Ambry Genetics

RESEARCH FOR YOUR PRACTICE

Defining Inherited Ovarian Cancer Risks

TAKING ACTION AND PREVENTING DISEASE WITH GENETIC TESTING RESULTS

A recent collaboration between Ambry Genetics, Mayo Clinic, and Huntsman Cancer Institute published in Gynecologic Oncology[1] uncovers useful information about ovarian cancer risks.

WHY THIS MATTERS TO YOU

Understanding precise inherited ovarian cancer risks is vital for providers to better manage patients and their family members. To date, this collaboration is the largest of its kind and provides critical data to further clarify ovarian cancer risks associated with results from multigene panel testing.

BACKGROUND

- Up to 25% of ovarian cancer is thought to be hereditary with up to 40% of those cases attributed to *BRCA1/2*
- Genetic testing helps to identify women with an increased risk for ovarian cancer
- Due to limited screening options, risk-reducing salpingo-oophorectomy (RRSO) is often recommended for women at increased risk for ovarian cancer
- We studied associations of germline mutations in 19 cancer susceptibility genes. Updated ovarian cancer risks were estimated in an analysis of patients with ovarian cancer compared to Exome Aggregation Consortium (ExAC) reference controls

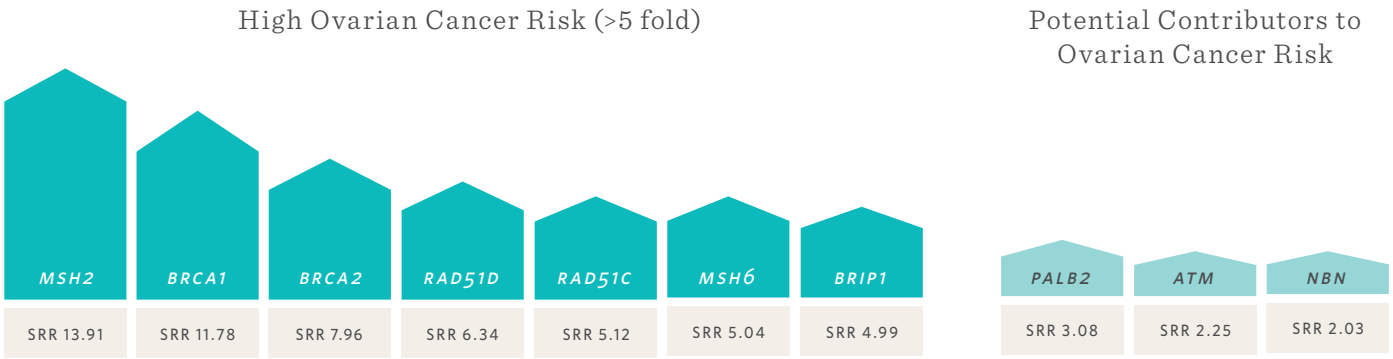
7,768
women with ovarian cancer studied

POINTS FOR YOUR PRACTICE

- All studied genes with defined ovarian cancer risks are found on several of Ambry's cancer panels, including OvaNext and CancerNext.
- According to NCCN® guidelines, women with mutations in *BRCA1/2, RAD51C, RAD51D, BRIP1, MSH2*, and *MSH6* should consider RRSO[2]. All of these genes were found to be associated with a high risk of ovarian cancer (>5-fold) in this study.
- Mutations in *ATM, PALB2,* and *NBN* were established as potential contributors to ovarian cancer risk, therefore, testing for these genes should be considered for patients with a personal and/or family history of ovarian cancer.

SIGNIFICANT FINDINGS

- Study results established or confirmed the likelihood of developing ovarian cancer, known as standardized risk ratios (SRR), for several genes



- Gene-specific findings:
  - Mutations in *PALB2* were only associated with ovarian cancer risk when there was a personal or family history of breast cancer
  - *BRCA1, MSH6*, and *MSH2* were observed more frequently in earlier-diagnosed cases of ovarian cancer
  - Mutations in two of the genes causative of Lynch syndrome, *MLH1* and *PMS2*, were not associated with an increased risk of ovarian cancer in this study, and additional research is needed to further evaluate these genes in relation to ovarian cancer risk

- *BARD1, CHEK2, MRE11A* and *RAD50* showed no evidence of increased ovarian cancer risk

Learn more about our research here.

REFERENCES

1. Lilyquist J *et al:* Frequency of mutations in a large series of clinically ascertained ovarian cancer cases tested on multi-gene panels compared to reference controls. Gynecologic Oncology
2. NCCN Clinical Practice Guidelines in Oncology (NCCN Guidelines ®). Genetic/Familial High-Risk Assessment: Breast and Ovarian. V2. 2017. Available at nccn.org.