

2nd International Congress on **Bacteriology & Infectious Diseases**

November 17-19, 2014 DoubleTree by Hilton Hotel Chicago-North Shore, USA

Multi-drug resistance in coliforms from a wastewater treatment plant of a community in Lagos, Nigeria

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Antibiotic-resistant bacteria may survive the biological treatment process of wastewater treatment plants and enter the distribution system. This may represent significant reservoir for antibiotic-resistant organisms which could be disseminated in the community. This study was aimed at isolating and identifying bacteria from a wastewater treatment plant and to determine their antibiotic resistance profile. Ten wastewater samples were aseptically collected at different points of a wastewater treatment plant and immediately transferred to the laboratory for microbiological analysis. Isolates were identified using API 20E kit and species were confirmed using ABIS ONLINE software. Identified organisms were assessed for resistance to common antibiotics following Kirby-Bauer disk diffusion method and the Multiple Antibiotic Resistance (MAR) Index was calculated. Thirteen bacterial species were detected from the wastewater samples collected which include *Enterobacter species* (3), *Klebsiella spp.* (3), *Escherichia spp.* (3), *Rahnella aquatilis* (1), *Edwardsiella tarda* (1) and *Buttiauxella ferruginea* (1). The total coliforms ranged from 3.2×10^4 cfu/ml to 2.0×10^2 cfu/ml at the point of discharge to the environment. None of the isolates had 100% susceptibility to all the antibiotics investigated. The most prevalent multiple antibiotic resistance phenotype observed was TET, GEN, COT. The MAR values ranged from 0.16 to 0.83; 92% of the isolates had MAR > 0.2 suggesting their origin from a high risk source of contamination where antibiotics are often used. The presence of antibiotic resistant bacteria in the treatment plant could pose a potential threat to human health as it could get into the food chain.

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