



**CALIFORNIA STATE SCIENCE FAIR
2002 PROJECT SUMMARY**

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Project Title Monitoring Gene Expression in Pulmonary Carcinoma Using Oligonucleotide Arrays	
<p style="text-align: center;">Abstract</p> <p>Objectives/Goals Our purpose is to monitor the differences in gene expression between a cell line of pulmonary carcinoma (HTB174), a normal cell line (HTB175), and normal tissue using oligonucleotide arrays. We hope to target the specific involvement of individual genes and gene combinations that are involved in transforming normal tissue into carcinogenic tissue. By chance, we may also discover some genes not previously associated with the development of carcinogenic tissue. On top of this, we are looking to check any differences in gene expression in the normal tissue and the normal lab-produced cell line.</p> <p>Methods/Materials We first extract total RNA from the samples and isolate the messenger RNA. We then perform a reverse transcription reaction with the mRNA to make complimentary DNA, which is then made into double stranded cDNA in an effort to clean it. Once the cDNA is cleaned, we perform an in-vitro transcription to obtain a single stranded cRNA strand. Once this cRNA strand is cleaned, it is fragmented into smaller pieces, each containing a specific gene. These small segments containing individual genes are then hybridized on oligonucleotide arrays. Once hybridized, we scan the arrays and analyze the data using special software.</p> <p>Results Upon preliminary analysis, we have found that a few oncogenes and cell-cycle related genes are overexpressed in the cancerous cell line relative to the normal tissue sample. We are noticing that tumor suppressor related genes are underexposed in the HTB174 sample relative to the same normal tissue sample. Furthermore, we are noticing a number of genetic differences between the normal cell line, which is produced in a lab, and the tissue. However, these differences are not major and are not cancer-related. Due to some unpredicted "errors" in the processing of the data, we have not yet completed our analysis. Nevertheless, we will have comprehensive results by the time of the fair.</p> <p>Conclusions/Discussion Our results thus far are pointing us in the direction of conventional thought pertaining to pulmonary carcinoma. In terms of comparing normal cell lines to normal tissue, our results so far reaffirm the notion that synthetic cells are not exactly the same as naturally occurring ones - in a lab, these cell lines can multiply more, thus expanding the possibilities of genetic mutations. However, we still need more time to analyze the final results to make absolute conclusions.</p>	
Summary Statement We are monitoring and attempting to explain the differences in the over-expression and under-expression of certain genes in carcinogenic lung cells and normal cells.	
Help Received Used lab equipment and basic protocols at Affymetrix, Inc. under the direction of Ms. Angelyn Tracy and Dr. Garry Miyada.	