MULTI-DRUG RESISTANT (MDR) *ESCHERICHIA COLI* ORIGINATED FROM CLINICAL AND ENVIRONMENTAL SOURCES IN ISMAILIA-EGYPT

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ABSTRACT

The exaggerated use of antibiotics has led to the selection of new strains of bacteria that resist to antibiotics, a situation which is found in the case of *Escherichia coli* strains. This study was conducted to evaluated the antibiotic resistance profiles of *Escherichia coli* (*E. coli*), isolated from different Clinical and Environmental sources in Egypt. A total of 384 samples from human, animal and environmental sources were collected from different locations in Ismailia, Egypt. *E. coli* isolates (n = 283) were identified by conventional microbiology culture and were phenotypically characterized using biochemical and motility tests. From the overall number of *E. coli* isolates, 31.4% (89/283) were isolated from stools of humans with diarrhea, 17.3% (49/283) from stools of sheep, cattle and chicken with diarrhea, 16.6% (47/283) from urine of humans with urinary tract infection, 17.3% (49/283) from surfaces water, 6.4% (18/283) from sea-food, 6% (17/283) from processed meat products, 3.9% (11/283) from dairy products and 1.1% (3/283) from poultry products (liver). The antibiotic resistance patterns showed that the isolates carried multi-drug resistance (MDR) phenotype to at least four commonly used antibiotics belonging to different classes: Erythromycin (E), Gentamicin (CN), Cefazolin (CZ), Thiampinicol (TP), Vancomycin (VA), Ciprofloxacin (CIP) and Ampicillin (AM).

Keywords: *Escherichia Coli*, Antibiotics, Egypt, MDR.