

PDF - ANTIBIOTICS RESISTANCE PROFILE OF ESCHERICHIA COLI ISOLATED FROM APPARENTLY HEALTHY DOMESTIC LIVESTOCK IN SOUTH-WEST NIGERIA (OSUN STATE, NIGERIA) -

researchcub.info **ABSTRACT**

This study was conducted to determine the antibiotic resistance profile of Escherichial Coli isolate from apparently healthy domestic livestock viz: cow, goats and chicken from Osun State Nigeria. E. Coli was isolated using Eosin methylene Blue Agar (EMB) and identified by conventional microbiological technique. The isolate were tested against 14 antibiotics using the disc diffusion method. A total of 42 different antibiotics resistance profile were observed with each isolate showing resistance to at least four or more drugs tested. Generally, the E. coli isolates showed resistance rates of 93.8% to Ampicilin; 15.3% to Chloramphenicol, 52.7% to cloxacillin, 74.3% Erythromycin, 20.9% to Gentamicin, 53.8% to Penicillin, 17.7% to Streptomycin, 67.3% to Tetracyclin, 21.1% to Ceftazidime 70.7% to Cefuroxime, 20.5% to Cefixine, 28.8% to Ofloxacin, 58.6% to Augmentin, 27.2% to Nitrofurantion 27.3% to Ciprofloxacin. Statistical analysis showed that average number of resistance phenotypes per isolate was significantly higher for cow compared with poultry. A significant public health concern observed in this study is that multi drug resistant: commensal E. Coli strains may constitute a potential reservoir of resistance genes that could be transferred to pathogenic bacteria.

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CHAPTER ONE

INTRODUCTION

Antibiotic usage is considered the most important factor promoting the emergence, selection and dissemination of antibiotic-resistant microorganisms in both veterinary and human medicine (Daniel et al, 2009). Antibiotic usage selects for resistance not only in pathogenic bacteria but also in the endogenous flora of exposed individuals (animals and humans). Antibiotics are used in animals as in humans for therapy and control of bacterial infections. In intensively reared food animals, antibiotics may be administered to whole flocks rather than individuals animals, and antimicrobial agents may be continually fed to food animals such as poultry, goats and cattle as growth promoters. Therefore, the antibiotic selection pressure for resistance in bacteria in poultry is high and consequently their faecal flora contains a relatively high proportion of resistant bacteria (Literak et al, 2010).

The mechanism of spread of antibiotic resistance from animals to humans remains controversial. Colonization of the intestinal tract with resistant *Escherichia coli* from chicken has been shown in human volunteers and there is historical evidence that animals are a reservoir for *E. coli* found in humans (Akwar et al, 2008). Spread of an antibiotic resistance plasmid in *E. coli* from chickens to human handlers was described by Levy et al. Other have also presented evidence of spread of antibiotic – resistant microorganisms from poultry to humans in various countries (Fang et al, 2008).

Resistance has been found in organisms common to both humans and animals such as *E. coli* salmonella

spp., campylobacter spp and Enterococcus among others (Davis et al, 2009). Due to the intricate balance of microflora of different habitats within the ecosystem, the transfer of resistance genes among bacteria occupying different habitats has the potential to occur frequently.

Widespread reliance on antimicrobials in food animal production has resulted in an considerable rise of the treatment of infectious diseases in livestock, companion animals and humans. This has led to important changes in the perceptions and priorities of regulatory agencies with regard to antimicrobial usage, particularly agents. The selective pressure from the use of antimicrobial agents at sub therapeutic levels in dairy cattle could result in the selection of those strains that contains genes for antimicrobial resistance (Call et al, 2008).

Molecular tools have been used to correlate animal associated pathogens with similar pathogens affecting humans and to clearly demonstrate transferable resistant gene carried by plasmid common to both animals and humans (Pitout et al, 2009). The possibility of antibiotic resistance genes circulating among humans, animals and the environment constitutes a direct to public health. This threat prompts research into emerging resistance mechanisms novel approaches to antimicrobial efficacy and stringent control measures in the prudent use of antimicrobials in animal medicine.

In the developed world, the extensive use of antibiotics in agriculture, especially for prophylactic and growth promoting purposes, has generated much debate as to whether this practice contributes significantly to increased frequencies and dissemination of resistance genes into other ecosystems. In developing countries like Nigeria, antibiotics are used only when necessary, especially, if the animals fall sick, and only the sick ones are treated in such cases. However, even in the absence of heavy use of antibiotics it is important to identify and monitor susceptibility profiles of bacterial isolates, particularly of commensal organisms. This, according to John and Fishman (1997) will provide information on resistance trends including emerging antibiotics which are essential for clinical practice.

This work was therefore, undertaken to investigate the antibiotic resistance profile of E. coli isolates from apparently healthy domestic livestock.

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