



Introduction

Porcine nasal microbiota constitutes a potential source of drug-resistant pathogens. Recent studies proved that in animals, coagulase-negative staphylococci also harbor antibiotic resistance determinants playing an important role in drug-resistance development.

Aim of the study

The aim of the study was to investigate the species distribution of *Staphylococcus* spp. present in porcine nasal microbiota and to determine the antimicrobial resistance profile of collected strains.

Materials & methods

COLLECTION OF STUDIED MATERIAL

Studied group consisted of 50 male pigs (Yorkshire x Danish Landrace crossbred) from one age group (approx. 2.5 months; 70 kg of weight) in a farm located in Poland (Łódź Voivodeship). Nasal swabs were collected with the use of sterile cotton swabs with a transport medium from both nostrils.

IDENTIFICATION

The swabs were transported to the laboratory of the Department of Animal Hygiene and Environmental Hazards, plated on Mannitol Salt Agar and Baird-Parker Agar, and incubated at 35°C for 24–48 h. After plating, colonies with distinct morphology were isolated and identified with the use of the Vitek 2 Compact System and GP cards.

ANTIMICROBIAL SUSCEPTIBILITY TESTING

The antimicrobial resistance profile was determined with the use of automatic and/or disc diffusion methods against the following antimicrobials: oxacillin, gentamycin, linezolid, daptomycin, rifampicin, vancomycin, tetracycline, tigecycline, ticoplanin, trimethoprim/sulfamethoxazole and tobramycin.

RESULTS

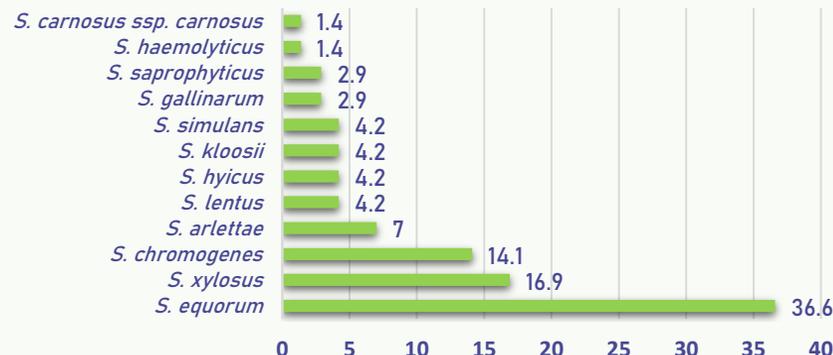


Fig. 1. The percentage of staphylococci isolated from the nasal cavity of pigs (n = 71).



Fig. 2. The percentage of staphylococci resistant to studied antimicrobials.

No resistance was observed for gentamycin, daptomycin, teicoplanin, vancomycin, tigecycline, rifampicin and trimethoprim/sulfamethoxazole (n = 71).

There were 6 strains (8.5%) resistant to three or more classes of antimicrobials (MDR; multidrug-resistant) – *S. kloosii* and *S. xylosus*

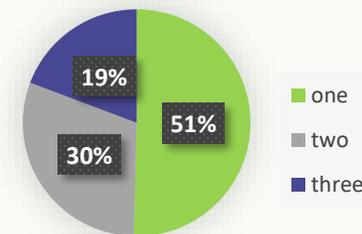


Fig. 3. The percentage of colonization with one, two or three different staphylococci species among colonized pigs (n = 42).

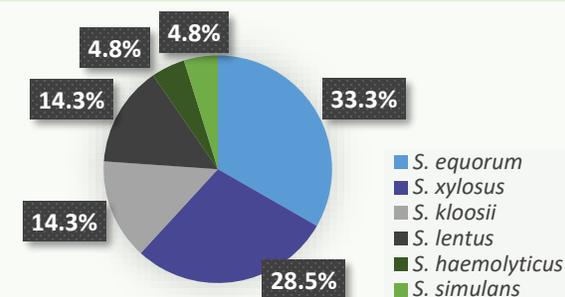


Fig. 4. Resistance to oxacillin according to staphylococci species isolated from pigs (n = 21).

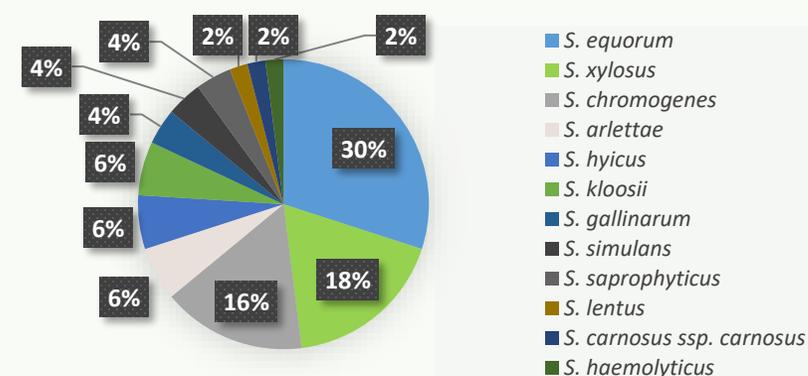


Fig. 5. Resistance to tetracycline according to staphylococci species isolated from pigs (n = 50).

CONCLUSIONS

1. The most common *Staphylococcus* spp. isolated from porcine nasal microbiota are *S. equorum* (36.6%), *S. xylosus* (16.9%) and *S. chromogenes* (14.1%).
2. Staphylococci isolated from pigs are most often resistant to tetracycline (70.4%) and oxacillin (29.6%).
3. The most common staphylococci resistant to tetracycline and oxacillin were *S. equorum* and *S. xylosus*.
4. 8.5% of isolated *Staphylococcus* spp. were classified as MDR.
5. Further research should study the presence of drug-resistance genes in non-susceptible strains of *Staphylococcus* spp. isolated from pigs.

