

Evolution of antibiotic resistance of coagulase-negative staphylococci isolated from healthy turkeys in Egypt: First report of linezolid resistance

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Coagulase-negative Staphylococcus (CoNS) species were considered as non-pathogenic organisms for a long time in humans and animals. Recently, they are gaining much attention as causative agents of serious nosocomial infections in humans. This study aimed to determine the prevalence, magnitude of phenotypic antimicrobial resistance and determination of resistance-associated genes among CoNS isolated from turkey farms in northern Egypt.

Two hundred and fifty cloacal swabs were collected from apparently healthy turkeys reared in Egypt. The collected samples were microbiologically investigated and the antibiotic susceptibility was tested.

Thirty-nine CoNS were identified. All isolates were phenotypically resistant to trimethoprim/sulphamethoxazole, penicillin, ceftazidime and fusidic acid. The resistance rates to streptomycin and erythromycin were 97.4%, moxifloxacin and chloramphenicol 94.9%, oxacillin, tigecycline and daptomycin 92.3% and to fosfomycin and tetracycline 89.7%. Thirty-four isolates were resistant to linezolid (87.2%). Low resistance rates (30.8%) were detected for imipenem and vancomycin.

The *erm(C)* gene was identified in all phenotypically resistant isolates to erythromycin whereas two phenotypic resistant isolates possessed three resistance conferring genes *erm(A)*, *erm(B)* and *erm(C)*. The *cfr* and *optrA* genes were detected in 11 (32.4%) and 12 (35.3%) of 34 linezolid-resistant isolates. The *mecA*, *aac-aphD* and *blaZ* genes were identified in 22.2%, 39.4%, and 2.6% of phenotypically resistant isolates to oxacillin, gentamicin and penicillin, respectively. Two different species of CoNS with variable phenotypic and genotypic resistance profiles were isolated from an individual bird.

These findings highlight the potential risk of the increased prevalence of antibiotic-resistant CoNS in healthy turkeys in Egypt.

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