

Characterization of Antibiotic Resistance in Cultivable Enterobacteriaceae Isolates from Different Ecological Niches in the Eastern Cape, South Africa

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Abstract : Evolution and rapid dissemination of antibiotic resistance from one ecosystem to another has been responsible for wide-scale epidemic and endemic spreads of multi-drug resistance pathogens. This study assessed the prevalence of Enterobacteriaceae in different environmental samples, including river water, hospital effluents, abattoir wastewater, animal rectal swabs and faecal droppings, soil, and vegetables, using standard microbiological procedure. The identity of the isolates were confirmed using matrix-assisted laser desorption ionization-time of flight mass spectrophotometry (MALDI-TOF) while the isolates were profiled for resistance against a panel of 16 antibiotics using disc diffusion (DD) test, and the occurrence of resistance genes (ARG) was determined by polymerase chain reactions (PCR). Enterobacteriaceae counts in the samples range as follows: river water $4.0 \times 10^1 - 2.0 \times 10^4$ cfu/100 ml, hospital effluents $1.5 \times 10^3 - 3.0 \times 10^7$ cfu/100 ml, municipal wastewater $2.3 \times 10^3 - 9.2 \times 10^4$ cfu/100 ml, faecal droppings $3.0 \times 10^5 - 9.5 \times 10^6$ cfu/g, animal rectal swabs $3.0 \times 10^2 - 2.9 \times 10^7$ cfu/ml, soil $0 - 1.2 \times 10^5$ cfu/g and vegetables $0 - 2.2 \times 10^7$ cfu/g. Of the 700 randomly selected presumptive isolates subjected to MALDI-TOF analysis, 129 (18.4%), 68 (9.7%), 67 (9.5%), 41 (5.9%) were *E. coli*, *Klebsiella* spp., *Enterobacter* spp., and *Citrobacter* spp. respectively while the remaining isolates belong to other genera not targeted in the study. The DD test shows resistance ranging between 91.6% (175/191) for cefuroxime and (15.2%, 29/191) for imipenem. The predominant multiple antibiotic resistance phenotypes (MAR_P), (GM-AUG-AP-CTX-CXM-CIP-NOR-NI-C-NA-TS-T-DXT) occurred in 9 *Klebsiella* isolates. The multiple antibiotic resistance indices (MAR_I) the isolates (range 0.17-1.0) generally showed >95% had MAR_I above the 0.2 thresholds, suggesting that most of the isolates originate from high-risk environments with high antibiotic use and high selective pressure for the emergence of resistance. The associated ARG in the isolates include: bla_{TEM} 61.9 (65), bla_{SHV} 1.9 (2), bla_{OXA} 8.6 (9), CTX-M-2 8.6 (9), CTX-M-9 6.7 (7), sul 2 26.7 (28), tet A 16.2 (17), tet M 17.1 (18), aadA 59.1 (62), strA 34.3 (36), aac(3)A 19.1 (20), (aa2)A 7.6 (8), and aph(3)-1A 10.5 (11). The results underscore the need for preventative measures to curb the proliferation of antibiotic-resistant bacteria including Enterobacteriaceae to protect public health.

Keywords : enterobacteriaceae, antibiotic-resistance, MALDI-TOF, resistance genes, MAR_P, MAR_I, public health

Conference Title : ICATAD 2019 : International Conference on Antibiotic Therapy and Antimicrobial Dosing

Conference Location : Rome, Italy

Conference Dates : November 11-12, 2019