Breast Cancer Care-It’s Time to Rethink and Redesign

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Summary

Notoriosly recognized as the principal cause of mortality among women worldwide, breast cancer calls for an immediate redressal in order to devise combative strategies. Currently, Northern America and Western Europe experience more than half of the global burden of breast cancer [1]. However, as recently reported by International Agency for Research on Cancer (IARC), rapid societal and economic transitions herald an epidemiological shift in the incidence, with more low income countries projected for an increased burden of breast cancer [2]. Although the incidence rates remain higher in more developed countries, mortality and morbidity are higher in less developed regions, attributable to late detection and lack of access to advanced medical amenities. Regardless of epidemiological prevalence, the etiological determinants of breast cancer development remain common and include age, family history, genetic risk factors such as BRCA1 and BRCA2 mutations and hormonal risk factors [3]. Although viruses have been etiologically associated with many cancers, a viral etiology to breast cancer is at best speculative. There is conflicting evidence of roles of viruses such as human mammary tumor virus, human papillomavirus, Epstein-Barr virus, human cytomegalovirus, herpes simplex virus and measles virus in breast cancer development [4]. Nonetheless, a recent development that levels of mutagenic antiviral enzyme APOBEC3B are elevated in a majority of breast cancers warrants a re-visit to the role of viruses in breast cancer pathogenesis [5]. Keeping in view the current scenario, there is an urgency to assess the worldwide trends and risk factors for prediction of future scenarios with the ultimate goal of developing effective, affordable and prioritized approaches for breast cancer control.

On the basis of gene expression profiling, breast cancers are classified into four major subtypes: luminal A, luminal B, HER2+ and basal-like [6] which incidentally also form the basis for breast cancer therapy, responsiveness and patient outcome. Endocrine therapies that target the estrogen and estrogen receptor (ER) signaling pathways are the cornerstone of breast cancer treatment for the majority of patients. However, 25%–30% of breast tumors do not express ER and do not develop. In developed countries, mortality and morbidity are higher in less developed regions, attributable to late detection and lack of access to advanced medical amenities. Regardless of epidemiological prevalence, the etiological determinants of breast cancer development remain common and include age, family history, genetic risk factors such as BRCA1 and BRCA2 mutations and hormonal risk factors [3]. Although viruses have been etiologically associated with many cancers, a viral etiology to breast cancer is at best speculative. There is conflicting evidence of roles of viruses such as human mammary tumor virus, human papillomavirus, Epstein-Barr virus, human cytomegalovirus, herpes simplex virus and measles virus in breast cancer development [4]. Nonetheless, a recent development that levels of mutagenic antiviral enzyme APOBEC3B are elevated in a majority of breast cancers warrants a re-visit to the role of viruses in breast cancer pathogenesis [5]. Keeping in view the current scenario, there is an urgency to assess the worldwide trends and risk factors for prediction of future scenarios with the ultimate goal of developing effective, affordable and prioritized approaches for breast cancer control.

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Breast cancer diagnosis relies on combinatorial approach consisting of clinical and physical examinations, imaging mammography and immuno-histochemical analysis. Improved imaging methods and screening programs as well as emergence of novel prognostic and predictive biomarkers have brought about a dramatic change in the field of breast cancer diagnosis and therapeutic decision procedures. Biomarkers used in routine breast cancer assessment include ER, progesterone receptor (PgR) and HER2 [10]. In addition, multiple panels of novel biomarkers are currently under assessment for their clinical competence. Major efforts including proteomics-based approaches are underway to simplify breast cancer diagnosis through identification and validation of biomarkers which can be accessed with minimally invasive procedures such as serum biomarkers, circulating tumor cells, circulating cell-free DNA (mitochondrial or nuclear) and tumor-specific microRNA [10]. Another attractive concept currently under evaluation is utilization of integrated microarray-led transcriptomic and magnetic resonance spectroscopy based metabolomic profiling of breast cancer samples as diagnostic, prognostic or predictive tool for molecular classification of the disease [11]. Development and diffusion of such breakthrough strategies has revolutionized breast cancer diagnostics, however critical questions have arisen about the translation of these approaches from bench to the bedside. The answer lies in following a multi-omics’ line of action that includes proteomics, transcriptomics, genotyping and metabolite profiling of patient samples, for complete molecular dissection of the disease, which can prove to be invaluable in routine breast cancer therapy decision making. However, such thorough approach, informative and ingenious as it may be, presents an uphill challenge to financially-stretched healthcare systems worldwide. Thus it is paramount that med-tech companies prioritize their R & D goals
and chase cost-saving ideas, so that only the most cost-effective technology gets to the market and is able to offset the overall cost of medical treatment and improve patient outcome.

Although the incidence of breast cancer is on a rise, the mortality rates are declining, owed to earlier diagnosis, better surgical and radiotherapy techniques and improved adjuvant therapies. The proposition of cancer immunotherapy has met with overwhelming enthusiasm, several studies have demonstrated importance of cytotoxic and immuno-suppressive T cells in therapeutic response and clinical outcomes. The role of noncoding RNAs such as the differential ratios of antisense-to-sense transcripts in normal and breast cancer cells is being increasingly appreciated. Undoubtedly, these are exciting times for breast cancer research, which can inspire collaborations among oncologists, surgeons, geneticists and drug developers, to understand and assimilate the research trends, in order to guarantee a future with improved diagnostic, prognostic and therapeutic regimes aimed at better clinical outcome and patient care.

References