Investigate the Side Effects of Patients With Severe COVID-19 and Choose the Appropriate Medication Regimens to Deal With Them

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Abstract : In December 2019, a coronavirus, currently identified as SARS-CoV-2, produced a series of acute atypical respiratory illnesses in Wuhan, Hubei Province, China. The sickness induced by this virus was named COVID-19. The virus is transmittable between humans and has caused pandemics worldwide. The number of death tolls continues to climb and a huge number of countries have been obliged to perform social isolation and lockdown. Lack of focused therapy continues to be a problem. Epidemiological research showed that senior patients were more susceptible to severe diseases, whereas children tend to have milder symptoms. In this study, we focus on other possible side effects of COVID-19 and more detailed treatment strategies. Using bioinformatics analysis, we first isolated the gene expression profile of patients with severe COVID-19 from the GEO database. Patients' blood samples were used in the GSE183071 dataset. We then categorized the genes with high and low expression. In the next step, we uploaded the genes separately to the Enrichr database and evaluated our data for signs and symptoms as well as related medication regimens. The results showed that 138 genes with high expression and 108 genes with low expression were observed differentially in the severe COVID-19 VS control group. Symptoms and diseases such as embolism and thrombosis of the abdominal aorta, ankylosing spondylitis, suicidal ideation or attempt, regional enteritis were observed in genes with high expression and in genes with low expression of acute and subacute forms of ischemic heart, CNS infection and poliomyelitis, synovitis and tenosynovitis. Following the detection of diseases and possible signs and symptoms, Carmustine, Bithionol, Leflunomide were evaluated more significantly for high-expression genes and Chlorambucil, Ifosfamide, Hydroxyurea, Bisphenol for low-expression genes. In general, examining the different and invisible aspects of COVID-19 and identifying possible treatments can help us significantly in the emergency and hospitalization of patients.

Keywords : phenotypes, drug regimens, gene expression profiles, bioinformatics analysis, severe COVID-19