

The Gut Microbiome as a Reservoir of Pathogens and Antimicrobial Resistance in Orthopaedic Infection

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INTRODUCTION

The origin of organisms identified in orthopaedic infection remains incompletely understood. The gut microbiome represents a potential endogenous reservoir of both pathogens and antimicrobial resistance genes (ARGs). This study aimed to evaluate overlap between gut microbiome taxa and orthopaedic infection isolates, and to compare the prevalence of ARGs between these environments.

METHODS

A prospective pilot cohort of 21 patients undergoing surgery for hip fracture provided stool samples for shotgun metagenomic sequencing. Microbial taxonomic composition was assessed at genus level, and ARGs were identified by alignment to the ResFinder database. These findings were compared with microbiological data from a retrospective cohort of 166 patients undergoing surgical treatment for orthopaedic infection; the two cohorts were analysed independently and were not matched. Organisms were classified as skin-associated, gut-associated, or other, based upon their prevalence within microbiome niches. Associations between gut-associated organisms and polymicrobial infection were assessed. For each genus, prevalence in the gut microbiome was compared with prevalence in infection samples. ARG prevalence was compared with published datasets of orthopaedic infection isolates.

RESULTS

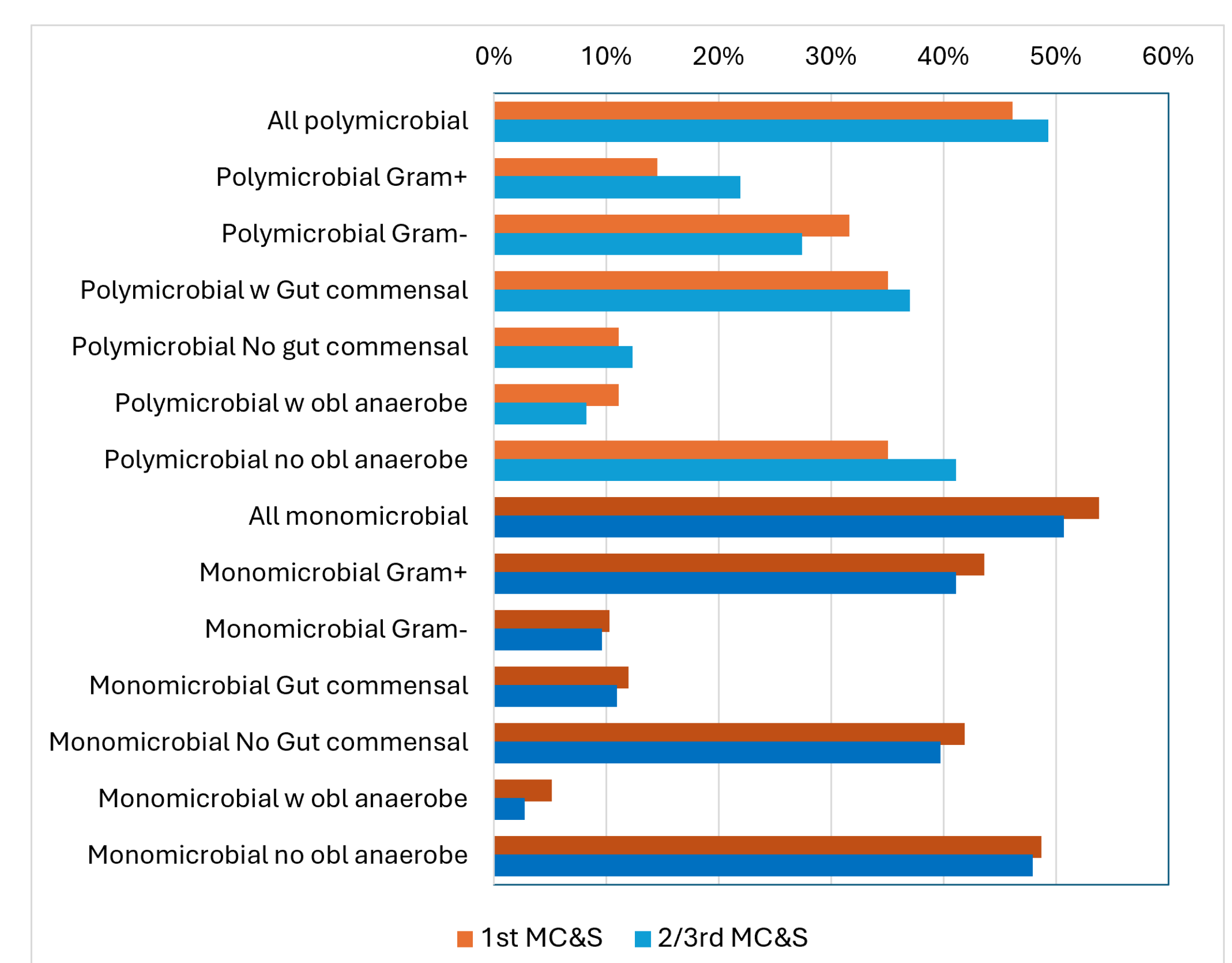
Within the orthopaedic infection cohort, a total of 166 index procedures and 100 subsequent procedures were performed, of which 190 yielded culture-positive results and were included in analysis. Gut-associated organisms were identified in 87/190 (45.8%) culture-positive procedures. A strong association was observed between gut-associated organisms and polymicrobial infection. Among polymicrobial procedures, 68/92 (73.9%) contained gut-associated organisms compared to 19/98 (19.4%) monomicrobial procedures ($p < 0.001$; odds ratio 11.6, 95% CI 5.7–24.8). This association remained significant when restricted to index procedures ($p < 0.001$).

Several genera identified in orthopaedic infections were highly prevalent in the gut microbiome, including *Streptococcus* (100%), *Escherichia* (95%), *Bacteroides* (95%), and *Clostridium* (95%). The gut microbiome demonstrated a high prevalence of antimicrobial resistance genes across multiple antibiotic classes. In particular, resistance determinants associated with macrolide-lincosamide-streptogramin antibiotics and tetracyclines were significantly more prevalent in gut microbiome samples compared to orthopaedic infection datasets (e.g. *erm*(B) 86.4% vs 3.8%, $p < 0.001$; *tet*(M) 72.7% vs 3.8%, $p < 0.001$). In contrast, resistance genes associated with staphylococcal infection were more commonly identified in infection isolates.

CONCLUSION

There is substantial overlap between bacteria identified in orthopaedic infection and those present within the gut microbiome, supporting the plausibility of an endogenous microbial reservoir contributing to orthopaedic infection. The high prevalence of antimicrobial resistance genes within the gut microbiome may potentially influence orthopaedic infections under selective antimicrobial pressure. These findings support the evaluation of therapies to optimise the perioperative gut microbiome.

A



B

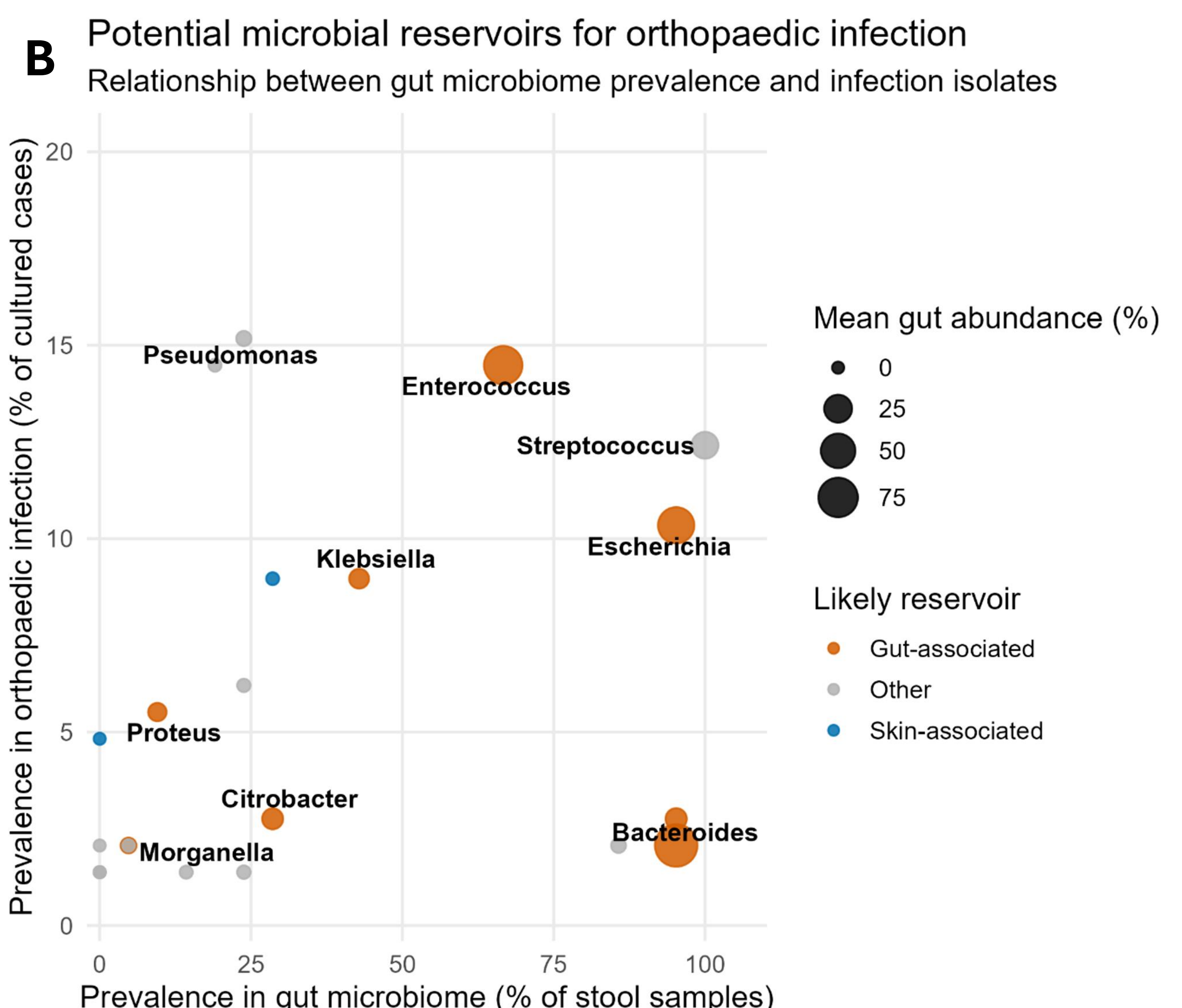


Figure 1: (A) Proportion of Polymicrobial Infections and Cases Positive for Gut-Commensal Bacteria (B) Prevalence of Bacterial Genera in SSI and Gut Microbiome Cohorts