REVIEW

SNP array technology: an array of hope in breast cancer research

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Abstract

Breast cancer is the most common malignancy in women worldwide. The incidence of breast cancer in Malaysia is lower compared to international statistics, with peak occurrence in the age group between 50 to 59 years of age and mortality rates of 18.6%. Despite current diagnostic and prognostic methods, the outcome for individual subjects remain poor. This is in part due to breast cancers' wide genetic heterogeneity. Various platforms for genetics studies are now employed to determine the identity of these genetic abnormalities, including microarray methods like high-density single-nucleotide-polymorphism (SNP) oligonucleotide arrays which combine the power of chromosomal comparative genomic hybridization (cCGH) and loss of heterozygosity (LOH) in the offering of higher-resolution mappings. These platforms and their applications in highlighting the genomic alteration frameworks manifested in breast carcinoma will be discussed.

Keywords: breast carcinoma, microarray, single-nucleotide-polymorphism, comparative genomic hybridization, loss of heterozygosity

INTRODUCTION

Worldwide, breast cancer remains the most common form of malignancy in women with approximately 1.38 billion cases reported in the year 2008.1 In the United States of America, breast carcinoma was the most prevalent non-cutaneous form of malignancy in 2010, accounting for about 207,090 new cases,2 and contributing to a total of 40,230 cases of projected mortality amongst female patients. In Malaysia, 31.3% of the total number of new cancer cases in female patients was breast cancer, and the highest age-standardized rate (ASR) (59.9 per 100,000) was seen in the Chinese community, followed by Indians (54.2 per 100,000) and Malays (34.9 per 100,000).3 Although Malaysia's breast cancer incidence was lower when compared to Western statistics,4 the incidence was high when compared with other prominent Asian countries such as China (Beijing), Japan (Hiroshima), Korea (Seoul), and India (Chennai).5 The peak incidence in Malaysia was in the age group of between 50 to 59 years old,6 except for Indian patients who peak after the age of 60 years old.7 The mortality of breast carcinoma in Malaysia have been documented at a disconcerting number of 1,716, which is approximately 18.6% of the total cases.8

In current practice, clinical factors (anatomy, morphology and pathology) are utilized to categorize breast carcinomas for diagnostic, prognostic, and therapeutic purposes. Despite the well-established criteria in the assessment of these clinical factors, outcome for individual subjects remain difficult to predict. Even with well-worked out diagnoses, current existing therapeutic plans could not optimally treat all breast carcinoma cases.9 This is because, like most human cancer, breast carcinoma's heterogeneous nature is underpinned by a wide array of genetic alterations. These encompass those that extend from gross and structural-based chromosomal aberrations to diminutive point mutations. The alterations involved manifest at the molecular level to affect established equilibrium on the controlling and functional aspects of individual genes, as well as impinge upon the appropriate cellular network which ultimately leads to chaotic genomic behaviour that favours carcinogenesis. Uncovering these