An investigation of cytokines and chemokines interaction using network analysis in covid-19

ABSTRACT

The emergence of a pandemic coronavirus disease 2019 (COVID-19) caused by infection with SARS-CoV-2 have become threats to humanity. In terms of their physio pathological pathways, a wide variety of biomolecules have been activated, based on immunological responses. It is therefore relevant to compare the human respiratory cell lines to infections with the SARS-CoV-2 and other respiratory viruses. In this study, we examined gene expression profiles of GSE147507 from the Gene Expression Omnibus (GEO) were used to explore the transcriptional response of SARS-CoV-2 with other respiratory viruses, including human parainfluenza virus 3 (HPIV3), respiratory syncytial virus (RSV), and influenza A virus (IAV), in human respiratory cell lines. Network Analyst 3.0 software was used to perform this gene expression data via intuitive web interface. Through its well-established statistical procedures with state- of-the-art data visualization techniques, it allows us to navigate large complex gene expression data sets to determine important features, patterns, functions and connections that would lead us to a new biological hypothesis. The raw RNA-sequencing data undergoes data processing, including filtering, quality check and normalization before it corresponds to data analysis and interpretation. The edger package was used to identify differentially expressed genes (DEGs) on respiratory viruses infected in human lung epithelium- derived cell lines, such as lung alveolar cells (A549), A549 cells expressing ACE2 (A549-ACE2) and cultured human airway epithelial cells (NHBE). P |2| were set as thresholds for identifying DEGs. Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) analyses were applied for the functional annotation and pathway analysis. Interpretation of gene expression data obtained from the visualization of volcano plot and analysis of protein-protein interaction (PPI) to reveal the functional associations between proteins on a genome-wide scale using STRING interactome.