



# ACCESS MICROBIOLOGY

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## Gambian poultry isolates from hyperendemic group of AMR *Escherichia coli* strains in sub-Saharan Africa

Ebenezer Foster-Nyarko<sup>1</sup>, Nabil-Fareed Alikhan<sup>1</sup>, Anuradha Ravi<sup>1</sup>, Nicholas Thomson<sup>1</sup>, Sheikh Jarju<sup>2</sup>, Arss Secka<sup>3</sup>, Martin Antonio<sup>2</sup>, Mark J. Pallen<sup>1</sup>

 View Affiliations

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Chickens and guinea fowl are commonly reared in Gambian homes as affordable sources of protein. Using standard microbiological techniques, we obtained 68 caecal isolates of *Escherichia coli* from ten chickens and nine guinea fowl in rural Gambia. After Illumina whole-genome sequencing, 28 sequence types were detected in the isolates (four of them novel), of which ST155 was the most common (22/68, 32%). These strains span four of the eight main phylogroups of *E. coli*, with phylogroups B1 and A being most prevalent. Nearly a third of the isolates harboured at least one antimicrobial resistance gene, while most of the ST155 isolates (14/22, 64%) encoded resistance to  $\geq 3$  classes of clinically relevant antibiotics, as well as putative virulence factors, suggesting pathogenic potential in humans. Furthermore, hierarchical clustering revealed that several Gambian poultry strains were closely related to isolates from humans. Although the ST155 lineage is common in poultry from Africa and South America, the Gambian ST155 isolates sit within a tight genomic cluster (100 alleles difference) of strains from poultry and livestock in sub-Saharan Africa (the Gambia, Uganda and Kenya). Continued surveillance of *E. coli* and other potential pathogens in rural backyard poultry from sub-Saharan Africa is warranted.

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