Abstract and Introduction summary

.In this work, we present new studies to solve the problem of the spread of the Corona virus , by using existing drugs to identify drugs that can treat this disease .

.The problem is that , this disease has caused the destruction of families and children , the death of more than two million people in a single day , and the injury of more than 108 million , krona virus is a health crisis all over the world.

.Therefore, we will try to present a new platform for drug reuse and also by researching the genes of old diseases in cooperation with bioinformatics.

.how to extract data for highly similar diseases based on the genetic similarity of the diseases as a bioinformatics team with experts in pharmacology discover this similarity to try to find a drug for the virus.

.SARS-cov-2, caused by the covid-19, is a disease of a health crisis all over the world, but the construction of SARS-cov-2 was the knowledge about its similarity with other viruses.

. Despite the availability of many vaccines, it remains a major challenge due to combating the epidemic of emerging mutated strains of the virus.

▪ During an outbreak, network bioinformatics allows for quick therapy analysis.

▪ COVID-19 was linked to 34 genes, 24 pathways, and 5 modules using this method.

. SARS-CoV-2 was unknown at the time of the initial outbreak , but its relation to other viruses contributed to its discovery.

. We began by examining the genome sequence of SARS-CoV-2 , which revealed SARS to be the nearest virus in terms of genome similarity , followed by MERS and other human coronaviruses . We obtained 34 COVID-19-related genes using text mining and database searches to seed the development of a molecular network , where our module identification and drug prioritization algorithms found 24 disease-related human pathways. There are five modules to repurpose , as well as 78 drugs . 30 theoretically repurposable medication were re-prioritized against COVID-19 based on scientific information.

Related Work:

. *COVID-19 outpatients: early risk-stratified treatment with zinc plus low-dose hydroxychloroquine and azithromycin: a retrospective case series study. The first COVID-19 outpatient trial focused on risk stratification and antiviral therapy early in the disease's course. Combining low-dose hydroxychloroquine with zinc and azithromycin proved to*

be a successful treatment for COVID-19. The recovery group's hospitalisation rates were much lower. The recovery party has a lower death rate.

. Escape from neutralizing antibodies by SARS-CoV-2 spike protein variants. *Neutralizing antibodies elicited by prior infection or vaccination are likely to be key for future protection of individuals and populations against SARS-CoV-2. Moreover , passively administered antibodies are among the most promising therapeutic and prophylactic anti-SARS-CoV-2 agents. However, the degree to which SARS-CoV-2 will adapt to evade neutralizing antibodies is unclear. Using a recombinant chimeric VSV/SARS-CoV-2 reporter virus, we show that functional SARS-CoV-2 S protein variants with mutations in the receptor-binding domain (RBD) and N-terminal domain that confer resistance to monoclonal antibodies or convalescent plasma can be readily selected. Notably, SARS-CoV-2 S variants that resist commonly elicited neutralizing antibodies are now present at low frequencies in circulating SARS-CoV-2 populations.*

. Recognition of the SARS-CoV-2 receptor binding domain by neutralizing antibodies. *Immediately from the outset of the COVID-19 pandemic, researchers from diverse biomedical l and biological disciplines have united to study the novel pandemic virus, SARS-CoV-2. The antibody response to SARS-CoV-2 has been a major focus of COVID-19 research due to its clinical relevance and importance in vaccine and therapeutic development . Isolation and characterization of antibodies to SARS-CoV-2 have been accumulating at an unprecedented pace. Most of the SARS-CoV-2*

neutralizing antibodies to date target the spike (S) protein receptor binding domain (RBD), which engages the host receptor ACE2 for viral entry. Here we review the binding sites and molecular features of monoclonal antibodies that target the SARS-CoV-2 RBD, including a few that also cross-neutralize SARS-CoV.

Methodology:

-Genome sequence analysis suggests SARS as the most similar disease

After performing a BLASTn search using the SARS-CoV-2, genome sequence against the NCBI GenBank database, representative sequences from top results , all being coronaviruses either in humans or other animals , to build a phylogenetic tree using the neighbor-joining method, With an 80 percent sequence similarity , SARS-CoV was shown to be the evolutionarily closest sequence to SARS-CoV-2.

-Text mining and database searches yield a list of 34 seed genes

In this step , we aimed to identify a list of human genes that are involved in the COVID-19 disease and built a literature searching-engine-based web tool which is freely accessed in http://literature.tasly.com/covid19. Considering SARS-CoV as the closest virus to SARS-CoV-2 , we used SARS as the first keyword for text mining against the database of NCBI PubMed . We searched for all human genes co-occurring with the keyword “SARS-COV-2” within any sentence . We then ranked all genes based on their SARS co-occurrences count .

-Network bioinformatics approach helps to predict 30 repurposable drugs

In order to contextualize and better understand , at a systems level , the molecular and physiological role of the COVID-19-related genes we found , we applied an in-house developed algorithm to build a molecular network taking these 34 genes as seeds . This algorithm repeats subnetwork expanding , merging , and pruning in an iterative manner, controlled by pathway enrichment analysis , In this way , we obtained a final protein network of 1344 genes and 24 enriched pathways . The Newman greedy heuristic module detection algorithm was applied on the network, leading to five modules , At last , Drug Bank's drug-target interactions were added to the protein network , resulting a heterogeneous molecular network , over which proximity-based network analysis identified a list of 78 repurposable drugs . Having obtained these 78 drugs , we looked for more informationand adverse effect and traditional Chinese medicine usage and theory.

Through a literature review , we identified a list of important symptoms and mechanisms linked to SARS-CoV-2, including fever , fatigue , cough , breathing difficulty , septic shock , viral proliferation , immunodeficiency and pulmonary fibrosis We also filtered out drugs for which there is little scientific knowledge . After removing these drugs we obtained a list of 30 drugs.

-Results sharing and case analysis

To help fight COVID-19 as quickly as possible , we first shared our list of 78 drugs and our list of 24 enriched

pathways and we briefly explained our approach with healthcare professionals and hospitals .