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Genomic and Transcriptomic Analysis of Antibiotic Resistance Genes in Biological Wastewater Treatment Systems Treating Domestic and Hospital Effluents

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Abstract : The discharge of antibiotics and its residues into the wastewater treatment plants (WWTP's) create a conducive environment for the development of antibiotic resistant pathogens. This presents a risk of potential dissemination of antibiotic resistant pathogens and antibiotic resistance genes into the environment. It is, therefore, necessary to study the level of antibiotic resistance genes (ARG's) among bacterial pathogens that proliferate in biological wastewater treatment systems. In the current study, metagenomic and meta-transcriptomic sequences of samples collected from the influents, secondary effluents and post chlorinated effluents of three wastewater treatment plants treating domestic and hospital effluents in Durban, South Africa, were analyzed for profiling of ARG's among bacterial pathogens. Results show that a variety of ARG's, mostly, aminoglycoside, β-lactamases, tetracycline and sulfonamide resistance genes were harbored by diverse bacterial genera found at different stages of treatment. A significant variation in diversity of pathogen and ARGs between the treatment plant was observed; however, treated final effluent samples from all three plants showed a significant reduction in bacterial pathogens and detected ARG's. Both pre- and post-chlorinated samples showed the presence of mobile genetic elements (MGE's), indicating the inefficiency of chlorination to remove of ARG's integrated with MGE's. In conclusion, the study showed the wastewater treatment plant efficiently caused the reduction and removal of certain ARG's, even though the initial focus was the removal of biological nutrients.

Keywords : antibiotic resistance, mobile genetic elements, wastewater, wastewater treatment plants

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