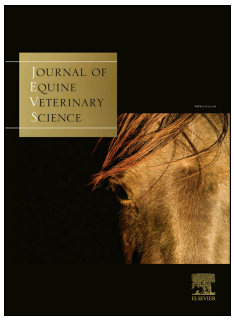
Accepted Manuscript



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

Katarzyna Wolny-Koładka

PII: S0737-0806(17)30696-2

DOI: 10.1016/j.jevs.2017.11.010

Reference: YJEVS 2424

To appear in: *Journal of Equine Veterinary Science*

Received Date: 19 October 2017

Revised Date: 23 November 2017

Accepted Date: 24 November 2017

Please cite this article as: Wolny-Koładka K, 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, *Journal of Equine Veterinary Science* (2017), doi: 10.1016/j.jevs.2017.11.010.

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.

Katarzyna Wolny-Koładka
Department of Microbiology, University of Agriculture in Cracow

Corresponding author: Katarzyna Wolny-Koładka, Department of Microbiology, University of Agriculture in Cracow, Mickiewicza Ave 24/28, 30-059 Cracow, Poland; Phone.: +48 12 662 40 96; Fax:+48 12 633 13 56; ORCID ID: 0000-0003-2994-8842, E-mail: katarzyna.wolny@urk.edu.pl

Abstract

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

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