First outbreak due to Vancomycin Resistant Enterococcus (VRE) epidemic Clone ST796 in Europe

Introduction

- **Vancomycin-resistant enterococci (VRE)** are multidrug-resistant microorganisms that can cause healthcare-associated infections and increase risk of mortality and length of hospital stay.
- An outbreak with VRE affected several hospitals within the Bern University hospital group since the end of December 2017, due to a new VRE clone ST796 characterized by rapid intra- and inter-hospital dissemination.
- This clone has recently emerged in Australia and New Zealand and quickly spread between hospitals (L2).
- Here, we describe a large outbreak of this clone in our hospital group and illustrate the genetic relationship of the Swiss and Australian isolates.

Case work-up

- Assessment of epidemiological linkage by a line list and identifying contacts by chart review.

Microbiology

- Identification of E. faecium (MALDI-TOF) mass spectrometry.
- Screening for VRE and confirmation with detection of vanB and vanA resistance genes.
- Phenotypic susceptibility testing by CLSI disk diffusion and Etest.

Whole genome sequencing

- VRE isolate analysis by whole genome sequencing (WGS) for epidemiological linkage.
- WGS sequencing was performed using a MiSeq (llumina platform) from different ST isolates and sequencing after Nextera XT library preparation. Mean coverage of 30-fold.
- Read assembly and analysis by cgMLST.
- Additional ST796 strain genome sequences were downloaded from databases for comparison (2).

Table 1: Characteristics epidemic VRE clone versus others

<table>
<thead>
<tr>
<th>All patients*</th>
<th>Patients with VRE ST796 +/- other ST (n = 121)</th>
<th>Patients with VRE other than ST796 (n = 136)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean age</td>
<td>66 ± 15</td>
<td>66 ± 13</td>
</tr>
<tr>
<td>Gender</td>
<td>46 (38%)</td>
<td>46 (38%)</td>
</tr>
<tr>
<td>VRE isolation</td>
<td>216 (90%)</td>
<td>90 (74%)</td>
</tr>
<tr>
<td>Susceptible infection</td>
<td>12 (5.4%)</td>
<td>12 (5.4%)</td>
</tr>
<tr>
<td>Clinical infection</td>
<td>49 (35%)</td>
<td>49 (36%)</td>
</tr>
</tbody>
</table>

Table 2: Outbreak description

- The outbreak was characterized by two waves, between which the management strategy was adapted. After the outbreak was declared on 4 January 2018, the following outbreak investigation and management strategy was undertaken:

Strategy I

- **VRE outbreak team formation**
- **Temporary admission stops in affected wards**
- **Cohorting of VRE-colonized or infected patients, contact precautions, and staff cohorting**
- **Active contact tracing, targeted screening and preemptive contact precautions**
- **Taging of outpatient contacts**
- **Cross-sectional screening of patients on high-risk wards**
- **Environmental disinfectant cleaning on high-risk wards**
- **Hand hygiene compliance reinforcement on all occasions**

Strategy II

The outbreak seemed to near containment by April 2018, when another wave in VRE cases and transmissions was observed from May on. The following points were identified as follows:

- **Discontinuation of preemptive contact isolation precautions of contacts**
- **Cohorting of patients and ward staff, managed by wards in their own responsibility**
- **Environmental disinfectant cleaning expanded to entire bed tower (with few exceptions)**

Discussion

To the best of our knowledge, we report the first description of VRE ST796 clonal dissemination across several hospitals in Europe. *E. faecium* ST796 was first recognized at an Australian hospital during 2011 and spread rapidly throughout Australia and New Zealand, implying an effective transmission ability of this clone (1,2). The WGS analyses revealed a clear genomic relationship between isolates from the outbreak in the Bern University Hospital group described here and those from Australia. In Switzerland, VRE incidence is not systematically monitored for infection prevention purposes, national surveillance data are lacking. In collaboration with the National Center of Infection Control (Swissnoso), and the Swiss Centre for Infection Research (LANNES), a national program for VRE epidemiology and the corresponding outbreak management has been launched on 29 June 2018.

Acknowledgements: Infection control team, Bern University Hospital

Conclusions

- We report the first VRE ST796 outbreak in Europe.
- Close genetic relationship among VRE confirmed the epidemiological links between patients.
- Extended and rapid interventions are warranted on an interdisciplinary basis to control such an outbreak.

References:

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Figure 1: Epidemic curve

- **Epidemic curve of VRE cases (Bern University hospital group, Switzerland).** 80 beds. **Number of Patients:** Red line. **Number of screenings:** Black line.

Figure 2: Core genome Multi Locus Sequencing Typing

- **Core genome multi locus sequencing typing (cgMLST) analyses based on 643 loci, performed in Rabin Medical Centre, Haifa, Israel. **Number of isolates belonging to each cluster is shown in the circles.** If more than one cluster was found, cluster indicative of recombination is indicated.**

Outbreak management

- WGS sequencing was performed using a MiSeq (llumina platform) from different ST isolates and sequencing after Nextera XT library preparation. Mean coverage of 30-fold.
- Read assembly and analysis by cgMLST.
- Additional ST796 strain genome sequences were downloaded from databases for comparison (2).
- We report the first VRE ST796 outbreak in Europe.
- Close genetic relationship among VRE confirmed the epidemiological links between patients.
- Extended and rapid interventions are warranted on an interdisciplinary basis to control such an outbreak.
- By the end of August 2018 the (biphasic) epidemic curve indicates a decline of new VRE detections.
- The rapid spread of this multidrug-resistant clone warrants strengthening and timely execution of infection control procedures.
- National guidance on the prevention and management of VRE has been issued on 12 September 2018.

References: