ABSTRACT

BRCA1 and BRCA2 are the most important breast and ovarian cancer susceptibility genes. Biallelic mutations in BRCA2 can lead to Fanconi anemia and predisposition to cancers, whereas biallelic BRCA1 mutations have not been confirmed, presumably because one wild-type BRCA1 allele is required during embryogenesis. This study describes an individual who was diagnosed with ovarian carcinoma at age 28 and found to have one allele with a deleterious mutation in BRCA1, c.2457delC (p.Asp821Ilefs*25), and a second allele with a variant of unknown significance in BRCA1, c.5207T>C (p.Val1736Ala). Medical records revealed short stature, microcephaly, developmental delay, and significant toxicity from chemotherapy. BRCA1 p.Val1736Ala cosegregated with cancer in multiple families, associated tumors showed loss of wild-type BRCA1, and BRCA1 p.Val1736Ala showed reduced DNA damage localization. These findings represent the first validated example of biallelic deleterious human BRCA1 mutations and have implications for the interpretation of genetic test results.

SIGNIFICANCE: Accurate assessment of genetic testing data for BRCA1 mutations is essential for clinical monitoring and treatment strategies. Here, we report the first validated example of an individual with biallelic BRCA1 mutations, early-onset ovarian cancer, and clinically significant hypersensitivity to chemotherapy. Cancer Discov; 3(4); 399–405. ©2012 AACR.

INTRODUCTION

Hereditary breast and ovarian cancer syndrome is predominantly caused by heterozygous, germline mutation in the BRCA1 or BRCA2 genes (1). Several forms of Fanconi anemia, characterized by bone marrow failure and malignancy, can be a consequence of biallelic mutations in BRCA2 (2) or biallelic mutations in genes encoding BRCA2- and BRCA1-associated proteins PALB2 and BRIP1 (3–7). Despite a frequency of approximately 1.5% in the Ashkenazi Jewish population for biallelic deleterious mutations in BRCA2, individuals with such mutations may not present with Fanconi anemia. The biallelic BRCA1 mutations found in this patient were not previously known to be deleterious.

BRCA1 and BRCA2 are the most important breast and ovarian cancer susceptibility genes. Biallelic mutations in BRCA2 can lead to Fanconi anemia and predisposition to cancers, whereas biallelic BRCA1 mutations have not been confirmed, presumably because one wild-type BRCA1 allele is required during embryogenesis. This study describes an individual who was diagnosed with ovarian carcinoma at age 28 and found to have one allele with a deleterious mutation in BRCA1, c.2457delC (p.Asp821Ilefs*25), and a second allele with a variant of unknown significance in BRCA1, c.5207T>C (p.Val1736Ala). Medical records revealed short stature, microcephaly, developmental delay, and significant toxicity from chemotherapy. BRCA1 p.Val1736Ala cosegregated with cancer in multiple families, associated tumors showed loss of wild-type BRCA1, and BRCA1 p.Val1736Ala showed reduced DNA damage localization. These findings represent the first validated example of biallelic deleterious human BRCA1 mutations and have implications for the interpretation of genetic test results.

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See related commentary by D’Andrea, p. 376.
the BRCA1 mutations, 185delAG [Human Genome Variation Society (HGVS) c.68_69delAG] and 5382insC (HGVS c.5266dupC), no homozygous or compound heterozygote carriers of these mutations have been reported. Although Brca1 nullizygosity results in embryonic lethality in mice (8), genetically engineered mice harboring biallelic mutations that correspond to human cancer-associated missense mutations within the BRCA1 carboxyl-terminal (BRCT) domain are viable through adulthood and display highly penetrant cancer susceptibility (9). These findings raise the possibility that a partially functional BRCA1 allele in trans with a deleterious truncating mutation (or with a similarly partially functioning mutation) in BRCA1 could be present within the same individual and could contribute to familial cancer susceptibility in humans. Herein, we document the presence of a functionally deleterious BRCA1 BRCT domain missense alteration in trans with a pathogenic BRCA1 alteration in a woman with dysmorphic features and early-onset ovarian carcinoma.

RESULTS

The proband (Fig. 1A, ego 28, arrow) presented at age 28 with stage IV papillary serous ovarian carcinoma. Medical records revealed a history of microcephaly, short stature (adult height of 150 cm), and developmental delay with limited speech at age 4 years. A review of pictures provided by the family showed coarse features with low anterior hairline, macroglossia, a prominent nasal bridge, and small alae nasi. She did not have obvious abnormalities of her thumbs.
Biallelic BRCA1 mutations

and had a normal blood count at the time of her cancer diagnosis. Neither ataxia nor telangiectasias were documented. This individual was found to have a known deleterious mutation in BRCA1 reported as 2576delC (HGVS c.2457delC; p.Asp821Ilefs*25) and a variant of unknown significance (VUS) in BRCA1 (HGVS c.5207T>C) p.Val1736Ala, as well as a VUS in BRCA2 (HGVS, c.971G>C; p.Arg324Thr).

Treatment with carboplatin [target area under the concentration versus time curve in mg/mL × min (AUC) of 5] and paclitaxel (175 mg/m²) resulted in significant toxicity requiring hospitalization due to fever and grade 4 neutropenia [absolute neutrophil count (ANC) nadir of 160/mm³], as well as grade 4 red blood cell and platelet transfusions. She also developed grade 2 nausea, diarrhea, and mucositis. As a result of the excess toxicity, carboplatin and paclitaxel were discontinued after 2 cycles. She received no further therapy and died 6 months after her diagnosis. Extreme sensitivity to the interstrand crosslinking agent carboplatin is not typically observed in heterozygous BRCA1 mutation carriers (10–12), but it is seen in biallelic BRCA1-mutant cells and mice, suggesting that both BRCA1 alleles were compromised for DNA repair function.

The mother of ego 28 was diagnosed with ovarian cancer at age 53 and died at 55. A maternal great aunt (Fig. 1A, Family A, ego 1) was diagnosed with breast and ovarian cancers at ages 59 and 69, respectively, and a contralateral breast cancer at age 76. A second maternal great aunt (ego 9, sister of ego 1) was diagnosed with primary peritoneal cancer at age 67 and died at 68. Notably, both carried the BRCA1 p.Val1736Ala variant VUS and the paternal lineage also had multiple cases of early-onset breast cancer. To investigate this variant further, we were able to obtain pedigrees on 11 additional families with the BRCA1 p.Val1736Ala VUS. Nine of these pedigrees that had additional genotyping of family members were used to assess cosegregation using methods described by Thompson and colleagues (ref. 13; a representative pedigree is shown in Fig. IB, and characteristics of the families are detailed in Supplementary Table S1). The combined OR in favor of p.Val1736Ala being pathogenic was 234:1, assuming the age-specific penetrance estimated in Antoniou and colleagues (14). Loss of heterozygosity (LOH) analysis was conducted on genomic DNA extracted from BRCA1 p.Val1736Ala mutation-positive tumors using a custom designed TaqMan assay (Table 1 and Supplementary Fig. S1). Ovarian/primary peritoneal cancer tumor blocks from Family A egos 1 and 9 showed LOH at the wild-type BRCA1 allele with retention of the p.Val1736Ala allele. Conversely, in ego 28, who carried germline BRCA1 2576delC and p.Val1736Ala alterations in trans, the ovarian tumor did not display LOH at either allele.

Abbreviation: LOH, loss of heterozygosity; WT, wild-type.

### Table 1. Loss of heterozygosity from the index family

<table>
<thead>
<tr>
<th>Sample ID</th>
<th>Description</th>
<th>Germline BRCA1</th>
<th>Taqman result</th>
<th>Interpretation</th>
</tr>
</thead>
<tbody>
<tr>
<td>S2504</td>
<td>Cell line</td>
<td>WT/WT</td>
<td>A/A</td>
<td>No LOH</td>
</tr>
<tr>
<td>S2366</td>
<td>Tumor (breast)</td>
<td>WT/WT</td>
<td>A/A</td>
<td>No LOH</td>
</tr>
<tr>
<td>Ego 1</td>
<td>Lymphoblasts</td>
<td>WT/p.Val1736Ala</td>
<td>A/G</td>
<td>No LOH</td>
</tr>
<tr>
<td>Ego 10</td>
<td>Lymphoblasts</td>
<td>WT/p.Val1736Ala</td>
<td>A/G</td>
<td>No LOH</td>
</tr>
<tr>
<td>Ego 9</td>
<td>Tumor (Ovarian)</td>
<td>WT/p.Val1736Ala</td>
<td>G/G</td>
<td>LOH at WT</td>
</tr>
<tr>
<td>Ego 9</td>
<td>Tumor (Ovarian)</td>
<td>WT/p.Val1736Ala</td>
<td>G/G</td>
<td>LOH at WT</td>
</tr>
<tr>
<td>Ego 28</td>
<td>Tumor (Ovarian)</td>
<td>p.2576delC/p.Val1736Ala</td>
<td>A/G</td>
<td>No LOH</td>
</tr>
</tbody>
</table>

NOTE: Ovarian/primary peritoneal cancer tumor blocks from Family A egos 1 and 9 showed that LOH had occurred at the wild-type BRCA1 allele with retention of the p.Val1736Ala allele. “A” at position 5207 represents the wild-type allele and “G” at position 5207 represents the Val1736Ala allele. Conversely, in ego 28, who carried germline BRCA1 2576delC and p.Val1736Ala alterations in trans, the ovarian tumor did not display LOH at either allele.
Figure 2. Analysis of the BRCA1 p.Val1736Ala mutation. A, partial sequence alignment of a BRCA1 BRCT domain from different species showing that BRCA1 V1736 and P1749 residues (highlighted in red) are completely conserved across all vertebrate species. Numbers on top of the alignment indicate amino acid positions of the human BRCA1 protein. Conservation below describes sequence conservation (*, identical; ≥80% conservation; ., ≥60% conservation). B, modeling (based on protein data bank [pdb] code 1t15) of the interaction between the BRCA1 BRCT domains and a peptide of BACH1. BRCA1 is gray, with disease-causing mutants of the conserved residues in red. The BACH1 peptide is purple. C, WT BRCA1 (shown as a green focus) but not the p.Val1736Ala or p.Pro1749Arg mutant efficiently colocalized with mcherryLacIFokI fusion endonuclease-induced DNA DSBs. D, percentage of cells with BRCA1 (WT or mutant) colocalizing to FokI was quantified. At least 100 cells were assessed for each data point (n > 100). Measurements were obtained in triplicate and reported as means of 3 replicates. P values were calculated using Student t test; P < 0.05 for all comparisons. Error bars, SEM. E, Coimmunoprecipitation of epitope-tagged BRCA1 (Myc-BRCA1) WT or mutants from 293T cells at room temperature for 2 hours followed by immunoblot for RAP80.
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Figure 3. Resequencing of BRCA1 c.2681_2682delAA mutation carrier. A, chromatogram showing the WT BRCA1 sequence in lymphocyte DNA from a noncarrier individual. B, chromatogram from lymphocyte DNA showing the heterozygous status of the Scottish woman previously reported as homozygous for the BRCA1 c.2681,2682delAA mutation. Both the mutant and WT alleles are clearly present.

and B). Therefore, the purported homozygous carrier was in actuality heterozygous for a BRCA1 mutation.

DISCUSSION

Here, we report the first individual with validated biallelic mutations in BRCA1. Compelling evidence is presented that BRCA1 p.Val1736Ala is both pathogenic and can support viability through adulthood in trans to a deleterious mutation in exon 11 of BRCA1 (BRCA1 2576delC). BRCA1 p.Val1736Ala diminishes protein–protein interaction with RAP80 and localization to DSBs and imparts cancer susceptibility independent of other BRCA1 or BRCA2 alterations. LOH analysis was also consistent with pathogenicity. Loss of the WT allele occurred in both tumors that carried the p.Val1736Ala VUS in trans to WT BRCA1; however, LOH did not occur in the ovarian cancer of the proband (ego 28), which was compound heterozygous for p.Val1736Ala and 2576delC, indicative of a scenario in which selective pressure did not exist to delete either pathogenic allele.

Several features of the index patient were uncharacteristic for monoallelic BRCA1 mutation carriers. In addition to the aforementioned developmental delay, microcephaly, and short stature, ovarian cancer was diagnosed earlier than the age of 30, which is unusual for BRCA1 mutation carriers (19). The patient also had extreme sensitivity to the interstrand crosslinking agent carboplatin, a characteristic not typically displayed in BRCA1 mutation carriers (10–12, 20).

Although complete BRCA1 deficiency results in early embryonic lethality in mice, it should be considered that certain biallelic BRCA1 mutations that mimic human cancer-associated mutations can support viability through adulthood in mice (9). Genetically engineered mice harboring biallelic BRCT domain mutations (p.Ser1598Phe) that correspond to a known cancer-causing allele in humans (p.Ser1655Phe) were viable through adulthood and displayed similar cancer susceptibility to that of mice completely lacking BRCA1 gene function in the mammary gland (9). Moreover, complete deletion of exon 11 or introduction of a mutation that produces a stop codon in the BRCA1 exon 11 region, as predicted in the 2576delC allele, disrupts full-length BRCA1 protein leaving intact an evolutionarily conserved exon 10 to exon 12 splice variant. The BRCA1 delta 11 splice product contains the BRCA1 RING domain and BRCT repeats, localizes to DNA damage sites, and can support viability in certain mouse backgrounds, yet still confers cancer susceptibility (21–23). The BRCA1 delta 11 splice isoform is expressed at both the RNA and protein levels in human cells (24); however, it is not known whether this is the case in the context of the 2576delC mutation. Therefore, it is likely that partial DNA repair function of p.Val1736Ala (c.5207T>C), and possibly 2576delC (c.2457delC), or both of these mutant alleles is permissive for viability in humans.

Structural modeling suggests that p.Val1736Ala is unique when compared with other BRCT domain mutations in that it lies distal to the phosphopeptide-binding pocket. Prior studies have shown that p.Val1736Ala exhibits thermal instability and partial loss of function in transcriptional reporter assays (25, 26). Our results also show that p.Val1736Ala is a hypomorphic alteration with respect to biochemical and cellular function. Although BRCA1 p.Val1736Ala is predicted to be hypomorphic in terms of DNA repair function, whether this variant has reduced penetrance with respect to cancer susceptibility is not evident. Collectively, these findings, together with observations from genetically engineered mouse models (9), strongly suggest that viability and tumor suppression phenotypes are not completely concordant among BRCA1-mutant alleles.

Apart from the biologic implications, the findings in this study have importance to the interpretation of genetic variants. VUSs are a common finding in genetic testing for inherited cancer syndromes and pose challenges in counseling and management (27). Cooccurrence of a VUS in trans with a known deleterious BRCA1 mutation is considered a strong indication that the VUS is not clinically important (28). Our findings suggest that the presence of a BRCA1 VUS in trans with an established deleterious BRCA1 mutation should not be considered as definitive evidence against pathogenicity. This work also highlights the importance of examining multiple distinct lines of evidence when interpreting a VUS, including clinical phenotype. This lesson is particularly pertinent in the era of massively parallel DNA sequencing, as a large number of VUSs will be identified with the use of this methodology and caution will be needed in interpreting these results for clinical use.

METHODS

LOH Analysis

DNA was extracted from either cell lines or tumors following microdissection of cancer tissue to over 70% tumor (Supplementary Fig. S3). LOH was assessed by the University of Pennsylvania Genomics Facility using a custom-designed TaqMan assay to distinguish a single nucleotide alteration at nucleotide position 5207, codon 1736 from the WT allele (Table 1 and Supplementary Fig. S1).

BRCA1 c.2681_2682delAA Resequencing

Lymphocyte DNA from the patient was amplified by PCR using the primers F1: 5′-AACCACAGTCGGGAAACAAG-3′ and R2: 5′-AACCACAGTCGGGAAACAAG-3′ using the primers F1: 5′-AACCACAGTCGGGAAACAAG-3′ and R2:
5′-TGATGGGAAAAGTGGGTGGT-3′ and the Qiagen HotStar Plus PCR system according to the manufacturer’s instructions. PCR products were sequenced by Sanger sequencing using the 3730xl DNA Analyzer technology (Applied Biosystems), and the traces were visualized using Chromas software (Technelysium).

Immunofluorescence

Immunofluorescence was conducted in the DSB reporter cells as described previously (15). No additional authentication on cell lines was conducted. All analyses were carried out on unmodified images that were captured with a QImaging RETIGA-SRv camera connected to a Nikon Eclipse 80i microscope.

Disclosure of Potential Conflicts of Interest

D.E. Goldgar has an ownership interest (including patents) and royalties from BRCA1/2 gene patents. No potential conflicts of interest were disclosed by the other authors.

Authors’ Contributions

Conception and design: S.M. Domchek, K.L. Nathanson, W. Foulkes, R.A. Greenberg

Development of methodology: S.M. Domchek, R.A. Greenberg

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Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): S.M. Domchek, J. Stopfer, K.L. Nathanson, R.A. Greenberg

Study supervision: S.M. Domchek, R.A. Greenberg

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Biallelic BRCA1 mutations


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