

Ocular microbiota types and longitudinal microbiota alterations in patients with chronic dacryocystitis with and without antibiotic pre-treatment

Shengru Wu^{1,3,*}, Limin Zhu^{2,*}, Tingting Wang^{2,4,*}, Chengguang Zhang¹, Jiaqi Lin², Yanjin He², Junhu Yao¹, Tingting Lin^{2,#}, Juan Du³

1. College of Animal Science and Technology, Northwest A&F University, Yangling 712100, Shaanxi, China

2. Tianjin Key Laboratory of Retinal Functions and Diseases, Tianjin Branch of National Clinical Research Center for Ocular Disease, Eye Institute and School of Optometry, Tianjin Medical University Eye Hospital, Tianjin 300384, China

1. Department of Microbiology, Tumor and Cell Biology, Karolinska Institutet, Solna 17165, Stockholm, Sweden

2. Dep. of Ophthalmology of the First Hospital of Xi'an, Shanxi Ophthalmological Institute, Xi'an 710002, Shaanxi, China.



Shengru Wu, Limin Zhu, Tingting Wang, Chengguang Zhang, Jiaqi Lin, Yanjin He, Junhu Yao, Tingting Lin, Juan Du. 2024. Ocular microbiota types and longitudinal microbiota alterations in patients with chronic dacryocystitis with and without antibiotic pretreatment.

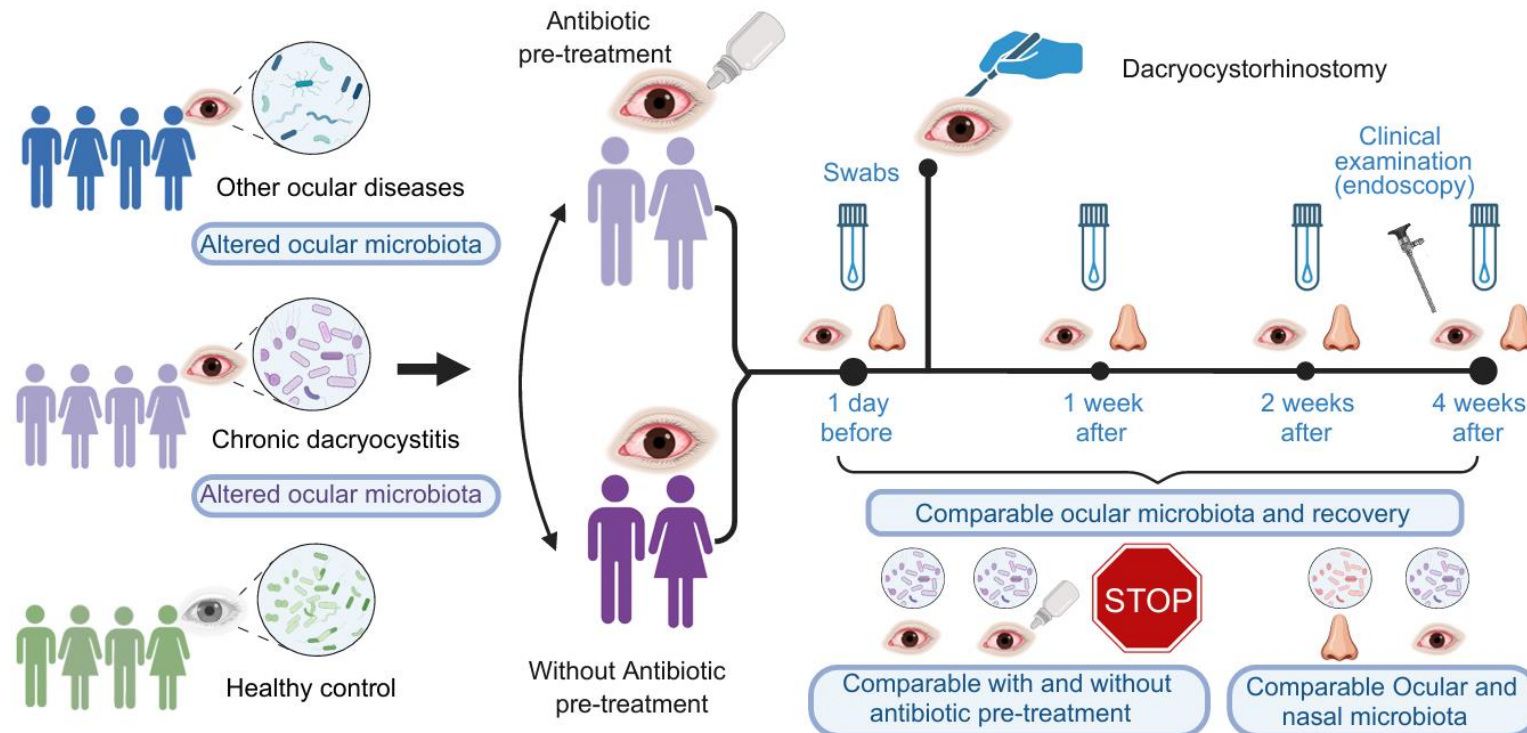
iMetaOmics 1: e17. <https://doi.org/10.1002/imo2.17>



INTRODUCTION

Chronic dacryocystitis (DC) is caused by an obstruction of the nasolacrimal duct leading to accumulation of tear fluid in the lacrimal sac and secondary bacterial infection. Dacryocystorhinostomy (En-DCR) is a surgery that creates a new path for tears to drain between the eyes and nose^[1,2]. Preoperative antibiotics are often used to treat DC, especially levofloxacin pre-treatment, is one of the most commonly applied antibiotics^[3-6]. The effect of this treatment on the prognosis of DC needs to be thoroughly investigated^[7-9].

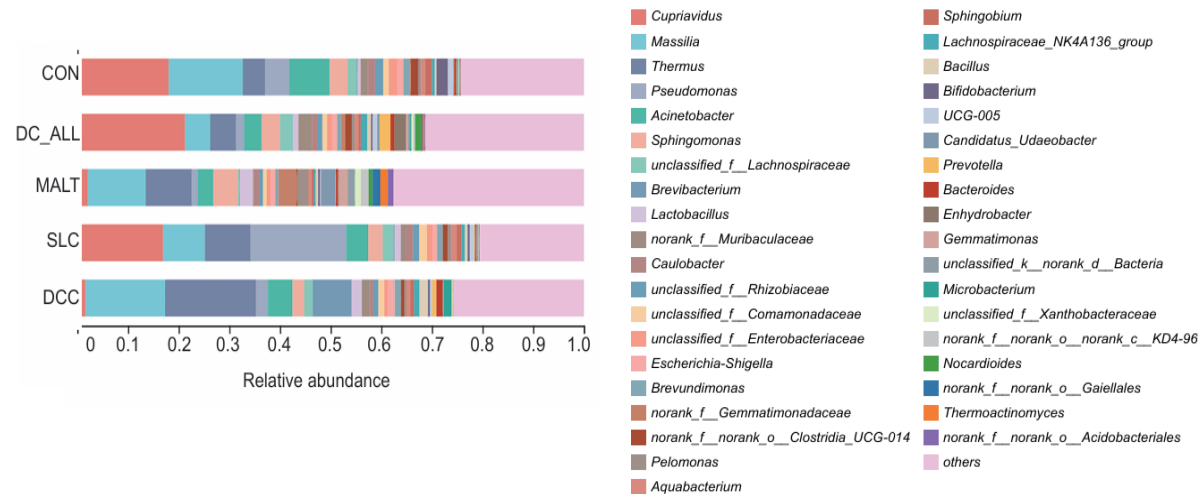
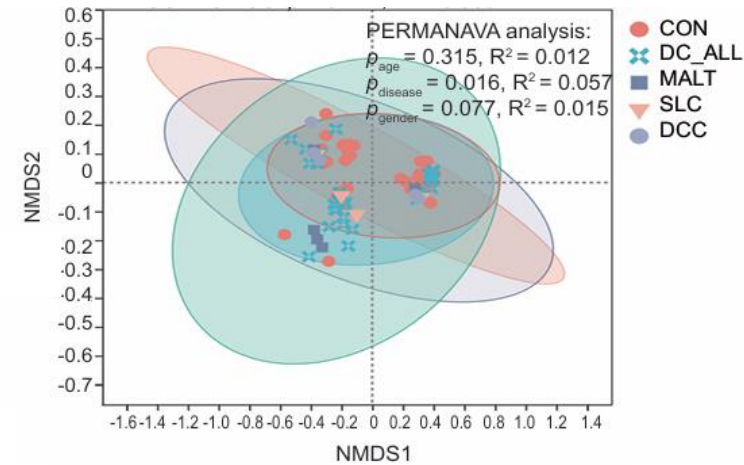
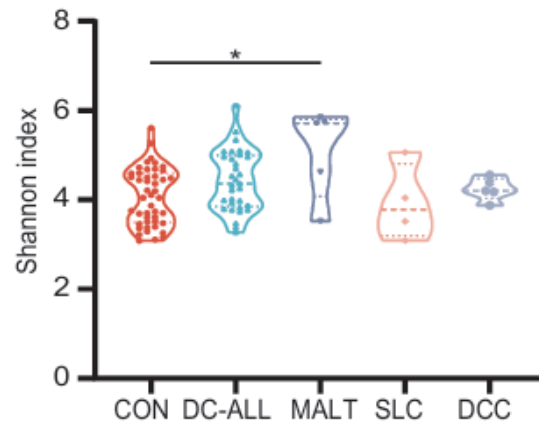
This study is a prospective clinical cohort study. Ocular and nasal microbiota samples obtained at different times after En-DCR were collected, as well as microbiota data from healthy controls and patients with other ocular disorders including chronic dacryocanaliculitis (DCC), stenosis of the lacrimal canaliculus (SLC), and ocular mucosa-associated lymphoid (MALT). Observations were made to compare the relationship between the use of preoperative antibiotics and the microbiota distribution and clinical recovery after surgery.



HIGHLIGHT 1

Different Ocular diseases have different ocular microbiota

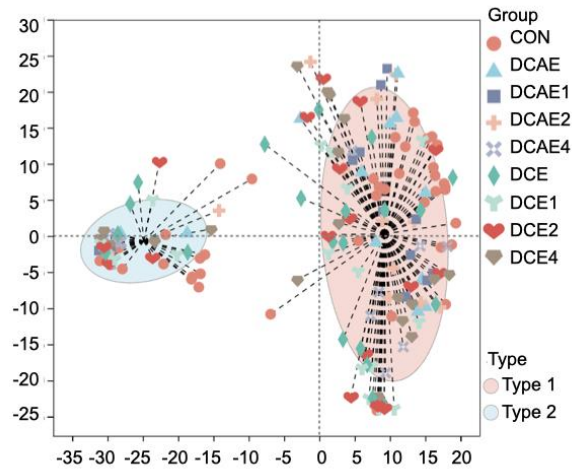
According to the beta diversity analysis, there were significant differences between the disease groups and healthy controls. *Cupriavidus*, *Massilia*, *Thermus*, *Pseudomonas* and *Acinetobacter* were at the forefront of each group, with varying abundance in different diseases.



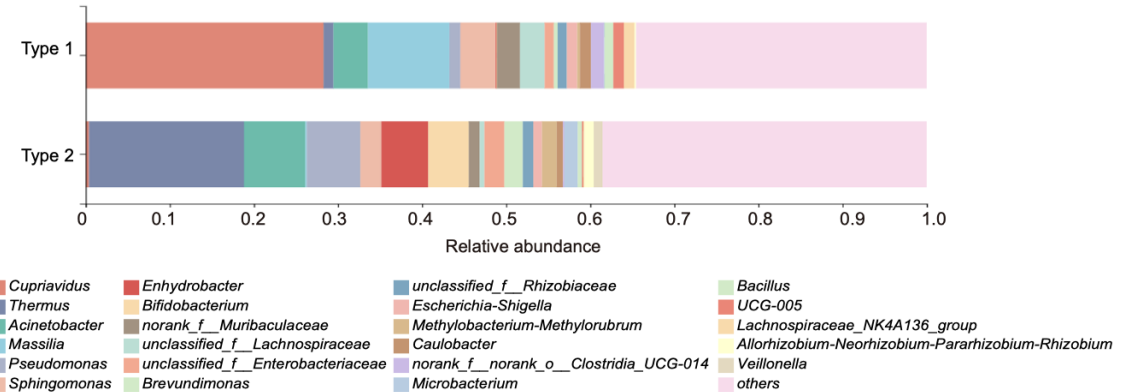
HIGHLIGHT 2

Two types of ocular microbiota and three types of nasal microbiota were demonstrated among patients with DC

1. The ocular microbiota tended to form two clusters according to the beta diversity analysis.

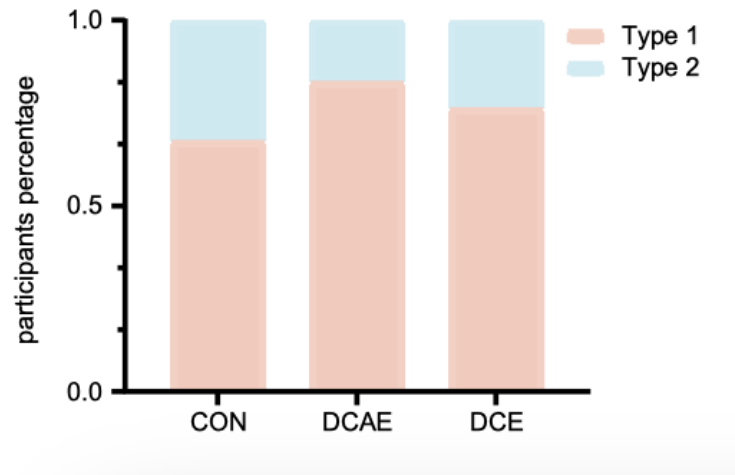


2. Type 1 contained a high abundance of *Cupriavidus* and *Massilia*, and type 2 contained more *Thermus* and *Acinetobacter*.

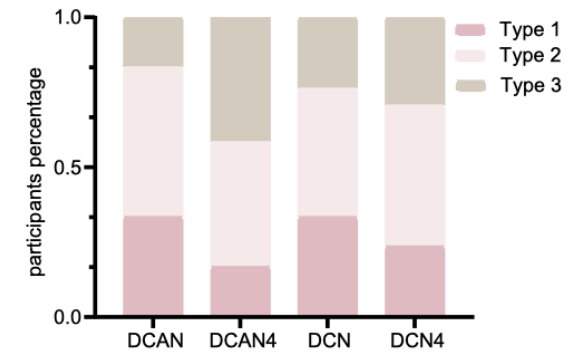
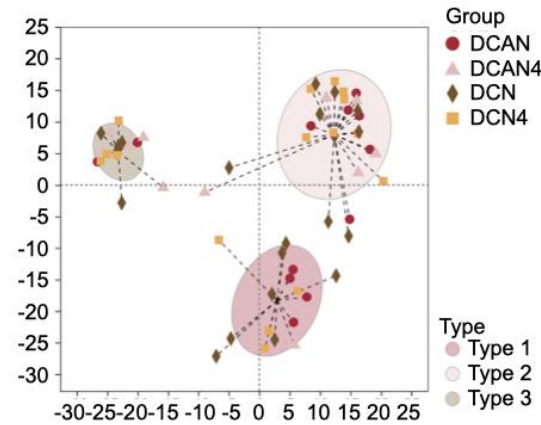


HIGHLIGHT 2

3. A higher prevalence of type 1 among DC patients than healthy participants, there was no significant distribution difference among the groups.



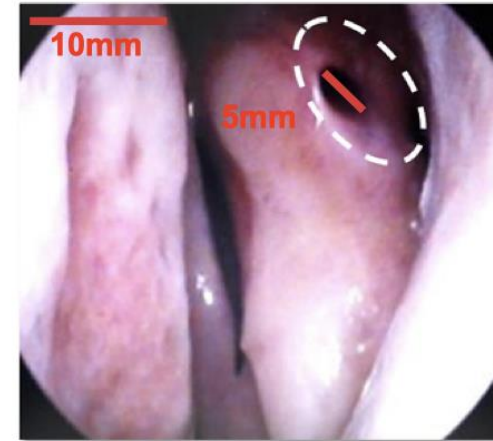
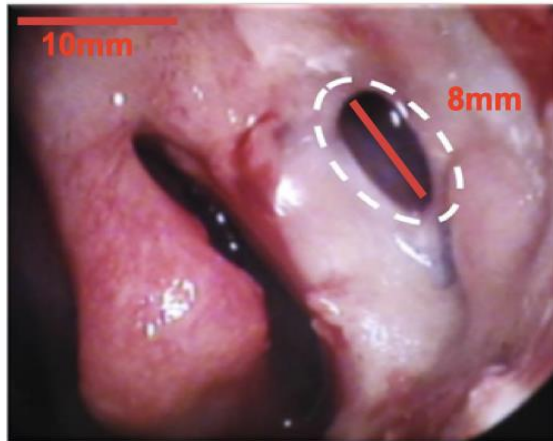
4. The three nasal microbiota types were distributed similarly among all the groups.



HIGHLIGHT 3

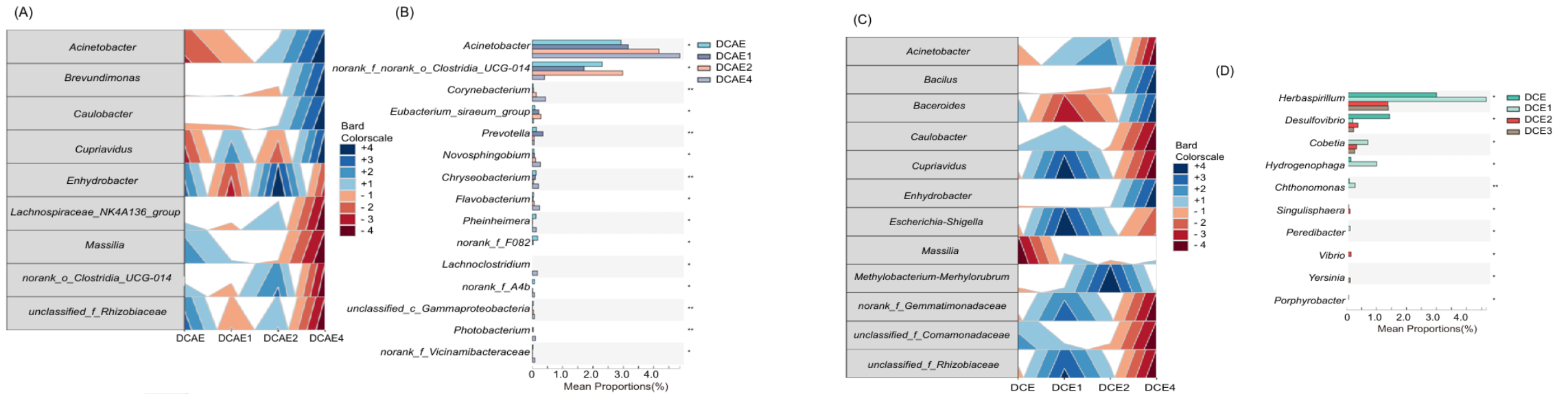
Although clinical recovery is comparable, the antibiotic pre-treatment significantly changed the ocular microbiota 4 weeks after En-DCR, which suggested the antibiotic is not needed for recovery from En-DCR

1. By the fourth week, clinical examination revealed no symptoms of lacrimation or ocular discharge from DC patients either with (left) or without (right) antibiotic pre-treatment. Hence, antibiotic pre-treatment will not affect the recovery of DC patients after endoscopic dacryocystorhinostomy.



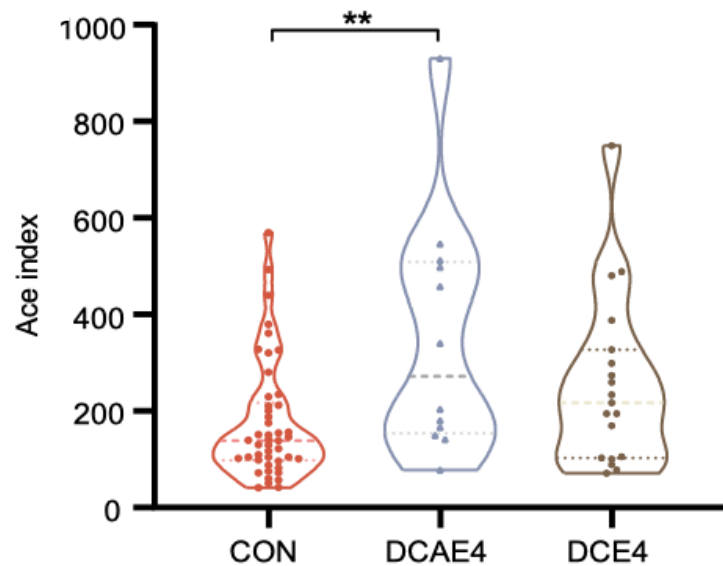
HIGHLIGHT 3

2. The changes in bacterial abundance in the longitudinal samples were different between the groups with or without antibiotic pre-treatment. The alteration tendencies of *Acinetobacter*, *Massilia*, and *Cupriavidus* were opposite in the DC patients with (left) or without (right) antibiotic pre-treatment, while the alteration tendencies of *Pseudomonas*, *Shingomonas* and *Thermus* were similar.

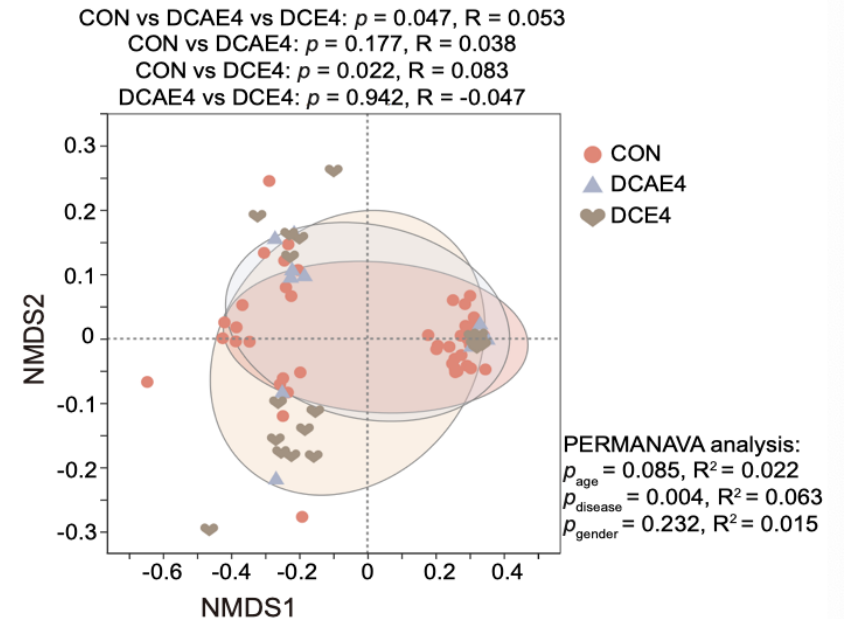


HIGHLIGHT 3

3. When compared with the control group, significantly increased microbial community diversity was observed in DC patients with antibiotic at four weeks postoperatively. A similar trend was observed in the microbial community richness, although it did not reach the significant level.



4. The comparison of microbiota beta diversity presented a significant dissimilarity ($p_{ANOSIM} = 0.047$).



SUMMARY

- 1. Different eye diseases (e.g. DC, DCC, SLC, MALT) have different ocular microbiota.**
- 2. Two types of ocular microbiota and three types of nasal microbiota were demonstrated among ocular diseases patients.**
- 3. Although clinical recovery is comparable, the antibiotic pre-treatment significantly changed the ocular microbiota 4 weeks after En-DCR, which suggested the antibiotic is not needed for recovery from En-DCR.**

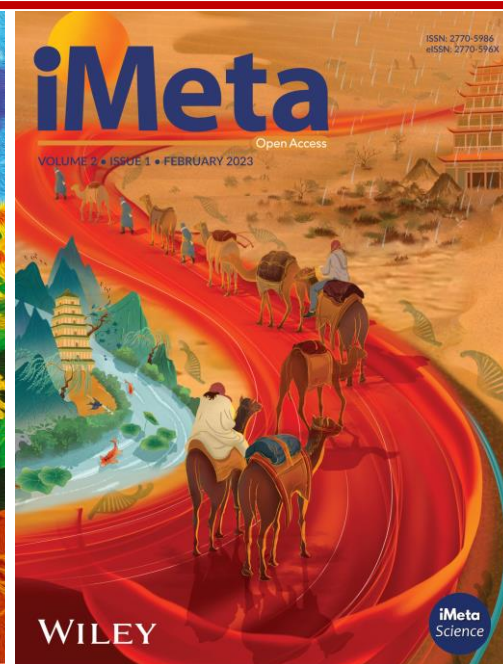
Shengru Wu, Limin Zhu, Tingting Wang, Chenguang Zhang, Jiaqi Lin, Yanjin He, Junhu Yao, Tingting Lin, Juan Du. 2024. Ocular microbiota types and longitudinal microbiota alterations in patients with chronic dacryocystitis with and without antibiotic pretreatment.

iMetaOmics 1: e17. <https://doi.org/10.1002/imo2.17>



iMeta: Integrated meta-omics to change the understanding of the biology and environment

WILEY



“***iMeta***” is a Wiley partner journal launched by iMeta Science Society in 2022, receiving its first impact factor (IF) of **23.7** in 2024, ranking 2/165 in the microbiology field. It aims to publish innovative and high-quality papers with broad and diverse audiences. Its scope is similar to *Nature Biotechnology*, *Nature Microbiology*, and *Cell Host & Microbe*. Its unique features include video abstract, bilingual publication, and social media dissemination, with more than 500,000 followers. It has published 200+ papers and been cited for 4000+ times, and has been indexed by [ESCI/WOS/JCR](#), [PubMed](#), [Google Scholar](#), and [Scopus](#).

“***iMetaOmics***” is a sister journal of “***iMeta***” launched in 2024, with a target IF>10, and its scope is similar to *Microbiome*, *ISME J*, *Nucleic Acids Research*, *Briefings in Bioinformatics*, *Bioinformatics*, etc. All contributes are welcome!

Society: <http://www.imeta.science>
Publisher: <https://wileyonlinelibrary.com/journal/imeta>

 office@imeta.science
imetaomics@imeta.science

 [iMetaScience](#)

Submission: <https://wiley.atyponrex.com/journal/IMT2>
<https://wiley.atyponrex.com/journal/IMO2>

 [Promotion Video](#)

 [iMetaScience](#)