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Prevalence and characterization of human mecC methicillin-resistant Staphylococcus aureus isolates in England

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Objectives: There are limited data available on the epidemiology and prevalence of methicillin-resistant Staphylococcus aureus (MRSA) in the human population that encode the recently described mecA homologue, mecC. To address this knowledge gap we undertook a prospective prevalence study in England to determine the prevalence of mecC among MRSA isolates.

Patients and methods: Three hundred and thirty-five sequential MRSA isolates from individual patients were collected from each of six clinical microbiology laboratories in England during 2011–12. These were tested by PCR or genome sequencing to differentiate those encoding mecA and mecC. mecC-positive isolates were further characterized by multilocus sequence typing, spa typing, antimicrobial susceptibility profile and detection of PBP2a using commercially available kits.

Results: Nine out of the 2010 MRSA isolates tested were mecC positive, indicating a prevalence among MRSA in England of 0.45% (95% CI 0.24%–0.85%). The remainder were mecA positive. Eight out of these nine mecC MRSA isolates belonged to clonal complex 130, the other being sequence type 425. Resistance to non-β-lactam antibiotics was rare among these mecC MRSA isolates and all were phenotypically identified as MRSA using oxacillin and cefoxitin according to BSAC disc diffusion methodology. However, all nine mecC isolates gave a negative result using three different commercial PBP2a detection assays.

Conclusions: mecC MRSA are currently rare among MRSA isolated from humans in England and this study provides an important baseline prevalence rate to monitor future changes, which may be important given the increasing prevalence of mecC MRSA reported in Denmark.

Keywords: MRSA, mec genes, S. aureus, surveillance

Introduction

Staphylococcus aureus is a versatile, opportunistic pathogen able to cause a wide range of diseases in humans, from minor skin infections to severe illnesses such as sepsicaemia, toxic shock, endocarditis and pneumonia. It is also able to colonize and infect a variety of other host species, including farm and companion animals and wildlife. The emergence and dissemination of methicillin-resistant S. aureus (MRSA) since the early 1960s has posed a major challenge to the treatment of S. aureus infections. Methicillin resistance in S. aureus is conferred by the acquisition of one of several staphylococcal cassette chromosome mec (SCCmec) elements, which carry the mecA gene encoding a penicillin-binding protein homologue (PBP2a) with reduced affinity for β-lactam antibiotics. We identified a novel mecA homologue, mecA LGA251, encoded in a new SCCmec element, designated type XI, among human and bovine MRSA isolates in the UK and Denmark. This mecA homologue, subsequently named mecC, exhibits only 69% identity at the DNA level and 63% identity at the protein level to the previously described mecA/PBP2a. As a result, it is not detectable by routine mecA-specific PCR approaches or PBP2a slide agglutination tests. mecC MRSA have now been isolated in small numbers from humans and a wide range of other host species in several European countries: Republic of Ireland, France, Sweden, and the
Isolate collection and assessment of mec gene status

Three hundred and thirty-five sequential MRSA isolates from individual patients were identified according to local procedures from screening and clinical samples at five hospital clinical microbiology laboratories from October 2011 to August 2012 (Table 1). These were sent to Cambridge for PCR detection of mecA and mecC, as described previously.17 These were isolates drawn from hospitals and other healthcare providers in the catchment area of each laboratory, including community-based general practitioners. Methicillin resistance was based on phenotypic resistance (cefoxitin disc diffusion, Vitek 2 or chromogenic agars) in all cases and not on molecular detection of mecA or PBP2a. Isolates from a sixth hospital (Addenbrooke's Hospital, Cambridge; Table 1) were collected as above and genome sequenced as part of an independent study. These were not assessed by PCR but by interrogation of their genome sequences using BLAST analysis to identify mecA and mecC MRSA isolates with confirmation of the presence of femB as a species marker of S. aureus. The analysis of 2010 isolates provides the power to detect mecC MRSA prevalence at a lower limit of 0.05% at the 95% confidence level.

Antimicrobial susceptibility testing and slide agglutination for PBP2a

All mecC MRSA isolates were analysed using the Vitek 2 system (bioMérieux, Basingstoke, UK). In brief, suspensions of cultures were made in 0.45% sodium solution from growth on Columbia blood agar, adjusted to a turbidity equivalent to that of a 0.5 McFarland standard and used to load the test cards, which were used in accordance with the manufacturer’s instructions. The Staph AST-P620 card was automatically filled, sealed and inserted into the Vitek 2 reader–incubator module (incubation temperature 37°C), and fluorescence measurements were performed every 15 min for up to 18 h. Cefoxitin and oxacillin resistances were also assayed by disc diffusion following BSAC guidelines (version 11.1 May 2012) and the MICs of cefoxitin and oxacillin were determined using Etest strips (bioMérieux). All mecC MRSA isolates identified were tested with three commercially available mecA microarrays (Vitek 2 reader–incubator module; Mectasystm Kit, bioMérieux, France; AlereTM PBP2a Culture Colony Test (Alere Ltd, Stockport, UK). The mecA-positive MRSA strain NCTC12493 was used as a positive control.

Methods

Genome sequencing and spa typing

All mecC MRSA isolates underwent whole genome sequencing using the HiSeq2000 platform (Illumina, Little Chesterford, UK) to confirm their mec gene status and determine their multilocus sequence type (ST). Isolates that were PCR negative for either mecA or mecC were also genome sequenced to confirm their mec gene status. The species identity of isolates negative by PCR for femB was tested by assessing their growth and morphology on Staph Brilliance 24 and MRSA Brilliance 2 agar plates (both Oxoid) and by PCR to detect nuc.20 Spa typing was performed using the primers spo-1113f (5′-TAA AGA AGA TCC TCC GTG GAG C-3′) and spo-1514r (5′-CAG CAG TAG TGC CGT TTG CTT-3′) as described by Ridom GmbH (Würzburg, Germany).

Results and discussion

PCR (or genome sequence analysis in the case of Addenbrooke's Hospital, Cambridge) revealed that 9 isolates out of a total of 2010 MRSA collected were mecC MRSA. These mecC MRSA isolates were largely from screening samples (six isolates), but included three isolates from skin and soft tissue infections. The remaining MRSA isolates were mecA positive, which provides a prevalence rate of mecC MRSA among all MRSA collected of 0.45% with a 95% CI of 0.24%–0.85%. All 2010 isolates were confirmed to be S. aureus. In the majority of cases this identification was based on the presence of femB as detected by PCR or genome sequencing. However, 12 out of the 1675 isolates (0.72%) tested by PCR for femB were negative for an amplicon and were instead confirmed to be S. aureus based on their growth on Staph Brilliance and MRSA Brilliance agar plates and all were positive for nuc. The basis for the negative femB PCR result is under investigation and may relate to divergence in the femB primer binding sites. Indeed, a small number of S. aureus isolates negative for femB using alternative PCR approaches have been reported previously.21,22 Two isolates were negative by PCR for both mecA and mecC, but genome sequencing revealed that they were indeed mecA positive and carried previously described mecA genes (NCBI accession numbers FJ390057 and AF411935) with divergence in the primer binding sites used in this study.

Genome sequencing confirmed that each isolate positive for mecC by PCR encoded mecC within an SCCmec type XI. Multilocus ST derived from the genome sequences revealed five different STs among the nine isolates, including a novel ST, ST2574. Eight of the isolates belonged to clonal complex (CC) 130, with the remaining isolate belonging to ST425. Five spa types were represented:

Table 1. Contributing hospitals

<table>
<thead>
<tr>
<th>Clinical microbiology laboratory</th>
<th>Location (city and county)</th>
<th>First sample date</th>
<th>Last sample date</th>
<th>Number of mecA/mecC MRSA</th>
</tr>
</thead>
<tbody>
<tr>
<td>Royal Preston Hospital</td>
<td>Preston, Lancashire</td>
<td>October 2011</td>
<td>June 2012</td>
<td>335:0</td>
</tr>
<tr>
<td>Countess of Chester Hospital</td>
<td>Chester, Cheshire</td>
<td>November 2011</td>
<td>August 2012</td>
<td>335:0</td>
</tr>
<tr>
<td>Nottingham Universities Hospitals</td>
<td>Nottingham, Nottinghamshire</td>
<td>January 2012</td>
<td>May 2012</td>
<td>333:2</td>
</tr>
<tr>
<td>Musgrove Hospital</td>
<td>Taunton, Somerset</td>
<td>November 2011</td>
<td>May 2012</td>
<td>333:2</td>
</tr>
<tr>
<td>Royal Cornwall Hospitals Trust</td>
<td>Truro, Cornwall</td>
<td>November 2011</td>
<td>July 2012</td>
<td>333:2</td>
</tr>
<tr>
<td>Addenbrooke's Hospital</td>
<td>Cambridge, Cambridgeshire</td>
<td>April 2012</td>
<td>June 2012</td>
<td>332:3</td>
</tr>
</tbody>
</table>
t843, t6220, t9280, t11702 and t11706 (Table 2). All mecC MRSA isolates were resistant to cefoxitin and oxacillin using BSAC guidelines for disc diffusion, while MICs varied from 8 to 32 mg/L for oxacillin and from 8 to 16 mg/L for cefoxitin (Table 2). Antimicrobial susceptibility testing using Vitek 2 revealed that resistance to non-β-lactam antibiotics was rare, the only example being a single isolate, Ta222, displaying resistance to erythromycin and inducible resistance to clindamycin (Table 2). All nine isolates displayed the unusual Vitek 2 resistance profile of being resistant to cefoxitin, but susceptible to oxacillin. This feature of mecC MRSA, likely caused by structural differences between the mecA- and mecC-encoded PBP2a, has been described previously and may be helpful in the identification of mecC MRSA isolates.  

The susceptibility to oxacillin seen using Vitek 2 is in disagreement with our oxacillin disc diffusion results. mecC-encoded PBP2a has been shown to be less stable at 37°C than at 30°C, which may explain this discrepancy. oxacillin disc diffusion being performed at 30°C, but Vitek 2 analysis at 37°C. Cefoxitin resistance is presumably still seen using Vitek 2, even at 37°C, because of the higher affinity of mecC-encoded PBP2a for cefoxitin versus oxacillin. All nine mecC MRSA isolates gave negative results when assayed with three different commercial PBP2a slide agglutination assays, confirming the difficulty of detecting mecC MRSA using this approach.

This is the first formal prospective prevalence study of mecC MRSA performed in the UK and these data provide a baseline prevalence for the future surveillance of mecC MRSA in England. Continued monitoring of mecC is potentially important given the increase in prevalence of mecC MRSA reported in Denmark. There are few other data on mecC MRSA prevalence elsewhere, but in Germany a large multicentre prospective study identified a single mecC isolate among 1604 tested in 2004–05 and again a single isolate from 1603 tested in 2010–11. This indicates a prevalence of 0.06% with no change between the study periods. In contrast, the prevalence in Denmark was both higher and increasing, rising from 1.91% in 2010 to 2.78% in 2011. A survey of 565 human MRSA isolates in Switzerland failed to find any mecC MRSA, indicating that the prevalence there is lower than in Denmark. Clearly, there are significant and as yet unexplained differences in mecC MRSA prevalence between different countries, and the recent increase reported in Denmark suggests that it would be prudent to monitor prevalence in the UK and elsewhere.

None of the hospitals used oxacillin to identify MRSA, which has been shown to be less reliable than cefoxitin for the detection of mecC MRSA. Nonetheless, it is possible that some mecC MRSA may have been missed during primary isolation. For instance, small numbers of mecC MRSA isolates grow poorly on MRSA-selective agars, presumably due to their having low cefoxitin/oxacillin MIC values. An area for future study may be the comparison and standardization of primary isolation methods in relation to mecC MRSA.

The majority of mecC MRSA isolates found in our survey belonged to CC130, which agrees with the data of Garcia-Alvarez et al. showing that CC130 was the most common lineage among their retrospective testing for mecC MRSA among human isolates in the UK and Denmark. Both CC130 and ST425 are the predominant lineages among mecC MRSA isolates found not only in humans but also in other host species elsewhere, and genome sequencing has provided strong evidence of cross-species transmission of mecC MRSA between humans and livestock. Of the five spa types recovered in this study, neither t11702 nor t11706 appear to have been reported previously among mecC MRSA, whilst the other three, t843, t6220 and t9280, have. There were multiple CCs belonging to the same spa type and multiple spa types within the same CC, illustrating the difficulty of inferring CC from spa type data.

As reported for mecC MRSA isolated elsewhere in Europe and from different host species, resistance to non-β-lactam antibiotics was uncommon among these English mecC MRSA isolates.

The origins of mecC MRSA and SCCmec type XI are unclear, but mecC has also been detected in Staphylococcus xylosus and Staphylococcus sciuri. This suggests a possible origin for mecC in coagulase-negative staphylococci, as proposed for mecA and clinical microbiology laboratories should therefore be aware not only of mecC MRSA but of the possible occurrence of mecC in other pathogenic species of methicillin-resistant staphylococci.
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Transparency declarations
Competing interests: none to declare.

References