ERVK3-1 as a Prognostic Marker for Invasive Ductal Carcinoma

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Human endogenous retroviruses (HERVs) are remnants of germline infections that constitute 5-8% of the human genome. HERVs have been suggested as potential oncogenic drivers. One HERV, HML-6 encodes a protein, ERVK3-1. However, there is no data on the impact of ERVK3-1 on invasive ductal carcinoma, a type of breast cancer. Mean expression of ERVK3-1 was analyzed in two breast cancer cell lines (T47D and MCF7) relative to normal breast epithelial cells. Gene expression data were obtained from the ENCODE database. Clinical survival data were collected from the Cancer Genome Atlas (TCGA). Expression analyses were performed in R, and patient data was queried using the R package TCGA Biolinks. T47D cell line had higher average gene expression relative to MCF7 ($p<0.0001$) and normal cell lines ($p<0.0001$). Gene expression analysis identified that ERVK3-1 was significantly increased in both the T47D (fold change=8.06, $p=0.039$) and MCF7 cell lines (fold change=3.13, $p=0.04$). Patients with high ERVK3-1 expression had lower overall survival relative to patients with lower ERVK3-1 expression ($p=0.021$). Stage II and III cancers had significantly higher mean ERVK3-1 expression relative to Stage I tumors ($p<0.0001$ and $p=0.0003$, respectively). ERVK3-1 expression was significantly higher in tumor samples that had low immunocyte infiltration relative to tumor samples with high immunocyte infiltration ($p<0.0001$). ERVK3-1 is overexpressed in breast cancer cells relative to healthy cells, and increased ERVK3-1 expression is associated with lower overall survival in breast cancer patients. Lower overall immunocyte infiltration was seen in breast cancer samples with high ERVK3-1 expression, suggesting that ERVK3-1 may reduce normal immune responses to cancer, which may lower patient survival.

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