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ePoster Viewing

Basic science: biofilm pathophysiology

MOLECULAR INVESTIGATION OF BACTERIAL COMMUNITIES ON INTRAVASCULAR CATHETERS: NOT JUST STAPHYLOCOCCUS ANYMORE

L. Zhang¹, G. John², M. Morrison³, L. Krause⁴, C. Rickard¹

¹Griffith Health Institute, Griffith University, Brisbane, Australia ; ²Intensive Care Medicine, Royal Brisbane Women's Hospital, Brisbane, Australia ; ³Diamantina Institute, University of Queensland, Brisbane, Australia ; ⁴Bioinformatics Laboratory, Queensland Institute of Medical Research, Brisbane, Australia

Objective: Intravascular catheter-related bloodstream infections are associated with significant morbidity and mortality. Early detection and adequate treatment of causative pathogens is critical for a favourable outcome. Metagenomics approaches can reveal and capture the genetic potential present in complex microbial communities without having to first isolate and culture the microorganisms. The cultivation-independent approaches inherent to metagenomics are now being used to reveal 'new' pathogens as well as the polymicrobial nature of some infections.

Methods: Patients (over 18 years of age) with IVCs (pairs of concurrently sited arterial and central venous catheters) were examined by 454 GS FLX Titanium 16S rRNA sequencing. The whole genome of the predominant bacterial species was sequenced and analysed.

Results: An average of 100 operational taxonomic units (OTUs, phylotypes) on each IVC was reported. *Ralstonia* (53% of 16S rRNA sequences), *Shigella* (16%), *Propionibacterium* (5%), *Staphylococcus* (5%), and *Streptococcus* (2%) were the most abundant genera present. There was no statistically significant difference in the bacterial communities examined from arterial and central venous catheters; from those with and without antibiotic treatment; or from colonised and uncolonised IVCs. The genome of the predominant species, *R. pickettii* AU12-08, was found to encode resistance to antimicrobial drugs of different classes via alternative mechanisms including 23 multidrug resistance efflux pump systems. In addition, many genes encoded quorum sensing and biofilm formation that would further contribute to increased antimicrobial drug resistance. In total, these findings suggest that *R. pickettii* AU12-08 can act as a reservoir of antimicrobial drug resistance determinants in a clinical environment - an issue of considerable concern.

Conclusion: Our results highlight the complex diversity of microbial ecosystems on vascular devices. Metagenomics offers an insight into the pathogenesis of IVC-related infections and opens up scope to improve diagnosis and management.