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Clonal diversity and antibiotic resistance among coagulase-negative *staphylococci* recovered from birds of prey in Portugal

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The aim of the present study was to evaluate the antibiotic resistance of coagulase-negative staphylococci (CNS) strains, isolated from birds of prey, and their clonal diversity. Briefly, samples from the nasopharynx of all birds of prey were collected when they were admitted into CRAS (wild birds' recovering center from the Veterinary Medical Hospital at UTAD). Swabs were inoculated into BHI broth containing 6.5% NaCl and incubated for 24h at 37°C; then, 150 µL was seeded on MSA (manitol salt agar) and ORSAB [2 mg/L oxacillin]. Presumptive *Staphylococcus* spp. colonies were isolated and identified by microbiological, biochemical and molecular methods. The phenotype of resistance was determined according to CLSI, 2014. Selected CNS strains were analyzed by PFGE to study their clonal diversity. These strains showed susceptibility to 14 of the antibiotics tested and diminished susceptibility against fusidic acid, clindamycin, tetracycline, penicillin and chloramphenicol. The PFGE patterns showed a high genetic heterogeneity among these isolates with the exception of 3 *S. xylosus* that were genetically related, although, from 2 different animal species. Also, we observed that 2 *S. sciuri* recovered from *Strix aluco* and *Milvus migrans* were genetically related. CNS strains from birds of prey also carried genetic determinants to various antibiotics. We observed a high frequency of resistance to fusidic acid, clindamycin, tetracyclines, penicillin and to chloramphenicol. Overall, the results suggest a high rate of clonal diversity among CNS from wild animal populations, which can be a reservoir of some antimicrobial resistance determinants related to the most used antibiotics in veterinary clinical practice.

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