



## Environmental resistome risks of wastewaters and aquatic environments deciphered by shotgun metagenomic assembly

MD.Ekwanzala

Florida Campus, Johannesburg, South Africa

### Abstract:

In this paper, we deciphered the core resistome disseminating from hospital wastewater to the aquatic environment by characterising the resistome, plasmidome, mobilome and virulome using metagenomic analysis. This study also elucidated different environmental resistome risks using shotgun-metagenomic assembly. The results showed that clinically relevant taxa were found in assessed matrices (*Salmonella* spp., *Acinetobacter* spp, *Escherichia-Shigella* spp., *Pseudomonas* spp., *Staphylococcus* spp. and *Vibrio* spp.). For the plasmidome, we found 249 core plasmidome sequences that were shared among all assessed matrices. The core mobilome of 2 424 mobile genetic elements shared among all assessed matrices was found. Regarding the virulome, we found 148 core virulence factors shared among all assessed samples, and the core virulome content was consistently shared across the most abundant bacterial genera. Although influent of wastewater showed considerable higher relative bacterial abundance ( $P = 0.008$ ), hospital wastewater showed significant higher environmental resistome risk scores against all other assessed matrices, with an average of 46.34% ( $P = 0.001$ ). These results suggest hospital wastewater, effluent and sewage sludge should be subjected to stringent mitigating measures to minimise such dissemination.

### Biography:

Mutshiene.D.Ekwanzala is a fresh scholar and an erudite research enthusiast. He received his first degree in Microbiology from Analysis of swabs and water in Benoni Area South Africa. Doctor of Philosophy (PhD)Field Of StudyWater



Science and Technology Dates attended or expected graduation 2017 - 2019. Activities and Societies: Antimicrobial resistance, metagenomics, NGS, Whole genome sequencing, Biological network Analysis, Phylogenetics, Bioinformatics, Biological App development.

### Recent Publications:

1. Phylogenomic analysis of vancomycin-resistant *Pedococcus acidilactici* and *P. pentosaceus* isolated from the environment
2. Systematic review in South Africa reveals antibiotic resistance genes shared between clinical and environmental settings
3. Options for Microbiological Quality Improvement in African Households
4. Genetic relatedness of faecal coliforms and enterococci bacteria isolated from water and sediments of the Apies River, Gauteng, South Africa

[Webinar on Vaccine Research and Development, December 13, 2020](#)

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