WS21.5 A comparative study of motility and biofilm production in cystic fibrosis (CF) and environmental Pseudomonas aeruginosa (Pa) isolates

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Objectives: In the CF airway Pa uses motility mechanisms for adherence and biofilm (BF) formation. There are few studies which compare Pa motility and BF formation among isolates from CF patients and other ecological niches. It is also unclear if shared (genotypically indistinguishable) and unique strains of Pa from CF patients display similar motility and BF capabilities. The aim of this study was to compare the motility characteristics and BF formation capabilities of shared and unique strains Pa strains cultured from the CF airway and isolates collected from other ecological settings.

Methods: Motility (swim, swarm and twitch) and short-term microtitre based BF assays performed under aerobic, microaerophilic and anaerobic conditions were determined for isolates collected from CF patients (n=60, including AUST-02 [n=26]), animal infections (n=14), non-CF clinical infections (n=20) and the environment (n=34).

Results: Environmental isolates displayed higher rates of motility and BF formation in all three atmospheric conditions when compared to all other isolates. In contrast, strains cultured from CF patients displayed the lowest rates of motility and biofilm production when compared with isolates from other ecological settings. In particular, the shared AUST-02 strains demonstrated significant reductions in motility and BF formation when compared to environmental isolates. Further long-term biofilm and mechanistic studies are being conducted to investigate the significance of these findings.

WS21.6 Comparison of the CF airway microbiome obtained by bronchoscopy vs. sputum

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Objectives: Diverse bacterial communities exist in CF airways and molecular studies seem to indicate decreasing diversity with increasing age and disease severity.

Aim: To ascertain and compare airway microbiome composition sampled by bronchialalveolar lavage (BAL) or sputum from children and young adults using aerobic and anaerobic cultures.

Methods: In a cross-sectional, 3 centre study BAL and sputa were obtained and immediately processed using enhanced culture methods [1]. Bacterial identification was by full-length 16sRNA sequencing. Species diversity, prevalence and fraction of anaerobic cfu/total cfu were compared by sample types.

Results: A total of 85 BAL and 57 sputum samples were included. Sputum producers were significantly older: 16 (5.4) vs. 5.2 (6.2) years (p < 0.001). A total of 47 genera (range per sample 0–14) were cultured across all samples and CF centres (Table 1).

Table 1. T-test to compare BAL vs. sputum

<table>
<thead>
<tr>
<th>Descriptor</th>
<th>P. aeruginosa positive</th>
<th>S. aureus positive</th>
<th>No. (#) of bacterial species, mean (SD)</th>
<th>Anaerobe positive samples</th>
<th>Anaerobe cfu/total cfu, mean (SD)</th>
</tr>
</thead>
<tbody>
<tr>
<td>BAL</td>
<td>25.9%</td>
<td>36.5%</td>
<td>3 (3.5)</td>
<td>47.1%</td>
<td>0.07 (0.26)</td>
</tr>
<tr>
<td>Sputum</td>
<td>49.1%</td>
<td>50.9%</td>
<td>5 (2.9)</td>
<td>59.6%</td>
<td>0.137 (0.19)</td>
</tr>
</tbody>
</table>

# of bacterial species, p = 0.16; fraction anaerobe cfu/total cfu, p = 0.04.

Conclusion: Anaerobic bacteria were highly prevalent in both BAL and sputum but their density compared to aerobic bacteria was lower in BAL. A similar number of bacterial species were detected by culture in BAL and sputum thus showing a similar diversity in our subset.

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Reference(s)