

Antibiotic resistant bacteria and -genes in raw water, and the implications for drinking water production

Rinaldo Kritzinger

North-West University, South Africa

Abstract

Antibiotic resistance threatens the success of modern medicine. Antibiotic resistant bacteria in drinking water distribution systems (DWDS) in South Africa has recently been demonstrated. The aim of this study was thus to determine the general drinking water quality and antibiotic resistance profiles of isolated heterotrophic bacteria in two DWDS in South Africa. Samples were collected in 2016 and 2017 and included raw water, treated water and sampling points in the distribution water. Selected physico-chemical properties were measured for each sample. Heterotrophic plate count (HPC) bacteria were enumerated and subjected to the Kirby Bauer disc diffusion method for antibiotic susceptibility tests. 16S rRNA gene sequencing was used to identify the bacteria. The potential pathogenicity of isolates was determined by testing for the production of haemolysins, proteinase, lecithinase, lipase and DNase. The physico-chemical properties mostly complied to the SANS 241 (2015) except for the turbidity and nitrite levels that were very high. Identification of HPC isolates showed that *Bacillus* spp. represented more than 30% of HPC bacteria in the raw water and more than 70% in drinking water at both DWTP. 47% - 100% of the isolates showed resistance against ampicillin, cephalothin, penicillin and trimethoprim. Antibiotic resistance increased from the raw water into the drinking water. The average multiple antibiotic resistance (MAR) index showed values higher than 0.2 which indicates antibiotic pollution. 76% of isolates tested positive for haemolysins, proteinase and lecithinase whereas between 19% and 50% of the isolates tested positive for lipase and DNase. The presence of antibiotic resistant bacteria in drinking water is prevalent together with the possibility and potential to be pathogenic.

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Biography

Rinaldo Kritzinger has completed his MSc in Microbiology in 2018 at the North-West University. He is currently self-

employed.