Clonal expansion of community-associated methicillin-resistant Staphylococcus aureus in people who inject drugs from 2012 to 2017: prevalence, risk factors and molecular epidemiology

Simon Packer, Field Epidemiology Service (FES), Public Health England (PHE)
Background

- Large increase in MRSA infections in people who inject drugs (PWID) resident in Bristol (South West of England).
- PWID at particular risk of MRSA infection through colonisation

Aim:
- to estimate the prevalence of MRSA in PWID,
- explore the genetic relatedness of these samples,
- establish whether specific interventions are required.

* Data only up until August 2016
Methods: study design and recruitment

Study Design

• Cross sectional survey – Unlinked Anonymous Monitoring (UAM) survey

Recruitment

• Central and mobile needle exchange services in Bristol
• Non-probability quota sampling – age and sex weighted
• Inclusion criteria: reporting injecting drugs in the past year

Ethics

• Ethical approval from London research ethics committee
Methods: data collection and analysis

Data collection

• Adapted unlinked anonymous monitoring (UAM) survey questionnaire
• Microbiological data for whole genome sequencing:
  • Nasal and groin swabs from study participants
  • Bristol PWID MRSA bacteraemia samples
  • Bristol hospital admission screening swabs positive for MRSA (non-PWID)

Data analysis

• Descriptive statistics, univariable analysis, and risk group classification
• Phylogenetic analysis of whole genome sequencing data
• Cluster analysis
Results: descriptive

Demographics

• 153 persons recruited 149 eligible

• Majority male and aged between 35 and 44 years

MRSA colonisation

• MRSA colonisation prevalence of 9% (13/149)
### Results: univariable and risk groups

<table>
<thead>
<tr>
<th>Variable</th>
<th>Positive</th>
<th>OR</th>
<th>95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Report most frequently Inject in group of three or more</td>
<td>50% (3/6)</td>
<td>15.8</td>
<td>2.51 99.28</td>
</tr>
<tr>
<td>Report most frequently injecting outside</td>
<td>23% (5/22)</td>
<td>5.5</td>
<td>1.34 22.73</td>
</tr>
<tr>
<td>Hospital contact in past month</td>
<td>19% (7/36)</td>
<td>4.3</td>
<td>1.34 13.8</td>
</tr>
<tr>
<td>Injected into groin past month</td>
<td>14% (10/74)</td>
<td>3.8</td>
<td>0.99 14.23</td>
</tr>
<tr>
<td>Homeless within the past year</td>
<td>14% (9/65)</td>
<td>3.2</td>
<td>0.94 10.96</td>
</tr>
<tr>
<td>Skin and soft tissue infection (SSTI) in the past year</td>
<td>15% (7/47)</td>
<td>2.8</td>
<td>0.89 8.85</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Risk grouping</th>
<th>Positive</th>
<th>OR</th>
<th>95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hospital contact, SSTI, or outside injecting</td>
<td>15% (12/78)</td>
<td>12.6</td>
<td>1.77 551.65</td>
</tr>
<tr>
<td>Hospital contact, SSTI, group injecting or outside injecting</td>
<td>15% (12/80)</td>
<td>11.9</td>
<td>1.67 520.34</td>
</tr>
<tr>
<td>Hospital contact or SSTI</td>
<td>16% (11/69)</td>
<td>7.3</td>
<td>1.51 70.36</td>
</tr>
<tr>
<td>Hospital contact, SSTI or group injecting</td>
<td>15% (11/72)</td>
<td>6.7</td>
<td>1.38 64.35</td>
</tr>
</tbody>
</table>
Results: phylogenetic analysis

Phylogenetic tree of CC5 isolates – 80% of study colonisation samples and 32% of hospital admission screening swabs.

Clinical group
- Bacteraemia
- Non-invasive
- Carriage

Tree scale: 0.001

<table>
<thead>
<tr>
<th>Region</th>
<th>Color</th>
</tr>
</thead>
<tbody>
<tr>
<td>East</td>
<td>purple</td>
</tr>
<tr>
<td>South East</td>
<td>dark blue</td>
</tr>
<tr>
<td>East Midlands</td>
<td>teal</td>
</tr>
<tr>
<td>London</td>
<td>light blue</td>
</tr>
<tr>
<td>North West</td>
<td>orange</td>
</tr>
<tr>
<td>South West</td>
<td>red</td>
</tr>
<tr>
<td>Yorkshire &amp; Humbers</td>
<td>brown</td>
</tr>
<tr>
<td>Wales</td>
<td>dark red</td>
</tr>
</tbody>
</table>

- isolates from same patient
- bootstrap value > 80%
Limitations

• Sample size
  • Insufficient power for multivariable analysis

• Non-random sampling
  • Sampling bias likely present
  • Sample comparable to routine demographic data

• Cross sectional design
  • Cannot determine temporality of MRSA colonisation
Conclusions

• High colonisation prevalence in Bristol PWID
• Establishment of an epidemic clone of MRSA in Bristol PWID
• Transmission occurring within the PWID community
• Potential links to the non-injecting population
• Large number of invasive infections associated with specific clade
• Certain groups at greater odds of colonisation
Recommendations

• Local stakeholders (clinical commissioning groups, NHS, local councils) implement interventions to reduce bacterial infections in Bristol’s injecting population and these are evaluated.

• Determine the cost to the NHS related to MRSA in people who inject drugs in Bristol.

• Further research to understand the epidemiology of bacterial infections (with a focus on MRSA) in people who inject drugs in the United Kingdom.
Acknowledgements

This study would like to thank for their hard and invaluable work Bristol Drugs Project, Public health laboratory in Bristol and the Antimicrobial Resistance and Healthcare Associated Infections Reference Unit London.

This work was supported by the Elizabeth Blackwell Institute for Health Research, University of Bristol and the Wellcome Trust Institutional Strategic Support Fund.
Thank you for listening, any questions?
References

