Cough swab versus cough plate in non-expectorating patients with Cystic Fibrosis

T. Orska1, M. Graver2, J.J. Wade2, J. Dinigan3, K. Ferguson1, C. Bossley1, H. Wyatt1. 1Kings College Hospital, 2HFA London Region Lab, London, UK

Aims: The use of cough swabs (CS) which trap respiratory secretions produces false negatives and are poorly tolerated. Using cough plates (CP) was proposed as an alternative sampling method [1]. This study compares CS with CP in non-expectorating CF pts.

Methods: 45 pts, 4–16 yrs were enrolled into the study over 4 months. The pts had to be able to cough voluntarily and be unable to expectorate a sputum sample. Each pt had a CS inserted into the back of the oropharynx, following a cough; it was withdrawn. The pt then coughed deeply twice over 4 CP at 5 cm from their mouth. The CP were blood agar, chocolate agar, Sabouraud's medium and Rubaldi[1]; only 1 CP grew Staph aureus while the CS grew yeast.

Results: The variety and frequency of micro-organisms was greater in CS compared to CP of the 48 samples that had concurrence between CS and CP. There were 4 staphylococcus aureus, 2 Aspergillus spp. The following numbers of CS grew organisms for which the CP did not: 9 Staph aureus, including 2 MRSA; 14 Pseudomonas aeruginosa; 1 Burkholderia cepacia. Only 1 CP grew Staph aureus while the CS grew yeast.

Conclusion: Our results do not confirm those of Mayja et al, who concluded that CP are more sensitive than CS. However their pt group differed from ours in that their pts were able to expectorate, while ours were excluded from the study if they were not able to expectorate sputum. There may have been a potential source of bias as there was no randomisation of CS and CP, but this alone cannot explain the difference between the results. Our results suggest CS are far superior to CP in the non-expectorating CF pt.

References


Microbiology of the pulmonary secretions in cystic fibrosis (CF) in a pediatric center: 18 years experience

L. Galanter[1], J. Hererra[2], A. Pecorari[1], C.N. Macri[2]. 1Microbiology Laboratory, 2Respiratory Center Hospital de Niños “Dr Ricardo Gutierrez” (HRGCU) – Giadol, Buenos Aires, Argentina

The aim of this study was to analyse microbiological findings in respiratory tract samples in CF patients (pts) in 3 different periods. Sputum, oropharyngeal swab and BAL from 256 pts aged 0–16 yrs, taken in 1987, 1995 and 2004 were analysed. Samples were plated on 5% blood agar, chocolate agar, CLED agar and mannitol salt agar. Since 2001 BCSA agar was used, to enhance B. cepacia recovery.

In 1987, 115 samples (sam) from 77 pts were studied (x =2 sams/pts; r = 1M). In 1995, 238 sam from 92 pts were studied (76 new regarding 1987, x = 2 sams/pts; r = 1-9). The 2004 group of pts contained 348 sam from 131 pts (103 new regarding 1987 and 1995) (x = 2 sams/pts; r = 1-8).

The percentage of pts isolates were:

<table>
<thead>
<tr>
<th>Year</th>
<th>P. aeruginosa (Pan)</th>
<th>S. aureus (SA)</th>
<th>M. catarrhalis SA</th>
<th>H. influenzae</th>
<th>B. cepacia</th>
<th>A. ventilatorum</th>
</tr>
</thead>
<tbody>
<tr>
<td>1987</td>
<td>75.3</td>
<td>51.9</td>
<td>5.2</td>
<td>1.9</td>
<td>2.6</td>
<td>0.0</td>
</tr>
<tr>
<td>1995</td>
<td>72.8</td>
<td>79.3</td>
<td>23.8</td>
<td>20.2</td>
<td>1.1</td>
<td>0.0</td>
</tr>
<tr>
<td>2004</td>
<td>56.5</td>
<td>77.1</td>
<td>34.4</td>
<td>22.9</td>
<td>9.9</td>
<td>5.3</td>
</tr>
</tbody>
</table>

The predominant species by age groups were:

<table>
<thead>
<tr>
<th>Age Group</th>
<th>0-12m</th>
<th>1-2y</th>
<th>2-5y</th>
<th>5-10y</th>
<th>10-15y</th>
<th>15-20y</th>
<th>&gt;20y</th>
</tr>
</thead>
<tbody>
<tr>
<td>1987</td>
<td>50.5%</td>
<td>75.5%</td>
<td>76.5%</td>
<td>83.1%</td>
<td>100%</td>
<td>85.7%</td>
<td>67.5%</td>
</tr>
<tr>
<td>1995</td>
<td>66.7%</td>
<td>84.8%</td>
<td>85.6%</td>
<td>99.4%</td>
<td>100%</td>
<td>86.1%</td>
<td>65.6%</td>
</tr>
<tr>
<td>2004</td>
<td>61.5%</td>
<td>73.7%</td>
<td>76.8%</td>
<td>96.8%</td>
<td>100%</td>
<td>89.4%</td>
<td>75.5%</td>
</tr>
</tbody>
</table>

Conclusions:

1. In the last two periods, a lower P. aeruginosa colonization was observed in all age groups, perhaps due to recent better treatments.
2. The increase of H. influenzae is due to inadequate search in the 1st period.
3. The high colonization in the last period by B. cepacia is probably associated to incorporation of a new selective media.
4. Prevalence of A. ventilatorum will be evaluated in the future.

Comparison of bacterial composition in spontaneous and successively induced sputum samples

G. Rogers1, D. Serisier2, M. Carroll3, K. Bruce1. 1Molecular Microbiology Laboratory, King’s College London, UK; 2St Mater Adult Hospital, Brisbane, Australia; 3Southampton University Hospital, UK

The degree to which the bacterial content of sputum samples represents the composition of lower airway infections in CF remains the subject of debate. Studies looking at induced sputum have suggested successive induction of sputum significantly affects its cellular and biochemical composition, in a manner suggesting that large airways are sampled at the beginning of sputum induction.

In this study, we applied molecular-based bacterial community analysis to successively induced sputum samples to determine whether there were significant changes in the sample composition. Five adult CF patients provided a spontaneous sputum sample, followed by four induced sputum samples at 5 minute intervals. T-RFLP analysis was then used to characterise the bacterial community.

On average, 8.2 separate T-RF bands were detected in each of the sputum samples analysed, with an average standard deviation of ± 2.11. No any significant differences between induced sputum and spontaneous sputum, or between the 4 induced sputum samples. There is some indication that species richness may be higher in the first induced sputum sample compared to either later induced sputum samples or spontaneous sputum samples. Variations in the species detected occurred, but these were not consistent with duration of induction.

These data do suggest that due to the variability of sputum samples, induced or otherwise, and the commonness of samples with anomalous profiles, it would be unwise to rely on a single sputum sample to characterise a CF lung infection. We conclude, therefore, that the analysis of several spontaneous samples may provide the most convenient and informative type of sputum sample.

References


Multilocus sequence typing databases for CF pathogens: identification of global epidemic clones, novel species, natural reservoirs, and relationships between environmental and clinical isolates

C.G. Dowson1, A. Baldwin3, E. Mahenthiralingam2, E. Vanlaere2, P. Vandamme3, D. Honeybourne4, P. Mills5, B. Carran1. 1Department of Biological Sciences, University of Warwick, 2Department of Microbiology, University of Cardiff, UK; 3Laboratorium voor Microbiologie, Ghent University, Belgium; 4Respiratory Medicine, Heartlands Hospital, Birmingham; 5HR, University of Warwick, UK

Aims: The Burkholderia cepacia complex and Pseudomonas aeruginosa are both important CF pathogens yet they both present problems when using classical typing methods. Unambiguous characterization and typing is an essential prerequisite for effective identification, national and international epidemiology studies. Using modern molecular approaches to bacterial typing our aim is to identify global clones of these organisms, novel species, natural reservoirs and relationships between environmental and clinical isolates.

Methods: Our recent multi locus sequence typing (MLST) databases for these organisms has revolutionized the potential for global epidemiological studies and helps inform virulence studies using invertebrate models of infection.

Results: MLST has revealed several major novel groups that fall outside of current Bcc taxonomy. Furthermore, we have identified new globally distributed clones of Bbc and expanded our understanding of clones within P. aeruginosa. It is apparent, using MLST and invertebrate models of infection that isolates of P. aeruginosa present in high numbers (104-107) on commercial mushrooms across Europe are not ‘benign’ environmental isolates.

Conclusions: This highlights the need for unified approaches in typing, the value of a common exchangeable database and the power that such an approach can bring to better understanding globally important infectious disease.