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First detection of livestock-associated meticillin-resistant Staphylococcus aureus CC398 in bulk tank milk in the United Kingdom, January to July 2012

G K Paterson1, J Larsen2, E M Harrison1, A R Larsen2, F J Morgan1, S J Peacock3,4, J Parkhill2, R N Zadoks5, M A Holmes (mahi@cam.ac.uk)1

1. Department of Veterinary Medicine, University of Cambridge, Cambridge, United Kingdom
2. Microbiology and Infection Control, Statens Serum Institut, Copenhagen, Denmark
3. School of Clinical Medicine, University of Cambridge, Cambridge, United Kingdom
4. The Wellcome Trust Sanger Institute, Wellcome Trust, Cambridge, United Kingdom
5. Moredun Research Institute, Penicuik, United Kingdom

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Antimicrobial Susceptibility Testing (EUCAST) guidelines [3].

Molecular and phenotypic characterisation of LA-MRSA CC398 from dairy cattle in the United Kingdom

Multi-locus sequence typing found all seven isolates belonged to sequence type ST398, and CC398-specific PCR based on the restriction–modification system saus–hsdS1 confirmed that all the isolates belonged to clonal complex CC398 [4]. Isolates from three farms exhibited spa type t011 and carried a composite staphyloccocal cassette chromosome mec (SCCmec) V(5C2&5)c element, whereas isolates from the remaining two farms had spa types t011 and t2546 and harbour SCCmec IVa. All isolates lacked the lukS-PV and lukF-PV genes encoding Panton-Valentine leukocidin and the scn gene (Table). Antimicrobial susceptibility testing using disk diffusion according to the EUCAST guidelines revealed that all isolates were resistant to tetracycline, and PCR [10] demonstrated the presence of the tetracycline resistance gene tet(M) in all seven, and of tet(K) in three isolates (Table).

Discussion

Here we describe the first isolation of LA-MRSA CC398 from dairy cattle in the UK. This is only the second published instance of LA-MRSA CC398 in this country following the report of isolates (t011 and SCCmec IVa) from two horses in south-eastern England [11]. In many countries in continental Europe and elsewhere, LA-MRSA CC398 poses an occupational risk for those in close contact with livestock, particularly pigs and veal calves. For instance, significantly higher rates of MRSA nasal carriage by humans in contact with pigs (farm workers, abattoir workers, veterinarians) have been noted in several epidemiological studies, with the isolates typically belonging to CC398 [12-16]. Further
studies have shown an association between clinical disease resulting from LA-MRSA CC398 infection and contact with pigs or pig farms [16-20]. The impact of this can be significant locally, and this lineage can be imported into healthcare settings. For example, in a German hospital in an area with a large number of pigs, 22% of patients colonised with MRSA at admission carried ST398 [21]. Nosocomial transmission has also been reported [22]. LA-MRSA CC398, like other MRSA, may be responsible for life-threatening infections during long or frequent hospitalisations, or following wound or surgery site infections, and also increases healthcare costs resulting from screening, isolation of carriers, and decolonisation. Although pasteurisation of milk should ensure that CC398 MRSA will not enter the food chain, our finding of LA-MRSA CC398 in dairy cattle has clear public health implications for the UK. Workers on dairy farms, or individuals with regular contact with dairy cows, are likely to have a higher risk of colonisation or infection with LA-MRSA CC398 compared to the general population in the UK. LA-MRSA CC398 isolates from three of the farms where isolated were found carried SCC\textit{mec} type IVa. The isolates from the other two farms carried SCC\textit{mec} type V(5C2&5)c. Both of these SCC\textit{mec} types have previously been found in LA-MRSA CC398 isolates [23].

Heterogeneity is seen in \textit{S. aureus} CC398, with human and livestock-associated lineages being differentiated by the presence or absence of specific resistance and virulence-related genes [23-24]. In all of our isolates the absence of the \textit{scn} gene, encoding the human-specific staphylococcal complement inhibitor, and the presence of \textit{tet}(M) suggested that they were all livestock-associated, as opposed to \textit{S. aureus} CC398 strains which circulate in the human population independent of a livestock reservoir [23-24]. Likewise, all seven isolates lacked the \textit{lukS}-\textit{lukF} genes encoding Panton-Valentine leukocidin which is absent in LA-MRSA CC398, but is present in some, but not all, human-associated CC398 isolates [23]. Three consecutive samples from the same farm over a seven-month period were positive for LA-MRSA CC398 isolates with identical \textit{spa} (t011) and SCC\textit{mec} types (IVa), suggesting that this strain is able to persist in dairy herds over prolonged periods. While there are relatively few reports of LA-MRSA CC398 from dairy cattle compared to pig farms, it has been found to cause bovine mastitis [25-27]. Our findings therefore have significance to veterinary medicine, in addition to public health. The relative absence of CC398 MRSA from the UK prior to this study, when it is widespread in the rest of Europe suggests that the geographical separation of the UK.

TABLE
Molecular and phenotypic characteristics of meticillin-resistant \textit{Staphylococcus aureus} CC398 from bulk tank milk in the United Kingdom, January to July 2012 (n=7)

<table>
<thead>
<tr>
<th>Farm</th>
<th>Location</th>
<th>Date of sampling</th>
<th>Strain</th>
<th>CC398a</th>
<th>spa type</th>
<th>SCC\textit{mec} typeb</th>
<th>\textit{lukS}-\textit{lukF}</th>
<th>\textit{Scn}c</th>
<th>\textit{tet}(M)d</th>
<th>\textit{tet}(K)e</th>
<th>Resistance profilef</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Dumfries and Galloway</td>
<td>Jan 2012</td>
<td>17-51</td>
<td>+</td>
<td>t011</td>
<td>IVa</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>TET, NOR, KAN</td>
</tr>
<tr>
<td>1</td>
<td>Dumfries and Galloway</td>
<td>Jul 2012</td>
<td>17-57</td>
<td>+</td>
<td>t011</td>
<td>IVa</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>TET, NOR, KAN</td>
</tr>
<tr>
<td>1</td>
<td>Dumfries and Galloway</td>
<td>Jul 2012</td>
<td>34-179</td>
<td>+</td>
<td>t011</td>
<td>IVa</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>TET, NOR, KAN</td>
</tr>
<tr>
<td>2</td>
<td>Worcestershire</td>
<td>May 2012</td>
<td>22-79</td>
<td>+</td>
<td>t011</td>
<td>V(5C2&amp;5)c</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>TET, NOR</td>
</tr>
<tr>
<td>3</td>
<td>Berkshire</td>
<td>May 2012</td>
<td>25-26</td>
<td>+</td>
<td>t011</td>
<td>V(5C2&amp;5)c</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>ERY, CLI, TET, NOR</td>
</tr>
<tr>
<td>4</td>
<td>Warwickshire</td>
<td>May 2012</td>
<td>30-59</td>
<td>+</td>
<td>t2346</td>
<td>IVa</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>TET, KAN</td>
</tr>
<tr>
<td>5</td>
<td>Wrexham</td>
<td>Jul 2012</td>
<td>31-07</td>
<td>+</td>
<td>t011</td>
<td>V(5C2&amp;5)c</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>TET, NOR, KAN</td>
</tr>
</tbody>
</table>

CC: clonal complex; ERY: erythromycin; CLI: clindamycin; TET: tetracycline; NOR: norfloxacin; KAN: kanamycin.
a CC398 as determined by the method of Stegger et al. [4].
b As determined by the method described in [5-7], V(5C2&5)c; SCC\textit{mec} V harbouring the czrC gene in the J1 region.
c As determined by the method described in [8].
d As determined by the method described in [9].
e As determined by the method described in [10].
f Also tested (but all strains susceptible) were linezolid, rifampicin, fusidic acid, trimethoprim/sulfamethoxazole and mupirocin.
from continental Europe may have delayed the spread of this lineage to the UK rather than there being any fundamental difference in husbandry or biosecurity in the UK. The authors are aware of unpublished surveys looking for potential LA-MRSA in UK dairy and pig herds that have been negative before now. These CC398-positive samples were not part of a formal prevalence study, and it is therefore unclear how common LA-MRSA CC398 isolates are in UK dairy farms or if they are present in other livestock. However, the five farms with positive samples were identified from a sample of ca. 1,500 farms, indicating a low prevalence currently.

Conclusions

This is the first description of LA-MRSA CC398 in food-producing animals in the UK. The ability of this lineage to colonise a wide range of host species, coupled with its zoonotic potential, make this finding of significance to both veterinary and human health. Future surveillance for this LA-MRSA CC398 strain in all food-producing animal species in the UK and the evaluation of occupational risk factors for MRSA carriage and infection should be considered.

Acknowledgments

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