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Antibiogram survey of enterobacteriaceae species isolated from fecal droppings of pigeon birds in four local government of Sokoto state, Nigeria

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Abstract

The threat of antibiotic- resistant bacteria in the public health sector has been on the rise throughout the world especially in the developing and underdeveloped world probably due to rising population and poverty. The main habitats and carriers of *Enterobacteriacea* species are humans, plants and animals such as birds, food stuff, soil and fecal matter This work is aimed at finding epidemiological studies and antibiogram survey of some members of Enterobacteriaceae isolated from fecal droppings of domesticated (pigeon) birds. fecal droppings of domesticated (pigeon) birds from 60 houses were collected from each of the four local government areas making a total of 60 samples. The samples were then investigated for the presence of Enterobacteriaceae species. The isolated species were then subjected to antimicrobial susceptibility test using twelve antibiotic discs. The results showed that 10(16.66) sample analyzed using biochemical characterization reveal *Salmonella*, *E. Coli*, *Klebsiella* and *Proteus* species. The overall isolation rate of *Salmonella* (50%), *E. Coli* (20%), *Klebsiella* (20%) and *Proteus* (10%). Sensitivity test reveal that five isolates from fecal droppings of pigeon birds were resistant to more than five antibiotics applied, which include Augmentine, gentamycin, nalidixic acid, Nitrofuranton, Ampiclox and cefexime. The result also showed that out of 10 isolates, five (5) are multidrug resistant. Among the five multi drug resistant isolates only three harbor blaTEM gene,but bla SHV and bla CTX were not detected in the study.The presence of the bla TEM gene indicated that the gene may allow the spread of resistant gene to other bacteria This resistance profile aligns with global concerns regarding antibiotic efficacy, as highlighted by the World Health Organization, particularly with growing resistance to essential antibiotics. These findings underscore the role of domesticated birds as potential vectors of multidrug-resistant pathogens, which could have significant public health implications. Given the risk of transmission to humans and animals, these results highlight an urgent need for intervention strategies aimed at controlling the spread of resistant bacteria within environmental and domestic settings.

Keywords: Antibiogram survey; Enterobacteriaceae; Pigeon birds; Antibiotic resistant bacteria; Pathogens; Sokoto State

1. Introduction

Antibiotic resistant bacteria are microorganisms that have developed mechanisms to survive exposure to antibiotics (drugs designed to kill or inhibit bacrerial growth) (Olinda 2012). This resistance allows bacteria to evade the effects of antibiotics. Antibiotic-resistant bacteria have been the focus of much research due to their potential health risks as well as their potential economic effects. Research has demonstrated that domesticated and wild birds are becoming more important hosts for bacteria harboring antibiotic-resistance genes (Smith et al., 2014; Carroll et al., 2015). These animals are thought to play a significant role in the establishment of multidrug resistance in many global habitats and

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in the dissemination of resistant bacteria to various hosts and locations (Hasan et al., 2012). These birds are known to host a variety of newly developing zoonotic infections and to spread arthropod vectors (Godoy, 2007).

A wide range of bacterial diseases, including those caused by pathogens from the family Enterobacteriaceae, can affect birds (Joseph 2003). The Enterobacteriaceae is a vast family of Gram-negative bacteria (Quinn et al., 2016), also known as Enterobacteria. These, however, are regarded as secondary, and in order for the illness to manifest, predisposing conditions must exist. In birds that are clinically healthy, these predisposing factors are linked to direct human interaction (Asterino 1996). Birds are sensitive to enteropathogens, much like all other vertebrates, and few thorough surveys have been conducted for both wild and domesticated birds (Reed et al., 2003).

Enterobacteria belonging to the Klebsiella genera were discovered in wild birds and have been documented in past research (Gibbs et al., 2007; Santos et al., 2010). This bacterium can sometimes cause infections and occasionally act as the major pathogen (Davides et al., 2016).

The gastrointestinal tracts of warm-blooded animals serve as the natural habitat for the numerous members of the Enterobacteria. According to Shabarinath et al., (2007) and Lopez et al., (2010), several bacterial species in this family are highly pathogenic and may be involved in food deterioration. According to Lindberg et al., (1998), pathogens such as Shigella spp., *Salmonella* spp., and some strains of *E. Coli* can cause severe diarrhea. Intestinal tracts of Humans and animals (farm animals, birds, and reptiles) are primarily infected with *Salmonella*. Many natural areas, such as water reservoirs and coastal waters tainted by human or animal waste, are home to *Salmonella* species, which are responsible for outbreaks all over the world. According to the Centers for Disease Control and Prevention nearly 400 infected persons each year die from acute Salmonellosis (CDCP, 2013).

The occurance of bacteria that are resistant to antimicrobial agents in natural environments poses a risk to the health of people and animals. It is known that wild and domesticated birds can harbor enteric human pathogens such as *Escherichia coli* and *Salmonella* which can produce toxins (Abulreesh et al., 2007, Magda et al., 2013). They have a significant impact on the epidemiology of zoonoses that affect humans. Despite few interactions with antimicrobial agents, these birds' fecal deposits may serve as reservoirs and potential dispersers of resistant bacteria in the environment (Guenther et al., 2010, Jarhult et al., 2013). According to Allen et al., (2010), there is a risk to human and animal health when multidrug-resistant bacteria appear in natural settings. As noted by Abdulreesh et al., (2007), Bonnedahl et al., 2009, Guenther et al., 2010, Radhouani et al., (2012), Water contact and acquisition via food are the supposed ways of transmission of resistant bacteria of human and veterinary origin to domesticated birds (Abdulreesh et al., 2007). In the study area, domesticated birds such as pigeon are raised unrestrained in and around the home and as a result, food and the surroundings can become contaminated by their feces. Such droppings may contain pathogens some of which may have developed resistance to medications frequently employed to treat illnesses they cause. Resistance to antibacterial agents by Entrobacteriacea species has been reported by many authors (Hur et al., 2012, Hassan et al., 2012and Foti et al.,2009). Several clones of multidrug resistant Entrobacteriacea been reported and their prevalence has expanded worldwide (Shah and Korejo 2012, Abiodun et al., 2014, Niki et al., 2017 and Kambo et al.,2018). In the study area, limited report exists on the prevalence of multidrug resistant Entrobacteriacea species of domestic origin (especially pigeon birds), and literature on antibiotic surveillance which is supposed to serve as a basis for diseases control programs in the state is very scanty in Sokoto. Therefore, this study seeks to add data to the existing available information on Entrobacteriacea species transmission via domesticated (pigeon) birds in the Study area, and the role played by these birds in spreading these bacteria in the environment.

2. Materials and methods

2.1. Collection of fecal droppings from pigeon birds

Sample of fecal droppings of pigeon were collected from households in Sokoto North, Sokoto South, Wamakko and Kware local government areas. Samples are collected from households randomly selected from each local government area. A total of 60 dried fecal droppings were collected and placed in sterile airtight container and transferred to the Microbiology Laboratory UDUS for analysis.

2.2. Isolation of bacteria

Entrobacteriacea species were isolated from fecal droppings of pigeon, turkey and dove birds according to the procedure described by Raufu et al. (2013). Ten grams (10g) of each fecal sample was weighed and transferred to 100mls of Selenite broth in 200mls conical flasks and incubated over night at 37^{o}C. 1ml of the pre-enriched sample was transferred aseptically in to 9 mls of buffered peptone water, and reincubated at 37 °C for 24 hrs. A loop full of the

buffered peptone water culture was sub-cultured onto deoxycholate citrate agar (DCA) agar, and *Salmonella*–Shigella agar, and Macconkey agar using spread plate method. All inoculated plates were incubated aerobically at 37 °C for 24 h. After 24hrs, the plate was examined for typical colonies growth characteristics. On Macconkey, DCA and SSA agar (Cheesbrough, 2002). The suspected colonies were sub- cultured on Nutrient Agar to obtain the pure isolates.

2.3. Identification and characterization of isolates

Identification of Entrobacteriacea isolates was done based on the morphology (Gram staining) and biochemical characterization according to the methods described by Oyeleke and Manga (2008).

2.4. Antibiotic Susceptibility Tests

The susceptibility of the isolates to Amoxicillin Clavulanate 30µg, Cefotaxine 25µg, Imipenen/Cilastatin10/10 µg, Ofloxacin 5 µg, Gentamycin 10µg, Nalidixic acid – 30 µg, Nitrofuranton 300 µg cefuroxime – 30 µg, Ceftriazone sulbactin-45 µg, Ampiclox – 10 µg, Cefexime - 5µg and Lexofloxacin - 5µg was determined according to the specifications described by the Clinical and Laboratory Standards Institute (CLSI 2016). The inoculum was prepared at a density adjusted to a 0.5 McFarland turbidity standard solution. Bacterial suspension was inoculated on Mueller Hinton Agar (MHA) using sterile swab stick. Plates were dried for 15 minutes and commercially available antibiotic discs were applied on the plate surface and allowed to stand for 30 minutes to allow the antibiotics to diffuse in to the agar medium. Each plate was incubated in an upright position overnight at 37 °C. Sensitivity were recorded after 24 hours of incubation by measuring the zone of inhibition formed around the antibiotic disc (CLIS, 2016).

2.4.1. DNA Extraction

DNA was extracted from the isolate growing in broth media by using DNA Extraction kit (DNA/RNA isolation kit Qiagen U.S.A) according to the manufacturer`s instruction/ specification, is follows:

- The bacterial isolates were grown in LB medium for 24 hours, 1000µl aliquot was retrieved and centrifuged at 4°C, 1000rpm for 10 minutes.
- About 300 µl of the cultured sample was transferred to 1.5ml Eppendort tube.
- Twenty microliter of proteinase K was added and 600µl of lysis buffer were added, the mixture was vortex to mixed and incubated at 56oc for 10 mins,
- Six hundred microliter of absolute ethanol were also added and vortex to mix. The sample was shake and transferred in to spin column and centrifuged at 12000rpm for 1 minute. The supernatant was discarded and binding column was put back into the collection tube.
- About 500 µl of washing buffer A were added and centrifuged at 12000rpm for 1 minute. The supernatant was discarded and
- Five hundred microliter of washing buffer W was added and centrifuged at 12000rpm for 1 minute again. The supernatant was discarded
- the sample was transferred into fresh effendorf tube, and centrifuged at 12000rpm for 3 mins to dry the membrane, and the supernatant was discarded.
- About 50 µl Elution buffer was added to the middle of the adsorption membrane, and place at room temperature for 5 min. This was centrifuged at 12000rpm for 1 min The extracted DNA was used for PCR amplication.

2.4.2. PCR amplication of resistant gene

PCR was used to amplify class 3 multi drug resistance genes (blaTEM, bla CTX and bla SHV) associated with drug resistance in beta- lactamase antibiotics, and annealing temperature shown in table 1 with conditions as previously described by Skyberg et al., 2006. PCR was carried out using Top Taq master mix (Qiagen, USA) following manufacturer`s instruction, as follows:

A total of 25 µl reactions were prepared in a 0.2ml nuclease free microtube (treflabs). The mix were containing 12.5µl of Toptaq master mix, 2.5 µl of Coral Load, 0.5 µl each of forward and reverse primers (table 1), 2.5 µl nuclease free water (Qiegen, USA), 5 µl of DNA template. The mixtures were vortexes briefly to mix, and then transferred to thermo cycler (applied biosystems 9700) programmed with the following cycling conditions:

The PCR reaction condition for bla TEM, bla SHV and bla CTX were consisted of initial denaturation at 940C for 3 minutes, followed by 40 cycles of denaturation at 940C for 30 seconds, annealing at 500C for 1 minute and extensions at 720C for 1 minute followed by final extension at 720C for 10minutes.

The PCR products were analyzed on 1% agrose gel in 1x TBE buffer, run at 90 volts for 50 minutes. Gel was stained with ethidium bromide and photographed (Hughes et al., 2008).

Table 1 Primers for detecting integrin class 1 genes and class A β-lactamse genes of Entrobacteriacea species isolated from Study samples

Target gene	Primer sequence (5`-3`)	Temp(0c)	size (bp)	Reference
	BlaCTX-M F: CGATGTGCAGTACCAGT R: TTAGTGACCAGAATCAGCGG	50	192	Roschanski *et al* 2014
	blaTEM F: GCATCTTACGGATGGCATGA R: GTCCTCCGATCGTTGTCAGAA	50	100	Roschanski *et al* 2014
	blaSHV F: TCCCATGATGAGCACCTTTAAA R: TCCTGCTGGCGATAGTGGAT	50	104	Roschanski *et al* 2014

3. Results

Entrobacteriaceae species were isolated from sixty (60) fecal samples of pigeon from the study areas. Ten isolates were obtained from fecal samples of pigeon, Wamakko Local Government had nine isolates (WMK 1, 2, 3, 4, 5, 12,13,17 and 20), and Sokoto North had six isolates (S/N1, 2, 3, 4,10 and 14). Some isolates displayed a colorless, smooth, shiny, and translucent surfaces with black center, some appear red without bile and others species display pale mucoid colonies All colonies were Gram-negative, rod-shaped bacteria after gram staining and viewed at x100 objective.

Fecal droppings sample collected from pigeon birds, shows that, the most frequent species was *Salmonella* spps 5 (50) followed by *E. Coli* 2(20) and Klebsilla 2(20), while Proteus has zero 1(10) occurrences in a total of 60 samples.

The sensitivity pattern of the bacterial isolates from fecal droppings of pigeon birds from four sample areas is presented in Table 4.8. One isolate from Wamakko, two from Sokoto North and one from Sokoto South were resistant to two antibiotics (WMK3 S/N 1,2 and S/S2). While one isolate from Sokoto South, two from Wamakko and two from kware were resistant to nine antibiotics that applied (S/S3, WMK4and 5, KWR1 and KWR2). While four isolates, one from Wamakko, one from Sokoto South and two from Sokoto North were resistant to two antibiotic discs (WMK3, S/N1, S/N2 and S/S2).

Table 2 Result of Biochemical Reaction of isolates obtained from fecal droppings of pigeon collected in four L/Government areas

Samples	Macroscopy	Microscopy				Biochemical tests					Suspected isolates
	Morphology	Gram RXN	Indole	Citrate Utilization	MR	VP	Sugar Production	H_2S	Motility	Urease	
WMK 3	Colorless colonies with black center	-	-	+	+	-	+	+	+	+	*Salmonella*
WMK4	Mucoid colonies	-	-	+	+	-	+	+	+	+	*Klebsiella*
WMK5	Mucoid colonies	-	-	+	+	-	+	+	+	+	*Klebsiella*
WMK6	Colorless coloniesw ith black center	-	-	+	+	-	+	+	+	+	*Salmonella*
S/N1	Colorless colonieswith black center	-	-	+	+	-	+	+	+	+	*Salmonella*

S/N2	Colorless colonieswith black center	-	-	+	+	-	+	+	+	+	*Salmonella*
S/S2	Colorless colonieswith black center	-	-	+	+	-	+	+	+	+	*Salonella*
S/S3	Smooth colorless colonies	-	+	-	+	-	+	+	+	+	*Proteus*
KWR1	Non lactose fermenters	-	-	-	+	-	+	+	-	+	*E. Coli*
KWR2	Non lactose fermenters	-	-	-	+	-	+	+	-	+	*E. Coli*

Key: WMK= Wamakko, S/North= Sokoto North, S/South= Sokoto South, KWR= Kware, MR= Methyl red, VP= Vagues Pokesvuer, H2S= Hydrogen Sulphide production

Table 3 Frequency and Percentage of occurrence of bacterial isolates from fecal dropping of pigeon birds collected from four Local Government (Sample areas)

Isolated Entrobacteriacea	Frequency of occurrence	Percentage of occurrence %
Salmonella spp	5	50
E. Coli spp	2	20
Klebsiella spp	2	20
Proteus spp	1	10
Total	10	100

Table 4 The Antibiogram pattern of isolates obtained from fecal droppings of pigeon birds collected from four local governments

Isolates	Count	Pattern	AUG	CTX	IMP	OFX	GN	NA	NF	CRO	CXM	ACX	LBC	ZEM
Salmonella	5	R	2(40.0)	1(20.0)	5(100)	0(0)	0(0)	0(0)	0(0)	0(0)	1(20.0)	1(20.0)	0(0.0)	0(0)
		S	3(60)	4(80.0)	0(0)	5(100)	5(100)	5(100)	5(100)	5(100)	4(80.0)	4(80.0)	5(100)	5(100)
Klebsiella	2	R	2(100)	2(100)	2(100)	1(50.0)	2(100)	2(100)	2(100)	2(100)	2(100)	1(50)	1(50)	2(100)
		S	0(0)	0(0)	0(0)	1(50)	0(0)	0(0)	0(0)	0(0)	0(0)	1(50)	1(50)	0(0)
Proteus	1	R	0(0)	0(0)	1(100)	1(100)	1(100)	1(100)	1(100)	0(0)	1(100)	1(100)	0(0)	1(100)
		S	1(100)	1(100)	0(0)	0(0)	0(0)	0(0)	0(0)	1(100)	0(0)	0(0)	1(100)	0(0)
E. Coli	2	R	0(0)	0(0)	0(0)	1(50)	1(50)	1(50)	0(0)	2(100)	0(0)	0(0)	2(100)	1(50)
		S	2(100)	1(50)	2(100)	1(50)	1(50)	1(50)	2(100)	0(0)	2(100)	2(100)	0(0)	1(50)

Key: AUG = Amoxicilin Clavulanate 30µg; CTX=Cefotaxine 25µg; IMP = Imipenen/Cilastatin 10/10µg; OFX =Ofloxacin - 5µg GN = Gentamycin - 10µg; NA = Nalidixic acid – 30µg; NF = Nitrofuranton 300µg; CXM =Cefuroxime - 30µg; CRO =Ceftriazone sulbactin-45µg; CX =Ampiclox - 10µg; ZEM = Cefexime - 5µg; LBC =Lexofloxacin - 5µg; Antibiotic dics= 6mm

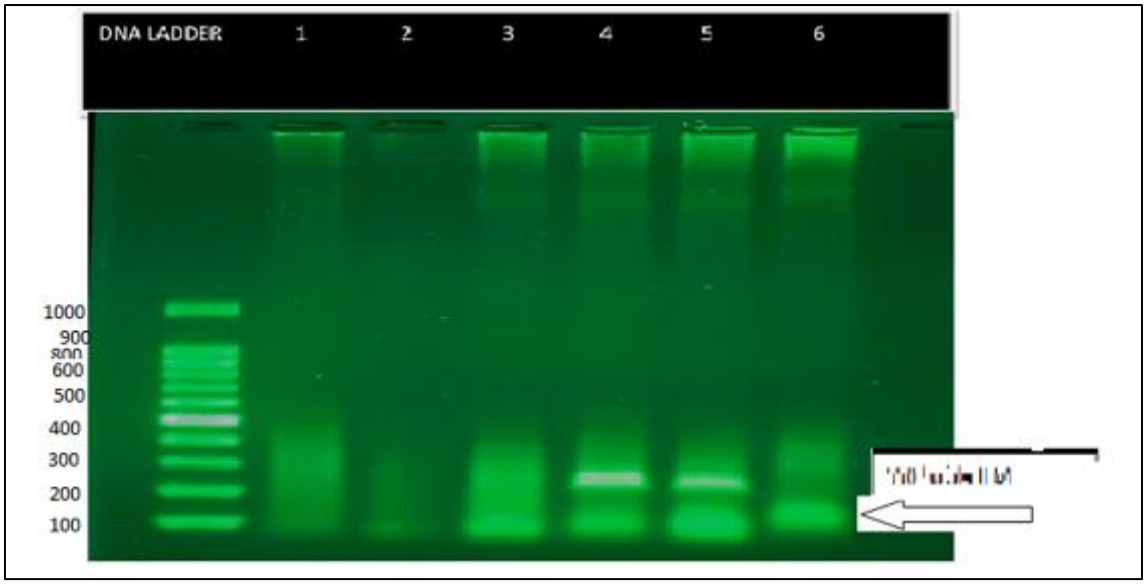

Figure 1 PCR result of Six Blatem gene amplification from Fecal Dropping of pigeon birds. ;[A] *Escherichia coli* strain U5/41 (isolate 4); [B] *Salmonella enterica subs. Enterica* Serovar typhi strain BKQU3X(isolate 5); [C] *Klebsiella pneumoniae* strain Kpn555 (isolate 6)

Table 5 shows the sequencing result for the isolates, out of five isolate that are multidrug resistant three (3) had possess bla TEM gene, and none of the isolates had bla SHV and bla CTX.

Table 5 Blast results for Blatem genes fragments amplified using PCR of Bacteria isolated from Fecal Dropping of pigeons, turkey and dove.

Isolates	**Products size (bp)**	**Match sequence title**	**% Query Cover**	**% Identity**	**Accession Number**
Escherichia coli strain U5/41	550	Blatem	90%	100	CP719746.1
Salmonella enterica Subs enterica Serovar typhi srainBKQU30	550	Blatem	80%	100	CP160063.1
Klebsiella pneumoniae strain Kpn555	550	Blatem	49%	79.52	CP015130.1

4. Discussion

In the current investigation, fecal droppings from pigoen birds in Wamakko, Sokto North, Sokoto South, and Kware Local Government area of Sokoto state were collected to isolate Kleibsiella, Proteus, *E. Coli*, and *Salmonella* species. Only 10 (16) of the 60 samples that were examined for the presence of Entrobacteriaceae members revealed positive results using biochemical characterisation.

Overall, 50% of *Salmonella*, 20% of *E. Coli*, 20% of *Klebsiella*, and 10% of Proteus were isolated. Although these microbes normally act as opportunistic organisms that infiltrate the normal intestinal microbiota, they are rarely capable of causing illness. The most isolated bacterial species is *Salmonella*. As the main cause of typhoid fever and gastroenteritis, it is considered as a significant human pathogen. Birds can acquire this bacterium from contaminated environments in which they inhabit and may also serve as disseminators. As the third most isolated organism, *E. Coli* is also a common organism that is present in soil, water, and plants. Sometimes, like when they acquire virulence genes, its existence does not necessarily indicate that they are ill. This bacterium has the ability to create pathogenic issues in both humans and animals, including birds.

This study's findings were in line with those of Traore (2003), who discovered that chicken intestines in Côte d'Ivoire had a 55.66% *Salmonella* contamination level. Similarly, Dione et al. (2011) found a high prevalence of 67% from chicken fecal samples in the Gambia. Fagbamila et al. (2017) also discovered that commercial poultry farms in Nigeria had significant *Salmonella* prevalence rates (43.6%). Also, Ameh et al., (2001), state prevalences ranging from 11.1 to 65.4%.

The result of this finding is different from Abdoulaye (2000) who reported 15% prevalence rates of *Salmonella* from apparently healthy local chickens sold and slaughtered at a retail market in Zaria. Also, it is line with the work of Beleza et al., (2024) who find high frequency of *E. Coli* (36.0%), among wild birds in brazil followed by *Salmonella*, Proteus mirabilis and *Klebsiella pneumoniae* (1.8%). The morphological characteristic of the isolated *Salmonella* species exhibited Gram- negative, small rod, singular paired an arrangement under a microscope which was in line with the work of Wayne et al., (2001) Since almost every *Salmonella* serotype does not generate indole, hydrolyze urea, or deaminate tryptophan or phenylalanine, all of the isolates were indole and voges-proskaver negative (Popoff and Minor, 2005). Although every isolate was discovered to be mobile, they all used citrate, fermented carbohydrates, and produced urease, methyl red, and hydrogen sulfide.

The sensitivity tests show the five isolates from fecal droppings of pigeon birds were resistant to more than five antibiotics applied (Table 4.7). *E. Coli*, Klebsiella amd Proteus exhibit a high level of resistance (50-100) to the antibiotics tested which include Augmentine, Cefotaxine, Imipinen/Cilastatin, gentamycin, Nalidic acid, Nitrofuranton, Ampiclox and Cefexime, Ceftriazone Sulbactin,Cefexime and Lexofloxacin.

The World Health Organization has raised an alarm that approved antibiotics and those in the clinical pipeline are suitable to reduce the threat of antibiotic resistance. Augmentin, cefuroxine, and ceftazine are essential antibiotics for treating infections caused by these organisms. Increasing reports of resistance to these agents are a public health concern.

In comparison to some of the aminoglycoside antibiotics studied, the majority of isolates from this study show greater resistance to augmentine, gentamycin, and nalidixic acid. This is also consistent with Antonio et al.'s (2021) findings. The fact that these bacteria can produce beta-lactamase may have nothing to do with this.

Over the decades under study, the resistance problem has essentially stayed the same. Despite being an ecological phenomenon, the main cause of antimicrobial resistance in members of the Entrbacteriaceae family is the natural competition among microbes. Low resistance to the antimicrobials was found in Levy's (1983) research on antibiotic-resistant bacteria in human and animal food from 1920 and from African wild animals, however plasmids that transmit resistance elements were found. Lying birds become infected in a series because to the fact that they share virulence elements with other enthropathogens such *Salmonella*, *E. Coli*, Proteus, and Klebsiella species (Albert et al., 1992).

Numerous studies have demonstrated the potential for wild birds to serve as carriers of bacteria resistant to antibiotics. Additionally, there are instances where the movement of wild birds has been linked to the spread of diseases, including the West Nile Virus in the United States (Reed et al., 2003). Similarly, *Salmonella* strains resistant to antibiotics were identified from black-headed gulls by Palmgren et al. (1997), indicating that the bacterium was dispersed by migration. Birds from isolated and preserved habitats have also been found to harbor antibiotic-resistant bacteria, including ESBL-producing *E. Coli* (Guenther et al., 2012). Although this might be seen as a potential human activity tract, in certain instances, it seems more plausible that it spreads through bird migration (Hermandez et al., 2010: Chiu et al., 2002).

Additionally, 13 (34.6%) of the isolates had multiple antibiotic resistance, which was consistent with the findings of Oaks et al. (2010), who found that more than half of the isolates (57.9%) were resistant to at least three antibiotics, and 97.5% of the *E. Coli* strains were resistant to at least one antibiotic, with multiple resistance detected in 74.1% of the isolates, while Majewski et al. (2021) found only 10% and 38% of the isolates to be sensitive to the two antimicrobials, respectively.

Additionally, the study identified 13 (34.6%) cases of multiple antibiotic resistance. It should be noted that the study by Majewski et al., (2014) concerned Klebsiella spp. isolated from hens, which may point to differences in bacterial resistance between different species of poultry.

Since Wu et al. (2016) found that 96.7% of Klebsiella spp. isolated from chickens were multidrug resistant, compared to 20% in our investigation, we can also use their findings as additional evidence of the species factor. The study was consistent with Majewski et al. (2021).

In terms of medication prescription, this is concerning because these bacterial strains have the potential to become cross-resistant, making it difficult and potentially fatal to treat infections caused by them with antibiotics. Beta – lactemase comprises a widely used of cephalosporin antibiotic in human. The most significant β-lactamase genes are variants of CTX-M, SHV, TEM, VEB, GES, PER, TLA and OXA which have broadened the substrate specificity against ceftazidime, cefotaxime and ceftriaxone (Oteo et al., 2016). These genes have broad host range but are predominantly found in *Escherichia coli* and Klebsiella spp. (Bajpai et al., 2007)'The dissemination of extended spectrum beta-lactamase (ESBL) producing among the family of Entrobactriacea in human and animals has increasingly around the glove. Bla TEM, SHV and CTX genes comprise the key forms of ESBL, and are present in wide range of clinically important pathogens worldwide.

Among the five (5) multi drug resistant isolates only three harbor bla TEM gene, but bla SHV and Bla CTX were not detected in the study. BlaTEM, Bla CTX and blaSHV also confer resistance to beta-lactam classes of antibiotics in humans, birds, livestock, and other animals (Ngaiganam, 2019). The presence of beta-lactamase genes in *E. Coli*, *Salmonella* typhi, and Klebsiella pneumoniea isolated from pigeon birds poses a serious threat to human health. This is because pigeon birds are directly connected to environmental features, especially water, and contaminated water plays an important role in the dissemination of beta-lactamase producing Enterobacteriacea in the human community According to this finding, the pigeon birds are highly exposed to antibiotics, most likely as a result of the accumulation of animal and human waste, including household waste.

5. Conclusion

The result of this finding reveals that fecal droppings of pigeon birds host members of Entrobacteriaceae family and *Salmonella* is the most frequent isolates followed by *E. Coli* then Klebsiella and Proteus. Most of these isolates shows high resistant rate to antibiotics tested, presence of these multidrug resistant bacteria in fecal droppings of domesticated birdis , can serve as vehicle of transmission of pathogen from entrobacteriacea group is a matter of great concern from public health point of view because this source can accidentally serve as a potential vehicle for transmission of these spps. to animals and human beings.

Recommendation

Intervention studies are required to control this pathogen from spreading in the environment. A comprehensive approach, involving responsible antibiotic use, enhanced biosecurity, robust surveillance, and public education, is essential to mitigate the impact of MDR Enterobacteriaceae on global health.

Compliance with ethical standards

Disclosure of conflict of interest

No conflict of interest to be disclosed.

Statement of ethical approval

The present research work does not contain any studies performed on animals/humans' subjects by any of the authors

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