

Transcriptomics Analysis on Comparing Non-Small Cell Lung Cancer versus Normal Lung, and Early Stage Compared versus Late-Stages of Non-Small Cell Lung Cancer

Authors : Achitphol Chookaew, Paramee Thongsuksai, Patamarerk Engsontia, Narongwit Nakwan, Pritsana Raugrut

Abstract : Lung cancer is one of the most common malignancies and primary cause of death due to cancer worldwide. Non-small cell lung cancer (NSCLC) is the main subtype in which majority of patients present with advanced-stage disease. Herein, we analyzed differentially expressed genes to find potential biomarkers for lung cancer diagnosis as well as prognostic markers. We used transcriptome data from our 2 NSCLC patients and public data (GSE81089) composing of 8 NSCLC and 10 normal lung tissues. Differentially expressed genes (DEGs) between NSCLC and normal tissue and between early-stage and late-stage NSCLC were analyzed by the DESeq2. Pairwise correlation was used to find the DEGs with false discovery rate (FDR) adjusted p-value ≤ 0.05 and $|\log_2 \text{fold change}| \geq 4$ for NSCLC versus normal and FDR adjusted p-value ≤ 0.05 with $|\log_2 \text{fold change}| \geq 2$ for early versus late-stage NSCLC. Bioinformatic tools were used for functional and pathway analysis. Moreover, the top ten genes in each comparison group were verified the expression and survival analysis via GEPIA. We found 150 up-regulated and 45 down-regulated genes in NSCLC compared to normal tissues. Many immunoglobulin-related genes e.g., IGHV4-4, IGHV5-10-1, IGHV4-31, IGHV4-61, and IGHV1-69D were significantly up-regulated. 22 genes were up-regulated, and five genes were down-regulated in late-stage compared to early-stage NSCLC. The top five DEGs genes were KRT6B, SPRR1A, KRT13, KRT6A and KRT5. Keratin 6B (KRT6B) was the most significantly increased gene in the late-stage NSCLC. From GEPIA analysis, we concluded that IGHV4-31 and IGKV1-9 might be used as diagnostic biomarkers, while KRT6B and KRT6A might be used as prognostic biomarkers. However, further clinical validation is needed.

Keywords : differentially expressed genes, early and late-stages, gene ontology, non-small cell lung cancer transcriptomics

Conference Title : ICMOO 2020 : International Conference on Molecular Oncology and Oncogenesis

Conference Location : Bangkok, Thailand

Conference Dates : December 15-16, 2020