

Low prevalence of antibiotic-resistant gram-negative bacteria isolated from rural south-western Ugandan groundwater

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Abstract

The objective of this study was to determine antibiotic resistance patterns and specific resistance genes in Gram-negative enteric bacteria recovered from 42 different drinking water sources servicing 2 rural villages in south-western Uganda. These water sites were prone to contamination by both human and cattle activity. Of the 52 isolates examined, 26 carried antibiotic resistance genes with 25 being ampicillin resistant, 21 carrying the *bla*_{TEM} gene, and no isolate carrying genes coding for extended-spectrum β -lactamases. Twelve isolates were tetracycline resistant and these bacteria carried between 1 and 3 different *tet* genes, with the *tet*(A) gene the most common. Six isolates carried the macrolide resistance *mef*(A) and/or the macrolide-lincosamide-streptogramin B resistance *erm*(B) genes. Four isolates carried the *sulI* gene, and 4 isolates carried the *sulI* and *intI* genes indicating the presence of Class 1 integrons. The Ugandan isolates in this study had lower than expected carriage rates of antibiotic and multi-drug resistance genes, carriage of Class 1 integrons and lacked genes coding for extended-spectrum β -lactamases as compared to antibiotic resistance carriage in clinical African isolates.

Keywords: drinking water, antibiotic resistance, resistance genes, Gram-negative, conjugal transfer