Stratification of chronic rhinosinusitis with nasal polyps by distinct sinonasal microbial communities and their clinical and pathological correlations

Bixing Fang[1,2,3#], Yanmin Liu[4,5#], Qing Bao[1], Lin Sun[1], Hexin Chen[1],
Qingxiang Meng[6], Linyi Jiao[1], Xiaoyan Ye[1], Jian Li[1,2*], Tao Ding[5,7*], Chunwei Li[1*]

[1] Department of Otolaryngology, Department of Allergy,
The First Affiliated Hospital, Sun Yat-sen University, Guangzhou, China
[2] Guangxi Hospital Division of The First Affiliated Hospital,
Sun Yat-sen University, Nanning, China
[3] Department of Otolaryngology, The Second Affiliated Hospital,
Zhejiang University School of Medicine, Hangzhou, China
[4] State Key Laboratory of Dampness Syndrome of Chinese Medicine
[5] Department of Immunology and Microbiology, Zhongshan School of Medicine,
Sun Yat-sen University
[6] Department of Otorhinolaryngology Head and Neck Surgery, Guangzhou First People’s Hospital
[7] Key Laboratory of Tropical Diseases Control (Sun Yat-sen University), Ministry of Education

Bixing Fang, Yanmin Liu, Qing Bao, Lin Sun, Hexin Chen, Qingxiang Meng, Linyi Jiao, et al. 2025. Stratification of chronic rhinosinusitis with nasal polyps by distinct sinonasal microbial communities and their clinical and pathological correlations. ***iMetaOmics*** 2: e70076. https://doi.org/10.1002/imo2.70076

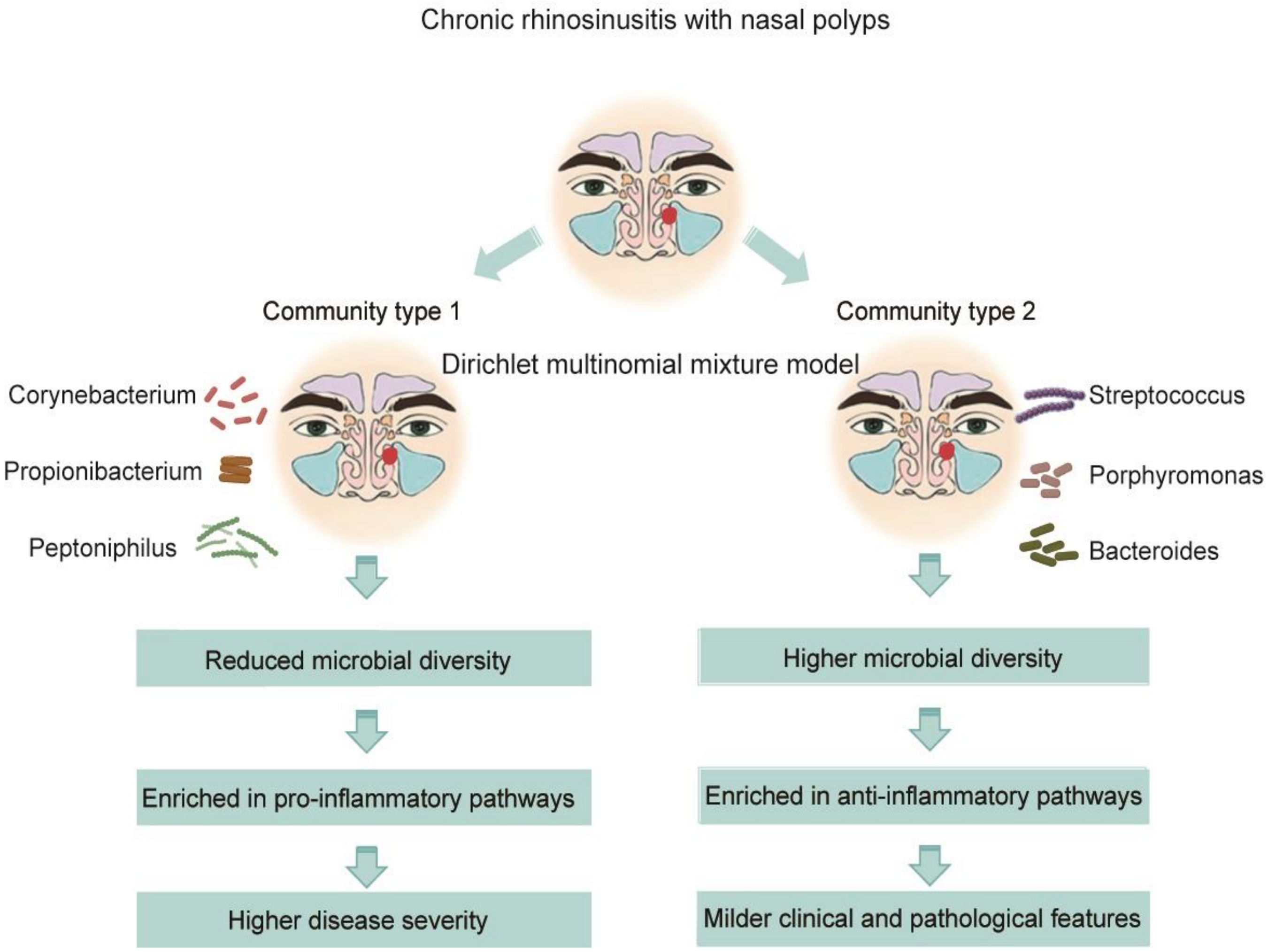
Introduction

1. Chronic rhinosinusitis (CRS) is a complex, multifactorial inflammatory disease of the upper airway. Studies have shown that the sinonasal microbiome plays a key role in CRS, with reduced microbiota diversity, or “Microbial dysbiosis,” being a common feature among patients.

2. It has been proposed that CRS patients could be stratified according to specific sinonasal microbial compositions, illuminating phenotypic heterogeneity.

3.This study aims to identify sinonasal microbial communities in CRSwNP patients, categorize them based on microbial phenotypes, and explore associations with clinical and pathological characteristics.

Highlights



1.Two distinct sinonasal microbial community subtypes (CT1/CT2) in CRSwNP patients were first identified via 16S rRNA sequencing, dominated by Corynebacterium-related and Streptococcus-related genera respectively, with significant differences in microbial diversity and inflammation-associated metabolic pathways.

2.Microbial community stratification strongly correlates with CRSwNP clinicopathology: CT1 links to severe disease, higher eosinophil infiltration, and CT2 to a mild phenotype. Validated by an independent dataset, this stratification provides a key microbiological basis for tailored therapies.

Two distinct sinonasal microbial community types in CRSwNP Patients

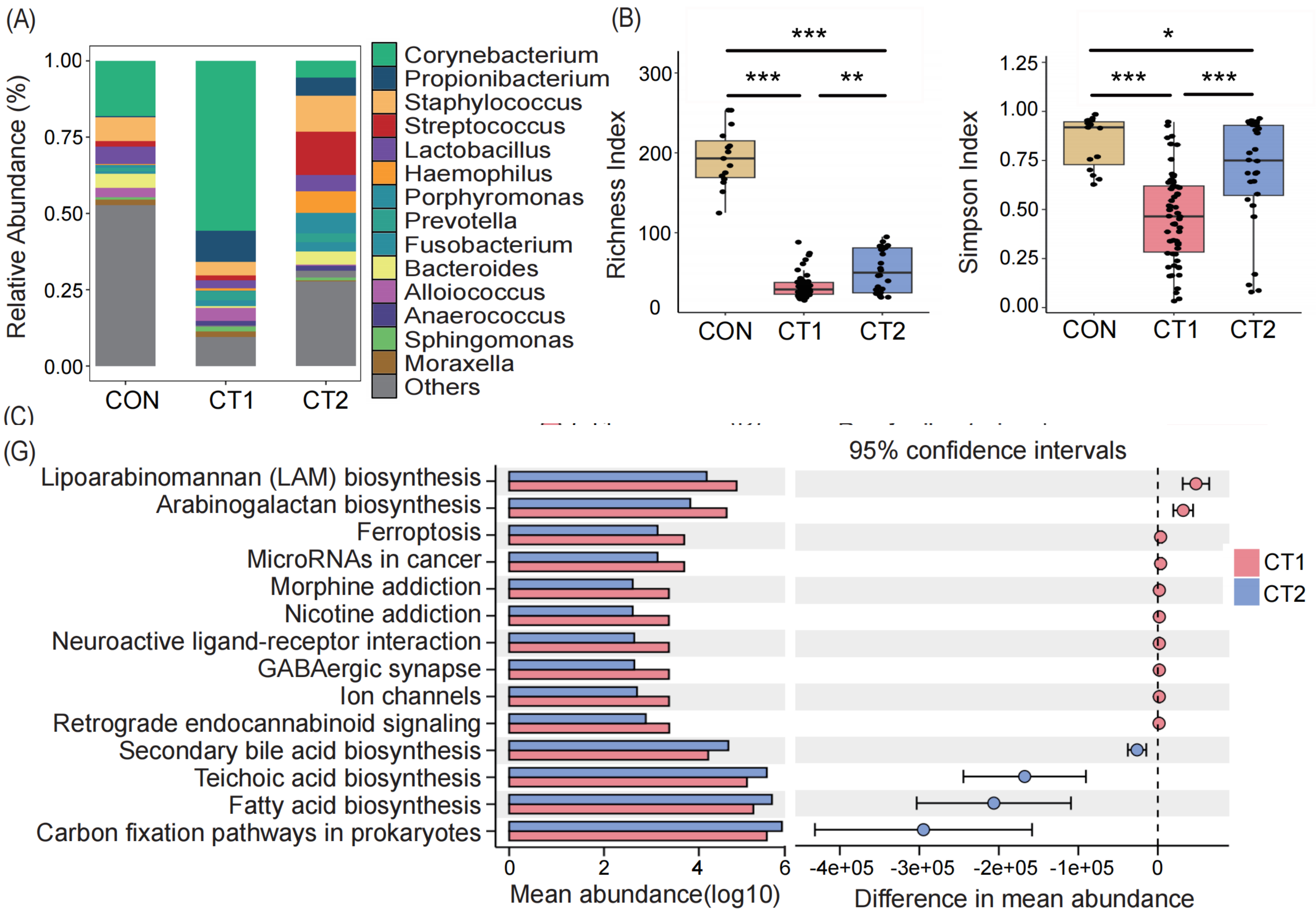


Figure 1. Characteristics of microbial community types among nasal samples and functional predictions.

1. Unsupervised clustering approach using the Dirichlet Multinomial Mixtures model revealed two distinct microbial community types (CT1 and CT2). CT1 showed significantly diminished microbial diversity (Simpson index) and richness compared to CT2 and control subjects, with the control group exhibiting the highest diversity and richness. This suggests that the microbial environment in CT1 patients may be more prone to dysbiosis (Figures 1A−1D)

Two distinct sinonasal microbial community types in CRSwNP Patients

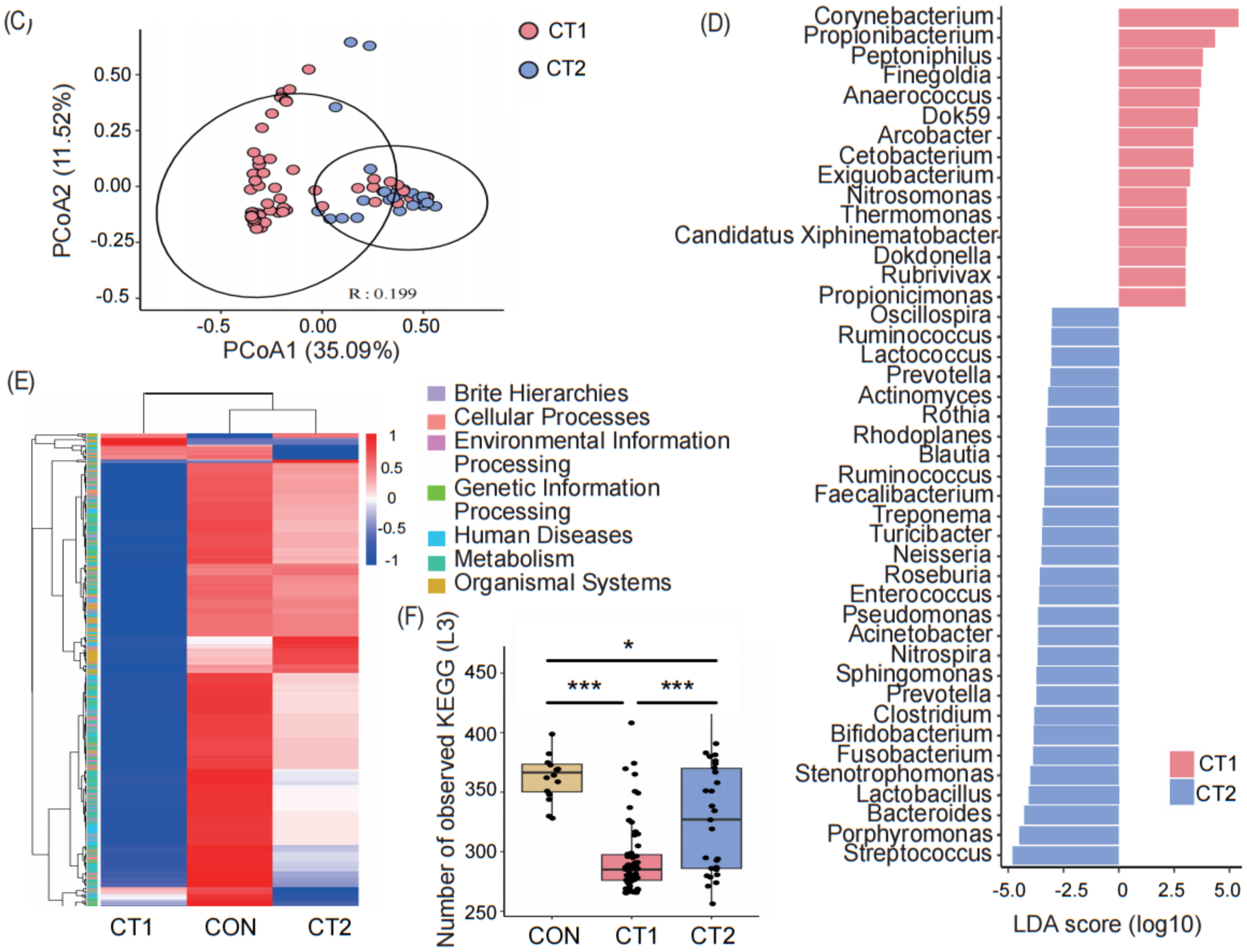


Figure 1. Characteristics of microbial community types among nasal samples and functional predictions.

2. The functional potential of the microbiota was predicted using the PICRUSt algorithm. These findings suggest that CT2 harbors enhanced anti-inflammatory and antimicrobial functions, whereas CT1 microbiota may contribute to a more pathogenic state.

Validation of Microbial Communities in a Separate Dataset

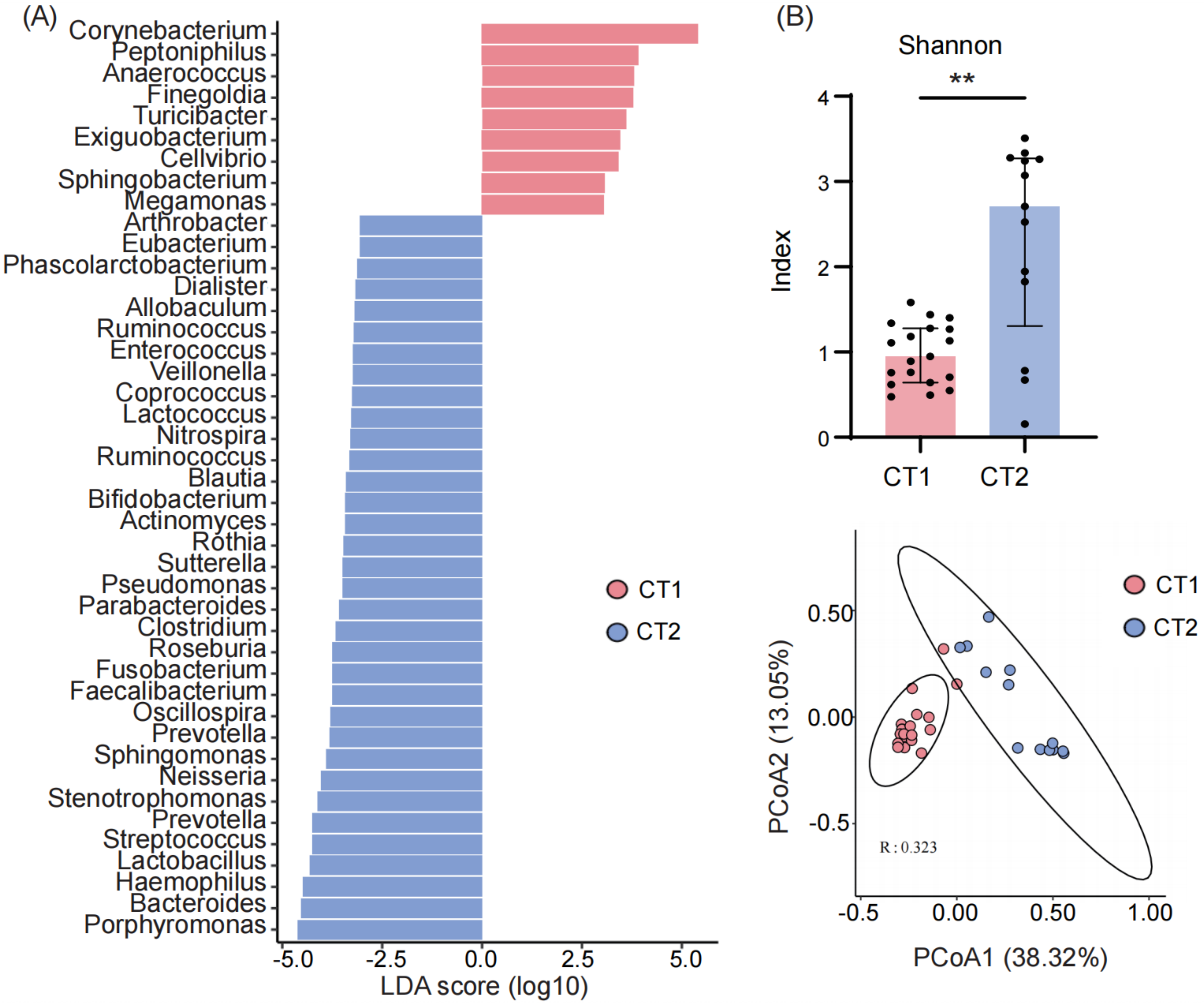


Figure 2. Validation of a predictive model based on nasal microbiome typing and its corresponding clinical and pathological features.

1. Validation cohort samples were clustered independently without prior model training, and then a semi-supervised clustering approach identified two subtypes; Cluster 1, dominated by Corynebacterium, resembled CT1; Cluster 2, enriched in Porphyromonas, Bacteroides, and Streptococcus, mirrored CT2.

Validation of Microbial Communities in a Separate Dataset

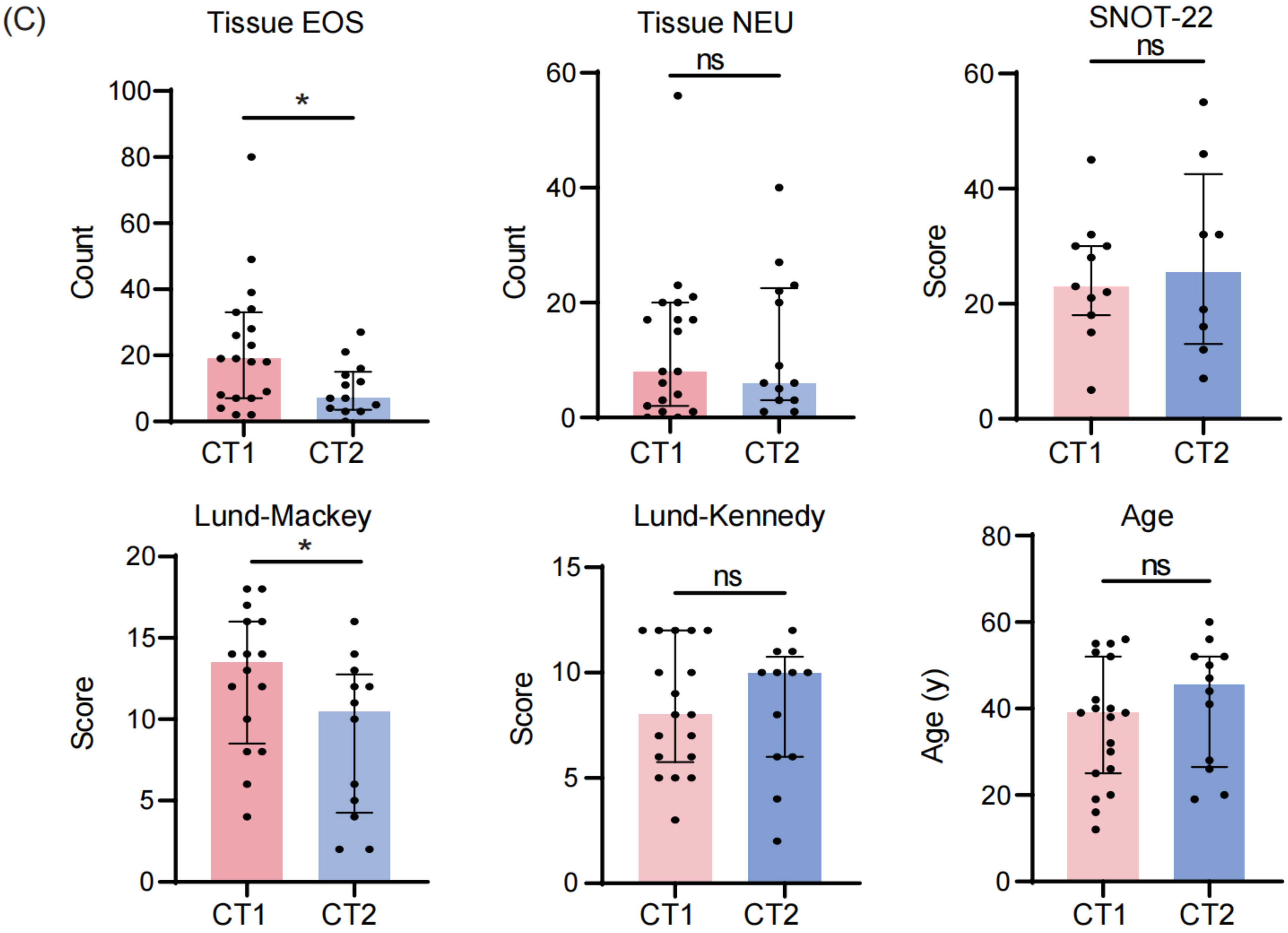


Figure 2. Validation of a predictive model based on nasal microbiome typing and its corresponding clinical and pathological features.

2. Higher CT scores and eosinophil levels were associated with Cluster 1, validating the clinical and pathological characteristics observed in CT1 and CT2.

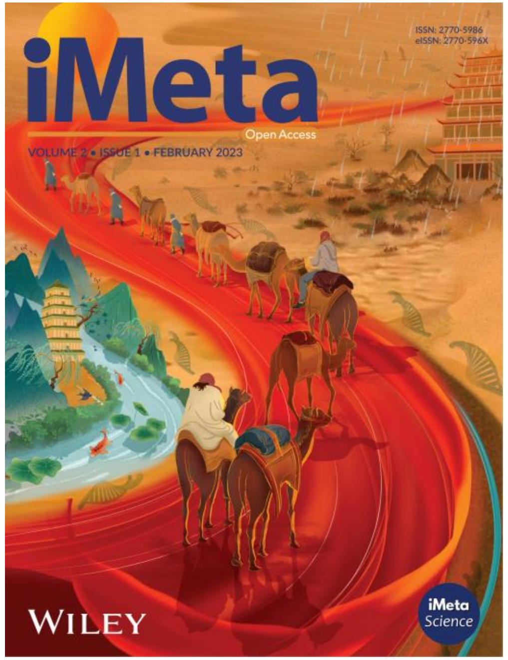
Summary

- ☐ CRSwNP patients can be stratified into two distinct microbial communities, each with specific clinical and pathological profiles.
- ☐ Microbial-based stratification may inform tailored therapeutic strategies to address the diverse clinical and pathological manifestations of CRSwNP.

Bixing Fang, Yanmin Liu, Qing Bao, Lin Sun, Hexin Chen, Qingxiang Meng, Linyi Jiao, et al. 2025.
Stratification of chronic rhinosinusitis with nasal polyps by distinct sinonasal microbial communities and their clinical and pathological correlations. ***iMetaOmics*** 2: e70076. https://doi.org/10.1002/imo2.70076

iMeta: To be top journals in biology and medicine

WILEY



"***iMeta***" launched in 2022 by iMeta Science Society, impact factor (IF) **33.2**, ranking top 65/22249 in world and 2/161 in the microbiology. It aims to publish innovative and high-quality papers with broad and diverse audiences. **Its scope is similar to *Cell*,** *Nature Biotechnology/Methods/Microbiology/Medicine/Food*. Its unique features include video abstract, bilingual publication, and social media with 600,000 followers. Indexed by **SCIE/ESI**, **PubMed**, **Google Scholar** etc.

"***iMetaOmics***" launched in 2024, with a **target IF>10, and its scope is similar to *Nature Communications***, ***Cell Reports***, *Microbiome, ISME J, Nucleic Acids Research, Briefings in Bioinformatics,* etc.

"***iMetaMed***" launched in 2025, with a **target IF>15, similar to *Med, Cell Reports Medicine***, *eBioMedicine, eClinicalMedicine* etc.

Society: http://www.imeta.science
Publisher: https://wileyonlinelibrary.com/journal/imeta
iMeta: https://wiley.atyponrex.com/journal/IMT2
Submission: iMetaOmics: https://wiley.atyponrex.com/journal/IMO2
iMetaMed: https://wiley.atyponrex.com/journal/IMM3

iMetaScience
iMetaScience

office@imeta.science
imetaomics@imeta.science

Promotion Video

Update
2025/7/6