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Original Article

Chromosome aberrations [dup(1q)] in endometrial cancer: Gene analysis of 54 surgical specimens in Turkey

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ABSTRACT

Objective: We aimed to evaluate the frequency of chromosomal aberrations and mutations in the *k-ras* or *Her-2/neu* genes in surgical specimens of endometrial carcinoma and their association with clinicopathological findings.

Materials and methods: Fifty-four patients who were treated for endometrial cancer between April 2010 and May 2011 at the Kocaeli University Obstetrics and Gynecology Department, Kocaeli, Turkey were enrolled in a prospective study. Clinical and histopathological findings were recorded. Genetic analysis, which included the detection of chromosomal deletions and duplications, as well as *k-ras* and *Her-2/neu* mutations, was performed on endometrial samples from surgical specimens.

Results: In 70% of cases, tumor size was >2 cm or covered the entire uterine cavity, affecting mostly corpus (76%) and invading less than half of the myometrium (80%). Forty-six cases (86%) had endometrioid-type carcinoma, and early stage (Stage I, 65%) and higher grade (Grade II–III, 66%) tumors were predominant. Lymph node and lymphovascular involvement was positive in 11% and 28% of the patients, respectively. Chromosomal aberrations (deletion or duplication) and *Her-2/neu* and *k-ras* mutations were encountered in 44%, 15%, and 13% of surgical specimens, respectively. The most common chromosomal aberration was dup(1q) ($n = 16$). Oncogenic mutations in *Her-2/neu* or *k-ras* had no association with the severity of endometrial cancer, but the presence of chromosomal aberrations, as a whole or dup(1q) alone, were associated with higher tumor size, deeper myometrial invasion, advanced stage or grade, lymphovascular invasion, and lymph node involvement ($p < 0.05$ for all).

Conclusion: Chromosomal aberrations, particularly dup(1q), are related to advanced disease in endometrial cancer. Genetic analysis of cancer tissues may provide important insights in determining disease prognosis.

Introduction

Endometrial cancer is one of the most common malignant tumors of the genital tract in women, causing ~74,000 deaths globally per year [1]. Although there is no effective screening test, 75% of cases can be diagnosed at an early stage due to the symptomatic nature of the disease [1,2]. This is the main reason why current treatment has a good response. However, therapeutic success is poorer in advanced stages, emphasizing the need for better prognostic markers that aid in the planning of treatment [3]. Furthermore, disease recurrence in early stage endometrial cancer that cannot be explained by known prognostic factors has led researchers to investigate new prognostic markers [1,4]. As a result, the need for prognostic factors that can estimate the prognosis of patients with endometrial cancer has become an intense focus of attention in recent years.

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Histopathological analysis and tumor spread play a major role in determining the prognosis of endometrial cancer [5,6]. Other factors known to have a prognostic role in endometrial cancer, include age, histological type, histological grade, myometrial invasion, lymphovascular and lymph node involvement, tumor size, peritoneal cytology, hormone receptor status, cervical and adnexal spread, intraperitoneal disease, and the type of treatment [2,7,8].

As with many cancers, genetic changes play a role in the etiology of endometrial cancer, and in some cases, they have been suggested to be useful in the early diagnosis of endometrial cancer. For example, mutations in the *k-ras* or *Her-2/neu* oncogenes has been reported in 19–46% or 9–30% of endometrial cancer cases, respectively [9,10]. In addition, previous studies have shown that chromosomal duplication and deletion frequently occurs at chromosomes 1, 3, 8, 10, and 20 in endometrial cancers [11].

Thus, chromosomal abnormalities, such as *k-ras* and *Her-2/neu* oncogenic mutations, play an important role in the genetics of endometrial cancer, and may be useful to estimate the prognosis of disease and plan therapeutic management strategies.

In this study, we determined the frequency of chromosomal deletions or duplications and *k-ras* and *Her-2/neu* oncogenic mutations in endometrial tissue samples from endometrial cancer patients, as well as assessing the potential relationship between genetic results and clinicopathologic findings.

Materials and methods

Study design and patients

This was a prospective, single-arm study from a single institution in Turkey. Fifty-four patients who were diagnosed with endometrial cancers and treated at Kocaeli University Obstetrics and Gynecology Department, Kocaeli, Turkey between April 1, 2010 and May 31, 2011 were included in the study. Other inclusion criteria included complete staging studies, adequate tissue sample, and regular postoperative follow-up. Patients who received neoadjuvant therapy were excluded from the study.

The surgical operation was a total abdominal hysterectomy (TAH) with a bilateral salpingo-oophorectomy (BSO; TAH + BSO) in eight patients, TAH + BSO + bilateral pelvic lymph node dissection (LND) + omentectomy in 14 patients, TAH + BSO + pelvic and paraaortic LND + omentectomy in 14 patients, TAH + BSO + bilateral pelvic LND in 16 patients, and TAH + BSO + omentectomy in two patients.

The study protocol was approved by the Institutional Ethics Committee of Kocaeli University and was conducted in accordance with the latest version of the Helsinki Declaration. Each patient was informed on the study and signed the consent form before participation.

Clinical and histopathological findings

Clinical and histopathological findings included menopausal status, age at diagnosis, concomitant diseases and therapies, clinical outcome, endometrioid versus nonendometrioid type, tumor size, extent of myometrial invasion, stage, and histopathologic grade (according to the International Federation of Gynecology and Obstetrics system) [12], and lymph node and lymphovascular involvement.

Genetic analysis

Surgical uterine specimens from all patients were sent to the Pathology Department of Kocaeli University for frozen-section examination. Endometrial sampling was performed on uterine specimens with adequate tumoral tissue, and samples were stored at −80°C until they were evaluated in the Laboratory of the Medical Genetic Department, Kocaeli University. Sampling and storing was performed under sterile conditions.

Detection of chromosomal deletions and duplications

An array-based comparative genomic hybridization (aCGH) method was used to determine the chromosomal deletions and duplication in tissue samples. Genomic DNA was isolated using the DNeasy Blood and Tissue kit (Qiagen, Hilden, Germany). The quality and quantity of DNA was determined using agarose gel electrophoresis and a spectrophotometer (NanoDrop ND-1000; NanoDrop Technologies, Wilmington, DE, USA), respectively. CytoChip Focus Constitutional (BlueGnome, Cambridge, UK) was used as an aCGH platform. DNA with adequate quantity and quality, as well as reference DNA (Human Genomic DNA, Female; Promega Corporation, Madison, WI, USA), were marked, combined, and hybridized with aCGH microchips at 47°C for 20 hours in accordance with CytoChip protocol. The microchips were then washed with different dilutions of 20× saline-sodium citrate according to the protocol and scanned with an Agilent Microarray Scanner (Agilent Technologies, Palo Alto, CA, USA). Scanned images were evaluated quantitatively, and all of the chromosomal copy number variations were analyzed for deletion and duplication with fixed CytoChip algorithm settings in BlueFuse Multi software (version 2.2, BlueGnome, Cambridge, UK; Figure 1).

Detection of k-ras mutations

Genomic DNA was scanned for seven *k-ras* mutations located in codons 12 and 13 on a LightCycler 480 real-time polymerase chain reaction device (Roche Diagnostic GmbH, Mannheim, Germany) with a TheraScreen *k-ras* Mutation kit (Diagnostic Innovations Ltd., St. Asaph, UK). The difference between the threshold cycle of the sample assay and the threshold cycle of the corresponding endogenous reference was calculated. The cut-off corresponding endogenous reference value for positive mutations was defined as < 1%.

Detection of Her-2/neu mutations

In genomic DNA, 101-bp *Her-2/neu* fragments were amplified with specific primers in accordance to the Way2Gene protocol and analyzed using marked probes compared with standard samples in LightCycler 480 real-time polymerase chain reaction device (Roche Diagnostic GmbH). An amplification ratio of <2 was considered to be negative, whereas those >2 were considered positive.

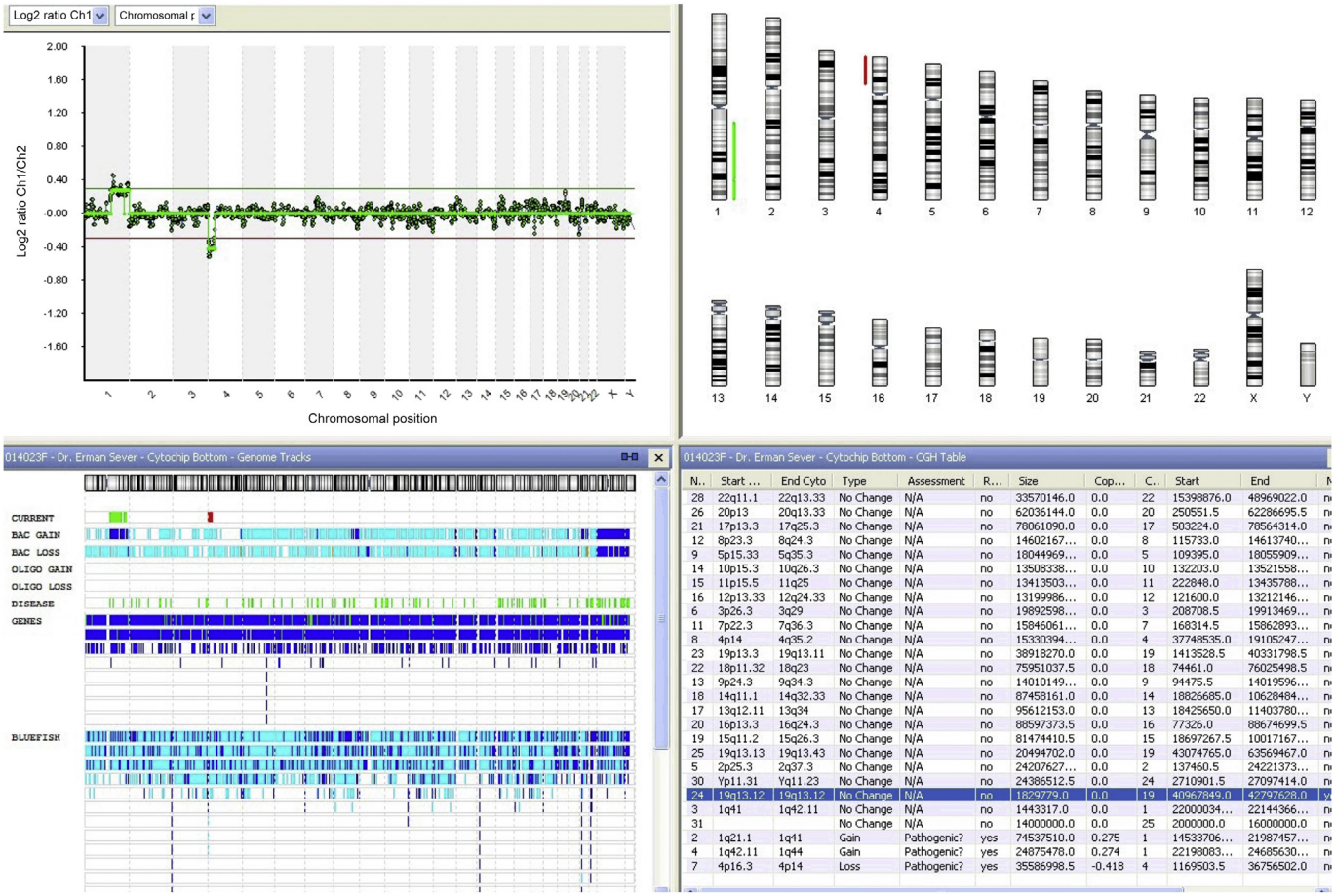
Statistical analysis

The study data were summarized with descriptive statistics, e.g., mean, standard deviation, number, and percentage. The frequency of the oncogenic mutations and chromosomal aberrations were analyzed with respect to the histopathological findings using the Chi-square and Mann–Whitney tests for two subgroups, as well as analysis of variance for more than two subgroups. The statistical analysis was performed using the SPSS 12 (SPSS Inc., Chicago, IL, USA) software package. Odds ratios and 95% confidence intervals were calculated. The statistical significance level was set to $p < 0.05$.

Results

Study population

The mean age of the 54 study patients at the time of diagnosis was 62.5 ± 14.5 years (range, 33–85 years), and most patients (80%)



N..	Start ...	End Cyto	Type	Assessment	R...	Size	Cop...	C..	Start	End
28	22q11.1	22q13.33	No Change	N/A	no	33570146.0	0.0	22	15398876.0	48969022.0
26	20p13	20q13.33	No Change	N/A	no	62036144.0	0.0	20	250551.5	62286695.5
21	17p13.3	17q25.3	No Change	N/A	no	78061090.0	0.0	17	503224.0	78564314.0
12	8p23.3	8q24.3	No Change	N/A	no	14602167...	0.0	8	115733.0	14613740...
9	5p15.33	5q35.3	No Change	N/A	no	18044969...	0.0	5	109395.0	18055909...
14	10p15.3	10q26.3	No Change	N/A	no	13508338...	0.0	10	132203.0	13521558...
15	11p15.5	11q25	No Change	N/A	no	13413503...	0.0	11	222848.0	13435788...
16	12p13.33	12q24.33	No Change	N/A	no	13199986...	0.0	12	121600.0	13212146...
6	3p26.3	3q29	No Change	N/A	no	19892598...	0.0	3	208708.5	19913469...
11	7p22.3	7q36.3	No Change	N/A	no	15846061...	0.0	7	168314.5	15862893...
8	4p14	4q35.2	No Change	N/A	no	15330394...	0.0	4	37748535.0	19105247...
23	19p13.3	19q13.11	No Change	N/A	no	38918270.0	0.0	19	1413528.5	40331798.5
22	18p11.32	18q23	No Change	N/A	no	75951037.5	0.0	18	74461.0	76025498.5
13	9p24.3	9q34.3	No Change	N/A	no	14010149...	0.0	9	94475.5	14019596...
18	14q11.1	14q32.33	No Change	N/A	no	87458161.0	0.0	14	18826685.0	10628484...
17	13q12.11	13q34	No Change	N/A	no	95612153.0	0.0	13	18425650.0	11403780...
20	16p13.3	16q24.3	No Change	N/A	no	88597373.5	0.0	16	77326.0	88674699.5
19	15q11.2	15q26.3	No Change	N/A	no	81474410.5	0.0	15	18697267.5	10017167...
25	19q13.13	19q13.43	No Change	N/A	no	20494702.0	0.0	19	43074765.0	63569467.0
5	2p25.3	2q37.3	No Change	N/A	no	24207627...	0.0	2	137460.5	24221373...
30	Yp11.31	Yq11.23	No Change	N/A	no	24386512.5	0.0	24	2710901.5	27097414.0
24	19q13.12	19q13.12	No Change	N/A	no	1829779.0	0.0	19	40967849.0	42797628.0
3	1q41	1q42.11	No Change	N/A	no	1443317.0	0.0	1	22000034...	22144366...
31			No Change	N/A	no	14000000.0	0.0	25	2000000.0	16000000.0
2	1q21.1	1q41	Gain	Pathogenic?	yes	74537510.0	0.275	1	14533706...	21987457...
4	1q42.11	1q44	Gain	Pathogenic?	yes	24875478.0	0.274	1	22198083...	24685630...
7	4p16.3	4p14	Loss	Pathogenic?	yes	35586998.5	-0.418	4	1169503.5	36756502.0

Figure 1. Outcome of choromosomal copy number variation analysis by BlueFuse Multi software (BlueGnome, Cambridge, UK).

were postmenopausal. The mean body weight index (34 ± 9.07 kg/m^2; range, 23.4–48.2 kg/m^2) indicated that the majority of patients were obese. Of the patients, 40% had concomitant hypertension, 7.2% had diabetes mellitus, and 21.8% had hypertension and diabetes mellitus. Thirty-two patients (59%) received postoperative radiotherapy. Upon follow-up, endometrial carcinoma recurrence was observed in 11% of patients, and three patients (5%) died due to the disease (Table 1).

Histopathology of surgical specimens

In 70% of cases, the tumor size measured >2 cm or covered the entire uterine cavity, affecting mostly corpus (76%) and invading less than half of the myometrium (80%). Histopathological findings on surgical specimens showed that 46 patients (86%) had endometrioid-type carcinoma. Early stage (Stage I, 65%) and higher grade disease (Grade II–III, 66%) were predominant among the cohort. Lymph nodes and lymphovascular involvement was positive in 11% and 28% of the patients, respectively (Table 1).

Genetic analysis

Chromosomal aberrations (deletion or duplication) or mutations in *Her-2/neu* or *k-ras* were encountered in 44%, 15%, and 13% of surgical specimens, respectively (Table 2). The observed chromosomal aberrations were as follows: duplication of chromosome 1 [dup(1q), $n = 16$], duplication of chromosome 10 [dup(10q), $n = 7$], mixed aneuploidy ($n = 4$), duplication of chromosome 7 [dup(7q),

Table 1
Demographic, clinical, and histopathological characteristics of patients.

Parameter		Outcome ($n = 54$)
Age (y)		62.6 ± 11.5
Body mass index (kg/m^2)		34 ± 9.07
Menopause status	Premenopausal	11 (20)
	Postmenopausal	43 (80)
Recurrent disease		6 (11)
Death due to disease		3 (5)
Histological type	Endometrioid (Type 1)	46 (86)
	Nonendometrioid (Type 2)	8 (14)
Stage	I	35 (65)
	II	9 (16)
	III	7 (13)
	IV	3 (6)
Grade	I	18 (34)
	II	22 (40)
	III	14 (26)
Myometrial invasion	<1/2	43 (80)
	>1/2	11 (20)
Lesion site	Corpus	41 (76)
	Fundus	8 (15)
	Fundus-corpus	5 (9)
Tumor size (cm)	<2	16 (30)
	>2	27 (50)
	Entire cavity	11 (20)
Lymphovascular invasion	Positive	15 (28)
	Negative	39 (72)
Lymph node involvement	Positive	6 (11)
	Negative	48 (89)
Cytology of abdominal fluid	Positive	4 (8)
	Negative	50 (93)

Data are presented as n (%) or mean ± standard deviation.

$n = 3$], deletion of chromosome 16 [del(16q), $n = 2$], trisomy 8 ($n = 2$), monosomy 4, 9, 18, X ($n = 1$ for each), trisomy 4, 6, 11 ($n = 1$ for each), and deletion of chromosome 4 [del(4p), $n = 1$]. No significant correlation was observed between the patient's age and mutation in either *k-ras* or *Her-2/neu* ($p = 0.610$ and $p = 0.555$, respectively). However, the frequency of chromosomal aberrations was shown to increase significantly with age ($p = 0.014$).

No significant relationship was observed between oncogenic mutations in either *k-ras* or *Her-2/neu* and the following histopathological findings: histological type, stage, grade, myometrial invasion, tumor size, lymph node involvement, or lymphovascular invasion ($p > 0.05$ for all; Table 3). No significant difference in *k-ras* or *Her-2/neu* oncogenic mutations or chromosomal aberrations was detected between early and advanced disease stages (Stage I vs. II–IV) and grades (Grade I vs. II–III). Importantly, however, samples with a higher rate of chromosomal aberrations and dup(1q) was associated with larger tumor size, deeper myometrial invasion, advanced disease stage or grade, lymphovascular invasion, and lymph node involvement ($p < 0.05$ for all; Table 3). Clinicopahological parameters, chromosome aberrations, and abnormality of *k-ras* and *Her-2* genes are evaluated in Type I and Type II endometrial cancers. The values are shown in Table 3.

Chromosomal aberrations were regarded as significant risk factors for stage, grade, myometrial invasion, tumor size, and lymph node involvement ($p < 0.05$) by univariate analysis. Tumor size was an independent risk factor on multivariate analyses (Table 4).

Discussion

Endometrial cancer is a tumor characterized by the invasion of endometrial tissue into the underlying stroma, myometrium, and vascular tissues. Microscopically, endometrial cancer presents as a marked hyperplasia and anaplasia of glandular elements [13]. Understanding the molecular biology and genetics of endometrial cancer has recently become a major focus of research to develop novel therapies, better estimate the relative risk and prognosis of the disease, and more accurately predict treatment response [3,5,14,15]. Although genetic polymorphisms that are associated with endometrial cancer risk or prognosis have been identified in various studies, the clinical significance of these genetic polymorphisms is currently unclear [4,15].

To assess the underlying genetics and their effects on clinical endometrial cancer, we characterized chromosomal aberrations, including deletions, duplications, or oncogenic mutations in *k-ras* or *Her-2/neu*, in endometrial tissue samples that were harvested from patients diagnosed with endometrial cancer and assessed whether a relationship exists between specific genetic events and clinicopathologic findings. Our study population consisted mostly of patients with endometrioid types of endometrial cancer at early stages but with advanced histopathological grade. Although the majority of patients had tumors larger than 2 cm, we observed that lymph node and lymphovascular involvement, as well as myometrial invasion were limited. Chromosomal aberrations (deletion or duplication events) or mutations in *Her-2/neu* or *k-ras* were detected in 44%, 15%, and 13% of surgical specimens, respectively.

Table 2
Mutations in *k-ras* and *Her-2/neu* oncogens and chromosomal aberrations.

		n (%)
k-ras mutation	Positive	7 (13)
	Negative	46 (87)
Her-2/neu mutation	Positive	8 (15)
	Negative	46 (85)
Chromosomal aberrations	Positive	24 (44)
	Negative	30 (56)

Previous data suggests that the frequency of oncogene mutation in endometrial cancer differs by race [16]. Therefore, local data may represent an important factor when evaluating oncogenic mutations in endometrial cancer. Here, we evaluated the frequency of *k-ras* and *Her-2/neu* oncogene mutations in endometrial cancer samples. It is known that mutations in the *k-ras* oncogene plays an important role in the tumorigenesis of female genital tract cancers [17,18]. However, conflicting data in literature has questioned the prognostic value of mutant *k-ras* in endometrial cancer. While work done by Alexander-Sefre et al [6] suggests that *k-ras* mutations correlate with myometrial invasion depth, a study done by Esteller et al [19] showed that although point mutations at codon 12 of the *k-ras* oncogene occurred in eight of 55 (14.5%) tumor specimens, no correlation was observed between *k-ras* oncogene mutation and prognosis. However, studies from Japan, where endometrial cancer has a lower incidence but a higher mortality rate than Europe and the USA, reported higher rates of *k-ras* mutation, ranging from 12.2% to 40% [20–23]. In addition, these studies suggested that *k-ras* mutations are related to advanced disease, aggressiveness, and mortality [20–23].

Ito et al [24] found a significant association between *k-ras* mutations and the presence of lymph node metastases and negative disease outcome in 221 cases of endometrioid endometrial cancer. Similar to previous reports from the USA and Europe, we detected *k-ras* mutations in 13% of surgical specimens. In contrast to reports from Japan, we did not find any significant effect of *k-ras* mutations on the histological type of tumor, grade, surgical stage, depth of myometrial invasion, lymphovascular invasion, lymph node involvement, and tumor size. Furthermore, *k-ras* mutations were not detected in three out of the 54 patients who died during follow-up.

Mutations in the *Her-2/neu* oncogene are also a potential carcinogenic mechanism of endometrial cancer [25]. Overexpression of *Her-2/neu* occurs in 10–21% of endometrial cancer and correlates with intraperitoneal spread of disease and poor survival [26–29]. Oncogenic aberrations in *Her-2/neu* have also recently been suggested as an independent prognostic factor in Type I endometrial adenocarcinoma [30,31], and *Her-2/neu* amplification correlates with histological grade of endometrium cancer [32,33]. In our study, *Her-2/neu* mutations were detected in 15% of the surgical specimens. However, in contrast to previous reports, our findings did not indicate a prognostic value of *Her-2/neu* in endometrium cancer, as no significant relationship was observed between *Her-2/neu* mutations and the histological type of tumor, grade, surgical stage, depth of myometrial invasion, lymphovascular invasion, lymph node involvement, or tumor size.

The role of genetics in endometrial carcinogenesis was first demonstrated by the cytogenetic analysis of the total cellular DNA content (ploidy). Genomic alterations are commonly manifested by chromosomal aberrations. A recent study by Nesina et al [34] demonstrated that the number of damaged chromosomes present in the peripheral blood T-lymphocytes was increased in patients with endometrial cancer compared with healthy individuals. In line with this, Falck et al [35] reported recurrent numerical and structural chromosomal changes and chromosomal translocations have been frequently detected in rat endometrial carcinomas.

Interestingly, ~20% of endometrial cancers with advanced stage and undifferentiated histology have been shown to harbor cytogenetic abnormalities [36,37]. In an analysis of 174 endometrial cancer patients, Susini et al [38] reported that aneuploidy was the strongest independent predictor of poor prognosis. We detected chromosomal aberrations (deletion or duplication), including the most common dup(1q), in 44% of our cases. In our study population, histological grade, surgical stage, depth of myometrial invasion,

Table 3
Correlation of histopathological findings to oncogen mutations and chromosomal aberrations.

		k-ras mutation (+)	*Her-2*/neu mutation (+)	Chromosomal aberration (+)	Dup(1q) (+)
Histological type	Endometrioid	7 (15)	8 (17)	20 (44)	14 (30)
	Nonendometrioid	0 (0)	0 (0)	4 (50)	2 (25)
	p	0.577	0.336	0.732	0.756
Endometrioid type	Type I	7 (18.9)	7 (18.9)	15 (40.5)	6 (20)
	Type II	0 (0)	1 (5.9)	9 (52.9)	6 (40)
	p	0.055	0.210	0.694	0.153
Stage	I	4 (17)	5 (14)	12 (34)	8 (23)
	II	0 (0)	1 (11)	4 (44)	2 (22)
	III	2 (43)	2 (43)	4 (60)	4 (60)
	IV	0 (0)	0 (0)	3 (100)	2 (66)
	p	0.065	0.585	0.044	0.035
Grade	I	3 (16)	2 (11)	4 (22)	2 (11)
	II	4 (18)	4 (18)	12 (54)	9 (40)
	III	0 (0)	2 (14)	8 (57)	5 (36)
	p	0.102	0.818	0.041	0.08
Myometrial invasion	<1/2	5 (12)	6 (14)	15 (35)	10 (23)
	>1/2	1 (9)	2 (18)	9 (82)	6 (54)
	p	0.621	0.621	0.04	0.043
Tumor size	<2 cm	2 (13)	3 (19)	1 (6)	1 (6)
	>2 cm	4 (13)	5 (16)	18 (58)	12 (39)
	Entire cavity	1 (14)	0 (0)	5 (71)	3 (43)
	p	0.993	0.291	0.001	0.029
Lymphovascular invasion	Positive	1 (7)	1 (7)	10 (66)	7 (46)
	Negative	6 (15)	7 (18)	14 (35)	9 (23)
	p	0.363	0.281	0.041	0.089
Lymphnode involvement	Positive	1 (17)	0 (0)	5 (83)	4 (66)
	Negative	6 (13)	8 (17)	19 (40)	12 (25)
	p	0.775	0.279	0.042	0.037

Data are presented as *n* (%) or mean ± standard deviation.

Table 4
Logistic regression analysis. Outcomes of the 54 patients analyzed by univariate and multivariate analyses using clinicopathological parameters and the genomic markers.

	Univariate model				Multivariate model			
	OR	% 95 CI		*p*	OR	% 95 CI		*p*
		Lower	Upper			Lower	Upper	
Chromosomal aberration (+)								
Histological type	1.30	0.29	5.85	0.732				
Endometrioid type	1.65	0.52	5.25	0.396				
Stage	1.31	1.04	1.65	0.023				
Grade	2.16	1.02	4.58	0.044				
Myometrial invasion	8.40	1.60	43.98	0.012				
Tumor size	6.76	1.95	23.35	0.003	6.76	1.95	23.35	0.003
Lymphovascular invasion	7.63	0.83	70.52	0.073				
Lymph node involvement	3.57	1.02	12.56	0.047				

CI = confidence interval; OR = odds ratio.

lymphovascular invasion, lymph node involvement, and tumor size were significantly associated with the presence of chromosomal aberrations. Furthermore, chromosomal aberrations were detected in all three patients who died during follow-up. Therefore, our findings support the predictive value of chromosomal aberrations as a bad prognostic marker in endometrium cancer.

Previous studies suggest that dup(1q) is an independent predictor of tumor aggressiveness and poor survival [39]. Therefore, we analyzed the prognostic value of dup(1q) alone in endometrium cancers. Similar to the data reported in the literature, we found that dup(1q) was associated with higher tumor size, deeper myometrial invasion, advanced stage or grade, lymphovascular invasion, and lymph node involvement. Additionally, dup(1q) was present in two of three patients who died during follow-up.

We acknowledge that the main limitation of our study was the small sample size. This precludes us from reaching a definitive conclusion on the prognostic value of oncogene mutations in endometrial cancer. Therefore, the findings of the study will need to be confirmed with larger prospective studies.

In conclusion, we showed that chromosomal aberrations, particularly dup(1q), are related to advanced disease and poor prognosis in endometrial cancer. Given that endometrial cancer is the most common gynecologic cancer, and can be diagnosed definitively by tissue biopsy via local intervention, the genetic analysis of cancer tissue is important to determine disease prognosis. As chromosomal analysis tests become more cost-effective via technological advances, these tests will likely play a significant role in the management of endometrial cancer.

Conflicts of interest

The authors have no conflicts of interest relevant to this article.

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