

TEK and TIE1 Downregulation in Smokers and Nonsmokers with Lung Adenocarcinoma

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Introduction

Lung cancer is the leading cause of cancer deaths in men and women, causing 1.59 million deaths worldwide in 2012 (World Health Organization). The disease is classified into two major categories, small cell lung cancer (SCLC) and non-small cell lung cancer (NSCLC), the latter of which accounts for 85% of all cases. This study investigated differences in gene expression in smokers and nonsmokers with lung adenocarcinoma, a subset of NSCLC and the most common type of lung cancer in nonsmokers.

Methods

This study utilized dataset GSE10072 (provided by NCBI), which contains a total of 180 lung adenocarcinoma and normal tissue samples (control) from 20 never smokers, 26 former smokers, and 28 current smokers. This study focused on 15 tissue samples from never smokers with lung adenocarcinoma and 16 control samples from healthy never smokers. The gene expression between the lung adenocarcinoma and control samples was compared using GEO2R. Genes with a p value of less than $1.01E-10$ (250 genes) were then introduced into String database to search for pathway connections. Afterwards, the GEO2R analysis was repeated on the same dataset to compare the results to gene expression in current smokers.

Results

In String, TEK and TIE1, genes expressed in endothelial cells with common functions such as cell proliferation and migration, showed many interactions. The genes had low p-values ($7.93E-16$ and $1.88E-14$, respectively). Both TEK and TIE1 were significantly downregulated in the lung adenocarcinoma samples. These genes were also downregulated in current smokers with lung adenocarcinoma. After observing these similarities, we compared the expression levels of other genes between smokers and nonsmokers with lung adenocarcinoma to look for differences specific to nonsmokers. However, we found no differences in the top 250 genes.

Conclusion

Based on the statistical significance we observed between TEK and TIE1 downregulation and lung adenocarcinoma, we concluded that targeting the expression of these genes may allow for restoration of functions that will limit disease progression. In addition, the pattern we observed between gene expression in smokers and nonsmokers with lung adenocarcinoma suggests that this disease arises by similar genetic mechanisms in both populations. Further research into genetic causes of this disease specific to nonsmokers would benefit from information on the patient's family history of cancers and exposure carcinogens.

Keywords: TEK, TIE1, nonsmoker, lung adenocarcinoma, endothelial cells

References

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