Metabolic Analysis as a Method of Breast Cancer Diagnosis

Bronars, Matthew

Provol, Jason

This project takes a novel approach to breast cancer metabolomics to reveal biomarkers with the potential to be used in a breast cancer diagnostic test. This test, unlike current methods, will be noninvasive and cost-effective. Data was compiled from 20 studies examining metabolites 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 common across all three domains and known to be associated with breast cancer. Metabolites were also analyzed for their ability to diagnose breast cancer subtypes and predict gene regulation. In development of a breast cancer screening test, urinary samples provided by San Diego State University (SDSU) were run through a Nuclear Magnetic Resonance (NMR) machine at SDSU. Results reveal that 6 Metabolic Pathways and 5 genes are the same between domains. Metabolic concentrations predicted the expression of 15 genes. Metabolites also revealed pathways and gene connections for each breast cancer subtype. NMR spectra show consistent results and relative high concentrations for 13 critical metabolites. The metabolites in the common networks and pathways show the most promise for breast cancer diagnosis. Accurate prediction of gene inhibition/activation and the visual distinctions in the pathways and genes tied to each breast cancer subtype, reveal that metabolic changes can be used to predict gene expression and breasts cancer subtype. Both factors will allow for better treatment by personalized prescriptions. Urine metabolites show great promise in being employed for a noninvasive breast cancer screening test. Current work is focused on developing methods for detecting the critical urinary metabolites.

Awards Won: