Analysis of immune infiltration and cuproptosis-related genes in acute myocardial infarction

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Background: Acute myocardial infarction (AMI) is a major global health concern. The identification of key genes associated with AMI and cuproptosis is crucial for developing effective diagnostic and prognostic tools.

Purpose: To identify differentially expressed genes (DEGs) associated with AMI, and investigate their correlation with cuproptosis and immune infiltration to improve diagnosis and prognosis.

Methods: Six datasets (GSE48060, GSE83500, GSE97320, GSE974, GSE19339, and GSE66360) containing normal control and AMI samples were integrated from the Gene Expression Omnibus (GEO) database. DEGs between AMI and control samples were identified and cross-referenced with ferroptosis-associated genes. GO and KEGG analyses were performed to explore the functions and pathways associated with the identified genes. Immune infiltration analysis was also conducted to investigate the correlation between the genes and immune infiltration. An AMI prediction model was constructed using statistical analysis.

Results: Fifteen DEGs were identified, including nine upregulated and six downregulated genes. Among these genes, 11 were found to be associated with cuproptosis, including SLC31A1, PDHB, PDHA1, LIPT1, LIAS, FDX1, DLS1, DLD, DLAT, DBT, and ATP7B. These genes were mainly enriched in the TCA cycle, pyruvate metabolism, glycolysis/gluconeogenesis, and carbon metabolism pathways. Immune infiltration analysis revealed significant differences in macrophages, Th1 cells, Th2 cells, tumor-infiltrating lymphocytes, cytolytic activity, and MHC class 1 between normal and AMI samples. A correlation between these genes and immune infiltration was also observed. The AMI prognostic model constructed had an AUC of 0.61047.

Conclusion: Cuproptosis-related genes (SLC31A1, PDHB, PDHA1, LIPT1, LIAS, FDX1, DLS1, DLD, DLAT, DBT, and ATP7B) may play significant roles in AMI and its immune infiltration. The identified genes and pathways could potentially serve as biomarkers for improving the diagnosis and prognosis of AMI.

Flow chart of research design
Cuproptosis-related AMI genes