Outer membrane protein and biotype analysis of non-serotypable strains of *Haemophilus influenzae*

CHRISTINE H COVERDALE, G S TEMPLE

*From the Department of Microbiology, Hull Royal Infirmary*

SUMMARY Strains of *Haemophilus influenzae* (n = 161) were isolated from inpatients with symptoms of pulmonary infection. Conventional tests showed that 144 strains were non-serotypable and all belonged to one of eight biotypes. The common biotypes were 2 (41%), 3 (27.1%), 1 (13.2%) and 5 (10.4%). The outer membrane protein (OMP) profiles of 59 non-serotypable strains were examined by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE). A comparison of OMP profiles suggested a possible association between several strains belonging to biotype 2. Although no clear correlation was established between biotype or OMP profile cluster groups and the age or clinical state of the patients from whom the strains were isolated, SDS-PAGE analysis was a useful technique for the epidemiological study of non-serotypable *H influenzae*.

Non-serotypable (non-encapsulated) strains of *Haemophilus influenzae* are now regarded as a major cause of respiratory infection in adults and have been implicated in other infections which include urogenital disease, meningitis, bacteremia and otitis media in children.1 A scheme for the differentiation of *H influenzae* into a number of biotypes was described by Kilian.2 This biotyping scheme has been used in several studies3-7 in an attempt to understand the epidemiology of diseases caused by non-serotypable strains. It lacked sensitivity to strain variation, however, as only six biotypes were recognised.8 Recently the biotyping scheme has been extended to include an additional two biotypes.9,10

A subtyping scheme, based on sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) of outer membrane protein (OMP) profiles has been used to further differentiate non-serotypable strains of *H influenzae*.11 Although non-serotypable strains have exhibited considerable variation in the number and relative molecular mass (Mr) of their OMPs, it has been suggested that non-serotypable strains from the same anatomical site may be related.12 A possible association between biotype and subtype remains unclear.

Material and methods

Over five months 161 strains of *H influenzae* were isolated from sputum specimens of inpatients with pulmonary infection on 10% cholocatised horse blood agar (with 5 µg/ml cloxacillin) incubated at 37°C in 7.5% carbon dioxide for 18 hours.

The identity of each isolate was determined by its colonial morphology and growth requirement for nicotinamide adenine dinucleotide (NAD) and haemin (Sigma Chemicals Ltd). Isolates were serotyped by slide agglutination with antiserum against capsular antigen types a to f (Wellcome Diagnostics Ltd). Non-serotypable strains were assigned to one of eight biotypes on the basis of indole production, urea hydrolysis, and ornithine decarboxylation.29,10

Fifty nine non-serotypable strains of *H influenzae* were subjected to OMP subtyping. They included 15 strains each of biotypes 1, 2, and 5, and 14 strains of biotype 3. The strains representative of biotypes 1, 2, and 3 were chosen at random. Outer membranes were prepared by a modification of the rapid microprocedure of Carlone et al13 for the isolation of detergent-insoluble OMPs. Briefly, bacterial strains were cultured in 20 ml of brain heart infusion broth (Oxoid Ltd, supplemented with 10 µg each of NAD and haemin) and incubated at 37°C for 18 hours on an orbital shaker (100 rpm). The optical density of the culture (600 nm) was adjusted to between 0.5 and 0.6 with sterile broth. The cells were harvested by centrifugation at 6000 × g for 10 minutes at 4°C. The pellet was washed once in cold (4°C) 10 mM HEPES (N-2-hydroxyethylpiperazine-N'-2-ethanesulfonic acid, Sigma Chemicals Ltd) buffer (pH 7.4)
and, while kept on ice, sonicated (eight bursts, 10 seconds each burst at 40 W, with 30 seconds between each burst). The cell membranes were sedimented at 15000 × g for 30 minutes at 4°C. Cytoplasmic membranes were solubilised with 2% sodium N-lauroylsarcosine (Sigma Chemicals Ltd) for 30 minutes at 23°C, and centrifuged at 15000 × g for two minutes to remove cellular debris. The membrane pellets were centrifuged at 15000 × g for 30 minutes, washed once, and resuspended in 50 μl of 10 mM HEPES buffer.

Extracts of OMPs were prepared by boiling the membrane suspension with an equal volume of solubilising buffer for 10 minutes. Aliquots of the mixture were examined by PAGE. Electrophoresis was performed in the presence of SDS using the discontinuous buffer system of Laemmli with 15% (w/v) polyacrylamide as the resolving gel. Low molecular weight standards (Pharmacia Ltd) were included with each run. Gels were run at a constant current of 8 mA until the blue marker reached the bottom of the plate. The proteins were stained by immersion in 0.25% (w/v) Coomassie brilliant blue G (Sigma Chemicals Ltd) in a mixture of glacial acetic acid/methanol/distilled water (10:45:45, v/v) for 30 minutes. The gels were destained in the above solvents in the ratio 7:5:5:87.5 (v/v), respectively.

Protein profile comparisons were made using the Dice coefficient of similarity. The diversity index was determined by the method of Shannon and Weaver.

### Results

Most (144, 89.4%) of the strains were non-serotypable. All strains were biotypable and eight distinct biotypes were represented.

Of the non-serotypable strains, (91, 63.2%) were isolated from patients between 60 and 89 years of age. The number of biotypes of H influenzae isolated from patients of each age group is shown in Table 1. For all

### Table 1  Biotypes isolated from different age groups

<table>
<thead>
<tr>
<th>Age (years)</th>
<th>No of patients</th>
<th>No of strains isolated</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Biotype</td>
</tr>
<tr>
<td>0–9</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>10–19</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td>20–29</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td>30–39</td>
<td>7</td>
<td></td>
</tr>
<tr>
<td>40–49</td>
<td>12</td>
<td></td>
</tr>
<tr>
<td>50–59</td>
<td>12</td>
<td></td>
</tr>
<tr>
<td>60–69</td>
<td>12</td>
<td></td>
</tr>
<tr>
<td>50–79</td>
<td>8*</td>
<td></td>
</tr>
<tr>
<td>80–89</td>
<td>17</td>
<td></td>
</tr>
<tr>
<td>90–99</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td>Unknown</td>
<td>5</td>
<td></td>
</tr>
</tbody>
</table>

*The same biotype strain isolated from one patient on two separate occasions; †strains of biotype 6 and biotype 8 were isolated from consecutive samples from one patient; ‡ the same biotype strain was isolated from one patient on three successive occasions; ††strains of biotype 1 and biotype 2 were isolated from consecutive samples from one patient.

### Table 2  Biotypes associated with pulmonary infection

<table>
<thead>
<tr>
<th>Clinical diagnosis</th>
<th>No of patients</th>
<th>No of strains isolated</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Biotype</td>
</tr>
<tr>
<td>Pulmonary infection</td>
<td>84</td>
<td></td>
</tr>
<tr>
<td>Infection associated with:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bronchial disease†</td>
<td>17</td>
<td></td>
</tr>
<tr>
<td>Chronic asthma</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>Cystic fibrosis</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>Carcinoma (lung or bronchus)</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td>Cardiac disease</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>Surgery</td>
<td>21</td>
<td></td>
</tr>
</tbody>
</table>

*The same biotype strain isolated from one patient on two separate occasions; †strains of biotype 6 and biotype 8 were isolated from consecutive samples from one patient; ††this group of diseases included bronchitis, bronchiectasis and chronic obstructive airways disease; ‡strains of biotype 1 and biotype 2 were isolated from consecutive samples from one patient; ††the same biotype strain isolated from one patient on three successive occasions.
patients, biotype 2 was the most common isolate (59; 41%), followed by biotypes 3 (39; 27-1%), 1 (19; 13-2%), and 5 (15; 10-4%). Examination of the clinical diagnosis (table 2) showed that most strains of biotypes 2 (34; 57-6%), 3 (30; 76-9%), and 5 (nine; 60-0%) were isolated from patients with symptoms of pulmonary infection without underlying disease. A significant number of biotype 1 strains (nine; 47-4%) were also isolated from this group of patients.

The OMP profile was determined for 59 non-serotypable strains of *H. influenzae*. Fifteen strains each of biotypes 1, 2, and 5, and 14 strains of biotype 3 were examined by SDS-PAGE. Each strain contained 10 to 20 OMPs. The OMP profiles of 15 strains of biotype 2 are shown in the figure. The major proteins of biotype 2 strains had M, values between 1·6 × 10⁴ and 5 × 10⁴. Similar OMP profiles were obtained for strains of biotypes 1, 3, and 5 (results not shown). Several minor bands of similar electrophoretic mobility were present in most of the strains studied.

The OMP profiles of strains within the same biotype were compared using the Dice equation. The similarity matrix for biotype 2 strains is shown in table 3. A large cluster, defined by a similarity coefficient of greater than 90%, contained six strains. Three smaller cluster groups each containing two strains were observed. Biotype 5 strains showed three cluster groups, each containing three strains. Three cluster groups (of three, two, and two strains, respectively) were seen in biotype 1. One cluster group of two strains was observed in biotype 3. The diversity index calculated for each biotype showed that the order of decreasing diversity was 3 > 1 > 5 > 2.

**Discussion**

Non-serotypable strains of *H. influenzae* have been established as important aetiological agents in cases of sinusitis, respiratory infection in the presence of chronic bronchitis and obstructive lung disease, and bronchopneumonia in elderly men. Our results confirm the assertions of other workers that most strains of *H. influenzae* in the respiratory secretions of both adults (81-8%) and children (72-5%) with serious chest infections are non-serotypable. Most strains (82-6%) were isolated from patients over the age of 40 years. In this group of patients biotypes 2 and 3 predominated (table 1). Similar findings were made by Oberhofer and Back.

The OMP profiles of isolates of both non-serotypable and serotypable strains of *H. influenzae* have been the subject of previous studies. Analysis of the OMP profiles of *H. influenzae* (serotype b) has shown only a limited number of subtypes. Non-serotypable strains have been reported to include a greater variety of subtypes, the OMP profiles of which are independent of growth phase and remain stable after several subcultures.

Generally, the OMP profiles of the non-serotypable strains were similar to those reported in earlier studies (figure). Six major proteins were resolved with M, values between 1·6 × 10⁴ and 5 × 10⁴ (figure). In most strains pairs of major protein bands were seen with M, values in both the 1·6 × 10⁴ to 3·0 × 10⁴ and the 3·2 × 10⁴ to 4·2 × 10⁴ regions. The OMP profile patterns could not be assigned to a previously published subtyping scheme which was based on only two OMP bands for each subtype.

Dice analysis of strains within each of the common biotypes (1, 2, 3 and 5) was carried out. A value of 90% was taken as the limiting value for each cluster group. Separate cluster groups were identified in biotypes 1 (three groups), 2 (four groups, table 3), 3 (one group) and 5 (3 groups). All the other strains within a biotype had individual OMP profile patterns (<90% similarity). A comparison of OMP profile...
diversity within each biotype showed that biotype 3 was the most diverse group and biotype 2 was the least diverse. With the exception of cluster group 1 of biotype 2, a clear association was not observed between a particular biotype and an individual OMP profile. Another study has also failed to detect an association between biotype and OMP subtype. The large number (40%) of biotype 2 strains with the same OMP profile (table 3) suggests that there may be less genetic diversity within this biotype than has been found among other strains of H influenzae. A direct comparison of the OMP profiles of strains from different biotypes was not possible due to the problems associated with inter-gel variability.

No clear correlation was observed between either the clinical state or age of the patient and the OMP profile cluster groups belonging to biotypes 1, 2, 3 or 5. Interestingly, five of the strains belonging to cluster group 1 of biotype 2 were isolated from patients with pulmonary infection that was associated with other underlying conditions.

Subsequent isolates from individual patients over a period of seven days showed identical OMP profiles (results not shown). Similar results have been reported by other workers. Our results confirm that the determination of OMP profiles by SDS-PAGE is a useful technique for the epidemiological study of this group of organisms.

The present study has shown a tentative association between a number of biotype 2 strains of H influenzae and their OMP profile. These strains were isolated from adult patients with symptoms of pulmonary infection, but a clear association between biotype, OMP cluster group, and disease cannot be confirmed. Other factors such as the immunological properties of the individual strain may also be important. Further studies are required to determine the possible association of pulmonary disease with non-serotypable biotype 2 strains of H influenzae.

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References

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Outer membrane protein subtyping of Haemophilus influenzae


Requests for reprints to: Dr C H Coverdale, Microbiology Laboratory, York District Hospital, Wigginton Road, York YO3 7HE, England.
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C H Coverdale and G S Temple

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