

Gene expression pattern in severely progressing covid-19 patients is related to diabetes mellitus type 1: A functional annotation analysis

Alipour Mohsen, Javeshghani Danesh, Roustazadeh Abazar

Abstract

Aims: The aim of this study was to extract the signaling mediators or biological pathways that link covid-19 to other diseases such as type 1 diabetes mellitus (T1DM).

Methods: Microarray data of covid-19 (GSE164805) was extracted from Gene Expression Omnibus (GEO) and analyses were performed by R package and GEO2R. Functional enrichment analysis was done to extract enriched molecular pathways (MP), biological process (BP) and molecular function (MF). Then commonly up- and down-regulated genes in covid-19 and T1DM were extracted by comparing differentially expressed genes (DEGs) of GSE164805 and GSE9006.

Results: Down-regulated DEGs in the severely progressing covid-19 patients (SPCP) had a link to T1DM. Major histocompatibility system (MHC) class II, gamma interferon (IFN γ), and IL-1B were enriched in extracted pathway that leads to T1DM. In addition, comparing extracted DEGs from GSE164805 and GSE9006 indicated that MTUS1, EGR1 and EGR3 are the genes that are up-regulated in both SPCP and T1DM.

Conclusion: The findings of this study indicate that coincidence of SARS-COV-2 infection and T1DM may increase the severity of both diseases. Although covid-19 reduced the T cell mediated immune response, but increased mediators of T-cell signaling pathway such as IL-1 in both diseases. This could potentiate the inflammation response and worsens the severity of covid-19 cytokine storm or increase the resistance to insulin.

Keywords: Annotation analysis Diabetes mellitus Microarray SARS-COV-2