

Species distribution and antimicrobial susceptibility of *Staphylococcus* spp. in the porcine nasal microbiota

Mateusz Ossowski¹, Martyna Kasela², Maria Malm³, Sylwia Andrzejczuk², Weronika Słotwińska^{2*}

1. Department of Animal Hygiene and Environmental Hazards, University of Life Sciences in Lublin, Poland

2. Department of Pharmaceutical Microbiology, Medical University of Lublin, Poland

3. Department of Informatics and Medical Statistics with e-Health Lab, Medical University of Lublin, Poland;

*Student Scientific Circle

mateusz.ossowski@up.lublin.pl

Porcine nasal microbiota constitutes a potential source of drug-resistant pathogens. Although studies have focused mainly on the *Staphylococcus aureus* pathogenicity, other staphylococci species also harbor antibiotic resistance determinants playing an important role in drug-resistance development. We aimed at determining the species profile of staphylococci isolated from porcine nasal microbiota and at evaluation of their antimicrobial susceptibility.

Nasal swabs were collected from 50 pigs from one age group located on a single farm in Poland. After plating, colonies with distinct morphology were isolated and identified with the use of the Vitek 2 Compact System. The antimicrobial resistance profile was determined with the use of automatic or disc diffusion method against oxacillin, gentamycin, linezolid, daptomycin, teicoplanin, vancomycin, tetracycline, tigecycline, rifampicin, trimethoprim/sulfamethoxazole, and tobramycin.

In total, we identified 71 strains of staphylococci represented by 12 different species: *S. equorum* (36.6%), *S. xylosus* (16.9%), *S. chromogenes* (14.1%), *S. arlettae* (7%), *S. lentus* (4.2%), *S. hyicus* (4.2%), *S. kloosii* (4.2%), *S. simulans* (4.2%), *S. gallinarum* (2.9%), *S. saprophyticus* (2.9%), *S. haemolyticus* (1.4%) and *S. carnosus* ssp. *carnosus* (1.4%). Among 42 (84%) pigs colonized with the above-mentioned staphylococci, 21 (50%) were colonized by one strain, 13 (30.1%) by two strains, and 8 (19.1%) by three strains. We detected resistance against tetracycline (70.4%), oxacillin (29.6%), rifampicin (9.9%), tobramycin (4.2%), and linezolid (1.4%).

The high share of resistance to tetracycline and oxacillin in staphylococci from porcine nasal microbiota is alarming and requires further investigation of the resistome.

Keywords: *Staphylococcus*, antibiotics, swine, microbiota