



## **High Prevalence of Antibiotic Resistant *Escherichia coli* Serotype O157: H7 among Pastoral Communities in Rural Uganda**

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### **Authors' contributions**

*This work was carried out in collaboration among all authors. Author AW performed the laboratory work, data entry and analysis, and wrote the primary draft of the manuscript. Author JSI supervised the laboratory work, advised on the data analysis plan and was a major contributor in writing the manuscript. Author HKM participated in data analysis and writing of the manuscript. Author CFN participated in construction of the research idea, supervision of laboratory work and manuscript writing. Author DA participated in conducting laboratory work. Author HK provided some of the laboratory supplies and was a major contributor in writing the manuscript. Author BBA was the senior advisor and supervisor in the study, availed the necessary funds, was a major contributor in writing the manuscript and performed final editing of the manuscript. All authors read and approved the final manuscript.*

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## ABSTRACT

**Background:** Non-prescribed use of antimicrobials in Agriculture incurs a transfer risk of resistant pathogens to humans, complicating treatment. The aim of this study was to determine the potential of Zoonotic *E. coli* to serve as drivers of antimicrobial resistance (AMR) among animals and humans in pastoralist communities in Kasese district, so as to protect the community.

**Materials and Methods:** A laboratory based cross-sectional study was done using archived *E. coli* isolates previously obtained from humans in pastoralist communities of Kasese district, Uganda. Recovery of the isolates was done by conventional culture, and Identification by biochemical methods, serotyping and PCR. Kirby Bauer disc diffusion method was adopted for AMR profiling. Isolates were screened for resistance mechanisms including Extended Spectrum  $\beta$ -lactamase (ESBL), Carbapenemases and AmpC production using disc diffusion based methods.

**Results:** The prevalence of Enterohemorrhagic *E. coli* (EHEC) was 16% (28/180). These EHEC isolates belonged to phylogroups; B<sub>1</sub> (94%, 26/28), B<sub>2</sub> (3%, 1/28) and A (3%, 1/28). All the 28 EHEC isolates possessed the virulence gene *stx1*, 26 of the 28 EHEC isolates contained the virulence gene *stx2e*, but none of the 28 possessed the virulence gene *stx2*. Highest resistance was seen to Cotrimoxazole (89%, 25/28), Tetracycline (71%, 20/28), Ampicillin (65%, 18/28) and Nitrofurantoin (28%, 8/28), these are the most commonly used antimicrobials in the agricultural sector in Uganda. Minimal resistance was observed to the antimicrobials that are commonly used in human medicine especially  $\beta$ -lactams,  $\beta$ -lactam+inhibitors and Carbapenems. Of the 28 zoonotic *E. coli* isolates, 17%, (5/28) were ESBL positive and among these 1 (3%, 1/28) was a Carbapenemase producer.

**Conclusion:** There is a high prevalence of highly pathogenic, drug resistant *E. coli* O157:H7 among humans in pastoralist communities in Uganda. We suspect that these were acquired from animals because they mostly contained vero toxin gene *vt2e* which is animal specific, predominantly swine. Also majority of these EHEC isolates belonged to phylo-group B<sub>1</sub> which has been documented to inhabit domestic animals. We recommend future studies to investigate relatedness of drug resistant isolates from humans and animals to ascertain the zoonotic spread of resistant enterohemorrhagic *E. coli* in pastoralist communities.

**Keywords:** Antibiotic resistance; *Escherichia coli* O157:H7; pastoralist communities; PCR.

## ABBREVIATIONS

AMR : Antimicrobial Resistance;  
ATCC : American type culture collection;  
CLSI : Clinical and laboratory standard Institute;  
ESBL : Extended-spectrum  $\beta$ -lactamase;  
MDR : Multi-drug resistance;  
SPSS : Statistical package for social sciences

## 1. INTRODUCTION

Globally, the incidence of antimicrobial resistant pathogens is increasingly manifesting its self [1, 2]. This has continued to make the treatment of infections caused by these pathogens very difficult and expensive, imparting a great risk of death [3]. Uncontrolled use of antimicrobials in farming is a major factor causing the emergence of resistant bacterial pathogens [4]. The emergent zoonotic strains may pass on to humans via the food chain [5-7]. At present, *E. coli* O157:H7 is one of major pathogens implicated in the zoonotic spread of antimicrobial resistance (AMR) globally [8]. In East Africa, and

Uganda in particular, antimicrobial resistant *E. coli* with the potential for transmission from animals to humans are commonly implicated in human diarrheal diseases [9,10].

In Kasese district, western Uganda, farmers in and around Queen Elizabeth National park graze domestic animals within the Park. The interactions between domestic animals, wild animals and humans create a porous interface for zoonotic transfer of drug resistant pathogens [11]. This district has for long suffered outbreaks of antimicrobial resistant diarrheal diseases caused by zoonotic bacterial agents [10]. Though studies about these zoonotic pathogens have been done [9,12], little is known about the prevalence of antimicrobial resistant *E.coli* O157:H7, and the potential role of this strain in the zoonotic spread of antimicrobial resistance among pastoralist communities in this area.

This study aimed to determine the prevalence, population structure, and antimicrobial resistance profiles of zoonotic *E. coli*, among bacterial