Abstract

Background: Carbapenemase-producing organisms (CPO) are a growing healthcare problem. We are reporting an outbreak of a New Delhi metallo-beta-lactamase (NDM-1) producing Klebsiella pneumoniae that occurred at a major tertiary care facility in British Columbia from November 2013 to March 2014.

Objectives: Gram-negative bacteria from clinical and surveillance specimens were tested for carbapenem susceptibility by VITEK 2. Carbapenem non-susceptible organisms were further tested by Etest and RODOS Neo Sensitive. PCR for carbapenem genes was done on all carbapenem non-susceptible isolates. Pulsed field gel electrophoresis (PFGE) was performed on the isolates. Plasmid restriction fragment length polymorphism (RFLP) was done for carbapenemase producing plasmas using RFLP.

Methods: A total of eleven patients were considered part of the K. pneumoniae NDM-1 outbreak on a medical unit. PCR showed that the patients’ isolates had 2 main clonal patterns. Plasmid analysis by RFLP and RFLP was done and showed that 10 of the 11 cases had an NDM plasmid that belonged to the same major cluster (pNDM-BC-5). Two ICU patients had NDM-1 producing K. pneumoniae in clinical isolates but the plasmid belonged to a different major cluster (pNDM-BC-7) and they were not considered part of the outbreak. All patients colonized or infected with NDM producing K. pneumoniae were placed on contact precautions in single rooms. All positive patients were cohorted into one side of the outbreak unit. Nursing staff were also cohorted into a clean cohort and an outbreak cohort. Weekly point prevalence surveys were conducted. Targeted surveillance of all admitted patients was started in March 2014 within all hospitals in the health authority. These combined measures resulted in halting transmission and the outbreak was declared over on March 10, 2014.

Conclusions: Infections that serve populations who frequently travel to regions where carbapenemase-producing organisms are endemic would have a robust surveillance and containment system for these organisms. Active surveillance and staff cohorting are important infection control measures. Molecular tools are helpful in understanding the patterns of transmission of these organisms and assisting with control measures.

Introduction

One particular carbapenemase, NDM, attracts significant attention because the gene encoding this metallo beta-lactamase (MBL), is located on a very mobile genetic element (1). The gene has moved from India and Pakistan to the United Kingdom, United States, Kenya, Japan, and other countries. This gene, thus has the potential to be a worldwide public health problem (2). Hospitals that serve populations who frequently travel to regions where NDM genes have high prevalence can be vulnerable to outbreaks due to organisms harboring this gene. Unless a robust surveillance system (3) and adequate laboratory detection protocols are in place, transmission within these facilities becomes inevitable. We describe a K. pneumoniae outbreak in a large tertiary care centre in BC that took place from November 2013 to March 2014.

Methods

Broth enrichment of rectal swabs, followed by subculture to MacConkey agar with Ertapenem and Meropenem discs.

Plasmid Analysis by RFLP

Molecular testing for CPE genes

ROSICO discs: phenotypic detection of enzymes

N.B. In December 2014, FH switched to SUPERCARBA plate (4) for carbapenemase producing Enterobacteriaceae (CPE) surveillance cultures.

Outbreak Control Measures

Contact Precautions in single rooms for all CPE positive patients.

Co-horting of CPE positive patients to one side of the unit and co-horting staff with a separate nursing station in the outbreak section of the unit.

Enhanced environmental cleaning and dedicated patient equipment.

Active Surveillance for CPE. FHA implemented surveillance in mid-2013 beginning with the higher risk sites. It was in place in all sites by March 2014

Chlorhexidine bathing of CPE positive patients.

Results

Table 1: Plasmid Analysis Profiles and PFGE results of NDM K. pneumoniae strains isolated from outbreak patients.

<table>
<thead>
<tr>
<th>Date of positive specimens</th>
<th>Source of specimen</th>
<th>CPE Gene</th>
<th>PFGE typing</th>
<th>Order on Image</th>
<th>Plasmid Analysis Profile</th>
</tr>
</thead>
<tbody>
<tr>
<td>11-Dec-13</td>
<td>rectal</td>
<td>K. pneumoniae</td>
<td>NDM-1</td>
<td>BCkPXA1.0056</td>
<td>pNDM-BC-5-1</td>
</tr>
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<td>17-Nov-13</td>
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<td>K. pneumoniae</td>
<td>NDM-1</td>
<td>BCkPXA1.0056</td>
<td>pNDM-BC-5-1</td>
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<td>pNDM-BC-5-1</td>
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<td>pNDM-BC-5-1</td>
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<td>K. pneumoniae</td>
<td>NDM-1</td>
<td>BCkPXA1.0050</td>
<td>pNDM-BC-6-1</td>
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<td>22-May-14</td>
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<td>K. pneumoniae</td>
<td>NDM-1</td>
<td>Not Done</td>
<td>pNDM-BC-5-6</td>
</tr>
</tbody>
</table>

Figure 1: PFGE and RFLP results of K. pneumoniae strains isolated from outbreak patients.

Green = pNDM-BC-7; Red = pNDM-BC-6; Purple = pNDM-BC-5; Blue = pNDM-BC-5.

Discussion and Conclusions

- The outbreak involved eleven patients. One patient had a UTI due to NDM-1 K. pneumoniae and the remaining patients were colonized with the organism. (Table 1).
- PFGE showed the isolates had 2 main clonal patterns. Plasmid analysis by PCR and RFLP was done and showed that 10 of the 11 cases had an NDM plasmid that belonged to the same major cluster (pNDM-BC-5).
- One patient (Figure 1: blue rectangle and arrow) had a different strain by PFGE but the plasmid analysis belonged to the same major cluster (pNDM-BC-5).
- Another patient (Figure 1: red rectangle and arrow) had a strain with a PFGE pattern related to that of the outbreak strain but the plasmid analysis profile belonged to a different major cluster (pNDM-BC-6).

References