

Identification and antimicrobial resistance of *Staphylococcus* spp. isolated from a swine waste treatment plant

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Staphylococcus spp. colonize the skin and mucosa of animals and humans and are responsible for several opportunistic infections. The excessive use of antibiotics contributes to the selection of resistant strains. In addition, in livestock, they are used in the treatment and prevention of infections, and as growth promoters. In pig farming, antimicrobials are used in different stages of the production chain. In this work, we analyzed the species distribution and antimicrobial susceptibility profile of *Staphylococcus* species along different points of a swine manure treatment plant. A total of 116 isolates, suspected of belonging to the genus *Staphylococcus*, were isolated using mannitol salt agar. Catalase test and Gram staining were initially performed. All presumptive staphylococcal strains were analyzed by mass spectrometer analysis (MALDI-TOF) for the identification of species. Ten species were identified: *Staphylococcus cohni* (36%, n=30), *Staphylococcus simulans* (22%, n=26), *Staphylococcus saprophyticus* (5%, n=6), *Staphylococcus equorum* (4%, n=5), *Staphylococcus xylosus* (4%, n=5), *Staphylococcus nepalensis* (4%, n=5), *Staphylococcus arlettae* (3%, n=3), *Staphylococcus lentus* (3%, n=3), *Staphylococcus warneri* (0.5%, n=1), *Staphylococcus sciuri* (0.5%, n=1) and *Staphylococcus* spp. (18%, n=21). Nine antimicrobials were tested by the agar diffusion using BrCAST/EUCAST recommendations. The isolates did not show resistance to mupirocin, but they were resistant to other antibiotics tested: chloramphenicol (89%, n=103), erythromycin (75%, n=87), tetracycline (74%, n=86), gentamicin (47%, n=54), ciprofloxacin (41%, n=47), ceftiofur (18%, n=21), sulfamethoxazole-trimethoprim (11%, n=13) and linezolid (1%, n=1). After the determination of the antimicrobial susceptibility profile, we analyzed all genomes of swine staphylococci origin available from public databases to build a pan-resistome with Resfinder 4.1. From that pan-resistome, we chose the most prevalent antimicrobial genes to search in our isolates, by PCR. Of the 87 erythromycin resistant isolates, 16 (18%) carry the *erm(A)* gene and of the 86 tetracycline resistant isolates, 83 (97%) carry the *tet(K)* gene. The other genes are still being tested. The presence of resistant bacteria along a manure treatment plant highlights the potential risk of contamination people in direct contact with these animals and the soil, since the effluent is used as biofertilizer in the surrounding soil.

Keywords: *Staphylococcus*, pig farming, antimicrobial resistance.