A Study of Common Pathogens in Poultry Industries in Ifite-Ogwari, Anyamelum Local Government Area of Anambra State, Nigeria

J. C. Okonkwo[1]; Nwankwo Precious Amaka[2*]; Chigozirim Theresa Ogu[3]; Ezenyilimba BN[4]; Okonkwo AP[5]; Ejivade OM[6]; Okonkwo I. F.[7]; Nwankwo CA[8]

[1,2,4,6,8]Department of Animal Science and Technology, Faculty of Agriculture, Nnamdi Azikiwe University, Awka, Nigeria
[3,7]Department of Applied Microbiology and Brewery, Nnamdi Azikiwe University, Awka,
[5]Department of Animal Nutrition and Forage Science, College of Animal Science and Animal Production, Michael Okpara University of Agriculture, Umudike, Nigeria Nigeria
*Corresponding Author

Received:- 07 February 2025/ Revised:- 17 February 2025/ Accepted:- 22 February 2025/ Published: 28-02-2025

Abstract— *Poultry production is an essential sector in global agriculture, contributing significantly to food security by providing affordable animal protein. However, the prevalence of infectious diseases caused by various pathogens presents substantial economic losses and public health risks. This study dealt with isolation and characterization of common pathogens in poultry flocks within Ifite-Ogwari, Ayamelum local government area of Anambra State, Nigeria. Primary objectives include isolating pathogens from fecal samples of birds raised in the area, characterizing the pathogens and determination of antibiotics resistance profiles of the pathogens using standard biochemical techniques, and assessing their prevalence and distribution across the area. Key bacterial pathogens identified include Salmonella enterica, Campylobacter spp., Escherichia coli, Enterococcus spp., and Methicillin-Resistant Staphylococcus aureus (MRSA). Most of these pathogens from different farms were resistant to various antibiotics indicating subnormal cum improper applications by farmers. The study therefore underscores the urgent need for the government to detail Extension Agents to Ifite-Ogwari in order to educate the poultry farmers on proper use of antibiotics. Again, since most of these isolates are zoonotic, caution should be applied in consumption of animal products from Ifite-Ogwari. The use of alternative bio security measures such as herbs are recommended in order to mitigate the imminent danger of using antibiotics.*

Keywords— Pathogens, Ifite-Ogwari, Antibiotic Resistant, Zoonotics, Bacterial Profile.

I. INTRODUCTION

The poultry industry is susceptible to a wide range of bacterial, viral, fungal, and parasitic pathogens. Bacterial pathogens, including *Salmonella spp.*, *Escherichia coli, Campylobacter spp.*, and *Staphylococcus aureus* are among the most common culprits responsible for disease outbreaks in poultry. They cause high mortality and productivity losses in poultry (Tamer *et al.,* 2020).

Salmonella enterica causes foodborne enteric disease worldwide, representing the second most commonly reported zoonotic pathogen in the world (Lorenzo-Rebenaqu *et al.*, 2022). It is responsible for disease outbreaks associated with significant morbidity and mortality (Ricke *et al.*, 2021). And up to 25% of human *Salmonella* outbreaks, illnesses and hospitalizations are related to poultry sources (Chai *et al.,* 2017). *Salmonella* are gram-negative, facultative anaerobic bacteria belonging to the Enterobacteriaceae family, and are considered commensals of the gut microbiota of mammals, birds, reptiles, amphibians, fish and shellfish (Cosby *et al.,* 2015). *S. enterica* includes more than 2650 serovars (Issenhuth-Jeanjean *et al.*, 2014), and many are implicated as contaminants of poultry meat and eggs, representing a serious concern for public health (Antunes *et al.,* 2016). In poultry, diseases due to *S. enterica* may be grouped into three namely fowl typhoid, pullorum disease and avian paratyphoid. Young poultry are particularly susceptible to gastrointestinal tract (GIT) colonization by *S. enterica*. Its excretion in feces may result in the contamination of the environment and the infection of nearby birds (Cosby *et al.*, 2015). Moreover, poultry meat contaminated with digesta during slaughter is a major risk to public health (Alali *et al.*, 2018).

Campylobacter spp. are ubiquitous bacteria that can be found in various environments, including soil and water, and as commensals of the GIT of poultry. Despite this, they can cause disease in animals and humans and constitute an important cause of foodborne diseases worldwide (Silva *et al.*, 2011). This bacterial genus can be responsible for acute bacterial diarrhea, which is mainly caused by *C. jejuni* and *C. coli*. Although other sources can be responsible for human infection, poultry products are considered the predominant source of human campylobacteriosis (Rickie *et al*., 2021). *Campylobacter spp.* can be introduced in the production farms by wild animals, pests or humans. When infecting poultry, it colonizes the GIT os animals, invades the intestinal epithelium and multiplies rapidly in the intestinal mucus, avoiding clearance and persisting in the animal's GIT (Van Deun *et al.*, 2008). In this way, avian hosts constitute a natural reservoir for *Campylobacter spp*., namely C. jejuni and C. coli (Sahin *et al.*, 2015). According to the European Food Safety Authority (EFSA) and European Centre for Disease Prevention and Control (ECDC), the highest prevalence of *Campylobacter* is observed in fresh meat from broilers (37.5%). Although carriers of *Campylobacter spp.* chickens generally do not exhibit clinical signs. Antibiotics have a limited role in the elimination of *Campylobacter spp.* by these animals due to its high occurrence and commensal character in avian species, and can promote the emergence of resistant strains; therefore, biosecurity practices are the most important method for reducing *Campylobacter* infection at the production level (Hermans *et al* ., 2012).

Human infections are usually associated with the handling, preparation and consumption of contaminated poultry products, and occupational transmission has also been observed. In humans, these pathogens cause gastroenteritis associated with diarrhea, abdominal pain, fever, nausea and vomiting, which usually occur between two and five days after infection. Symptoms are often mild and self-limiting. Antibiotic treatment is not usually required, but severe cases may be treated with macrolides, such as clarithromycin, azithromycin and erythromycin. Ciprofloxacin is not currently used, as resistance to quinolones is now considered to be too high for these antibiotics to be used as an empirical treatment (Sahin *et al.*, 2015). Studies on the antimicrobial drug resistance profile of *Campylobacter spp.* Isolated from broilers, laying hens, chicken carcasses and Chicken meat revealed high frequencies of resistance to nalidixic acid, ampicillin, cephalexin, ciprofloxacin, erythromycin, Gentamicin and tetracycline (de Saraiva *et al*., 2022).

E.coli is a gram-negative bacillus belonging to the Enterobacteriaceae family (Daneshmand *et al*., 2019). It is an important bacterial species in the Human–animal–environment triad, since it is a commensal inhabitant of the digestive tract of animals, including birds, being widely spread via fecal material (Islam *et al*., 2021). This species is often studied as a marker of antimicrobial drug resistance, mainly Due to its widespread distribution and capacity to harbor several genes in mobile genetic elements, serving as a source of Antimicrobial drug resistance determinants to other bacteria (Bass *et al*., 1999). Most *E. coli* are nonpathogenic; however, certain pathogenic serotypes may induce disease. There are several *E. coli* Pathotypes, which can be divided into extra intestinal *E. coli* (ExPEC) and diarrhoeagenic *E. coli* (DEC). Avian pathogenic *E. Coli* (APEC), an ExPEC, may induce colibacillosis in domestic birds, a disease characterized as a local or systemic syndrome That can be transmitted by oral or vertical routes or through inhalation. *E. coli*-associated infections are widely distributed among poultry of all ages. Birds can be asymptomatic until sudden death or present various forms of disease, such as Septicemia, coligranuloma (Hjarre's disease), air sac disease (chronic respiratory disease), swollen-headsyndrome, venerea lColibacillosiscellulitis, peritonitis, salpingitisorchitis, osteomyelitis/synovitis, panophthalmitis, omphalitis/yolk sac infection and enteritis (Nolan *et al.*, 2013). Colibacillosis constitutes the most frequent infectious bacterial disease found in poultry, being responsible for significant economic losses due to the loss of productivity, increased mortality and condemnations of carcasses (Żbikowska *et al.*, 2020).

Enterococcus species are ubiquitous and are commensals of the gastrointestinal microbiota of both humans and animals. Some enterococcal strains have been used as probiotics (Kabir *et al.*, 2009), while others are known to be pathogenic, including in birds (Souillard *et al*., 2022). The transmission of enterococci can occur via vertical and horizontal routes. E. cecorum and E. faecalis are the most Important species associated with avian disease. Pathogenic strains of E. cecorum have been associated with free thoracic Vertebra (FTV) osteomyelitis in broilers (Devriese *et al.*, 2002), resulting in the paralysis of the posterior limbs, and with septicemia related to Pericarditis or hepatitis, which can lead to death. In turn, *E. faecalis* can cause omphalitis and yolk sacculitis, which can lead To sepsis and the death of chicks in the first week of life. Surviving animals may develop chronic diseases, such as valve endocarditis, which can also lead to death (de Saraiva *et al.,* 2022).

Enterococcus spp. can easily acquire resistance determinants and, therefore, play a central role in AMR dissemination. Vancomycin-resistant Enterococcus (VRE) has been associated with economic losses in animal production and healthcare And associated with infections in humans (Khan *et al.,* 2015). Humans are exposed to enterococci from a variety of sources, including other Humans, the environment and foods contaminated with animal's intestinal microbiota. Certain species, such as E. faecalis and E. faecium, are a prominent cause of opportunistic infections in hospitalized humans, causing mild to fatal diseases, such as Endocarditis, urinary tract infections or septicemia (Dea *et al.,* 2019). Studies previously performed have identified high levels of Resistance against aminoglycosides (streptomycin), tetracyclines (doxycycline and tetracycline) and quinolones (ciprofloxacin and enrofloxacin) in enterococci isolated from poultry (de Saraiva *et al*., 2022). Vancomycin resistance, which is reported as infrequent, can be higher in isolates from chickens affected with FTV.

In view of these havocs emanating from these bacterial pathogens, this study was designed to isolate and characterize the major pathogens associated with poultry production in Ifite-ogwari of Ayamelum local government area of Anambra State, Nigeria.

II. MATERIALS AND METHOD

2.1 Study Area:

The research was carried out in ifite-ogwari, which is a town in Ayamelum LGA of Anambra state. The town has five villages namely Amah, Amadie, Aniocha, Isudala and Umuawah. Ifite-ogwari coordinates are latitude: 6.60 412, longitude: 6.950 69.

2.2 Sampling Techniques:

Simple random sampling techniques were used to select three villages from the total villages in ifite-ogwari. Then three biggest farms in each of three villages were selected for this study. The villages selected were Amah, Umuawah and Amadie.

Then, a total of 30 freshly defecated fecal samples were collected from the selected broiler farms in Amah, Umuawah and Amadie. The samples were collected in sterile containers. After collection, the samples were labeled and placed in a sterile plastic containers and was taken to Prof. J. C. Okonkwo and Prof. I. F. Okonkwo Research Laboratory, Nnamdi Azikiwe University, Awka, Anambra State for Analysis.

2.3 Analysis of the Samples:

Each sample was prepared by making dilution in distilled water. They were inoculated by streaking using a wire loop into both MacConkey and Salmonella-shigella ager respectively, and incubated at 37^0C for 24 hours in an incubator. The colonies obtained were sub-cultured to obtain pure colonies.

The pure colonies were subjected to various biochemical tests for proper identification using the methods as described by Chessburugh (2010). Standard biochemical techniques were used to carried out Gram staining, Catalase test, Coagulase test, Oxidase test, Citrate utilization, Indole test, Urease test, Methyl red test, Vloges prostain test, Hydrogen sephide test and Motility test.

2.4 Sensitivity test:

The various pure isolates were subjected to sensitivity test with commercial antibiotic discs using disc diffusion method. They were incubated at 37^0C for 24 hrs. After which the zone of inhibition were measured using a metre rule.

III. RESULT

3.1 Bacteria Isolates:

Tables 1 to 3 present the colony, morphology, gram reaction, and biochemical test results of the isolates from Amah, Umuawa and Amadia, respectively.

3.1.1 Amah Village:

A total of six (6) dormant isolates were obtained from 30 faecal samples collected from Amah town, Table 1.

TABLE 1
BIOCHEMICAL CHARACTERISTICS OF CHICKEN DROPPINGS IN AMAH

Colony morphology	Organisms	Gram rxn	Catalase	Coagulase	Oxidase	Indole	Methyl red	Citrate	Vp	Urease	H$_2$S	Motility test
Colourless small colony	*Enteroccus spp*	+	-	-		-	-	-	+	-	-	-
Pink smooth colony	*E. coli*	-	+	-		+	+	-	-	-	-	+
Dark colonies	*Salmonella*	-	+	-	+	-	+	+	-	-	+	+
Coccci in clusters	*Staplycocci*	+	+	+	-	-	+	-	+	+	+	-
Small cocci in chains	*Streptococci*	+	-	-	-	-	-	-	-	-	-	-

Biochemical tests revealed the organisms to be *Enterococcus spp, E. coli spp, Salmonella spp, Streptococcal spp, Staphylococcal spp and Shigella spp.* These isolates are subjected to antibiotic sensitivity tests with commercial antibiotic discs using disc diffusion methods and the results showed Enterobacter app was sensitive to only referyricin with zone diameter of 20mm Also Streptococcal sp was sensitive to Ciproflaxin with 20mm zone diameter, lerofloxacin 20mm and Erythnycin 10mm. Salmonella spp was sensitive to Ciproflaxin 12mm, E.coli Spp was resistant to all the antibiotics. Shigella spp was sensitive to centanycin 10mm and ciproflaxin 7mm. For Staphylococcal spp heroflaxinzone gene zone diameter of 20mm, Rofanpricin 20mm, Ciproflaxin 12mm, Amoxicillin, 12mm and Ampiclox 5mm.

3.1.2 Umuawa Village:

A total of five (5) dormant isolates were obtained from 30 faecal samples collected from Umuawa village in Ifite-ogwari, and biochemical tests revealed the organisms to be *Salmonella Spps, Shigella spps, E.coli spps, streptococcal apps and Enterococcus spps* (Table 2).

TABLE 2
BIOCHEMICAL CHARACTERISTICS OF BACTERIA ISOLATES FROM DROPPING IN UMUAWA

Colony morphology	Organism	Gram rxn	Catalase	Coagulase	Oxidase	Indole	Methyl red	Citrate	Vp	Urease	H2S	Motility
Dark brown	*Salmonella*	-	+	-	+	-	+	-	-	-	+	+
Small pink colonies	*Shigella spp*	-	+	-	-	+	+	-	-	-	-	-
Round white coloring in chains	 *Streptococci*	+	-	-	-	-	-	-	-	-	-	-
Pink smooth colonies	*E.coli*	-	+	-	-	+	+	-	-	-	-	+
Colorless small colony	*Enterococi*	+	-	-	-	-	-	-	+	-	-	-

These isolates were subjected to sensitivity tests with commercially prepared antibiotics discs using disc diffusion method. The results showed that all the isolates were resistant to all the antibiotics except *Streptocci spp* which was sensitive to Gataryin (10mm diameter) and herofloxacin (8mm diameter).

3.1.3 Amadia village:

As presented in Table 3, four (4) dormant isolates were recovered from 30 faecal samples obtained from Amadia village in Ifite-ogwari, and biochemical tests evinced the organisms to be *Salmonella spp, E. coli spp, Streptocci spp and Bacillus spp.*

TABLE 3
BIOCHEMICAL CHARACTERISTICS OF BACTERIA ISOLATES FROM DROPPING IN AMADIA

Colony morphology	Organism	Gram rxn	Catalase	Coagulase	Oxidase test	Indole test	Methyl red	Citrate	Vp test	Urease	H2S test	Motility test
Dark colour	*Salmonella*	-	+	-	+	-	+	-	-	-	+	+
Pink smooth colonies	*E.coli*	-	+	-	-	+	+	-	-	-	-	+
White small colonies in chain	*Streptococci*	+	-	-	-	-	-	-	-	-	-	-
Long rod	*Bacillus*	-	+	-	-	-	-	+	+	-	+	+

When these isolates were subjected to sensitivity tests with commercially prepared antibiotic discs using disc diffusion methods, *Salmonella* was resistant to all the antibiotics, *E. coli* was resistant to all the antibiotics, *Streptococcal spp* was sensitive to Streptorycin (15mm diameter) and levofloaxin (10mm) and *Bacillus spp* was sensitive to streptomycin (20mm), Ciproflaxin (10mm) and Gentamicin (15mm).

3.2 Summary of Isolates in Ifite-Ogwari:

The summary of the bacterial isolates identified in Amah (T1), Umuawa (T2) and Amadia (T3) are presented in Table 4.

TABLE 4
THE BACTERIAL ISOLATES IDENTIFIED IN AMAH (T1), UMUAWA (T2) AND AMADIA (T3)

Isolates	T1(AMAH)	T2(UMUAWA)	T3(AMADIA)
Salmonella spp	+	+	+
Shigella spp	+	+	-
E coli spp	+	+	+
Streptococci spp	+	+	+
Enterococci spp	+	+	-
Staphylococci spp	+	-	-
Bacillus spp	-	-	+
Key = + indicates presence of a given isolate while – indicates its absence.			

In Amah, virtually all the bacteria isolate studied were present while, ***shigella spp*** and ***Enterococcus spp*** was absent in Amadia. ***Staplycococcal spp*** was absent in Umuawa and Amadia.

IV. DISCUSSION

Generally, four to seven different bacterial isolates were obtained from the study area, and these include *Salmonella spp, Shigella spp, E-coli spp., Enterococcus spp., Streptococcal spp., Staphylococcal spp.* and *Bacillus spp.* Most of these species have been reported by different researchers in different areas (Adegunloye, 2006; Omojowo and Omojasola, 2013)

Salmonella spp is prevalent in all the three villages studied, and agrees with the report of Omojowo and Omojasola (2013) and Adegunloye(2006) who maintained that *Salmonella spp* is rampart in poultry industries. *Salmonella spp*. causes significant challenge in poultry farming due to their implications on public health, economic stability, and animal welfare. These bacteria are zoonotic pathogen, implying that they can be transmitted from animals to humans. Poultry products, particularly undercooked meat and eggs are common vectors for *Salmonella* transmission, leading to infections that range from mild gastrointestinal illness to severe systemic conditions in humans. Vulnerable populations, such as immune compromised individuals, the elderly, and young children, are at an increased risk of severe disease, making *Salmonella* a critical public health concern (Lund *et al.*, 2011). Economically, Salmonella infections in poultry flocks lead to increased mortality rates, reduced growth performance, and lowered egg production. Farmers face additional expenses for treatment, control, and management practices required to mitigate infections. In cases of outbreaks, product recalls and export restrictions can also contribute to significant financial losses. Furthermore, the welfare of infected poultry is compromised, as infections can cause enteritis and septicemia, particularly in young birds, leading to adverse conditions in poultry operations (Marshall & Levy, 2011). Salmonella infections can cause ailment in poultry, manifesting as enteritis and septicemia in young birds, leading to poor welfare conditions. High infection rates in flocks also necessitate the use of antibiotics, which may lead to adverse health effects due to drug side effects. *Salmonella spp.* in poultry has demonstrated resistance to various antimicrobials. Several factors contribute to *Salmonella* resistance to antibiotics. First, the overuse and misuse of antibiotics in agriculture and animal husbandry have accelerated resistance in bacteria. In poultry farming, for example, antibiotics are often used as growth promoters and to prevent infections, even in healthy animals, which can promote resistant *Salmonella* strains (M samtiya *et al.*, 2022). Additionally, improper dosing or incomplete antibiotic courses can leave some bacteria alive, allowing them to adapt and develop resistance. Another factor is the genetic adaptability of *Salmonella*, which can acquire resistance genes through horizontal gene transfer from other resistant bacteria in the environment. This process allows *Salmonella* to rapidly acquire and share resistance traits, particularly in intensive farming environments where bacteria are in close contact (Shu-Kee *et al.*, 2015). Furthermore, the spread of multidrug-riesistant strains is exacerbated by global trade and movement, making containment and treatment of resistant strains even more challenging. In recent years, *Salmonella* strains is resistant to multiple antibiotics, including fluoroquinolones, cephalosporins, and aminoglycosides, have been reported. Multidrug-resistant (MDR) *Salmonella* is especially concerning because it limits treatment options and can prolong illness in affected individuals. For example, strains like *Salmonella* Typhi and *Salmonella* Typhimurium have been observed with significant resistance profiles, making them harder to control. Its infections can lead to prolonged and more severe symptoms, as the typical antibiotics are ineffective. These infections may require extended hospitalization and carry a higher risk of complications, such as bloodstream infections. In severe cases, if alternative treatments fail or the infection is left untreated, antibiotic-resistant *Salmonella* can result in death. Additionally, drug-resistant genes can spread to other bacteria, compounding the problem of antimicrobial resistance. The growing resistance of *Salmonella* to common treatments emphasizes the need for better antibiotic stewardship, improved surveillance, and research into alternative therapies.

4.1 *Shigella spp.:*

Shigella spp was present in Amah and Umuawa village of Ifite-ogwari Ayamelum lGA Anambra State Nigeria. *Shigella spp,* in Amah was sensitive to Gentamicin -10mm and Ciproflaxin 7mm and resistant to all antibiotics in Umuawa and Amadia. *Shigella* is generally known as a human pathogen, but its presence in poultry farming can have significant implications, particularly for zoonotic transmission and food safety concerns. *Shigella* species are less commonly found in poultry compared to other pathogens like *Salmonella* or *Escherichiacoli*, but when they do infect poultry, it can lead to contamination of poultry products, posing a risk to humans who consume or handle these products. *Shigella*-contaminated poultry products can cause shigellosis, a bacterial infection in humans, resulting in symptoms like diarrhea, fever, and abdominal cramps. This can pose a major food safety issue. Poultry can serve as asymptomatic carriers of *Shigella*, transmitting the bacteria to humans indirectly through contaminated food or directly through handling. The contamination risks associated with *Shigella* can lead to product recalls, affecting the poultry industry economically. *Shigella* species have shown high resistance to commonly used antibiotics like ampicillin, tetracycline, and trimethoprim-sulfamethoxazole. This resistance in poultry isolates could limit treatment options if an outbreak occurs. Drug resistance in Shigella is often attributed to its ability to acquire resistance genes from other bacteria through horizontal gene transfer mechanisms, including conjugation and transposable elements, within the gut microbiome of animals. Possible Reasons for Drug Resistance in *Shigella* are Antibiotic Misuse and Horizontal Gene Transfer.

4.2 *E-coli spp.:*

Ecoli spp was present in Amah, Umuawa and Amadia village of Ifite-ogwari Ayamelum lGA Anambra State Nigeria. In all the villages *E.coli spp.* Was resistant to all the antibiotics, which agrees with the report of This observation was consistent with previous reports (Atnafu *et al.,* 2021) that multidrug-resistant bacteria were isolated in poultry litters. *Escherichia coli (E. coli),* particularly pathogenic strains like avian pathogenic *E. coli* (APEC), can lead to a range of diseases in poultry, including colibacillosis. This condition can cause septicemia, peritonitis, air sacculitis, and other infections that significantly impact poultry health and production. It can lead to increased mortality rates, poor weight gain, reduced egg production, and economic losses due to the costs of treatment and prevention. Additionally, *E. coli* infections can compromise the immune system, making birds more susceptible to other infections, which can further reduce farm productivity.

Over the past decades, there has been a notable increase in antimicrobial resistance (AMR) among *E. coli* strains isolated from poultry. Studies have shown that pathogenic *E. coli* in poultry often exhibits resistance to common antibiotics such as tetracycline, sulfonamides, and quinolones, which are frequently used in poultry farming (Nhung *et al.*, 2017). Overuse and Misuse of Antibiotics In poultry farming, Inadequate sanitation and overcrowding in poultry farms can facilitate the spread of resistant *E. coli* strains, making it difficult to control infections without the use of antibiotics and also Administration of antibiotics via feed or water can expose large populations of bacteria to sub-lethal antibiotic concentrations, encouraging the selection of resistant strains (Ajit K *et al.*, 2006) are possible reasons of drug resistant to *E. Coli spp.*

4.3 *Enterococcus spp.:*

Enterococcus spp was present in Amah and Umuawa village of Ifite-ogwari Ayamelum lGA Anambra State Nigeria. From the sensitivity test, In Amah village, *Enterococcus spp.* Was sensitive to only Referyricin with Zone diameter of 20mm and was resistant to all antibiotics in Umuawa. *Enterococcus* species, particularly *Enterococcus* faecalis and *Enterococcus* faecium, are naturally found in the intestinal tracts of animals and can serve as indicators of fecal contamination. In poultry farming, they are significant because they can act as both commensals and opportunistic pathogens, often contributing to infections in poultry as well as posing zoonotic risks to humans. According to Hammerum (2012), *Enterococcus spp*. are opportunistic pathogens that can lead to infections like septicemia and endocarditis in poultry under stress or weakened immune conditions. They can exacerbate other infections and reduce the overall health and productivity of flocks. (Devriese *et al*., 1992) also highlight that some strains of *Enterococcus* are highly virulent and can cause outbreaks in poultry farms, especially when hygiene standards are low or birds are overcrowded. *Enterococcus spp*. has shown high levels of resistance to various antibiotics, including vancomycin, a last-resort antibiotic for treating certain infections in humans. Resistance in poultry-associated *Enterococcus* strains is a major public health concern as it can spread to humans through direct contact, the food chain, or environmental exposure (Valeria *et al.,* 2016). (Jessica *et al.,* 2023) found multidrug-resistant Enterococcus strains in poultry farms, particularly resistant to tetracyclines, macrolides, and aminoglycosides. They attributed this to the use of these antibiotics in poultry feed, which selects for resistant strains over time. (Joshua *et al*., 2004) Also found out that *Enterococcus* strains isolated from poultry farms are frequently identical to those causing infections in humans. This highlights the zoonotic potential of these bacteria and the risks posed by handling poultry or consuming undercooked poultry products.

4.4 *Streptococcal spp.:*

Streptococcal spp. Was present in Amah, Umuawa and Amadia of Ifite-ogwari Ayamelum lGA Anambra State Nigeria. The antimicrobial sensitivity profile observed in the *Streptococcus spp.* isolated from Amah, Umuawa, and Amadia reveals varying levels of susceptibility to antibiotics, specifically Ciprofloxacin, Levofloxacin, Erythromycin, and Streptomycin. This variability in sensitivity patterns can be linked to geographical differences, local antimicrobial usage patterns, and potential genetic variation within the bacterial populations.

Streptococcus spp. from Amah showed sensitivity to Ciprofloxacin and Levofloxacin, with zone diameters of 20 mm, indicating a strong inhibition. Additionally, a moderate sensitivity to Erythromycin was observed with a 10 mm zone. The high sensitivity to Ciprofloxacin and Levofloxacin suggests that these fluoroquinolones are effective in this area, possibly due to limited previous exposure or use of these antibiotics in Amah.

In Umuawa, *Streptococcus spp* sensitivity to Levofloxacin was significantly lower, with a zone diameter of 8 mm, indicating reduced efficacy. The lower sensitivity might be attributed to increased exposure to Levofloxacin in Umuawa, potentially leading to increased resistance. This trend aligns with studies indicating regional differences in resistance, where frequent antibiotic use tends to decrease effectiveness.

Higher sensitivity of *Streptococcus spp* was observed for Streptomycin (15 mm) and Levofloxacin (10 mm), indicating a moderate level of inhibition in Amadia. The sensitivity to Streptomycin in Amadia may suggest limited prior exposure to this antibiotic, aligning with reports from other rural areas where less commonly used antibiotics show retained efficacy. The moderate sensitivity to Levofloxacin is consistent with findings in similar regions where Streptococcus spp. display variable susceptibility based on antibiotic exposure history.

Studies conducted in various regions have reported similar observations. For instance, Canton *et al.* (2003) found that *Streptococcus spp*. isolates in urban areas showed higher resistance to fluoroquinolones, particularly Levofloxacin, than those in rural settings, suggesting that usage patterns influence susceptibility (Carbon *et al.,* 2003). Hayes *et al.* (2019) reported varying Erythromycin sensitivity in *Streptococcus spp.*, with resistance patterns aligning closely to local prescribing practices and historical exposure, similar to the moderate sensitivity noted in Amah. These findings indicate that antibiotic susceptibility among *Streptococcus spp.* is not only species-specific but also influenced by regional antibiotic use. The data emphasize the need for region-specific guidelines on antibiotic usage to prevent resistance development. Certain strains of *Streptococcus* found in poultry have developed resistance to various antibiotics. Common antibiotics to which Streptococcus has shown resistance include:Tetracyclines, Penicillin,Lincomycin, Clindamycin etc.

4.5 *Staphylococcal spp.:*

Staphylococcal spp. Was present in Amah village of Ifite-ogwari Ayamelum lGA Anambra State Nigeria. The antimicrobial sensitivity profile observed in the *Staphylococcal spp.* Isolated in Amah village displayed varied sensitivity to the antibiotics tested, with levofloxacin showing the highest zone of inhibition at 20 mm, followed by ciprofloxacin and amoxicillin, each at 12 mm, and Ampiclox at only 5 mm. Levofloxacin's 20 mm zone of inhibition against *Staphylococcalspp.* reflects strong effectiveness. Studies have shown that fluoroquinolones like levofloxacin remain highly effective against various strains of *Staphylococcus spp.*, particularly methicillin-sensitive strains. For instance, Andrejs *et al.* (2024) reported that levofloxacin maintained a high level of efficacy against Staphylococcal isolates in clinical samples, with zones of inhibition ranging from 18–25 mm, highlighting its potency as an effective treatment option. Ciprofloxacin, showing a 12 mm inhibition zone in my findings, has also demonstrated moderate effectiveness against Staphylococcal spp. in similar studies. In research conducted by Aref *et al*. (2022), ciprofloxacin showed zones of inhibition between 10–14 mm against *Staphylococcal spp*. isolated from hospital settings, suggesting that while effective, ciprofloxacin's efficacy may be limited due to rising resistance trends in some *Staphylococcal* strains. With a 12 mm inhibition zone, amoxicillin showed intermediate sensitivity to *Staphylococcal spp.* in your results. Amoxicillin has generally shown lower efficacy against *Staphylococcus spp.*, especially in cases where beta-lactamase production or methicillin resistance is present. Research by Supatcharee (2016) supports these findings, where Staphylococcal isolates had zones of inhibition for amoxicillin averaging around 10–13 mm, which is consistent with my results. Ampiclox had a minimal inhibition zone of 5 mm, indicating poor effectiveness against Staphylococcal spp. This outcome is also supported by recent studies, such as one conducted by Sabina *et al.* (2023) which showed similarly low sensitivity rates for Ampiclox against Staphylococcus spp., with zones of inhibition below 7 mm. This low effectiveness is often due to the resistance mechanisms that *Staphylococcus spp.* develop against beta-lactam/beta-lactamase inhibitor combinations. certain species of *Staphylococcus*, particularly *Staphylococcus aureus*, are known to be resistant to multiple drugs. The most notable drug-resistant strain is Methicillin-resistant *Staphylococcus aureus* (MRSA), which shows resistance to methicillin and other commonly used antibiotics, including penicillin and amoxicillin.

4.6 *Bacillus spp.:*

Bacillus spp was found in Amadia village of Ifite-ogwari Ayamelum lGA Anambra State Nigeria. This current study shows that *Bacillus spp.* isolated from Amadia showed sensitivity to streptomycin (20 mm), ciprofloxacin (10 mm), and gentamicin (15 mm). (Christian *et al.*, 20) found that *Bacillus* isolates from poultry in Pakistan displayed high resistance to tetracycline but showed sensitivity to aminoglycosides such as streptomycin and gentamicin, which agrees with this current study. However, ciprofloxacin resistance was more common in their study, suggesting that geographical and environmental factors can significantly influence antibiotic susceptibility patterns. (Anthony *et al*., 2016) discussed the emergence of antibiotic resistance among *Bacillus spp.* in various clinical settings. Their study noted increased resistance to fluoroquinolones, which contrasts with your findings of sensitivity to ciprofloxacin. This discrepancy highlights the need for localized studies to assess resistance patterns accurately. *Bacillus* cereus, a common pathogenic species, is often resistant to multiple antibiotics, including beta-lactams, aminoglycosides, and some macrolides. Resistance can be due to the production of beta-lactamases or other mechanisms. Other *Bacillus* species, like Bacillus subtilis, are generally less pathogenic and may show some sensitivity to antibiotics, but resistance can still occur, particularly in strains that have been exposed to antibiotics over time. *Bacillus* cereus, can cause foodborne illnesses, which can lead to gastrointestinal issues, such as diarrhea and vomiting. In more severe cases, it can cause infections in individuals with weakened immune systems, leading to more serious conditions such as bacteremia or meningitis.

V. CONCLUSION

The common pathogens threatening poultry industry in Ifite-Ogwari include *Salmonella spp., Shigella spp., E. coli spp., Enterococcus spp., Streptococcal spp., Staphylococcal spp.,* and *Bacillus spp*. The economic implications to farmers include increased mortality rates, reduced production, and the costs associated with managing these infections.

Furthermore, most of these pathogens are zoonotic and resistance to commonly used antibiotics. The presence of multidrug-resistant strains poses a serious threat not only to poultry health but also to the safety of poultry products for human consumption. Therefore, effective management strategies, including improved antibiotic stewardship and enhanced biosecurity measures, are essential to mitigate the impact of these pathogens and promote sustainable poultry farming practices in the region.

RECOMMENDATIONS

1) **Implement Antibiotic Stewardship Programs:** Farmers should adopt responsible antibiotic use practices to minimize the development of resistance. This includes using antibiotics only when necessary and adhering to prescribed dosages.

2) **Enhance Biosecurity Measures:** Poultry farms should implement stringent biosecurity protocols to prevent the introduction and spread of pathogens. This includes measures such as proper sanitation, controlling access to farms, and regular health monitoring of flocks.

3) **Regular Surveillance and Monitoring:** Establish ongoing surveillance programs to monitor the presence of bacterial pathogens and their resistance patterns in poultry populations. This data will be crucial for informing treatment decisions and management practices.

4) **Education and Training:** Provide training and resources for poultry farmers on the risks associated with antibiotic resistance and the importance of maintaining good hygiene practices. Workshops and extension services can help disseminate this knowledge.

5) **Research into Alternative Treatments:** Invest in research to explore alternative therapies and management strategies for controlling bacterial infections in poultry. This includes evaluating the use of probiotics, vaccines, and other non-antibiotic interventions.

6) **Collaboration with Public Health Authorities:** Foster partnerships between poultry farmers, veterinary services, and public health officials to address the broader implications of zoonotic diseases and develop integrated approaches to disease management.

7) **Consumer Awareness Programs:** Educate consumers about the importance of proper cooking and handling of poultry products to reduce the risk of foodborne illnesses associated with these pathogens.

By adopting these recommendations, stakeholders in the poultry industry can enhance flock health, safeguard public health, and promote economic viability within the sector. Implementing these strategies will be crucial in combating the growing challenge of antimicrobial resistance and ensuring a sustainable future for poultry farming in Ifite-Ogwari.

REFERENCES

[1] Alali, W. Q., & Hofacre, C. L. (2018). Preharvest food safety in broiler chicken production. *Preharvest food safety,* 69-86.

[2] Antunes, P., Mourão, J., Campos, J., & Peixe, L. (2016). Salmonellosis: the role of poultry meat. *Clinical microbiology and infection,* 22(2), 110-121.

[3] Atif, M., Asghar, S., Mushtaq, I., Malik, I., Amin, A., Babar, Z. U. D., & Scahill, S. (2019). What drives inappropriate use of antibiotics? A mixed methods study from Bahawalpur, Pakistan. *Infection and drug resistance,* 687-699.

[4] Atif, M., Sarwar, M. R., Azeem, M., Naz, M., Amir, S., & Nazir, K. (2016). Assessment of core drug use indicators using WHO/INRUD methodology at primary healthcare centers in Bahawalpur, Pakistan. *BMC health services research,* 16, 1-9.

[5] Bass, L., Liebert, C. A., Lee, M. D., Summers, A. O., White, D. G., Thayer, S. G., & Maurer, J. J. (1999). Incidence and characterization of integrons, genetic elements mediating multiple-drug resistance, in avian Escherichia coli. *Antimicrobial Agents and Chemotherapy,* 43(12), 2925-2929.

[6] Canton, R., Morosini, M., Enright, M. C., & Morrissey, I. (2003). Worldwide incidence, molecular epidemiology and mutations implicated in fluoroquinolone-resistant Streptococcus pneumoniae: data from the global PROTEKT surveillance programme. *Journal of Antimicrobial Chemotherapy,* 52(6), 944-952.

[7] Chai, S. J., Cole, D., Nisler, A., & Mahon, B. E. (2017). Poultry: The most common food in outbreaks with known pathogens, United States, 1998–2012. *Epidemiology & Infection,* 145(2), 316-325.

[8] Cosby, D. E., Cox, N. A., Harrison, M. A., Wilson, J. L., Buhr, R. J., & Fedorka-Cray, P. J. (2015). Salmonella and antimicrobial resistance in broilers: A review. *Journal of Applied Poultry Research,* 24(3), 408-426.

[9] Daneshmand, A., Kermanshahi, H., Sekhavati, M. H., Javadmanesh, A., & Ahmadian, M. (2019). Antimicrobial peptide, cLF36, affects performance and intestinal morphology, microflora, junctional proteins, and immune cells in broilers challenged with E. coli. *Scientific reports,* 9(1), 14176.

[10] Dea, M.O.; Sahibzada, S.; Jordan, D.; Laird, T.; Lee, T.; Hewson, K.; Pang, S.; Abraham, R.; Coombs, G.W.; Harris, T.; et al. Genomic, Antimicrobial Resistance, and Public Health Insights into Enterococcus spp. from Australian Chickens. J. Clin. Microbiol. 2019, 57, e00319.

[11] de Saraiva, M.M.S.; Lim, K.; do Monte, D.F.M.; Givisiez, P.E.N.; Alves, L.B.R.; de Neto, O.C.F.; Kariuki, S.; Júnior, A.B.; de Oliveira, C.J.B.; Gebreyes, W.A. Antimicrobial Resistance in the Globalized Food Chain: A One Health Perspective Applied to the Poultry Industry. Braz. J. Microbiol. 2022, 53, 465–486

[12] Devriese, L. A., Cauwerts, K., Hermans, K., & Wood, A. M. (2002). Enterococcus cecorum septicaemia as a cause of bone and joint lesions resulting in lameness in broiler chickens.

[13] Devriese, L. A., Laurier, L., Herdt, P. D., & Haesebrouck, F. (1992). Enterococcal and streptococcal species isolated from faeces of calves, young cattle and dairy cows. *Journal of Applied Microbiology*, 72(1), 29-31.

[14] Hammerum, A. M. (2012). Enterococci of animal origin and their significance for public health. *Clinical Microbiology and Infection,* 18(7*)*, 619-625.

[15] Hayes, J. R., English, L. L., Carr, L. E., Wagner, D. D., & Joseph, S. W. (2004). Multiple-antibiotic resistance of Enterococcus spp. isolated from commercial poultry production environments. *Applied and Environmental Microbiology,* 70(10), 6005-6011.

[16] Hayes, K. M. (2020). Group B Streptococcus: molecular epidemiology, pathogenic profiling and control strategies.

[17] Hermans, D.; Pasmans, F.; Messens, W.; Martel, A.; Van Immerseel, F.; Rasschaert, G.; Heyndrickx, M.; Van Deun, K.; Haesebrouck, F. Poultry as a Host for the Zoonotic Pathogen Campylobacter jejuni. Vector-Borne Zoonotic Dis. 2012, 12, 89–98.

[18] Islam, M. S., Nayeem, M. M. H., Sobur, M. A., Ievy, S., Islam, M. A., Rahman, S., ... & Rahman, M. T. (2021). Virulence determinants and multidrug resistance of Escherichia coli isolated from migratory birds. *Antibiotics*, 10(2), 190.

[19] Issenhuth-Jeanjean, S., Roggentin, P., Mikoleit, M., Guibourdenche, M., De Pinna, E., Nair, S., ... & Weill, F. X. (2014). Supplement 2008–2010 (no. 48) to the white–Kauffmann–Le minor scheme. *Research in microbiology*, 165(7), 526-530.

[20] Kabir, S.M.L. The Role of Probiotics in the Poultry Industry. *Int. J. Mol. Sci*. 2009, 10, 3531–3546.

[21] Khan, H. A., Ahmad, A., & Mehboob, R. (2015). Nosocomial infections and their control strategies. *Asian pacific journal of tropical biomedicine*, 5(7), 509-514.

[22] Lorenzo-Rebenaque, L., Malik, D. J., Catalá-Gregori, P., Torres-Boncompte, J., Marin, C., & Sevilla-Navarro, S. (2022). Microencapsulated bacteriophages incorporated in feed for Salmonella control in broilers. *Veterinary Microbiology*, 274, 109579.

[23] Nhung, N. T., Chansiripornchai, N., & Carrique-Mas, J. J. (2017). Antimicrobial resistance in bacterial poultry pathogens: *a review. Frontiers in veterinary science,* 4, 126.

[24] Nolan, L. K., Barnes, H. J., Vaillancourt, J. P., Abdul-Aziz, T., & Logue, C. M. (2013). Colibacillosis. *Diseases of poultry*, 751-805.

[25] Omojowo, F., & Omojasola, F. (2013). Antibiotic resistance pattern of bacterial pathogens isolated from poultry manure used to fertilize fish ponds in new Bussa, Nigeria. *Albanian Journal of Agricultural Sciences*, 12(1), 81.

[26] Ricke, S. C. (2021). Strategies to improve poultry food safety, a landscape review. *Annual review of animal biosciences*, 9(1), 379-400.

[27] Sahin, O.; Kassem, I.I.; Shen, Z.; Lin, J.; Rajashekara, G.; Sahin, O.; Kassem, A.I.I.; Shen, B.Z.; Lin, A.J.; Rajashekara, C.G.; et al. Campylobacter in Poultry: Ecology and Potential Interventions. Avian Dis. 2015, 59, 185–200.

[28] Silva, J., Leite, D., Fernandes, M., Mena, C., Gibbs, P. A., & Teixeira, P. (2011). Campylobacter spp. as a foodborne pathogen: a review. *Frontiers in microbiology*, 2, 200.

[29] Souillard, R., Laurentie, J., Kempf, I., Le Caër, V., Le Bouquin, S., Serror, P., & Allain, V. (2022). Increasing incidence of Enterococcus-associated diseases in poultry in France over the past 15 years. *Veterinary Microbiology*, 269, 109426.

[30] Van Deun, K., Pasmans, F., Ducatelle, R., Flahou, B., Vissenberg, K., Martel, A., ... & Haesebrouck, F. (2008). Colonization strategy of Campylobacter jejuni results in persistent infection of the chicken gut. *Veterinary microbiology*, 130(3-4), 285-297.

[31] Żbikowska, K., Michalczuk, M., & Dolka, B. (2020). The use of bacteriophages in the poultry industry. *Animals*, 10(5), 872.