**Manuscript title:** Identification of COVID-19 and dengue host factor interaction networks based on integrative bioinformatics analyses

**First author:** Zheng Wenjiang

The First Clinical Medical School of Guangzhou University of Chinese Medicine.

**Corresponding author:** Xiaohong Liu

The First Affiliated Hospital of Chinese Medicine, Guangzhou University of Chinese Medicine

**Contact Information:** 20202120031@stu.gzucm.edu.cn

Supplementary material for the manuscript including potential host factors between COVID-19 and dengue, and bioinformatics analysis result of the manuscript.

It is being made public to act as supplementary data for publications in order for other researchers to use this data in their own work.

**Description of the data in this data set:**

**Supplementary material lists:**

**01 common host factors between COVID-19 and dengue**

The host factors for COVID-19 and dengue are not clear at present, thus we collected the targets through searching in databases and analyzing the transcriptomic. After searching for COVID in CTD, DisGeNET, and PubChem, selecting the top 500 genes in accordance with relevance scores. And from three transcriptomics analysis data, 524 factors were collected. Eventually, we included 1721 host-related genes. Similarly, on the basis of searches of the CTD，DisGeNET, and GeneCards databases, and analysis of three transcriptome data, we included 1901 related factors. After collating the targets, ultimately, 460 common host factors were obtained.

**02 host factors in PPI**

To generate the protein-protein interaction (PPI) network, we inserted the common host factors between COVID-19 and dengue in STRING website (version 11.0, <https://string-db.org/>). Subsequently, the network topology analysis was performed through the cytoHubba (<http://apps.cytoscape.org/apps/cytohubba>).

**03 relevant factors in module analysis with MCODE**

Molecular Complex Detection (MCODE) in Metascape (<https://metascape.org/>) was applied to complete the module analysis of the PPI network.

**04 GO BP, 05 GO MF, 06 KEGG, and 07 WIKI**

R software was used for further enrichment analysis. Network of genes and KEGG pathways interaction was conducted by Network Analyst (<https://www.networkanalyst.ca/>). Besides, the ShinyGO v0.61 platform (<http://bioinformatics.sdstate.edu/go/>) was used to obtain GO terms and pathway enrichment analysis.

**08 pathway activity inference with SPEED2**

SPEED2 (<https://speed2.sys-bio.net/>) was used to presume upstream pathway activity of the host factor interaction networks, which was related to the Z-value and p-value, afterwards, the ranked lists were obtained. The method is important to infer the signaling pathways.

**09 candidate drug from STITCH**

Search tool for interactions of chemicals (STITCH) (<http://stitch.embl.de/>) was utilized to predict the potential drugs for the co-infection, which was on the basis of the chemical protein interactions and drug-target relationships.