Gene Expression Biomarkers for Epilepsy: Identification Through Integrative Evidence-Based Genomics Analysis

Vishruth M. Nagam (1,2,3)

1. Duke University School of Medicine, Durham, NC
2. Master of Management in Clinical Informatics (MMCi), Duke University School of Medicine, Durham, NC
3. University of California, Riverside School of Medicine, Riverside, CA

Abstract

Epilepsy is a neurological condition affecting 50 million individuals worldwide. This study performs neuroinformatics research, utilizing a novel blood "omics" informatics approach to analyze large-scale gene expression data from the blood transcriptome and identify consistent gene expression profiles and novel biomarkers for epilepsy. These findings enhance our understanding of epilepsy's molecular mechanisms and contribute to precision health informatics solutions, such as genetic tests that could expedite diagnosis and improve treatment strategies.

Introduction

Epilepsy affects approximately 50 million individuals globally, manifesting as seizures without identifiable medical causes. Differentially expressed genes are valuable candidate biomarkers to facilitate early detection and diagnosis of epilepsy via genetic tests[1,2]. This work represents research to identify such biomarkers for epilepsy and was conducted as part of a University Honors capstone project.

Methods

This study performs neuroinformatics research and integrative evidence-based genomics analyses to analyze differential gene expression in epilepsy between 21 epilepsy disease patients and 234 healthy control patients from the PltDB database, utilizing large-scale gene expression data from the blood transcriptome, and identify a consistent gene expression profile for epilepsy[3]. This research represents a novel blood "omics" informatics approach to epilepsy and involved the use of both genomic and evidence-based functional databases (Gene Ontology, GeneCards, etc.), strengthening the novelty and rigor of the findings.

Results

The data (including Figure 1 and Tables 1-5) for this research can be found here (link: https://tinyurl.com/vnagam-data; QR code below). A consistent gene expression profile and novel biomarkers were discovered for epilepsy from the blood platelet transcriptome. The strongest biomarkers for epilepsy are identified as the CD163, SLC25A39, SH3BP5L, SOCS1, and IRAK3 genes.

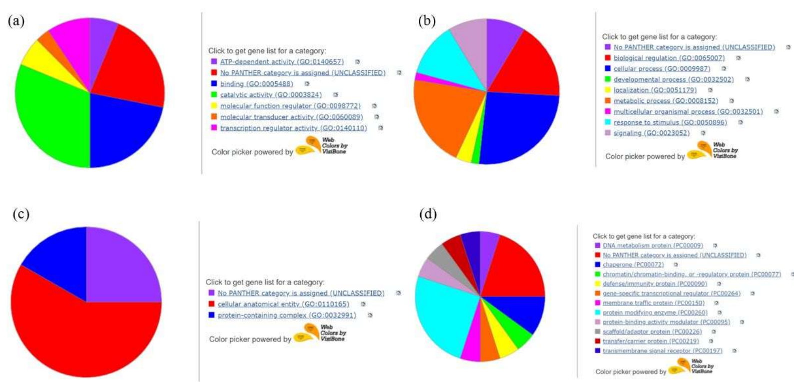

Figure 1. Pie charts of Gene Ontology classifications of the mRNAs differentially expressed in epilepsy, with (a), (b), (c), and (d) showing molecular function, biological process, cellular component, and protein class classifications, respectively.

Discussion and Conclusions

These findings enhance our understanding of the molecular mechanisms underlying epilepsy and contribute to the development of precision health solutions, such as genetic tests, that could improve and expedite diagnosis and treatment of epilepsy[4].

References

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