



CALIFORNIA SCIENCE & ENGINEERING FAIR 2019 PROJECT SUMMARY

Name(s) Jibiana Jakpor	Project Number S1512
Project Title Comparison of Gene Expression in Pancreatic Cancer with and without Perineural Invasion	
<p style="text-align: center;">Abstract</p> <p>Objectives Pancreatic cancer is the third leading cause of cancer death. Perineural invasion (PNI) which is cancer cells invading the surrounding nerves, is associated with a poor prognosis. Understanding the gene expression of perineural invasion in pancreatic cancer will help in the development of precision medicine to treat this deadly disease. I hypothesized that gene expression would be different in the patients with PNI than in the patients without PNI.</p> <p>Methods The dataset (GSE102238) is a deidentified public dataset from the NIH s Gene Expression Omnibus (GEO). I performed statistical analysis with GEO2R on the gene expression of two groups: all of the samples without PNI, and all of the samples with PNI. I downloaded the output of GEO2R as a spreadsheet and used R to convert the microarray probe IDs to HGNC Gene IDs. From the top 2000 genes with the most statistically significant gene expression differences (those with the smallest p-values), I used R to select the genes with log₂-fold change values greater than 0. This means that the genes were downregulated in the samples with PNI. I studied the functional enrichments of those genes using STRING, a protein interaction database. I studied some of the specific genes in the enriched function using GeneCards.</p> <p>Results In the patients with perineural invasion, more than 232 genes were downregulated. Among the 20 Gene Ontology (GO) biological processes with the lowest false discovery rates enriched in these downregulated genes, 7 processes were directly related to immune function. The GO biological process with the lowest false discovery rate (1.00E-5) was "positive regulation of immune system process." There are 34 downregulated genes from this process.</p> <p>Conclusions There are differences in gene expression between pancreatic cancer patients with PNI and without. It is known that PNI in cancer is associated with a poor prognosis. With PNI, I found downregulation in 34 genes associated with "positive regulation of immune system process." Perhaps perineural invasion is associated with a weakened immune system. Understanding gene expression is essential to applying precision medicine to treat pancreatic cancer.</p>	
Summary Statement This study compared the gene expression in pancreatic cancer patients with and without perineural invasion and found downregulation in more than 34 genes associated with immune function.	
Help Received I asked questions of Dr. Inhan Lee of MiRcore, UCSD undergrad student Aaron Ta, and UCSD graduate student Alex Sharp, who taught me these transcriptome research techniques last summer at the MiRcore computational biology camp in San Diego.	