



Tropentag, September 14-16, 2022, hybrid conference

“Can agroecological farming feed the world?
Farmers’ and academia’s views”

One Health: Epidemiology of antimicrobial resistance in children, food and livestock in a low-income setting

NOAH OKUMU¹, JOSEPH NGERANWA², OLIVER CUMMING³, ELIZABETH COOK¹

¹*International Livestock Research Institute (ILRI), Animal and Human Health, Kenya*

²*Kenyatta University, Kenya*

³*London School of Hygiene and Tropical Medicine, United Kingdom*

Abstract

In developing countries, foodborne disease (FBD) is a threat to human health with children under 2 years particularly vulnerable. This is so because from 6 months, they begin to consume weaning foods and water that may be contaminated. This often causes diarrhea, the second leading cause of infant mortality after pneumonia. Bacteria such as *Escherichia coli* and *Salmonella* spp. have been implicated in FBD as the major causes of illness and death in children, often requiring therapeutic interventions.

Inappropriate use of antimicrobials in human and animal health, inadequate water, sanitation and hygiene and poor infection control in hospitals and clinics select for antimicrobial resistance (AMR) in these pathogens, transferrable between people, animals and the environment. Antimicrobial resistance is one of the biggest threats to global health, food security and development. Globally, 700,000 deaths are attributable to drug-resistant infections every year with low-income countries being the most affected. Increasing rates of AMR in these pathogens will limit therapeutic options in the future.

In this study, we isolated and identified *E. coli* pathotypes and *Salmonella* spp. from stool collected from 541 children (6–24 months), 296 livestock, and 860 food samples (from farm-to-fork) from a low-income peri-urban setting in Nairobi, Kenya. We are currently pathotyping isolates and testing for their sensitivity to commonly used/prescribed antibiotics and profiling their resistome by Polymerase Chain Reaction (PCR) and Whole Genome Sequencing (WGS). Results will be used to determine the phylogeny and virulome amongst epidemiologically related isolates to understand spread and pathogenic potential and the burden of AMR in children.

This project will provide valuable data on strain diversity and circulating *Salmonella* and *E. coli* clones in Kenya. Information on AMR in childhood diarrheal infections will contribute to AMR surveillance in Kenya and inform treatment guidelines. Further, detected AMR reservoirs in food and in contact animals may help evaluate risks to children, information that can be used to design interventions.

Keywords: Antimicrobial resistance, diarrhea, food-borne disease