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Letter to the Editor

Methicillin-resistant staphylococci isolated from animals

Sir,

We read with interest the recent article in *Veterinary Microbiology* 'Methicillin-resistant staphylococci isolated from animals' (Duijkeren et al., 2004). The authors report on the isolation of methicillin-resistant *Staphylococcus aureus* (MRSA) from two animals in the Netherlands and state it was unusual that one of the isolates showed homology to a human MRSA strain.

We recently reported the isolation of MRSA from companion animals causing clinical infections (Rich and Roberts, 2004). Further to our preliminary investigations, we now report the isolation of MRSA from 210 companion animals (mainly dogs and cats) from various geographical locations throughout the UK, primarily associated with postoperative and wound infections. Of these isolates, 31 were randomly selected for detailed characterisation using a range of phenotypic and genotypic tests, including biotyping, tube coagulase testing, phage typing, antimicrobial susceptibility testing, PCR-based detection of the *mecA* gene and pulsed field gel electrophoresis (PFGE). The data show that, in contrast to the findings of Duijkeren et al. (2004), 29 (93.5%) of the animal isolates in our study were indistinguishable from human healthcare-associated epidemic MRSA (EMRSA) strains currently prevalent in the UK.

These apparently conflicting results may be explained by the considerable difference in the prevalence of MRSA between the Netherlands and the UK. MRSA is an important cause of healthcare-associated infection in the UK, where in excess of 40% *S. aureus* bacteraemias are due to MRSA (Anonymous, 2004). In contrast, <1% of clinical *S. aureus* strains in the Netherlands are methicillin resistant (Duijkeren et al., 2004). To date, 17 epidemic strains of methicillin-resistant *Staphylococcus aureus* (EMRSA) have been described in the UK (Aucken et al., 2002) and the predominant MRSA clones currently found in humans are EMRSA-15 and EMRSA-16, accounting for over 95% of isolates (Johnson et al., 2001; Hardy et al., 2004.). Twenty-nine of the strains from animals that we have so far characterised are representatives of these genetic lineages (EMRSA-15, $n = 25$; EMRSA-16, $n = 4$), which have spread throughout Europe and worldwide. Variations in PFGE banding patterns showed various sub-types of these epidemic strains, indicating different strains were able to cause infection in companion animals and that no single sub-type was predominant.

MRSA was first described from a canine source in 1994 (Cefai et al., 1994) and recent reports have shown that MRSA infection in companion animals is much more widespread that previously thought (Boag et al., 2004; Rich and Roberts, 2004). Evidence also suggests that, rather than the emergence of specific host-adapted resistance among staphylococci in companion animals, common human strains are involved. In order to establish the MRSA types involved in areas of low endemicity, detailed characterisation of such strains to include antimicrobial susceptibility testing and genotyping may be prudent not only from a public health perspective but also to provide insights into the transmission dynamics of MRSA in human and animal populations. In addition, these data highlight the need for continued

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vigilance and systematic studies to further our understanding of the origins and epidemiology of MRSA in companion animals.

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