Phenotypical and genotypical antimicrobial resistance of coagulase-negative staphylococci isolated from cow mastitis

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Abstract

The objectives of this study were to determine the prevalence and antimicrobial resistance of coagulase-negative staphylococci (CNS) isolated from dairy cows with subclinical mastitis. Antimicrobial resistance in staphylococci were evaluated by breakpoint values specific to the species (EUCAST). The presence of resistance-encoding genes was detected by multiplex PCR. A total of 191 CNS isolates were obtained. The CNS isolates were typically resistant to penicillin (67.4%), tetracycline (18.9%), and erythromycin (13.7%). CNS isolates (78.0%) were resistant to at least one antimicrobial compound, and 22.0% were multiresistant. The multiresistant isolates were predominantly Staphylococcus chromogenes (28.6%), Staphylococcus warneri (19%) and Staphylococcus haemolyticus (14.3%). According to MIC pattern data, multiresistant isolates showed the highest resistance (p<0.05) rates to penicillin (85.7%), tetracycline (66.7%), and erythromycin (48.2%), but all of them were sensitive to daptomycin, oxacillin, quinupristin/dalfopristin, and vancomycin. S. chromogenes (9.5%), S. haemolyticus (4.8%), and S. capitis ss capitis (2.4%) strains were resistant to methicillin; their resistance to oxacillin and penicillin was more than 8 mg/l. A high rate of resistance to penicillin was linked to a blaZ gene found in 66.6% of the isolated multiresistant CNS strains. Resistance to tetracycline via the tetK (38.1%) gene and penicillin via the mecA (23.8%) gene were detected less frequently. Gene msrAB was responsible for macrolides and lincosamides resistance and detected in 28.6% of the CNS isolates. Antimicrobial resistance genes were identified more frequently in S. epidermidis, S. chromogenes, and S. warneri.

Key words: coagulase-negative staphylococci, mastitis cows, antimicrobial resistance, gene