy. There were no treatment-related deaths. The median overall survival (OS) period was 47.5 months (range: 6-65). The reasons for protocol termination were as follows: eight patients were due to finish adjuvant therapy; two patients

Table II. Characteristics of the eligible patients.

	No. of patients	(%)
Overall	14	100
Age (years)		
Median (range)	57 (39-70)	
WHO performance status score		
0	5	36
1	9	64
Histology		
Adenocarcinoma of the uterine cervix	8	57
Adenosquamous carcinoma of the uterine cervix	3	21
Clear cell adenocarcinoma of the ovary	2	14
Mucinous adenocarcinoma of the ovary	1	7
Prior therapy		
None	2	14
Simple hysterectomy	3	21
Radical hysterectomy	9	64
No. of cycles		
1	10	71
2	3	21
3	1	7

were due to undergo surgical procedures; three patients requested to discontinue the study therapy and one patient with clear cell carcinoma of the ovary had increased ascites during the treatment period. Among the 14 patients, only two patients who had been diagnosed with adenocarcinoma of the cervix with stage Ib and IIb disease died of the disease at 21 months and 30 months after this protocol therapy, respectively.

**Toxicity observed in cycle 1.** Tables III and IV list the major toxicities encountered during the first cycle. At dose level 1, three patients developed grade 3 leukopenia and two of them received G-CSF. Two patients experienced grade 2 diarrhea and one of them received loperamide and hangeshashinto. Only one patient was not administered CPT-11 and MMC on day 15, because grade 2 leukopenia was still present. At dose level 2, one patient developed grade 3 leukopenia and administration of CPT-11 and MMC was not carried out on day 15. At dose level 3, one patient developed grade 3 neutropenia and grade 2 diarrhea and the patient received G-CSF and hangeshashinto. Another patient showed grade 3 leukopenia and grade 4 neutropenia and was administered G-CSF. At dose level 4, two out of the three patients developed grade 3 leukopenia and the administration of CPT-11 and MMC was cancelled on day 15. As mentioned above, leukopenia was the major toxicity, but no DLTs were observed at any of the dose levels. Therefore, the MTD had not been reached and the maximum dose level (CPT-11/MMC, 150/7 mg/m<sup>2</sup>) was considered to be the recommended dose for further study.

Table III. Hematological toxicity: Cycle 1.

Dose level	No. of patients	Leukopenia					Anemia					Thrombocytopenia					
		G1	G2	G3	G4	G 3/4 (%)	G1	G2	G3	G4	G 3/4 (%)	G1	G2	G3	G4	G	3/4 (%)
1	4	0	1	3	0	75	2	2	0	0	0	1	0	0	0	0	0
2	4	0	3	1	0	25	2	1	0	0	0	0	0	0	0	0	0
3	3	0	1	1	0	33	0	2	0	0	0	0	1	0	0	0	0
4	3	0	1	2	0	67	1	0	0	0	0	0	1	0	0	0	0

Table IV. Nonhematological toxicity: Cycle 1.

Dose level	No. of patients	Diarrhea				Nausea/vomiting				Hepatotoxicity				Alopecia			
		G1	G2	G3	G4	G1	G2	G3	G4	G1	G2	G3	G4	G1	G2	G3	G4
1	4	0	2	0	0	2	1	0	0	0	0	0	0	3	1	0	0
2	4	0	1	0	0	1	0	0	0	2	0	0	0	3	1	0	0
3	3	1	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0
4	3	1	0	0	0	0	1	0	0	1	0	0	0	1	0	0	0

Table V. Hematological toxicity: Overall.

Dose level	No. of cycles	Leukopenia					Anemia					Thrombocytopenia					
		G1	G2	G3	G4	G 3/4 (%)	G1	G2	G3	G4	G 3/4 (%)	G1	G2	G3	G4	G	3/4 (%)
1	7	1	3	3	0	47	3	3	0	0	0	3	0	0	0	0	0
2	4	0	3	1	0	25	2	1	0	0	0	0	0	0	0	0	0
3	5	0	1	3	0	60	0	3	1	0	20	0	1	1	0	0	20
4	3	0	1	2	0	67	1	0	0	0	0	0	1	0	0	0	0

Table VI. Nonhematological toxicity: Overall.

Dose level	No. of cycles	Diarrhea				Nausea/vomiting				Hepatotoxicity				Alopecia			
		G1	G2	G3	G4	G1	G2	G3	G4	G1	G2	G3	G4	G1	G2	G3	G4
1	7	3	2	0	0	4	1	0	0	0	0	0	0	4	3	0	0
2	4	0	1	0	0	1	0	0	0	2	0	0	0	3	1	0	0
3	5	1	1	0	0	0	2	0	0	0	0	0	0	1	0	0	0
4	3	1	0	0	0	0	1	0	0	1	0	0	0	1	0	0	0

Toxicity observed in overall treatment cycles. In our series, grade 3 leukopenia was noted in 9 cycles (47%), but no grade 4 leukopenia occurred (Table V). Grades 3 and 4 neutropenia were observed in 7 out of 11 (63%) estimated cycles and 4 cycles (36%), respectively. G-CSF was administered in 6 out of 19 (32%) cycles. Only one patient in the second cycle treated with dose level 3 demonstrated grade 3 anemia and thrombocytopenia and none of the patients had any other hematological grade 4

toxicities. Grade 1 diarrhea was observed in 5 out of the 19 cycles and grade 2 diarrhea was observed in 4 out of the 19 cycles (Table VI). Three patients were treated with loperamide and/or hangeshashinto. No grade 3 or 4 non-hematological toxicities occurred in any of the cycles. Fifteen out of the 19 cycles (79%) completed the full scheduled dosage, while CPT-11 and MMC were omitted in 4 cycles (21%) on day 15 because of the delay in the recovery of toxicities.

## Discussion

Cervical cancer is the second most common cancer among women worldwide. Histological analysis revealed that the incidence of adenocarcinoma has risen in recent years (37, 38). It is commonly accepted that the prognosis for advanced or recurrent cervical adenocarcinoma is poorer than that of squamous cell carcinoma (10, 11, 13). Eifel *et al.* demonstrated that the overall 5-year survival rates for FIGO stage Ib patients with squamous cell carcinoma and adenocarcinoma were 81% and 72%, respectively, and that adenocarcinoma of the cervix had an estimated risk of death 1.9 times that of patients with squamous cell type (11). The efficacy of chemotherapy for advanced or recurrent adenocarcinoma of the cervix has been examined because radiotherapy is less effective. Papadimitriou *et al.* reported that clinical responses of the combination of PTX and CDDP occurred in 6 out of 10 (60%) patients with metastatic and recurrent non-squamous carcinoma (19). However, advanced and recurrent cervical carcinoma is often complicated by ureteral stenosis or obstruction and it seems to be difficult to use CDDP. In our preliminary study (unpublished data), the response rate was 2 out of 17 (11.8%) patients for adenocarcinoma of the cervix treated with CPT-11 and 5-FU. These previous reports of chemotherapy for cervical adenocarcinoma have only been studied in a small population and the efficacy of chemotherapy is controversial. Therefore, a new effective regimen without CDDP would be desirable in patients with non-squamous cell carcinoma of the cervix.

The incidence of clear cell carcinoma is higher in Japan (15-20%) than that in Europe and the United States (5-10%). Sugiyama *et al.* reported that CDDP-based chemotherapy was effective in only 3 out of 27 (11%) cases of clear cell carcinoma, but was effective in 79 out of 109 (73%) cases of serous adenocarcinoma (1). Enomoto *et al.* showed that the response rate with TC was significantly lower in clear cell (18%, 2/11) and mucinous (13%, 1/8) carcinomas than in serous (81%, 61/75) and endometrioid (89%, 16/18) carcinomas (2). Thus, there is a need to evaluate potentially more effective regimens for mucinous and clear cell carcinoma of the ovary.

In the current phase I study against non-squamous cell carcinoma of the cervix and clear cell and mucinous carcinoma of the ovary, DLTs were not observed in any of the three patients studied at dose level 4 (CPT-11, 150 mg/m<sup>2</sup>; MMC, 7 mg/m<sup>2</sup>; 5-FU, 600 mg/m<sup>2</sup>). Therefore, the MTD had not been reached and that dose level was recommended for further study. The incidence of grade 3 leukopenia in the first cycle was 7 out of 14 (50%) cycles. Other grade 3/4 adverse events were not observed. Diarrhea was the most important non-hematological toxic effect of CPT-11. Grade 2 diarrhea occurred in 3 out of 14 (21%) cycles, but no grade 3/4 diarrhea was observed during cycle 1. Only one patient treated with dose level 2 showed grade 1 renal toxicity in the first

cycle. Therefore, this new regimen can be well tolerated for gynecological malignancies. In the present series, one patient with cervical adenocarcinoma was diagnosed as FIGO stage Ib with a tumor 8.5 cm in diameter showed a cervical lesion reduced by 18% after 2 cycles of protocol treatment, and was still alive without disease for 61 months after radical surgery. Another patient who had stage IIB disease showed a partial response (50% reduction) after this therapy, and has survived over 25 months without disease after radical surgery and adjuvant radiotherapy. These data suggested that this protocol regimen may be effective for cervical adenocarcinoma.

The combined chemotherapy with CPT-11 (15 mg/m<sup>2</sup> on days 1 and 15), MMC (7 mg/m<sup>2</sup> on days 1 and 15) and 5-FU (600 mg/m<sup>2</sup> from days 3 to day 7) is well tolerated for non-squamous cell carcinoma of the cervix and mucinous and clear cell carcinoma of the ovary. It is possible that this protocol treatment may be an option for gynecological malignancy with renal disorders and platinum resistance. A phase II study using this protocol regimen will be required to evaluate the response rate and survival benefit for advanced or recurrent gynecological malignancies, especially for non-squamous cell carcinoma of the uterine cervix.

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## Antiproliferative effects of the major tea polyphenol, (–)-epigallocatechin gallate and retinoic acid in cervical adenocarcinoma

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### Abstract

**Objective.** To investigate the combined effect of the major tea polyphenol, (–)-epigallocatechin gallate (EGCG) and retinoic acid (RA) on cervical adenocarcinoma.

**Methods.** Cell growth rate was examined after treatment for 4, 7 and 10 days with 0–100 μM EGCG and/or 1 μM RA in two cervical adenocarcinoma cell lines, HeLa and TMCC-1. The effect of EGCG treatment was examined for the induction of apoptosis by DNA ladder assay and caspase-3-related protease activity in cell lysate. Telomerase activity was detected by stretch PCR telomere extension assay. hTERT expression levels were quantified by a real-time PCR system.

**Results.** Combining EGCG and RA increased the antiproliferative effect in adenocarcinoma cell lines, whereas EGCG or RA treatment alone caused a less sensitive response in these cells. Neither EGCG nor RA treatment alone affected apoptosis and telomerase activity. The combination treatment of EGCG and RA induced apoptosis and inhibited telomerase activity in adenocarcinoma cell lines. These results were consistent with those of an antiproliferative effect of EGCG and/or RA in cervical adenocarcinoma cells.

**Conclusion.** Our data suggest that EGCG and RA combined to prevent the carcinogenesis of cervical adenocarcinoma, induce apoptosis and inhibit telomerase activity. The treatments of combining EGCG and RA may be effective in preventing or treating cervical adenocarcinoma.

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**Keywords:** EGCG; Retinoic Acid; Cervical adenocarcinoma

### Introduction

Cervical cancer is the second most common cancer in the world. Adenocarcinoma, including adenosquamous carcinoma, represents only 15–20% of all primary carcinoma of the cervix, but this percentage is increasing greatly [1,2]. It has been suggested that adenocarcinoma of the uterine cervix tends to metastasize earlier to lymph nodes and is less sensitive to radiation therapy and to chemotherapy than is squamous cell carcinoma [3,4]. Radical surgery seems to be the treatment of choice for this tumor; however, treatments for advanced or recurring cases have been most often unsuccessful.

Green tea is one of the most common beverages consumed worldwide, and its possible beneficial health effects have received much attention. A number of epidemiological and rodent carcinogenesis studies have provided evidence that green tea has chemopreventive effects for a wide range of malignancies [5–7]. Green tea contains a variety of polyphenols known as catechins. (–)-Epigallocatechin gallate (EGCG) is a major component of polyphenols in green tea [8]. The antitumor effect of EGCG has been demonstrated [5,6,8–11]. Previously, we reported that the treatment with EGCG prevented the carcinogenesis of cervical cancer, induced apoptosis and inhibited telomerase activity [12,13]. It is also reported that EGCG inhibits the growth of human squamous cervical cancer cell lines through apoptosis [12]. EGCG was effective in HPV-18 immortalized endocervical cell lines (pre-malignant cell) but less effective in cervical adenocarcinoma cell lines. These results suggest that the sensitivity to

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Table 1  
Origin and human papillomavirus status of cervical cells and cell lines

Cell line	Origin	HPV DNA type	Tumorigenicity
HEN-18	Endocervix	HPV-18	(-)
HEN-18-S*	Endocervix	HPV-18	(-)
HeLa	Cx, adenocarcinoma	HPV-18	(+)
TMCC-1	Cx, adenocarcinoma	HPV-18	(+)

HEN=human endocervical cells; - =negative; + =positive.

\* Non-tumorigenic, adapted to growth in serum.

EGCG decreases with the progression of the carcinogenic process [12]. The inhibitory effect in cell lines derived from cervical adenocarcinoma cells was less than that from cervical squamous carcinoma cells [12], although several studies have shown that EGCG possesses anticarcinogenic effects in adenocarcinoma, including stomach, colon and breast cancer [5–10]. Recently, Tachibana et al. [14] reported that the combination of EGCG and vitamin A increased expression of the receptor that mediates the anticancer activity of EGCG and enhances the anticancer activity of EGCG.

In the present study, we investigated whether the combined use of EGCG and retinoic acid (RA), the direct acting vitamin A metabolite, possesses growth inhibitory properties in human cervical adenocarcinoma cell lines. Furthermore, we investigated whether the mechanism involves the induction of apoptosis and inhibition of telomerase activity.

## Materials and methods

### Cells, cell culture and cell growth assay

Primary human end cervical cells (HEN) were prepared as described previously [15,16]. Cervical cell lines are summarized in Table 1. Keratinocyte serum-free medium (K-SFM, GIBCO, Grand Island, NY) was used for growth of HEN; HPV-18-immortalizes HEN. Other cell lines were cultured in Dulbecco's modified Eagle's medium plus 10% fetal calf serum (GIBCO). The uterine cervix adenocarcinoma cell line, TMCC-1, was kindly provided by M. Sakamoto (Tokyo Medical College, Tokyo, Japan). For growth assay, EGCG (Wako Pure Chemical Industries, Osaka, Japan) and RA (Sigma, St. Louis, NY) were diluted in 100% ethanol and stored at -20 °C before use. Cells seeded at  $2 \times 10^5$  cells per 5 cm plate were incubated with or without 0–100  $\mu$ M EGCG and/or 1  $\mu$ M all-trans RA, which was changed every other day. Cell growth rate was determined by counting the number of cells with a Coulter counter and expressed with the following formula:

$$\text{Growth rate (\%)} = \frac{\text{cell number (experiment)}}{\text{cell number (control)}}$$

### DNA ladder apoptosis assay

Cells were cultured in medium with 0  $\mu$ M (control) EGCG and 50–100  $\mu$ M EGCG and/or 1  $\mu$ M all-trans RA for 4 days. High molecular weight DNA was extracted, resolved by 1.5% agarose gel electrophoresis and stained using an apoptosis ladder detection kit (Wako Pure Chemicals Industries, Osaka, Japan).

### Caspase-3 activity

Caspase-3-related protease activity in cell lysate was determined using a caspase-3 assay kit, fluorometric (Sigma, St. Louis, MO). Briefly, cell lysate was

mixed with assay buffer and the caspase-3 substrate, Ac-DEVD-AMC, followed by incubation at room temperature for 1.5 h. Absorbance was then read with a plate fluorometer. The excitation and emission wavelengths were 360 nm and 460 nm, respectively. Caspase-3 activity was expressed as the fluorescence value relative to that for untreated cells (control).

### Telomerase assay

Telomerase activity was quantified with the overlap extension PCR assay method using TeloChaser (Toyobo Co., Osaka, Japan). Briefly,  $2 \times 10^4$  cells grown in medium with 0  $\mu$ M (control) EGCG and 50–100  $\mu$ M EGCG and/or 1  $\mu$ M all-trans RA for 4 days were obtained and suspended in Lysis solution. Cell extracts were assayed in extension mixture. After 30 min incubation at 30 °C for telomerase extension, the telomerase products were purified by Clean-Up solution, followed by isopropyl alcohol precipitation. Recovered pellets were mixed with 30  $\mu$ l of PCR mixture, heated at 95 °C for 150 s and then subjected to 30 PCR cycles of 95 °C for 30 s, 68 °C for 30 s and 72 °C for 45 s. PCR products were resolved by electrophoresis in a 7% polyacrylamide gel and visualized with SYBR Green I nucleic acid stain (Molecular Probes, Inc., Eugene, USA).

### Quantitation of hTERT mRNA

hTERT expression levels were quantified by a real-time PCR system, Light Cycler Telo TAGGG hTERT Quantification kit (Roche Molecular Biochemicals, Indianapolis, IN) according to the manufacturer's instructions. Briefly, cells grown in medium with 0  $\mu$ M (control) EGCG and 50–100  $\mu$ M EGCG and/or 1  $\mu$ M all-trans RA for 4 days were obtained. Two hundred nanograms total RNA of each sample was analyzed. hTERT encoding mRNA was reversely transcribed and amplified in a one-step RT-PCR protocol using the LightCycler instrument. Relative expression levels were calculated by dividing the amount of the housekeeping gene PBGD. The resulting ratio is an hTERT value normalized to the expression of PBGD. Duplicates for each sample were performed. PCR products were resolved by electrophoresis in a 7% polyacrylamide gel and visualized with SYBR Green I nucleic acid stain (Molecular Probes, Inc., Eugene, USA).

Table 2  
Effect of epigallocatechin gallate (EGCG) and/or retinoic acid on cell growth rate of endocervical and cervical adenocarcinoma cell lines

Cell line	Treatment	Growth rate (% of untreated control)		
		Day 4	Day 7	Day 10
HEN-18	EGCG 100 $\mu$ M	15.4 $\pm$ 4.1*	9.5 $\pm$ 0.8*	9.0 $\pm$ 0.8*
	EGCG 50 $\mu$ M	35.3 $\pm$ 1.8*	10.9 $\pm$ 0.3*	8.2 $\pm$ 1.4*
	EGCG 10 $\mu$ M	51.4 $\pm$ 4.1*	9.2 $\pm$ 4.8*	7.8 $\pm$ 1.3*
HEN-18S	EGCG 100 $\mu$ M	42.1 $\pm$ 0.8*	14.6 $\pm$ 0.8*	8.6 $\pm$ 0.9*
	EGCG 50 $\mu$ M	94.2 $\pm$ 1.8****	68.2 $\pm$ 6.9****	66.6 $\pm$ 3.1****
	EGCG 10 $\mu$ M	120 $\pm$ 12.6****	89.3 $\pm$ 1.5****	91.1 $\pm$ 4.3****
TMCC-1	EGCG 100 $\mu$ M	72.8 $\pm$ 4.5****	92.5 $\pm$ 1.1**	108 $\pm$ 2.1****
	EGCG 50 $\mu$ M	89.8 $\pm$ 4.5****	106.2 $\pm$ 2.3**	99.5 $\pm$ 3.1****
	RA	79 $\pm$ 5.1**	57.7 $\pm$ 2.3*	62.2 $\pm$ 4.2*
	EGCG 50 $\mu$ M+ RA	53.0 $\pm$ 0.0**	22.4 $\pm$ 0.0*	25.4 $\pm$ 0.0*
HeLa	EGCG 100 $\mu$ M	78.3 $\pm$ 5.6***	93.2 $\pm$ 1.6****	63.1 $\pm$ 1.2*
	IEGCG 50 $\mu$ M	89.5 $\pm$ 3.8****	103 $\pm$ 1.5****	101.4 $\pm$ 3.8****
	RA	66.4 $\pm$ 5.8**	80.1 $\pm$ 3.8**	78 $\pm$ 4.3**
	EGCG 50 $\mu$ M+ RA	62.1 $\pm$ 7.2**	17.5 $\pm$ 5.4*	20.2 $\pm$ 6.3*

HEN-18=human papillomavirus type 18-immortalized human endocervical cell; HEN-18S=non-tumorigenic serum adapted HEC-18; RA=retinoic acid; EGCG=epigallocatechin gallate. The results represent the mean $\pm$ standard deviation of percent. P is the statistical significance of difference in cell growth rate between each day treated and untreated control cells. \* $P$ <0.001, \*\* $P$ <0.01, \*\*\* $P$ <0.05, \*\*\*\*not significant.

## Results

To investigate the effect of EGCG and/or RA on premalignant and malignant cervical adeno cell lines (Table 1), we treated cells for 4, 7 and 10 days with EGCG and/or RA. Cell growth inhibition assays demonstrated that the combination of EGCG and RA treatment inhibited 75–80% growth in cervical adenocarcinoma cell lines, HeLa and TMCC-1, whereas EGCG or RA treatment alone caused a less sensitive response in these cells (Table 2). TMCC-1 was less sensitive than HeLa in EGCG treatment, but the inhibitory effect of RA in TMCC-1 was more than that in HeLa.

The effect of EGCG or RA treatment on apoptosis was examined by DNA ladder apoptosis assay. Cells treated with 0 and 100  $\mu$ M EGCG or 1  $\mu$ M RA for 4 days showed that neither EGCG nor RA treatment resulted in the formation of DNA fragments in HeLa and TMCC-1 (Fig. 1, lanes 2, 3, 6 and 7). In comparison with these treatments, the combination of EGCG and RA treatment induced the formation of DNA fragments (Fig. 1, lanes 4 and 8). These results are consistent with those of an antiproliferative effect of EGCG and/or RA in these cell lines.

As caspase-3 plays an important role in apoptotic events, the influence of EGCG and RA on the caspase-3 activity was examined by using a specific fluorogenic substrate for caspase-3. The TMCC-1 and HeLa treated with the combination of EGCG and RA had significantly higher activity of caspase-3 than that of no treatment (Fig. 2). These results showed that the activation of caspase-3 was associated with the induction of apoptosis in the combination treatment of EGCG and RA.

Telomerase has been proposed to represent a novel and potentially selective target for cancer therapy. It is also reported that the inhibition of telomerase is one of the major mechanisms

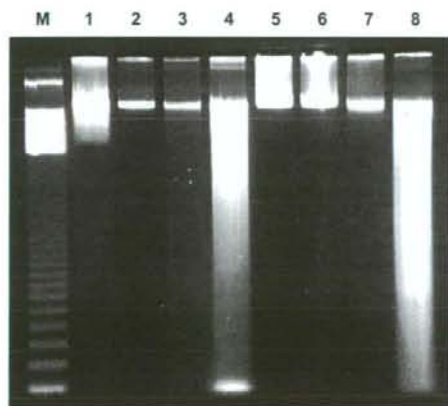


Fig. 1. Effect of epigallocatechin gallate (EGCG) and/or retinoic acid (RA) on apoptosis in TMCC-1 and HeLa. Apoptosis was assayed by DNA ladder formation analysis. TMCC-1 (lanes 1, 2, 3 and 4) and HeLa (lanes 5, 6, 7 and 8) were cultured in medium with EGCG and/or RA. M: 123 bp ladder marker; lanes 1 and 5: control medium; lanes 2 and 6: 1  $\mu$ M of RA; lanes 3 and 7: 100  $\mu$ M of EGCG; lanes 4 and 8: 1  $\mu$ M of RA and 100  $\mu$ M of EGCG. DNA by ladder formation obtained from cells after EGCG and RA treatment confirmed apoptosis.

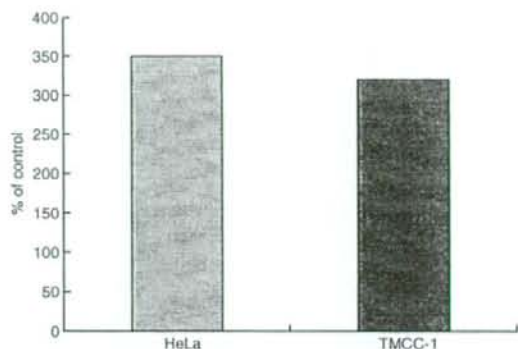


Fig. 2. Effect of epigallocatechin gallate (EGCG) and/or retinoic acid (RA) on caspase-3 activity in HeLa and TMCC-1.

of the anticancer effects of EGCG. We studied whether EGCG and RA inhibit telomerase activity by the stretch PCR assay methods. Telomerase was dramatically decreased in HeLa with the combination of EGCG and RA treatment (Fig. 3, lanes 4). Neither EGCG nor RA treatment inhibited the telomerase activity.

A strong correlation between telomerase activity and the expression level of hTERT mRNA has been described in cancer cells. We investigate hTERT expression level by a real-time PCR system. EGCG and RA treatment showed that hTERT expression was decreased in HeLa and TMCC-1 (Fig. 4, lanes 2 and 4). These

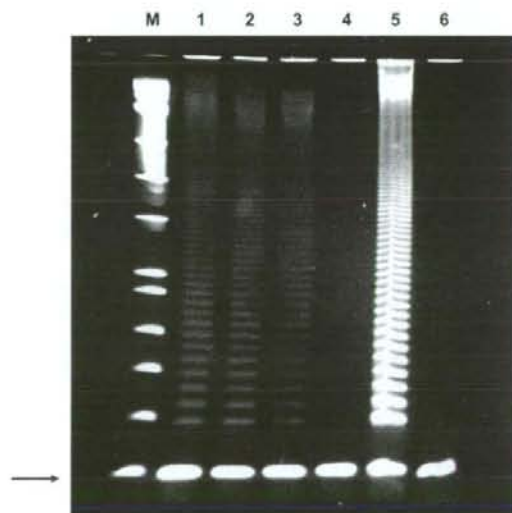


Fig. 3. Effect of epigallocatechin gallate (EGCG) and/or retinoic acid (RA) on telomerase activity in HeLa. Semiquantitative telomerase activity was assayed by stretch PCR assay method. HeLa was cultured in medium with 1  $\mu$ M of RA and/or 100  $\mu$ M of EGCG M:  $\phi$ X174/Hinf I marker; lane 1: control medium; lane 2: 1  $\mu$ M of RA; lane 3: 100  $\mu$ M of EGCG; lane 4: 1  $\mu$ M of RA and 100  $\mu$ M of EGCG; lane 5: positive control (HeLa cell); lane 6: negative control. The arrow indicates the internal standard DNA (65 bp).