

Integrated One Health Genomic Evidence of Carbapenem-Resistant *Escherichia coli* Transmission Across Food, Clinical, and Sewage Sources in Hong Kong

Iain Chi-Fung NG*, Ivan Tak-Fai WONG, Jake Siu-Lun LEUNG, Franklin Wang-Ngai Chow, Polly Hang Mei Leung, Gilman Kit-Hang SIU

Department of Health Technology and Informatics, The Hong Kong Polytechnic University, Hong Kong Special Administrative Region, China

Background: The World Health Organization has classified carbapenem-resistant Enterobacterales as a critical priority pathogen because of limited treatment options and severe clinical outcomes. Over the past 16 years, carbapenem-resistant *Escherichia coli* (CR-E. coli) has evolved from a rarely detected resistance phenotype into an emerging public health concern in Hong Kong. We used a One Health surveillance approach to investigate the genomic relatedness of CR-E. coli from food, clinical, and sewage sources and to assess potential transmission at the cross-sector transmission.

Methods: From 2022 to 2025, 4,917 food samples and, from 2024 to 2025, 165 sewage samples were collected across Hong Kong for CR-E. coli surveillance. In addition, 186 clinical isolates were included for comparative analysis. Species identification used MALDI-TOF MS, antimicrobial susceptibility testing used disk diffusion, and whole-genome sequencing used Oxford Nanopore, followed by MLST, resistance gene detection, plasmid typing, cgSNP phylogeny, and comparative genomic analysis.

Results: A total of 561 CR-E. coli isolates were recovered from food samples. Prevalence was highest in pork (30.8%) and chicken (29.0%), followed by beef (9.1%) and ready-to-eat foods (0.4%). Predominant food-associated lineages were ST69, ST10, ST155, ST101, ST93, and ST48, with ST69 the most common. Phylogenetic analysis of ST69 isolates from food, clinical, and sewage sources (n=72; 43 food, 26 clinical, 3 sewage) identified three clusters, including one containing isolates from all three sectors within a 13-SNP threshold. blaNDM-5 was the major carbapenemase gene, and shared resistance genes and Inc11 plasmids supported both clonal and plasmid-mediated dissemination.

Conclusion: CR-E. coli ST69 in Hong Kong showed substantial genetic overlap across food, clinical, and sewage sources, supporting cross-sector dissemination through clonal spread and plasmid-mediated transfer. These findings highlight the public health relevance of integrated genomic AMR surveillance within a One Health framework.

Keywords: Carbapenem-resistant *Escherichia coli*, One Health surveillance, Antimicrobial resistance, Whole-genome sequencing, E.coli ST69, blaNDM-5