CDH1 mutations in gastric cancers are not influenced by family history

Sangjoon Choi

Samsung Medical Center <https://orcid.org/0000-0003-2108-0575>

Jiryeon Jang

Sungkyunkwan University

You Jeong Heo

Sungkyunkwan University

So Young Kang

Samsung Medical Center

Seung Tae Kim

Samsung Medical Center

Jeeyun Lee

Samsung Medical Center

Won Ki Kang

Samsung Medical Center

Jong-Won Kim

Samsung Medical Center

Kyoung-Mee Kim (✉ kkmkys@skku.edu)

<https://orcid.org/0000-0002-1162-9205>

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Abstract

Background: *CDH1* mutation is the most frequent genetic alteration in hereditary diffuse gastric cancer (GC) and early onset diffuse GC patients. However, the incidence of *CDH1* mutations in sporadic GC with or without family history has not been studied.

Methods: This retrospective study includes a total of 993 Korean patients with primary advanced GC who underwent surgery and received palliative chemotherapy. Targeted deep sequencing was performed in all cases and family history of GC was searched with survival analysis.

Results: We found *CDH1* alterations in 146 of 993 patients (14.7%) and 8 were germline (0.8%). Out of 146 patients with *CDH1* mutations, 25 (17.1%) had a family history of GC in one of their first relatives, and 12 patients (8.2%) were diagnosed with familial GC (FGC). All cases with FGC were diffuse type by Lauren classification, and only one harbored a previously reported germline mutation of *CDH1* (c.2638G>A) and the remaining 11 harbored known somatic *CDH1* mutations. Among all patients with *CDH1* mutation, there was no significant survival difference between patients with family history or FGC. In the 847 patients without *CDH1* mutation, 189 (22.3 %) had a family history of GC and 92 patients (10.9%) were FGC. *CDH1* mutations were more frequent in patients with early onset (<45 years) GC (45.5%) compared with patients with late onset GC (10.9%) ($p = 0.001$), but were not significantly associated with the family history of GC ($p > 0.05$).

Conclusions: *CDH1* mutations are mostly somatic and typically are not associated with family history.

Background

CDH1 gene encodes the protein E-cadherin, which is a cell-cell adhesion protein that plays an important role in tumor development, epithelial invasion, and progression of tumor cells in gastric cancer (GC). Germline mutation of *CDH1* is the most frequently found genetic alteration in hereditary diffuse gastric cancer (HDGC) patients and is detected in 25–30% of cases fulfilling the clinical criteria of International Gastric Cancer Linkage Consortium [1]. A total of 122 *CDH1* germline mutations has been reported worldwide, and the types of mutations include deletions, insertions and splice site, nonsense, and missense mutations [2]. Most previous studies identified germline mutations through polymerase chain reaction and sequencing [3–7] with multiplex ligation-dependent probe amplification [8–11] or high-resolution melting analyses [12] using DNA from patients with familial gastric cancer (FGC), HDGC, or early-onset gastric cancer (EOGC). From these studies, *CDH1* germline mutations were identified in 10% of FGC cases [10, 11], 0 ~ 19% of HDGC cases [3–5, 8], and 0 ~ 8.9% [5–7, 9] of EOGC cases with diffuse or mixed histologic types [6]. Germline mutations of *CDH1* were also reported in 1.7% of patients with sporadic GC [12].

The recent advent of and use of multigene cancer panel testing using next-generation sequencing (NGS) has dramatically improved testing by enabling simultaneous evaluation of many patients for multiple high-risk cancer syndromes as well as moderate-risk cancer-associated genes such as *CDH1* [13]. While this strategy has resulted in significant increases in identification of individuals at risk, it has also led to clinical conundrums regarding management of nonsyndromic carriers of an unexpected or unanticipated genetic mutation [14], such as patients with *CDH1* mutation [15]. With NGS, somatic mutations of *CDH1* are found in 9%~36% of GC cases [16–22] and are highly prevalent in sporadic early-onset diffuse-type GC (EODGC) (53.2% of cases) [17]. Somatic mutations of *CDH1* have been suggested as a poor prognostic marker in diffuse-type GC [22, 23]. Although a few studies have investigated the frequency and impact of *CDH1* mutations in HDGC and EODGC [9, 10, 17, 24] the incidence of *CDH1* mutations in sporadic GC with or without family history has not been studied. Although familial aggregation is found in about 10% of GC cases, the prevalence of *CDH1* alterations in patients with familial aggregation is unclear [25].

In the present study, we studied *CDH1* alterations with deep targeted sequencing and investigated the association with family history in 993 GC patients in a GC-prevalent country.

Methods

Patients

This study involved retrospective analysis of patients with GC at Samsung Medical Center in Seoul, South Korea. All patients were diagnosed with GC by pathologic examination and provided written informed consent. The 993 patients included 647 male and 346

female patients, and the patient age ranged from 18 to 80 years (mean 60.8). By Lauren classification, diffuse type was found in 463 cases. Patients < 45 years old were defined as EOGC, and 110 cases in the total patient group were classified as EOGC. Among these 110 cases, 81 were diffuse type and were diagnosed as EODGC.

Patients who had family history of GC in first- or second-degree relatives were considered as GC with family history. Patients with family history were defined as FGC if they met the following criteria: (1) GC in 2 or more first/second-degree relatives, with at least one diagnosis before age 50 or (2) GC in 3 or more first/second-degree relatives, independent of age. The remaining patients were classified as sporadic GC, as previously described [26].

DNA extraction and targeted deep sequencing

Genomic DNA was extracted from fresh tissues using QIAamp DNA mini kits (Qiagen, Valencia, CA, USA) and from formalin-fixed paraffin-embedded (FFPE) tissues using the QIAamp DNA FFPE Tissue kit according to the manufacturer's instruction. DNA concentration was measured by spectrophotometry (ND1000, Nanodrop Technologies, Thermo Scientific, MA, USA). Sample purity was assessed using a Qubit Fluorometer (Life Technologies, Grand Island, NY, USA).

Genomic DNA (~ 250 ng) from each tissue was sheared in a Covaris S220 ultrasonicator (Covaris, Woburn, MA, USA) and used with CancerSCAN™ probes and a SureSelect XT reagent kit HSQ (Agilent Technologies) for construction of a library according to the manufacturer's protocol. This panel is designed to enrich 381 exons, covering 366.2 kb of the human genome [23]. After enriched exome libraries were multiplexed, the libraries were sequenced on a HiSeq 2500 sequencing platform (Illumina). Briefly, a paired-end DNA sequencing library was prepared through gDNA shearing, end-repair, A-tailing, paired-end adaptor ligation, and amplification. After hybridization of the library with bait sequences for 27 h, the captured library was purified and amplified with an index barcode tag, and the library quality and quantity were assessed. Sequencing of the exome library was performed using the 100-bp paired-end mode of the TruSeq Rapid PE Cluster Kit and TruSeq Rapid SBS Kit (Illumina).

Variant detection

Sequence reads were mapped to the human genome (hg19) using Burrows-Wheeler Aligner (BWA) [27]. Duplicate read removal was performed using Picard and SAMtools [28]. Local alignment was optimized using the Genome Analysis Toolkit (GATK) [29]. To detect single nucleotide variants (SNVs), we integrated the results of three variant callers to increase sensitivity [30–32]. For insertion and deletions (indels), Pindel was used [33]. Copy number variations were calculated for targeted regions by dividing read depth per exon by estimated normal reads per exon using an in-house reference.

Single nucleotide polymorphisms (SNPs) of CDH1 were removed based on dbSNP (<http://www.ncbi.nlm.nih.gov/SNP>), established by the National Center for Biotechnology Information (NCBI).

Analyses of CDH1 variants

Lists of CDH1 variants were assembled from the literature and a search using the ClinVar [34], Human Gene Mutation Database (HGMD) [35], the Genome Aggregation Database (gnomAD) (<https://gnomad.broadinstitute.org/>), the single nucleotide polymorphism database (dbSNP) (<https://www.ncbi.nlm.nih.gov/snp/>), 1000 genome project, Exac03, ESP5400, and KRDGB_1100. For somatic alterations, Catalogue of Somatic Mutations in Cancer (COSMIC v85) and TCGA databases were used. The predisposition discovery process of CDH1 variants in the 993 GC cases is described in Fig. 1.

Statistical analysis

SPSS ver. 23.0 statistical software program (SPSS Inc., Chicago, IL, USA) was used for statistical analyses. Chi-square and linear by linear test were performed to analyze correlations of clinicopathological features between patients with or without family history, and FGC patients. Overall survival (OS) rates were calculated by the Kaplan-Meier method and differences in survival were compared using log-rank test. A p-value < .05 indicated a statistically significant result.

Results

Mutations types of CDH1

We identified 146 (14.7%) CDH1 mutations from 993 GC cases by NGS analysis. The 146 patients with CDH1 mutations included 69 male and 77 female patients, and patient age ranged from 18 to 80 years (mean 49.6 years). Diffuse-type by Lauren classification was identified in 127 cases (Table 1). Patients < 45 years were defined as EOGC; a total of 50 cases was classified as EOGC, and 47 of these cases were EODGC. CDH1 mutations were more frequent in patients with EOGC (45.5%) compared with patients with late onset GC (10.9%) ($p = < 0.001$) (Table 2).

Table 1
Characteristics of patients with gastric cancer harboring CDH1 mutation (n = 146)

	Familial gastric cancer (n = 12)	GC with family history (n = 13)	GC without family history (n = 121)	p value
Age, year				
Median (range)	47 (30–68)	57 (50–71)	50 (18–80)	
Sex				0.485
Male	5	10	54	
Female	7	3	67	
Differentiation				0.050
Well or moderate	0	5	5	
Poor	9	4	61	
Signet ring cell	3	4	46	
Others	0	0	9	
Lauren histology				0.081
Intestinal	0	5	5	
Diffuse	12	8	107	
Mixed	0	0	6	
Indeterminate	0	0	3	
CDH1 mutations				0.229
Germline	1	2	5	
Somatic	11	11	116	

Table 2
Characteristics of gastric cancer patients with or without CDH1 mutation

	GC with CDH1 mutation (n = 146)	GC without CDH1 mutation (n = 847)	p value
Age			< 0.001
< 45	50	60	
≥ 45	96	787	
Family history			0.370
FGC	12	92	
GC with FHx	13	97	
Absent	121	658	
GC gastric cancer, FGC familial gastric cancer, FHx Family history			

To rule out the possibility of deamination effects of formalin, the nucleotide changes were analyzed, and the prevalence of C > G alterations (2.74%) was not significantly frequent ($p > 0.05$) (Fig. 2A). Mutations of CDH1 included nonsynonymous SNVs (n = 99, 67.8%), stopgain SNV (n = 14, 9.6%), frameshift deletion (n = 12, 8.2%), and frameshift insertion (n = 4, 2.7%), frameshift substitution (n = 1, 0.7%), nonframeshift deletion (n = 15, 10.3%), and nonframeshift substitution (n = 1, 0.7%). The distribution of CDH1 mutation is shown in Fig. 2B. The distributions of somatic mutations within the CDH1 gene are depicted in Fig. 3.

With a cut-off value for variant allele frequency (VAF) of > 50% [36], germline mutations were identified in 8 patients (0.8%) and 2 of them were novel: c.1424T > A in exon 10 and c.1839_1841delCAT in exon 12. The two novel CDH1 mutations were validated as germline mutations by Sanger sequencing of paired normal tissue. Remaining 6 mutations have been reported previously as uncertain significance. The precise mutation profiles of germline CDH1 alteration with clinicopathologic characteristics are described in Table 3.

Table 3
Mutation profiles with clinicopathologic characteristics of 8 germline CDH1 alteration

Case	Age/Sex	Exon	cDNA sequence changes	Function	Clinical significance in ClinVar	Lauren's classification	Histologic type	Family history
1	65/M	exon10	c.1424T > A*	nonsynonymous SNV	Uncertain significance	Diffuse	SRCC	No
2	53/M	exon10	c.1418T > A	nonsynonymous SNV	Uncertain significance	Diffuse	Tubular PD	No
3	45/F	exon10	c.1478T > C	nonsynonymous SNV	Uncertain significance	Diffuse	Tubular PD	No
4	59/M	exon12	c.1839_1841delCAT*	nonframeshift deletion	Uncertain significance	Diffuse	SRCC	No
5	47/M	exon16	c.2638G > A	nonsynonymous SNV	Uncertain significance	Diffuse	Tubular PD	FGC
6	47/F	exon05	c.546A > C	nonsynonymous SNV	Uncertain significance	Diffuse	Mucinous ADC	No
7	50/M	exon14	c.2246G > A	nonsynonymous SNV	Uncertain significance	Intestinal	Papillary WD	FHx
8	70/F	exon02	c.76G > C	nonsynonymous SNV	Uncertain significance	Diffuse	Tubular PD	No
*These two mutations are considered as novel ones								
AA Amino acid, F/U Follow up, SNV Single nucleotide variant, SRCC Signet ring cell carcinoma, DOD Dead of disease, PD poorly differentiated, Del Deletion, FGC Familial gastric cancer, ADC Adenocarcinoma, FHx Family history								

Mutations of CDH1 in patients with and without family history

In the 146 patients with CDH1 mutations, 25 (17.2%) had a familial history of GC in one of their first relatives, and 12 patients (8.2%) were diagnosed with FGC with CDH1 mutation (Table 1). All cases with FGC were diffuse-type by Lauren classification, and only one harbored germline mutations of CDH1 (c.2638G > A); the remaining 12 had known somatic CDH1 mutations. No FGC patients met the clinical criteria or histologic features of HDGC. Unexpectedly, we found germline mutations of CDH1 in 6 patients without a family history of GC. Among all patients with CDH1 mutation, there was no significant survival difference between patients with family history or FGC (Fig. 4). In the 847 patients without CDH1 mutation, 189 (22.3%) had a family history of GC in one of their first relatives, and 92 patients (10.9%) were diagnosed as FGC (Table 2). We could not find any statistical significance in CDH1 mutations with family history of GC ($p > 0.05$).

Discussion

Although familial aggregation is found in about 10% of GC cases [25], the incidence of CDH1 alterations in patients with or without family history of GC is unclear. We explored CDH1 alterations with NGS and investigated the association with family history in 993 GC patients. We found that occurrence of CDH1 mutation was not significantly associated with family history.

After the first report of germline CDH1 mutation in GC [37], various types of CDH1 mutations have been reported in HDGC or diffuse type GC by polymerase chain reaction and sequencing [3–7] aided with multiplex ligation-dependent probe amplification [8–11] or high-resolution melting analyses [30] from patients with FGC, HDGC, or EOGC. CDH1 germline mutations were identified in 10% of FGC cases [10, 11], 0 ~ 19% of HDGC cases [3–5, 8] and 0 ~ 8.9% [5–7, 9] of EOGC cases [6], as well as in 1.7% of patients with sporadic GC [12]. With NGS, somatic mutations of CDH1 are found in 9%~36% of GC cases [16–22] and are highly prevalent in sporadic EODGC (53.2% of cases). Somatic CDH1 mutation has also been suggested as a poor prognostic marker in diffuse-type GC [17, 22, 23]. The previously reported germline and somatic CDH1 mutations detected in patients with gastric cancer by various

technologies are summarized in Table 4. Although a few studies have investigated the frequency and impact of CDH1 mutations in HDGC and EODGC [9, 10, 17, 24], the incidence of CDH1 mutations in sporadic GC patients with or without family history is unclear [25]. To the best of our knowledge, this is the first study exploring CDH1 mutations in association with family history. Our results showed that CDH1 mutations are not influenced by family history.

Table 4
CDH1 mutations found in patients with gastric cancer

Mutation Type	Number of samples	Country	History	Method	Frequency	References
Somatic	32	Chinese	Signet-ring cell carcinoma: sporadic	WGS	15.60%	[16]
Somatic	109 EOGC 115 LOGC	Korean	DGC	WES/RNA sequencing	early 53.2%, late 36.0%	[17]
Somatic	200	Hong Kong	100 pairs of GC	WGS	10%	[18]
Somatic	87	Japan	DGC	WES	32%	[19]
Somatic	22	Hong Kong	GC	WES	9%	[20]
Somatic	295	TCGA data	GC	WES/RNA sequencing	11%	[21]
Sporadic	544	Chinese	DGC	Targeted sequencing	11.60%	[22]
Germline	499 families, 578 individuals	Netherlands	HDGC	PCR, Sanger sequencing	HDGC, 13.5%	[3]
Germline	183	Portugal	HDGC	Cancer panel, MLPA	19%	[8]
Germline	25 EODGC 23 HDGC	Korean	EODGC HDGC	PCR, MLPA	EODGC, 8% (2 cases) HDGC, 4.3% (1 case)	[9]
Germline	236 GC: 175 sporadic, 61 hereditary, 240 cancer free	Chinese	Sporadic	PCR, HRM analysis	1.70%	[12]
Germline	22	Italy	EOGC	Direct sequencing	8.90%	[6]
Germline	86	Poland	HDGC	Sanger sequencing	0	[4]
Germline	HDGC 9 EODGC 16	Portuguese	HDGC EOGC	PCR-SSCP	HDGC, 11.1% (1 case) EODGC – 0	[5]
Germline	66	North America	EOGC	PCR-SSCP	7.60%	[7]
Germline	6 families, 19 patients	Korean	FDGC	PCR-SSCP	10.06%	[10]
Germline	6 families, 30 patients	Caucasian	FGC	PCR-SSCP	10%	[11]
GC gastric cancer, DGC diffuse gastric cancer, HDGC hereditary diffuse gastric cancer, EODGC early-onset diffuse gastric cancer, EOGC early-onset gastric cancer, LOGC late-onset gastric cancer, FGC familial gastric cancer, WGS whole genome sequencing, WES whole exome sequencing, PCR polymerase chain reaction, MLPA multiplex ligation-dependent probe amplification, SSCP single-strand conformation polymorphism						

In the present study, we identified 146 CDH1 mutations in 993 patients. Eight CDH1 mutations were germline (0.8%, 8/993), and this incidence is similar to a previous study in a Chinese population (1.7%, 4/236), the only study investigating CDH1 germline mutation in sporadic GC patients [12]. In previous studies in EODGC patients, CDH1 germline mutation rates were higher in Korean (8%, 2/25) [9] and Italian populations (7.2%, 19/264) [6]. In a meta-analysis study, GC occurring in a high-prevalence area harbored less frequent CDH1 germline mutations than that in a low-incidence area [2]. Based on these observations, our low incidence of CDH1 germline mutations may be due to patient age (more frequent CDH1 germline mutations in younger patients) and because the present study was performed in a GC-prevalent area.

In GC-prevalent areas, the ratio of missense mutations was higher than that of non-missense (deletion, insertion, truncating, and nonsense) mutations [2]. In addition, non-missense mutations were reported to be likely pathogenic compared with missense mutations. We also found that the frequency of missense mutation was higher (67.8%) compared with that of non-missense mutation, and this result is similar to the previous analysis. A recent comprehensive genomic study demonstrated that RhoGAP domain-containing fusions or PPAPDC1A fusions, which are mostly somatic mutations, are common in GC of diffuse-type [38]. In addition, germline mutations in genes such as CTNNA1 were observed at a similar frequency as CDH1 germline mutation [39]. These findings suggest that GC might be frequently caused by somatic mutations rather than germline alterations of CDH1 in GC-prevalent areas such as Korea, as previously suggested [2].

Unlike previous studies that focused exclusively on HDGC patients, we compared the distribution of CDH1 alterations in patients with and without family history of GC. As a result, most CDH1 alterations in both groups were somatic mutations. Thus, CDH1 somatic mutation appears to play a more important role than germline mutation regardless of family history;

The limitation of this study is that the patient's family history was investigated only through electronic medical records. Therefore, the age of onset and histological information of GC in the patient's family could not be accurately identified. In addition, there is a possibility of missed records. Further studies might be required to analyze the family information about GC more in detail with pedigree analysis.

Conclusions

In conclusion, we found 146 CDH1 mutations in 14.7% of GC patients. CDH1 mutations were not associated with family history. Rare germline mutations in sporadic and familial GC patients suggest that somatic CDH1 mutation may play an important role in pathogenesis of GC in GC-prevalent areas.

Abbreviations

GC: Gastric cancer; HDGC: hereditary diffuse gastric cancer; FGC: Familial gastric cancer; EOGC: Early-onset gastric cancer; NGS: Next-generation sequencing; EODGC: Early-onset diffuse-type gastric cancer; FFPE: Formalin-fixed paraffin-embedded; SNV: Single nucleotide variants; Indels: Insertion and deletions; SNP: Single nucleotide polymorphisms; NCBI: National Center for Biotechnology Information; HGMD: Human Gene Mutation Database; gnomAD: Genome Aggregation Database; dbSNP: single nucleotide polymorphism database; COSMIC: Catalogue of Somatic Mutations in Cancer; TCGA: The Cancer Genome Atlas; OS: Overall survival; VAF: Variant allele frequency;

Declarations

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Author's contributions

JWK and KMK conceived and designed the study. JJ, YJH, and SYK performed data analysis. SC generated tables and figures. SC and JJ drafted the manuscript. STK, JL, WKK, JWK, and KMK revised the manuscript and contributed to knowledge.

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Availability of data and materials

All data generated or analyzed during this study are included in this published article.

Ethics approval and consent to participate

The Institutional Review Board of Samsung Medical Center approved this study and waived informed consent.

Consent for publication

Not applicable

Competing interests

The authors declare no competing interests.

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Figures

Figure 1

Flow charts of CDH1 variants filtered by public databases

A

Mutation Type	Samples	
	N	%
A>C	6	4.11%
A>G	18	12.33%
A>T	6	4.11%
C>A	7	4.79%
C>T	13	8.90%
C>G	4	2.74%
G>A	18	12.33%
G>C	8	5.48%
G>T	10	6.85%
T>A	7	4.79%
T>C	7	4.79%
T>G	8	5.48%
other	34	23.29%
Total numbers	146	100.00%

B

Mutations		Samples	
		n	%
SNV	Nonsynonymous	99	67.8%
	Stopgain	14	9.6%
Frameshift	Deletion	12	8.2%
	Insertion	4	2.7%
	Substitution	1	0.7%
Nonframeshift	Deletion	15	10.3%
	Substitution	1	0.7%
Total		146	100.0%

Figure 2

(A) Distribution of nucleic acid changes in CDH1 mutations. (B). Distribution of amino acid change

Figure 3

Distributions of somatic mutations within the CDH1 gene. The figure was created using the cbiportal mutation mapper program. (https://www.cbiportal.org/mutation_mapper)

Figure 4

Overall survival of gastric cancer patients with CDH1 mutation with and without family history

Supplementary Files

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- [Supplementarydata.xlsx](#)