Poly-microbial biofilms – prevalence and importance in infections

Trine Rolighed Thomsen[1,2]* Yijuan Xu[1,2] Lone Heimann Larsen[1,3] Jan Lorenzen[2]

1: Center for Microbial Communities, Department of Chemistry and Bioscience, Aalborg University, 9200 Aalborg, Denmark.
2: The Danish Technological Institute, Life Science Division, 8000 Aarhus C, Denmark.
3: Department of Clinical Microbiology, Aalborg University Hospital, 9000 Aalborg, Denmark

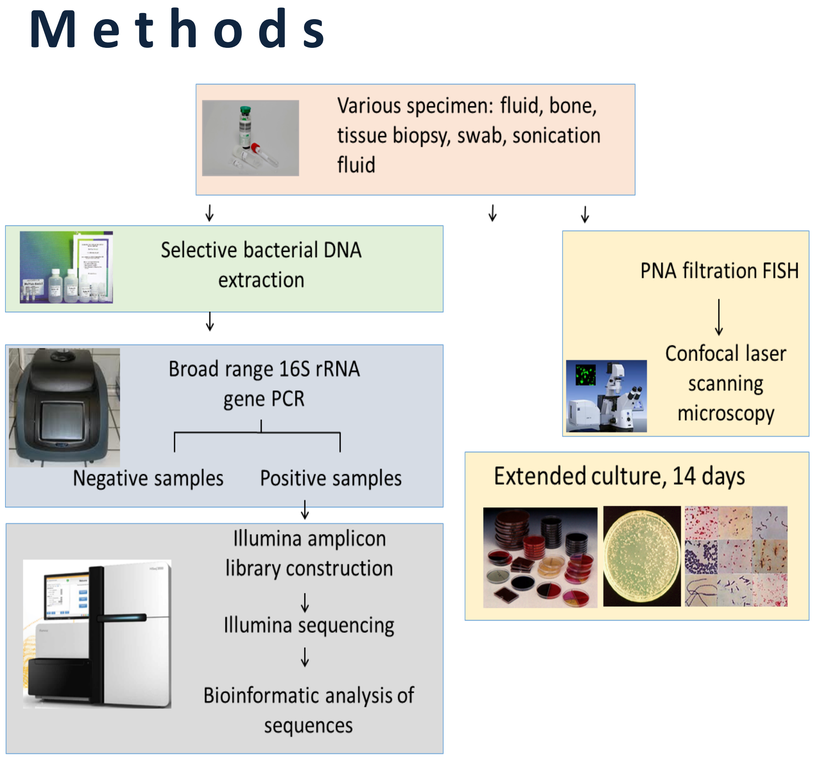
Introduction

Infections cause one-third of all death in the world and 60% of all infections are biofilm related. Formation of biofilm constitutes a challenge to current sampling, culture and treatment procedures. Standard microbiological cultures often underestimate the diversity of pathogens present in chronic infections. This is often due to a combination of inadequate growth conditions and presence of slow, fastidious, anaerobic or unculturable bacteria growing in biofilms.
Application of various molecular techniques is often able to identify less common pathogens that may not grow readily on laboratory culture media.

Aim

The objective was to study the prevalence and importance of poly-microbial communities in different biofilm-related diseases.

Methods



- The presence of microorganisms was investigated using traditional culture-dependent methods and a range of culture-independent molecular methods including cloning, Sanger sequencing, amplicon sequencing, fluorescence *in situ* hybridisation and quantitative PCR.
- Improved sampling was performed using the "All in a box" concept


Larsen et al. BMC Research Notes 2014, 7:418
http://www.biomedcentral.com/1756-0500/7/418

BMC Research Notes

TECHNICAL NOTE Open Access

'All in a box' a concept for optimizing microbiological diagnostic sampling in prosthetic joint infections

Lone Heimann Larsen[1,2*], Yijuan Xu[2], Ole Simonsen[4], Christian Pedersen[4], Henrik C Schønheyder[1,3], Trine Rolighed Thomsen[2,3] and PRIS Study Group

Abstract

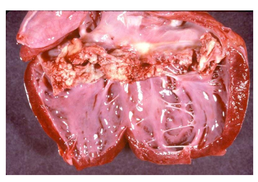
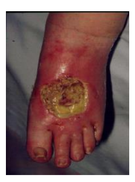
Background: Accurate microbial diagnosis is crucial for effective management of prosthetic joint infections. Culturing of multiple intraoperative tissue samples has increased diagnostic accuracy, but new preparatory techniques and molecular methods hold promise of further improvement. The increased complexity of sampling is, however, a tough challenge for surgeons and assistants in the operation theatre, and therefore we devised and

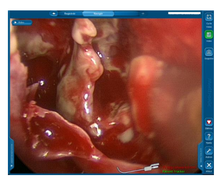
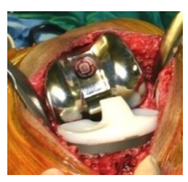
Conclusions

- **Inclusion of standardised sampling and several techniques improves diagnosis.**
- **Heterogeneous distribution of polymicrobial biofilm.**
- **Results are used for improvement of sampling and analysis in the clinic.**

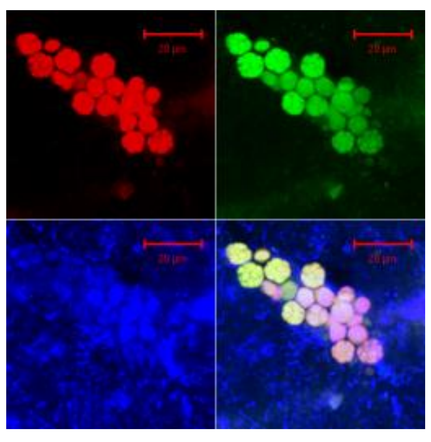
Results

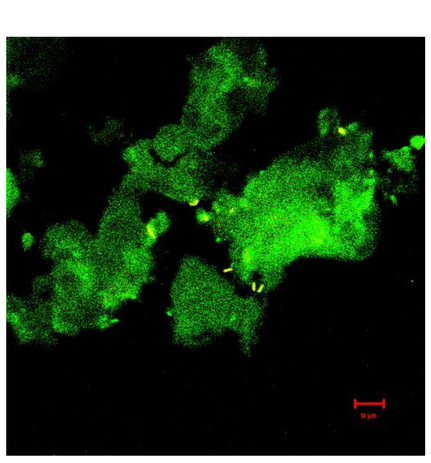
- Number of specimens analysed were: endocarditis (n=18), chronical wound (n=14), central venous catheter (n=18), sinus samples from cystic fibrosis patients (n=19) and prosthesis-related infections (n=42) .

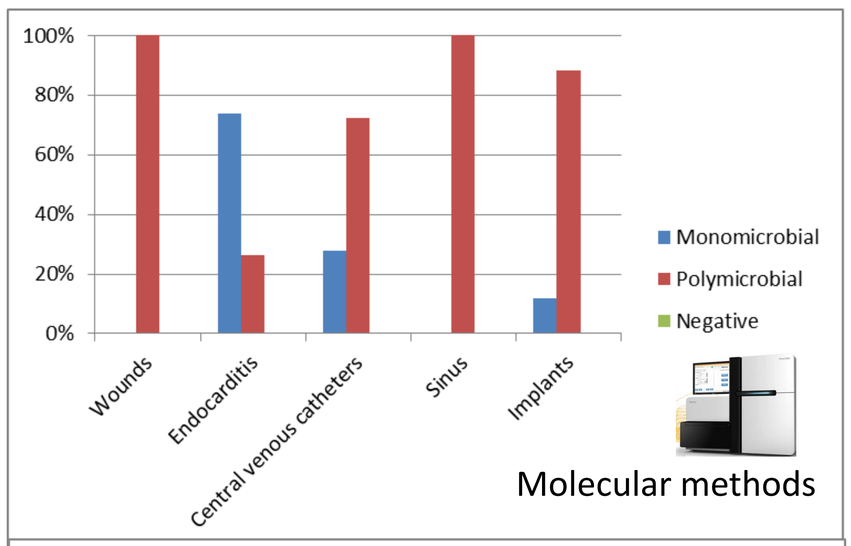



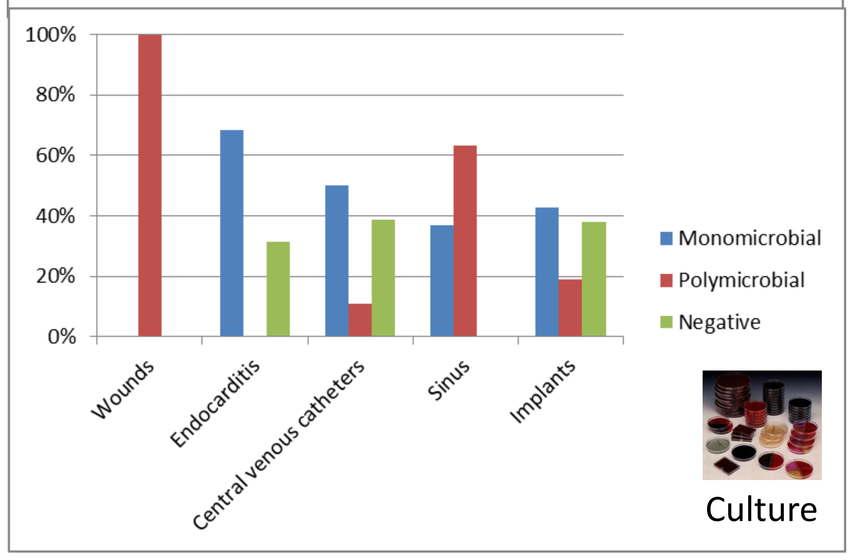
- All species detected by cultivation were also identified by molecular methods.
- Poly-microbial communities were detected in 64% and 32% of the samples by molecular methods and culture, respectively.
- Molecular methods illustrated that all chronical wounds and sinus samples were poly-microbial as opposed to only 26% of endocarditis samples.
- Using standardised sampling and investigation of several specimens from each patient a heterogeneous distribution of the bacteria in the infections was clearly illustrated.
- Some specimen types were shown to be more appropriate than others for sampling of poly-microbial biofilm. For example, a larger bacterial diversity was generally observed in sonicated joint implants compared to joint fluid.
- Tendencies were observed in numerous implant samples, where *E. faecalis* co-existed with *Finegoldia magna*, *P. acnes* in several cases was overlooked by culture, and some normally easily cultured bacteria e.g. *S. aureus, S. epidermidis* and *E. faecalis* were not detected by culture methods which might be caused by biofilm mode of growth.





Mono- and polymicrobial communities determined by culture and molecular methods, respectively





Acknowledgement

This study was supported by a grant for the PRIS Innovation Consortium from The Danish Council for Technology and Innovation (no. 09–052174) and by the Danish PWT Foundation- Investment in Public Welfare Technology (ABT-fonden). Collaborators are greatly acknowledged.

trt@teknologisk.dk www.cmc.aau.dk