

Deconstructing Breast Cancer Heterogeneity: Clinical Implications for Women With Basal-Like Tumors

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One in eight women in the United States will develop breast cancer in her lifetime, and breast cancer is the second leading cause of cancer death among women (DeSantis, Ma, Bryan, & Jemal, 2013). Breast cancer embodies several clinically distinct diseases that result from the interaction of varied genetic and environmental influences, many of which are not yet well understood. The inherent clinical and molecular heterogeneity of breast cancer poses a challenge for researchers and clinicians. Breast tumors consist of several pathologic subtypes with different clinical presentations and outcomes, and patients show a diverse range of responses to a given treatment (Sorlie, 2004). Because of the aggressive and treatment refractory nature of basal-like breast cancer (BLBC), the goal of the current article is to investigate BLBC in depth, with a particular focus on genetic and environmental risk factors and current clinical targets for this tumor subtype. A brief overview of the five main breast cancer subtypes will also be provided to understand BLBC within the broader context of breast cancer heterogeneity.

Historically, breast tumors were classified via immunohistochemical (IHC) protein staining for estrogen receptor (ER), progesterone receptor (PR), or human epidermal growth factor receptor 2 (HER2), but the advent of gene expression microarrays has made a more comprehensive molecular assessment possible (Litsas, 2013). Major breakthroughs in the understanding of breast cancer heterogeneity have been made by Perou et al. (2000) and Parker et al. (2009) by showing that multiple types of breast tumors exist, each with distinct prognosis and risk indicators defined by differential gene expression (see Table 1). The five main subtypes of breast cancer that reflect distinct gene-expression patterns are luminal A, luminal B, normal-like, HER2-enriched, and basal-like (Yehiely, Moyano, Evans, Nielsen, & Cryns, 2006). More than 95% of all breast cancers arise within the milk ducts of the breast

Purpose/Objectives: To compare and contrast the molecular and environmental factors contributing to basal-like breast cancer and highlight the clinical implications for women with this phenotype.

Data Sources: CINAHL® and PubMed databases, journals, and citation indices were searched using the key word *basal-like* in combination with *breast cancer*, *epigenetic*, *treatment*, *subtype*, *risk factor*, and *BRCA1* to synthesize the literature on the multiple underpinnings of basal-like breast cancer.

Data Synthesis: Research findings related to the molecular foundation of basal-like breast cancer were integrated with knowledge of nongenetic contributing risk factors. Approved therapies and those under development were summarized with the goal of improving understanding for research and practice.

Conclusions: Of the five subtypes of breast cancer, the basal-like subtype has the shortest survival and poorest prognosis. The development of gene expression assays with epigenetic studies has enabled reliable identification of the basal-like subtype and has shed light on novel therapeutic possibilities. Clinical trials for basal-like breast cancer are underway, and the potential for individualized treatments for women with this subtype show promise.

Implications for Nursing: The main difficulties with basal-like breast cancer are its aggressive course, treatment refractory nature, and complex biology, all of which pose real challenges for clinical management and patient education. Oncology nurses play a pivotal role in providing holistic care and patient support. Therefore, nurses must understand the complexity of the clinical presentation and the underlying biology of this cancer subtype.

Key Words: basal-like; breast cancer; risk factors; epigenetic; treatment; BRCA1

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(Tomaskovic-Crook, Thompson, & Thiery, 2009). The origin of the terms *luminal* and *basal* refer to the location of either secretory (inner lumen) or basal (outer lumen) epithelial cell types, which have distinct hormone responsiveness and gene expression patterns (Creighton, 2012; Millikan et al., 2008).