Leukocyte Transendothelial Molecules in NSCLC

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Introduction

Lung cancer is the second most commonly diagnosed cancer in the United States in both men and women. An estimated 224,390 new cases are expected in 2016, making up around 14% of all cancer diagnoses. 1 out of 4 cancer deaths in both men and women are from lung cancer, making it the leading cause in cancer death. There are three main types of lung cancer: non-small cell (NSCLC), small cell, and lung carcinoid tumor. NSCLC and is the most common, making up 85% of lung cancer cases. The later the stage the cancer is diagnosed in, the lower the 5-year survival rate. Although there are many treatment options for those who are diagnosed with lung cancer that has already metastasized, the 5-year survival rate is 1%.Some treatment options include surgery, chemotherapy, and radiation therapy. For those whose cancer has spread to more than one site, a target therapy drug will be used depending on the gene that is mutated. Determining which genes are upregulated or downregulated in NSCLC is essential to earlier diagnoses and the development of more effective genetically tailored treatment options.

Methods

I found the dataset GSE19804 from NCBI that compared tissue samples from 60 female non-smoking NSCLC patients to tissue samples of 60 healthy females. I used GEO2R to find which genes were upregulated and downregulated. Then, I looked at the top 250 genes on STRING to see which genes interacted with one another. I used GO Biological Process to determine which genes had similar functions. Noticing that the 45 genes involved in either the regulation of cell adhesion or cell adhesion interacted with each other, I found a KEGG Pathway on cell adhesion molecules. Many of these genes were also involved in a KEGG Pathway on leukocyte transendothelial migration.

Results

JAM2, JAM3, CDH5, PECAM1, and CD99 were genes responsible for cell adhesion and leukocyte transendothelial migration. Looking at the t-test values revealed that CD99, a gene involved in T-cell death, was the only gene out of the five to be upregulated in cancer. All of these genes bind to leukocytes to facilitate their migration across the endothelium from the blood to tissue.

Conclusion

Leukocytes are unable to travel where they are needed due to the downregulation of some of the genes listed above. T-cells determine what immune response is needed depending on the antigen. A specific type of T-cell called a Cytotoxic T-cell directly bind to and kill cancer cells. In NSCLC, T-cell death is increased because of the upregulation of CD99. There are less Cytotoxic T-cells present to combat the cancer. More research into these genes as well as creating drugs that can upregulate JAM2, JAM3, CDH5, and PECAM1 or downregulate CD99 can be ways to create more effective gene-specific treatment options for NSCLC patients.