

**PREVALENCE AND ANTIBIOTIC RESISTANCE PATTERNS
OF *Aeromonas* SPECIES FROM DRINKING WATER IN
RURAL HOUSEHOLDS' CONTAINERS IN VHEMBE
DISTRICT OF SOUTH AFRICA.**

by

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ABSTRACT

Aim of the study: The aim of this study was to determine the prevalence and antibiotic resistance patterns of *Aeromonas* species from drinking water collected from rural households' drinking water containers in rural areas of Vhembe district, South Africa.

Methods: 100 drinking water and biofilm samples were collected from households' storage drinking water storage containers in Ngudza and Dzingahe rural villages in Vhembe district and analysed for the presence of *Aeromonas* spp. Membrane filtration technique was used for the isolation of *Aeromonas* species. API 20E biochemical tests were used to identify isolates to *Aeromonas* species level based on their biochemical characteristics and 16S rRNA gene sequencing method was used to confirm the identities of *Aeromonas* based on their genotypic content. Haemolysin production on blood agar was performed to determine haemolytic activity of the isolates. The virulence genes targeted to determine potential pathogenic ability of the isolates include *asa1*, *cylA*, *gelE* and *hyl*. The antibiotic resistance patterns of the isolates were determined using the Kirby Bauer disk diffusion method.

Results: *Aeromonas* prevalent in accordance to API 20E biochemical identification system was shown in 73 (44%) of the drinking water isolates and 45 (54%) of biofilm isolates. 15% of the drinking water and 23% biofilm *Aeromonas* prevalent was confirmed by 16S rRNA sequencing molecular identification method. β haemolytic activity was displayed in 57% of all isolates (of which 40% were biofilm and 17% were drinking water). α haemolytic activity was displayed in 43% (of which 20% were biofilm and 23% were drinking water) isolates. None of the isolates displayed gamma haemolytic activity in all confirmed isolates. Gelatinase gene (*gelE*) was detected in 67% out of which 20% was of drinking water and 47% of biofilm isolates. Aggregation substance (*asa1*) was observed in 50% out of which 17% was from drinking water and 33% biofilm from isolates. Cytolysin (*cylA*) and hyaluronidase (*hyl*) genes were not detected in both drinking water and biofilm isolates. Ampicillin, Amoxicillin and Erythromycin were highly resistant to all tested isolates. The most dominant antibiotic phenotype in this study was AP-A-C-E-KF-OT.

Conclusion: The presence of *Aeromonas* spp. and virulence factors from households' drinking water signifies a health risk to the community. High level of antibiotic resistance and even multidrug resistance patterns observed in this study to antibiotics commonly used for treatment of bacterial infections lessen the choice of antibiotics used for treatment of associated infections and thus increases public health risk.

Keywords: *Aeromonas* spp., drinking water, biofilms, and antibiotic resistance patterns.