# **Titre d’article**: Molecular Characterization of Multidrug-Resistant Escherichia coli Isolated from Milk of Dairy Cows with Clinical Mastitis in Algeria

**Abstract :**

 The objective of this study was to investigate the occurrence of multidrug-resistant Escherichia coli in cows with clinical mastitis in 42 different dairy farms located in the Bordj Bou Arreridj region of Algeria. Milk samples were cultured on Columbia blood agar, and isolates were then identified by matrix-assisted laser desorption ionization–time of flight mass spectrometry. In total, 200 samples were screened and 52 E. coli strains confirmed as causative agents were obtained. The antimicrobial susceptibility testing was performed by disk diffusion method. Antibiotic resistance genes, including those conferring resistance to extended-spectrum β-lactamases (i.e., blaTEM, blaSHV, and blaCTX-M), tetracyclines (tetA, tetB, tetC, and tetJ), aminoglycosides [aph(30 ), aac(30 ), aac(60 ), ant, aad, and armA], and quinolones (qnrA and qnrB) were amplified by standard PCR and sequenced when positive. Transferability of resistance genes has been investigated by conjugation experiments and multilocus sequence typing. The most frequently observed resistance was to amoxicillin (86.5%), followed by tetracycline (75%), amoxicillin–clavulanic acid (59.6%), trimethoprim-sulfamethoxazole (36.5%), doxycycline (13.5%), and ciprofloxacin (13.5%). Multidrug resistance was observed in 38.4% of isolates. Genotypic characterization showed that tetA (44.2%) and blaTEM-1 (30.7%) genes were the most prevalent. Screening for plasmid-mediated quinolone resistance genes demonstrated that seven isolates (13.5%) expressed qnrB and one isolate (1.9%) harbored qnrA. In addition, aminoglycoside resistance determinants including aadA1 and aac(3)-Id were detected in seven and two isolates, respectively. Moreover, blaTEM, tetA, tetB, qnrB, and aadA1 were successfully transferred horizontally to transconjugant strains. The multilocus sequence typing revealed the presence of three different sequence types (ST162, ST371, and ST 949).