

**BIODIVERSITY OF *SALMONELLA* STRAINS ISOLATED FROM SELECTED
WATER SOURCES AND WASTEWATER DISCHARGE POINTS IN THE
EASTERN CAPE PROVINCE OF SOUTH AFRICA**

BY

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SCIENCE (MICROBIOLOGY)**

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DECLARATION

I, NWABISA MAFU hereby declare that the work on which this dissertation is based, is original (except where acknowledgements indicate otherwise) and that neither the whole work nor any part of it has been, or is being submitted for another degree at this university or tertiary educational institution or examining body.

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GENERAL ABSTRACT

In this study, the diversity of forty *Salmonella* isolates from selected drinking water and wastewater sources in the Eastern Cape Province of South Africa was assessed using parameters such as protein and lipopolysaccharide profile analysis, DNA fingerprinting and antibiotic susceptibility profile as test indices. Wastewater samples from Amalinda, Shornville and Fort Hare wastewater plants, and water samples from Gogogo and Tyume rivers were collected on ice and *transported* to the laboratory of the department of Microbiology and Biochemistry, University of Fort Hare for processing. The DNA dendograms of *Salmonella* and the applied UPGMA revealed 4 similarity groups of the strains. Most of the strains recovered from Amalinda, Shornville, Fort Hare wastewater plants, Gogogo and Tyume rivers show a high percentage of genetic similarity. On the other hand, protein dendograms of *Salmonella* isolates revealed 2 similarity groups which varied widely. Also, the lipopolysaccharide dendograms revealed three similarity groups with the first similarity groups showing a very high relatedness between strains from different water sources. The second similarity group included 16 strains which formed a rather homogenous group, and the third similarity group formed a distinct group. Of the seven antibiotics and sulfonamides tested against the *Salmonella* species, five namely, neomycin, chloramphenicol, kanamycin, streptomycin and cotrimoxazole were significantly inhibitory, while the bacteria showed considerable resistance to doxycycline and sulphamethoxazole. Our results based on restriction digestion, SDS/PAGE and dendogram construction show that there is a high similarity between the forty *Salmonella* strains studied, and that these methods are valuable tools for evaluating the relatedness of

Salmonella species. Our observations have proffered a veritable reference point on the diversity of *Salmonella* strains in the studied area

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