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Abstract (publication only)

**Diversity of antimicrobial and biocide susceptibility patterns among equine methicillin-resistant staphylococci**

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**Objectives:** Antimicrobial and biocide susceptibility characterization was performed in 14 methicillin-resistant staphylococci isolates (8 *Staphylococcus sciuri*, 2 *S. aureus*, 1 *S. lentus*, 1 *S. fleurettii*, 1 *S. haemolyticus* and 1 *S. cohnii cohnii*) previously isolated from 71 sick and healthy horses. **Methods:** MICs of the study strains towards several antimicrobial agents, biocides and dyes were determined by broth microdilution according to the CLSI standard. Beta-lactamase production was tested after cephalosporin induction by using the nitrocefin test. PCR amplification was used to detect antimicrobial resistance and plasmid-encoded efflux-pump genes. *S. sciuri* strains were subjected to PFGE. All isolates were characterized by dru-typing. **Results:** Beta-lactamase production was detected in three strains and confirmed by the presence of the blaZ gene. Only the *S. lentus* isolate was resistant to chloramphenicol due to the presence of the gene cat pC221. Likewise only one *S. aureus* showed a high MIC (>256 mg/L) to trimethoprim and the dfrK gene was detected. Eight strains were resistant to tetracycline due to the presence of the genes tet(K) (n=7) and tet(M) (n=1). The erm(C) gene was seen in two isolates, which showed resistance to both, erythromycin and clindamycin. High MICs to gentamicin and kanamycin were observed in two strains which were encoded by the bifunctional enzyme aacA-aphD (n=2), and also by aph(3')-IIIa (n=1). Fusidic acid resistance and the gene fusC were detected in a single *S. aureus* strain. Two strains had high MICs to ethidium bromide ( $\geq 64$  mg/L), benzalkonium chloride (2 mg/L) and triclosan (2 mg/L) and carried qac genes (*S. haemolyticus* harbouring qacA and *S. cohnii cohnii* carrying both qacB and a qacH-like gene). The same *S. sciuri* clone, with an undistinguishable PFGE profile, was isolated from different horses. The dru type dt11a was the most frequently identified type (n=7), two single strains (*S. lentus* and *S. haemolyticus*) harboured novel dru types one *S. aureus* had dt10q and three strains were non-typeable. **Conclusions:** This study showed that methicillin-resistant staphylococci are important reservoirs of antimicrobial and biocide resistance genes, which circulate in different staphylococcal species, including MRSA. These bacteria/genes seem to be disseminated in the equine population and can be transmitted to humans in close contact, which raises the question of potential interspecies and zoonotic spread.