

P-1256 - THALAMIC ANTERIOR NUCLEUS MICROARRAY SCREENING IN SCHIZOPHRENIA

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Multiple cortical and subcortical regions have been shown to exhibit altered transcriptional states in association with schizophrenia (SZ) through gene expression studies. Select nuclei of the thalamus, a subcortical region, have been previously shown to have neuron and volume loss. These thalamic regions are reciprocally connected with areas of cortex which have been implicated in SZ. The thalamic anterior nucleus (AN) is of particular interest due to its reciprocal connectivity with the SZ-associated anterior cingulate cortex (ACC). To identify SZ-related gene expression changes we used whole genome microarray screening to compare transcriptional profiles of two thalamic regions, the AN and VPL (a lateral tier nucleus not considered SZ-impacted) in the same subject with SZ. The same microarray screening comparison was performed with the same regions in non-psychiatric controls (NC) subjects. Differentially expressed genes common to both analyses were removed from the SZ list to sharpen focus on disease-related genes. One-hundred thirty-six gene expression changes were identified. This list was used with DAVID functional annotation and Ingenuity pathway tools which indicated their involvement in endocytosis, neuron projection morphogenesis, and cytoskeleton organization. These findings further support the notion of schizophrenia being a “disease of the synapse.”