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Identification of central genes and pathways associated with stroke and ferroptosis by comprehensive transcriptome analysis

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This study aimed to find important genes and pathways related to stroke and ferroptosis (Ferr), and estimate the possible pathways by which Ferr affects stroke rehabilitation. The GSE102541 dataset is from the gene expression omnibus database (GEO), which contains six samples of patients with poor prognosis of acute cerebral infarction and three samples of healthy volunteers. The limma package was used to identify differentially expressed genes (DEGs). Meanwhile, Ferr related DEGs (Ferr-DEGs) were found using the Ferr database. Ferr DEGs were enriched by Gene Ontology (GO) and Kyoto Encyclopedia of genes and genomes (KEGG). The protein-protein interaction (PPI) network was constructed using the string database, and the cytohubba plug-in in Cytoscape helped identify hub genes. Finally, the miRNA-TF-mRNA regulatory network of these central genes was established. A total of 43 Ferr-DEGs were obtained. These genes are mainly concentrated in cellular response to metal ion, response to virus, cellular response to chemical stress, cellular processes, human diseases, environmental information processing et al. Eight Central genes regulating ferroptosis in stroke have been identified, SOCS1, PTPN6, IFNA10, IFNA6, GSK3B, ATF4, BECN1 and HMGB1. According to the miRNA-TF-mRNA regulatory network, SOCS1, as a target of STAT3, is regulated by upstream hsa-mir-4324. As a target of NFKB1, GSK3B is regulated by upstream hsa-mir-484, hsa-miR-3156-5p, hsa-miR-769-5p, hsa-miR-4443, hsa-miR-4484, hsa-miR-4269, hsa-miR330-3p, has miR-4674, hsa-miR-193a-3p, hsa-miR-4797-5p, hsa-miR-762.

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