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Editorial

Forecast the potential SARS-CoV-2 variants in the future and predict their biological properties and social impacts from bioinformatics and public health perspectives

Yixue Li [a,1,*], Yuming Guo [b,*], Tao Huang [c,*]

[a] Guangzhou Laboratory, Guangzhou 510005, China
[b] Monash University, Clayton, Australia
[c] Shanghai Institute of Nutrition and Health, Chinese Academy of Sciences, Shanghai 200031, China

The evolutionary nature of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a topic of concern, as it is anticipated that additional variants will emerge in the future. The likelihood of these variants and their biological properties are difficult to predict, as are the rates of transmission, incidence, and mortality. The current vaccines may not be sufficient in protecting against these new variants, as demonstrated by the recent delta and omicron strains. It is imperative that we prepare for future outbreaks by forecasting the evolution of SARS-CoV-2, identifying potential variants, and predicting their biological properties. In this special issue, we aim to provide a comprehensive view on the effects of new SARS-CoV-2 variants on transmission, pathogenicity, and fatality. A wide range of multimodal data have been analyzed, including genomics of SARS-CoV-2 variants, transcriptomics of SARS-CoV-2 infection, single cell omics during vaccination and drug treatment, and public health data. Our objective is to support epidemic prevention and control efforts. This special issue comprises nine papers:

Zhang et al. [1] conducted surveillance of the first variant of concern (VOC)/Omicron subvariant BA.2.75 in China, originating from an imported case on July 15, 2022. The variant had nine additional mutations in the S protein in comparison to BA.2, three of which (W152R, G446S, and R493Q reversion) are posited to contribute to higher transmissibility and immune evasion.

He et al. [2] analyzed the genomic variations of SARS-CoV-2 during a flight-associated cluster outbreak of coronavirus disease 2019 (COVID-19) in Shenzhen, China. Results indicate that the intra-host diversity of SARS-CoV-2-infected individuals increased rapidly with time.

Zhao et al. [3] established a highly efficient platform that integrates 17-plex assays with matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS), which allows for the targeting of 14 different mutation sites of the spike gene. The multiplex approach is both sensitive and high throughput, successfully detecting all known SARS-CoV-2 variants and tracking their evolution.

Chen et al. [4] investigated the efficacy of hetero-chimeric RBD-dimer mRNA vaccines as booster jabs in mice, following two doses of inactivated vaccine (IV). The researchers found that these chimeric vaccines were effective in significantly boosting neutralizing antibody levels and specific T-cell responses against variants. Moreover, PT-Beta was found to be superior to Delta-BA.1 RBD as a booster in mice, which has important implications for the design of next-generation COVID-19 vaccines.

Cen et al. [5] reviewed the current state of the field and discussed future directions for globalized and precision medicine of COVID-19. Omics, including genomics, proteomics, single-cell multi-omics, and clinical phenomics, have been increasingly utilized to address biological and clinical questions about COVID-19.

Xie et al. [6] developed a novel predictive tool named Emvirus for studying human-virus protein–protein interactions (PPIs), including human-SARS-CoV-2 PPIs. The tool employs an embedding-based neural framework with convolutional neural network (CNN) and bi-directional long short-term memory unit (Bi-LSTM) architecture. This work has important implications for the study of human-virus PPIs.

Huang et al. [7] proposed a computational framework to comprehensively study the roles of TLR7 in COVID-19 and pan-cancers at various levels, including genetic, gene expression, protein, epigenetic, and single-cell levels. These findings may have important implications for preventing SARS-CoV-2 infection and alleviating cytokine storms in infected cancer patients.

Ren et al. [8] conducted a comprehensive review on emerging infectious viruses and their variants, focusing on forecasting and early warning. It included the multi-dimensional information integration and database construction of emerging infectious viruses, virus mutation spectrum construction and variant forecast model, analysis of the affinity between mutation antigen and the receptor, propagation

* Corresponding authors: Guangzhou Laboratory, Guangzhou 510005, China (Y. Li); Monash University, Clayton, Australia (Y. Guo); Shanghai Institute of Nutrition and Health, Chinese Academy of Sciences, Shanghai 200031, China (T. Huang).

E-mail addresses: yxli@sibs.ac.cn (Y. Li), Yuming.Guo@monash.edu (Y. Guo), huangtao@sibs.ac.cn (T. Huang).

[1] Given his role as Editorial Board Member, Yixue Li had no involvement in the peer-review of this article and had no access to information regarding its peer-review. Full responsibility for the editorial process for this article was delegated to Editor Di Qu.

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model of virus dynamic evolution, and monitoring and early warning for variants.

Ma et al. [9] provided an informative overview of the resources available for SARS-CoV-2 genome data deposition. They also highlighted the challenges faced in integrating SARS-CoV-2 genome data, including issues with low-complexity, inconsistency, and absence of isolate name, sequence inconsistency, asynchronous update of genome data, and mismatched metadata.

Overall, the studies presented in this special issue offer valuable insights into the evolution of SARS-CoV-2 variants and the potential effects of new mutations. Given the complexity of COVID-19 and its association with other diseases and symptoms, more attention should be paid to addressing long COVID, especially since a significant proportion of the world's population has been infected.

Conflict of interest statement

The authors declare that there are no conflicts of interest.

Author contributions

Yixue Li, Yuming Guo: Writing - review & editing. **Tao Huang:** Writing - original draft.

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