Commentary
Volume 13:4, 2022

Journal of Molecular Biomarkers & Diagnosis

ISSN: 2155-9929 Open Access

Insights of Breast Cancer in Women

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Description

Breast cancer (BC) is the fifth leading cause of cancer-related deaths worldwide, with an estimated lifetime risk of 8-12%. Although the cancer-related mortality rate has decreased in several countries, this benefit has not been shared equally by young women with cancer in many parts of the world. Because it has been applied to BC in women aged 35, 40, or 50 years, as well as BC in premenopausal women, the operational definition of BC in young women (BCYW) is generally flexible. In this study, we defined BCYW as BC in women aged 40 years old, based on a recent consensus based on tumour clinical features. The current trend of a high incidence of aggressive BC in women aged 40 or 35 years, on the other hand, calls into question the validity of growing age as a risk factor for BCYW. The prevalence of BCYW is approximately 2-6% in Western countries and 10-20% in Asian countries, indicating that BCYW is becoming a growing concern globally, including in countries with a large young population, such as India.

The increased relapse rate in BCYW is also likely to be influenced by pathways involved in tumour dormancy regulation and bi-directional tumor–stroma interactions. This area of BC research has received little attention, particularly in relation to hormone receptors, nuclear oestrogen signaling, and non-genomic oestrogen signaling. Many studies have been conducted in the literature to investigate the role of stromal cell types in the modification of BC phenotypes. A study on age-related genes derived from normal breast tissues, for example, found that a subset of aggressive breast tumours in young patients express genes that are upregulated in young normal breast tissues [1-3]. The reason for this up regulation, as well as the significance of tumor-associated genes in normal breast tissues, are unknown. Another large study found 1408 and 1150 unregulated and down regulated genes, respectively, in normal breast tissues from donors aged 27-66 years with no history of breast cancer, indicating the importance of adipogenesis and inflammation in BC progression.

Because the nature of the mammary gland stroma is known to be markedly modified by ovarian hormones, growth factors, and soluble factors in both normal and cancerous tissues, the genomic landscape of the normal mammary gland (as well as breast tumours) is expected to be further modified by menstrual cycle phases, breast-feeding status, and pregnancy phase - all of which are components of women's reproductive years. In this context, a genomic study described the nature of differentially expressed genes (DEGs) in the normal mammary glands of young women during the luteal and follicular stages of the menstrual cycle. This study discovered that 221 genes were up regulated during the luteal phase, many of which are known to play established roles in BC progression [4,5].

These genomic studies on normal breast tissues highlight the importance of altered gene or gene set expression in the biology of the mammary gland and BC. These studies, however, have not taken into account BCYW 40 years. The current study was undertaken to determine the nature of genomic overlaps between age-specific unique genes in BCYW and matched adjacent normal or normal breast tissues, as well as to explore changes in the function of BC subtypes and BC laterality using BC genomic datasets. We focused the TCGA breast invasive carcinoma database and selected the mRNA expression z-scores relative to diploid samples (RNA Seq V2 RSEM) and protein level z-scores (mass spectrometry by CPTAC) with 2 as the expression cut-off value to validate the expression of 60 genes uniquely upregulated in breast tumours from patients aged 40 years from differential expression analysis. After removing genes with no mRNA or protein expression, we chose 15 genes with data at both mRNA and protein levels as an example of mRNA–protein correlation and displayed the expression pattern as a heatmap.

Conflict of Interest

None.

References

1. Sung, Hyuna, Jacques Ferlay and Rebecca L. Siegel, et al. "Global cancer statistics 2020: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries." *CA A Cancer J Clin* 71 (2021): 209-249.
2. Hendrick, R. Edward, Mark A. Helvie and Debra L. Monticciolo. "Breast cancer mortality rates have stopped declining in US women younger than 40 years." *Radiol 299* (2021): 143-149.
3. Kumar, Rakesh, Catarina Abreu and Masakazu Toi, et al. "Oncobiology and treatment of breast cancer in young women." *Cancer Metastasis Rev* (2022): 1-22.
4. Kim, Hee Jeong, Seonok Kim and Rachel A. Freedman, et al. "The impact of young age at diagnosis (age< 40 years) on prognosis varies by breast cancer subtype: A US SEER database analysis." *The Breast* 61 (2022): 77-83.
5. Woodward, Terry L, Jian Wei Xie and Sandra Z. Haslam. "The role of mammary stroma in modulating the proliferative response to ovarian hormones in the normal mammary gland." *J Mammary Gland Biol Neoplasia* 3 (1998): 117-131.

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Received: 02-Apr-2022, Manuscript No. Jmbd- 22-66892; **Editor assigned:** 04-Apr-2022, Pre QC No. P-66892; **Reviewed:** 18-Apr-2022, QC No.Q-66892; **Revised:** 23-Apr-2022, Manuscript No.R-66892; **Published:** 30-Apr-2022, DOI: 10.37421/2155-9929.2022.13.523.

How to cite this article: Richard, Forbes. "Insights of Breast Cancer in Women." *J Mol Biomark Diagn* 13 (2022): 523.