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***Human Brain Proteomics in the Systems Biology of Epilepsy Project (SBEP)***

Epilepsy is a neurological disorder that manifests as recurrent seizures. Many cases are resistant to antiepileptic drugs and may benefit from surgical procedures to identify and remove the epileptic foci.

The project takes advantage of unique human surgical specimens, removed from electrophysiologically mapped brains to compare electrically active brain to adjacent quieter normal regions of the same individuals. We present a pilot proteomic study and initial integration with the project's database of clinical, histological, genomic and metabolomic information. We used Differential in Gel Electrophoresis (DiGE) to compare protein abundances in three fractionated cellular compartments of six patients.

About 4400 protein isoform spots were resolved for each patient and the identities of a subset of 400 significantly changing spots was determined by LC-MS/MS. Hierarchical clustering of the spot expression patterns was used to group changing proteins, followed by gene ontology enrichment analysis. Combination of the two analysis tools allowed for enhanced interpretation of the changes in cellular processes taking place in the tissues that trigger seizures. Changes in cell populations and increased vascularity, predicted from the proteome, were validated by histology. Integrating the findings to develop human epilepsy models seeks to deepen understanding of the disorder and suggest new drug targets.