

In silico analysis of angiogenesis associated gene expression in lung cancer stem cells

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Abstract

Angiogenesis is a process that leads to the formation of blood vessels and is an important feature of malignancies and can occur at different stages of tumour progression. Angiogenesis is regulated by the balance between pro-angiogenic and anti-angiogenic factors. Lung cancer is the cause of many cancer-related deaths in the world. In the present study, we adopted three high-throughput GEO data sets with 18 different stages of lung cancer and 18 control samples which they have been classified into up and down-regulated genes. The four most up regulated genes in lung cancer patients, which are filtered, based on their regulation role in angiogenesis and have been confirmed in signal transductions of carcinogenesis and progression have been selected. Our analysis demonstrated up regulated EPhB2 in lung cancer. The expression of Wnt7b and TGF-beta1 in health and disease in different lung cell types depend on Wnt7B and TGF- β 1 concentration in their microenvironments and may also be affected by their neighbouring cells' changes in expression. This *in silico* analysis showed a higher expression of Wnt7b in both LUSC and LUAD. The differential expression level of Wnt7b in LUAD has been analysed by violin plot. Kaplan-Meier analysis of overall survival in both high and low Wnt7b TPM in LUAD has been investigated that observed 50% decrease in overall survival percentage within 50 months in both low and high Wnt7b TPM. Gene expression association between angiogenesis progress and lung cancer invasively has been proven by this study.

Biography

Mahsa Ghorbani has completed her MSc at the age of 24 years from Shahid Chamran University of Ahwaz, Iran. She spends her Internship at NIGB. She is interested in Lung cancer and Lung cancer stem cell research.



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