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LETTER TO THE EDITOR

Bioinformatics Analysis for Screening of Therapeutic Drugs in COVID-19

To the Editor:

We would like to share ideas on the publication Therapeutic Drugs in Coronavirus Disease 2019 (1). Wang T, et al. concluded that *some drugs selected through our methods have been proven to have antiviral effects in previous studies* (1). Indeed, the bioinformatics tools are helpful for analyzing on the possible alternative drugs for the new diseases. The approaches might be the genomics, proteomics, expressional analysis, or interaction analysis (2). Wang T, et al. performed a screening and reported the feasibility that some studied drugs/herbs might be useful. Some previous reports on new COVID-19 drug search based on the bioinformatics techniques are also published (3–4). Nevertheless, the limitation of the in silico study should be mentioned.

First, the bioinfoirmatics approach starts from available data. If there is no data, the bioinformatics manipulation, either clarification or prediction, might not effective. As a new disease, the data on the new pathogen is limited and the bioinformatics assessment based on limited primary data might not highly effective. The interaction screening, as used by Wang T, et al., might identify possible interaction but whether the interaction can really exist or not has to be further proven. Additionally, if the interaction really occurs, whether the interaction can result in final therapeutic effect is the point for further *in vitro* and *in vivo* analysis. Another part that is limited reported in bioinformatics based COVID-19 drug search studies is the toxicity or adverse effect of the studied drug alternative. There are ae limited informatics tolls that is applicable for analyzing the adverse effect due to the alternative drugs/herbs.

Conflict of Interest

None.

References

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