

MICROBIOME OF CONTACT LENS CASES FOLLOWING CORNEAL INFILTRATIVE EVENTS

INTRODUCTION

Microbiome is the collective genome of microorganisms that inhabit a particular site. Contact lens (CL) cases become contaminated with microbes during use [1,2] and are often implicated in corneal infiltrative events [3]. These cultivable microorganisms represent only a fraction of the microbiota and many bacterial species remain non-culturable with standard laboratory techniques.

AIM

To study the microbiome of contact lens cases following corneal infiltrative events using DNA sequencing.

METHODS

- Six contact lens storage cases were collected from five female patients attending the "Emergency Red Eye Clinic" at the School of Optometry & Vision Science, University of New South Wales.
- Using a sterile swab pre-soaked in phosphate buffered saline, both the wells of each lens case were swabbed.
- Aliquots of the swab solution from one well were placed on appropriate media plates to grow bacteria and fungi.
- Bacteria were identified using API strips (bioMérieux, Marcy l'Etoile, France) and fungi were identified by morphologies of their colonies and their conidia.
- Microbial DNA was extracted from the swabs of the other well using the QiAMP DNA minikit (Qiagen, Santa Clarita, CA), and 16S rRNA amplicon sequencing performed using PCR primers 515/806 targeting the V4 variable region of 16S rRNA gene.

RESULTS

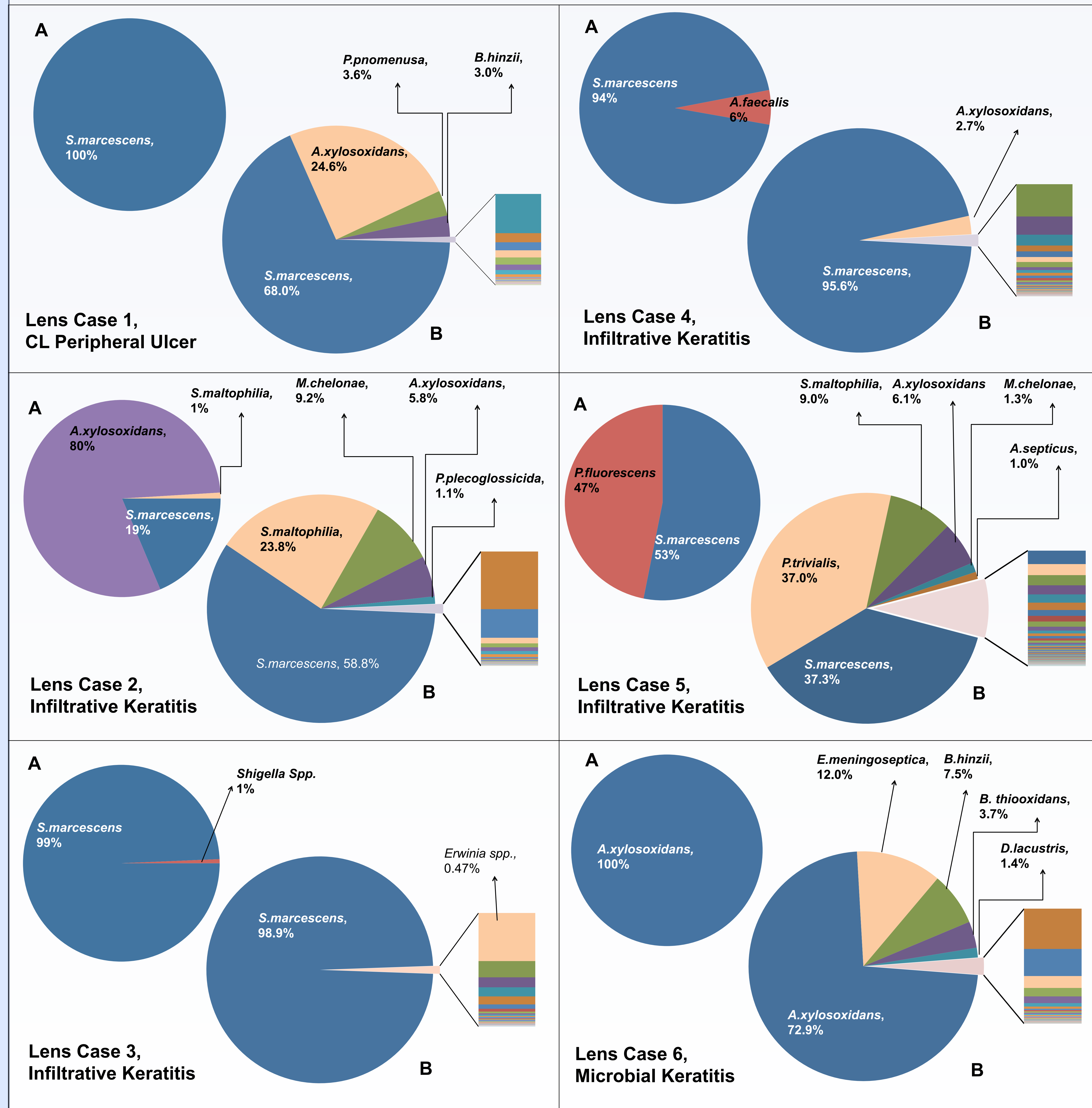


Figure 1: Bacterial culture (A) and relative abundance of bacteria (B) from contact lens cases following infiltrative keratitis

RESULTS

- Six lens cases were collected from five subjects (mean age 22 ± 4 years) with corneal infiltrative events: microbial keratitis (n=1), contact lens peripheral ulcer (n=1) and infiltrative keratitis (n=3).
- All six lens cases were culture positive for Gram-negative bacteria. Multiple bacterial strains were cultured from 4/6 of the lens case wells (Figure 1A).
- 16S rRNA sequencing of DNA from lens cases identified multiple bacterial species (median = 30, max = 79, min = 21) from each lens case (Figure 1B).
- Majority of the bacterial strains belonged to the phylum Proteobacteria (96%)

CONCLUSION

DNA analysis of the lens case revealed the presence of a large number of microbial contaminants that were not culturable using standard laboratory techniques. However, standard lab culture was able to identify the major contaminants present in the lens case. DNA analysis of lens cases can provide valuable information that may help understand the pathogenesis of contact lens related microbial keratitis and corneal infiltrative events.

REFERENCES

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