Detection of Pools of Bacteria with Public Health Importance in Wastewater Effluent from a Municipality in South Africa Using Next Generation Sequencing and Metagenomics Analysis

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Abstract

Wastewater effluents are always accompanied with possibilities for human health risks as diverse pathogenic microorganisms are harboured in them, especially if untreated or poorly treated. They allow the release of pathogens into the environment and these may find its way into food cycle. This paper reports the findings of our research work that focused on the characterization of microorganisms from a municipal final wastewater effluent that receives bulk of its spent water from a research farm. High throughput sequencing using Illumina MiSeq apparatus and metagenomics analysis showed a high abundance of microbial genes, which was dominated by Bacteria (99.88%), but also contained Archaea (0.07%) and Viruses (0.05%). Most prominent in the bacterial group is the Proteobacteria (86.6%), which is a major phylum containing wide variety of pathogens, such as Escherichia, Salmonella, Vibrio, Helicobacter, etc. Further analysis showed that the Genus Thauera occurred in largest amounts across all 6 data sets, while Thiomonas and Bacteroides propionicifaciens also made significant appearances. The presence of some of the detected bacteria like *Corynebacterium crenatum* showed degradation and/or fermentation in the effluent, which was evidenced by fouling during sampling. Notable pathogens classified with critical criteria by World Health Organization (WHO) for research and development including *Acinetobacter* sp., *Escherichia coli,* and *Pseudomonas* sp. in the effluent were being released to the environment. Our results suggest a potential influence of wastewater effluent on microbial community structure of the receiving water bodies, the environment as well as possible effects on the individuals exposed to the effluents. The evidences from the results in this study suggest an imminent public health problem that may become sporadic if the discharged effluent is not properly treated. This situation is also a potential contributor of antimicrobial resistance genes to the natural environments.
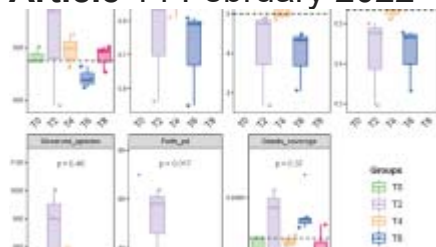
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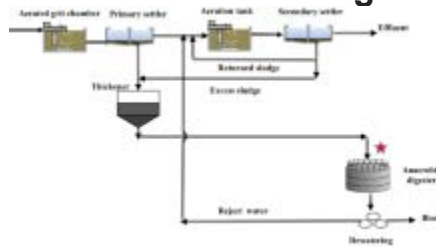
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