BreastNext can Identify More Patients with Hereditary Breast Cancer to Guide Medical Management

Studies support inclusion of moderate risk breast cancer genes when testing patients at-risk for hereditary breast cancer

**KEY STUDY FINDINGS**

1. A large-scale exome sequencing study of >11,000 breast and ovarian cancer patients confirmed ATM, CHEK2, and PALB2 as moderate risk breast cancer genes.¹

2. Based on a study of >89,000 breast cancer patients undergoing multigene panel testing, National Comprehensive Cancer Network (NCCN®) (v2.2017) BRCA1/2 testing criteria can help to identify patients with ATM, CHEK2, or PALB2 mutations.² ⁵

**Overall Clinical Sensitivity of NCCN® (v.2.2017) BRCA1/2 Testing Criteria by Gene**

<table>
<thead>
<tr>
<th>Gene</th>
<th>BRCA1/2 Testing Criteria</th>
<th>ATM</th>
<th>CHEK2</th>
<th>PALB2</th>
<th>BRCA1/2</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Meets BRCA1/2 testing criteria</td>
<td>92.4</td>
<td>91.3</td>
<td>93.6</td>
<td>95.7</td>
</tr>
<tr>
<td></td>
<td>Does not meet any BRCA1/2 testing criteria</td>
<td>7.6</td>
<td>8.7</td>
<td>6.4</td>
<td>4.3</td>
</tr>
</tbody>
</table>

% of Positive Patients Meeting Criteria
Studies show that multigene panels (MGP) identify more patients with hereditary cancer allowing for personalized medical management.

**KEY STUDY FINDINGS**

1. Retrospective review of >86,000 breast cancer patients indicated that compared to a 5-gene breast cancer panel, the positive rate increased by 25% with BRCAplus (8 genes) and by 44% with BreastNext (17 genes). This suggests that larger MGP increase the identification of patients with hereditary breast cancer.\(^3\)

2. Expanding testing beyond BRCA1/2 identifies more patients who may benefit from risk reducing surgical options for breast and other cancers.\(^4\)

**Surgically Actionable Findings (beyond BRCA1/2)**

*Based on NCCN v1. 2018*

<table>
<thead>
<tr>
<th>Procedure</th>
<th>Percentage</th>
<th>Count</th>
</tr>
</thead>
<tbody>
<tr>
<td>Risk-reducing mastectomy (TP53 or PTEN)</td>
<td>3.07% (N=83)</td>
<td></td>
</tr>
<tr>
<td>Risk-reducing mastectomy could be considered in the context of family history (ATM, PALB2, CHEK2, CDH1, NF1 or NBN)</td>
<td>54.22% (N=1465)</td>
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<tr>
<td>Non-breast surgical guidelines (Risk-reducing salpingo-oophorectomy: BRIP1, RAD51C, RAD51D; Hysterectomy: PTEN, Gastrectomy: CDH1)</td>
<td>7.18% (N=194)</td>
<td></td>
</tr>
<tr>
<td>No current surgical guidelines (BARD1, MRE11A, MUTYH-biallelic, or RAD50)</td>
<td>7.44% (N=200)</td>
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</tbody>
</table>

**POINTS FOR YOUR PRACTICE**

- Larger multigene panels, like BreastNext, can help you identify more patients with hereditary breast cancer.
- Several genes, including ATM, CHEK2, and PALB2 have been established as genes associated with a moderately increased risk for breast cancer.
- Maximizing identification of patients with hereditary breast cancer is important for early detection and prevention.

**REFERENCES**