Methicillin-resistant Staphylococcus aureus with the novel mecC gene variant isolated from a cat suffering from chronic conjunctivitis

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Sir,

Methicillin-resistant Staphylococcus aureus (MRSA) is of growing concern in public and animal health and it is important to ensure efficient and reliable methods for MRSA identification. Standard confirmatory tests include PCR for detection of the mecA gene and protein agglutination for identification of the penicillin-binding protein 2a (PBP2a). In 2011, a novel mecA homologue designated mecC (or mecA1GA251) was described in S. aureus. This MRSA variant will not be detected with the usual mecPCR approaches or with the PBP2a agglutination tests, representing a challenge to MRSA confirmation in diagnostic laboratories. Searching for mecC has recently been performed in several countries. Investigated isolates have either been part of historical collections or originated from current diagnostic submissions. The chosen candidates for mecC screening have typically been isolates with a phenotype corresponding to MRSA but lacking mecA, and/or isolates belonging to clonal lineages already associated with mecC carriage. So far the occurrence of the mecC gene has been confirmed in isolates from the typical hosts, humans and/or cattle, in several countries in Northern Europe: the UK, Denmark, Ireland, Germany, France, Sweden and Norway. Only two studies examining isolates from hosts other than humans and cattle are known; one of these studies investigated a historical isolate collection and mecC was found in S. aureus from a dog, a seal and a chaffinch (all from the UK), from a rabbit and rats from Belgium, and from sheep in Denmark. The other study, recently published by Walther et al., found mecC-positive MRSA from two dogs, seven cats and a guinea pig. The MRSA isolates investigated originated from samples submitted to a laboratory in Germany during the period 2008–11. Based on current knowledge, mecC seems to have a rather wide geographical and host distribution, but occurs at low frequencies. The Norwegian Veterinary Institute has recently detected mecC in an MRSA isolate from a submission to our diagnostic bacteriological service unit in Bergen. The isolate originated from a cat and represents the first finding from current diagnostic activity performed on samples from companion animals.

The mecC-positive MRSA (designated 2012-50-2037) was isolated from an eye swab from a 5-year-old house cat with chronic conjunctivitis and stomatitis. The cat had tested negative for all relevant viruses and Chlamyphila felis. Initial treatment with systemic clavulanate-potentiated amoxicillin and topical fusidic acid was ineffective, but improvement was seen after a change of treatment to systemic enrofloxacin and topical dexamethasone, neomycin and polymyxin B. The cat is currently living in a household with two adults, two children and another cat. The MRSA carrier status of the family members and the other cat is not known.

The isolate was routinely tested for susceptibility to antimicrobial agents following the disc diffusion method and breakpoints described by EUCAST (www.eucast.org, 7 November 2012, date last accessed). The isolate showed resistance to β-lactams only. MICs were subsequently determined by the use of a broth dilution method (Trek Diagnostics). The following antimicrobial agents were tested: penicillin, cefoxitin, ciprofloxacin, erythromycin, clindamycin, gentamicin, tetracycline, linezolid, fusidic acid, rifampicin, chloramphenicol, trimethoprim, vancomycin, quinupristin/dalfopristin and mupirocin. The isolate exhibited resistance to the β-lactams only, with a cefoxitin MIC of 16 mg/L. The MIC of oxacillin was 2 mg/L, determined by Etest (bioMerieux). The results were interpreted according to EUCAST. S. aureus ATCC 29213 was included as quality control.

DNA was prepared by the boil lysis method and subsequently subjected to PCR for detection of mecA, mecC, nuc and 16S rDNA with primers previously described. In addition to a negative control, positive control strains included S. aureus CCUG 29213 (nuc+), S. aureus CCUG 35603 (nuc+, mecA), Staphylococcus pseudintermedius CCUG 49543 (nuc+, mecA) and S. aureus SVA-AB-773 (nuc+, mecC). The PCR results confirmed MRSA with mecC. The sequence of the mecC amplicon was determined and showed 100% identity with the previously determined mecC sequence. The mecC gene was probably located on a type XI SCCmec element as PCRs with primers for the mecI, mecR, ccrA, ccrB and blaZ genes related to SCCmecX1 produced amplicons of correct sizes.

The spa typing showed that the isolate belonged to spa type t6902. This spa type has only one other recording in the Ridom spaserver (http://spaserver.ridom.de/, 7 November 2012, date
last accessed). This isolate (submitted in 2010) originated from Poland and is described as methicillin susceptible. Multilocus sequence typing showed that the isolate belonged to the novel sequence type ST2497, a single-locus variant of ST1943 with one nucleotide difference in the glpF gene.

The isolate described in this study represents the first detection of an mecC-containing MRSA from an animal host in Norway. The mecC gene has been detected recently in a total of eight MRSA isolates from humans in Norway and homologue mecA Pichon B, Hill R, Laurent F 355 methicillin-resistant blaZ and mecC have been described from other countries. 1,4 55

during 2006–12, belonged to CC130. The genotype of the feline isolate represents a new mecC-positive genotype identified in our country; however, isolates within this clonal lineage with mecC have been described from other countries. 1,4

The detection of mecC in an MRSA from a clinical sample from a cat submitted to our diagnostic bacteriological service unit demonstrates the importance of taking mecC into consideration in diagnostic units that examine samples from companion animals. Our finding extends our knowledge of MRSA carrying mecC from animals and demonstrates that detection of mecC is not only a rare event when screening historical isolate collections.

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References


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HIV-1 intregase variability and relationship with drug resistance in antiretroviral-naive and -experienced patients with different HIV-1 subtypes

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