

Antibiotic Resistance of Some *Enterobacteriaceae* Strains Isolated from Bovine in The West of Algeria

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Abstract

The misuse of antibiotics in cattle breeding is a phenomenon that still exists on some farms in the northwest of Algeria. This calls into question the effectiveness of available treatments and threatens human and animal health. The aim of this study is to try to determine the antimicrobial resistance (AMR) patterns of some *Enterobacteriaceae* to antibiotics in healthy cattle. Samples from bovine were taken using sterile swabs on the skin of cattle and different places in the stable and prepared for culture using conventional microbiological techniques. Isolates were identified biochemically using API 20E. In accordance with nccls guidelines, all isolates were identified and analyzed using the Kirby Bauer disk diffusion technique against 20 antibiotic disks. A total of 356 distinct species of *E. coli* were isolated. Twenty two agglutinable *E. coli* isolates with O157 :H7 were found using serotyping. *E. Coli* resistance to nalidixic acid (85.7%), tetracyclin (68.2%), streptomycin (53.5%), nitrofurantoin (75.4%), ampicillin (48.6%), ticarcillin (37.4%), piperacillin (41.8%), and chloramphenicol (19.2%) was highly prevalent when it came to antibiotic susceptibility. Some *Serratia* species present a resistance of 55.9% to nalidixic acid and ofloxacin, 52.3% to ciprofloxacin and 29.54% to streptomycin. *Enterobacter* isolated were resistant to ampicillin, and cefazolin, however no resistance was observed for gentamicin, amikacin and kanamycin. The *Klebsiella* species shows no resistance for gentamicin, amikacin and kanamycin, but 69% ciprofloxacin 42% ofloxacin, and a total resistance to tetracyclin and ampicillin. Resistance to more than four antibiotic classes, was present in 75.6% of the isolates. The PCR technique showed that all the twenty two *E.coli* O157 :H7 carried the *stx2* and the *ehxA* genes, 5 isolate carried *stx1* genes and 3 both *stx1* and *stx2*.

Key Words: Bovine, *Enterobacteriaceae*, Multidrug resistance, *E.coli* O157 :H7.