Integration of Genomics in Cancer Care

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Key words
Genetics, genomics, cancer, risk assessment

Abstract

Purpose: The article aims to introduce nurses to how genetics-genomics is currently integrated into cancer care from prevention to treatment and influencing oncology nursing practice.

Organizing Construct: An overview of genetics-genomics is described as it relates to cancer etiology, hereditary cancer syndromes, epigenetics factors, and management of care considerations.

Methods: Peer-reviewed literature and expert professional guidelines were reviewed to address concepts of genetics-genomics in cancer care.

Findings: Cancer is now known to be heterogeneous at the molecular level, with genetic and genomic factors underlying the etiology of all cancers. Understanding how these factors contribute to the development and treatment of both sporadic and hereditary cancers is important in cancer risk assessment, prevention, diagnosis, treatment, and long-term management and surveillance.

Conclusions: Rapidly developing advances in genetics-genomics are changing all aspects of cancer care, with implications for nursing practice.

Clinical Relevance: Nurses can educate cancer patients and their families about genetic-genomic advances and advocate for use of evidence-based genetic-genomic practice guidelines to reduce cancer risk and improve outcomes in cancer management.

The completion of the Human Genome Project in 2003 heralded a shift in cancer research focused on single genes, such as BRCA1 and BRCA2, to that of a broader perspective focused on the genome—a person’s entire genetic content and interacting factors that regulate or modify gene expression (Pasche & Absher, 2011). As a result, rapid discoveries in genetics and genomics (hereafter referred to as genomics unless specific to a single gene) are significantly impacting all aspects of health care across the life span, providing an unprecedented era of personalized medicine for persons with cancer or at increased risk for cancer (Speicher, Geigl, & Tomlinson, 2010). The National Cancer Institute (NCI) defines personalized medicine as “A form of medicine that uses information about a person’s genes, proteins, and environment to prevent, diagnose, and treat disease” (NCI, n.d., para 1). Understanding how genomics is currently influencing cancer prevention, screening, diagnosis, treatment, and survivorship is essential for optimal nursing care of patients and their families.

This article aims to introduce nurses to how genomics is currently integrated into cancer care from prevention to
Genomics in Cancer Care

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Figure 1. Four-generation pedigree with significant family history of colon and uterine cancers, in the paternal lineage; suspect for Lynch syndrome (fictitious case).

Case Study (Fictitious)

Mr. J. is a 41-year-old white man of Northern European ancestry. He presents to the hospital for a colon resection due to a biopsy-confirmed right-sided colon cancer detected during diagnostic colonoscopy for rectal bleeding. Two adenomatous polyps were also excised at that time. He has no prior cancer history and his medical history is unremarkable. His family history is significant for colon cancer in his father diagnosed at age 50, who died of disease at age 52, and in his paternal grandmother, who was diagnosed at age 51 and died of colon cancer at age 52. Additionally, one of two paternal aunts was diagnosed and died of uterine cancer at age 43 (Figure 1).

Etiology of Cancer: Sporadic, Familial, Hereditary

Genetic and genomic factors underlie the etiology of all cancer. The complexity of carcinogenesis has been attributed to accumulation of gene alterations (“mutations”), with progressive cell genome instability leading to abnormal cell proliferation, tumors, and cancer (Kinzler & Vogelstein, 1996). Abnormal genetic expression leading to cancer is most often multifactorial: genetic, infectious, radiation, environmental, hormonal, or lifestyle, due to acquired (nonhereditary) factors altering DNA structure in a specific area of the body, such as the skin, colon, breast, or blood. These tumors are referred
to as sporadic and account for about 75% of all cancers (Fletcher & Houlston, 2010). Sporadic cancers usually occur at an age of onset expected for the type of cancer (e.g., colon cancer at age 65).

The same type of cancer occurring at the expected age in more than one close relative on the same side of the family (e.g., two or more siblings with colon cancer after age 60) are sometimes referred to as familial. Familial cancer accounts for approximately 10% to 15% of cancer, likely due to the combination of environmental (sun exposure, smoking, diet, etc.) and genomic influences shared by close relatives. These genomic influences include single nucleotide polymorphisms (SNPs; pronounced “snips”) and genes of low to moderate penetrance, concepts described later in this article.

Approximately 5% to 10% of most cancers are hereditary, due to a single gene mutation in the germline (ovary or sperm) that predisposes an individual to developing certain cancers. Most germline mutations are transmitted to offspring by the mother or father during conception. The pattern of transmission is nearly always autosomal dominant, placing each first-degree relative (sibling, child, or parent) of a mutation carrier at 50% chance of inheriting the mutation. Earlier age at onset than normally expected for a particular cancer is the hallmark of hereditary cancer. Although germline mutations represent only a small proportion of cancer (Krepsich et al., 2012), the early age at onset and tremendously increased cancer risks associated with these syndromes warrant identifying mutation carriers to guide personalized prevention-focused health care. To date, more than 50 hereditary cancer predisposition syndromes have been described (Weitzel, Blazer, MacDonald, Culver, & Offit, 2011).

Penetrance refers to the proportion of individuals who will express a given trait, disorder, or disease, such as cancer. Most cancer predisposition genes are highly penetrant, meaning that the individual is likely to develop cancer at some point in their life unless risk reduction strategies are undertaken. In contrast, some genes and many SNPs are associated with low or moderate cancer risks. Genetic testing to identify carriers of a mutation or SNP conferring modestly increased cancer risk is generally of limited clinical utility in guiding care (Schwartz et al., 2008; Weitzel et al., 2011).

Differentiating between acquired and heritable genetic mutations resulting in cancer is essential in educating clients about cancer risk (MacDonald, 2011). Recognizing hereditary cancer predisposition syndromes is also key to appropriate referral of individuals to a genetics nurse-counselor-physician or other cancer genetics specialist for further evaluation.

Cancer Risk Assessment and Genetic Testing

Individual and family cancer risk can be evaluated through a CRA process. The objectives of CRA are to (a) better define cancer risks for clients and family members through the collection of detailed personal health and family history information; (b) identify individuals who may benefit from genetic-genomic testing; (c) provide risk-based cancer screening and risk-reduction strategies; (d) assess psychosocial and cultural implications of risk assessment and family communication of risk (including motivation for risk assessment; knowledge of cancer, prevention, and genetics; risk perception; health beliefs; social support; and coping strategies); and (e) provide education, counseling and psychosocial support to facilitate informed decision making (Aiello-Laws, 2011; Weitzel et al., 2011).

Genetic indicators for CRA include (a) earlier age of cancer onset than expected (e.g., breast cancer before age 45; colon cancer before age 50); (b) the same type of cancer in two or more close relatives in the same lineage; (c) two or more primary cancers in the same person; (d) constellation of cancers characteristic of a hereditary syndrome; (e) male breast cancer, ovarian cancer, or medullary thyroid cancer, at any age; (f) breast cancer in a woman of Jewish ancestry; and (g) a previously identified cancer-associated mutation in the family (Weitzel et al., 2011).

Genetic testing is medically necessary when the test result will assist in diagnosis or medical or surgical management of the client or family, including risk reduction through enhanced surveillance, chemoprevention, or surgery. Pre- and post-test counseling includes discussion of the potential costs, risks, benefits, and limitations of testing and early detection and risk reduction strategies (American Society of Clinical Oncology, 2003) and ethical, legal, and social implications (Badzek, Hanaghan, Turner, & Monsen, 2013).

Genomics of Tumor Profiling, Pharmacogenomics, and Targeted Cancer Therapy

Genomics of Tumor Profiling

Tumor profiling (also referred to as molecular profiling) includes the evaluation of genomic, proteomic (e.g., proteins), and epigenomic (see later discussion) expression factors, alone or in combination, for cancer diagnosis, prognosis, and therapeutics (Dacic, 2011). Tumors of the same histological type may have distinct mutations, resulting in differences in treatment response. Since cancers
are now known to differ molecularly as well as histologically, molecular markers in addition to tumor classification are increasingly identifying predictive and prognostic factors and guiding selection of therapy. Examples of tumor profiling techniques currently influencing clinical care include immunohistochemistry (IHC) staining, microsatellite instability (MSI) testing, and microarray analysis, each discussed in ensuing paragraphs.

**Immunohistochemistry**

IHC tumor profiling determines the level of genetic protein expression using a staining process. IHC is widely used in oncology for diagnosis, determining therapy, and identifying predictive and prognostic factors. One example of this use is the evaluation of protein expression of the human epidermal growth factor-like receptor 2 (HER2) in breast cancer tumors. Overexpression of HER2 is an important prognostic and predictive marker implicated in the pathogenesis and aggressive behavior of approximately 25% of invasive breast cancers (Mehta, Jain, & Badve, 2011). Personalized treatment of patients with HER2-positive breast cancer warrants specific therapy with trastuzumab to manage the disease (Dancey, Bedar, Onetto, & Hudson, 2012; Mehta et al., 2011).

IHC is also used in numerous other cancers to identify important biomarkers for diagnosis, subtyping of tumors, characterization of tumor site, and prognostic and therapeutic management (Luongo de Matos, Trufelli, Luongo de Matos, & da Silva Pinhal, 2010). In colorectal cancer, IHC can be used to assess protein expression of the mismatch repair genes MSH2, MLH1, MSH6, and PMS2. Absent or low expression of the protein product of these genes is useful in identifying tumors that are suspect for Lynch syndrome and warrant further evaluation, including consideration of germline testing (Beamer et al., 2012). For example, absence of MLH1 protein expression may be sporadic due to an acquired BRAF V600E gene mutation, or methylation (discussed in a later section), or hereditary due to a germline MLH1 mutation associated with Lynch syndrome (Boland, Koi, Chang, & Careythers, 2008). Lynch syndrome is a hereditary cancer syndrome characterized by high risk for colon and uterine cancers and increased risk for ovarian and other extracolonic malignancies.

**Microsatellite Instability**

MSI testing tumor profiling uses a panel of markers to assess repetitive sequences of DNA nucleotides that are part of the mismatch repair gene process. These repetitive sequences are highly fragile (unstable) and prone to DNA replication errors. MSI testing has two primary purposes in colon cancer: to determine the choice of chemotherapy in stage II and III disease (therapeutic) and to aid in identifying Lynch syndrome (predictive). Microsatellite unstable (i.e., MSI) tumors are sensitive to irinotecan-based chemotherapy but resistant to 5-fluorouracil (5-FU)-based chemotherapy. While not diagnostic for Lynch syndrome since about 15% of sporadic colon, uterine, and gastric cancers exhibit this instability, MSI-high tumors warrant evaluation of Lynch syndrome (Kohlmann & Gruber, 2004; Walsh et al., 2010). A number of cancer centers in the United States are performing reflex (automatic) MSI or IHC testing as screening tests for Lynch syndrome upon diagnosis of CRC (Beamer et al., 2012). Continuing with the case of Mr. J, an important strategy in his cancer care and for his family’s health care is determining if he has sporadic or Lynch syndrome-related hereditary colon cancer.

**Case Study– Tumor Profiling**

Mr. J underwent a partial colectomy for stage III adenocarcinoma of the right colon. MSI testing revealed the tumor to be unstable at all five markers used (MSI-H), which influenced his chemotherapy regimen (see later discussion). IHC revealed protein expression of MSH2, MSH6, and PMS2 but absence of the MLH1 protein. In accordance with the National Comprehensive Cancer Network (NCCN, 2012) standard of care for all patients diagnosed with colon cancer prior to age 50 (regardless of family history), he was referred for a genetics evaluation. An advanced practice nurse credentialed in genetics (APNG) obtained his personal and family history, including a detailed four-generation pedigree (see Figure 1). Given that his family history and the IHC and MSI results were consistent with Lynch syndrome, the patient was counseled about and provided informed consent for Lynch syndrome genetic testing. IHC helped to direct mismatch repair gene testing to only MLH1, a cost-effective strategy. Testing was performed using his blood sample as the source of DNA. Results identified an MLH1 gene mutation, which is diagnostic for Lynch syndrome. Mr. J has informed his paternal family members of the need for consideration of genetic counseling or testing to determine if they have the syndrome and guide risk-reduction strategies.

**Microarray Analysis and Global Expression Analysis**

Microarray is a method to evaluate the expression or genomic alteration of multiple genes simultaneously.
Microarray analysis can also be used to detect SNPs (see later discussion). In tumor profiling, microarrays are used to compare gene expression in a tumor to that of normal tissue (Cleator & Ashworth, 2004). These comparisons provide insights into the underlying genomic pathways involved in carcinogenesis in diverse populations, important in personalized health care. The use of microarray analysis has also led to the development of molecular signatures for predicting prognosis in several cancers. For example, Oncotype DX® (Genomic Health, Inc., Redwood City, CA, USA) molecular assays for multi-gene expression testing provide a score predicting the risk of disease recurrence. The score is used to help refine treatment decisions such as the benefit of chemotherapy for early stage breast and colon cancer patients (Genomic Health, 2004–2012). Microarray analysis also allows the classification of breast tumors into various subtypes such as HER2-like, basal-like, and luminal A or luminal B tumor characteristics, important data related to differences in survival (Mehta et al., 2011). Similarly, microarrays have helped explain the development of benign pheochromocytomas, medullary thyroid cancers, and skeletal abnormalities in multiple endocrine neoplasia syndromes (Jain et al., 2004) and have identified gene expression differences in papillary and follicular thyroid cancers that may be useful in diagnosis (Aldred et al., 2004).

### Single Nucleotide Polymorphisms

Single nucleotide polymorphisms are genetic variations resulting from a single nucleotide base (A, C, T, or G) change in the DNA sequence. SNPs account for approximately 90% of the genetic variation in humans. It is estimated that the human genome has more than 30 million SNPs (Diamandis, White, & Yousef, 2010; Reich, Gabriel, & Altshuler, 2003). Recent studies have contributed to understanding the role of specific SNPs in genetic predisposition to cancer, heart disease, diabetes, and other chronic diseases. In addition, SNP profiles play an important role in identifying cancer genes, risk, prognosis, and comorbidities associated with cancer, as well as drug responses and interactions.

### SNPs and cancer gene identification, cancer risk, prognosis, and comorbidities

One of the most robust approaches to identifying SNPs is through genome-wide association studies (GWAS). GWAS are presented in detail by Conley, Biesecker, Gonsalves, Merkle, Kirk, & Aouizerat (2013) in this issue. As an example, however, a meta-analysis of two large GWAS studies reported four new SNPs associated with risk for colorectal cancer. These four SNPs and six previously identified SNPs represent less than 1% of familial colorectal cancer risk but collectively could account for about 6% of familial colorectal cancer risk (Houlston et al., 2008). Genetic variants or SNPs have also been found to identify individuals who may be at risk for several other cancers. In addition, SNPs are associated with prognosis in various malignancies, including prostate (Gallagher et al., 2010) and head and neck cancers (Olivieri et al., 2009). An example of SNPs in relation to comorbidity is that multiple SNPs within three receptor genes are associated with lymphedema in women with breast cancer (Newman et al., 2012). These and future studies will pave the way toward personalized and improved cancer care.

### SNP and Drug Responses-Interactions and Pharmacogenomics

Pharmacogenomics is the study of how genomic factors (including SNPs) and acquired mutations in tumors determine an individual’s response or toxicity to drugs—directly impacting personalized health care, particularly in cancer management. Numerous genes and SNPs alter drug metabolism genetic pathways, resulting in increased (induced) or decreased (inhibited) metabolism (O’Donnell & Ratain, 2012). SNPs also affect drug transport, absorption, distribution, elimination, and action (Wang, McLeod, & Weinshilboum, 2011). The following discussion provides a few examples of pharmacogenomics in oncology.

A group of 40 enzyme families known as cytochrome P450 (CYP450) are responsible for a large segment of drug metabolism, with about 20% of drug metabolism attributed to a specific enzyme, CYP2D6. Endoxifen, the major active metabolite of tamoxifen, a drug used in the adjuvant treatment of women with estrogen receptor-positive breast cancer, is inhibited (decreased) by certain CYP2D6 variants, rendering it less effective in preventing disease recurrence (Kiyotani et al., 2010), resulting in shorter relapse time and a worse event survival rate (Schroth et al., 2007). In addition, CYP2D6 is inhibited by fluoxetine and paroxetine, medications frequently given to breast cancer patients for the control of hot flashes and depression. Venlafaxine may be a better choice for management of these symptoms because it does not interfere with tamoxifen metabolism (Prows, 2011). While genetic testing for variants in the CYP2D6 gene is available, it is not currently the standard of care (O’Donnell & Ratain, 2012). However, nurses can educate clients that these medications interfere with tamoxifen metabolism, reducing its effectiveness.

Nongenetic factors such as certain foods and herbal products may also adversely affect drug metabolism, transport, and response. For example, grapefruit juice...
Table 1. Selected Genetic Markers and Their Application in Cancer Treatment

<table>
<thead>
<tr>
<th>Tumor</th>
<th>Genetic marker</th>
<th>Description-application</th>
<th>Drug-implication</th>
</tr>
</thead>
<tbody>
<tr>
<td>Breast</td>
<td>HER2 amplification</td>
<td>HER2-positive tumors indicates need for additional therapy.</td>
<td>Trastuzumab, lapatinib</td>
</tr>
<tr>
<td>Breast</td>
<td>OncotypeDx®</td>
<td>Microarray analysis of 21 genetic markers. Identifies if patients with early stage ER-positive, lymph node negative, Her2-negative tumors may benefit from adjuvant chemotherapy.</td>
<td>Chemotherapy evaluation</td>
</tr>
<tr>
<td>Colorectal cancer</td>
<td>OncotypeDx®</td>
<td>Microarray analysis of 12 genetic markers. Identifies if patients with stage II disease may benefit from adjuvant chemotherapy.</td>
<td>Chemotherapy evaluation</td>
</tr>
<tr>
<td></td>
<td>KRAS mutation</td>
<td>Tumors with a KRAS mutation do not respond to treatment with EGFR monoclonal antibodies. KRAS status should be evaluated prior to treatment.</td>
<td>Cetuximab, panitumumab contraindicated</td>
</tr>
<tr>
<td></td>
<td>UGT1A1*28</td>
<td>Patients with a germline UGT1A1 variant are at risk for higher toxicity (especially neutropenia, diarrhea).</td>
<td>Irinotecan; consider dosage adjustment or alternate drug</td>
</tr>
<tr>
<td>Leukemia</td>
<td>BCR-ABL</td>
<td>Ph + CML; Ph + ALL. Presence of a BCR-ABL gene mutation indicates response to tyrosine kinase inhibitor therapy.</td>
<td>Imatinib, dasatinib, nilotinib</td>
</tr>
<tr>
<td>Non-small-cell lung cancer</td>
<td>EGFR mutation</td>
<td>EGFR mutation is associated with a better response to an EGFR-tyrosine-kinase inhibitor.</td>
<td>Erlotinib, gefitinib</td>
</tr>
<tr>
<td>Breast, ovarian</td>
<td>BRCA1/BRCA2 mutation</td>
<td>Patients with a germline BRCA gene mutation who have disease progression following initial therapy may respond to treatment with PARP inhibitors.</td>
<td>Olaparib, for example</td>
</tr>
<tr>
<td>Melanoma</td>
<td>BRAFT600E mutation</td>
<td>Tumors with this BRAFT6 mutation are sensitive to a kinase inhibitor</td>
<td>Vemurafenib indicated</td>
</tr>
</tbody>
</table>

Note. ER = estrogen receptor; EGFR = epidermal growth factor receptor; Ph = Philadelphia chromosome; CML = chronic myelogenous leukemia; ALL = acute lymphoblastic leukemia; PARP = poly ADP ribose polymerase.

inhibits the function of p-glycoprotein (important for absorption) and an intestinal enzyme (CYP3A4) important in the metabolism of many drugs (Dancey et al., 2012; Imai & Takaoka, 2006; O'Donnell & Ratain, 2012). Persons taking oral methotrexate, a drug affected by CYP3A4, should be cautioned to avoid grapefruit juice as doing so may raise plasma blood levels to that of toxicity (Prows, 2011).

Another example of genomic healthcare in oncology is in the use of irinotecan. Irinotecan is used to treat metastatic colorectal cancer. Its active metabolite, SN38, is inactivated by the genetic variant uridine diphosphatase glucorosyltransferase 1A (UGT1A). UGT1A*28 homozygotes (persons with two copies of the same genetic variant) are at risk for severe neutropenia and diarrhea. Testing is available to identify individuals with this variant prior to use of irinotecan (O'Donnell & Ratain, 2012).

Table 1 provides some examples of how the choice and dose of chemotherapeutic agents and other drugs may depend on a person's personal genome or the genome of their tumor. Nurses knowledgeable about pharmacogenomics can caution clients about drug interactions and help clients to understand why they may be receiving a different treatment for the same disease than another patient. Nurses can also alert patients to the importance of reporting use of prescription and nonprescription medications, herbal products, and foods that can interfere with effectiveness or increase drug toxicity (Prows, 2011).

Epigenetics

Factors other than DNA sequence variations may also influence gene functioning. These factors include epigenetics, nongenetic events occurring during cell development and proliferation that alter gene expression without changing the actual DNA sequence. An important type of epigenetics in carcinogenesis is methylation, a biochemical process by which a methyl (CH3) group attaches to cytosines (a DNA nucleotide base), thereby “turning off” the gene so that it is no longer expressed. Certain genes are frequently methylated in some cancers, such as the RB1 gene involved in retinoblastoma (Das & Singal, 2004).

As previously discussed, methylation testing helps differentiate sporadic colon cancers from Lynch syndrome. In sporadic colorectal cancer, aberrant MLH1 methylation leads to deficient expression of the MLH1 protein despite a normal MLH1 gene sequence. In Lynch syndrome, non-expression of the MLH1 protein results from an abnormal MLH1 gene sequence (not from methylation). Future methylation studies may provide additional clues to cancer diagnosis, targeted therapies, and survival (Das & Singal, 2004).
Cancer Management–Targeted Therapy and Pharmacogenomics

Targeted therapy encompasses providing personalized treatment based on molecular features of a patient’s tumor. Identification of these tumor-specific features allows the development of drug targets that reach signaling pathways associated with cell growth, proliferation, and survival. Targeted therapies may have a lower, more manageable, and tolerable toxicity profile than conventional chemotherapy (O’Donnell & Ratain, 2012).

Bevacizumab is an example of a targeted therapy used in conjunction with chemotherapy for treating metastatic colon, Her2-negative breast, and other solid tumors. This humanized monoclonal antibody binds to vascular endothelial growth factor, a key protein in tumor angiogenesis, thereby inhibiting blood supply to the tumor. Toxicities associated with bevacizumab include bleeding, hypertension, and proteinuria (Marrs & Zubal, 2009). Nurses who understand the mechanism of action and toxicities associated with these therapies are better able to identify and manage adverse reactions promptly. Table 1 presents examples of genetic markers and their application in cancer treatment and targeted therapy.

Case Study–Targeted Therapy

In addition to the colon resection, Mr. J underwent adjuvant chemotherapy with FOLFOX (5-FU, oxaliplatin, leucovorin) based on having high-risk stage III colon cancer and on his tumor profile. His hospitalization was uneventful and he responded well to treatment. His follow-up personalized care will be evidence based, focusing on his diagnosis of Lynch syndrome, genomic make-up, and his cultural values and beliefs.

Tumor profiling was integral to the treatment, targeted therapy, and personalized management of care for Mr. J. MSI was used to predict response to, and guide choice of, chemotherapy. Patients with MSI-H tumors do not benefit from single-agent 5-FU chemotherapy (Ng & Schrag, 2010). In a pooled analysis of several studies, patients with MSI-H stage II tumors who received adjuvant 5-FU fared worse in both disease-free and overall survival compared with those who received no adjuvant therapy (Sargent et al., 2010).

Case Discussion–Additional Management Considerations

MSI testing was important in determining the most effective adjuvant chemotherapy for Mr. J. Testing for Lynch syndrome was also important in his care because individuals with this hereditary cancer syndrome warrant earlier and enhanced surveillance to prevent an initial or subsequent cancer or detect cancer at an early stage when chemotherapy may not be needed. Furthermore, some patients may opt for full colectomy at the time of initial surgery due to the high risk for second primary colorectal tumors and to avoid frequent colonoscopies. Women with Lynch syndrome may also opt for a hysterectomy and oophorectomy due to the associated increased risk for uterine and ovarian cancers. Moreover, Mr. J’s first-degree relatives have a 50% chance of inheriting the same mutation. As such, it is important for nurses to discuss the personal and family implications of

Table 2. Clinical Resources

<table>
<thead>
<tr>
<th>Name</th>
<th>Purpose</th>
<th>Resources/link</th>
</tr>
</thead>
<tbody>
<tr>
<td>NCI–types of cancer</td>
<td>Accurate, up-to-date, comprehensive cancer information from the U.S. government’s principal agency for cancer research</td>
<td><a href="http://www.cancer.gov/">http://www.cancer.gov/</a></td>
</tr>
<tr>
<td>Gene reviews (University of Washington)</td>
<td>Expert-authored, peer-reviewed, current disease descriptions that apply genetic testing to the diagnosis, management, and genetic counseling of patients and families with specific inherited conditions. Includes reviews on numerous hereditary cancer syndromes (e.g., Lynch syndrome; hereditary breast and ovarian cancer; familial adenomatous polyposis).</td>
<td><a href="http://www.ncbi.nlm.nih.gov/projects/geneTests/static/about/content/reviews.shtml">http://www.ncbi.nlm.nih.gov/projects/geneTests/static/about/content/reviews.shtml</a></td>
</tr>
<tr>
<td>National Comprehensive Cancer Network</td>
<td>An alliance of 21 of the world’s leading cancer centers, and authoritative source of comprehensive cancer guidelines including cancers by site; guidelines for detection, prevention and risk reduction; guidelines for supportive care and guidelines for age-related care</td>
<td><a href="http://www.nccn.org/professionals/physician_gls/f_guidelines.asp">http://www.nccn.org/professionals/physician_gls/f_guidelines.asp</a> Requires free user login</td>
</tr>
</tbody>
</table>

Note. NCI = National Cancer Institute.

Journal of Nursing Scholarship, 2013; 45:1, 43–51. © 2013 Sigma Theta Tau International
Lynch syndrome with Mr. J, including the importance of informing his at-risk relatives (Maradiegue, Jasperson, Edwards, Lowstuter, & Weitzel, 2008).

**Summary**

Genomic care is no longer limited to a small group of patients but is central to the care for all individuals, including those diagnosed with cancer. The rapidly evolving field requires that nurses be aware of developments in genomics and its impact on risk assessment, prevention, diagnosis, and management. Knowledgeable nurses can incorporate evidence-based interventions and expert professional guidelines into practice to improve overall health, quality of life, and safety of patients. Table 2 provides some useful clinical resources to assist nurses in familiarizing and staying current with cancer genomic knowledge.

**Acknowledgments**

The authors thank Sandra Belderian, MPH, City of Hope, for editorial assistance.

**References**


Aldred, M. A., Huang, Y., Liyanarachchi, S., Pellegrata, N. S., Gimm, O., Jhiang, S., ... Eng, C. (2004). Papillary and follicular thyroid carcinomas show distinctly different microarray expression profiles and can be distinguished by a minimum of five genes. *Journal of Clinical Oncology*, 22(17), 3531–3539.


Krepischi, A., Achatz, M. I., Santos, E., Costa, S., Lisboa, B., Brentani, H., ... Rosenberg, C. (2012). Germline DNA copy...


