Antibiotic Susceptibility Profile of Bacterial Isolates from Commercial Poultry Farms in Ile-Ife, Nigeria

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Abstract: Nontherapeutic antimicrobial usage in animal farms has been associated with the development and spread of resistant bacteria. The emergence of serious life-threatening infections from veterinary and environmental sources and treatment failures occurring with the available antibiotics warrants investigation into resistance of antimicrobial agents in poultry farms. This study therefore provides information on antibiotic resistance pattern of bacteria isolated from five commercial poultry farms in Ile Ife, a peri-urban settlement in Nigeria. Isolation of bacteria from droppings, feed and water samples, was performed by spread plate method using all purpose and selective media. Morphological and biochemical characterization of isolates was done. The antibiotics sensitivity of the recovered isolates was determined by Kirby-Bauer disk diffusion method. A total 151 bacterial isolates, comprising 11 genera of 8 Gram negative and 3 Gram positive bacteria were recovered. *E. coli* had highest incidence rate of 21.19%, followed by *Bacillus* sp. with 15.23%; while the least recorded incidence of 1.32% was *Citrobacter* sp. All five farms recorded a 100% resistance to at least two (2) classes of antibiotics. A 100% resistance was recorded for augmentin in all five (5) farms, while 100% resistance in four (4) farms was recorded for cloxacilin. Furthermore a 100% resistance against erythromycin and cefixime respectively was documented in three farms. The least percentage resistance of 30% was against ciprofloxacin in only one farm, while the overall highest susceptibility of 39% was to ofloxacin. The multiple antibiotic resistance index (MARI) of isolates from all farms ranged from 0.3 to 1. Up to 9 bacterial genera had MARI 1, including *E. coli*, *Salmonella*, *Bacillus*, *Klebsiella*, and *Pseudomonas*. This study is a further indication that poultry farms represents an important reservoir of antibiotic resistance bacteria. It also serves as a pointer to the need for enforcement of regulatory antibiotics use in poultry farming by the government, and controlled usage by all stakeholders.

Keywords: Antibiotic, Resistance, Susceptibility, Bacteria, Poultry Farm, MARI

1. Introduction

There is an increasing demand for poultry meat mainly due to its acceptance by most societies and its relatively low cholesterol content and egg products [1]. Food and Agriculture Organization (FAO) reported a global increase in egg and poultry meat production, with a total of 87 million tons of eggs and 123 million tons of poultry meat (37% of meat production) in 2017 [2]. The poultry sub-sector is the most commercialized of all of Nigeria's agricultural sub-sectors; poultry meat and eggs being among the main source of protein in many households [3].

Domestic chickens are the most important poultry species in the world; contributing 89% of world poultry meat production [2]. However increasing world populations and urbanization have led to the bulk of production being in larger, more intensive specialist units. These are often situated close to where the feed is grown or to where the meat is needed, and result in cheap, safe food being made available for urban communities [4]. All over the world, more than 300 breeds of domestic chicken species (*Gallus domesticus*) exist [4]. There are basically three types of chicken. They are:

1) Layers: these are reared for egg production.
2) Broilers: are reared for meat production and are ready for

market from 8 weeks.

3) Cockerel: This is also reared for meat production. Cockerels grow slower and can take up to twenty four weeks before they are matured for marketing. Cockerels are reliable in terms of survival and withstanding bad weathers. They are more resilient, and can absorb shock far better than layers and broilers.

Nigeria has the second largest chicken population in Africa As a result, livestock in these environments commonly require aggressive infection management strategies, which often include the use of antibiotic therapy [5]. Most commercial farmers in particular, rearing chicken for meat or egg production, do so under intensive management system [6]. Under that condition antibiotics are used as therapeutic agents, prophylactic agents and growth promoters in feed [7]. It is to be stressed that in animals the antimicrobial agents are not used only for therapy and prevention of bacterial infections but also as growth promoters. In Europe, approximately 30% of all antibiotics used in animals are growth promoters [8]. Some of the commonly used antibiotics today in poultry industries in developing countries like Nigeria are tylosine, neomycin, gentamycin, tetracyclines (chlortetracycline, oxytetracycline), sulfonamides (sulfadimethoxine, sulfamethazine, sulfathoxazole), penicillin (ampicillin), arsenicals (roxarsone), enrofloxacin, erythromycin and vaccines [9].

There is growing scientific evidence that the use of antibiotics in food animals leads to the development of resistant pathogenic bacteria that can reach humans through the food chain [10]. The concern over microbial antibiotic resistance has led to the banning of antibiotic use in feeds for poultry and livestock in various countries of Europe as well as in the U.S.A [11]. It is now generally known that the main risk factor for an increase in bacterial resistance is an increased use of antibiotics, it is similar in humans and in animals [12]. These drug resistant bacteria can move from animals to humans through a variety of channels, the farmers, their families, or employees through direct contact with animals, their neighbors, or others through soil and water contamination or via airborne particles and consumers via contaminated meat. Bacteria also pass resistance genes back and forth, creating another mechanism by which antibiotic resistance could be transferred to human pathogens [13]. This study therefore provides information on antibiotic resistance pattern of bacteria isolated from droppings, feed and water samples, in commercial poultry farms in Ile-Ife, Osun State, Nigeria. The specific objectives were to isolate bacteria from poultry droppings, feed and water samples; characterize isolates based on morphological and biochemical tests, and carry out antibiotic susceptibility testing on the isolates.

2. Materials and Methods

2.1. Study Area

This study was carried out in Ile-Ife of Osun State, in the South-West region of Nigeria. Ile-Ife is a semi-urban town with two Local Government Areas, namely; Ife East and Ife Central. Geographically, Ile-Ife lies on longitude 4°69'E and latitude 70°50'N and has a humid tropical climate with distinct wet and dry seasons. Ile-Ife is an ancient town in Yoruba history of Western Nigeria, and is regarded as the cradle of civilization [14]. Conventional farming system is practiced by the populace.

2.2. Collection of Sample

Composite samples of water and feed in canisters and/or troughs, and chicken droppings were collected from 5 different commercial poultry farms in the months of April to June, 2019. These farms are distributed within Ile-Ife, Osun State in different districts (Table 1) namely Obafemi Awolowo University (OAU) campus (OAU farm), Sabo (Olabisi Farm), Opa (Adedapo farm), Adesanmi (Abdulrahman farm) and NASFAT (Rukol farm). The feed and droppings samples were collected in sterile ziplock bags using spatula, and water samples were collected in sterile bottles. All samples were immediately transported in ice packs to Oduduwa University microbiology laboratory for analysis.

Table 1. Description of the poultry farms.

SITE CODE	DESCRIPTION
A	This farm is a tertiary institution farm. A total of 1500 birds were in the poultry, which were all broilers kept in folds. Neomycin, Enrofloxacin were the major antibiotics used in the poultry farm
B	Is a private farm located in SABO, Ile-Ife. A total of 300 birds were kept in the poultry, which were all broilers reared in deep liter system. Antibiotics used were Tylodox, Keproceryl, tetracycline and doxygen.
C	This is a private owned poultry farm located at OPA, Ile-Ife. A total of 800 birds were kept in the poultry, which were all broilers reared in folds. Keproceryl, Cotrimoxazole and Neomycin were the antibiotics used.
D	This poultry is a private farm located at ADESANMI Ile-Ife Osun state. A total of 1000 birds were kept in the farm, which were all broilers kept in folds. The antibiotics used in the farm were Kenflux, Enrofloxacin and Cotrimoxazole.
E	The poultry is a private farm located at NASFAT Ile-Ife Osun state. A total of 500 birds were reared, which were kept in folds. Antibiotics used in the farm were Neomycin, Enrofloxacin and Cotrimoxazole

2.2.1. Preparation of Media Used

The media were aseptically prepared according to the manufacturer's instructions. All media were sterilized by autoclaving at 121°C for 15 minutes except Salmonella Shigella agar (SSA) which was heated to boiling point.

2.2.2. Microbiological Analysis

For the isolation of total heterotrophic bacteria. A 1 g sample each of feed or droppings, was dissolved thoroughly in 9 ml of peptone water and used in preparing fivefold serial dilutions. For water sample, 1 ml of each sample was added in

9 ml of peptone water and used to prepare fivefold serial dilutions. A fresh sterile tip was used to mix the contents of each dilution by sucking up and down several times, then 0.1 ml of each dilution for 10^2 to 10^5 was withdrawn and inoculated into nutrient agar (NA) plates, using spread plate method. A 10^1 and 10^2 dilutions were streaked on eosin methylene blue agar (EMB) agar for isolation of E. coli, and on SSA for isolation of *Salmonella* and *Shigella*. Two replicates of each dilution were made and were labeled. Inoculated plates were incubated in an inverted manner for 18h to 24 h at 37°C. The plates were observed, counted and the distinct colonies were re-streaked on the respective medium in order to obtain pure culture which were stored in nutrient agar slants at 4°C for further test.

2.2.3. Morphological and Biochemical Identification of Isolates

Gram staining was performed on microbial pure culture to differentiate organisms based on their cell wall structure [15]. Bacterial isolates were further identified based on their cultural, morphological and biochemical characteristics according to Bergey's Manual of Determinative Bacteriology [16]. Biochemical characteristics were determined using conventional biochemical tests such as methyl red-voges-Proskauer, catalase, indole and citrate tests [17].

2.3. Antibiotic Susceptibility Tests (AST)

The antibiotic susceptibility pattern of all the isolated bacteria from each farm was determined using the disk diffusion method according to the Bauer - Kirby technique [18]. A colony of pure isolate to be tested was picked with a sterile wire loop and was aseptically dissolved in 5ml sterile saline solution. It was mixed thoroughly and repeated until the turbidity of the saline solution visually matched that of 0.5 McFarland standard. A sterile swab was dipped into the saline solution of the isolate and was gently squeezed against the inside of the tube i n order to remove excess fluid. The swab was used to streak all through the surface Mueller Hinton agar plates to ensure a lawn of growth. After the streaking was completed, the plate was allowed to dry for 5 minutes. The Antibiotic discs used are presented in Table 2. The discs were placed on the surface of the agar using sterilized forceps and were gently pressed onto the surface of the agar. The inoculated plates was carefully inverted and incubated for 24 hours at 37°C. After incubation, a metric ruler was used to measure the diameter of the zone of inhibition for each antibiotic used. Zone of inhibition was interpreted according to the interpretative standard of the Clinical and Laboratory Standards Institute guidelines [18].

Table 2. *Antibiotics discs used and the concentration.*

S/N	Antibiotic and its concentration	Antibiotic Class
1	Amoxicillin/clavulanic acid (Augmentin/AUG– 30 μg)	Penicillins (β-Lactams)
2	Nitrofurantoin (NIT – 100 μg)	Nitrofurans
3	Ciprofloxacin (CIP – 5 μg)	Quinolones (Fluroquinolones)
4	Cefuroxime (CXM – 30 μg)	Cephalosporins
5	Ceftriaxone (CTR – 30 μg)	Cephalosporins
6	Gentamicin (GEN – 10 μg)	Aminoglycosides
7	Erythromycin (ERY– 5 μg)	Macrocyclics (Macrolides)
8	Ofloxacin (OFL– 5 μg)	Quinolones (Fluroquinolones)
9	Cloxacilin (CXC– 5 μg)	Penicillins (β-Lactams)
10	Cefixime (CFM– 5 μg)	Cephalosporins
11	Ceftazidime (CAZ– 30 μg)	Cephalosporins

The multiple antibiotic resistance index (MARI), is defined as a/b where;

'a' represents the number of antibiotics to which the isolate was resistant, and

'b' represents the number of antibiotics to which the isolate was exposed [19].

2.4. Data Analysis

Data collected were entered into Excel Spreadsheet. Descriptive statistics was used to examine resistance pattern in isolates and in the farms.

3. Results

3.1. Total Heterotrophic Bacterial Count

The total heterotrophic bacterial (THB) count of the poultry feed, water samples and droppings was noted and the result is presented in Table 3. The bacterial load of the samples showed that the highest heterotrophic bacterial count of feed samples was from Farm A with 2.01×10^7 cfu/g, feed sample from Farm E came next with 1.56×10^7 cfu/g counts while the least count was recorded in Farm D with 1.46×10^7 cfu/g. The THB count for water sample was highest in Farm D with 2.05×10^7 cfu/ml, followed by Farm A with 1.92×10^7 cfu/ml, the least recorded was in Farm C with a count of 1.4×10^7 cfu/ml. However the highest THB in droppings of 2.40×10^5 cfu/g was recorded in Farm C. A higher count of 1.92×10^5 cfu/g was also recorded in Farm A, while the least THB count in droppings 1.46×10^5 was in Farm D.

3.2. Morphological and Biochemical Tests Result

The isolated bacteria were presumed to be *Escherichia coli*, *Klebsiella* sp., *Bacillus* sp. *Staphylococcus* sp., *Proteus* sp., *Shigella* sp., *Salmonella* sp., *Enterobacter* sp., *Citrobacter* sp., *Pseudomonas* sp. and *Corynebacterium* sp. These genera were recovered from the farms at varying frequency as indicated in Figure 1. The highest frequency of 32 was recorded for *Escherichia coli* with an incidence rate of 21.19%, followed

by *Bacillus* sp. with frequency of 23 isolates and an incidence of 15.23%; while the least recorded frequency of 2 was *Citrobacter* sp. with 1.32% incidence. The incidence rate is shown in Figure 2.

Table 3. *Total heterotrophic bacterial count of the samples.*

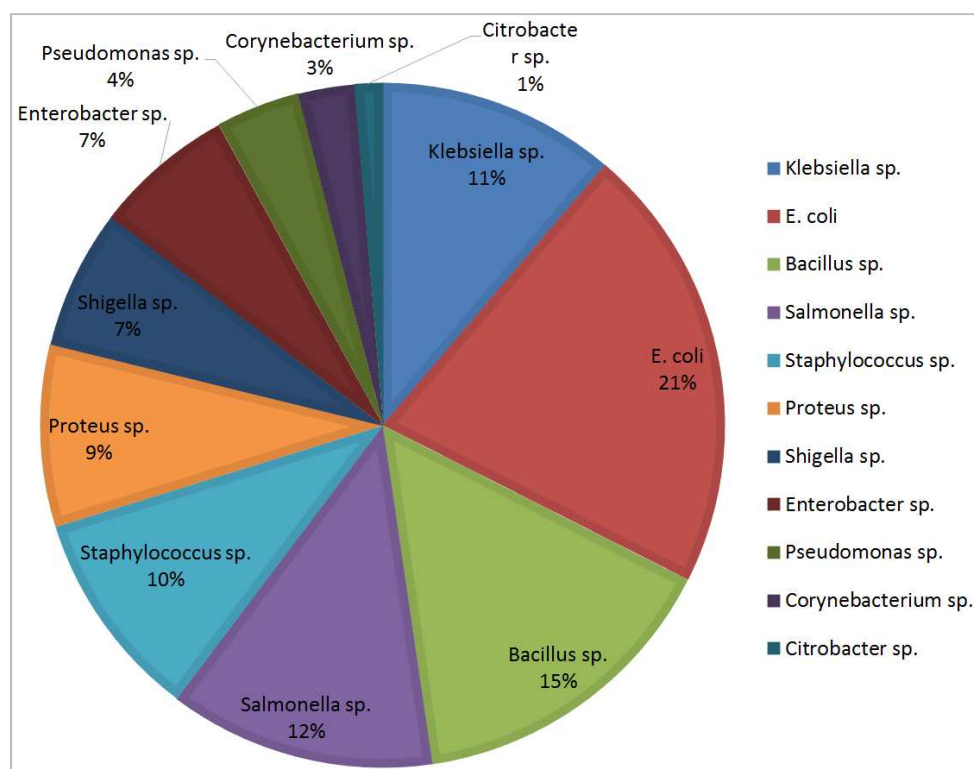| Sampling site	Total Viable Count (cfu/g)	Total Viable Count (cfu/g)	Total Viable Count (cfu/ml)
	Droppings	Feed	water
A	1.92×10^5	2.01×10^7	1.92×10^7
B	1.85×10^5	1.20×10^7	1.85×10^7
C	2.40×10^5	8.9×10^7	1.4×10^7
D	1.46×10^5	1.46×10^7	2.05×10^7
E	1.60×10^5	1.56×10^7	1.64×10^7

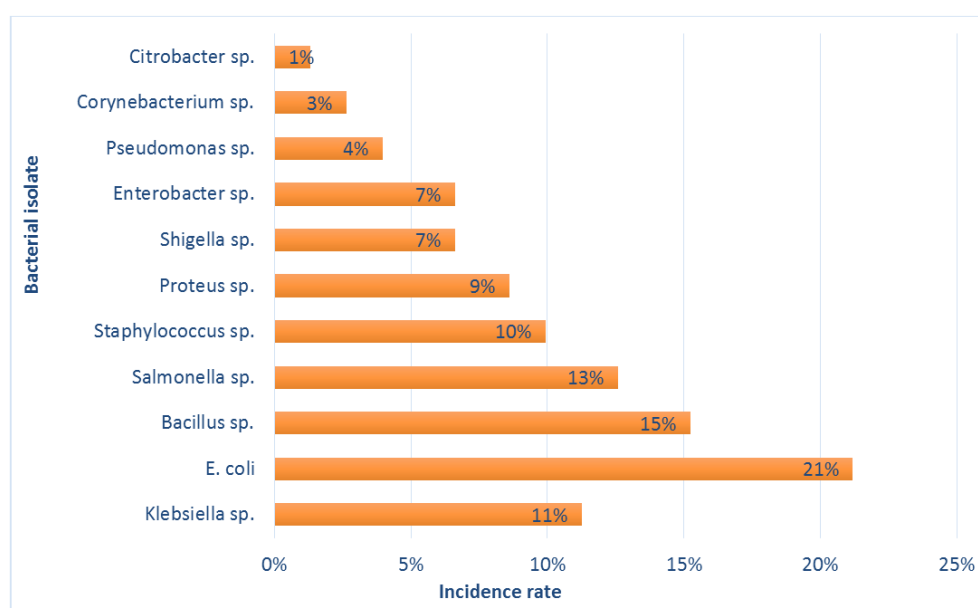***Figure 1.*** *Frequency of the isolated bacteria.*

Figure 2. *Incidence rate of bacterial isolates.*

3.3. Antibiotics Susceptibility Profile

Antibiotics susceptibility profile of the isolates from all farms indicated a susceptibility percentage (%) of 39, 38.4 and 37 to ofloxacin, gentamicin and cefuroxime respectively. On the other hand, a highest resistance of 100% against augmentin, followed by 98% resistance against cloxacilin, cefixime and erythromycin respectively was recorded; while the least resistance of 44% was against ofloxacin. In addition, the intermediate reaction varied from 0% towards cloxacilin and augmentin respectively to 26% towards ciprofloxacin. Result of the susceptibility profile is presented in Figure 3.
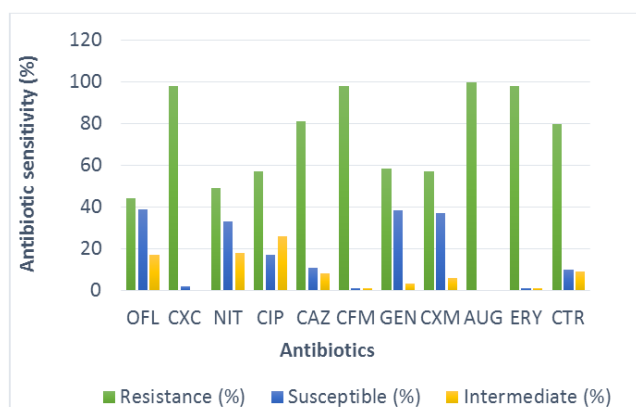

Figure 3. Susceptibility profile of isolates recovered from all farms.

The antibiotics resistance pattern in the farms showed that isolates from all five farms recorded a 100% resistance to at least two (2) classes of antibiotics. A 100% resistance was recorded for augmentin in all five (5) farms, while 100% resistance in four (4) farms was recorded for cloxacilin. Furthermore a 100% resistance against erythromycin and cefixime respectively was documented in three farms. Moreover resistance of 95% and 94% against erythromycin was recorded in farms D and B respectively. The least percentage resistance of 30% was against ciprofloxacin which occurred in farm C. The antibiotic resistance pattern is highlighted in Figure 4.
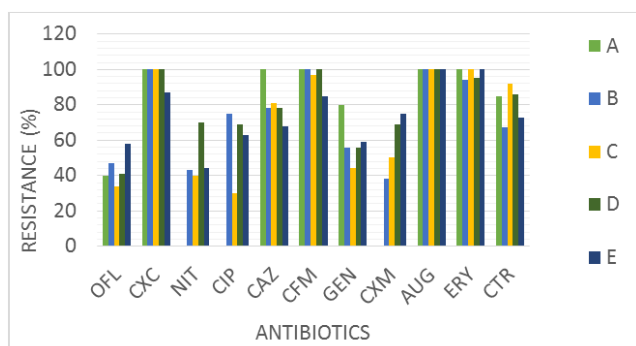

Figure 4. Antibiotics resistance pattern in the five farms.

Antibiotics resistance profile of bacterial isolates from individual farms differed from farm to farm. In farm A (Supplementary File 1), a 100% resistance was recorded for cloxacilin, ceftazidime, cefixime, augmentin and erythromycin; 85% resistance towards ceftriaxone and the least resistance of 40% was towards ofloxacin. The mean percentage resistance against the panel of antibiotics tested was 89±9.9%. On the other hand, a resistance of 100% against cloxacilin, cefixime and augmentin; 94% against erythromycin and the least resistance of 38% against cefuroxime by the isolates was observed in farm B (Supplementary File 2). Also in the farm B, a mean percentage resistance of 74±17.6% was recorded against the antibiotics tested. Likewise the isolates from farm C (Supplementary File 3) exhibited 100% resistance against three antibiotics comprising cloxacillin, augmentin and erythromycin followed by a 97% and 92% resistance against cefixime and ceftriaxone respectively, and the least 30% resistance was against ciprofloxacin. Furthermore, the resistance pattern of isolates from farm D (Supplementary File 4), showed that percentage resistance against cloxacilin, cefixime and augmentin was 100% followed by 95% resistance against erythromycin while the least percentage resistance of 41% was against ofloxacin. In addition, antibiotics resistance pattern of the isolates from Farm E (Supplementary File 5) indicated a 100% resistance against augmentin and erythromycin, 94% resistance against cefixime and a least percentage resistance of 44% against nitrofurantoin. A mean percentage resistance of 89±9.9 (%) and 74±17.6 (%) against the panel of antibiotics tested was recorded in Farms A and B respectively, while 68± 20 (%), 78.3± 20.4 (%) and 76.2± 20.2 (%) was the mean percentage resistance observed in Farms C, D and E respectively (Supplementary Files 1-5).
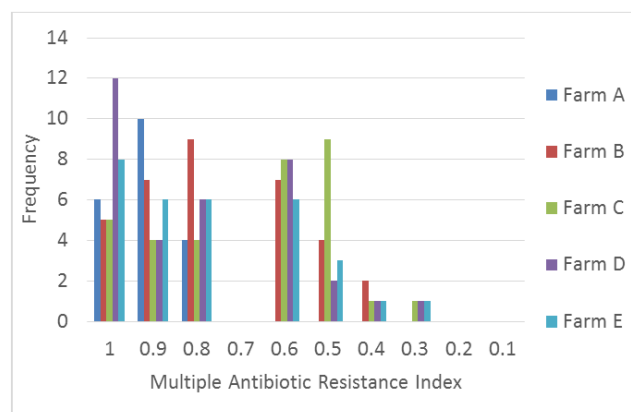

Figure 5. Frequency of Multiple Antibiotic Resistance Index.

The MARI of isolates from all farms ranged from 0.3 to 1. Farm A had the highest average of 0.9 ± 0.1, followed by an average of 0.8 ± 0.2 for Farms B, D and E respectively, and an average of 0.7 ± 0.2 for farm C (Supplementary Files 1-5). Frequency distribution of the MARI showed that Farm D had the highest frequency (12) of the MARI value 1. Bacterial isolates from all farms with MARI 1 comprised *E. coli*, and the genera *Salmonella*, *Proteus*, *Staphylococcus*, *Corynebacterium*, *Enterobacter*, *Bacillus*, *Klebsiella*,

Pseudomonas, as well as *Enterobacter*. The least MARI of 0.3 was recorded for *Staphylococcus* sp*., Enterobacter* sp. and *E. coli* in Farms C, D and E respectively. The result is presented in Figure 5.

4. Discussion

The level of microbial contamination in poultry farms is one of the most important sanitary and hygienic indicators. The main sources of microorganisms in poultry houses are birds, droppings, litter, feed, ventilation air, as well as employees [20].

The heterotrophic bacterial count (HTB) in this study showed the highest to be 2.05×10^7 cfu/ml which was from water sample, while another high HTB count of 2.01×10^7 cfu/g was from feed sample. However, the droppings had the least bacterial count of 1.46×10^5 cfu/g. According to Reference [21], water troughs left for 3-5 days uncleaned have increased high bacterial loads, which may be from regurgitated feed particles or from source water. Contrary to this findings however, Reference [22] reported a higher bacterial counts in litter than feed samples. Another study also reported a higher bacterial count in poultry litter than in soil samples of poultry farms and agricultural land [23]. Although a hundred and fifty-one (151) isolates comprising eleven (11) genera were isolated from the farms, these may not be a complete representation of the bacterial population due to viable but non-culturable (VBNC) condition of some bacteria. The highest frequency of *E. coli*, recorded in this study is similar to findings from previous studies on other poultry farms in Nigeria [22, 24] and other parts of the world [23, 25, 26]. This is not surprising since *E. coli* is ubiquitous in the gastrointestinal tracts of warm-blooded animals [27]. *E. coli* is an etiologic agent of collibacillosis, a global bacterial disease of poultry which is transmissible to humans; while some are capable of traversing into organs, causing fatal disease in birds [28]. Other bacterial species of high incidence in this study, by decreasing order include *Bacillus* sp., *Salmonella* sp., *Klebsiella* sp., *Staphylococcus* sp., *Proteus* sp. *Shigella* and *Enterobacter* sp. *Bacillus* species may include both free living non-pathogenic and pathogenic species including *B. cereus* which causes food poisoning and *B. anthracis*, the etiologic agent of anthrax. *Salmonella* species are wide spread in poultry production and are the etiological agent of salmonellosis and pullorum disease, characterized by high mortality and reduction in productivity [29]. *Klebsiella* species have commonly been isolated from both poultry birds, litters, droppings, feed, water and the poultry environment [23, 30-32]. Common pathogenic *Klebsiella* in humans and animals include *K. oxytoca*, *K. pneumonia* and *K. varricola* [30]. Staphylococcal infection can cause food poisoning in man when contaminated poultry meat is consumed. *Escherichia coli*, *Salmonella gallinarum*, and *Proteus* species have been implicated in chick mortality. Moreover, *Salmonella* and *Proteus*; *Streptococcus pluranimalium* and *Staphylococcus saprophyticus*; *S. aureus*; faecal Enterococci, *E. coli*, *S. typhi*, *S. aureus* and non-coagulase staphylococci

have all been identified in poultry air environment, hatcheries, and water sources used in poultry [33, 34]. Hence the poultry environment could serve as reservoir of pathogenic bacteria with the associated public health risks.

Poultry flocks are often raised under intensive conditions using large amounts of antimicrobials to prevent and to treat disease, as well as for growth promotion. For instance, the antibiotic usage pattern observed in a survey of poultry farms in Nigeria showed that poultry farmers relied heavily on antimicrobial medications, and most farms were multi-drug users for therapeutic, prophylactic and for growth promotion [35, 3]. The use of antimicrobials in intensive poultry production is becoming increasingly common at smaller scales within low-resource settings because of its high output of meat and egg products, and this is expected to intensify with the increased transition of low-to middle income countries to high incomes with the attendant demand for increased sources of animal protein [36]. However antimicrobial resistance (AMR) has become a global health threat, and nontherapeutic antimicrobial usage in animal production is one of its contributing sources [37, 38]. It has been suggested that the use of nontherapeutic antimicrobials be eliminated due to the substantial and increasing volume of direct and indirect evidence reporting animal-to-human transmission of resistant bacteria, and the growing environmental load of resistance [37].

In this study, isolates from all the five farms sampled showed varying percentage resistance to the eleven antibiotics tested. A complete (100%) resistance was recorded for augmentin, cloxacilin, erythromycin and cefixime in five (5), four (4), and three (3) farms respectively. The least percentage resistance of 30% (against ciprofloxacin) was recorded in only one farm (Farm C). All five farms recorded a 100% resistance to at least two (2) classes of antibiotics. Resistance against fluoroquinolones as recorded in this study is of great concern since they are the commonest class of antibiotics used in the poultry farms, they also serve as farmers' option in cases of refractory bacterial infections caused by bacterial resistance to the conventional older generation frontline antibiotics, and are also known to be highly successful and strategic in the treatment of infections such as salmonellosis caused by multiresistant *Salmonella* serotypes [35]. An earlier report on poultry farms droppings in Ile Ife documented *E. coli* strains to be more resistant than staphylococci and showed 100% resistance to nalidixic acid and amoxicillin but with lower resistance to gentamicin [3]. Another study on poultry droppings in Ilorin documented all the Gram positive bacteria to be resistant to ceftazidime, cefuroxime, ceftriaxone, cloxicillin and Amoxycillin-clavulinate (augmentin) while all the Gram negative bacteria were resistant to ceftazidime, gentamcin and Amoxycillin-clavulinate; and *S. aureus* and *Microbacterium holobium* were resistant to all the antibiotics tested [39]. A report on poultry farms in India stated more than 70% resistant *E. coli* to co-trimoxazole, penicillins and fluoroquinolones; 50-70% resistance against cefuroxime and ceftriaxone and less than 30% resistance to aminoglycosides [23]. Elsewhere, a statistically significant difference in

antibiotic resistant *E. coli* between both of conventional, no antibiotics poultry farming and chicken from humane family owned production schemes, with resistance against two of the antibiotics, ampicillin and erythromycin, has been reported [40]. Production birds, including broilers and laying hens, were reported to have high levels of resistance and a notably higher proportion of resistant isolates than household birds [41].

MARI tool is used to reveal the spread of bacteria resistance in a given population [19]. Any MARI value above 0.20 implies that such bacterial strain originates from an environment where several antibiotics are used or misused, have been exposed to several antibiotics, and have thereby developed resistance to these antibiotics [19, 42]. The bacterial isolates with MARI value of 1 in this study includes *E. coli*, and eight other genera comprising *Salmonella*, *Proteus*, *Staphylococcus*, *Corynebacterium*, *Enterobacter*, *Bacillus*, *Klebsiella*, as well as *Pseudomonas*. This implies exposure of these isolates to several antibiotics of which they have developed high resistance. This study corroborates an earlier report of a multiple antibiotics resistance of bacterial isolates from Farm A with MARI range of 0.1 to 1. Higher susceptibility to quinolone (ofloxacin) and aminoglycosides (gentamicin) recorded in this study however, is in contrast with the quinolones comprising ofloxacin, ciprofloxacin and pefloxacin which were the most effective of all the antibiotics used in that study [43]. Reference [24] reported 65.4% of the bacterial isolates from chicken litter as resistant to multiple antibiotics, with a MARI ≥ 0.2. Multidrug resistant bacteria have been found in poultry, poultry feed, water, poultry products, carcasses, litter and droppings [44, 45]. Reference [32] reported that commercial day-old chicks in Nigeria are already colonized by multidrug-resistant coliforms. These not only serve as sources of environmental reservoir of antibiotic resistance genes but also exposure potential to the farmers. For instance, a significantly higher antibiotics resistance prevalence and multidrug resistant *E. coli* has been reported among poultry workers [45].

Despite global control strategies, proper veterinary monitoring especially in the predominately small-scale poultry farming in Nigeria has been a challenge [22]. Moreover Nigeria also faces a hazard of poor antibiotic prescription monitoring and prescription-only medicines, including antimicrobials that are routinely sold Over-The-Counter (OTC) in pharmacies and by patent proprietary medicines vendors [17]. Furthermore, the high bacterial load observed, and the high incidence of pathogenic bacterial genera is a further indication of the potential public health hazard that might be associated with poultry farms.

Apart from the direct danger posed to humans by consumption of contaminated poultry products, there is also the risk of indirect transmission of the resistant genes. These would reduce the treatment options, increase the cost of treatment or risk of treatment failure thereby leading to a longer hospital stay. Additionally, poultry wastes are used in fish farming as feed, and also as soil enrichment manure. Study has shown that poultry waste can serve as

environmental reservoirs of multiple antibiotic resistant bacteria therefore their indiscriminate use and dumping in the environment could constitute health risks from drug resistant zoonotic pathogens [46].

5. Conclusion

Although further promotion of intensive poultry farming could address issues of food security, it may also increase risks of AMR exposure to poultry, other domestic animals, wildlife, and human populations. Given that intensively raised poultry and the environment can serve as reservoirs for AMR, constant surveillance is needed for assessment of the impacts on humans, other animals, and the environment at large. This study is a further indication that poultry farms represents an important reservoir of antibiotic resistance genes. It also serves as a pointer to the need for enforcement of regulatory antibiotics use in poultry farming by the government, and controlled usage by all stakeholders.

Acknowledgements

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