

The impact of physico-chemical water quality parameters on bacterial diversity in the Vaal River, South Africa

Karen Jordaan and Cornelius Carlos Bezuidenhout*

School of Biological Sciences, Subject Group: Microbiology, North-West University, Potchefstroom Campus,
Private Bag X6001, Potchefstroom 2520, South Africa

ABSTRACT

This study aimed to identify bacterial community structures in the Vaal River using PCR-DGGE (polymerase chain reaction denaturing gradient gel electrophoresis) and high-throughput sequencing. The impact of physico-chemical characteristics on bacterial structures was investigated through multivariate analysis. Samples were collected from 4 sampling stations along the Upper Vaal River during winter (June 2009) and summer (December 2010). Physico-chemical analysis was conducted on-site. Additional physico-chemical data were obtained from statutory bodies. DNA was directly isolated from water samples and PCR amplified using universal bacterial primer pairs. PCR products were subjected to DGGE fingerprinting and high-throughput sequencing, followed by Shannon-Weaver diversity calculations, cluster analysis and multivariate analysis. Physico-chemical parameters did not exceed the prescribed South African water quality standards for domestic use, aquatic ecosystems, livestock watering and irrigation. DGGE banding patterns revealed similar bacterial community structures for 3 of the 4 sampling stations. PCA and RDA indicated that pH, water temperature and inorganic nutrient concentrations could be used to explain changes in bacterial community structures. High-throughput sequencing data showed that bacterial assemblages were dominated by common freshwater groups: Cyanobacteria, Alphaproteobacteria, Betaproteobacteria, Gammaproteobacteria, Bacteroidetes and Actinobacteria. Other freshwater phyla such as Deltaproteobacteria, Epsilonbacteria, Acidobacteria, Verrucomicrobia, Firmicutes, Fusobacteria, Flavobacteria and Fibrobacteres were found in low proportions. This study provides an overview of the dominant bacterial groups in the Upper Vaal River and the impact of environmental changes on bacterial diversity.

Keywords: Vaal River, bacterial community structures, 16S rDNA PCR-DGGE, high-throughput sequencing, multivariate analysis

INTRODUCTION

Socio-economic growth and development of the Vaal River require continuous augmentation of this water resource to meet the growing water requirements of communities in Gauteng, the Free State, North West and Northern Cape provinces (DWAF, 2009b). Water quality has drastically deteriorated due to constant disposal of industrial and domestic waste into the river. Salinisation, eutrophication and microbiological pollution are currently the main problems affecting the water quality (DWAF, 2009a). The Department of Water Affairs and Forestry (DWAF) of South Africa, in line with the South African National Water Act (NWA), Act No. 36 of 1998, stipulated regulatory guidelines and criteria a water system must meet to ensure that the country's water resources are fit for use. A structured biomonitoring programme was implemented by the DWAF in 2009 to determine the exact sensitivity and health status of the Vaal River (DWAF, 2009a). Criteria routinely monitored to ensure sustainability, optimal water use and protection of the water resource include: physico-chemical characteristics, stream flow, discharge loads and microbiological pollutants, in particular, *Escherichia coli*

(DWAF, 2009a; 2009b). The detection of *Escherichia coli* only indicates the presence of faecal contamination and not necessarily the degree of industrial pollution. Therefore, in-depth studies on the microbial communities in the Vaal River are essential to understand the microbial processes underlying secondary pollution and changes in the physico-chemical quality of water.

DGGE has been applied in numerous research studies involving the assessment of microbial diversity of rivers, streams, lakes and sediment, to determine the water quality of the resource (De Figueiredo et al., 2010; Essahale et al., 2010; De Figueiredo et al., 2011; Haller et al., 2011). This method opened up new avenues of research on the diversity of microorganisms present in complex aquatic environments. Currently, metagenomic analysis of microbial ecology, such as high-throughput sequencing (HTS), has been the focus of several environmental studies such as soil, (Lemos et al., 2011), freshwater lakes (Marshall et al., 2008) and deep sea microbiota (Sogin et al., 2006). Metagenomic analysis provides extensive information on community structure and composition (Kakirde et al., 2010). In addition, phylogenetic and functional analyses of microorganisms can be determined at community level (Cowan et al., 2005).

The objectives of this study were (i) to identify the bacterial community structures in the planktonic phase of the Vaal River using 16S rDNA PCR-DGGE and high-throughput sequencing, and (ii) determine the impact of physico-chemical characteristics on bacterial community structures using principle component analysis (PCA) and redundancy analysis (RDA).

This paper was originally presented at the 2012 Water Institute of Southern Africa (WISA) Biennial Conference, Cape Town, 6–10 May 2012.

* To whom all correspondence should be addressed.

+27 18 299-2315; fax: +27 18 299-2330;

e-mail: carlos.bezuidenhout@nwu.ac.za

<http://dx.doi.org/10.4314/wsa.v39i3.7>

Available on website <http://www.wrc.org.za>

ISSN 0378-4738 (Print) = Water SA Vol. 39 No 3 WISA 2012 Special Edition 2013

ISSN 1816-7950 (On-line) = Water SA Vol. 39 No 3 WISA 2012 Special Edition 2013