INFECTIOUS DISEASES

COVID-19 prognosis from a longitudinal dataset

Cell Syst. https://doi.org/10.1016/j.cels.2021.05.005 (2021)

The coronavirus disease 2019 (COVID-19) is known to affect people differently, meaning that patients may show similar symptoms but with varying degrees of severity. At the onset of the disease, the physical symptoms are not enough to determine if a patient's condition will be stable, or if it will deteriorate, potentially leading to severe disease and organ failure and requiring extensive medical assistance. Alternatively, biomarkers and molecular signatures are promising tools that can enable prognosis of COVID-19 progression, but this requires a more comprehensive, detailed longitudinal patient dataset for accurate results. In order to address this gap, Damichev and colleagues established a dataset of biomarker profiles and diagnostic parameters for COVID-19 prognosis by performing an extensive longitudinal study. Based on this dataset, the authors were able to predict the treatment needs of patients, the recovery time and the risk of clinical deterioration of mildly ill patients.

In their study, the authors measured 86 diagnostic markers, such as blood cell and immune cell counts, at 687 sampling points at different times, and in 139 COVID-19 patients. The longitudinal study was carried out in Charité University Hospital, Germany, and it included patients from the World Health Organization (WHO) grade 3, who require inpatient care without supplemental oxygen therapy, to WHO grade 7, who require invasive mechanical ventilation. The interdependencies of the diagnostic parameters were studied using a correlation map. The results showed that changes were observed in 113 proteins and 55 diagnostic parameters across different WHO grades. Of the 113 proteins, 30 had not been associated with COVID-19 severity in earlier studies. The markers were also correlated with age, disease severity, and the therapy received by the patient.

Using the longitudinal dataset, the authors applied a machine learning algorithm based on gradient boosted trees to study how diagnostic parameters characterize treatment requirements. It was observed that both the proteomes and the clinical diagnostic parameters could identify patients needing invasive mechanical ventilation, and when the model was applied to a validation dataset obtained from a different hospital, they obtained an area under the receiver operating characteristic (AUROC) score of 0.97. The results also showed that the molecular signature of the initial host response is predictive of future clinical deterioration and could predict the remaining time needed in the hospital for mildly ill patients of WHO grade 3 or less. This study opens up the possibility of predicting potential COVID-19 outcome at the onset of the disease, allowing for better allocation of medical treatments.

Ananya Rastogi

Published online: 15 July 2021
https://doi.org/10.1038/s43588-021-00106-y