PLoS One. 2013;8(3):e58182. doi: 10.1371/journal.pone.0058182. Epub 2013 Mar 11.

Prevalence of BRCA1 mutations in familial and sporadic greek ovarian cancer cases.

Stavropoulou AV, Fostira F, Pertesi M, Tsitlaidou M, Voutsinas GE, Triantafyllidou O, Bamias A, Dimopoulos MA, Timotheadou E, Pectasides D, Christodoulou C, Klouvas G, Papadimitriou C, Makatsoris T, Pentheroudakis G, Aravantinos G, Karydakis V, Yannoukakos D, Fountzilas G, Konstantopoulou I.

Source

Molecular Diagnostics Laboratory, INRaSTES, National Center for Scientific Research Demokritos, Athens, Greece.

Abstract

Germline mutations in the BRCA1 and BRCA2 genes contribute to approximately 18% of hereditary ovarian cancers conferring an estimated lifetime risk from 15% to 50%. A variable incidence of mutations has been reported for these genes in ovarian cancer cases from different populations. In Greece, six mutations in BRCA1 account for 63% of all mutations detected in both BRCA1 and BRCA2 genes. This study aimed to determine the prevalence of BRCA1 mutations in a Greek cohort of 106 familial ovarian cancer patients that had strong family history or metachronous breast cancer and 592 sporadic ovarian cancer cases. All 698 patients were screened for the six recurrent Greek mutations (including founder mutations c.5266dupC, p.G1738R and the three large deletions of exon 20, exons 23-24 and exon 24). In familial cases, the BRCA1 gene was consequently screened for exons 5, 11, 12, 20, 21, 22, 23, 24. A deleterious BRCA1 mutation was found in 43/106 (40.6%) of familial cancer cases and in 27/592 (4.6%) of sporadic cases. The variant of unknown clinical significance p.V1833M was identified in 9/698 patients (1.3%). The majority of BRCA1 carriers (71.2%) presented a high-grade serous phenotype. Identifying a mutation in the BRCA1 gene among breast and/or ovarian cancer families is important, as it enables carriers to take preventive measures. All ovarian cancer patients with a serous phenotype should be considered for genetic testing. Further studies are warranted to determine the prevalence of mutations in the rest of the BRCA1 gene, in the BRCA2 gene, and other novel predisposing genes for breast and ovarian cancer.