Name(s)	Project Number
Alice R. Zhai	**J1420**

Project Title

Bad for One, or Bad for All? A Cancer Genome Anatomy Project

Abstract

Objectives/Goals

My project aims to identify highly over-expressed genes in one type of cancer and examine how over-expressed these genes are in other types of cancer.

Methods/Materials

Using the web-based software and bioinformatics tools from the Cancer Genome Anatomy Project (CGAP) developed by the National Cancer Institute (NCI), I identified 10 over-expressed genes in lung cancerous tissues. Then I searched for the expression frequency of these 10 genes in the normal and cancerous tissues of 17 human organs, and assigned each expression frequency a number between 1 and 10, which represents the base-2 logarithm of gene expression frequency. I subtracted the number assigned to normal tissue from the number assigned to cancerous tissue to indicate the level of over-expression of each gene. Next, I examined the statistics of the over-expression indices of each gene for all 17 types of cancer, including the counts of positive over-expression, the average, and the range of positive over-expression indices. I found that the highest over-expressed gene for lung cancer is not the highest over-expressed in other types of cancer. Instead, the moderately over-expressed genes tend to be more over-expressed in other cancers. I repeated the procedure using the 10 over-expressed genes from pancreatic cancer and found similar results. The 10 over-expressed genes from pancreatic cancer are generally more active in other cancers than the 10 genes from lung cancer. I concluded that some genes are unique to certain cancers, and some genes are universal for most types of cancer.

I used my laptop with high-speed Internet to access the online database. I also used Microsoft Excel to make tables and graphs. I used Microsoft Word to type up my report. Besides my computer, I used a printer to print out the charts, a glue-stick and a stapler to attach the print-outs to my lab notebook.

Results

I found that the highest over-expressed gene in either lung or pancreatic cancer is not the highest over-expressed gene for all 17 types of cancer together. Instead, the 4th (3rd) gene in lung (pancreatic) cancer ranks the highest for all 17 types of cancer together.

Conclusions/Discussion

I concluded that that some genes are unique to certain cancers, and some genes are universal for most types of cancer. The moderately-expressed genes in one type of cancer can be the highest over-expressed in all types of cancer. If sciences can identify these genes, they may be able to find a universal cure for all cancer. If I am to repeat the experiment, I would use the actual counts instead of the coarse color coding to indicate the expression frequency of each gene. I would also conduct the analysis using genes from other

Summary Statement

My project is to find out if over-expressed genes in one type of cancer are over-expressed in other types of cancer.

Help Received

After an experience in the kitchen with a skillet, I wanted to test four common metals and their resistance to a change in temperatures. My hypothesis is that the cast iron would cool the slowest due to my experience in the kitchen and the aluminum would cool the fastest.