INTRODUCTION: There is increasing evidence for a zoonotic background of MRSA harbouring mecC encoding an alternative gene for a penicillin-binding protein. In this study wildlife isolates were screened for mecA, mecC, and other resistance genes.

MATERIALS AND METHODS: Wildlife isolates of S. aureus from Germany, Austria, and Sweden were characterised by microarray analysis (Alore Technologies GmbH), VITEK-2 and MLST.

RESULTS: mecC was identified in CC130-MRSA-XI from two diseased Swedish hedgehogs (Erinaceus europaeus), from a fox (V. vulpes), two hares (Lepus europaeus) and a fallow deer (D. dama) from Germany. One CC399-MRSA-XI was found in a road-killed hedgehog from Germany. These isolates also harboured the SCCmec X1-associated beta-lactamase gene and several resistance genes.

The mecC gene was found in CC398-MRSA-IV from a mallard (Anas platyrhynchos), CC398-MRSA-V from a marten (Martes sp.) and ST5ST225-MRSA-II (Rhine-Hesse/New York-Japan Clone) from all, hare from Austria. These isolates also carried blaZ (beta-lactamase), qacA (organism resistance to macrolides, clindamycin), aadD (tobramycin).

CONCLUSION: mecC appears to be common in wildlife and mecC MRSA can be found in several distinct wildlife species. mecA MRSA can be expected in urban wildlife living in proximity to humans and their refuse. More systematic studies are needed as wild animals might serve as significant reservoir for resistant S. aureus with potential for transmission to domestic animals and humans.

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