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Título	Mass Spectrometry-Based Metabolomics Reveals a Salivary Signature for Low-Severity COVID-19
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Resumo	Omics approaches were extensively applied during the coronavirus disease 2019 (COVID-19) pandemic to understand the disease, identify biomarkers with diagnostic and prognostic value, and discover new molecular targets for medications. COVID-19 continues to challenge the healthcare system as the virus mutates, becoming more transmissible or adept at evading the immune system, causing resurgent epidemic waves over the last few years. In this study, we used saliva from volunteers who were negative and positive for COVID-19 when Omicron and its variants became dominant. We applied a direct solid-phase extraction approach followed by non-target metabolomics analysis to identify potential salivary signatures of hospital-recruited volunteers to establish a model for COVID-19 screening. Our model, which aimed to differentiate COVID-19-positive individuals from controls in a hospital setting, was based on 39 compounds and achieved high sensitivity (85%/100%), specificity (82%/84%), and accuracy (84%/92%) in training and validation sets, respectively. The salivary diagnostic signatures were mainly composed of amino acids and lipids and were related to a heightened innate immune antiviral response and an attenuated inflammatory profile. The higher abundance of thyrotropin-releasing hormone in the COVID-19 positive group highlighted the endocrine imbalance in low-severity disease, as first reported here, underscoring the need for further studies in this area.
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