BRCA1:185delAG found in the San Luis Valley probably originated in a Jewish founder

I Makriyianni, N Hamel, S Ward, W D Foulkes, S Graw

Three BRCA1/2 mutations (185delAG and 5382insC in BRCA1, and 617delT in BRCA2) are present in about 2.5% of the Ashkenazi Jewish population, and in 10–12% of Ashkenazi Jewish women with breast cancer. Mutations that become common in a population are often explained by the presence of a “founder effect”. This effect tends to exist when a population is established by a small group of ancestors. The members of the group are called founders and become isolated from the original population from which they are derived on account of geographical, cultural, or linguistic barriers. If this isolation persists, genetic drift can cause disease producing alleles present in the founders to become more frequent in subsequent generations.

The San Luis Valley (SLV) is a large, isolated valley situated on the border between New Mexico and Colorado. The first settlers were Spaniards of the de Oñate expedition in 1598, but today it has an admixed population descended from Native Americans, West Africans, and Europeans. A previous study in Colorado of breast cancer patients with SLV ancestry revealed the presence of a hereditary breast cancer mutation, BRCA1:185delAG. Many of these individuals came from areas of Spanish settlement in what is now northern New Mexico, an area known to have had a number of Spanish settlers with Jewish heritage. This population remained fairly coherent until the mid-1900s, which would have allowed the fixation of certain mutations in the population through the founder effect.

The 185delAG mutation (c.68_69del2) is a founder mutation in the Ashkenazi Jewish population and is the most common BRCA1 mutation in this population, with a frequency of 1%. Markers flanking this mutation have conserved alleles among Ashkenazi carriers, allowing for the construction of a distinct, linked haplotype.

In this study, we followed up on our original finding and set out to determine whether the BRCA1:185delAG mutation was also observed in breast cancer patients from the San Luis Valley (SLV) of Colorado and New Mexico. Seven nearby markers known to be conserved on the 185delAG Jewish haplotype were tested to determine whether the SLV mutation shares an origin with the Jewish mutation, or whether it arose independently. All 185delAG mutation carriers were found to share the conserved allele at each of the seven loci tested. These results suggest that individuals in the SLV who carry the 185delAG mutation share a common ancestor with Jews who also carry this mutation.

Table 1 shows the genotypes of the subjects for each marker in reference to the conserved Jewish haplotype. We found that all 185delAG mutation carriers share a conserved allele at each of the seven loci tested. Moreover, subject 7, a non-carrier, does not have the conserved alleles at any of the loci. These results are consistent with the hypothesis that individuals in the SLV who carry the 185delAG mutation share a common ancestor with Jews who also carry this mutation. This finding suggests that individuals in this population have at least one ancestor of Jewish origin.

**COMMENT**

The BRCA1:185delAG mutation has previously been observed on different haplotypes in both Jewish and non-Jewish mutation carriers, which implies that the mutation arose more than once. However, the existence of only one haplotype in the Ashkenazi Jews indicates a single origin within this population. Two previous studies also found that non-Jewish populations of Hispanic origin segregate the 185delAG mutation with the Ashkenazi Jewish haplotype. One study was on a Spanish gypsy population and another on a Chilean family with no known Jewish ancestry. Most recently, Weitzel et al found that BRCA1:185delAG is the most frequent deleterious BRCA1 mutation in women of Hispanic origin living in Los Angeles. All patients with the BRCA1:185delAG mutation from this area also show conservation of the common Ashkenazi haplotype at markers centromeric to and throughout the BRCA1 gene.

The linked haplotype is commonly referred to as the “Ashkenazi Jewish haplotype” because it was originally identified and has been extensively studied in Ashkenazi Jews. However, this does not mean that the haplotype is unique to this population. Indeed, other non-Ashkenazi
Jewish populations also carry the 185delAG mutation. One possible interpretation of this finding is that the mutation could have arisen at an ancient time before the dispersion of Jews. However, Neuhausen et al determined that the mutation occurred around 1235 CE (90% confidence interval ranging from 396 to 1536 CE) based on the 500 kb conserved region that they found centromeric to the mutation. Although one of our previous studies narrowed down the conserved region to 200 kb, suggesting that the mutation is actually older, its origin is still likely more recent than the last dispersion of the Jews in the Diaspora, estimated to be around 70 CE. A second possibility that the mutation could have arisen after the divergence of the Jews and the Spanish inquisition and considerably earlier than the recent Ashkenazi immigration to the Americas.

“Ashkenazi” founder mutations have also been observed in non-Ashkenazi Jewish populations in other syndromes. Examples of these are the mutations causing Bloom syndrome and Creutzfeldt–Jakob disease. Bloom syndrome is a rare autosomal recessive disorder that causes short stature, skin pigmentation anomalies, and immunodeficiency. A study of Bloom patients of non-Ashkenazi origin in America revealed an “Ashkenazi” mutation, present on an Ashkenazi haplotype, in about 5% of the patients. A study of Bloom patients of non-Ashkenazi origin in America revealed an “Ashkenazi” mutation, present on an Ashkenazi haplotype, in about 5% of the patients. Patients of this subgroup are from Spanish speaking Catholic families that have resided in south western United States, Mexico, or El Salvador for several generations. This study also implies Jewish ancestry in these Spanish immigrants. Haplotype analysis of the 200K PRNP mutation causing Creutzfeldt–Jakob disease also indicates a single origin of the mutation in Jewish populations. It was observed in 100% of patients from a Jewish population in Tunisia, in 47% of Libyan Jewish patients, and in 100%, 33%, and 43% of patients from non-Jewish populations of Spain, Italy, and Chile, respectively.

The results of this and previous studies on non-Jewish populations support the presence of well known Ashkenazi Jewish founder mutations in non-Jewish individuals. Specifically, these studies illustrate the presence of Jewish ancestry in patients with a personal or familial history of breast cancer who identify themselves as having Spanish origins. Future studies are necessary to evaluate the frequency of this mutation in the San Luis Valley population.

### Authors’ affiliations

I Makriyianni, Department of Human Genetics, McGill University, Montreal, Quebec, Canada

N Hamel, Department of Medicine, McGill University Health Centre, Montreal

W D Foulkes, Program in Cancer Genetics, Departments of Oncology and Human Genetics, McGill University

S Ward, University of Wyoming, Laramie, Wyoming, USA
Jewish founder mutations in Hispanic populations

S Graw, Eleanor Roosevelt Institute, University of Denver, Denver, Colorado, USA

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Correspondence to: Dr William D Foulkes, Montreal General Hospital, 1650 Cedar Avenue, Room L10-116, Montreal, Quebec, Canada H3G 1A4; william.foulkes@mcgill.ca

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