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Expression of stem cell marker BMI1 in invasive breast cancer and correlation with estrogen receptor, progesterone receptor, HER2/neu, and ki67

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Worldwide, breast cancer is the most common cancer in women. Currently, BMI1 has been linked to a stem cell-like 11 gene expression microarray signature, predictive of tumor relapse, metastasis, and resistance to therapy in multiple human cancers. The aim of this study was to evaluate immunohistochemical expression of BMI1 in invasive breast cancer, and its correlation with the clinicopathological features, hormone receptor status [estrogen receptor (ER) and progesterone receptor (PR)], HER2/neu score, Ki67 proliferation index, and molecular subtypes. 50 invasive breast carcinomas were studied for immunohistochemical demonstration of BMI1, ER, PR, HER2/neu, and Ki67. Cases were classified into four molecular subtypes (luminal A, luminal B, Her2-enriched, and triple negative). BMI1 expression was detected in 37 (74%) breast carcinoma cases, and a significant positive association with tumor size ($P=0.03$) and lymph node metastasis ($P=0.01$) was reported in this study. No significant correlation was detected between BMI1 expression and other variables such as age, histologic type, grade, hormone receptor status, Her2 status, Ki67, and molecular subtypes ($P>0.05$). In conclusion BMI1 stem cell marker was detected in a high percentage of breast cancer cells, and there was a significant positive association with tumor size and lymph node metastasis, which confirms its role in aggressiveness and dissemination of cancer cells. However, no correlations with ER, PR, Her2, Ki67 expressions, or molecular subtyping were found. Further studies are required to emphasize the prognostic value of cancer stem cell marker BMI1 and its therapeutic targeting.

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