A Computational Drug Repurposing Workflow to Prioritize Pharmacotherapeutics for COVID-19 and Other Infectious Diseases

By

Reham Abdel Rahman Kharmah

Supervisor

Dr. Rima Hajjo

Al-Zaytoonah University of Jordan, 2024

Abstract

Emerging and re-emerging viruses have been key players in causing major epidemics and pandemics worldwide. The current COVID-19 pandemic, caused by SARS-CoV-2, has threatened public health systems due to lack of effective drugs and vaccines. Host targeted drugs are considered promising alternatives to conventional antivirals which target viral proteins and found ineffective for COVID-19. This study employs a novel integrative informatics workflow to identify host-targeted pharmacotherapy for COVID-19. Our objective is to explore the network pharmacology of COVID-19, seeking disease-modifying treatments by analyzing disease signatures. Results unveiled blood coagulation as a critical underlying pathway for COVID-19 pathogenesis. This led to Von Willebrand Factor (VWF) prioritization as a promising drug target. Thus, known drugs for this target hypothesis could be repurposed for treating COVID-19 or its complications. Eighteen virtual screening hits, including PCA-8008, were identified as small molecule inhibitors for VWF awaiting experimental validation.

Keywords: Bioinformatics, cheminformatics, COVID-19, drug-repurposing, infectious diseases.