Methicillin-resistant (MR) staphylococci isolated from Austrian and German wildlife

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Introduction: Antimicrobial-resistant zoonotic pathogens are a major threat to the health of both humans and animals. While the presence of antimicrobial-resistant zoonotic pathogens in humans, companion animals and livestock has been well-documented, there is still little information on infections, carriage and role of these particular pathogens in wildlife. The objective of the present study was to assess the presence of methicillin-resistant Staphylococcus (S.) aureus (MRSA) as well as methicillin-resistant coagulase-negative staphylococci (MRCoNS) in Austrian and German wildlife.

Materials and Methods: Using enrichment step and selective media, MR staphylococci were obtained from 350 wild animals, and characterized by mecA/mecA1/mecC PCRs (Loncaric, JAC 2013; Harrison, AAC, 2014, Małyszko, JAC 2014), SCCmec typing and by DNA microarray analysis (Alere Technologies GmbH) (Monecke, FEMS 2008). Additionally, MRSA isolates were genotyped by spa typing, Multi-Locus-Sequence-Typing (MLST) (Enright, JCM 2000), and by two different multiple-locus variable-number of tandem repeat analyses (MLVA) (Loncaric, VETMIC 2014), and were further phenotypically subtyped and biotyped for capsular polysaccharide (CP) expression using Fourier Transform Infrared (FTIR) spectroscopy (Grunert, JCM 2013). Species allocation of MRCoNS isolates was conducted using a rpoB-based microarray* and confirmed by Vitek 2 and rpoB sequencing (Mellmann, EID 2006).

Results: Six MRSA isolates and 18 MRCoNS were detected. The mecA-positive MRSA isolates belonged to t011-CC398-IV-CP5 originating from mallard, t011-CC398-V-CPnt from beech marten, and t003-CC5-II-CPnt from European hare. Three clonally related mecC-positive MRSA from European hare belonged to 1843-CC130-XI-CP8. Fifteen out of 18 MRCoNS harbored the mecA gene, wherefrom two strains harbored mecA1 gene too. They belonged to 6 different staphylococccal species: S. fleurettii, S. sciuri subsp. sciuri, S. epidermidis, S. haemolyticus, S. lentus and S. saprophyticus and were isolated from various hosts. The mecC gene was found in two S. stepanovicii from European otter, and red fox, as well as in S. caprae from Eurasian beaver.

Conclusion: Even though the presence of MRSA and MRCoNS was low, isolates of various staphylococcal species, that carried either mecA or mecC genes, were detected in several distinct wildlife hosts. More systematic studies are needed (i) to determine the role of wild animals as reservoirs for MR staphylococci that may be transmitted to domestic animals and humans, and (ii) to unravel the role of wild animals in global spread of MR staphylococci.

* (http://alere-technologies.com/fileadmin/Media/Paper/Poster/Poster-ECCMID_2011_MILAN_CoNS_array.pdf)

![Figure 1. Geographic distribution of methicillin-resistant staphylococci.](image)

red – MRSA, yellow – mecC-poss. MRCoNS, blue – mecA-poss. MRCoNS

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