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Molecular identification of *Enterococcus* spp. associated with subclinical mastitis in goat, cow and camels in Algeria

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Abstract

Enterococcus genus is one of the opportunistic pathogens and responsible for mastitis in dairy animals. This study aimed to investigate the occurrence of enterococci associated with subclinical mastitis in goat, cow and camels in Algeria and to assess their antimicrobial resistance profiles. A total of 374 milk samples from udder quarters were tested for a subclinical mastitis (SCM) using the CMT. The positive samples were subjected to microbiological analysis for identification of *Enterococcus* spp. by biochemical and molecular techniques using 16S rDNA sequencing and phylogenetic analyses. Eight strains of enterococci were tested to their antibiotic sensitivity profiles. The data revealed that 34, 31% of samples showed the presence of SCM, meanwhile *Enterococcus* spp were occurred in 38.9% of positive milk. According to phenotypic criteria, 50 isolates were identified as *E. faecium* 70% (35/50) followed by *E. faecalis* 18% (9/50), 12 % (6/50) were non enterococci. Only eight isolates were confirmed to be *Enterococcus* spp using 16S rDNA sequencing technique. The antibiotic susceptibility showed that 85.5 % and 62.5% of *E. faecium* were resistant to Oxacillin and Penicillin respectively, while most of isolates were susceptible to Ciprofloxacin. In this study, Vancomycin-resistant enterococci (VRE) were found in 37.5% of isolates. Nevertheless, 62.5% of the tested strains displayed multi-drug resistances (MDR) across different patterns. This study highlights virulence and harmfulness of *Enterococcus* strains isolated from subclinical mastitic milk, which suggest continuous inspection and monitoring of dairy animals.

Keywords: Enterococci, 16 rDNA, Antimicrobial resistance, Phylogenetic, Dairy came.