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

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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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349 Patients infected with Omicron variant (PIOV)
262 Recovered patients who were infected with the Omicron variant (RP)
72 Patients infected with original strain (PIOS)
301 Healthy controls (HC)

Exclude
8 RP, 1 HC Sequencing failed
12 RP missing information

Tongue-coating samples
349 PIOV
242 RP
72 PIOS
300 HC

DNA extraction
Library construction
16S rRNA sequencing on illumina Miseq

Randomization

349 PIOV
242 RP
72 PIOS
300 HC

Discovery phase
200 HC
233 PIOV

Validation phase
100 HC
116 PIOV

Microbial phylogeny
Marker selection & model construction by RFC

Validate the effectiveness of the diagnostic model from microbial perspective
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