

Comprehensive assessment of side effects in COVID-19 drug pipeline from a network perspective

Ping Yin, Honghai Hong*

The Third Affiliated Hospital of Guangzhou Medical University

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*Author for Correspondence: Honghai Hong, The Third Affiliated Hospital of Guangzhou Medical University E-mail: gaolaosao@126.com.

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COVID-19 pandemic has raised increasing clinical needs for therapeutic agents, and the accelerated schedule prompt us to find more efficient ways to evaluate the safty profile of potential therapeutic agents comprehensively.

In this article, the authors developed a network-based framework to identify side effects of the ongoing drugs in COVID-19 pipeline. Specifically, after integration of drug-target network, drug-gene signatures, tissue-specific gene expression profiles from GTEx, and human protein-protein interactome, a systematic examination of the relationship between drug targets (or drug regulatory genes) and specific expression genes in each tissue from GTEx served as a foundation for generating predictive models to identify potential side effects in tissue. They established the associations between 116 COVID-19 drugs and 30 kinds of

human tissues. Moreover, the authors concentrated on side effects of four tissues including liver, kidney, lung and nerve, and validated several drug-tissue associations utilizing large-scale adverse drug event data and more than half of them supported their network-based prediction.

This article provides us with a fresh new and powerful way to predict the pharmacological and toxicity properties of investigational or experimental drugs for COVID-19 in clinical trials, which could benefit the discovery and clinical application of pharmacotherapy for COVID-19. Although the limitation was conceivable for the results were not completely based on experimental data, this computational framework could shorten the time to prioritize side effects associated with drugs and pre-alert the potential adverse effects during pharmacotherapy course of COVID-19.