

Escherichia Coli Antimicrobial Resistance Profile Obtained from Productive Livestock

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ABSTRACT

The goal of this research was to find out how multidrug-resistant bacterial *Escherichia coli* was recovered from healthy young household pets in 3 States of Nigeria, comprising cattle, goats, poultry, and pigs. On Methyl Red Blue agar, *Escherichia coli* were identified and purified using standard microbiological techniques (EMB). Disc diffusion was used to screen the isolates against 15 antibiotics. Every isolate strains resistant to at least a few of the 42 medicines examined 86% of the 80 *E. coli* excludes tested positive for Ampicillin, 91% for cotrimoxazole, and 91% for cephalothin; 78.6% for streptomycin, 63.6% for nitrofurantoin; 69.9% for ciprofloxacin; 57% for chloramphenicol; 57.5% for amoxicillin clavulanic acid; 59.9% for ceftiofloxacin; 48.6% for According to data techniques, the average number of susceptibility features per separation in goat and chickens was much larger than in livestock animals ($P < 0.0001$). According to the results, multidrug-resistant strains of *E. coli* might operate as storage for resistant strains that could be passed on to harmful bacteria, presenting a significant public health risk.

Keywords: Antibiotic, bacteria, Genes, Resistance

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INTRODUCTION

The indigenous flora of exposed persons along with pathogenic microbes show acquired resistance. Antibiotics may be provided to complete flocks instead of animals in the wild in intensively farmed food animals, while antibacterial medications can be given to chickens, goats, and cattle on a regular basis as growth promoters. As a result, the animal is subjected to significant antibiotic selective pressure for microbial chemo resistance, as well as its gut ecosystem is always dominated by resistant bacteria. It's unclear how antibiotic resistance spreads from animals to people and back again. Chickens have been infested with resistant *Escherichia coli*, and that there is documentary proof that animals act as a reservoir for *E. coli* identified in humans. Furthermore, in a number of countries, the transfer of drug resistance plasmid in *E. coli* through poultry to human operators, along with

antibiotic-resistant bacteria between animals to humans, has been demonstrated. *Enterococcus* is only a few of the species that have shown resistance. Due to its complicated equilibrium of microflora in many habitats within the ecosystem, transmission movement of resistance determinants across bacteria inhabiting distinct habitats has the potential of causing often. Vertical direction amongst bacteria belonging to distinct species and families, or diagonally between bacteria pertaining to the very same genus or family, resistance genes may be transmitted.

Antibiotic use in food-producing animals has led to a significant increase of antibiotic bacterial strains, providing a dilemma for treating infectious infections in cattle, household animals, and people. As a result, regulatory authorities' viewpoints and goals on antimicrobial use have altered dramatically, notably in the use of antimicrobial medicines as prebiotics and preventive agents. Selective pressure from sub therapeutic antimicrobial medication usage in milk production may lead to identification of strains containing antimicrobial resistance genes. Animal-associated illnesses have been linked to human-associated infections, and plasmid unique to both humans and animals have been found to contain

transferable resistance genes. Antibiotic resistance genes are found in people, animals, and the environment, presenting a direct danger to public health. Research into causes of resistance, innovative antimicrobial effectiveness measures, and strict antibiotic use security controls in animal medicine are all needed to combat this menace. The widespread use of antibiotics in agriculture, particularly for prophylactic and growth-promoting reasons, has sparked controversy in the industrialized world about whether this practice has a substantial impact on transgenic rates and dissemination into other ecosystems. Antibiotics are only given when absolutely required in poor nations like Nigeria, such as when pets get ill and that only the sick animals are treated. Even if medicines aren't widely used, it's critical to identify and analyse the challenging role of bacterial isolates, especially commensal species. According to John and Fishman, this would give information on antibiotic sensitivity as well as drug resistance development, both of which are significant in clinical practice. In the absence of significant antibiotic usage for both prevention and developmental promotion, this study examines the antibiotic resistant profile of *Escherichia coli* isolates from presumably normal domestic animals such as cows, goats, pigs, and poultry [1].

Food-borne illnesses infections are a significant public health problem that also has a significant financial impact in very many countries. Most food safety mechanisms must attempt to prevent tainted food from reaching customers. Milk provides a favorable habitat for bacterial growth, which destroys milk and associated products while also putting users at risk of sickness. It is difficult to completely eradicate microbe contamination in milk due to the unique manufacturing process; as a consequence, soil salinity of milk is a significant instrument for assessing its quality. Several bacteria, particularly *E. coli*, which is an indication of tainted milk mixed cranberry juice, might get entry to dairy as well as other milk products, posing a public health risk. *E. coli* infection is a disease that may be passed from animals to people either directly or indirectly. It's frequent in poorer countries like Ethiopia because of poor food handling and sanitary standards, insufficient food safety rules, lax regulation, a lack of financial resources to invest in safer technologies, and a lack of food handler training. Pathogens include *Aureus*, *Escherichia*, *Enterococcus*, and *Campylobacter taxa* have been found to be a substantial source of foodborne disease in nations where it has been studied and reported. These microorganisms have been linked to gastrointestinal disease and, in some cases, a more severe septicemic illness, which mostly affects children, the elderly, and those with compromised immune systems [2].

The capacity of these bacteria to live and flourish in low-nutrient conditions, including at sub-optimal temperature and poses a significant challenge to agriculture and nutrition. Raw animals, eggs, dairy items, vegetable sprouts, fresh fruits, and fruit drinks continue to be the most common sources of human foodborne diseases, rendering sector-based control efforts within

each industry challenging to coordinate. These fluids have already been reported to include bacterial pathogens such as *Escherichia coli*, *Staphylococcus sp.*, *Salmonella*, and *Staphylococcus aureus*. As a result of antibiotic usage in animal agriculture and human illness in developing nations, resistance to antibiotics has become a major worry for human health. Amoxicillin, minocycline, griseofulvin, and oxytetracycline are the most often used antibiotics in Ethiopian to treating animal and human illnesses. Despite the need for greater study into antibiotic usage in Ethiopia, this susceptibility diversity might be due to haphazard antiviral drug use in animal agriculture without medicine in the animal and human medical areas, which could promote selected pressures that favor pathogen resistance genes. There has been no research on *E. coli* frequency and drug susceptibility profiles in Mekelle, Ethiopia, to yet. We obtained *E. coli* and analyzed the antimicrobial resistance profile in this work [3].

REVIEW OF LITERATURE

In this research, Akwar et al. compare the existence and characteristics of bacterial obstruction in pigs from areas that treated their pig diets with who didn't. Using a breakpoint concentration approach, 940 *Escherichia coli* isolates were evaluated for resistance to 21 antimicrobials from 179 pooled waste samples derived from weiner dog and finisher pigs on 47 amazing walk-in closet swine farms. Resistance was found in a spectrum of antimicrobials, ranging from 0.0% to 81.3%. Antimicrobial resistance was discovered in 90% of the isolates tested. The most common multidrug resistance combinations included 4 to 8 antimicrobials. Resistance was much more prevalent on areas that used in-feed medication than on areas, and weaner pigs were substantially more common (P 0.01) than finishing pigs. The findings show that faecal matter *E. coli* samples from pigs on research farms were resilient to a broad range of antimicrobial drugs, and that this might be a source of obstructive genes that could spread to toxins. The findings add to the increasing body of evidence that resistance to antibiotics in *E. coli* in pigs is under selection pressure due to antibiotic usage in swine feeds [4].

According to Call et al. study, Livestock from traditional dairy products have just an increased concentration of antibiotic resistant (AMR) *E. coli* than farm animals from sustainably grown dairies or beef-cow operations which focuses on observational studies of cattle production systems. That's not surprising considering that dairies customarily include more antimicrobials. According to experimental studies, antimicrobial therapy causes a transitory rise in AMR microbial population in treated cattle. Despite the fact that most medicines are also used to treat mammary on dairy farms, antimicrobial resistance in mastitis bacteria is low. Other research has shown no link between antimicrobial use and the occurrence of AMR bacteria, particularly in situations wherein AMR microbes are antibiotic resistant treatment or stay high in the absence of antimicrobial use or other

clear selection pressures. As a result, AMR bacteria communities in cattle production systems are impacted by a variety of factors and influences. As per a heuristic model, antimicrobial selection pressure may enhance the likelihood of AMR genes being linked to niche-or development fitness traits. This link permits AMR bacteria to flourish at the herd level since subpopulations of AMR microbes may survive in host animals for extended periods of time in the absence of antibacterial selection pressure. This model emphasizes the need for a diversity of herd health management measures in order to minimize total antimicrobial consumption while meeting livestock welfare and public health objectives and lowering long-term expenses for owners and consumers [5].

Oluwasola et al. investigate Nigeria, *E. coli* resistance to regularly used medicines, and pathogenicity characteristics in this article. Standard procedures were used to evaluate 137 *E. coli* strains from bladder infections for antibiotics resistance and pathogenicity. It was also looked at their ability to convey resistance. All antibiotics examined, with the exception of Nitrofurantoin, showed significant and extensive susceptibility (51.2% to 94.4%) (7.4%). Eleven of the 12 drugs tested have been associated with resistance in 51 isolates (36.6%). 63% (64%) of the 108 trimethoprim-resistant *E. coli* transmitted their resistances while using penicillin, griseofulvin, amoxil, tetracycline, and glucophage. 1 or maybe more causative factors were detected in 51 (37.4%) of these multi-resistant individuals. Due to widespread resistance to commonly used antibiotics, the research discovered that bacterial infections pathogenic organisms in Ingilizce may possibly be resistant to empirical therapy except for nitrofurantoin. To minimize treatment failure and limit selection pressure that may lead to the emergence of uropathogenic *E. coli* in the environment, it is necessary to conduct culture and susceptibility testing on the infectious agent prior to therapy [6,7].

METHODOLOGY

Instruments

91% to cotrimoxazole, 91% to colistin, 78.6% to streptomycin, 64.6% to neomycin, 69.9% to tetracycline, 58% to cephalosporins, 59.4% to amoxicillin clarithromycin, 59.9% to cefpirome, 48.6% to gentamicin.

Sample collection

Freshly feces were gathered at randomness from goats, cattle, pigs, and chickens, with made concerted efforts to just not obtain upwards of one fecal specimen per each animal. The feces subsequently placed in a sterilized small container and transported in an ice box to the lab. Each animal's feces were crushed in 9 ml sterile distilled water, and the homogenate's volume was increased to 12 mL utilizing sodium chloride. The components were properly mixed and serially diluted 10-fold, with 0.2 ml inoculum served on Eosin Bleu agar (EMB) from each

dilution (Oxoid, England). After that, the infected plates were incubated at 37°C overnight. A single colony on EMB with such a turquoise glossy finish that has been identified as *Escherichia coli* was chosen for further investigation from a solitary fecal sample. Using standard microbiological tests, *E. coli* was completely identified.

Data collection

This has been performed by streaking 0.6 Mc Farland calibrated cell suspension across the surfaces of Mueller-Hinton agar (Oxoid, England) dishes, then introducing them to discs impregnated with defined amounts of antimicrobial compounds. Penicillin (11 g), Amoxycillin/Phenylactic acid (21/10 g), Trimethoprim (31 g), Amoxicillin (11 g), Ceftazidime (11 g), Ceftriaxone (31 g), Cefpirome (31 g), Gentamycin (11 g), Oxacillin (31 g), Sulfamethoxazoletrimethoprim (31 g).

Data analysis

ANOVA was used to compare the rates of the four animals. The tests were carried out as specified, and the findings were deemed significant at a 95% confidence level.

RESULTS

The bacterial resistance for such 80 *E. coli* strains were 86% for ampicillin, 91% for cotrimoxazole, 91% for cephalothin, 77.6% for streptomycin, 62.6% for nitrofurantoin, 68.9% for tetracycline, 56% for chloramphenicol, 56.4% for amoxicillin clavulanic acid, 58.9% for cefpirome. There have been 42 multiple antimicrobial resistance profiles detected in total. When susceptibility rates for ampicillin, cotrimoxazole, streptomycin, and cephalothin were examined by collection source, 94.7% of goat strains tested positive for each (Figure 1). Cephalothin has been the least effective treatment in cattle (93.1% resistance), although Gentamycin obstruction was really quite low (17.2%) (Figure 2). In chicken isolates, cotrimoxazole and cephalothin resistance was 100%, while streptomycin, nitrofurantoin, and amoxicillin clavulanic chemical resistance reached 66.7% (Figure 3). Pig isolates shows the lowest degree of resistance (to Ceftriaxone) in just this study, at 5.9%. Pig isolates, on the other hand, exhibited the same considerable antimicrobial activities and Cotrimoxazole as other sample sources, with around 88.2% sensitivity (each) reported (Figure 4). The overall amount of resistance traits per isolation in goats and chicken was significantly higher than those in cattle and pigs (P 0.0001), so according descriptive statistics.

Among the *E. coli* bacteria detected, penicillin, cotrimoxazole, ceftazidime, gentamycin, fluconazole, erythromycin, cefepime, and zithromax clavulanic chemical resistance was observed in large numbers. Deny the reality that now the farms under inquiry have never added antibiotics to their livestock feed as growth promoters or used medicines prophylactically, there's really substantial resistance. Although the domestic cattle studied in this study may not have access to

modern veterinary care, they may remain in close contact with humans who have now been treated to antibiotics in various ways (such as water). In many Nigerian communities, for example, people urinate mostly around adjacent compounds, bushes, or even at the corner of their homes. As a consequence of such insufficient and filthy human excrement disposal techniques, these animals are likely exposed to ordinary human enteric flora, which include novel resistance traits. Furthermore, Lipsitch et al., found that selective antibiotic use in infected humans in the very same context increased the risk of animal hosts obtaining resistant infections [8].

Taking susceptibility into consideration, there is significant proof that antibacterial usage in poultry industry may result in the growth and proliferation of resistant *E. coli*, which can then be transferred to people via diet or making interaction with the birds. The drug resistant strains found in *E. coli* isolates from chicken is alarming; bacteria from poultry demonstrated 100% sensitivity to Cotrimoxazole and Cephalosporins, respectively, which was not detected in other vertebrate hosts in this investigation. On a horse ranch where we collected these samples, early exposure to drugs seems to have altered events in colonizing microbes prior to specimen collection. Cotrimoxazole had such a 100% tension rate, Fluconazole used to have a 66.7% resistance % age, Triclosan had a 53.3% resistance rate, Ciprofloxacin had a 73.3% impedance rate, and Antibiotic had an 86.7% impedance rate, indicating that most of these antimicrobials were becoming severely damaged and are unlikely to be helpful in the evaluation of *E. coli* illnesses. This organism might serve as a massive store for antibiotic resistance genes, as well as a resistance propagation center [9].

However, a growing number of studies are demonstrating the migration and proliferation of resistance determinants throughout the environment, which might help bacteria, build antibiotic resistance. Our previous discoveries of narcotic symbiotic *Coli* from cattle operations that seldom utilize antibiotics corroborate our previous findings. Rysz et al., proved that soil bacteria may evolve resistance to naturally existing antibiotics as a result of environmental exposure, potentially establishing a reservoir of resistance determinants produced outside of the host, people, and animals. Agricultural environmental isolates, according to Sayah, were less sensitive to most drugs tested (as judged by disk diffusion method zone width) than faecal sample isolates. They hypothesized that quasi producers of resilience factors, such as farm workers and wildlife with access to the agro-ecosystem, may be generators of resistance considerations. The low usage of antibiotics in the broiler plant, as previously indicated, is most likely to blame for the high numbers of resistant bacteria seen in chicken isolates. Expect this since antimicrobial usage has been found to be the most significant selection variable in drug-resistant bacteria. The resistance data against fluoroquinolones in the latest research exemplify this point the best. Quinolones are a relatively wonderful addition to Nigeria pharmacology, and they are both

costly and difficult to come by for veterinary use. As a result, it's probable that the limited human use of these antibiotics is mirrored in the study's lowered levels of antibiotic resistance. These findings are concerning since promiscuous prescription usage, as well as inadequate sanitation and sickness management, are all potential drivers of antibiotic resistance in Nigerian microorganisms [10].

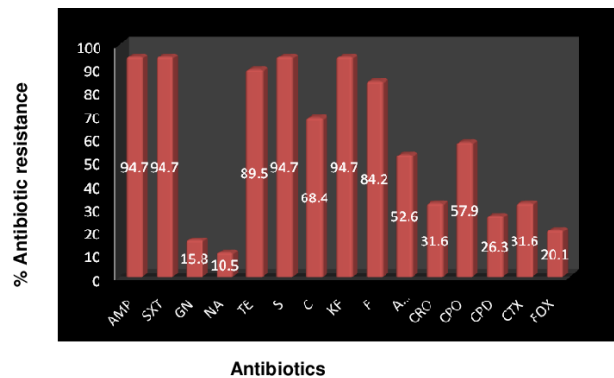


Figure 1: Antibiotic resistance patterns in goat *Escherichia coli* isolates.

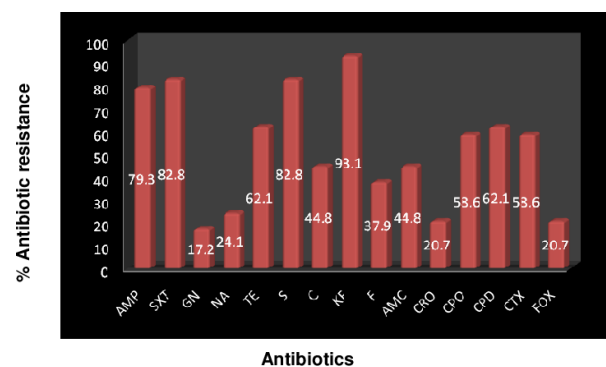


Figure 2: Antibiotic resistance patterns in cattle *Escherichia coli* isolates.

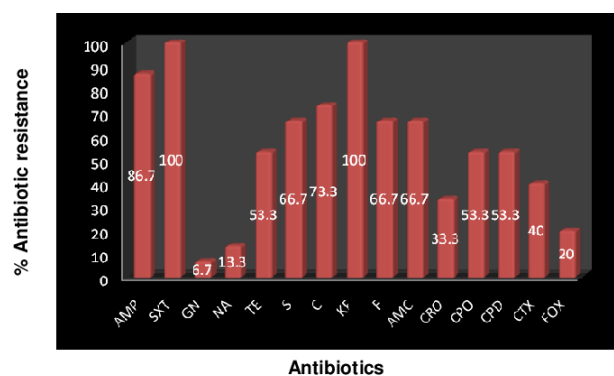


Figure 3: The antibiotic resistance pattern of *Escherichia coli* isolates from poultry.

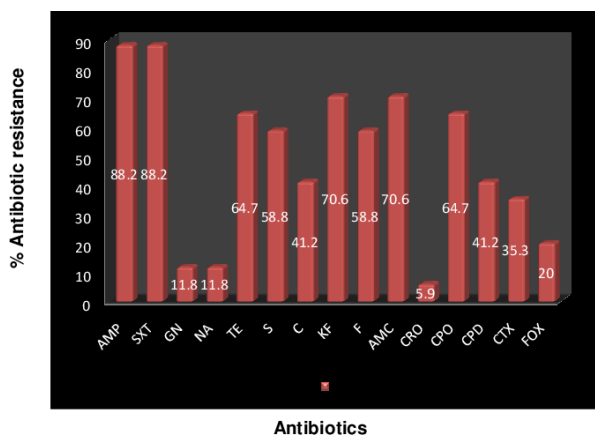


Figure 4: The trend of antibiotic resistance in Escherichia coli isolates from pigs.

CONCLUSION

Finally, rather than being host or context specific, resistance characteristics are dispersed among hosts in various settings, according to this research. The significant frequency of multidrug-resistant *E.coli* found in this research indicates that more education and communication about antibiotic usage in human and veterinary care is needed.

REFERENCES

1. van den Bogaard AE, London N, Driessen C, et al. Antibiotic resistance of faecal Escherichia coli in poultry, poultry farmers and poultry slaughterers. J Antimicrob Chemother. 2001;47:763-771.
2. Sayah RS, Kaneene JB, Johnson Y, et al. Patterns of antimicrobial resistance observed in Escherichia coli isolates obtained from domestic and wild-animal fecal samples, human septage, and surface water. Appl Environ Microbiol. 2005;71:1394-1404.
3. Schroeder CM, Zhao C, Debroy C, et al. Antimicrobial resistance of Escherichia coli O157

- isolated from humans, cattle, swine, and food. Appl Environ Microbiol. 2002;68:576-581.
4. Akwar HT, Poppe C, Wilson J, et al. Prevalence and patterns of antimicrobial resistance of fecal Escherichia coli among pigs on 47 farrow-to-finish farms with different in-feed medication policies in Ontario and British Columbia. Can J Vet Res. 2008;72:195-201.
5. Call DR, Davis MA, Sawant AA. Antimicrobial resistance in beef and dairy cattle production. Anim Health Res Rev. 2008;9:1515.
6. Olorunmola FO, Kolawole DO, Lamikanra A. Antibiotic resistance and virulence properties in escherichia coli strains from cases of urinary tract infections. African J Infect Dis. 2013;7:1.
7. Daniels JB, Call DR, Hancock D, et al. Role of ceftiofur in selection and dissemination of blaCMY-2- mediated cephalosporin resistance in Salmonella enterica and commensal Escherichia coli Isolates from cattle. Appl Environ Microbiol. 2009;75:2435.
8. Rysz M, Alvarez PJJ. Amplification and attenuation of tetracycline resistance in soil bacteria: Aquifer column experiments. Water Res. 2004;38:3705-3712.
9. Pitout JDD, Church DL, Gregson DB, et al. Molecular epidemiology of CTX-M-producing Escherichia coli in the calgary health region: Emergence of CTX-M-15-producing isolates. Antimicrob Agents Chemother. 2007;51:1377.
10. Pitout JDD, Gregson DB, Campbell L, et al. Molecular characteristics of extended-spectrum-β-lactamase-producing Escherichia coli isolates causing bacteremia in the calgary health region from 2000 to 2007: Emergence of clone ST131 as a cause of community-acquired infections. Antimicrob Agents Chemother. 2009;53:247-259.