



**CALIFORNIA STATE SCIENCE FAIR
2017 PROJECT SUMMARY**

Name(s) Matthew Bronars; Jason Provol	Project Number S0507
Project Title Metabolomic Analysis as a Method of Breast Cancer Diagnosis	
<p style="text-align: center;">Abstract</p> <p>Objectives/Goals The goal of this project is to take a novel approach to breast cancer metabolomics in order to reveal biomarkers with the potential to be used in a breast cancer diagnosis test that, unlike the current methods (mammogram and biopsy), is noninvasive, cost-effective, specific, and accessible.</p> <p>Methods/Materials Data was compiled from 20 studies examining which metabolites are significantly changed in the breast tissue, blood, and urine (sample domains) of breast cancer patients. The acquired metabolites were analyzed for metabolic pathways and gene networks both common across all three domains and known to be associated with breast cancer. The programs used for analysis of metabolic pathways and genes include MetaboAnalyst (free online program) and Ingenuity (program paid for by the San Diego Supercomputer Center) respectively. These programs were also used to investigate metabolites as a diagnostic tool for subtypes of breast cancer and prediction of gene regulation. In development of a test, urinary samples provided by San Diego State University were run through an Nuclear Magnetic Resonance (NMR) machine at SDSU.</p> <p>Results Metaboanalyst and Ingenuity results revealed that 6 Metabolic Pathways & 5 genes were found to be the same between domains. Tissue metabolite concentrations were used to predict the expression of 15 genes, 10 were predicted accurately, the other 5 genes have unknown breast cancer expression patterns. Blood metabolites were found to have distinct pathways and gene connections for each breast cancer subtype. In developing a portable test for urinary metabolites, NMR spectra show consistent results & relative high concentrations for 13 critical metabolites.</p> <p>Conclusions/Discussion The metabolites in the metabolic pathways and gene networks common between domains show the most promise for breast cancer diagnosis. Accurate prediction of gene inhibition/activation revealed that metabolic changes can predict expression of genes in breast cancer, which will allow for better treatment by personalized prescriptions. Metabolic changes can accurately distinguish between subtypes of breast cancer, which is necessary for determining which treatment methods will be effective. Urine metabolites especially show great promise in being employed for an easy-to-use, cost-effective breast cancer screening test. Current work is focused on developing portable methods for detecting the critical urinary metabolites.</p>	
Summary Statement This project takes steps towards developing a breast cancer diagnostic test that, unlike the current methods (mammogram and biopsy), is noninvasive, cost-effective, specific, and accessible.	
Help Received Dr. Gregory Holland (SDSU) Mr. Dillan Steigal (SDSU) Dr. Igor Tsigelny (UCSD) Dr. Valentina Kouznetsova (UCSD) for general project instructions	