

Introduction

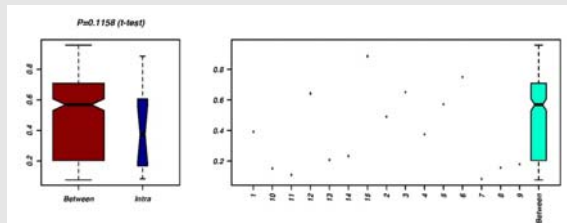
- Intravascular catheters (IVCs) are the most frequently used invasive medical devices in hospitals. However, IVCs are associated with life-threatening bloodstream infections (IVC-BSIs) [1].
- Early detection and adequate treatment of causative pathogens is critical for a favourable outcome, yet the majority of patients with a suspected IVC-BSI yield negative diagnostic investigations, necessitating empiric, rather than optimal, antimicrobial therapy [1].
- The next generation sequencing now provides a key approach by which to examine these complex microbial communities in a high-throughput manner [2].

Materials and Methods

- The study was carried out in the Intensive Care Unit of the Royal Brisbane and Women's Hospital, Queensland, Australia.
- Fifteen adult patients with concurrently sited arterial catheters and central venous catheters and with clinically suspected IVC-BSI were recruited for the study.
- All central venous catheters were ARROWgard Blue® (Arrow Int, Inc, Reading, PA, USA), and arterial catheters were Vygon Leader Cath brand (Ecouen, France).
- All IVCs were examined by high-throughput sequencing of microbial 16S rRNA.

Results

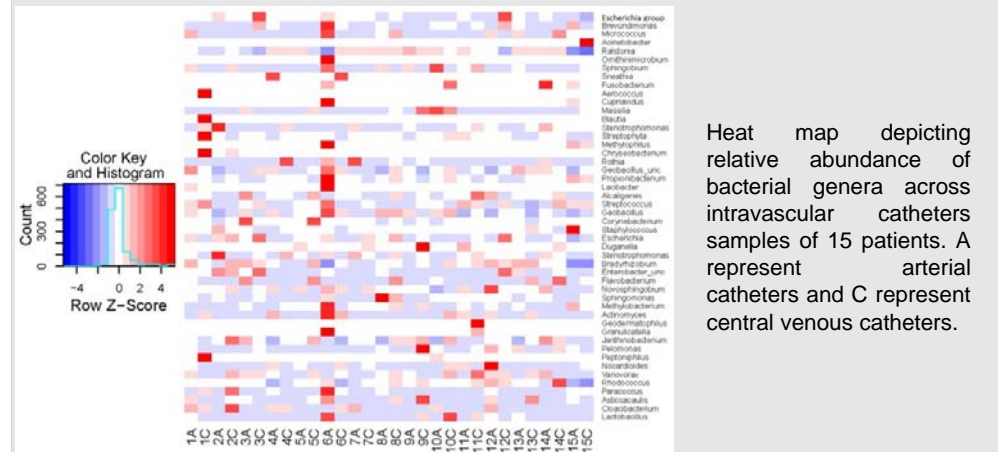
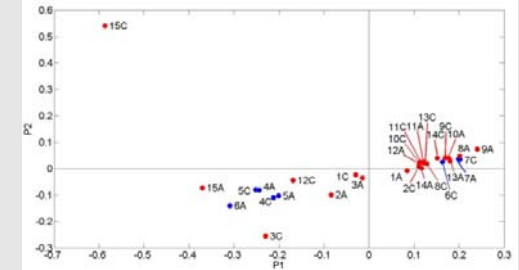
- An average of 100 operational taxonomic units (OTUs, phylotypes) was observed on each IVC, indicating that IVCs were colonized by complex and diverse bacterial communities.
- *Ralstonia* (53% of 16S rRNA sequences), *Escherichia* group (16%), *Propionibacterium* (5%), *Staphylococcus* (5%), and *Streptococcus* (2%) were the most abundant genera.
- There was no statistically significant difference in the bacterial communities examined from arterial and central venous catheters; from those with and without systemic antibiotic treatment.



Jaccard distance measuring dissimilarity between and intra 15 patients. The microbial communities found on the two different catheters were more similar than the average distance of microbial communities from different patients.

Results

Principal coordinate analysis of bacterial communities of intravascular catheters samples based on UniFrac distances. Antibiotic treatment (red balls) and without antibiotic treatment (blue balls). Each point corresponds to each IVC sample. A represent arterial catheters and C represent central venous catheters.



Conclusions

- Our results highlight the complex diversity of microbial ecosystems on intravascular catheters.
- High-throughput sequencing of 16S rRNA offers an insight into the pathogenesis of IVC-BSIs, and opens up scope to improve diagnosis and patient management.

References

1. Zhang L, Gowardman J, Rickard CM: Impact of microbial attachment on intravascular catheter-related infections. *Int J Antimicrob Agents* 2011, 38:9-15.
2. Zhang L, Morrison M, Nimmo GR *et al*: Molecular investigation of bacterial communities on the inner and outer surfaces of peripheral venous catheters. *Eur J Clin Microbiol Infect Dis* 2013, 32:1083-1090.