

Occurrence of diarrhoeagenic *Escherichia coli* virulence genes in water and bed sediments of a river used by communities in Gauteng, South Africa

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ABSTRACT:

In most developing countries, especially in Southern Africa, little is known about the presence of diarrhoeagenic *Escherichia coli* (DEC) pathotypes in riverbed sediments. The present study sought to investigate the presence of DEC virulence genes in riverbed sediments of the Apies River, a river used by many communities in Gauteng, South Africa. Water and sediment samples were collected from the river between July and August 2013 (dry season) and also between January and February 2014 (wet season) following standard procedures. Isolation of *E. coli* was done using the Colilert[®]-18 Quanti-Tray[®] 2000 system. DNA was extracted from *E. coli* isolates using the InstaGene[™] matrix from Bio-Rad and used as template DNA for real-time PCR. Water pH, temperature, dissolved oxygen, electrical conductivity and turbidity were measured in situ. Over 59% of 180 samples analysed were positive for at least one of the seven DEC virulence genes investigated. The *eaeA* gene was the most isolated gene (29.44%) while the *ipaH* gene the least isolated (8.33%). The *ipaH* gene ($p = 0.012$) and the ST gene (*stIa*, $p = 0.0001$, and *stIb*, $p = 0.019$) were positively correlated with temperature. The detection of diarrhoeagenic *E. coli* virulence genes in the sediments of the Apies River shows that the sediments of this river might not only be a reservoir of faecal indicator bacteria like *E. coli* but also pathogenic strains of this bacterium. These organisms could represent a public health risk for poor communities relying on this water source for various purposes such as drinking and recreational use. There is therefore an urgent need to monitor these DEC pathotypes especially in areas without adequate water supplies.