Molecular analysis of methicillin-resistant Staphylococcus pseudintermedius of feline origin from different European countries and North America

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Sir,

Staphylococcus pseudintermedius is the most frequent causative agent of canine pyoderma and may also be associated with wound infections, urinary tract infections and otitis externa in dogs. Although more rarely, S. pseudintermedius causes infections in cats and has also been identified in infections of humans. The latter observation highlights the zoonotic potential of S. pseudintermedius. S. pseudintermedius appears to be able to readily accumulate antimicrobial resistance genes and, in recent years, a rapid increase in methicillin resistance has been observed. A recent multicentre study on methicillin-resistant S. pseudintermedius (MRSP) of canine origin, obtained in different European countries as well as in the USA and Canada, revealed that most of the canine strains exhibited resistance to virtually all classes of antimicrobial agents approved for veterinary use. This represents a major therapeutic challenge for veterinarians in Europe and North America. Moreover, this multicentre study revealed that among MRSP from dogs two distinct, dominant clones—as identified by multilocus sequence typing (MLST), spa typing, SCCmec typing and Smal PFGE—have disseminated across Europe and North America. In contrast to the wealth of data available for MRSP isolates of canine origin, little data are available about MRSP from cats.

The aim of the present study was to characterize MRSP isolates from cats in different countries for their genetic relationships and antimicrobial resistance phenotypes and genotypes. Twelve epidemiologically unrelated MRSP isolates of feline origin were identified during 2006–08 in five different countries (Table 1). Eleven isolates were from clinical disease conditions, including septicemia, urinary tract infections, nephritis, rhinitis, wound infection and pneumonia. The remaining isolate was obtained from a nasal swab of an apparently healthy cat (Table 1). All isolates were confirmed to be S. pseudintermedius by MboI digestion of a PCR-amplified internal fragment of the pta gene. For a better comparison with data of canine MRSP isolates, MICs of 17 antimicrobial agents were determined using the VetMIC™ microdilution panels (National Veterinary Institute, Uppsala, Sweden) as previously described and evaluated using the breakpoints of the CLSI. MICs of rifampicin, mupirocin and quinupristin/dalfopristin were determined by Etest® (AB Biodisk, Solna, Sweden). Antibiotic resistance genes were detected using either a microarray or specific PCR assays as described previously.

All 12 feline S. pseudintermedius proved to be MRSP by oxacillin MICs of >16 mg/L and carriage of the mecA gene. Despite the diverse geographical origins, the 11 European MRSP isolates shared the same MLST type ST71, spa type 102 and SCCmec type II–III. SCCmec type II–III is a hybrid of SCCmec II (2A) from Staphylococcus epidermidis and SCCmec III from Staphylococcus aureus. PFGE analysis identified three different patterns J, N and O among these European feline MRSP isolates. The single MRSP isolate from Canada harboured an SCCmec type V element and exhibited spa type t23, MLST type ST100 and PFGE pattern B. A comparison with the data of the multicentre study on MRSP in dogs revealed that PFGE patterns B, N and O were exclusive to feline MRSP isolates whereas pattern J was the dominant PFGE pattern among European canine MRSP. The Canadian feline MRSP isolate also differed largely in its resistance phenotype and genotype from the European feline MRSP isolates. It was only resistant to β-lactam antibiotics via mecA and blaZ, and to tetracyclines via tet(M). In contrast, the European isolates
Table 1. Characteristics of the 12 MRSP isolates from cats investigated in this study

<table>
<thead>
<tr>
<th>Isolate no.</th>
<th>Country</th>
<th>Disease condition</th>
<th>SCCmec type</th>
<th>spa type</th>
<th>MLST type</th>
<th>PFGE pattern</th>
<th>Resistance phenotype</th>
<th>Resistance genotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>E028</td>
<td>I</td>
<td>septicaemia</td>
<td>II–III</td>
<td>t02</td>
<td>ST71</td>
<td>J</td>
<td>BLA, TET, ML, CHL, TMP, GEN, KAN, STR, FQ</td>
<td>mecA, blaZ, tet(K), erm(B), cat_{SC221}, dfrG, aac(6')-Ie/aph(2')-Ia, aac(3')-III, ant(6')-Ia</td>
</tr>
<tr>
<td>E029</td>
<td>I</td>
<td>nephritis</td>
<td>II–III</td>
<td>t02</td>
<td>ST71</td>
<td>N</td>
<td>BLA, TET, ML, CHL, TMP, GEN, KAN, STR, FQ</td>
<td>mecA, blaZ, tet(K), erm(B), cat_{SC221}, dfrG, aac(6')-Ie/aph(2')-Ia, aac(3')-III, ant(6')-Ia</td>
</tr>
<tr>
<td>E031</td>
<td>I</td>
<td>septicaemia</td>
<td>II–III</td>
<td>t02</td>
<td>ST71</td>
<td>J</td>
<td>BLA, TET, ML, CHL, TMP, GEN, KAN, STR, FQ</td>
<td>mecA, blaZ, tet(K), erm(B), cat_{SC221}, dfrG, aac(6')-Ie/aph(2')-Ia, aac(3')-III, ant(6')-Ia</td>
</tr>
<tr>
<td>E037</td>
<td>I</td>
<td>septicaemia</td>
<td>II–III</td>
<td>t02</td>
<td>ST71</td>
<td>J</td>
<td>BLA, TET, ML, CHL, TMP, GEN, KAN, STR, FQ</td>
<td>mecA, blaZ, tet(K), erm(B), cat_{SC221}, dfrG, aac(6')-Ie/aph(2')-Ia, aac(3')-III, ant(6')-Ia</td>
</tr>
<tr>
<td>E047</td>
<td>CH</td>
<td>rhinitis</td>
<td>II–III</td>
<td>t02</td>
<td>ST71</td>
<td>J</td>
<td>BLA, TET, ML, CHL, TMP, GEN, KAN, STR, FQ</td>
<td>mecA, blaZ, tet(K), erm(B), cat_{SC221}, dfrG, aac(6')-Ie/aph(2')-Ia, aac(3')-III, ant(6')-Ia</td>
</tr>
<tr>
<td>E051</td>
<td>CH</td>
<td>wound infection</td>
<td>II–III</td>
<td>t02</td>
<td>ST71</td>
<td>J</td>
<td>BLA, ML, CHL, TMP, GEN, KAN, STR, FQ</td>
<td>mecA, blaZ, erm(B), cat_{SC221}, dfrG, aac(6')-Ie/aph(2')-Ia, aac(3')-III, ant(6')-Ia</td>
</tr>
<tr>
<td>E053</td>
<td>CH</td>
<td>urinary tract infection</td>
<td>II–III</td>
<td>t02</td>
<td>ST71</td>
<td>J</td>
<td>BLA, TET, ML, TMP, GEN, KAN, STR, FQ</td>
<td>mecA, blaZ, tet(K), erm(B), cat_{SC221}, dfrG, aac(6')-Ie/aph(2')-Ia, aac(3')-III, ant(6')-Ia</td>
</tr>
<tr>
<td>E060</td>
<td>CH</td>
<td>urinary tract infection</td>
<td>II–III</td>
<td>t02</td>
<td>ST71</td>
<td>J</td>
<td>BLA, TET, ML, CHL, TMP, GEN, KAN, STR, FQ</td>
<td>mecA, blaZ, tet(K), erm(B), cat_{SC221}, dfrG, aac(6')-Ie/aph(2')-Ia, aac(3')-III, ant(6')-Ia</td>
</tr>
<tr>
<td>E072</td>
<td>CH</td>
<td>urinary tract infection</td>
<td>II–III</td>
<td>t02</td>
<td>ST71</td>
<td>J</td>
<td>BLA, TET, ML, CHL, TMP, GEN, KAN, STR, FQ</td>
<td>mecA, blaZ, tet(K), erm(B), cat_{SC221}, dfrG, aac(6')-Ie/aph(2')-Ia, aac(3')-III, ant(6')-Ia</td>
</tr>
<tr>
<td>E076</td>
<td>NL</td>
<td>urinary tract infection</td>
<td>II–III</td>
<td>t02</td>
<td>ST71</td>
<td>O</td>
<td>BLA, ML, CHL, TMP, GEN, KAN, STR, FQ</td>
<td>mecA, blaZ, erm(B), cat_{SC221}, dfrG, aac(6')-Ie/aph(2')-Ia, aac(3')-III, ant(6')-Ia</td>
</tr>
<tr>
<td>E114</td>
<td>D</td>
<td>healthy</td>
<td>II–III</td>
<td>t02</td>
<td>ST71</td>
<td>J</td>
<td>BLA, TET, ML, CHL, TMP, GEN, KAN, STR, FQ</td>
<td>mecA, blaZ, tet(K), erm(B), cat_{SC221}, dfrG, aac(6')-Ie/aph(2')-Ia, aac(3')-III, ant(6')-Ia</td>
</tr>
<tr>
<td>E132</td>
<td>CAN</td>
<td>pneumonia</td>
<td>V</td>
<td>t23</td>
<td>ST100</td>
<td>B</td>
<td>BLA, TET</td>
<td>mecA, blaZ, tet(M)</td>
</tr>
</tbody>
</table>

aI, Italy; CH, Switzerland; NL, the Netherlands; D, Germany; CAN, Canada.
bBLA, β-lactam antibiotics; CHL, chloramphenicol; FQ, fluoroquinolones; GEN, gentamicin; KAN, kanamycin; ML, macrolides/lincosamides; STR, streptomycin; TET, tetracyclines; TMP, trimethoprim.
exhibited three different expanded resistance phenotypes and 
genotypes (Table 1). All isolates were resistant to β-lactam anti-
biotics (mecaA, blaZ), macrolides/lincosamides [erm(B)], gentami-
cin/kanamycin [aac(6′)-Ie/aph(2′)-Ia], kanamycin [aph(3′)-III],
streptomycin [ant(6′)-Ia], trimethoprim [dfrG] and ciprofloxacin.
Moreover, all but one isolate from Switzerland and all but two 
isolates from Switzerland and the Netherlands were resistant to 
chloramphenicol (catPc221) and to tetracyclines [tet(K)], 
respectively. However, all feline MRSP isolates were susceptible 
to mupirocin, rifampicin, quinupristin/dalfopristin, linezolid and 
vancomycin, which are important for decolonization of humans 
or represent ‘antimicrobial agents of last resort’ for the treat-
ment of methicillin-resistant S. aureus (MRSA) infections in 
humans.

A comparison with the results of the genetic analysis of 
canine MRSP showed that the Canadian feline MRSP differed in 
all characteristics, except SCCmec type V, from the dominant 
canine MRSP clone in North America, which is characterized by 
ST68 (MLST)–C (PFGE)–t06 (spa).4 In contrast, 9 of the 11 
European feline MRSP isolates were identified as members of the 
previously described dominant clonal lineage among canine MRSP in Europe, which is characterized by ST71 (MLST)–J (PFGE)–t02 (spa)–II–III (SCCmec).6 This observation 
strongly suggested an exchange of MRSP isolates between 
dogs and cats in Europe. Whether the feline MRSP isolate from 
Canada represents a member of a new MRSP clone with a par-
ticular tropism for cats remains to be determined.

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provided MRSP isolates. We thank Fabiola Feltrin, Serena Lorenzetti, 
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expert technical assistance.

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participating institutions.

Transparency declarations

None to declare.

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Molecular characterization of plasmids 
encoding CTX-M-15 extended-spectrum 
β-lactamase associated with the ST131 
Escherichia coli clone in Belgium

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Keywords: ESBLs, B2 phylogroup, pEK499, pC15

Sir,

Previous studies performed in a large number of Belgian hospi-
tals showed the dissemination of a major clone of the virulent 
This E. coli ST131 clone has been reported worldwide and rep-
resents a major public health problem.2 The present study 
sought to characterize blaCTX-M-15-containing plasmids associ-
ated with ST131 E. coli CTX-M-15 isolates recovered in Belgian 
hospitals. This specific clone was detected from clinical speci-
mens of patients hospitalized at the Erasme hospital in Brus-
sels since 2001, as well as in 18 other Belgian hospitals

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