ANTIMICROBIAL RESISTANCE OF *STAPHYLOCOCCUS* SPP. ISOLATED FROM RIDING-HORSES NASAL MUCOSA

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Abstract. The aim of this study was to analyse *Staphylococcus* species distribution in the upper respiratory tract of riding horses and to determine antimicrobial resistance of the isolated staphylococci. Two hundred and ten isolates of *Staphylococcus* spp. were obtained (78.7 %) from the 267 healthy horses tested. A wide variety of the species was detected while the most prevalent were *S. aureus* (42.9 %), *S. lentus* (14.3 %), *S. pseudintermedius* (13.1 %), *S. cohnii* (9.5 %) and *S. xylosus* (9.5 %). Other species such as *S. sciuri, S. warneri* or *S. vitulinus* were detected only in a few cases. Eighty four isolates (40 %) demonstrated resistance to at least one antimicrobial. The most frequent resistance was demonstrated to penicillin G (66.7 %) and erythromycin (41.6 %). No strains resistant to vanocmycin, daptomycin and co-trimoxazole were detected. Ten isolates demonstrated phenotypical resistance to methicillin although only six of them (two isolates of *S. lentus* and the same amount of *S. sciuri* and *S. vitulinus*) carried the *mec*A gene while the *mec*C gene was not detected. In spite that resistance to macrolides and aminoglycosides was prevalent (35 and 5 isolates respectively), no genes encoding resistance to those classes of antibiotics (*aac(6')-Ie-aph(2')-Ia, aph(3')-III*, *aph(2')-Ic)* and macrolides (*msr*AB*, erm*A and *erm*C) were detected. Resistance to tetracycline was demonstrated in 33.2 % of the isolates attributed to *tet*K and *tet*M genes. This study revealed the first occasion of methicillin-resistant *Staphylococcus* spp. among horses in Lithuania.

Keywords: *Staphylococcus* spp., horse, antimicrobial resistance genes, multidrug resistance