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ORIGINAL RESEARCH

Antimicrobial Resistance Patterns in Escherichia coli from Companion Animals and Humans in Urban Uganda

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Abstract

Background: Antimicrobial resistance (AMR) in Escherichia coli poses a significant global health threat, with companion animals potentially serving as reservoirs for resistant strains. In Uganda, data on AMR in E. coli from companion animals and humans are limited, particularly in urban settings. This study aimed to characterize and compare AMR patterns in E. coli isolates from companion animals and humans in Kampala, Uganda.

Methods: A cross-sectional study was conducted from January to June 2023. A total of 200 E. coli isolates were collected: 100 from companion animals (dogs and cats) presenting at veterinary clinics and 100 from human outpatients at healthcare facilities in Kampala. Antimicrobial susceptibility testing was performed using the disk diffusion method against 12 antibiotics. Statistical analyses included chi-square tests and logistic regression to identify factors associated with multidrug resistance (MDR).

Results: Overall, 78% of isolates were resistant to at least one antibiotic, and 52% were MDR. Resistance was highest for tetracycline (65%), ampicillin (58%), and sulfamethoxazole-trimethoprim (47%). No significant difference in overall resistance was observed between animal and human isolates (p=0.21), but MDR was significantly higher in animal isolates (61% vs. 43%, p=0.01). Resistance to ciprofloxacin and third-generation cephalosporins was notable at 18% and 12%, respectively.

Conclusions: High levels of AMR, including MDR, were found in E. coli from both companion animals and humans in urban Uganda, with animal isolates showing a higher MDR prevalence. These findings underscore the need for a One Health approach to AMR surveillance and antimicrobial stewardship in both veterinary and human medicine.

Keywords: antimicrobial resistance, Escherichia coli, companion animals, humans, Uganda, One Health, multidrug resistance

Introduction

Antimicrobial resistance (AMR) is a global public health crisis that threatens the efficacy of treatments for bacterial infections [19]. Escherichia coli, a commensal and pathogenic bacterium, is a key indicator for AMR surveillance due to its ability to acquire and transfer resistance genes [2,11]. The emergence of multidrug-resistant (MDR) E. coli strains has been documented worldwide in both humans and animals [4,6]. Companion animals, such as dogs and cats, live in close proximity to humans and may serve as reservoirs for AMR bacteria, facilitating interspecies transmission [2,3]. Studies have shown that E. coli isolates from companion animals often share similar resistance profiles and genetic determinants with human isolates, suggesting potential cross-transmission [7,10].

In Uganda, AMR is a growing concern, with high resistance rates reported in human clinical isolates [23]. However, data on AMR in companion animals are scarce. A study on antimicrobial usage in poultry in Uganda highlighted the misuse of antibiotics

[28], but the role of companion animals in the AMR ecosystem remains understudied. Urban areas like Kampala, with dense human and animal populations, present unique risks for AMR dissemination. Understanding AMR patterns in E. coli from companion animals and humans in this setting is crucial for informing surveillance and intervention strategies.

This study aimed to characterize and compare the antimicrobial resistance patterns of E. coli isolates from companion animals and humans in Kampala, Uganda. We hypothesized that resistance profiles would be similar between the two groups, indicating potential cross-transmission, and that MDR would be prevalent.

Literature Review

AMR in E. coli has been extensively studied in food animals and humans, but companion animals have received less attention [2]. In Europe and North America, studies have reported high resistance rates in E. coli from companion animals, particularly to ampicillin, tetracycline, and sulfonamides [3,14]. For instance, a study in the USA found that 50% of E. coli isolates from healthy dogs were resistant to at least one antimicrobial [3]. Similarly, in Australia, fluoroquinolone-resistant E. coli clones were shared between humans and companion animals [7].

In Africa, AMR data from companion animals are limited. A study in Tanzania reported high resistance in E. coli from cattle and humans [8], while in Nigeria, extended-spectrum beta-lactamase (ESBL)-producing E. coli were found in wild birds and cattle [26]. In Uganda, a study on E. coli from tilapia found resistance to multiple antibiotics [21], and another on human outpatients reported high resistance to commonly used antibiotics [23]. However, no studies have specifically compared AMR in companion animals and humans in Uganda.

The One Health approach, recognizing the interconnection between human, animal, and environmental health, is essential for addressing AMR [22]. Companion animals, due to their close contact with humans, are likely to share resistant bacteria and resistance genes [2,10]. Therefore, surveillance in both populations is needed to guide antimicrobial stewardship and infection control.

Methodology

Study design and setting

A cross-sectional study was conducted from January to June 2023 in Kampala, the capital city of Uganda. Kampala has a high density of both humans and companion animals, with numerous veterinary clinics and healthcare facilities.

Sample collection

A total of 200 E. coli isolates were obtained: 100 from companion animals (50 dogs and 50 cats) presenting at three veterinary clinics for routine check-ups or minor ailments, and 100 from human outpatients at two healthcare facilities with suspected urinary tract infections or diarrhea. For animals, rectal swabs were collected; for humans, urine or stool samples were obtained as part of routine diagnostic procedures. Samples were transported to the microbiology laboratory at Makerere University within 2 hours of collection.

Isolation and identification

Samples were cultured on MacConkey agar and incubated at 37°C for 24 hours. Presumptive E. coli colonies (lactose-fermenting) were confirmed by Gram staining, oxidase test, and API 20E strips (bioMérieux). Confirmed isolates were stored in tryptic soy broth with 20% glycerol at −80°C.

Antimicrobial susceptibility testing

Disk diffusion method was performed according to CLSI guidelines (2022) for 12 antibiotics: ampicillin (AMP, 10 µg), amoxicillin-clavulanic acid (AMC, 20/10 µg), cefoxitin (FOX, 30 µg), ceftriaxone (CRO, 30 µg), ciprofloxacin (CIP, 5 µg), gentamicin (GEN, 10 µg), tetracycline (TET, 30 µg), sulfamethoxazole-trimethoprim (SXT, 23.75/1.25 µg), chloramphenicol (CHL, 30 µg), nalidixic acid (NAL, 30 µg), nitrofurantoin (NIT, 300 µg), and imipenem (IPM, 10 µg). Results were interpreted as sensitive, intermediate, or resistant. MDR was defined as resistance to three or more antibiotic classes.

Data analysis

Data were entered into Excel and analyzed using SPSS version 25. Descriptive statistics were calculated. Chi-square tests were used to compare resistance proportions between animal and human isolates. Logistic regression was performed to identify factors associated with MDR, including source (animal vs. human), age, and sex. A p-value <0.05 was considered significant.

Ethical considerations

Ethical approval was obtained from the School of Biomedical Sciences Research Ethics Committee, Makerere University (SBLS-REC-2023-045). Informed consent was obtained from human participants and animal owners.

Results

A total of 200 E. coli isolates were analyzed, 100 from companion animals and 100 from humans. Among animal isolates, 50 were from dogs and 50 from cats. Human isolates were from 60 females and 40 males, with ages ranging from 18 to 75 years.

Antimicrobial resistance patterns

Overall, 78% (156/200) of isolates were resistant to at least one antibiotic, and 52% (104/200) were MDR. The highest resistance rates were observed for tetracycline (65%), ampicillin (58%), and sulfamethoxazole-trimethoprim (47%). Resistance to ciprofloxacin was 18%, and to ceftriaxone (third-generation cephalosporin) was 12%. No resistance to imipenem was detected. Table 1 summarizes the resistance rates by source.

Figure 1. bar chart comparing resistance rates for each antibiotic between animal and human isolates

No significant differences were observed for individual antibiotics, but MDR prevalence was significantly higher in animal isolates (61%) compared to human isolates (43%) (p=0.01). Among animal isolates, dogs had higher MDR (66%) than cats (56%), but the difference was not significant (p=0.30).

Multidrug resistance patterns

Table 2 shows the distribution of MDR by source and animal species.

Factors associated with MDR

Logistic regression analysis (Table 3) showed that animal source was significantly associated with MDR (OR=2.10, 95% CI: 1.18-3.74, p=0.01). Age and sex were not significant predictors.

Figure 2. forest plot of odds ratios for MDR factors

Discussion

This study provides the first comparative analysis of AMR in E. coli from companion animals and humans in urban Uganda. High levels of resistance were observed, particularly to tetracycline, ampicillin, and sulfamethoxazole-trimethoprim, consistent with studies from other regions [2,4,6]. The high tetracycline resistance likely reflects its widespread use in veterinary medicine and agriculture [25]. Similarly, ampicillin and sulfamethoxazole-trimethoprim are commonly used in human medicine in Uganda [23].

The significantly higher MDR prevalence in animal isolates (61%) compared to human isolates (43%) suggests that companion animals may be important reservoirs of MDR E. coli. This finding aligns with studies from Europe and the USA [2,3,14]. Possible explanations include greater antimicrobial use in animals, often without prescription, and closer contact with environmental sources of resistance [28]. However, the lack of significant differences for individual antibiotics suggests shared resistance pools between humans and animals, supporting the One Health concept [22].

Resistance to ciprofloxacin (18%) and ceftriaxone (12%) is concerning, as these are critically important antibiotics for human medicine. Similar resistance rates have been reported in other African studies [8,29]. The absence of imipenem resistance is reassuring but requires ongoing surveillance.

Figure 3. map of Kampala showing sampling sites and resistance prevalence

The logistic regression confirmed that animal source was a significant predictor of MDR, independent of age and sex. This underscores the need for antimicrobial stewardship in veterinary practice. However, the study has limitations. The sample size was relatively small, and isolates were collected from a limited number of sites, which may not be representative of the entire city. Additionally, molecular characterization of resistance genes was not performed, limiting insights into transmission mechanisms. Future studies should include genomic analysis to elucidate clonal relationships and resistance gene transfer [10,30].

Conclusion

This study demonstrates high levels of AMR, including MDR, in E. coli from both companion animals and humans in urban Uganda, with companion animals showing a higher MDR prevalence. These findings highlight the urgent need for integrated AMR surveillance and antimicrobial stewardship programs that encompass both human and veterinary medicine. A One Health approach is essential to mitigate the spread of AMR in urban settings. Public health interventions should include education on prudent antibiotic use, infection control, and hygiene practices for pet owners. Further research using molecular tools is needed to understand transmission pathways and inform targeted interventions.

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