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Antimicrobial resistance at the human–animal interface in the Pastoralist Communities of Kasese District, South Western Uganda

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Intensive usage of antimicrobials in the management of animal diseases leads to selection for resistance among microorganisms. This study aimed to assess antimicrobial use and to describe factors associated with the transmission of antimicrobial resistance between humans and animals in pastoralist communities of Kasese district. A mixed-methods approach was employed in this study. Rectal swabs were collected from the participants and cattle and transported in Carry–Blair transport medium to the laboratory within 24 h of collection for culture and sensitivity to confirm carriage of multi-drug resistant bacteria. In-depth interviews were conducted among veterinary officers, veterinary drug vendors, human health facility in-charges in both public and private health facilities, and operators of human pharmacies and drug shops. Carriage of multi-drug resistant bacteria among humans was 88 (93%) and 76(80%) among cattle. Consumption of lakeshore water and carriage of multi-drug resistant bacteria in cattle were associated with carriage of multi-drug resistant bacteria in the human population. The prevalence of multi-drug resistance among organisms isolated from both humans and animals was high. There is a high likelihood of transmission of multi-drug resistance between humans and animals.

Abbreviations

AMR	Antimicrobial resistance
ESBL	Extended spectrum beta-lactamase
ECF	East coast fever
CBPP	Contagious Bovine pleuropneumonia
FMD	Foot-and-mouth disease
PPR	Peste des petits ruminants

Intensive usage of antimicrobials in the management of animal diseases may cause selection for resistance among microorganisms¹. Transmission of resistant bacteria from the wild and domestic food animals to humans may occur via the food chain, environment, or direct interaction with animals and this may lead to the emergence of infections that are challenging to manage². It is now estimated that antimicrobial resistance (AMR) among bacteria, viruses, or causes 700,000 deaths annually³ hence posing a significant public health challenge across the world. The resistant clones of bacteria have gained a global distribution with over 90% being resistant to commonly used antibiotics such as co-trimoxazole, penicillin, ampicillin, and gentamicin among others⁴. Most human diseases originate from animals with 61% being zoonotic⁵. Bacteria from animals are among the

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