

Breast and Ovarian Cancer Risks Beyond *BRCA1/2* from a Cohort of 15,000 Women Undergoing Multigene Panel Testing

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Multigene panel testing (MGPT) for hereditary cancer is increasing in popularity in the USA. Many panels include genes identified as hereditary breast and/or ovarian cancer (HBOC) genes despite limited data regarding the precise cancer risks associated with mutations in these genes. This study examined clinical histories, ethnicity, and test results from a cohort of 15,083 individuals who underwent MGPT of up to 20 genes (*ATM*, *BARD1*, *BRCA1*, *BRCA2*, *BRIP1*, *CDH1*, *CHEK2*, *MLH1*, *MRE11A*, *MSH2*, *MSH6*, *NBN*, *NF1*, *PALB2*, *PMS2*, *PTEN*, *RAD50*, *RAD51C*, *RAD51D*, *TP53*) using the BreastNext and OvaNext panels. The majority of individuals were from high-risk breast and/or ovarian (Br/Ov) cancer families, with 92.4% of all probands meeting National Comprehensive Cancer Network HBOC testing criteria. Pathogenic mutations were identified in 9.4% of the overall cohort. No ethnicity specific enrichment of mutations was observed. To further quantify gene-specific Br/Ov risks, a series of case-control analyses were performed comparing the frequencies of inactivating mutations and previously classified pathogenic or likely pathogenic missense alterations between cases from Br/Ov MGPT and controls from the Exome Aggregation Consortium (ExAC) database. Estimated risk ratios (RR) for Br/Ov cancer in well-studied genes were consistent with previous reports, including an increased breast cancer risk but no increased ovarian cancer risk associated with *CDH1*, *ATM*, and *CHEK2* mutations. Ovarian cancer risk was significantly ($p < 0.001$) increased for mutations in *RAD51D* (RR >9), *RAD51C* (RR >8) and *BRIP1* (RR >7). Additional results of interest included a significantly increased risk of breast cancer at age >50 for *NF1* carriers, breast cancer for *MSH6*, breast cancer <50 for *RAD51D*, and ovarian cancer for *PALB2*. This large breast and ovarian cancer case-control analysis provides useful data for many HBOC genes previously lacking risk estimates, and should prove useful for clinical risk management of patients after MGPT.