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PROGNOSTIC GENETIC MARKERS IN PRE- AND POSTMENOPAUSAL BREAST CANCER PATIENT COHORT FROM A TERTIARY CARE CENTER IN SRI LANKA

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Breast cancer is one of the major causes of morbidity among women in Sri Lanka, of which management is challenging due to the limited accuracy of existing classical prognostic markers. Therefore, prognostic molecular biomarkers for precise breast cancer diagnosis are vital. Dysregulated apoptosis plays a critical role in the pathogenesis of breast cancer. The members of the B-cell lymphoma 2 (*BCL2*) gene family are reported to have a prognostic significance in breast cancer. Epithelial-to-mesenchymal transition (EMT) is important in breast cancer metastasis. Epithelial Cadherin coded by *CDH1* is a marker for EMT. This study aimed to assess the expression of *BCL2*, *BAD* (*BCL-2* associated agonist of cell death) and *CDH1* genes in a breast cancer patient cohort in Sri Lanka. Gene expression analysis was carried out using Real-time quantitative PCR (RT-qPCR) in triplicates for 68 breast tumour specimens obtained from patients with histologically confirmed breast carcinoma in Sri Lanka. The gene expressions with the menopausal status and primary clinicopathological parameters were statistically analysed. Our results showed that only *CDH1* expression was significantly associated with the menopausal status ($p < 0.05$) and highly expressed in postmenopausal tumours. The *BCL2* expression was significantly associated with estrogen receptor (ER) status and tumour grade, while the *BAD* expression was associated with the ER status ($p < 0.05$). Moreover, *CDH1* expression was associated with human epidermal growth factor receptor 2 (HER2) status ($p < 0.05$). Therefore, *CDH1* may be suitable for prognosis based on menopausal status and HER2 status in Sri Lanka. *BCL2* may be suitable for ER status and tumour size-associated prognosis, while *BAD* may be suited for ER status-associated prognosis. However, analysis of patient survival data and an increased cohort size are required for establishing the suitability of these genes in the prognosis of breast cancer in Sri Lanka.

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Keywords: *BCL2* gene family, EMT markers, Prognostic biomarkers, Real-time quantitative PCR