



Aalborg Universitet

AALBORG UNIVERSITY
DENMARK

RNA-seqprofiling of pathogens in prosthetic joint infection

Xu, Yijuan; Nielsen, Kåre Lehmann; Nielsen, Per Halkjær; Nielsen, Jeppe Lund; Thomsen, Trine Rolighed

Publication date:
2013

Document Version
Early version, also known as pre-print

[Link to publication from Aalborg University](#)

Citation for published version (APA):

Xu, Y., Nielsen, K. L., Nielsen, P. H., Nielsen, J. L., & Thomsen, T. R. (2013). *RNA-seqprofiling of pathogens in prosthetic joint infection*. Abstract from The Danish Microbiological Society, Copenhagen, Denmark.
http://www.infection-research.de/events/view/detail/event/danish_microbiological_society_2013/

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal -

Take down policy

If you believe that this document breaches copyright please contact us at vbn@aub.aau.dk providing details, and we will remove access to the work immediately and investigate your claim.

RNA-seq profiling of pathogens in prosthetic joint infection



xuyijuan@bio.aau.dk

Xu, Yijuan¹; Nielsen, Kåre L.¹; Nielsen, Per H.¹; Nielsen, Jeppe L.¹; Thomsen, Trine R.^{1,2}
 1: Center for Microbial Communities, Aalborg University, Denmark
 2: Danish Technological Institute, Denmark



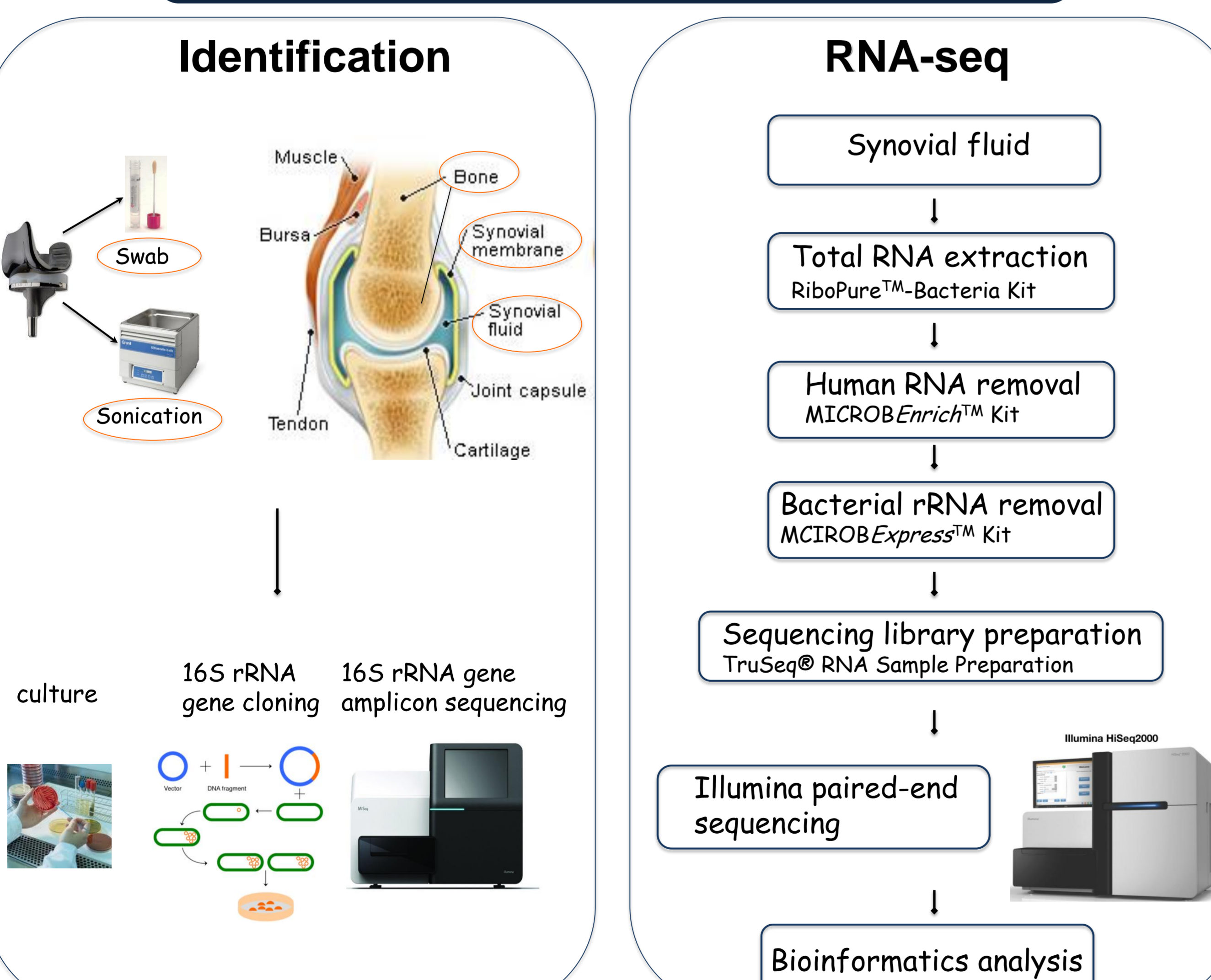
Introduction

Prosthetic joint infections (PJIs) are serious complications of joint alloplasties. These device-associated infections are typically caused by bacteria growing in biofilms, which protect them from antimicrobial agents and host immune responses in poorly vascularized joints. Our current knowledge of how pathogens cope with the complex conditions within the host is based on *in vitro* studies and animal models, which can differ substantially from their behavior in the human host. Studying gene expression of pathogens during infection is a way to understand pathogenesis. RNA sequencing (RNA-seq) is capable of characterizing the entire transcriptome, both quantitatively and qualitatively, of an organism.

Aim

To study the gene expression of pathogens directly in PJI in a human host using RNA-seq.

Methods



Acknowledgement

The study is part of the Danish "Prosthesis-related Infection and Pain" innovation Project, supported by a grant from the Danish Agency of Science and Technology (no. 09-052174).
www.joint-prosthesis-infection-pain.dk

Conclusions

This study indicates that RNA-seq is a challenging but powerful tool to profile the gene expression of pathogens *in vivo*.

Results

Identification

Monomicrobial infection: *Staphylococcus aureus* was identified by 3 independent methods (culture, 16S rRNA gene cloning, and 16S rRNA gene amplicon sequencing).

Mapping statistics

	Number of reads	Number of paired reads
Total reads	23.000.000	11.500.000
<i>S. aureus</i> reads ¹	270.000 (1.17%)	113.000 (0.98%)
<i>S. aureus</i> mRNA reads	17.000 (0.074%)	7.000 (0.061%)

¹Reference genome: *S. aureus* N315, 2.84 Mb, 2694 genes, 2613 proteins

Top 100 genes (ordered by RPKM)

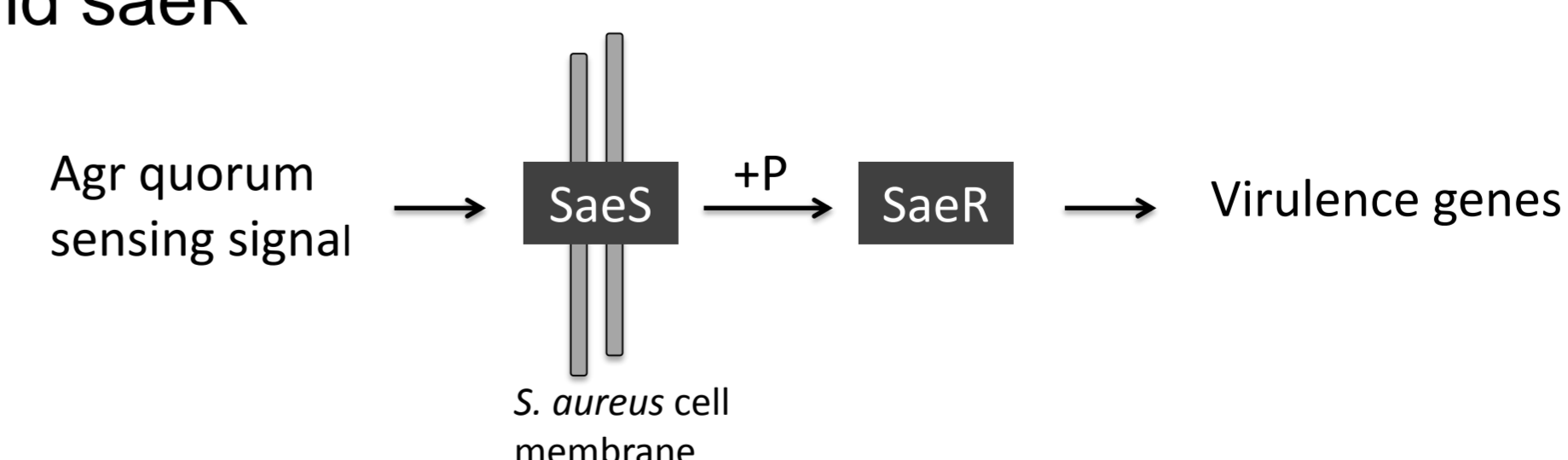
- 52 Essential genes
- 22 Hypothetical proteins
- 8 Infection related genes

Virulence factors:

- **hlgA, hlgB and hlgC** : form pores in immune cells
- **Sbi**: interferes with the host complement system

Virulence regulation genes:

saeS and *saeR*



Vancomycin resistance sensor/regulator:

vraS and *vraR*

