RNA-seq profiling of pathogens in prosthetic joint infection
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Publication date:
2013

Document Version
Early version, also known as pre-print

Link to publication from Aalborg University

Citation for published version (APA):

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Introductions

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.

Methods

Identification

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

Mapping statistics

<table>
<thead>
<tr>
<th>Number of reads</th>
<th>Number of paired reads</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total reads</td>
<td>23,000,000</td>
</tr>
<tr>
<td><em>S. aureus</em> reads&lt;sup&gt;1&lt;/sup&gt;</td>
<td>270,000 (1.17%)</td>
</tr>
<tr>
<td><em>S. aureus</em> mRNA reads</td>
<td>17,000 (0.074%)</td>
</tr>
</tbody>
</table>
<sup>1</sup>Reference 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*

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