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Analysis of Saudi Breast Cancer Patients' Primary Tumors using Array Comparative Genomic Hybridization

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Abstract : Breast cancer is the second most common cause of cancer death worldwide and is the most common malignancy among Saudi females. During breast carcinogenesis, a wide-array of cytogenetic changes involving deletions, or amplification, or translocations, of part or whole of chromosome regions have been observed. Because of the limitations of various earlier technologies, newer tools are developed to scan for changes at the genomic level. Recently, Array Comparative Genomic Hybridization (aCGH) technique has been applied for detecting segmental genomic alterations at molecular level. In this study, aCGH was performed on twenty breast cancer tumors and their matching non-tumor (normal) counterparts using the Agilent 2x400K. Several regions were identified to be either amplified or deleted in a tumor-specific manner. Most frequent alterations were amplification of chromosome 1q, chromosome 8q, 20q, and deletions at 16q were also detected. The amplification of genetic events at 1q and 8q were further validated using FISH analysis using probes targeting 1q25 and 8q (MYC gene). The copy number changes at these loci can potentially cause a significant change in the tumor behavior, as deletions in the E-Cadherin (CDH1)-tumor suppressor gene as well as amplification of the oncogenes-Aurora Kinase A. (AURKA) and MYC could make these tumors highly metastatic. This study validates the use of aCGH in Saudi breast cancer patients and sets the foundations necessary for performing larger cohort studies searching for ethnicity-specific biomarkers and gene copy number variations.

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