MSC VIRTUAL E-ABSTRACT
(E-Poster Presentation – Non-Clinical)
Malaysian Stroke Conference 2021

DOI: https://doi.org/10.32896/cvns.v3n3.36
Published: 30.09.2021

KEY MIRNAS AND TARGET GENES FOR ISCHEMIC STROKE

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ABSTRACT

Introduction: Ischemic stroke is caused by blockage in an artery that restricts normal flow of blood and oxygen within the brain. Most of the identified biomarkers for ischemic stroke are still at the pre-clinical stage, and yet to be cross validated. The objective of the current study is to elucidate differential expression microRNAs (DEmiRNAs) for ischemic stroke.

Methods: Raw miRNA datasets were obtained from NCBI GEO database. Bioinformatic analysis of the microarray datasets and RNA-seq dataset were carried out using limma and DESeq2 packages, respectively. The target genes for DEmiRNAs were predicted using TargetScan and miRDB. Cytoscape software was used to construct and visualize the miRNA-mRNA regulatory network. The functional enrichment analysis of the predicted target genes was performed using DAVID software.

Results: The present study has discovered 685 regulatory genes through the target prediction of which, three DEmiRNAs, namely, hsa-miR-320d, hsa-miR-139-5p, and hsa-miR-485-3p were overlapped by the highest number of genes. The regulatory genes were significantly enriched in regulation of transcription, nervous system development, and protein phosphorylation.

Conclusion: This study suggested that hsa-miR-320d, hsa-miR-139-5p, and hsa-miR-485-3p may be the potential diagnostic biomarkers for ischemic stroke.