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Antibiotic resistance pattern in bacterial isolates obtained from raw water which received treated effluent and treated water in Mafikeng, South Africa

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Problem Statement: Antibiotics are an important group of therapeutic agents used for the treatment of bacterial infections. Until recently, many of the enteric diseases, both bacterial as well as parasitic, in etiology could be treated with inexpensive antimicrobials. But today, the treatment has been made more costly and less effective due to the emergence and widely spread resistant enteric microorganisms. Development of antibiotic resistance in strains of bacteria otherwise sensitive is a major issue in antibacterial therapy. Exposure of bacteria to low doses of an antibiotic naturally selects for the survival of resistant organisms. The spread of these resistant strains of pathogenic bacteria from environment poses problems to treat infections.

Purpose of the study: Present study was designed to isolate indicator bacteria and opportunistic pathogens from surface and drinking water in Mafikeng to determine their antibiotic resistance phenotype.

Methodology: For the bacteriological analysis, organisms were isolated by membrane filtration using appropriate selective media, such as mFC agar, mEndo agar and *Aeromonas* selective media and incubated for 24 hours at appropriate temperatures. Antibiotic susceptibility test was performed using Kirby-Bauer disk diffusion method. DNA from the isolates was extracted using the bacterial DNA extraction kit. The identities of the presumptive *Pseudomonas* and *Aeromonas* were confirmed through amplicons of *gyrB* 222, *toxA* 367 and *ecfX*, 528 gene fragments respectively.

Findings: Multiple antibiotic resistance phenotypes were compiled and large proportion of the environmental isolates were resistant to erythromycin trimethoprim, amoxicillin, streptomycin and neomycin. Predominant multiple antibiotic resistant (MAR) phenotypes-

KF-AP-C-E-OT-K-TM-A

KF-AP-C-E-OT-K-TM-A-NE

KF-AP-E-OT-K-TM-A

Similar types of MAR phenotypes were observed in isolates from different sites.

Conclusion & Significance: The detection of MAR organisms especially *Aeromonas* and *Pseudomonas* species which possessed virulent genes was a cause for concern and this will provide suggestions that could help in controlling of antibiotic resistance.

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