Impact of a Protocol Implementation on Identification and Referral of Women At-Risk for Hereditary Breast Cancer

Chrysanthemum Davis Lawson
Valparaiso University, chrys.davis@valpo.edu

Follow this and additional works at: https://scholar.valpo.edu/gas

Recommended Citation
Davis Lawson, Chrysanthemum, "Impact of a Protocol Implementation on Identification and Referral of Women At-Risk for Hereditary Breast Cancer" (2020). Graduate Academic Symposium. 73.
https://scholar.valpo.edu/gas/73

This Poster Presentation is brought to you for free and open access by the Graduate School at ValpoScholar. It has been accepted for inclusion in Graduate Academic Symposium by an authorized administrator of ValpoScholar. For more information, please contact a ValpoScholar staff member at scholar@valpo.edu.
Impact of a Protocol Implementation on Identification and Referral of Women At-Risk for Hereditary Breast Cancer

Chrysanthemum Davis Lawson
MSN, APRN, CNS, FNP-C, DNP Student

Significance of Problem

- Breast cancer is the leading new cancer diagnosis & 2nd highest cause of cancer death in American women (American Cancer Society, 2020)
- Hereditary breast cancer is often caused by mutations in the BRCA 1 or 2 genes, with an associated 5 to 10-fold increase in breast cancer risk (Mayo Clinic, 2019)
- 10% of individuals with a gene mutation are aware of this diagnosis (Drohan et al., 2012)
- The USPSTF issued a Grade B recommendation & advised use of a breast cancer genetics referral screening tool (4)

Decision to Change Practice

- Breast Cancer Genetics Referral Screening Tool (B-RST™) received a high quality rating by USPSTF for assessing hereditary breast cancer risk (Nelson et al., 2019)
- B-RST™ Version 3.1 can be integrated in the EMR, has documented ease of use, & covers 1st & 2nd degree family history of breast & ovarian cancers, male breast cancer, & Ashkenazi Jewish heritage (Belcross et al., 2019)
- Offering medical management options to this at-risk group can promote breast cancer prevention or early detection to positively affect health outcomes (ACOG, 2019; Kiely & Schwartz, 2014)

PICOT Question

In women cared for in an obstetrical & gynecological practice (P) how does utilization of a breast cancer genetics referral screening tool (I) as compared to the current standard of care of collecting & reviewing family history in patients’ EMR (C) allow women at increased risk for hereditary breast cancer to be appropriately identified and referred for genetic counseling (O) within a twelve-week time frame (T)?

Review of Literature

Search Terms: (1) "breast neoplasm" or "breast cancer" and (2) "family history" or genetic or hereditary or "high risk" or inherited or "risk assessment" or tool and (4) refer"

Inclusion Criteria: English, female, published 2012-2019, academic journal, scholarly/peer reviewed

Exclusion Criteria: Only women with history of breast cancer, breast cancer tumor gene testing, breast cancer risk perception, risk tool used during mammography for ordering MRLs, chemoprevention

Accepted: 10 pieces of evidence were appraised (829 yielded from 6 databases, 100 reviewed, 10 duplicates)

Synthesis of Evidence

<table>
<thead>
<tr>
<th>EVIDENCE SUMMARY</th>
<th>Design</th>
</tr>
</thead>
<tbody>
<tr>
<td>Level</td>
<td>Total</td>
</tr>
<tr>
<td>I</td>
<td>2</td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td>II</td>
<td>1</td>
</tr>
<tr>
<td>III</td>
<td>5</td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td>IV</td>
<td>2</td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
</tbody>
</table>

The Evidence Level and Quality guide from the Johns Hopkins Nursing Evidence-Based Practice was used to appraise the evidence (Dang & Dearholt, 2017)

Evaluation

Primary Outcomes:
1. Identify women at-risk
2. Refer women at-risk

- Eligible: N = 1253
- Screened: n = 994
- Overall Protocol Adherence: 79.3% - achieved goal of ≥ 75%
- HRBC Candidates: n = 249
- Genetics Candidates: n = 174
- HRBC Referrals Provided: n = 57, 22.9%
- Genetics Referrals Provided: n = 32, 8.4%

Secondary Outcomes:
1. HRBC referral performance
2. Genetics referral performance

- HRBC Consultation Completed: n = 8 (14.0%)
- Genetics Consultation Completed: n = 7 (21.9%)
- HRBC Total Referrals Pre- to Post-Implementation: ↑ 51
- Genetics Total Referrals Pre- to Post-Implementation: ↑ 24

Evaluation

- Chi-Square Test for Independence: Pre- & post-implementation group demographic variables were independent, indicating sampling representative of office population for age, appt type, insurance, race, & religion
- Factorial ANOVA: Significant effects with increases in referrals to HRBC & genetics with providers using the B-RST™ to guide decision-making

Conclusion

- Use of the B-RST™ was an effective method at an Ob/Gyn office setting for identifying & providing referrals to women at-risk for hereditary breast cancer
- Continued B-RST™ use & improved participant referral performance necessary to support overall goal of medical management for promoting optimal health outcomes

Recommendations

- EBP Project Site: (1) Perform B-RST™ once yearly for all patients, (2) Improve referral provision rates & document if HRBC &/or genetics referrals were offered, accepted, &/or declined, & (3) Provide patient reported reasons for a referral being declined to aid in improving participation rates
- Health Care Community: (1) Educate nursing/APRN/PA medical students & health care providers about hereditary breast cancer risk & use of the B-RST™ & (2) Recognize & address barriers for providers ordering referrals & patients performing these consultations

Acknowledgements: I extend my most sincere gratitude to Dr. Lauren Winkler for her expertise, patience, & guidance, associates at the project health care system & colleagues at the Ob/Gyn site for their willingness to participate in this project, Dr. Cecelia Bellcross for her permission to use the B-RST™, Ms. Julia Allen for her assistance with the statistical analyses, & my network of family & friends for their incredible support.

References

Nelson et al., 2019
ACOG, 2019
Kiely & Schwartz, 2014
Belcross et al., 2019
Drohan et al., 2012
Dang & Dearholt, 2017