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Genetic characterization of antibiotic resistant *Enterococcus faecalis* isolated from groundwater in North West Province, South Africa

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Interococcus species are commercial organism usually inhabit the gastrointestinal tract of humans and animals. They are the Eindicators of faecal contamination in water and food and mostly enter into host through faecal-oral route. The presence of some pathogenic strains of Enterococci specifically vancomycin resistant Enterococcus faecalis cause nosocomial infection which become more prevalent in recent years and make situation more worse. In South Africa, mostly people in rural areas have no access to portable water and they depend on untreated water source. Therefore, they are at high risk of exposure to pathogenic microbes. Keeping this in view, present study was conducted to determine the presence of vancomycin resistant Enterococcus faecalis from the underground water from North West Province, South Africa. Enterococci were isolated from 60 borehole tap water samples on Bile Esculin agar. The presumptive isolates were analysed for the characteristics of *Enterococcus* faecalis using preliminary (Gram staining, catalase test, growth in 6.5% NaCl broth and haemolysis) and confirmatory (species specific 16S rRNA and ddl E. faecalis gene specific PCR) tests. The screened isolates were further subjected to antimicrobial susceptibility for 13 different antibiotics by standard disk diffusion method. Also, these isolates were screened for the presence of vancomycin resistant genes (vanA and vanB) and transposable elements (Tn1546 and Tn1547). A total of 253 presumptive isolates were obtained on Bile Esculin Agar and analysed for characteristics of Enterococcus faecalis using preliminary and confirmatory tests. A molecular typing confirmed 122 isolates as Enterococcus faecalis which were further screened for antimicrobial susceptibility. A large proportion of the isolates were multiple antibiotic resistant and showed resistance to vancomycin, penicillin, amoxicillin, ampicillin, tetracycline and erythromycin. The presence of vanB gene was observed in 83 isolates followed by 63 isolates harbouring vanA gene. Only 27 isolates which harbour vanA showed the presence of Tn1546 whereas none of the *vanB* positive isolates showed the presence of *Tn1547*.

Conclusions: This study showed the presence of vancomycin resistant *E. faecalis* (multiple antibiotic resistant) from the underground tap water which is a cause of concern. Therefore, there should be a regular surveillance to monitor antibiotic resistant bacteria to prevent its spreading in nature. Further, detailed molecular study is required to know the deep insight into the genetic jugglery in these bacteria as in the present study a high level incompatibility between phenotypes and genotypes were observed.

Biography

Collins Njie Ateba has completed his PhD from the North West University - South Africa. He also received professional training in the Centre for Medical Genetics, Yerevan State University, Yerevan – Armenia in 2006 in the Department of Microbiology- Tartu University Tartu – Estonia in 2007 and the Lethbridge Research Station – Lethbridge Alberta, Canada in 2014. He is currently an Associate Professor in the Department of Biological Sciences, Microbiology Division, North West University –Mafikeng Campus and is head of the Water, Food Safety and Phage Therapy/Biocontrol Research Laboratory. He is actively involved in research training and lecturing at both undergraduate and postgraduate levels. He has been serving as a host mentor for the DST/NRF internship program from 2011 till date. He has published more than 30 papers in reputed journals and serving as an Editorial Board Member of repute. He has presented research papers in a number of conferences locally and internationally.

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