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Changes in Plasma Metabolome Identify COVID-19 and Non-COVID-19 Pneumonitis

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DESCRIPTION

In Pneumonia is a common cause of morbidity and mortality that is primarily brought on by bacterial infections. COVID-19 is characterised by lung infection and the possibility for progressive organ failure. The systemic consequences of both illnesses on the blood metabolome are unknown. By contrasting the blood metabolomes of the two illnesses, we predicted that plasma metabolomics would be useful in identifying the systemic impacts of both disorders. Therefore, we profiled the plasma metabolomes of 26 controls, 23 cases of non-COVID-19 pneumonia, and 43 instances of COVID-19 pneumonia using a non-targeted approach.

The three groups could be separated by metabolic changes, with the two pneumonia groups being separated by specific metabolic changes. When plasma samples from the same participants' venous and arterial blood were analysed, the unique metabolic effects of pulmonary pneumonia were found. Additionally, a machine learning signature with four metabolites and an AUC of 86, 10% was able to predict the disease outcome in COVID-19 individuals. Overall, this study's findings point to systemic metabolic changes that may be connected to the causes of pneumonia caused by COVID-19 and pneumonia caused by other viruses.

The coronavirus disease (COVID-19) pandemic, which has affected millions of individuals globally over the previous two years, has been the main health problem. It was rapidly determined that the condition, which started with a number of pneumonia cases with an unidentified aetiology, resulted in severe acute respiratory syndrome. The primary symptom of COVID-19 is a respiratory infection, but it can develop into a systemic sickness that can be deadly and result in organ failure.

In addition, the build-up of saturated fatty acids, such as octadecanoic acid, indicates that the structural and functional features of the cells have been altered, leading to apoptosis or necrosis-mediated cell death. Other metabolic entities that have been identified as trans-pulmonary activities need more structural validation with regard to their function in the lung pathogenesis of COVID-19 pneumonia and non-COVID-19 pneumonia. Numerous cytokines show large trans-pulmonary gradients in both non COVID-19 pneumonia and COVID-19 illness, which are more prominent in the COVID-19 group. As was to be expected, there were no changes within the control group. A prior study found a correlation between the cytokine concentration in the vein and the severity of the disease and its outcome.

To find group-specific differences between the COVID-19 pneumonia, non COVID-19 pneumonia, and control groups in this investigation, we used a non-targeted plasma metabolomics technique. When compared to controls, COVID-19 pneumonia and non COVID-19 pneumonia groups both showed disease-specific metabolic abnormalities that can be used to create biomarker patterns that predict the likelihood of a patient dying from the disease. Numerous metabolites and cytokines were shown to have a trans-pulmonary gradient, indicating the function of the lung in regulating the effects of systemic illness.

Overall, our research provides novel insights into the metabolic differences that distinguish COVID-The study has both benefits and drawbacks. There may be bias because the patient sample contains more men than women. Initially, we included only male patients to account for female blood metabolome cyclic changes. As the COVID-19 pandemics started, we decided to address this novel disease by including female patients. Additionally, we did not address a number of underlying factors, such as medication or diet.

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CONFLICT OF INTEREST

The author declares there is no conflict of interest in publishing this article has been read and approved by all named authors.

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