

Virulence and antimicrobial resistance genes are enriched in the plasmidome of clinical *Escherichia coli* isolates compared with wastewater isolates from western Kenya.

Abstract

Many low-middle income countries in Africa have poorly-developed infectious disease monitoring systems. Here, we employed whole genome sequencing (WGS) to investigate the presence/absence of antimicrobial resistance (AMR) and virulence-associated (VA) genes in a collection of clinical and municipal wastewater *Escherichia coli* isolates from Kakamega, west Kenya. We were particularly interested to see whether, given the association between infection and water quality, the isolates from these geographically-linked environments might display similar genomic signatures. Phylogenetic analysis based on the core genes common to all of the isolates revealed two broad divisions, corresponding to the commensal/enterotoxigenic *E. coli* on the one hand, and uropathogenic *E. coli* on the other. Although the clinical and wastewater isolates each contained a very similar mean number of antibiotic resistance-encoding genes, the clinical isolates were enriched in genes required for in-host survival. Furthermore, and although the chromosomally encoded repertoire of these genes was similar in all sequenced isolates, the genetic composition of the plasmids from clinical and wastewater *E. coli* was more habitat-specific, with the clinical isolate plasmidome enriched in AMR and VA genes. Intriguingly, the plasmid-borne VA genes were often duplicates of genes already present on the chromosome, whereas the plasmid-borne AMR determinants were more specific. This reinforces the notion that plasmids are a primary means by which infection-related AMR and VA-associated genes are acquired and disseminated among these strains.

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