**TITLE:** *Escherichia coli* ISOLATED FROM BOVINE MILK AND INVESTIGATION OF ANTIMICROBIAL RESISTANCE GENES IN PARAÍBA

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**ABSTRACT**:

*Escherichia coli* represents about 15-20% of infectious bacterial mastitis cases, being the main cause among Gram-negative bacilli, as well as being environmentally ubiquitous, and an interface among humans, animals and environment. The production of carbapenemases enzymes, such as *Klebsiella pneumoniae* carbapenemase is an expected mechanism of resistance to beta-lactams in *E. coli* being responsible for the hydrolysis and inactivation of these antimicrobials. With the increased prevalence of strains carrying carbapenemases there was a reintroduction of polymyxins agents in medical and veterinary medicine to treat infections caused by multidrug-resistant bacteria. However, acquired resistance to polymyxins could be present in mobile genetic elements, *mcr* genes. This study aimed to study the diversity of *E. coli* strains and detect the presence of resistance determinant genes among bovine milk samples from the state of Paraíba. Thus, 15 mL of 20 milk samples were collected in industrial milk tanks of different regions. Subsequently, 200 µL of milk were seeded on MacConkey (MC) agar plates with and without supplementation with ceftriaxone (8 µg/mL), imipenem (1 µg/mL) and colistin (3.5 µg/mL). The identification at species level of *E. coli* was determined by performing biochemical and carbohydrate fermentation tests. The determination of the antimicrobial susceptibility profile was performed using the disk diffusion test following recommendations from the Brazilian committee on antimicrobial susceptibility testing (BrCast). The detection of the $bla_{SPM}$, $bla_{OXA-1}$, $bla_{OXA-10}$, $bla_{ACC}$, $bla_{KPC}$ and *mcr-1* genes were performed using the Polymerase Chain Reaction method followed by gel electrophoresis. The previous data show that among the samples seeded on MC media, 104 Gram-negative bacteria were isolated, of which 19 were identified as *E. coli*. The resistance prevalence were 15,8% for ceftriaxone, ceftazidime, cefotaxime, cefepime, aztreonam and amoxicillin+clavulanate, and 10,5% for imipenem and ertapenem. Were observed presence of $bla_{OXA-1}$ in two isolates and $bla_{ACC}$ in one, other genes were not detected among the analyzed isolates. Therefore, the importance of molecular phenotypic and molecular epidemiological analyzes is highlighted for the detection of the origin and spread of microorganisms, in order to develop preventive strategies to control the dissemination of bacteria resistance mechanisms.

**Keywords:** Enterobacterales, multi-drug resistance, one-health

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