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Abstract

Methylation Analysis of Genes for the T-type Voltage-Dependent Calcium Channels in Cervical Cancer Derived Cell Lines

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Abstract: Cervical cancer is the second cause of death in women worldwide. A positive correlation between increased gene methylation and increased pathological changes exists during the pathogenesis of cervical cancer. The intracellular calcium control allows orderly cell cycle progression, and play a vital role in growing and cell proliferation. T-type calcium channels play a fundamental role in the regulation of calcium in non-excitable cells. The expression of the T-type calcium channels isoforms has been reported in a wide range of cells including cancer cells. Our study has been aimed to evaluate the methylation in the promoter and regulatory regions of two genes encoding the main isoforms of T-type calcium channels: Ca_v 3.1 and Ca_v 3.2, and its correlation with their expression in cervical-cancer cells. Previously, it was reported no methylation of the T-type calcium channels in normal breast epithelial tissue, bone marrow, colon mucosa and placenta tissue suggesting that Ca_v 3.1 gene methylation is cancer specific. Using standard RT-PCR, the mRNA expression of the calcium channels was verified. Ca_v 3.1 mRNA was detected in CALO, while Ca_v 3.2 mRNA was detected in C-33A. After bisulfite DNA conversion the percentage of methylation was established, and correlated with the expression of the channels.

Keywords: T-type calcium channels, cervical cancer, methylation

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