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Non-human primates in the Gambia harbour human-associated pathogenic *Escherichia coli* strains 🔓

Ebenezer Foster-Nyarko[1], Nabil-Fareed Alikhan[1], Anuradha Ravi[1], Gaëtan Thilliez[1], Nicholas Thomson[1], David Baker[1], Gemma Kay[1], Jennifer D. Cramer[2], Justin O'Grady[1], Martin Antonio[3], Mark Pallen[1]

➕ View Affiliations

Increasing contact between humans and non-human primates provides an opportunity for the transfer of potential pathogens or antimicrobial resistance between different host species. We have investigated genetic diversity and antimicrobial resistance in *Escherichia coli* isolates from a range of non-human primates dispersed across the Gambia: patas monkey (n=1), western colobus monkey (n=6), green monkey (n=14) and guinea baboon (n=22). From 43 stools, we recovered 99 isolates. We performed Illumina whole-genome shotgun sequencing on all isolates and nanopore long-read sequencing on isolates with antimicrobial resistance genes. We inferred the evolution of *E. coli* in this population using the EnteroBase software environment. We identified 43 sequence types (ten of them novel), spanning five of the eight known phylogroups of *E. coli*. Many of the observed sequence types and phylotypes from non-human primates have been associated with human extra-intestinal infection and carry virulence characteristics associated with disease in humans, particularly ST73, ST217 and ST681. However, we found a low prevalence of antimicrobial resistance genes in isolates from non-human primates. Hierarchical clustering showed that ST442 and ST349 from non-human primates are closely related to isolates from human infections, suggesting recent exchange of bacteria between humans and monkeys. Our results are of public health importance, considering the increasing contact between humans and wild primates.

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