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Resistance to antibiotics and the occurrence of genes responsible for the development of methicillin resistance in *Staphylococcus* bacteria isolated from the environment of horse riding centres

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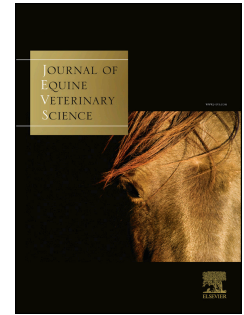
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14 Abstract

15 The purpose of the study was to identify species, to determine the drug resistance profile and
16 to evaluate the occurrence of genes responsible for the development of methicillin resistance
17 in *Staphylococcus* bacteria isolated from the environment of horse riding centres.
18 Staphylococci were isolated from air, manure and nostrils of horses located in three horse
19 riding centres, differing in horse stabling system – box stall stabling (OJK Pegaz and KJK
20 Szary) and free-range stabling (SKH Nielepice). The dominant species was *S. vitulinus*. A
21 large variation in the frequency of occurrence of individual species between horse riding
22 centres was determined. Resistance to antibiotics was determined by means of disc diffusion
23 method and PCR technique to detect *mecA* genes responsible for methicillin resistance. In
24 total, 408 strains were collected, most from SKH Nielepice, and least from OJK Pegaz. The
25 highest resistance was found to gentamicin and tetracycline. MDR isolates were also detected
26 in KJK Szary (10), in SKH Nielepice (5), and in OJK Pegaz (4). Methicillin resistance
27 determined by disk diffusion assay was found in 23 strains, while the *mecA* gene was detected
28 in 142 isolates. 137 strains holding the *mecA* gene are coagulase-negative staphylococci,
29 which, as shown by our own studies, may be a reservoir of methicillin resistance. Most
30 commonly, the *mecA* gene was found in staphylococci isolated in KJK Szary (61.70%). The
31 *mecA* gene was detected in 5 strains that belonged to *S. aureus* species and came from horses
32 in SKH Nielepice, indicating the presence of MRSA strains in these animals.

33 Keywords: *Staphylococcus* spp.; drug resistance; *mecA* gene; methicillin resistance; horses

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