

mRNA expression of steroidogenic enzymes, steroid hormone receptors and their coregulators in gastric cancer

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Abstract. Epidemiological and experimental findings suggest that the development of gastric cancer (GC) is regulated by steroid hormones. In postmenopausal women and older men, the majority of steroid hormones are produced locally in peripheral tissue through the enzymatic conversion of steroid precursors. Therefore, using reverse transcription-quantitative polymerase chain reaction analysis, the mRNA expression of genes encoding steroidogenic enzymes, including steroid sulfatase (STS), hydroxy-delta-5-steroid dehydrogenase 3 beta- and steroid delta-isomerase 1 (HSD3B1), 17 β -hydroxysteroid dehydrogenase type 7 and aromatase (CYP19A1), was investigated in primary tumoral and adjacent healthy gastric mucosa from 60 patients with GC. Furthermore, the mRNA levels for estrogen receptor α , estrogen receptor β (ESR2) and androgen receptor (AR), along with their coregulators, including proline, glutamate and leucine rich protein 1, CREB binding protein, nuclear receptor coactivator 1 (NCOA1), nuclear receptor corepressor 1 (NCOR1) and nuclear receptor subfamily 2 group F member 1 (NR2F1), were investigated. Additionally, the association between the mRNA expression of these genes and the clinicopathological features of patients with GC was examined. Significantly decreased levels of STS, HSD3B1, ESR2, AR, NCOA1 and NCOR1 mRNA, in addition to significantly increased levels of CYP19A1 mRNA were demonstrated in tumoral tissue samples compared with

adjacent healthy gastric tissue samples. Deregulated expression of these genes in the analyzed tissue samples was associated with certain clinicopathological features of GC, such as age and localization of the tumor. The results of the current study suggest that all of the genes analyzed are expressed in tumoral and adjacent healthy gastric mucosa. In addition, the results indicate that abnormal expression of STS, ESR2, AR, NCOA1 and NCOR1 may serve a role in the development and progression of GC, and may be associated with specific clinicopathological features in patients with GC.

Introduction

The global incidence and mortality rates of gastric cancer (GC) are amongst the highest for all malignant tumor types (1). Risk factors that may increase an individual's chance of developing GC include *Helicobacter pylori* infection, a diet high in salty/smoked food and low in fruit/vegetables, tobacco smoking and genetic susceptibility (2). Additionally, the incidence rate of GC is ~2 times higher in males compared with females, independently of known gender-specific variables (3). Therefore, it has been proposed that steroid hormone production influences the risk of developing GC (4,5). Furthermore, numerous studies have suggested a protective role of 17 β -estradiol (E2) in gastric carcinogenesis (6-12). Although the majority of E2 is produced in the ovaries, it is also synthesized locally in peripheral tissues in males and females (13).

There are two routes involved in the local synthesis of E2, the sulfatase and aromatase signaling pathways (13). The sulfatase signaling pathway involves the desulfation of dehydroepiandrosterone sulfate (DHEA-S) and estrone sulfate (E1-S) to DHEA and E1, respectively, by steroid sulfatase (STS). Subsequently, E1 is reduced to E2 by 17 β -hydroxysteroid dehydrogenases (HSD17Bs; types 1, 5 and 7). In addition, DHEA is converted to androstenedione (adione) by hydroxy-delta-5-steroid dehydrogenase 3 beta- and steroid delta-isomerase 1 (HSD3B1). In the aromatase signaling pathway, adione and testosterone are converted into E1 and E2, respectively, by

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aromatase (CYP19A1) (14). In recent studies, the mRNA and protein expression of enzymes belonging to the HSD17B family, including HSD17B1, 2 and 5 was demonstrated in healthy and tumoral gastric mucosa (15-17). In addition, it was revealed that the HGC-27 and EPG 85-257 GC cell lines were able to synthesize E2 *in vitro* (15).

In the present study, the mRNA levels of certain genes that participate in the synthesis of E2 through the sulfatase and aromatase signaling pathways, including STS, HSD3B1, CYP19A1 and HSD17B7, were investigated in primary tumoral and healthy adjacent gastric mucosa samples from patients with GC. Furthermore, considering the fact that the cellular functions of steroid hormones are mediated through binding to their receptors and that the abnormal expression of genes encoding nuclear estrogen receptors α (ESR1) and β (ESR2), and androgen receptor (AR) have been demonstrated in GC (18,19), the mRNA expression of coactivators and corepressors of steroid hormone receptors were also determined in the tissue samples. The following coactivators and corepressors were investigated: Proline, glutamate and leucine rich protein 1 (PELPI); CREB binding protein (CREBBP); nuclear receptor coactivator 1 (NCOA1); nuclear receptor corepressor 1 (NCOR1); and nuclear receptor subfamily 2, group F, member 1 (NR2F1). Additionally, the association between the mRNA expression of the genes investigated and the clinicopathological features of patients with GC was investigated.

Materials and methods

Patients and tissue specimens. Primary tumoral gastric mucosa specimens were collected between December 2012 and September 2015 from 60 patients with a mean age of 67.2 years old who underwent a total gastrectomy at the First Department of Surgical Oncology and General Surgery at the Greater Poland Cancer Centre or the Department of General and Endocrine Surgery and Gastroenterological Oncology, Heliodor Świącicki Clinical Hospital at the Poznań University of Medical Sciences (Poznań, Poland). The clinicopathological characteristics of the patients are presented in Table I; however, for certain patients not all the information was available. In addition, healthy gastric mucosa tissue samples located ≥ 10 cm away from the tumoral lesions was obtained from each patient. Specimens were snap-frozen in liquid nitrogen and stored at -80°C until required for RNA isolation. An experienced pathologist performed histopathological assessments of the tissue samples (Table I). The present study was approved by the Ethics Committee of Poznań University of Medical Sciences. Written informed consent was obtained from all patients.

Reverse transcription-quantitative polymerase chain reaction analysis. Total RNA from patient tissue samples was isolated according to Chomczynski and Sacchi's single-step method (20), which involves homogenization. The concentration and integrity of the RNA isolated was assessed using a Nano-100 Micro Spectrophotometer (Hangzhou Allsheng Instruments Co., Ltd., Hangzhou, China) and non-denaturing electrophoresis on a 1.5% agarose gel, respectively. RNA samples were treated with DNase I and reverse-transcribed into cDNA using a SuperScript[®] III First-Strand Synthesis

system (Thermo Fisher Scientific, Inc., Waltham, MA, USA) according to the manufacturer's protocol, using 1 μg of RNA as a template.

The target cDNA was quantified by the relative quantification method using a calibrator, as is described in the Relative Quantification Manual (Roche Diagnostics GmbH, Mannheim, Germany) (21). The calibrator was prepared as a cDNA mix from all of the patient samples and its successive dilutions were used to create a standard curve. qPCR reactions were performed using a LightCycler[®] 480 Real-Time PCR system (Roche Diagnostics GmbH, Mannheim, Germany). Each qPCR reaction contained 1 μl of total cDNA solution obtained in reverse transcription, 9 μl LightCycler 480 SYBR Green I Master mix (Roche Diagnostics GmbH) and 0.1 μM of the corresponding primer pair (Table II). Primers for ESR1, ESR2 and HSD17B7 were purchased from Sigma-Aldrich (Merck Millipore, Darmstadt, Germany) and the $\beta 2$ -microglobulin (B2M) primers were previously designed by Hashimoto *et al* (22). The primers for CYP19A1 were designed using the Universal ProbeLibrary website (Roche Diagnostics GmbH). All other primers were designed using OLIGO Primer Analysis Software (version 5.0; Molecular Biology Insights, Inc., Colorado Springs, CO, USA). qPCR thermocycling conditions consisted of a pre-denaturation step at 95°C for 7 min followed by 42 PCR cycles specific for each primer. Reaction conditions for each primer pair are detailed in Table II. The analyzed transcript levels were expressed as the ratio between the amount of target transcript in a sample and target transcript in the calibrator. The quantity of analyzed transcripts in each sample was standardized by the geometric mean of B2M, β -glucuronidase and porphobilinogen deaminase, and presented as the decimal logarithm.

Statistical analysis. Normality of data distribution was assessed using the Shapiro-Wilk test, followed by a Student's t-test (two-tailed) or Mann-Whitney U test to determine significant differences between mean values. $P < 0.01$ was considered to indicate a statistically significant difference. STATISTICA software (version 10; StatSoft, Inc., Tulsa, OK, USA) was used to perform all statistical analyses.

Results

mRNA expression of STS, HSD3B1, CYP19A1, HSD17B7, ESR1, ESR2, AR, PELPI, CREBBP, NCOA1, NCOR1 and NR2F1 in primary tumoral and healthy gastric mucosa of patients with GC. RT-qPCR was used to measure the mRNA expression of genes encoding steroidogenic enzymes (STS, CYP19A1, HSD3B1, HSD17B7), steroid hormone receptors (ESR1, ESR2, AR) and coregulators of steroid hormone receptors (PELPI, CREBBP, NCOA1, NCOR1, NR2F1), in primary tumoral and adjacent healthy mucosa tissue samples from 60 patients with GC (Fig. 1). Expression of STS and HSD17B7 mRNA was detected in all tissue samples examined, whereas expression of HSD3B1 mRNA was absent in one healthy tissue sample and CYP19A1 was not detected in seven healthy specimens (Fig. 1A). Furthermore, five cancerous tissue samples demonstrated no expression of HSD3B1 mRNA. There was no difference in the mRNA level of HSD17B7 in primary tumoral and adjacent healthy mucosa ($P = 0.2$; Fig. 1A). However,

Table I. Available clinicopathological characteristics of patients with gastric cancer.

Clinicopathological characteristic	No. of patients
Gender (male/female)	36/24
GC localization	
Multisite	31
Cardia	10
Trunk	6
Fundus	1
Lesser curvature	5
Pylorus	3
Histological type	
Diffuse	19
Intestinal	23
Undetermined	12
Tumor stage	
T1	2
T2	9
T3	32
T4	15
Lymph node metastasis stage	
N0	17
N1	8
N2	14
N3	19
Metastasis stage	
M0	45
M1	3
Histological grading	
G1	1
G2	17
G3	38

T, tumor; N, node; M, metastasis, G, grade.

significantly lower mRNA levels of STS ($P<0.00001$) and HSD3B1 ($P=0.0051$) were identified in tumoral tissue samples compared with healthy tissue samples. Tumoral tissue samples revealed a significantly increased expression of CYP19A1 mRNA compared with control samples ($P<0.00001$; Fig. 1A). However, despite the significant differences observed, HSD3B1 and CYP19A1 mRNA levels were maintained at low levels in primary tumoral and healthy gastric mucosa compared with STS and HSD17B7 mRNA (data not shown).

mRNA of the investigated steroid hormone receptors (Fig. 1B) and their coregulators (Fig. 1C) was detected in all 60 pairs of gastric tumor and adjacent healthy control samples. No significant difference was observed in the expression of ESR1 mRNA between primary tumoral and adjacent healthy mucosa ($P=0.26$; Fig. 1B). Furthermore, significantly decreased levels of ESR2 ($P=0.0097$) and AR ($P=0.00029$) mRNA were detected in GC specimens compared with adjacent healthy controls (Fig. 1B). Amongst the steroid hormone

receptors investigated, the expression levels of ESR2 and AR mRNA were the highest, with expression of ESR1 mRNA low in tumoral and adjacent healthy gastric tissue samples (data not shown). Amongst the coregulators of steroid hormones receptors examined, the expression of NCOA1 ($P=0.00021$) and NCOR1 ($P=0.00017$) mRNA was significantly reduced in tumoral mucosa compared with adjacent healthy mucosa (Fig. 1C). In addition, no significant differences were observed in the expression of PELP1 ($P=0.19$), CREBBP ($P=0.06$) and NR2F1 ($P=0.11$) mRNA between tumoral and healthy tissue samples (Fig. 1C).

Analysis of the clinicopathological characteristics of patients with GC and mRNA levels of STS, HSD3B1, CYP19, ESR2, AR, NCOA1 and NCOR1. Decreased expression of STS, HSD3B1, ESR2, AR, NCOA1 and NCOR1 mRNA, and increased expression of CYP19A1 mRNA in tumoral tissue samples compared with healthy controls, were associated with certain clinicopathological features of patients with GC (Table III). Expression of STS ($P<0.00001$), ESR2 ($P=0.0024$), AR ($P=0.0001$), NCOA1 ($P=0.00028$) and NCOR1 ($P=0.00067$) mRNA were significantly lower in tumoral tissue samples compared with the control in patients >60 years. Furthermore, males had significantly lower levels of AR ($P=0.0018$), NCOA1 ($P=0.00051$) and NCOR1 ($P=0.000095$) mRNA in tumoral tissue samples compared with control tissue samples, whereas in females the mRNA level of HSD3B1 was significantly lower in tumoral compared with control tissue samples ($P=0.004$).

The multisite localization of GC was demonstrated to be associated with a significantly lower level of HSD3B1 mRNA ($P=0.0034$) and tumors located in the cardia region had significantly lower STS ($P=0.0012$), AR ($P=0.0012$), NCOA1 ($P=0.001$) and NCOR1 ($P=0.0073$) mRNA, compared with healthy mucosa. However, only 10 patients with tumor localization in the cardia region were included in the analysis. Patients with the intestinal type of GC had significantly lower mRNA levels of AR ($P=0.000046$) and NCOA1 ($P=0.0007$) in tumoral tissue samples compared with the control mucosa. In addition, significantly lower levels of STS mRNA were identified in tumoral tissue compared with adjacent healthy tissue in patients with indeterminate GC ($P=0.0032$). Additionally, cancerous tissue samples of a T3 grade expressed significantly lower levels of STS ($P=0.00018$) and HSD3B1 ($P=0.0062$) mRNA compared with healthy tissue samples. A significantly lower level of AR mRNA was also identified in tumoral tissue graded as T4 compared with the control ($P=0.0086$). Expression of STS mRNA was significantly decreased in the tumoral tissue samples of patients with N3 lymph node metastases compared with the controls samples ($P=0.000089$).

The majority of patients were diagnosed with an M0 metastasis stage, thus no associations between the mRNA levels of the analyzed genes and metastasis grade were investigated. Significantly lower levels of AR ($P=0.00062$) and NCOA1 ($P=0.0027$) mRNA were identified in the tumoral tissue of patients with G2 stage GC compared with adjacent healthy tissue. In addition, STS ($P=0.000054$) and HSD3B1 ($P=0.0012$) mRNA expression was significantly lower in G3 histological grade tumors compared with healthy tissue

Table II. Primer sequences and qPCR conditions.

Gene	Sequence (5'-3')	Exon number	Product size (bp)	qPCR thermocycling conditions (denaturation; annealing; elongation)
STS	GCCAGAAGATTGATGAGCCAC AGGCGTTGCAGTAATGGAAGAG	ENSE00001203198 ENSE00001136339	174	95°C/8 sec; 62°C/8 sec; 72°C/8 sec
HSD3B1	GATGTCTTCGGTGTCACTCA GGCTACCTCTATGCTACTG	ENSE00001722296 ENSE00001846945	129	95°C/8 sec; 57°C/8 sec; 72°C/8 sec
CYP19A1	CAAACCCAATGAATTTACTCT ACCATGGCGATGTACTTTCC	ENSE00003683464 ENSE00001524808	111	95°C/6 sec; 58°C/6 sec; 72°C/6 sec
AR	GATCCTTCACCAATGTCAACT CTCATTCGGACACACTGGCT	ENSE00001282597 ENSE00001165458	109	95°C/10 sec; 60°C/10 sec; 72°C/10 sec
PELP1	GAGCATTTCAGCAGGTGTTAC AGGTGGTTCATGGAGATGTC	ENSE00003644127 ENSE00003476735	132	95°C/10 sec; 60°C/10 sec; 72°C/10 sec
CREBBP	TCTTCCATTGCCACCCACCT CTGTCTTCAGTTGCTTGTTTG	ENSE00003665970 ENSE00003538086	142	95°C/10 sec; 60°C/10 sec; 72°C/10 sec
NCOA1	GCTGGTATCCTTCTTAGTG TGGCGTTGCTTGTGTGGTG	ENSE00000808889 ENSE00000808890	136	95°C/10 sec; 60°C/10 sec; 72°C/10 sec
NCOR1	GCGTTATGATCAGCTCATGG ACTCCTAGCAATGGTGGCTG	ENSE00003681554 ENSE00003668751	202	95°C/10 sec; 62°C/10 sec; 72°C/10 sec
NR2F1	CGCATCTTCCAGGAGCAGGT GCAGTCGCAGCAGCAGTTTG	ENSE00001249995 ENSE00001250004	226	95°C/6 sec; 60°C/6 sec; 72°C/6 sec
GUSB	CGCCGACTTCTCTGACAAC ATCACCTCCCGTTCGTACC	ENSE00001799401 ENSE00003687473	174	95°C/10 sec; 60°C/10 sec; 72°C/10 sec
PBGD	GCCAAGGACCAGGACATC TCAGGTACAGTTGCCCATC	ENSE00003460195 ENSE00003609229/ ENSE00003610664	160	95°C/10 sec; 60°C/10 sec; 72°C/10 sec
B2M	CACCCCCACTGAAAAAGATG CCTCCATGATGCTGCTTACA	ENSE00003659794 ENSE00003459883/ ENSE00002538889	106	95°C/10 sec; 60°C/10 sec; 72°C/10 sec

qPCR, quantitative polymerase chain reaction; STS, steroid sulfatase; HSD3B1, hydroxy-delta-5-steroid dehydrogenase 3 beta- and steroid delta-isomerase 1; CYP19A1, aromatase; AR, androgen receptor; PELP1, proline, glutamate and leucine rich protein 1; CREBBP, CREB binding protein; NCOA1, nuclear receptor coactivator 1; NCOR1, nuclear receptor corepressor 1; NR2F1, nuclear receptor subfamily 2, group F, member 1; GUSB, β -glucuronidase; PBGD, porphobilinogen deaminase; B2M, β 2-microglobulin.

samples. However, the expression of CYP19A1 mRNA was significantly increased in tumoral tissue samples compared with the control in patients with multisite localization of GC ($P=0.00001$), a T3 tumor stage ($P=0.00001$), N0 ($P=0.0024$) or N3 ($P=0.001$) lymph node metastasis grades and G3 histological grade tumors ($P<0.00001$). The expression of CYP19A1 mRNA in primary tumoral tissue samples compared with healthy adjacent mucosa samples was significantly increased in all patients studied, regardless of age, gender, and histological type and localization of the tumor.

Discussion

In the present study, the mRNA levels of specific genes involved in the synthesis of E2, in addition to genes encoding steroid hormone receptors and their coregulators, were investigated in primary tumoral and adjacent healthy gastric mucosa samples obtained from patients with GC. The presence of mRNA was detected for all genes analyzed in the majority of gastric specimens examined. Furthermore, it was identified that the expression of STS, HSD3B1, ESR2, AR, NCOA1 and

Table III. Association between the expression of STS, HSD3B1, CYP19, ESR2, AR, NCOA1 and NCOR1 mRNA in tumoral and healthy gastric tissue samples and the clinicopathological characteristics of patients with GC.

Clinicopathological characteristic	Gene analyzed (P-value, GC vs. control tissue)						
	↓STS ^a	↓HSD3B1 ^b	↑CYP19A1 ^b	↓ESR2 ^a	↓AR ^a	↓NCOA1 ^b	↓NCOR1 ^b
All patients	<0.00001	0.0051	<0.00001	0.0097	0.00029	0.00021	0.00017
Age (years old)							
≤60	0.9	0.2	0.00074	0.89	0.35	0.27	0.22
>60	<0.00001	0.02	0.000012	0.0024	0.0001	0.00028	0.00067
Gender							
Male	0.0014	0.28	0.000072	0.08	0.0018	0.00051	0.000095
Female	0.000069	0.004	0.00023	0.056	0.04	0.11	0.48
GC localization							
Multisite	0.013	0.0034	0.00001	0.04	0.026	0.12	0.11
Cardia	0.0012	0.57	0.054	0.55	0.0012	0.001	0.0073
Body	-	-	-	-	-	-	-
Fundus	-	-	-	-	-	-	-
Lesser curvature	-	-	-	-	-	-	-
Pylorus	-	-	-	-	-	-	-
Histological type							
Diffuse	0.034	0.034	0.0018	0.73	0.69	0.36	0.038
Intestinal	0.037	0.022	0.0074	0.022	0.000046	0.0007	0.019
Indeterminate	0.0032	0.14	0.0009	0.047	0.47	0.71	0.98
Tumor stage							
T1	-	-	-	-	-	-	-
T2	0.57	0.96	0.11	0.79	0.19	0.093	0.077
T3	0.00018	0.0062	0.00001	0.022	0.027	0.016	0.038
T4	0.014	0.11	0.089	0.14	0.0086	0.046	0.074
Lymph node metastasis stage							
N0	0.17	0.11	0.0024	0.29	0.16	0.039	0.027
N1	0.18	0.27	0.052	0.76	0.035	0.014	0.024
N2	0.019	0.49	0.041	0.22	0.38	0.48	0.53
N3	0.000089	0.06	0.001	0.045	0.048	0.062	0.21
Metastasis stage							
M0	0.0021	0.003	<0.00001	0.014	0.00064	0.0028	0.0018
M1	-	-	-	-	-	-	-
Histological grading							
G1	-	-	-	-	-	-	-
G2	0.07	0.07	0.036	0.24	0.00062	0.0027	0.042
G3	0.000054	0.0012	<0.00001	0.027	0.044	0.021	0.0049

^aTwo-tailed Student's t-test, ^bMann-Whitney U test. GC, gastric cancer; STS, steroid sulfatase; HSD3B1, hydroxy-delta-5-steroid dehydrogenase 3 beta- and steroid delta-isomerase 1; CYP19A1, aromatase; ESR2, estrogen receptor β; AR, androgen receptor; NCOA1, nuclear receptor coactivator 1; NCOR1, nuclear receptor corepressor 1; T, tumor; N, node; M, metastasis; G, grade; ↓/↑, down/up-regulation in gastric cancer in compare to healthy controls.

an increase in the activity and expression of STS in breast cancer (28-33). Therefore, it has been suggested that upregulation of STS may be associated with higher concentrations of intratumoral E2 (28,30,32).

Desulfated DHEA that is converted into adione, typically by HSD3B1, may serve as a substrate of E2 synthesis through

the aromatase signaling pathway (25). However, low expression of HSD3B1 mRNA was observed in tumoral and healthy gastric tissue samples, with expression lower in the tumoral mucosa compared with the adjacent healthy tissue. Conversely to the results of the present study, increased expression of HSD3B1 mRNA has been identified in benign prostatic

hyperplasia compared with healthy adjacent prostate tissue samples (34), in addition to castration-resistant metastases compared with primary prostate tumors (35). HSD3B1 activity is essential for the production of androstenedione, which is subsequently used as a substrate for the synthesis of testosterone, an important hormone that regulates the proliferation of prostate cells (36). Furthermore, androstenedione and testosterone can be directly converted to E1 and E2, respectively, by CYP19A1 (25). In the current study, expression of CYP19A1 mRNA was demonstrated in the majority of healthy gastric tissue samples and all tumoral gastric tissue samples. A previous study identified the presence of CYP19A1 in 23/30 GC tissue samples; however, all healthy gastric mucosa specimens tested negative for this enzyme (37). The presence of CYP19A1 mRNA and protein has been revealed in healthy and tumoral gastric tissue samples, although no significant difference in the level of CYP19A1 mRNA was demonstrated between healthy and tumoral gastric tissue samples (38). These findings oppose the results of the present study; however, this may have been due to the fact that the previous study analyzed a total of five cases (38).

Numerous animal studies have demonstrated that parietal cells are capable of converting circulating androgens into estrogens, whilst simultaneously expressing CYP19A1 (39-44). Furthermore, the synthesis of E2 through the aromatization of exogenous testosterone has been demonstrated in various GC cell lines (38). Considering these findings and the numerous evidence for the protective role of E2 against GC (6-12), the increased level of CYP19A1 mRNA in tumoral tissue samples compared with the control group observed in the present study is difficult to explain. However, it was observed that the expression of CYP19A1 mRNA in cancerous and healthy tissues was maintained at a low level, indicating that the role CYP19A1 serves in estrogen synthesis in gastric tissue may be limited. Additionally, it has been demonstrated that E2 may inhibit CYP19A1 and STS activity in breast cancer cells (45,46), suggesting that the increased mRNA expression of CYP19A1 in GC could be due to lower intracellular concentrations of E2.

Cellular responses to steroid hormones are facilitated by steroid hormones binding to their receptors, such as ESR1, ESR2 and AR (47). Studies that investigated the association between these receptors and GC have produced inconsistent results (18,19,48). ESR1 has been suggested to mediate the cancer-promoting effects of E2 in breast (49,50), colon (51), prostate (52) and gastric (53-57) cells, whereas binding of E2 to ESR2 could inhibit cell proliferation in tumors of these tissues (51,53,55,57-61). In the current study, no significant difference in the expression of ESR1 mRNA was identified between healthy and tumoral gastric tissue samples; however, the expression of ESR2 mRNA was significantly lower in cancerous mucosa compared with the control. Thus, the results of the present study support the hypothesis that reduced ESR2 expression is associated with the development of GC. Conversely, Matsuyama *et al* (62) suggested that the role served by ESR2 in GC may differ depending on the subtype. Furthermore, Guo *et al* (63) demonstrated that certain splicing variants of ESR2 mRNA (ESR2-1, -2 and -5) are differentially expressed in GC and healthy tissue samples. Additionally, higher levels of ESR2-5 mRNA were detected in GC compared with healthy tissue samples, and were

associated with tumor-node-metastasis (TNM) staging, while decreased mRNA levels of ESR2-1 in GC did not correlate with any clinicopathological characteristics. In the current study, patients who were >60 years old had significantly lower levels of ESR2 mRNA in tumoral compared with healthy gastric tissue samples; however, all ESR2 splicing variants were analyzed simultaneously. A previous study suggested that ESR1 may exhibit antiproliferative activity, and reduce the motility and invasion of GC cells (64). Furthermore, ESR1 has been associated with an early TNM stage in GC (18). Thus, further studies investigating the role of ESRs in the etiology of GC are warranted.

In addition to investigating ESRs, the expression of AR mRNA was investigated in the current study. Previous studies have proposed that AR expression is an unfavorable factor in GC (19,65,66). In the present study, it was demonstrated that expression of AR mRNA was significantly decreased in GC tissue compared with controls. Similarly, decreased mRNA expression of AR in GC tissue samples has been reported by Gan *et al* (18). Low expression of AR and ESR1 mRNA was observed in cancerous and wild-type gastric mucosa, whereas the ESR2 mRNA was predominantly expressed in the both of these tissues. However, the expression of AR and ESR2 mRNA in GC tissue samples and matched controls was the highest amongst the analyzed steroid hormone receptors in the present study. The STS substrates E1-S and DHEA-S have been demonstrated to induce transactivation of ESRs and AR in a concentration-dependent manner in the MVLN invasive ductal carcinoma and CHO-K1 ovarian cell lines, respectively (67). The results of the current study suggest that DHEA-S is hydrolyzed by STS prior to AR activation, whereas E1-S may be active prior to STS-mediated hydrolysis. Thus, the decreased expression of AR mRNA in GC may have been due to reduced androgen synthesis caused by STS down-regulation. Notably, decreased expression of HSD3B1 mRNA, which is essential for androgen synthesis from DHEA, was detected in the present study.

The activity of nuclear steroid hormone receptors is regulated by various coactivators and corepressors (68). In the current study, NCOR1 and NCOA1 were demonstrated to be downregulated in GC tissue samples compared with healthy controls. Furthermore, mRNA and protein expression of NCOR1 has been identified to be downregulated in gastrointestinal stromal tumors, where it has been proposed to serve as a tumor suppressor through the SMAD signaling pathway (69). In contrast to these findings, another study identified increased mRNA expression of NCOR1 in malignant endometrial tissue samples compared with healthy tissue samples (70). Furthermore, high mRNA expression of NCOR1 has been associated with the improved prognosis of patients with breast cancer (71), whereas a loss of nuclear NCOR1 has been revealed to cause increased expression of cancer-associated genes and be significantly associated with the progression of invasive malignant melanoma (72). Upregulation of NCOR1 mRNA and protein expression, induced by progestins, has been associated with the suppression of estrogen-induced growth in T47D breast cancer cells (73).

In the present study, it was demonstrated that expression of NCOA1 mRNA was reduced in tumoral compared with healthy gastric tissue samples. Similarly, downregulation

of NCOA1 mRNA has been identified in cancerous bladder urothelium samples (74). Additionally, high mRNA levels of NCOA1 have been observed in healthy breast tissue samples, intermediate levels in tumoral tissue samples and low levels in breast cancer cell lines (75). However, numerous studies have identified an association between increased expression of NCOA1 and enhanced angiogenesis, cell proliferation and survival, disease recurrence, higher tumor grade and poor prognosis in breast cancer (76-81). Notably, upregulation of NCOA1 has been observed in patients with breast cancer treated with aromatase inhibitors (82). Thus, the decreased levels of NCOA1 mRNA in GC tissue identified in the present study may have been due to upregulation of CYP19A1 mRNA in tumoral gastric mucosa. Tai *et al* (83) demonstrated that overexpression of NCOA1 enhanced the E2-induced growth of MCF-7 breast cancer cells. Increased expression of NCOA1 has also been associated with the DHEA-mediated activation of AR in prostate cancer (84). Therefore, the decreased expression of AR and NCOA1 mRNA that were observed in cancerous gastric tissue samples in the present study may have been the result of limited desulfation of DHEA-S due to the downregulation of STS.

In conclusion, the presence of STS, HSD3B1, CYP19A1, HSD17B7, ESR1, ESR2, AR, PELP1, CREBBP, NCOA1, NCOR1 and NR2F1 mRNA was demonstrated in the majority of tumoral and adjacent healthy gastric mucosa tissue samples. Furthermore, significantly decreased mRNA levels of STS and HSD3B1, in addition to significantly increased expression levels of CYP19A1 mRNA, in tumoral gastric tissue samples compared with matched controls were identified. However, compared with STS, the expression of HSD3B1 and CYP19A1 mRNA was low in the majority of the examined tissue samples, indicating that their role in gastric carcinogenesis is limited. Additionally, tumoral gastric tissue samples exhibited decreased levels of NCOA1 and NCOR1 mRNA compared with adjacent healthy controls, suggesting that deregulated expression of these coregulators may serve a role in gastric carcinogenesis. A limitation of the current study was the use of homogenized tissue samples, and thus the possibility that the samples included non-cancerous cells, such as fibroblasts, endothelial cells, smooth muscle cells or blood cells, could not be excluded. Furthermore, mRNA abundance does not always correlate with protein expression. Therefore, further studies on the expression levels of the genes involved in the steroidogenesis pathway and their role in gastric carcinogenesis are warranted.

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