

# A New de novo *BRCA1* Mutation in a Young Breast Cancer Patient: A Case Report

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**Background:** *BRCA1* and *BRCA2* genes represent the most investigated breast and ovarian cancer predisposition genes. Ten cases of pathogenic de novo *BRCA1* variations and six cases of pathogenic de novo *BRCA2* variation have been reported at present. Here, we report a new case of a de novo *BRCA1* gene mutation.

**Case Presentation:** A 30-year-old woman with no health issues and no family history for hereditary breast and ovarian cancer was diagnosed with a hormone receptor positive/HER2 negative invasive breast cancer. Genetic testing revealed a pathogenic variant in *BRCA1* (c.4065\_4068delTCAA) which was not found in her parents or sister.

**Conclusion:** We report a new case of de novo *BRCA1* mutation, confirmed by repeated germline testing of the index patient and her parents. The published *BRCA1/2* de novo mutation rate is low. This is probably due – in part – to the strict testing criteria.

**Keywords:** *BRCA1* gene, breast cancer, de novo mutation, early onset, case report

## Background

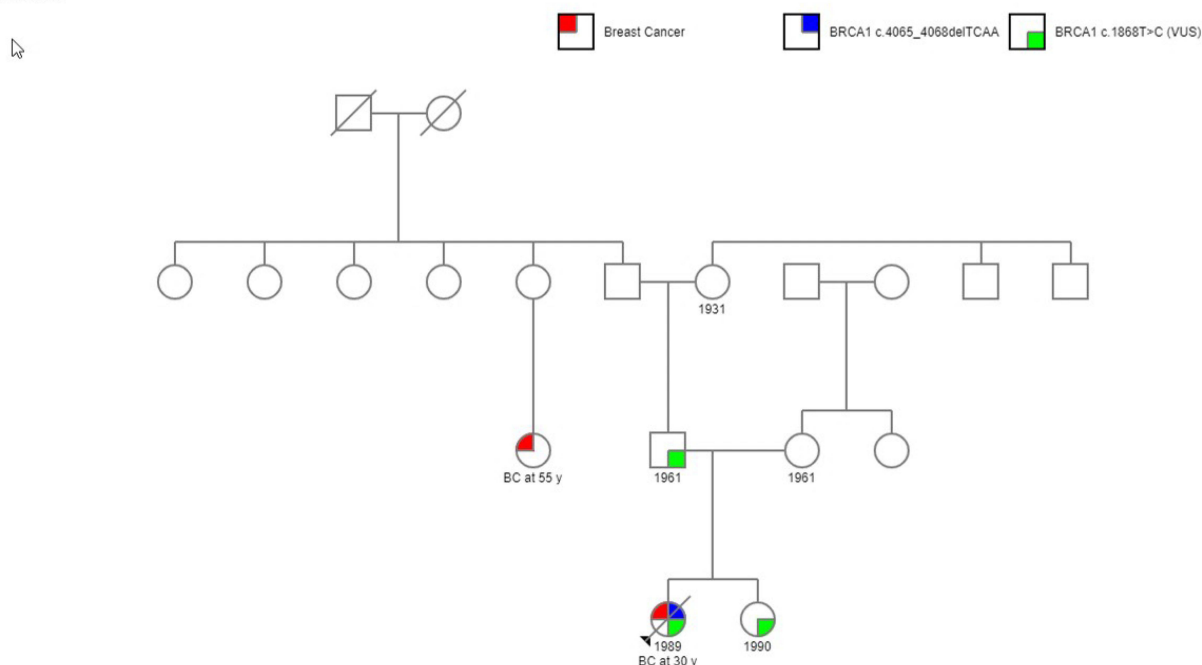
Hereditary cancer results from mutations in specific genes, such as those involved in regulating cell growth and DNA repair. Some of these mutations are inherited from one parent.<sup>1</sup> De novo mutations are genetic alterations arising for the first time in a germ cell (ie, ovum or sperm) or in the fertilized egg itself during early embryogenesis. The majority of hereditary breast and ovarian cancer cases are due to pathogenic or likely pathogenic variants in the *BRCA1/2* genes.<sup>2</sup> Pathogenic germline variants in the *BRCA1* or *BRCA2* gene lead to an increased lifetime risk of breast, ovarian and further less frequently present cancers in women and an increased lifetime risk of breast, prostate and other tumors in men.

*BRCA1* and *BRCA2* genes were discovered in 1994 and 1995, respectively,<sup>3,4</sup> and represent the most investigated breast and ovarian cancer predisposition genes. In recent years, numerous mutations have been described in these genes, of which very few cases involved de novo *BRCA1/2* alterations. In fact, only ten cases of de novo *BRCA1* mutations and six cases of de novo *BRCA2* mutations have been reported at present.<sup>5–15</sup> The *BRCA1/2* de novo mutation rate was previously estimated to be 0.3% (0.1–0.7%). In a French study population of 12805 patients diagnosed with breast and/or ovarian cancer, 1527 were found to be *BRCA1/2* mutated (12%), of whom three *BRCA1* mutations and one *BRCA2* mutation were de novo.<sup>6</sup> This is in contrast with other genes, ie, *TP53*, *NFI* and *RBI*.

We report a new case of a de novo *BRCA1* gene mutation in a woman with an early onset breast cancer without a relevant family history.

## Case Presentation

A 30-year-old woman with no health issues so far was diagnosed with a hormone receptor positive/HER2 negative invasive breast cancer. Her family history was not suggestive of a hereditary cancer syndrome (Figure 1). Only a cousin of her father had been diagnosed with a breast cancer at the age of 55 years. She underwent a neoadjuvant chemotherapy, followed by bilateral mastectomy and salpingo-oophorectomy. Regarding the early onset of her cancer, genetic testing was

de novo *BRCA1*

**Figure 1** Family pedigree chart for case.

offered to the patient. It revealed a pathogenic variant (c.4065\_4068delTCAA) and a variant of unknown significance (VUS) in the *BRCA1* gene. Her healthy sister and her father were tested thereafter and both were found to be carriers of the VUS – but not the pathogenic variant – in the *BRCA1* gene. In her mother neither the pathogenic *BRCA1* mutation (c.4065\_4068delTCAA) nor the described *BRCA1* VUS was detected. The findings were confirmed by an analysis of additional blood samples taken from each parent and the patient. In the absence of a germline mutation in both parents, we assume a de novo origin of the mutation during parenteral germ cell gametogenesis. A non-paternity event could be excluded by the detection of the VUS in the *BRCA1* gene, which was first reported in the patient and later in her father and sister. We concluded that our patient must be a carrier of a de novo *BRCA1* mutation.

## Materials and Methods

DNA extraction from blood leucocytes was done followed by PCR amplification and DNA sequencing (Cancer Panel V2, Illumina, MiSeq-Tec (Illumina), Alignment: NextGene V2.4.1.1 (Softgenetics)). A pathogenic mutation (NM\_007294.3:c.4065\_4068delTCAA/p.(Asn1355Lysfs\*10)) and a VUS (NM\_007294.3:c.1868T>C/p.Leu623Pro) were found in the *BRCA1* gene. The detected pathogenic variant was already reported by Friedman et al.<sup>16</sup> Recently, it has been also described by Rashid et al as founder mutation in breast cancer patients from Pakistan.<sup>17</sup>

This pathogenic variant NM\_007294.3:c.4065\_4068delTCAA/p.(Asn1355Lysfs\*10) results in a frameshift of the reading frame and, presumably, a premature stop codon. Thus, this deletion leads to a shortened protein and/or degradation of the transcript by NMD (nonsense mediated mRNA decay).

PCR amplification and Sanger sequencing were performed in the healthy sister and parents.

## Results and Discussion

Our patient with a pathogenic *BRCA1* variant is a Swiss citizen without a migration background. Neither the mother nor the father or sister are carriers of the pathogenic *BRCA* mutation, providing additional evidence for the de novo occurrence of this variant.

A search in PubMed (Search Terms: *BRCA*/germline/mutation/de novo) yielded 13 publications reporting 16 de novo *BRCA1/2* mutations.<sup>6–15,18–20,21</sup> The largest published clinical trial – from Golmard et al – detected – on

**Table 1** *BRCA1* and *BRCA2* de Novo Mutations Reported in the Literature and in This Case Report Updated and Revised from L Golmard et al 2015

| Gene                | Mutation                   | Clinical Features (Age at Diagnosis) | Family History                                         | Population                 |
|---------------------|----------------------------|--------------------------------------|--------------------------------------------------------|----------------------------|
| <i>BRCA1</i>        | c.3769_3770delGA           | BC (<40)                             | None                                                   | Australia <sup>7</sup>     |
| <i>BRCA1</i>        | c.5332+1G>A                | Bilateral IDBC (38, 43)              | Maternal aunt, BC (54)                                 | UK <sup>8</sup>            |
| <i>BRCA1</i>        | Exons 1–12 deletion        | IDBC (30)                            | None                                                   | China <sup>9</sup>         |
| <i>BRCA1</i>        | Gene deletion              | Bilateral BC (28, 37)                | None                                                   | Spain <sup>10</sup>        |
| <i>BRCA1</i>        | c.3494_3495delTT           | BC (52), OC (53)                     | None                                                   | Belgium <sup>11</sup>      |
| <i>BRCA1</i>        | Mosaic exon 16 deletion    | Bilateral BC (39, 47)                | Paternal cousin, BC (30)                               | UK <sup>12</sup>           |
| <i>BRCA1</i>        | c.5468–2 A>G               | OC (39)                              | Two paternal aunts, BC (57, 75)                        | France <sup>6</sup>        |
| <i>BRCA1</i>        | c.2296_2297delAG           | BC (31)                              | None                                                   | France <sup>6</sup>        |
| <i>BRCA1</i>        | Mosaic exons 1–13 deletion | IDBC (41)                            | Two sisters, BC (62, 63) Paternal grandmother, BC (75) | France <sup>6</sup>        |
| <i>BRCA1</i>        | c.5095C>T                  | IDBC (32)                            | None                                                   | Italy <sup>22</sup>        |
| <b><i>BRCA1</i></b> | <b>c.4065_4068delTCAA</b>  | <b>IDBC (30)</b>                     | <b>Paternal aunt, BC (55)</b>                          | <b>Case in this report</b> |
| <i>BRCA2</i>        | c.2808_2811del             | Multifocal BC (39)                   | Paternal cousin, BC (54)                               | Netherlands <sup>13</sup>  |
| <i>BRCA2</i>        | c.7260insA                 | Bilateral IDBC (35)                  | None                                                   | USA <sup>14</sup>          |
| <i>BRCA2</i>        | c.8754+1G>A                | IDBC (40)                            | Mother, BC (59)                                        | Denmark <sup>15</sup>      |
| <i>BRCA2</i>        | c.5301insA                 | IDBC (35)                            | Paternal grandmother, BC (42)                          | USA <sup>18</sup>          |
| <i>BRCA2</i>        | c.51dupA                   | Bilateral IDBC (27, 37)              | None                                                   | Spain <sup>19</sup>        |
| <i>BRCA2</i>        | c.6082_6086delGAAGA        | Bilateral BC (40, 48)                | Daughter, BC (31)                                      | France <sup>6</sup>        |

**Abbreviations:** BC, breast cancer; IDBC, invasive ductal breast carcinoma; OC, ovarian cancer.

a series of 12805 consecutive unrelated patients diagnosed with breast and/or ovarian cancer who met the inclusion criteria for *BRCA1/2* gene analysis according to French guidelines – a *BRCA1* or *BRCA2* variation in 1527 (12%) patients. A total of 801 (6.3%) *BRCA1* and 726 (5.7%) *BRCA2* mutation carriers were identified. In this study, de novo status was found for three *BRCA1* mutations and one *BRCA2* mutation, resulting in de novo mutation rates of 0.4% and 0.1% for *BRCA1* and *BRCA2* genes, respectively, and an overall *BRCA1/2* de novo mutation rate of 0.3%.

de novo mutations are generally identified in sporadic cases in most genetic diseases. However, in the 2015 study by Golmard et al, cases with a family history of breast cancer significantly outnumbered, while in the other published cases, half were found to have a family history of breast cancer (Table 1). The authors attribute this observation to the high incidence of breast cancer in the normal population, bias for family cancer cases due to the strong impact of family history as a criterion for *BRCA1/2* genetic testing, and genetic heterogeneity in breast cancer.

## Conclusion

We report a new case of de novo *BRCA1* mutation, confirmed by repeated germline testing of the index patient and her parents. The published *BRCA1/2* de novo mutation rate is low. This is probably due – in part – to the strict testing criteria, which are not uniform internationally and the restrictions regarding the cost coverage by the insurance companies. Most described de novo *BRCA1/2* variations were found in patients with early-stage breast cancer and without a family history

of the disease. Genetic testing of breast cancer patients based on their young age or family history does not allow detection of all *BRCA1/2* carriers who may benefit from preventive interventions. In our opinion, we should focus on identifying as many carriers of a pathogenic *BRCA* variant as possible. Genetic testing based on selection criteria mainly considering family history, age of onset and tumor characteristics may underestimate the prevalence of de novo mutations. By detecting a larger number of de novo mutations, more patients could benefit from preventive interventions and tailored treatments. Genetic testing for a pathogenic variant in offspring of a carrier of a de novo variant is useful in identifying individuals at high risk for malignancies.

## Abbreviations

*BRCA1*, BReast Cancer Gene 1; *BRCA2*, BReast Cancer Gene 2; *NF1*, Neurofibromatosis Gene 1; *RBI*, Retinoblastoma Gene 1; *TP53*, Tumor Protein P53 Gene; VUS, Variant of unclear significance; PCR, Polymerase chain reaction; DNA, Deoxyribonucleic acid; HER2, Human epidermal growth factor receptor 2.

## Data Sharing Statement

The datasets used during the current study are available from the corresponding author on reasonable request.

## Ethics Approval and Consent to Participate

Patient/Proband gave informed consent to tests as well as to use data/material for further anonymous use according to local and national guidelines.

## Consent for Publication

Patient/Proband gave informed consent to tests as well as to use data/material for further anonymous use including publication according to local and national guidelines. Institutional approval was given (KEK – Kantonale Ethikkommission für die Forschung am Menschen, Bern, Switzerland).

## Author Contributions

All authors made substantial contributions to conception and design, acquisition of data, or analysis and interpretation of data; took part in drafting the article or revising it critically for important intellectual content; agreed to submit to the current journal; gave final approval of the version to be published; and agree to be accountable for all aspects of the work”.

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## Disclosure

The authors declare no conflicts of interest.

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