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Altered expression profile revealing long-term effects in parietal and temporal cortex after mild-to-moderate traumatic brain injury via bioinformatics method

Background & Aim: Traumatic brain injury (TBI) initiates a complex pathological cascade of secondary insults following the initial mechanical injury. The present study was aimed at identifying the potential key genes, pathways and possible mechanisms in parietal and temporal cortex after mild-to-moderate TBI.

Methods: The array data of GSE104687 were downloaded from the Gene Expression Omnibus (GEO) database, including 98 postmortem cortex tissues from donors experienced mild-to-moderate TBI and 91 samples from donors without TBI. We performed Gene Ontology annotation, the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analyses and constructed a protein-protein interaction (PPI) network for the identified differential expression genes (DEG).
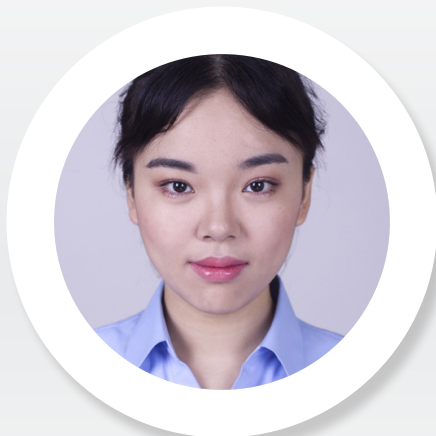
Results: Thirty three (33) DEGs with a±2-fold change (p<0.01) were obtained between TBI groups and non-TBI groups, including seven upregulated and 26 down-regulated genes. The altered genes were enriched in cytosol, translational initiation and structural constituent of ribosome. The protein-protein interaction (PPI) network consists of 14 nodes and 63 edges. Nine genes (RPL41, RPS4X, RPS7, RPL17, RPL27, RPL23, RPS15A, RPL24, and RPL7A) were identified as the hub genes with the most significant meaning.

Conclusion: We have demonstrated a global view of the altered genes, interactions, and their related pathways in traumatically injured cortex using bioinformatics methods. The present paper helps to contribute a more detailed understanding of the long-term pathophysiologic process after TBI, which might be transformed into clinical practice

Biography

Bao Wangxiao has completed her graduation from China Medical University in 2014 and is currently a PhD student majoring in Neurology at Zhejiang University School of Medicine, China. Her research interests focus on exploring the novel biomarkers for TBI patients using quantitative proteomics and integrative bioinformatics method. She has published eight papers in journals of related areas.

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