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Aim

To improve sampling and diagnosis of prosthetic joint infections (PJI) and chronic wounds, especially considering the biofilm issue.

Introduction

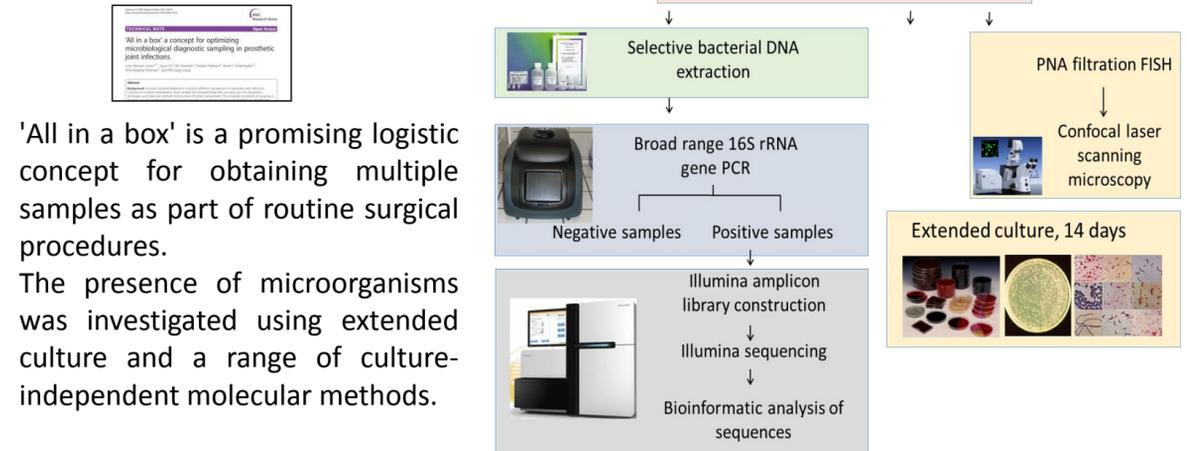
Recent evidence suggests that the microbial community, its spatial distribution and activity play an important role in the prolongation of treatment and healing of chronic infections. Standard bacterial cultures often underestimate the microbial diversity present in chronic infections. This lack of growth is often due to a combination of inadequate growth conditions, prior usage of antibiotics and presence of slow-growing, fastidious, anaerobic or unculturable bacteria living in biofilms. Thus, diagnosis of chronic infections is challenged by lack of appropriate sampling strategies and by limitations in microbiological testing methods.

Conclusion

- Diagnosis of chronic biofilm related infections required multiple specimen types, standardized sampling, extended culture and molecular analysis.
- Our results are useful for improvement of sampling, analysis and treatment in the clinic.

Diagnosis

Material and methods

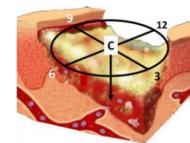
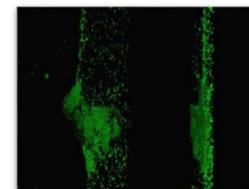
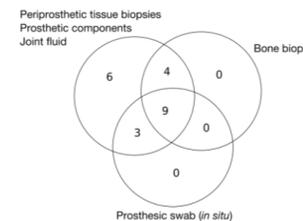


'All in a box' is a promising logistic concept for obtaining multiple samples as part of routine surgical procedures.

The presence of microorganisms was investigated using extended culture and a range of culture-independent molecular methods.

Results

- Investigation of several specimens from each patient illustrated clearly a heterogeneous distribution of the bacteria in the infections.
- We found multiple tissue biopsies, prosthetic component(s) and joint fluid to form the optimal specimen for both acute and chronic PJI.
- Some PJI 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.
- 1131 of 1191 scheduled PJI samples were obtained (completeness 95%).
- All species detected by cultivation were also identified by molecular methods.
- In chronic wounds, multiple biopsies from the same ulcer showed large differences in the abundance of fx *S. aureus* and *P. aeruginosa* at different locations by qPCR.

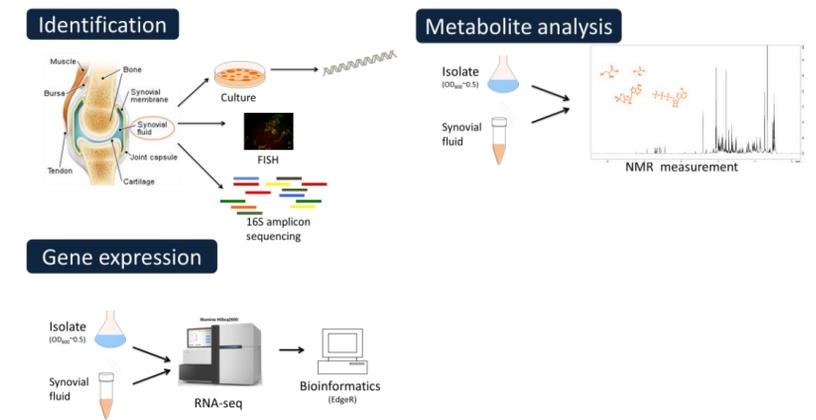


Picture from homepage of Montana State University

Position	Wound 1	Wound 2
C	510±18%	920±9%
3	No sample	300±13%
6	760±7%	8200±8%
9	47±9%	800±10%
12	280±3%	15±5%

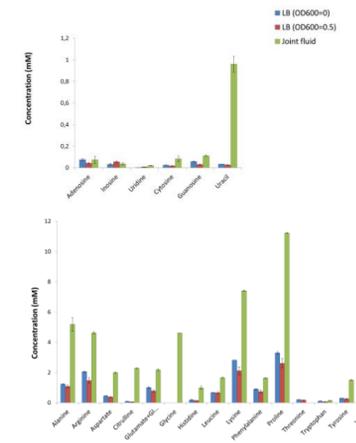
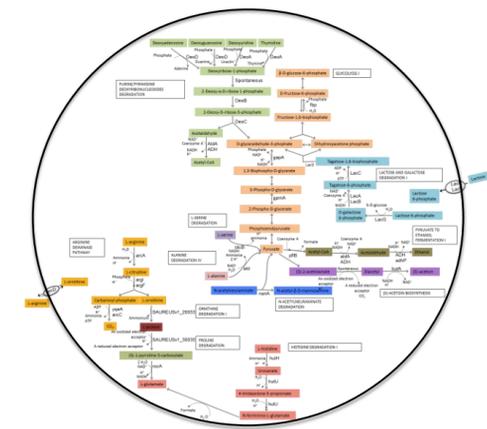
Function

Material and methods



Results

- Many, but not all, of the known virulence factor genes were upregulated *in situ*.
- *S. aureus* sustained on a versatile human-cell-based diet consisting of amino acids, glycans and nucleosides in the hypoxic joint fluid during human prosthetic joint infection. Examples of metabolites concentrations determined by NMR analysis are illustrated.



ACKNOWLEDGEMENT

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