ABSTRACT

The provision of safe and sanitary water is a constitutional right and above all, a necessity of life. As a result of the rapid urbanisation and the past policies of apartheid, a large population of South Africa dwell in informal settlements, where there is very little hope of development, as the government does not possess the resources that are necessary for a full-scale sanitation programme. Therefore, on-site treatments have been considered to provide sanitation in these dense peri-urban areas. The anaerobic baffled reactor (ABR) is one such sanitation system. This reactor utilises the phenomenon of anaerobic digestion to degrade substrates.

One of the major disadvantages of any anaerobic treatment processes is the extreme sensitivity of the bacterial communities, thus inducing slow recovery rates following toxic shocks. Therefore, an understanding of these microbial consortia is essential to effectively control, operate and optimise the anaerobic reactor. Fluorescence *in situ* hybridization and DNA sequencing techniques were applied to determine the microbial consortium, as well as their reactions to daily operating conditions. With an understanding of these populations and their responses to perturbations within the system, it is possible to construct an anaerobic system that is successful in its treatment of domestic wastewater.

In situ hybridizations were conducted for three operating periods, each characterised by a specific flow rates. Results showed Eubacterial population dominance over the Archaeal population throughout both of the operating periods investigated. However, these cells cumulatively consisted of 50% of the total biomass fraction. Group-probes utilised revealed a high concentration of fermentative acidogenic bacteria, which lead to a decrease in the pH values. It was noted that the ABR did not separate the acidogenic and methanogenic phases, as expected. Therefore, the decrease in pH further inhibited the proliferation of Archaeal acetoclastic methanogens, which were not present in the second operating period. DNA sequencing results revealed the occurrence of the hydrogenotrophic *Methanobacterium* and *Methanococcus* genera and confirmed the presence of *Methanosarcina.* Sequencing of the bacterial DNA confirmed the presence of the low G+ C Gram Positives (*Streptococcus*), the high G+C Gram Positives (*Propionibacterium*) and the sulfate reducing bacteria (*Desulfovibrio vulgaris*). However, justifications were highly subjective due to a lack of supportive analytical data, such as acetate, volatile fatty acids and methane concentrations. Despite this findings served to add valuable information providing details on the specific microbial groups associated with ABR treatment processes.