



ISSN 2278 – 0211 (Online)

Prevalence of Salmonella Isolated from Poultry Farms and Domestic Chicken Coops in Southern Taraba, North-East, Nigeria

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Abstract:

Salmonella remains a public health menace responsible for reoccurring cases of gastroenteric disorders and morbidity. Poultry sources, including eggs, meat, and excretes, are significant sources of zoonotic *Salmonella* transmission in the environment. This first-of-its-kind prevalence research in Southern Taraba was conducted in Donga, Takum, Wukari, and Ibi communities. A total of 500 fecal samples collected from small-scale poultry farms and domestic chicken coops were examined using standard microbiological techniques. The highest number of *Salmonella* isolates from this research was recorded in Wukari, with 36. This was closely followed by Takum, with a total of 27 isolates, while Ibi and Donga had 19 and 16 isolates, respectively. Overall, a total of ninety-six (96) of all samples examined were positive for *Salmonella*, polling a high prevalence of 19.6%. The considerable risk factors identified in this study were:

- Unhygienic poultry feed processing,
- Farm economic activities coupled with poor biosafety decisions, and
- Attitudes of farm attendants in the farms sampled

As observed in this research, high prevalence has necessitated the imperative need for molecular characterization, and antibiogram analysis of *Salmonella* isolates from the area studied.

Keywords: *Salmonella*, poultry, chicken coop, prevalence, Taraba

1. Introduction

Amid the emergence of new strains of *Salmonella* species, the onerous effect of its implications on food poisoning has remained a global public health issue [1], contributing to world morbidity and mortality rates. This has resulted in a significant global economic loss owing to the money spent on combating the cumbersome symptoms of the infection [2]. In the year 2010 alone, over 150,000 deaths were attributed to over 80 million cases of reported food-borne *Salmonella* [3]. The genus *Salmonella* belongs to the order *Enterobacteriales*, a member of the family *Enterobacteriaceae* [4]. Members of the genus *Salmonella* consist of peritrichous, motile, Gram-negative, non-spore-forming rod-shaped bacteria [5]. *Salmonella* predominantly lives in the intestinal tracts of humans and other warm and cold-blooded animals as their natural habitats [5, 6]. *Salmonella* is disseminated into natural habitats such as soil, water bodies, and food plants through fecal contamination from infected persons. Under favorable temperature, pH, and humidity, *Salmonella* can survive several weeks inside water bodies and several years in the soil but does not significantly multiply in these natural habitats, except in the digestive tract of humans and animals [7]. However, the *Salmonella* bacterium remains viable in the natural environment and can cause infection. According to the spectrum of disease they cause, Serovars of *Salmonella enterica* sub-species are divided into two main groups: Typhoidal Serovars (TS) and Non-Typhoidal Serovars (NTS). TS is responsible for typhoid and paratyphoid fever in humans, while the NTS *Salmonella enteritidis* and *Salmonella typhimurium* are responsible for over 95% of clinical cases of *Salmonella* gastroenteritis in humans and other animals. Nonetheless, other serovars of specie *enterica* may be pathogenic to man and domestic animals but are rarely isolated from clinical specimens, while serovars of *S. bongori* specie are predominant in birds and other cold-blooded vertebrates [7]. *Salmonella* infections are collectively termed Salmonellosis.

Symptoms of *Salmonella* infection are more rapid and fatal among immune-compromised patients, infants, and individuals with blood diseases [5]. TS is transmitted from an infected human to a non-infected human, and the infections are limited to humans and do not occur in animals [8]. NTS are commonly classified as zoonotic pathogens because; they are often transmitted from infected animals to humans by direct contact [9]. However, consumption of NTS-contaminated

food can also increase the risk of transmitting the infection [10]. Chickens are important animals that harbor the NTS and readily disseminate it into the environment [11]. The poultry business is very lucrative in Nigeria for its value-added chain relevance [12], which is why more zoonotic *Salmonella* contamination is often linked to chicken sources [13]. Hence, this research became necessary as we investigated the prevalence of *Salmonella* species isolated from animal sources, particularly in small-scale poultry farms and domestic chicken coops.

For this research, a domestic chicken coop is defined as a homemade structure where chickens are kept safe for rearing and often allowed to roam around the immediate environment to scavenge for daily survival and later return to roost. Moreover, small-scale poultry is a poultry farm where chicken is kept safe for the purpose of commercial production of meat and eggs, requiring minimal resources and labor.

2. Methods

This *in-vitro* experimental study was conducted to investigate the prevalence and antibiogram of *Salmonella* species isolated from poultry sources in selected locations in Southern Taraba, particularly Donga, Wukari, Ibi, and Takum, of which the majority of occupants are mostly farmers.

2.1. Sample Collection and Culturing

A total of 400 Chicken droppings were collected from 40 small-scale poultry farms, and 100 Chicken droppings were sampled from 20 domestic chicken coops in Donga, Wukari, Ibi, and Takum areas of Southern Taraba State. A semi-structured questionnaire was administered to attendants in all farms sampled to investigate their waste disposal strategy and the attitude towards sanitary standards observed in the poultry.

1g of each sample (chicken dropping) was dissolved in 10ml of sterile water. Using the pour plate method, 1ml each of the samples was poured into already prepared Nutrient and MacConkey agar, respectively, and incubated at 37°C for 24 hours for further examination. Noticeable colonies were sub-cultured on nutrient agar and incubated for 37°C for 24 hours to obtain pure isolates. Gram staining and other biochemical tests such as Catalase, Indole, Methyl red, Citrate, and Triple Sugar Fermentation (TSI) were carried out on all isolates. The stock culture was taken for further molecular analysis.

3. Results

Table 2 shows the distribution of *Salmonella-positive* poultry farms in the selected communities across Southern Taraba State. Of the 500 chicken fecal samples examined from both small-scale poultry farms and domestic chicken coops, 98 were positive for *Salmonella* with a farm prevalence of 50%, while domestic poultry coop prevalence was pegged at 30%. The actual prevalence of chicken poop sampled is 18.5% and 24% for small-scale poultry and domestic poultry coop, respectively, as shown in table 2 below. Looking at the prevalence of *Salmonella* per surveyed community, the highest prevalence was recorded in Wukari with 28.8%, which was closely followed by Takum with a total prevalence of 21.6. Besides, Ibi and Donga had the lowest prevalence of 15.2% and 12.8, respectively. The morphological and biochemical characteristics of isolated and identified bacterial pathogens are presented in table 1.

Isolate	Morphological Characteristic	Gram Stain Reaction	Biochemical Test						Organism
			CAT	INDO	MR	LAC	SUC	GLU	
A	Smooth, low convex, greyish white, and translucent	Negative bacilli	+	-	+	-	-	+	<i>Salmonella</i>

Table 1: Identification of *Salmonella* Species Isolated from Poultry Droppings

Location of Study	Small Scale Poultry Surveyed	No. of Samples Collected	Domestic Chicken Coop Surveyed	No. of Samples Collected	Salmonella Positive Small Scale Poultry		Prevalence in Small Scale Poultry (A)		Salmonella Positive Domestic Chicken Coop		Prevalence in Domestic Chicken Coop (B)		Total Positive Sample	Total Prevalence of A and B
					Count	%	Count	%	Count	%	Count	%	Count	%
					Wukari	10	100	5	25	6	60	29	29	2
Ibi	10	100	5	25	4	40	15	15	1	20	4	16	19	15.2
Donga	10	100	5	25	4	40	11	11	1	20	5	20	16	12.8
Takum	10	100	5	25	6	60	19	19	2	40	8	32	27	21.6
4	40	400	20	100	20	50%	74	18.5%	6	30%	24	24%	98	19.6%

Table 2: *Salmonella* Prevalence in Poultry Farms and Chicken Coops in Southern Taraba

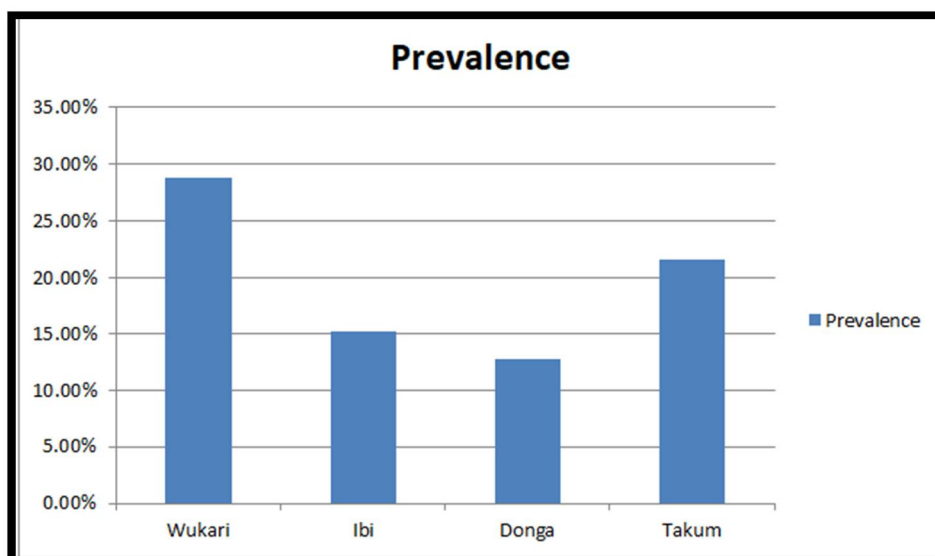


Figure 1: Chart Representing Salmonella Prevalence Distribution in Southern Taraba

4. Discussion

This is an unprecedented study heralding baseline information on *Salmonella* activity in poultry sources in Taraba State, Nigeria. Of the 500 chicken fecal samples examined from small-scale poultry farms and domestic chicken coops, 98 were positive for *Salmonella*, giving a prevalence of 19.6%. Similar findings have been documented by [11] for neighboring Bauchi State in a study investigating *Salmonella* serovars and their distribution in Nigerian commercial chicken layer farms. Among the findings is the prevalence of *Salmonella* infection among chickens in Bauchi, established at 18.1%, with a corresponding farm prevalence of 57.1%. Bauchi State is a North Eastern State like Taraba State, where this current study was undertaken. Additionally, [14] discovered 15.9% *Salmonella* prevalence in commercial poultry farms in selected States in Northern Nigeria. The prevalence recorded from this study, as well as that of [11, 14], is relatively high compared to the low prevalence of less than 3% zoonotic *Salmonella* contamination in most European Union member countries [11]. Nonetheless, industrialized and developed worlds like the United States of America (USA) still experience high rates of *Salmonella* infection in poultries. Environmental and personal behavioral factors have been highlighted severally as blameable for the discrepancies in the recorded prevalence rates among populations [11]. Contamination from poor preservation of poultry feed components and unhygienic packaging coupled with the temperate weather conditions in the area under study is a prime contributor to the high rates of *Salmonella* prevalence recorded in this study. This is because the flagellate organism *Salmonella* thrives very well and multiplies in a humid and warm environment [15]

Unhygienic practices of farm attendants have shown to remarkably contribute to high *Salmonella* contamination in farms. Simple and safe hygienic poultry farm practices, such as cleaning, sanitizing, and disinfecting surfaces, utensils, protective equipment, and other objects, as well as hand washing, were observed in this study to be stoically ignored by farm attendants. This essential biosafety protocol ignored by attendants was also observed by [16] as a significant facilitator of *Salmonella* contamination and spread in farms and environments. Furthermore, the transmission of *Salmonella* from poultry farms to chickens in a domestic coop is believed to be possible due to indiscriminate and improper waste disposal practices of poultry farms. This hypothetical view is supported by findings by [17] which established that rodent activities in farms and environments have increased the shedding of *Salmonella* in environments leading to contamination of other domestic animals and humans. This is because homegrown chickens will get contaminated as they scavenge for food in poultry waste disposal sites and other areas where rodent excretes has contaminated. Similarly, cattle rearing and livestock trade have an increased chance of the spread of *Salmonella* infection among Chickens [12]. The nomadic movement of cattle and other animals coupled with intense commercialized farming, including fishing, as observed in the areas under investigation, necessitates indiscriminate defecation and indecorous waste disposal, respectively. These wastes may contain *Salmonella* and contaminate the immediate environment. Interstate trade of chicken livestock and inter-border smuggling of livestock has shown to significantly increase the chances of vertical and horizontal transmission of *Salmonella* among chickens in poultry farms and domestic coops.

The high prevalence of *Salmonella*, as documented in this research, together with similar activities of other pathogenic microorganisms, has raised the urgent necessity for a proper antibiogram analysis of isolates with the discovery of alternative antimicrobials, particularly of plant origin. Plant extracts have been suggested by [18] to be the future of curative medicine. This research is limited by poor sample size and small geographical coverage. However, futuristic aggressive research is being considered to investigate the molecular characterization and antibiogram patterns of isolates.

5. Conclusion

This study has unearthed baseline information on *Salmonella*. More importantly, its high prevalence in southern Taraba, Nigeria. Therefore, molecular characterization of isolates and exploration of in-vitro analysis of phytochemicals as an alternative to chemotherapy is recommended. This will undoubtedly proffer guidelines to experts and professionals

towards a wilder public health consultation in the management of Salmonellosis in Southern Taraba environments in particular and, extensively, Nigeria at large. Hence, further research is recommended.

6. References

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