

# Alterations in oral microbiomes in SARS-CoV-2 Omicron Variant Infected and Recovery Patients

Chunfu Zheng<sup>1</sup>, Zhigang Ren<sup>2</sup>, Junyi Sun<sup>2</sup>, Qi Liu<sup>2</sup>, Jiyuan Xing<sup>2</sup>, Ning Xu<sup>2</sup>, Liwen Liu<sup>2</sup>, Guizhen Zhang<sup>2</sup>, Ying Sun<sup>2</sup>, Yawen Zou<sup>2</sup>, Haiyu Wang<sup>2</sup>, Benchen Rao<sup>2</sup>, Xinyue Zhang<sup>2</sup>, Zu-Jiang Yu<sup>2</sup>, and Guangying Cui<sup>2</sup>

<sup>1</sup>University of Calgary

<sup>2</sup>The First Affiliated Hospital of Zhengzhou University

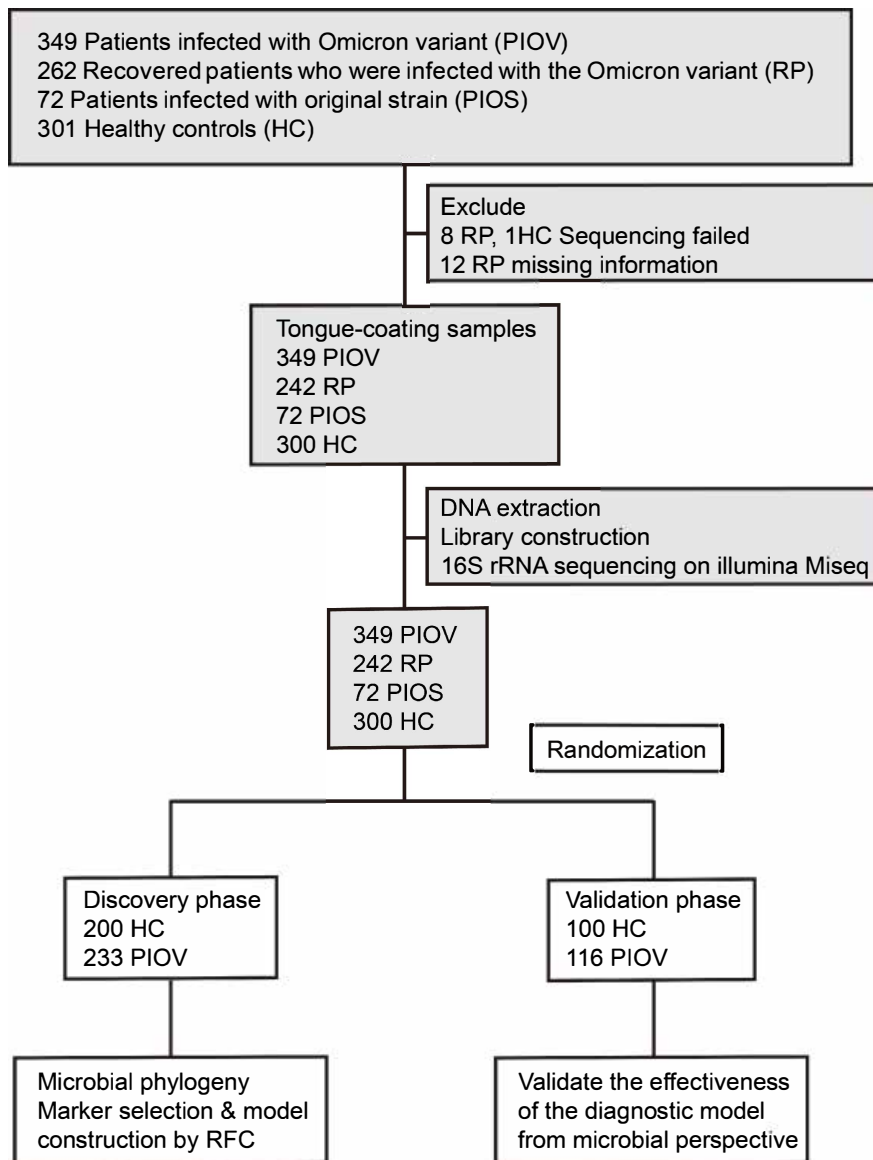
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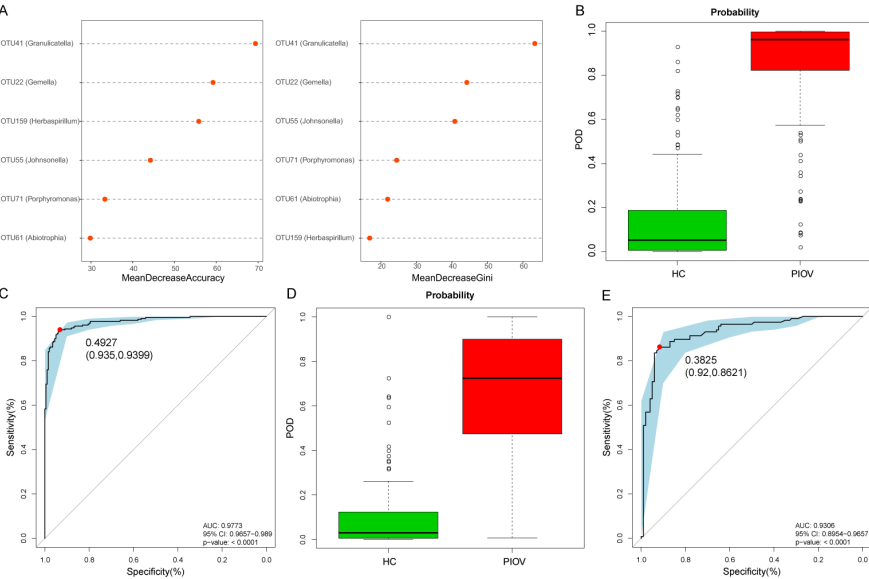
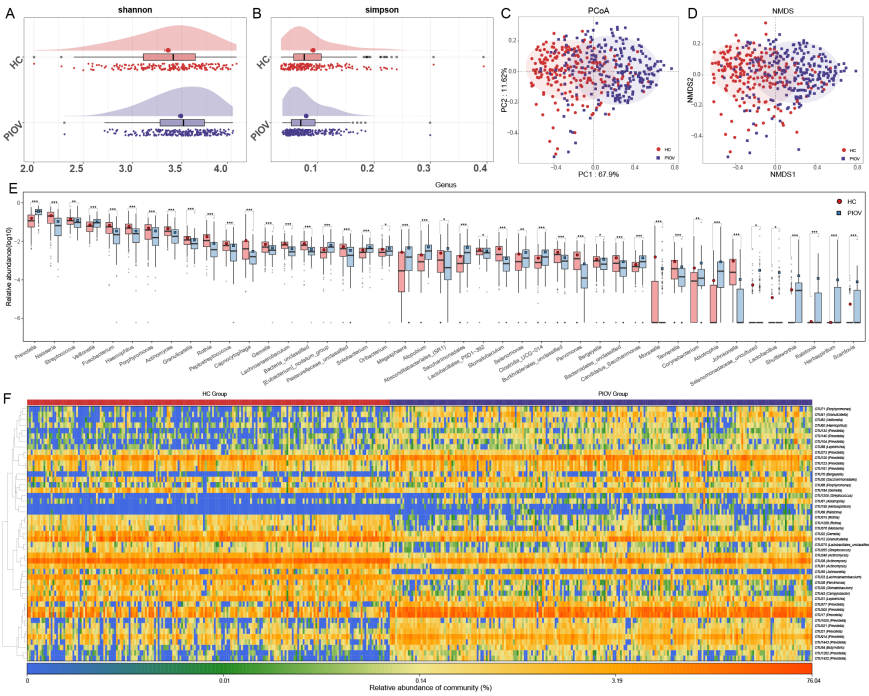
## Abstract

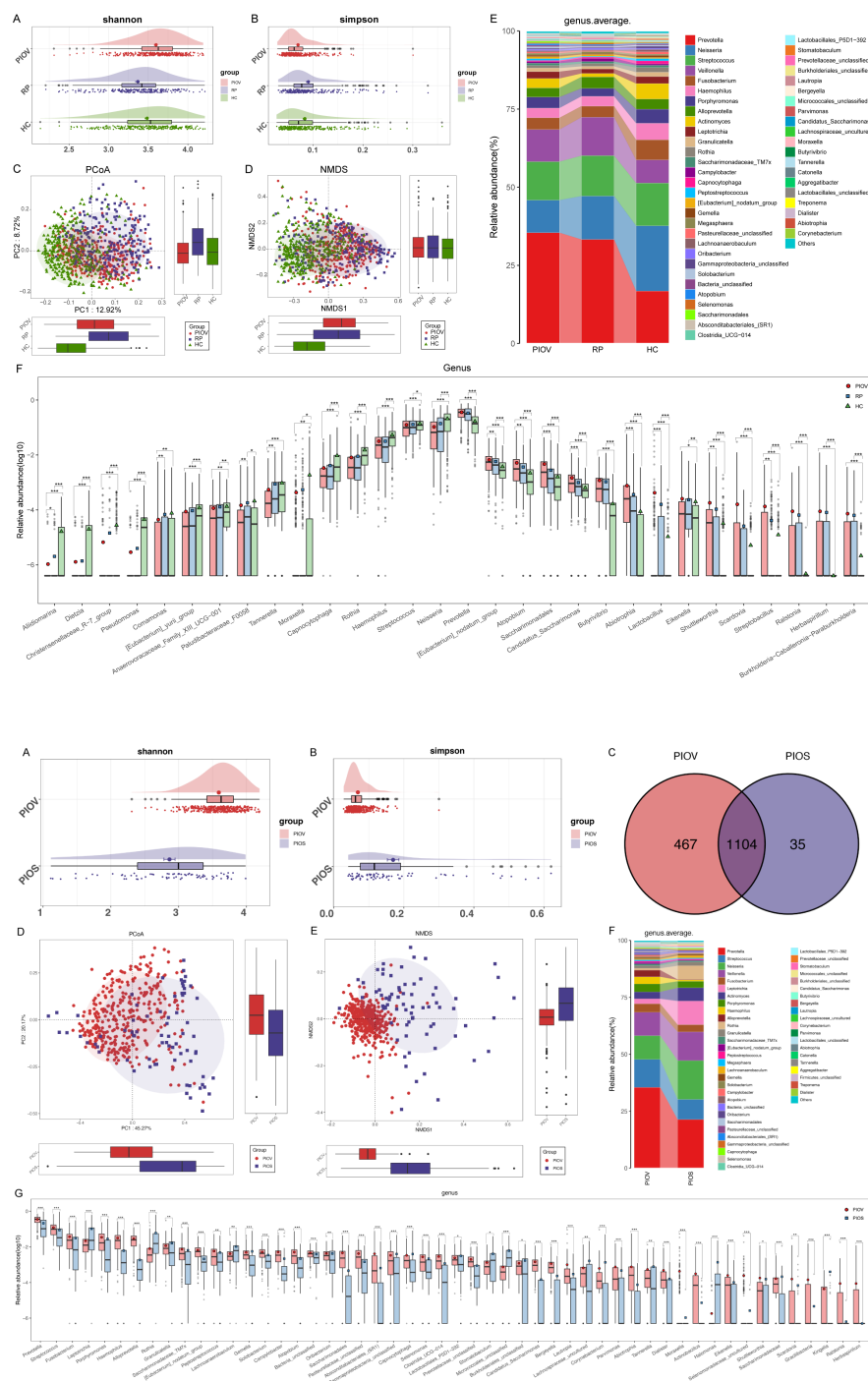
**Objective** Our study aimed to investigate the oral microbiome of patients infected with the Omicron variant (PIOV) and the changes in oral microbiota during the recovery of infection, compared to those infected with the original strain (PIOS) and provide a theoretical foundation for early diagnosis and disease prognosis of PIOV from the perspective of microecology. **Design** We collected 963 samples of tongue-coating prospectively, including 349 samples of PIOV, 242 samples of recovered patients from PIOV (RP), 300 samples of healthy controls (HC), and 72 samples of PIOS. We randomly selected tongue-coating samples from PIOV and HC at a ratio of 2:1, respectively, as the discovery cohort and validation cohort. **Results** Oral microbial diversity was significantly increased in PIOV. Compared to HC, conditional pathogenic bacteria were increased in PIOV. The classifier based on 6 optimal oral microbial markers had high diagnostic efficiency in both cohorts. Oral microbiota numbers were changed as the disease recovered. **Conclusion** For the first time, our study characterizes the oral microbiota of PIOV and RP, successfully establishes and validates the noninvasive diagnostic model of PIOV, and outlines the correlation between the OTUs of microbiota and clinical indicators.

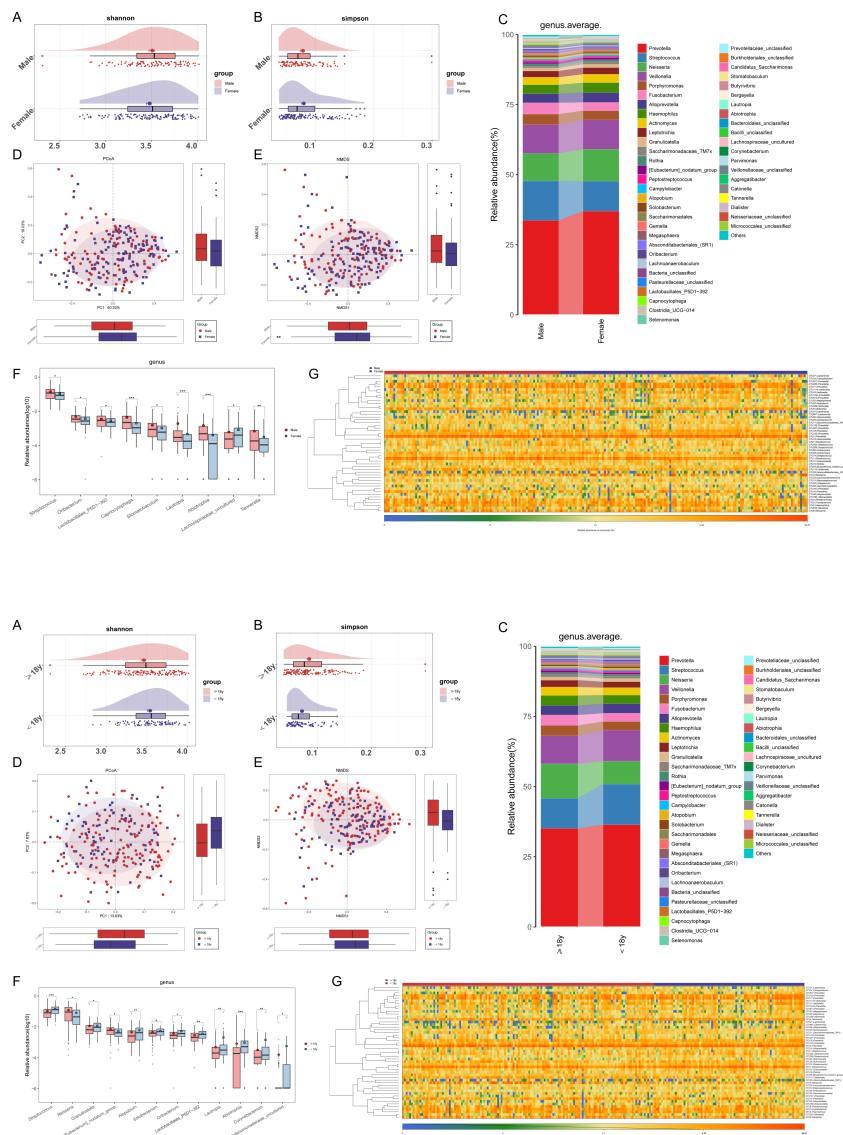
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