Staphylococcus aureus Isolates from Meat Products Legally and Illegally Introduced to Germany from non-EU countries harbor a variety of antimicrobial resistances and virulence factors

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Introduction

• Products of animal origin (POAO) can serve as a vector for Staphylococcus (S.) aureus and international trade with such products can facilitate the spread of S. aureus around the globe.
• Illegally imported POAO are of particular concern since hygienic standards during production and transportation are often insufficient.

Material, methods and results

Fig. 1: Examples of confiscated meat products

Origin of the isolates:

<table>
<thead>
<tr>
<th></th>
<th>Illegal</th>
<th>Legal</th>
</tr>
</thead>
<tbody>
<tr>
<td>Poultry</td>
<td>(n=14)</td>
<td>(n=5)</td>
</tr>
<tr>
<td>Pork</td>
<td>(n=3)</td>
<td>(n=1)</td>
</tr>
</tbody>
</table>

Molecular typing:

- 23 isolates were examined, among them 9 methicillin-resistant S. aureus (MRSA)
- Isolated from meat and meat products introduced to Germany from non-EU countries from January 2014 through January 2015
- Samples from legally imported meat as well as from confiscated meat seized from air passengers in the course of routine controls

Fig. 2: Distribution of spa types and clonal complexes

- 10 different spa types and 9 MLST sequence types were detected among the isolates with t127/CC1 being the most prevalent.
- Two novel dru types (dt10dg, dt11dc) and three novel MLST sequence types (ST3216, ST3217, ST3218) were identified.
- All MRSA were isolated from illegally imported poultry meat.

Antimicrobial resistances:

<table>
<thead>
<tr>
<th>Resistance Phenotype</th>
<th>Number of isolates</th>
<th>Resistance genes</th>
</tr>
</thead>
<tbody>
<tr>
<td>β-lactams</td>
<td>19</td>
<td>mecA (n=9)</td>
</tr>
<tr>
<td>MLS2-antibiotics</td>
<td>8</td>
<td>erm(C) (n=7)</td>
</tr>
<tr>
<td>Tetracycline</td>
<td>6</td>
<td>tet(K) (n=3)</td>
</tr>
<tr>
<td>Aminoglycosides</td>
<td>6</td>
<td>aacA-aphD (n=3)</td>
</tr>
<tr>
<td>Trimethoprim</td>
<td>2</td>
<td>dfrA (n=2)</td>
</tr>
<tr>
<td>Chloramphenicol</td>
<td>1</td>
<td>fosA (n=1)</td>
</tr>
</tbody>
</table>

- 14 isolates carried genes conferring resistance to ≥ 3 classes of antimicrobial agents

Virulence-associated genes:

- seh in all 10 t127/CC1 isolates
- sea in two isolates and sed in one isolate
- Enterotoxin gene cluster in 5 isolates
- Further detected genes include sek (n=2), seq (n=2), sej (n=1), sep (n=1), ser (n=1)
- luk-PV detected in 6 MRSA isolates
- tst1 in 2 methicillin-sensitive CC5 isolates
- edinB and etD in 3 CC80 isolates

Conclusion:

- A plethora of virulence factors and antimicrobial resistances could be detected among the isolates examined in this study.
- The presence of major virulence factors constitutes the potential for severe diseases in the consumer.
- A distribution of antibiotic resistance genes as well as virulence-associated genes among the local S. aureus population could occur.

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