Introduction

- Worldwide spread of antibiotic resistance to Streptococcus pneumoniae (pneumococci) is a major public health concern
- The introduction of pneumococcal conjugate vaccines (PCVs) in children has been associated with a decline in antibiotic resistance. However, data from West and Central Africa are scanty
- The World Health Organization Collaborating Center (WHOCC) for New Vaccines Surveillance at The MRCG supports African countries to monitor pneumococcal antimicrobial resistance as part of surveillance for vaccine preventable invasive bacterial diseases
- We report data collected between 2007 and 2016

Methods and study isolates

- Pneumococcal isolates (185) recovered from suspected meningitis patients aged 0-59 months, were shipped to the WHO CC MRCG (Figure 1)
- Serotyping and antibiotic resistance were performed by latex slide agglutination and E-test methods, respectively
- Sequence types (STs) and resistance genotypes (tetM, pbp, mef1, folA, cat1) were inferred from the genome and displayed on the phylogeny (Figure 3)

Results

Table 1: Characteristics of study population (N=185)

<table>
<thead>
<tr>
<th>Category</th>
<th>SEN (%)</th>
<th>CAE (%)</th>
<th>RDC (%)</th>
<th>SMA (%)</th>
<th>CN (%)</th>
<th>NEG (%)</th>
<th>IIE (%)</th>
<th>SEN (%)</th>
<th>GAM (%)</th>
<th>TOC (%)</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Male</td>
<td>1 (20)</td>
<td>11 (38)</td>
<td>1 (100)</td>
<td>4 (15)</td>
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<td>14 (58)</td>
<td>0 (0)</td>
<td>24 (44)</td>
<td>9 (42)</td>
<td>16 (70)</td>
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<tr>
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<td>0 (0)</td>
<td>6 (23)</td>
<td>0 (0)</td>
<td>2 (8)</td>
<td>1 (100)</td>
<td>22 (46)</td>
<td>11 (55)</td>
<td>6 (28)</td>
<td>55 (30)</td>
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<tr>
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<td>11 (58)</td>
<td>1 (100)</td>
<td>4 (15)</td>
<td>0 (0)</td>
<td>5 (13)</td>
<td>0 (0)</td>
<td>5 (13)</td>
<td>4 (10)</td>
<td>2 (5)</td>
<td>22 (12)</td>
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<tr>
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<td>11 (38)</td>
<td>1 (100)</td>
<td>4 (15)</td>
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<td>6 (23)</td>
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<td>4 (17)</td>
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<td>3 (13)</td>
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<td>11 (22)</td>
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<td>0 (0)</td>
<td>0 (0)</td>
<td>1 (2)</td>
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<tr>
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<td>0 (0)</td>
<td>0 (0)</td>
<td>0 (0)</td>
<td>7 (32)</td>
<td>6 (31)</td>
<td>0 (0)</td>
<td>1 (5)</td>
<td>13 (7)</td>
<td>185 (100)</td>
</tr>
</tbody>
</table>

- Age in months
- Serotyping and antibiotic resistance were performed by latex slide agglutination and E-test methods, respectively
- Sequence types (STs) and resistance genotypes (tetM, pbp, mef1, folA, cat1) were inferred from the genome and displayed on the phylogeny (Figure 3)

Results continued

- Resistance of pneumococci to cotrimoxazole and tetracycline was shown in 59% and 65% of all serotypes, respectively (Figure 2)
- Multi-drug resistance (resistance to more than three antibiotics) occurred in 80% of vaccine serotypes recovered
- No resistance to ceftriaxone was observed

Figure 2: Pneumococcal antibiotic resistance by serotype

- Resistance
- Sensitive
- Intermediate
- Unknown
- Vaccine type
- Non-PCV serotype
- PCV serotype
- Era
- Post-PCV
- Pre-PCV
- Unknown

Tree scale: 0.1

Genotypic resistance by prediction

- Resistance genes

Figure 3: Phylogeny of pneumococcal isolates associated with bacterial meningitis in West and Central Africa

- The phylogeny showed resistance genes were associated with clonal lineages (Figure 3)
- The pcp and cat genes identified in 20.5% and 9.7% of isolates, respectively were associated with vaccine types (VTs) as well as emerging non-vaccine types (NVTs)

Concluding remarks

The increased prevalence of NVTs e.g. serotype 12F carrying the chloramphenicol resistance gene in the post-PCV era poses a significant public health threat

Acknowledgements

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