Identifying a Novel Gene Signature to Predict Drug Resistance in Epilepsy Patients

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One in twenty-six people worldwide develops epilepsy during their lifetime, including myself. Around 30% of epilepsy patients are nonresponsive to medication. It is important to identify these patients using less invasive and low-cost methods. This study aims to use gene expression profiles derived from blood cells to identify potential gene signatures to predict drug response in epilepsy patients. To determine whether expression profile changes in blood samples can reflect epilepsy pathogenesis, a weighted gene coexpression network analysis (WGCNA) was performed using samples from drug-naive epilepsy patients and healthy controls. A differentially expressed network was identified through this analysis, suggesting a link between epileptogenesis and gene expression in blood samples. Patients with epilepsy were grouped based on 3 medications: Carbamazepine, Valproate, and Phenytoin. Responders and non-responders were compared with each other, establishing a list of differentially expressed genes. The lists were also analyzed with pathway enrichment and gene ontology analyses. Pathways enriched in all three drug groups were identified. Gene ontology analysis identified Regulation of Response to Biotic Stimulus as commonly enriched across all 3 gene lists. It has been reported that ‘Regulation of Response to Biotic Stimulus’ was related to the immune system. This result suggests an association between drug-resistant epilepsy and the immune system. In conclusion, multiple differentially expressed genes, pathways, and ontologies were identified from the expression profiles derived from blood samples of epilepsy patients. These gene signatures have the potential to be utilized as a biomarker to predict drug response in epilepsy patients.