Critical Care Surveillance: Ventilator Associated Pneumonia

Annual report:
Cardiff & Vale University Health Board

2018

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Data considerations

Data is captured at unit level in Ward Watcher across Wales. Once a month data is extracted and emailed to Public Health Wales. The information found in this report may differ slightly from that found in the quarter 4 report issued 31/1/19. This may be due to additional data being received for the annual report subsequently. For this reason the annual report should be referenced when mentioning annual VAP data.

This report includes data for University Hospital of Wales (2009-2018) and University Hospital Llandough (2009-2012).

Ventilator-Associated Pneumonia (VAP) definitions

*The below details are a summary guide only, and should not be used to determine infection status. For a more detailed breakdown of the criteria, please see the HELICS definitions for ICU-acquired pneumonia.*

To be classified as a ventilator-associated pneumonia, an invasive respiratory device must have been present (even intermittently) in the 48 hours preceding the onset of infection; there must be two or more serial chest X-rays (CXR) or CT scans with a suggestive image of pneumonia (only one definitive CXR or CT scan is sufficient if there is no underlying cardiac or pulmonary disease). Additionally, there will be a combination of symptoms which include fever, leucopenia, leucocytosis, purulent sputum (or a change in sputum), cough, dyspnoea, tachypnoea, suggestive auscultation, ronchi, wheezing, and/or worsening gas exchange.

In addition to the clinical criteria, the following criteria determine which category the infection falls under:

- **PN1** – Protected sample + quantitative culture (10⁴ CFU/ml BAL/10³ PB, DPA).
- **PN2** – Non-protected sample (ETA) + quantitative culture (10⁶ CFU/ml).
- **PN3** – Alternative microbiological criteria.
- **PN4** – Sputum bacteriology or non-quantitative ETA.
- **PN5** – No microbiological criterion met (only clinical criteria).
- **PNX** – Meets all requirements for PN1-4, but no CXR or CT scans have been done. Does not meet ECDC HELICS definition (but will be included for a Welsh VAP rate).
Cardiff & Vale UHB: Compliance

This section shows compliance by year for Cardiff & Vale UHB. We would expect to receive one export per month (12 per year per hospital). During 2014 the methods of data capture changed which may account for the decreased compliance.

During 2018 compliance for Cardiff & Vale UHB was 100%. Prior to 2013 data includes University Hospital Llandough.

Figure 1: Compliance trend for Cardiff & Vale UHB (2009-2018)
Cardiff & Vale UHB: Annual VAP rates (HELICS definition)

The European Centre for Disease Prevention and Control (ECDC) classifies VAPs according to the HELICS criteria. This section of the report details VAPs according to the HELICS criteria (PN1-PN5).

Figure 2: Cardiff & Vale UHB HELICS VAP trend rate compared with all Wales (2009-2018)

There were 26 infections and 7,342 ventilator days in 2018, giving a VAP rate of 3.54 per 1,000 ventilator days. This is higher than the 2017 rate of 3.17 VAP per 1,000 ventilator days.

The rate for Cardiff & Vale UHB is higher than the all Wales rate for all years after 2010.

*Excluding infections recorded as PNX (PN0) on WardWatcher.
Cardiff & Vale UHB: Welsh VAP rates (including PNX)

In 2016 a new PN code was added to capture infections meeting all requirements for PN1-4, but where no CXR or CT scans have been done. This was following reported incidence of VAPs in Wales being lower than other European regions and a study which was conducted by Public Health Wales.²

This section details all VAPs recorded including PNX and compares the rates with and without the additional code.

For 2018 there were an additional 17 VAPs recorded when the PNX type was included, giving a total of 43 VAPs across the health board (26 HELICS). This gives a VAP rate per 1,000 ventilator days of 5.86. This was higher than the rate for 2017 (4.76).

Since the introduction of the PNX code, the VAP rate for Cardiff & Vale UHB has increased each year.
Cardiff & Vale UHB UHB: VAP types

The following figure shows the number of VAPs broken down by type of VAP recorded by the surveillance. The VAP types include those as noted by HELICS (PN1- PN5), and includes the Welsh PNX type from 2016 onwards.

![Figure 4: VAPs recorded by type for Cardiff & Vale UHB (2009-2018)](image)

Table 1: VAP types for Cardiff & Vale UHB (2018)

<table>
<thead>
<tr>
<th></th>
<th>2018 Healthboard</th>
<th>2018 NHS Wales</th>
</tr>
</thead>
<tbody>
<tr>
<td>PN1</td>
<td>25</td>
<td>26</td>
</tr>
<tr>
<td>PN2</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>PN3</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>PN4</td>
<td>1</td>
<td>13</td>
</tr>
<tr>
<td>PN5</td>
<td>0</td>
<td>3</td>
</tr>
<tr>
<td>Total (HELICS)</td>
<td>26</td>
<td>42</td>
</tr>
<tr>
<td>PNX</td>
<td>17</td>
<td>24</td>
</tr>
<tr>
<td>Total (inc. PNX)</td>
<td>43</td>
<td>66</td>
</tr>
</tbody>
</table>

During 2018, the most common VAP type reported in Cardiff & Vale was PN1, followed by PNX. This is similar to the trend across Wales.
Cardiff & Vale UHB: Associated organisms

Infections categorised as PN1, PN2, PN3, or PN4 have microbiology data provided. Up to 3 organisms can be captured per infection.

Where only 1 organism is recorded we can deduce that this was the causative organism.

In 2018 there were 43 infections reported for Cardiff & Vale UHB. 23 of these had just one organism recorded as associated with the infection and thus we can deduce that these were the causative organisms. The most common causative organisms were Enterobacter sp. (other), MRSA, and Staphylococcus aureus.

Table 2: Causative organisms in Cardiff & Vale UHB (2018)

<table>
<thead>
<tr>
<th>Organism</th>
<th>Number of VAPS</th>
<th>Proportion of total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Enterobacter sp. (Other)</td>
<td>3</td>
<td>13.0</td>
</tr>
<tr>
<td>MRSA</td>
<td>3</td>
<td>13.0</td>
</tr>
<tr>
<td>Staphylococcus aureus</td>
<td>3</td>
<td>13.0</td>
</tr>
<tr>
<td>Candida albicans</td>
<td>2</td>
<td>8.7</td>
</tr>
<tr>
<td>Escherichia Coli</td>
<td>2</td>
<td>8.7</td>
</tr>
<tr>
<td>Pseudomonas aeruginosa</td>
<td>2</td>
<td>8.7</td>
</tr>
<tr>
<td>Candida sp. (Not specified)</td>
<td>1</td>
<td>4.3</td>
</tr>
<tr>
<td>Enterobacter sp. (Not specified)</td>
<td>1</td>
<td>4.3</td>
</tr>
<tr>
<td>Haemophilus influenzae</td>
<td>1</td>
<td>4.3</td>
</tr>
<tr>
<td>Klebsiella sp. (Not specified)</td>
<td>1</td>
<td>4.3</td>
</tr>
<tr>
<td>Klebsiella sp. (Other)</td>
<td>1</td>
<td>4.3</td>
</tr>
<tr>
<td>Pseudomonadaceae family (Not specified)</td>
<td>1</td>
<td>4.3</td>
</tr>
<tr>
<td>Serratia marcesecens</td>
<td>1</td>
<td>4.3</td>
</tr>
<tr>
<td>Staphylococcus epidermidis</td>
<td>1</td>
<td>4.3</td>
</tr>
<tr>
<td>Total</td>
<td>23</td>
<td>100.0</td>
</tr>
</tbody>
</table>

Table 3 (overleaf) shows all organisms recorded as associated with VAP infections in Cardiff & Vale UHB in 2018. The most common organisms associated with infections were Staphylococcus aureus, Escherichia coli, Candida albicans, and MRSA.
### Table 3: Associated organisms in Cardiff & Vale UHB (2018)

<table>
<thead>
<tr>
<th>Organism</th>
<th>Number of VAPs</th>
<th>Proportion of total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Staphylococcus aureus</td>
<td>10</td>
<td>14.9</td>
</tr>
<tr>
<td>Escherichia Coli</td>
<td>7</td>
<td>10.4</td>
</tr>
<tr>
<td>Candida albicans</td>
<td>6</td>
<td>9.0</td>
</tr>
<tr>
<td>MRSA</td>
<td>5</td>
<td>7.5</td>
</tr>
<tr>
<td>Enterobacter sp. (Other)</td>
<td>4</td>
<td>6.0</td>
</tr>
<tr>
<td>Candida sp. (Not specified)</td>
<td>4</td>
<td>6.0</td>
</tr>
<tr>
<td>Streptococcus sp. (Other)</td>
<td>4</td>
<td>6.0</td>
</tr>
<tr>
<td>Haemophilus influenza</td>
<td>4</td>
<td>6.0</td>
</tr>
<tr>
<td>Pseudomonas aeruginosa</td>
<td>4</td>
<td>6.0</td>
</tr>
<tr>
<td>Klebsiella sp. (Other)</td>
<td>3</td>
<td>4.5</td>
</tr>
<tr>
<td>Corynebacterium sp.</td>
<td>3</td>
<td>4.5</td>
</tr>
<tr>
<td>Klebsiella sp. (Not specified)</td>
<td>2</td>
<td>3.0</td>
</tr>
<tr>
<td>Staphylococcus epidermidis</td>
<td>2</td>
<td>3.0</td>
</tr>
<tr>
<td>Gram negative bacilli other</td>
<td>2</td>
<td>3.0</td>
</tr>
<tr>
<td>Pseudomonadaceae family (Not specified)</td>
<td>1</td>
<td>1.5</td>
</tr>
<tr>
<td>Enterococcus sp. (Not specified)</td>
<td>1</td>
<td>1.5</td>
</tr>
<tr>
<td>Stenotrophomonas maltophilia</td>
<td>1</td>
<td>1.5</td>
</tr>
<tr>
<td>Other coagulase negative staphylococci (CNS)</td>
<td>1</td>
<td>1.5</td>
</tr>
<tr>
<td>Streptococcus pneumonia</td>
<td>1</td>
<td>1.5</td>
</tr>
<tr>
<td>Serratia marcesecens</td>
<td>1</td>
<td>1.5</td>
</tr>
<tr>
<td>Enterobacter sp. (Not specified)</td>
<td>1</td>
<td>1.5</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>67</strong></td>
<td><strong>100</strong></td>
</tr>
</tbody>
</table>

### References


2) [https://www.frontiersin.org/articles/10.3389/fmicb.2016.01271/full](https://www.frontiersin.org/articles/10.3389/fmicb.2016.01271/full)