Alteration of Epithelial-to-Mesenchymal Transition Gene Expression in Periostin-treated Cholangiocarcinoma

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ABSTRACT

Periostin (PN) is increased in cholangiocarcinoma (CCA) tissues and relates to patient poor prognosis. Epithelial-to-mesenchymal transition (EMT) is a process characterized by changes of carcinoma to mesenchymal cell and essential for cancer progression. This study aims to investigate the expression of EMT-related genes in PN-induced CCA cell migration. Nine EMT genes including two matrix metalloproteinase genes (MMP-10, MMP-13), two mesenchymal genes (ASMA, VIM), epithelial (CK19, CDH1) and transcription factors (SNAIL1, SLUG, TWIST2) were explored expression levels in cells with and without PN treatment by real time PCR. The results showed the up-regulated expressions (>1.2 fold) of MMP-10, SNAIL1, TWIST2, ASMA, and VIM whereas CK19 was significantly down-regulated (≤0.8 fold) in PN-treated CCA cells. No alterations of SLUG and CDH1 were observed. The different results in PN- and transforming growth factor-β-treated CCA cells reveal specific EMT gene expression pattern depending on the stimulant. The understanding of EMT genes in PN-induced CCA cells helps to inhibit cancer progression.

Keywords: epithelial-to-mesenchymal transition, periostin, cholangiocarcinoma