

CD63 as a Potential Diagnostic Marker of Depression and Its Correlation with Immune Infiltrates

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Abstract

Major depressive disorder (MDD) is the most common severe mental illness and the leading cause of suicide and disability. The study attempted to screen the diagnostic markers of peripheral blood of MDD and their relationship with immune infiltration. From the differential gene intersection set of the two data sets (GSE98793 and GSE76826), we screened to 72 up-regulated genes and 139 down-regulated genes. Gene Ontology (GO) enrichment analysis revealed that identified genes were primarily related to mononuclear cell differentiation, lymphocyte differentiation and T cell selection. Protein-Protein interaction (PPI) network analysis, random forest algorithm and Lasso regression algorithm obtained the hub genes: CD63. ROC analysis showed that CD63 had a good diagnostic and predictive effect on MDD patients. The CIBERSORT algorithm was used to assess immune cell infiltration and identify common immune characteristics in MDD. We analyzed the proteins that interact with CD63 using GeneMANIA databases, the miRNAs that interact with CD63 using RNAInter, miRWalk and starBase databases, and the traditional Chinese medicine ingredients that regulate CD63 using the COREMINE databases. Finally, we further verified the expression of CD63 using qPCR and WB on MDD patients' plasm, depressive model mice, and in vitro cells. These findings indicate that CD63 associated the infiltration of immune cells may be potential diagnostic indicators for MDD.

Keywords

Major Depressive Disorder, Bioinformatic Analysis, Diagnostic Marker, Immune Infiltrates