Identification of Co-Expressed Genes to BDNF and trk-B as Major Depressive Disorder Related Biomarkers Using Microarray Data

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Depression is a leading cause of death and disability with more than 264 million people of all ages suffering from the disorder worldwide. Understanding how brain function is altered in depressed patients is crucial for determining novel biological targets that can be used to prevent suicidal behavior. This project aims to identify potential biomarkers for major depressive disorder by finding co-expressed genes with brain-derived neurotrophic factor (BDNF) and receptor tyrosine kinase B (trk-B), two genes that contribute to the pathophysiology of depression through neuron growth and survival (neuroplasticity). 3055 probes for genes involved in nervous system development were screened from public microarray data in the Allen Human Brain Atlas. Average gene expression level and Pearsons correlation coefficient were calculated for each probe using Java programming and Excel to determine correlations between either BDNF or trk-B and a potential gene biomarker. A total of 93 and 27 co-expressed genes were identified for trk-B and BDNF respectively with a significant Pearsons correlation of above +0.5 (trk-B: 0.82>x>0.50, BDNF: 0.68>x>0.50). In addition, 72 biomarkers were further identified by gene function and trends in data as especially important to depression research. These biomarkers may give new insight into genetic factors for vulnerability to depression involving brain neuroplasticity and can be used to create new therapies as drug targets or to improve the remission rates of existing therapies.

Awards Won:

Fourth Award of $500