OvaNext Identifies More Patients with Hereditary Ovarian Cancer

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OvaNext, a 25-gene hereditary gynecologic cancer panel, increases diagnostic yield of clinically actionable results in patients with ovarian cancer. Testing genes beyond BRCA1 and BRCA2 can significantly increase detection of patients with hereditary ovarian cancer.

**KEY STUDY FINDINGS**

1. By comparing mutations by gene in 7768 ovarian cancer cases and reference controls, BRCA1, BRCA2, BRIP1, MSH2, MSH6, RAD51C, and RAD51D were confirmed as high-risk genes, with >/=5-fold increased risk of ovarian cancer.

2. ATM was identified as a moderate risk ovarian cancer gene with >2-fold increased risk of ovarian cancer observed.

3. Using multigene panel testing increases the detection rate for ovarian cancer patients meeting BRCA1/2 testing criteria, by 62.5%.

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**Frequency of Pathogenic Variants in BRCA1/2 Relative to Other Genes Among Patients Meeting BRCA1/2 Testing Criteria**

Pathogenic/likely pathogenic variant frequency

*ATM, BRIP1, MSH2, MSH6, NBN, PMS2, RAD51C, RAD51D, TP53*
**KEY FINDINGS**

- >12,000 patients with a personal history of ovarian cancer were tested for hereditary breast and/or ovarian cancer through multigene panel testing.
- The combined frequency of pathogenic mutations in breast and/or ovarian cancer risk genes beyond BRCA1/2 was 8.3%.
- 92.9% of positive findings were clinically actionable.\(^4\)\(^5\)

**POINTS FOR YOUR PRACTICE**

- OvaNext can help you identify more patients with hereditary ovarian cancer, including those who could be missed by current testing criteria.
- Maximizing the identification of patients with hereditary cancer is critical for guiding personalized management for patients diagnosed with ovarian cancer.
- Identification of patients with hereditary cancer allows for cascade testing of at-risk relatives and tailored medical management to increase early detection and prevention of cancer.
  - For example, guidelines indicate that prophylactic oophorectomy can be considered for women with mutations in genes such as BRCA1, BRCA2, BRIP1, EPCAM, MLH1, MSH2, RAD51C and RAD51D.\(^4\)\(^5\)

**RESULTS: IMPACT ON MEDICAL MANAGEMENT**

<table>
<thead>
<tr>
<th>NCCN(^\circ) management guideline for at least one cancer type</th>
<th>92.9%</th>
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<tbody>
<tr>
<td>Consider prophylactic oophorectomy</td>
<td>47.3%</td>
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<tr>
<td>Management recommendation for non-ovarian cancer(s)</td>
<td>68.4%</td>
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**REFERENCES**

1. J. Lillyquist, et al., Frequency of mutations in a large series of clinically ascertained ovarian cancer cases tested on multigene panels compared to reference controls, Gynecol Oncol (2017).
2. Couch F et al. Expanding BRCA1/2 testing criteria to include other confirmed breast and ovarian cancer susceptibility genes. Poster Presentation ASCO 2018.