Germline variants and phenotypic spectrum in a Canadian cohort of individuals with diffuse gastric cancer

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ABSTRACT

Background CDH1 pathogenic variants (pv) cause most cases of inherited diffuse gastric cancer (DGC), but have low detection rates and vary geographically. In the present study, we examined hereditary causes of DGC in patients in Ontario.

Methods CDH1 testing through single-site or multi-gene panels was conducted for patients with DGC meeting the 2015 International Gastric Cancer Linkage Consortium (IGCLC) criteria, or with isolated DGC at less than 50 years of age, or with a strong family history of cancer identified at the Zane Cohen Centre (ZCC). All CDH1-positive patients at ZCC, regardless of cancer history, were summarized.

Results In 15 of 85 patients with DGC (17.6%), a pv or likely pv was identified through CDH1 single-site (n = 43) or multi-gene panel (n = 42) testing. The detection rate was 9.4% overall (8 of 85) and 11% using IGCLC criteria (7 of 65). No CDH1 pvS were identified in patients with isolated DGC at less than 40 years of age, but 1 pv was identified in a patient with isolated DGC at less than 50 years of age. Multi-gene panels identified 9 pvS (21.4%), including CDH1, STK11, ATM, BRCA2, MLH1, and MSH2. Review of 81 CDH1 carriers identified 10% with DGC (median age: 48 years; range: 38–59 years); 41% were unaffected (median age: 53 years; range: 26–89 years). Observed malignancies other than DGC or lobular breast cancer (LBC) included colorectal, gynecologic, kidney or bladder, prostate, testicular, and ductal breast cancers. Lobular-breast cancer was seen only in 3 families.

Conclusions In Ontario, the detection rate of CDH1 pvS in patients with DGC was low: no pvS were identified in patients with isolated DGC at less than 40 years of age, and 1 was identified in a patient with isolated DGC at less than 50 years of age. Isolated LBC with no DGC was observed in CDH1-positive families, as were pathology-confirmed non-DGC or non-LBC malignancies, which had not previously been reported. Given a phenotype that overlaps with other hereditary conditions, multi-gene panels are recommended for all patients with DGC at less than 50 years of age and for those meeting IGCLC criteria.

Key Words Hereditary diffuse gastric cancer; HDGC; early-onset disease; breast cancer, lobular

INTRODUCTION

Gastric cancer arises in 1 of 3500 Canadians yearly¹. Hereditary gastric cancer is rare: 10% of individuals with gastric cancer have a positive family history, but only 1%–3% are found to have a hereditary condition². The most common hereditary condition associated with diffuse-type gastric cancer (DGC) is hereditary diffuse gastric cancer syndrome (HDGC), which is caused by a heterozygous germline pathogenic or likely pathogenic variant (pv) in the CDH1 gene. The syndrome is associated with a lifetime risk for DGC of 70% in men and 56% for women, and a risk for lobular breast cancer (LBC) in women of 42%³. The penetrance of DGC declines when clinical CDH1 families are not ascertained based on multiple cases of DGC, with the cumulative risk up to age 80 for gastric cancer being 42% for men and 33% for
women, and for LBC being 55%\(^4\). Signet-ring-cell colorectal cancer\(^2\) has been associated with CDH1 variants, as have cleft lip and palate\(^6,7\). The incidences of intestinal-type gastric cancer and ductal breast cancer are not described to be higher in HDGC\(^8\).

In 2015, genetic testing criteria for CDH1 were updated by the International Gastric Cancer Linkage Consortium (IGCLC)\(^9\) to include affected individuals in families with

- 2 gastric cancers at any age, 1 confirmed as DGC; or
- DGC diagnosed at less than 40 years of age (DGC<40), regardless of family history; or
- personal or family history of DGC and LBC (1 diagnosed at less than 50 years of age).

Those criteria were revised from earlier versions outlined in 1999 and 2010 so as to broaden the eligibility of families with DGC. As a result, the detection of CDH1 pvs declined to approximately 10%–20% from 25%–30% based on the original criteria\(^8,10\). To date, more than 150 CDH1 pvs have been reported in HDGC\(^11\).

Although CDH1 is the most common cause of hereditary DGC, other hereditary conditions have been associated with DGC, including pvs in CTNNA1 and BRCA2; Lynch syndrome caused by mismatch repair genes; and Li–Fraumeni syndrome and polyposis conditions such as familial adenomatous polyposis, Peutz–Jeghers syndrome, and juvenile polyposis\(^3,12\). Still, causes in most families suspected of having a hereditary DGC syndrome remain unidentified.

Because the prevalence of CDH1 variants can vary geographically, studying the detection rate in various populations is important. The aim of the present study was to determine the frequency of CDH1 and other germline pvs in individuals with DGC who underwent genetic testing in Ontario and to summarize the phenotype of a large cohort of CDH1-positive carriers from the only Canadian clinical gastrointestinal cancer registry.

**METHODS**

Individuals with gastric cancer referred for genetic consultation at the Zane Cohen Centre (zcc) for Digestive Diseases at the Sinai Health System, Toronto, Ontario, between 1997 and 2018 were identified from a prospectively maintained database. The Familial Gastrointestinal Cancer Registry at the zcc is the only active hereditary gastrointestinal cancer registry in Canada\(^13\). Individuals with a pathology confirmation of DGC were offered genetic testing if they met zcc eligibility criteria: DGC diagnosed at less than 50 years of age (DGC<50), family history meeting IGCLC criteria, or family history suggestive of other hereditary cancer syndromes. Before 2016, genetic testing included CDH1 sequencing and deletion or duplication testing by multiplex ligation-dependent probe amplification and by single-site testing for other hereditary conditions based on family history. Families tested after 1 January 2016 were offered multi-gene panels processed using next-generation sequencing. Those panels included these genes at minimum: CDH1, CTNNA1, APC, MUTYH, mismatch repair genes, STK11, BMPR1A, SMAD4, BRCA1/2, and PALB2. Attempts at re-contact with individuals tested before 2016 were made to offer updated testing. All individuals who accepted underwent CDH1 screening through either single-site or multi-gene testing. For all individuals tested, a 3-generation family history was obtained.

The Familial Gastrointestinal Cancer Registry prospectively follows individuals identified with CDH1 pvs. Biennial follow-up includes results of Helicobacter pylori testing, development of malignancy, prophylactic surgery, and oncologic resection. The present study was approved by the Mount Sinai Hospital institutional ethics review board.

**RESULTS**

**Genetic Testing for Individuals with DGC**

In the zcc database, 208 individuals diagnosed with gastric cancer were identified, of whom 124 had pathology-confirmed DGC. Of those 124 patients, 119 met genetic testing criteria, but 34 did not consent to genetic testing or died before testing could occur. Genetic testing was performed for 85 individuals from 80 families when they met either the IGCLC criteria (n = 65), the zcc criteria of isolated DGC diagnosed at 40–49 years of age (n = 14), or DGC diagnosed at 50 or more years of age with family history suggestive of a hereditary condition (n = 6). In 43 individuals, testing consisted of single-site CDH1 sequencing and multiplex ligation-dependent probe amplification; in 42 individuals, it consisted of a multi-gene panel.

Ethnicity was available for 83 of the 85 patients, with 48% reporting European ancestry (n = 40), 24% Asian ancestry (n = 20), and 9% Canadian ancestry (n = 8), including First Nations, French Canadian, and Newfoundland. The remaining 19% of families were ethnically Middle Eastern (n = 5), African (n = 5), Ashkenazi Jewish (n = 4), and Latino (n = 1).

The 15 pvs or likely pvs identified in 85 individuals with DGC meeting eligibility criteria (17.6%) included 8 CDH1 pvs or likely pvs, and 7 pvs leading to other hereditary conditions. Of the 8 CDH1 variants identified in this cohort (9.4%), 6 were found through single-site testing, and 2 (1 pv, 1 likely pv), through a multi-gene panel. The multi-gene panel testing (42 individuals) identified 9 pvs or likely pvs (21.4%), including ATM (n = 1), CDH1 (n = 2), BRCA2 (n = 2), MLH1 (n = 1), MSH2 (n = 2), and STK11 (n = 1). Table I summarizes the demographics and variant results for the positive families. Table II summarizes genetic testing results for the entire cohort by age and eligibility criteria.

In the 65 individuals who met the IGCLC criteria, the positive CDH1 diagnostic yield was 10.8% (n = 7). No mutations were identified in individuals meeting the criterion of isolated DGC<40 (n = 18), or in individuals with LBC and DGC (n = 3), or in those meeting the combined criteria of LBC and DGC<40 (n = 1).

Notably, 1 individual in the group 40–49 years of age who was diagnosed with isolated DGC did not meet the IGCLC criteria, but rather met the sole zcc criterion of isolated DGC<50. Of the individuals meeting the IGCLC criteria, 4 were noted to also have other variants with hereditary implications, including BRCA2, MLH1, and ATM. Figure 1 outlines the IGCLC criteria, showing a breakdown of sole and group criteria met by the families and the resulting germline genetic results.
| ID | Ethnicity | Gene | Variant | Cancer diagnosis | Other history of cancer | Unaffected CDH1 carriers | Reference |
|----|-----------|------|---------|-----------------|------------------------|--------------------------|-----------|
|    |           |      |         | Proband         | Known or obligate carriers | (n) | Age (years) | IGCLC criteria |          |
|    |           |      |         | Type | Age (years) | Type | Age (years) | Type | Age (years) |                  |
| 1  | Italian   | CDH1 | EX16del (novel) | DGC | 49 | Ductal BCa, ovarian, ovarian | 49 | 27, 52, 59 | Brain, ovarian | None |
| 2  | Italian   | CDH1 | EX16del (novel) | DGCx3, Testicular | 47 | 27, 37 | Ductal BCa, ovarian, ovarian, DGC | 49 | 72 | Prostate, Gastric NOS, Bladder, Ovarian, BCa NOS | 1 |
| 3  | German    | CDH1 | c.187C>T | DGC, Lobular BCa | 57 | 50 | Lobular BCa, Lobular BCa, CRC, Prostate, Lobular BCa, Lobular BCa | 29, 63 | 51 | CRCx3, Bladder, Endometrial, CRCx2, Ureterx2, Prostate | 1, 3 |
| 4  | Chinese   | MLH1 | c.1558+1G>A | DGCx2 | CRC | 77 | 77 | CRCx2, CRC, Bladder | 70 | 63, 70 | CRC (multiple) | 1 |
| 5  | White     | MSH2 | c.1165C>T | DGC, CRC, Bladder | 70 | 63, 70 | Endometrial | 57 | CRC (multiple) | NA |
| 6  | Ashkenazi | Jewish | MSH2 | c.1906G>C | DGC | CRC Prostate | 68 | 33, 67, 77 | NA | None |
| 7  | Japanese  | CDH1 | c.1212delC | DGC, DGC | 44 | 59 | Lobular BCa, Lobular BCa, CRC, Prostate, Lobular BCa, Lobular BCa | 29, 53, 55, 56, 57 | 42 | CRC, Gastric NOSx3, Bladder | 1, 3 |
| 8  | British   | STK11 | c.910C>T | DGC, Lobular BCa | 67 | 64 | Lobular BCa | 51 | 51 | Gastric NOSx2 | NA |
| 9  | British   | CDH1 | c.1901C>T | DGC | 38 | Lobular BCa, Lobular BCa, CRC, Prostate, Lobular BCa, Lobular BCa | 27, 27 | 53, 57 | Gastric NOS, DGC | 1 |
| 10 | French    | CDH1 | c.2100delT | DGC | 38 | Lobular BCa, Lobular BCa, LCIS, DCIS | 47 | 52 | BCa, Gastric NOS | 1 |
| 11 | Italian   | CDH1 | EX1_2del | DGC | 42 | Lobular BCa, Lobular BCa, DGC, Lobular BCa, LCIS, DCIS | 47 | 52 | BCa, Gastric NOS | 0 |

**Table I** Demographic and genetic information from 15 patients with mutation-positive diffuse gastric cancer (DGC).
### TABLE I  Continued

| ID  | Ethnicity | Gene | Variant | Cancer diagnosis | Other history of cancer | Unaffected CDH1 carriers | IGCLC criteria | Reference<sup>b</sup> |
|-----|-----------|------|---------|------------------|-------------------------|--------------------------|----------------|---------------------|
|     |           |      |         |                  |                         |                          |                |                     |
|     |           |      |         |                  |                         |                          |                |                     |
| 12  | Italian   | CDH1 | EX1_2del | DGC, Lobular BCa |                         |                          |                |                     |
|     |           |      |         |                  |                         |                          |                |                     |
|     |           |      |         |                  |                         |                          |                |                     |
| 13  | Italian   | BRCA2| c.6591_6592delTG | DGC                  |                         |                          |                |                     |
|     |           |      |         |                  |                         |                          |                |                     |
|     |           |      |         |                  |                         |                          |                |                     |
| 14  | Ashkenazi Jewish | ATM | c.5932G>T | DGC                  |                         |                          |                |                     |
|     |           |      |         |                  |                         |                          |                |                     |
|     |           |      |         |                  |                         |                          |                |                     |
| 15  | Chinese   | BRCA2| c.7480C>T | DGC                  |                         |                          |                |                     |
|     |           |      |         |                  |                         |                          |                |                     |
|     |           |      |         |                  |                         |                          |                |                     |

<sup>a</sup> (1) Diagnosis of 2 gastric cancers not otherwise specified, with 1 confirmed DGC at any age; (2) diagnosis of DGC at less than 40 years of age; (3) diagnosis of DGC and lobular breast cancer, 1 diagnosis at less than 50 years of age.

<sup>b</sup> If variant was previously reported in other families.

PTG = prophylactic total gastrectomy; IGCLC = International Gastric Cancer Linkage Consortium; BCa = breast cancer; NOS = not otherwise specified; CRC = colorectal cancer; NA = not applicable.

### TABLE II  Detection of CDH1 and other genes in all patients with diffuse gastric cancer (DGC) by age and International Gastric Cancer Linkage Consortium (IGCLC) criteria

| Age at DGC diagnosis | IGCLC criteria | CDH1 detection | Other genes | Detection rate (%) |
|----------------------|----------------|----------------|-------------|-------------------|
|                      | (A)            | (B)            | (C)         | Tested (n) Pathogenic variants (n) Detection rate (%) |
|                      | 2 Gastric cancers NOS, with 1 being DGC | DGC at <40 years | Lobular BCa and DGC, 1 at <50 years | Tested (n) Pathogenic variants (n) Detection rate (%) |
| <40 Years            | √ Only         | √              | ±√          | 17 0 0 10 0 0 4 1 (BRCA2) 25 |
| 40–49 Years          | —              | —              | —           | 14 1 7 8 0 0 5 1 (BRCA2) 20 |
| ≥50 Years            | —              | —              | —           | 5 0 0 4 3 (2 MSH2, 1 STK11) 80 |
| TOTAL                | 85             | 8              | 42<sup>a</sup> 7 |

<sup>a</sup> Of 85 individuals, 42 underwent multigene testing.

NOS = not otherwise specified.
GERMLINE VARIANTS AND PHENOTYPIC SPECTRUM IN DGC, Aronson et al.

**DISCUSSION**

In the present study, we report the results of genetic testing for hereditary causes of DGC in a large Canadian cohort. In our series of 85 individuals with DGC meeting the ZGCC criteria of isolated DGC diagnosed at 40–49 years of age or meeting the IGCLC criteria, or with DGC diagnosed at 50 years of age or older and a family history suggestive of a hereditary cancer syndrome, we identified 15 (17.6%) with PVs or likely PVs, with more than half the variants (n = 8) being found in CDH1 (9.4%). Overall, we identified 65 individuals who met the 2015 IGCLC eligibility criteria, in whom the CDH1 mutation detection rate was 10.8% (n = 7). We found 1 HDGC carrier missed by the IGCLC criteria who was diagnosed with DGC at 49 years of age (no other DGC or LBC had been reported in the family at the time of diagnosis).

Our CDH1 mutation detection rate of 10.8% in Ontario patients who met the 2015 IGCLC criteria is slightly lower than rates reported in other countries with populations having a low incidence of gastric malignancies. In 1999, criteria for CDH1 genetic testing were published. Families were included if they had 2 cases of pathologically confirmed DGC in 1st- or 2nd-degree relatives, 1 DGC<50, or 3 or more pathology-confirmed DGC cases in 1st- or 2nd-degree relatives regardless of age. Those criteria were developed based on the understanding of CDH1 developed from highly penetrant families in New Zealand, leading to an ascertainment bias. Using those original criteria, the CDH1 detection rate was reported to be 25%–50%. In 2010, the criteria were revised based on the acknowledged difficulty.
### TABLE IV  Remaining 12 families in the registry who were CDH1-positive

| ID  | Ethnicity         | Variant                  | Cancer diagnosis                          | Other history of cancer                  | Unaffected CDH1 carriers | IGCLC criteria<sup>a</sup> | Reference<sup>b</sup> |
|-----|------------------|--------------------------|-------------------------------------------|------------------------------------------|--------------------------|---------------------------|-------------------------|
| 16  | Iranian          | c.2029C>T (novel, likely pathogenic) | Lobular BCa | 46 | BCa NOS, Prostate, Leukemia, Kidney | 1, 2<sup>c</sup> | None |                           |
| 17  | Pakistani        | c.1792C>T                | 58 | Gastic NOSx2, BCa NOS | 40 | 1, 2<sup>c</sup> | Gayther et al., 1998<sup>14</sup> |
| 18  | White            | c.1792C>T                | BCa NOS, Gastic NOSx2, Lobular BCa, Urethral | 34 | 1, 2<sup>c</sup> | Caldas et al., 1999<sup>23</sup> |
| 19  | Italian          | c.832+1G>A                | Lobular BCa, BCa NOS | 41, 50 | Esophageal, BCa NOSx2 | 3 | 35, 47, 69 | None | Oliveira et al., 2002<sup>26</sup> |
| 20  | Ashkenazi Jewish | c.2398delC               | 29 | None | 1, 2<sup>c</sup> | Oliveira et al., 2002<sup>26</sup> |
| 21  | White            | c.2398delC               | CRC | 77 | Gastric NOSx3, BCa NOS, Esophageal | 56 | 1, 2<sup>c</sup> | Oliveira et al., 2002<sup>26</sup> |
| 22  | White            | c.2398delC               | CRC | 77 | Gastric NOSx4, Gastric NOS | 63 | 1, 2<sup>c</sup> | Oliveira et al., 2002<sup>26</sup> |
| 23  | Canadian (NL)    | c.2398delC               | 28, 29, 48 | Unknown primary, BCa NOS | 64 (with PTG at 54) | 1, 2<sup>c</sup> | Brooks-Wilson et al., 2004<sup>4</sup> |
| 24  | Jordanian        | c.1137G>A                | Lobular BCa | 50 | Unknown primary, Gastric NOS, Leukemia, GEJx2 | 42 | 3 | Oliveira et al., 2006<sup>27</sup> |
| 25  | Canadian (NL)    | c.1189A>T                | Lobular BCa | 48, 28 | None |                           |                           | Hansford et al., 2015<sup>1</sup> |
| 26  | White            | c.2100delT               | Gastric NOS, CRC, Lobular BCa, Bladder, Kidney, Prostate | 35, 46, 54, 50s, 65, 71, 80 | DGC, CRC, BCa NOSx4, Gastric NOS | 53, 53, 62, 88 | 1, 2, 3 | Hansford et al., 2015<sup>1</sup> |
| 27  | British          | c.1064dupT               | DGC, Gastric NOS | 40 | 1, 2 | Hansford et al., 2015<sup>1</sup> |

<sup>a</sup> Diagnoses of 2 gastric cancers not otherwise specified, with 1 confirmed DGC at any age; (2) diagnosis of DGC at less than 40 years of age; (3) diagnosis of DGC and lobular breast cancer, 1 diagnosis at less than 50 years of age.

<sup>b</sup> If variant was previously reported in other families.

<sup>c</sup> Even though the gastric cancer pathology unavailable, families were known to have multiple cases of gastric cancer and were known to have published founder mutations with DGC confirmed. The IGCLC criteria were based on the relevant references.

DGC = diffuse gastric cancer; PTG = prophylactic total gastrectomy; IGCLC = International Gastric Cancer Linkage Consortium; BCa = breast cancer; NOS = not otherwise specified; GEJ = gastroesophageal junction; CRC = colorectal.
in obtaining pathology confirmation for multiple cases of DGC in the family and included 3 cases of DGC in a family, 1 confirmed by pathology, 2 cases of DGC, 1 confirmed by pathology and being DGC<50; a case of DGC<40 regardless of family history; or individuals with a personal or family history of DGC and LBC, 1 case diagnosed at less than 50 years of age. In 2015, the first two criteria were collapsed to include 2 cases of DGC at any age, 1 pathology-confirmed to be DGC. The remaining criteria of isolated DGC<40 or of DGC and LBC, 1 diagnosed at less than 50 years of age, remained the same. Given the slight difference between the 2010 and 2015 criteria, an evaluation considering both found comparable sensitivity, with decreased specificity for the 2015 version. Benusiglio et al. found CDH1 mutations in 19% of probands in France meeting the criteria (41 of 216), and van der Post et al. reported a mutation rate of 14% for individuals in the Netherlands who met testing criteria (16 of 118). The highest positive CDH1 detection rates have occurred in areas with known founder mutations, such as Newfoundland and New Zealand. To date, a few small series are investigating CDH1 mutations in populations with high incidences of gastric cancer, reporting relatively low positive yields of 7% (Japanese population) and 8% (Korean population). We examined each criterion from the 2015 IGCLC recommendations individually and then in combination to determine the most effective criteria. The highest yield of CDH1-positive detection using a single criterion was 2 cases of DGC in a family, where 2 of 26 tested positive for CDH1 mutation (7.7%). Using criteria in combination, the highest yield occurred in families with multiple cases of DGC with or without LBC and with early age of onset. In our cohort, 5 of 16 individuals (31%) from families with either 2 cases of DGC (1 being DGC<40) or 2 cases of DGC and LBC (1 being diagnosed at less than 50 years of age) were found to have pathogenic CDH1 variants. The combination of family history and early age of onset was shown to be most effective considering the positive rates in the original 1999 criteria. That finding was also supported when comparing the 2010 with the 2015 criteria, where a high CDH1 detection rate of 39%–42% was observed in individuals having family history of DGC with or without LBC and with a young age of onset. The detection rate dropped to 28% once the age restriction was removed.

The least successful single criterion in our cohort was the sole criterion for DGC<40. No mutation was identified in those patients. More than half our mutation-positive index cases (5 of 8) were diagnosed with DGC between ages of 40 and 49 years. In our larger cohort of CDH1 carriers, the median age of diagnosis with invasive DGC was 48 years. That age of onset is older than the median age of 40 years cited in previous reports, but it might be reflective of a clinical population in a low-incidence country that lacks some of the early ascertainment biases, and it is more comparable with similar studies reporting an age of DGC onset of 46.7 years. Sporadic gastric cancer rarely affects young people, and only 5% of cases are diagnosed at less than 40 years of age. The underlying cause of isolated DGC<40 is not well-understood, and geographic differences might be a factor affecting the mutation rate in young patients with DGC. Hakkaart et al. reported that, in New Zealand, 67% of individuals from the Maori population diagnosed with DGC at less than 45 years of age had a CDH1 mutation. The authors hypothesized a survival advantage of CDH1 mutation, with carriers having an innate resistance to the foodborne pathogen *Listeria monocytogenes*, which has been linked to gastroenteritis, meningitis, and miscarriage. Other studies have reported a low yield of mutations in isolated DGC<40, with the exception of Benusiglio et al., who reported a 15% positive pick-up rate of CDH1 in patients with isolated early-onset DGC. Although the criterion of isolated DGC<40 was not successful at identifying CDH1 carriers in our patients, the ZCC criteria of isolated DGC<50 was able to identify a carrier who would have been missed by the IGCLC criteria. Given certain of our observations (the lack of mutations in individuals with DGC<40, the small increase in the number of patients with DGC diagnosed between 40 and 49 years of age, and evidence of an older onset of DGC in the HDGC cohort), it is worth considering whether the age limit for the criterion of DGC<40 should be increased to 50 years of age.

*H. pylori* has long been seen as the most significant risk factor associated with intestinal-type gastric cancer. It has increasingly been associated with DGC, and recent studies in Italian, Japanese, Indian, and Korean populations suggest that it may contribute to early-onset DGC, especially in individuals with current infections. In our series, *H. pylori* was identified in 13 of 20 individuals with DGC<40 (65%). The estimated rate of *H. pylori* seropositivity in the Ontario population is less than 25%, and although causation cannot be determined, that rate would seem to support the role of *H. pylori* infection, possibly in conjunction with a host-related factor, as leading to early-onset DGC not explained by known disease susceptibility genes.

Positive family history of DGC or of DGC and LBC was an important factor in the CDH1 detection rate, with 14 of 18 CDH1-positive families in our series meeting those IGCLC criteria. The exceptions were 3 families having a history of LBC only, and 1 family with a case of DGC diagnosed at 49 years of age and no other history of DGC or LBC. Notably, although the latter family did not have the hallmark cancers of HDGC, known carriers in the family had been diagnosed with brain, testicular, ovarian, endometrial, and ductal breast cancers at younger ages. We also reported the lack of a personal history of cancer in 41% of CDH1 carriers (*n* = 33; median age: 53.5 years; range: 26–89 years), which might contribute to a lack of family history when kin are still young. Other challenges in fulfilling the testing criteria include limited knowledge of cancer diagnoses, lack of pathology confirmation, possible inaccurate diagnoses (gastroesophageal junction or esophageal cancer), and new diagnoses that might arise after the index case is first assessed.

Pathogenic CDH1 variants were identified in 4 families presenting with LBC only. After 3-generation pedigrees were obtained, only 1 case of DGC was identified. Traditionally, families with LBC in the absence of DGC have not been considered at high risk for CDH1 mutations, but incidental mutations have been identified in such families with the increased use of multi-gene panels. Nicula et al. recently reported that 36% of 113 HDGC families had cases of breast cancer in the absence of a family history of
gastric cancer, noting that full pedigrees were available on 38 families. Whether the genotype–phenotype correlation from variants identified in LBC-only families is associated with a reduced risk of DGC is unknown. However, caution is advised because an extensive family history might reveal DGC, and online databases might report DGC associated with those particular variants in other families. Several studies describe LBC-only families that are found to have signet-ring-cell carcinoma on endoscopy or examination of the resected specimen after prophylactic total gastrectomy. Published case reports might also provide information leading an evolved understanding. For example, one of our LBC-only families having the variant c.832+1G>A had no DGC history. However, that particular variant has been reported in a family with DGC diagnosed at 40 years of age and with 3 relatives affected by gastric cancer at ages 36, 48, and 50 years.

Several other inherited syndromes have been associated with DGC, including Lynch syndrome, Peutz–Jeghers syndrome, juvenile polyposis, Li–Fraumeni syndrome, and familial adenomatous polyposis. Hansford et al. identified PVs in CTNNA1 and BRCA2, and likely or possible PVs in MSRI, PRSSI, and in DGC families who were tested using a 55-gene comprehensive panel. Indeed, we identified 7 families with other hereditary cancer predisposition genes (Peutz–Jeghers syndrome, n = 1; Lynch syndrome, n = 3; BRCA2, n = 2; and ATM, n = 1), 4 of whom met IGCLC criteria. The families with the ATM and MLH1 mutations met IGCLC criteria, as did both families with pathogenic BRCA2 variants, 1 member of which was a 19-year-old with DGC who had 5 close relatives with early-onset gastric cancer (no breast cancer reported). Three families did not meet IGCLC criteria, but were tested based on family histories suggestive of hereditary conditions, namely Lynch syndrome and Peutz–Jeghers syndrome. The individual with the pathogenic STK11 mutation presented with 2 primary LBCs and DGC; however, the malignancies were diagnosed after 50 years of age, thereby not meeting the IGCLC criteria because of the age limitation. Although the patient underwent genetic testing because of mucopigmentation, the case highlights an overlapping of the phenotype with various hereditary syndromes and supports the need for multi-gene panel testing in at-risk families.

Our study has important limitations that warrant mention. Although this study is the first of hereditary DGC in Ontario, it is limited by the small number of patients with DGC. Another limitation was that only single-site CDH1 testing was performed for members in the earlier part of the cohort, and although attempts were made to retest individuals with larger multi-gene panels, many whom we tried to contact were deceased.

CONCLUSIONS

In individuals meeting IGCLC criteria, we found detection rates for CDH1 PVs that were lower than previously reported, and no CDH1 PVs in individuals with DGC<40 as the sole eligibility criterion. We added to the literature observing LBC in the absence of DGC within CDH1-positive families despite obtaining 3-generation pedigrees, supporting the need to better integrate that phenotype into the CDH1 diagnostic criteria. We also reported on pathology-confirmed malignancies in CDH1 carriers not previously associated with HDGC patients. In CDH1 carriers, DGC was observed at a slightly older age of onset, prompting our suggestion that age as the sole criterion in DGC be raised to 50 years from 40 years. Multi-gene panel testing is the recommended testing method, because several syndromes—such as Peutz–Jeghers syndrome—have been linked to both DGC and LBC and could have overlapping phenotypes. Despite comprehensive testing, most patients with high-risk DGC have no identifiable hereditary cause for their cancer. More research is needed to elucidate novel genes and risk factors for DGC.

CONFLICT OF INTEREST DISCLOSURES

We have read and understood Current Oncology's policy on disclosing conflicts of interest, and we declare that we have none.

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