



Prevalence and Antimicrobial Resistance of *Streptococcus dysgalactiae* in Commercial Broiler Farms in Barishal, Bangladesh

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ABSTRACT

Streptococcus dysgalactiae (*S. dysgalactiae*) is a significant pathogen affecting veterinary and public health. However, data on its presence and antimicrobial resistance in poultry production in Bangladesh are scarce. The present study aimed to investigate the prevalence, identification methods, and antibiotic susceptibility profiles of *S. dysgalactiae* in poultry, water, and feed samples collected from poultry farms in the coastal regions of Barishal, Bangladesh. A total of 64 samples were randomly collected, including poultry samples (heart, intestine, feces) and farm-associated sources (water and feed). These samples were analyzed using conventional phenotypic methods, including culture characteristics, hemolytic activity on blood agar, Gram staining, and catalase testing. Antimicrobial susceptibility was determined by the Kirby-Bauer disk diffusion method. Molecular confirmation by polymerase chain reaction (PCR) was not performed. *S. dysgalactiae* was found in 26 (40.62%) samples, with a significantly higher occurrence in poultry samples (52.63%) compared to environmental samples (23.08%). Among poultry samples, intestinal specimens exhibited the highest isolation frequency. All isolates were resistant to ampicillin and penicillin, while moderate resistance was observed to amoxicillin, azithromycin, streptomycin, doxycycline, and oxytetracycline. Comparatively lower resistance rates were detected for ciprofloxacin, levofloxacin, and gentamicin. Multidrug resistance was identified among isolates collected from poultry and environmental samples. The current findings demonstrated the presence of multidrug-resistant *S. dysgalactiae* in poultry production systems in coastal Barishal and provided baseline epidemiological data for Bangladesh. The study highlighted the need for prudent antimicrobial use, stronger farm biosecurity, and continuous surveillance.

Keywords: Antibiotic resistance, Broiler chicken, Poultry, Prevalence, *Streptococcus dysgalactiae*

INTRODUCTION

Avian streptococcosis is an important bacterial disease of poultry caused by different *Streptococcus* species, including *Streptococcus dysgalactiae* (*S. dysgalactiae*; McDougall et al., 2014; Watanabe et al., 2016). Streptococci are Gram-positive, catalase-negative, chain-forming cocci that commonly inhabit the skin and mucosal surfaces of animals as opportunistic pathogens (De Vos et al., 2009). Under favorable conditions, *S. dysgalactiae* can cause septicemia and a range of systemic infections affecting the cardiovascular, reproductive, musculoskeletal, and ocular systems, leading to significant morbidity and mortality in poultry (Watanabe et al., 2016; Idalan et al., 2026). Of the more than 60 recognized *Streptococcus* species, only a few, such as *S. dysgalactiae*, have been identified in poultry, underscoring its growing significance in veterinary settings (McDougall et al., 2014; Watanabe et al., 2016).

S. dysgalactiae is traditionally classified into two subspecies, including *S. dysgalactiae* subsp. *dysgalactiae* and *S. dysgalactiae* subsp. *equisimilis*. The subspecies *dysgalactiae* typically demonstrates alpha-hemolysis or is non-hemolytic on blood agar and is frequently associated with Lancefield group C (Vandamme et al., 1996). In contrast, *S. dysgalactiae* subsp. *equisimilis* typically forms β -hemolytic colonies and is most often categorized within Lancefield groups C and G (Vieira et al., 1998). *S. dysgalactiae* subsp. *equisimilis* has been identified as a pathogen affecting humans and different domestic mammals. However, recent reports have documented its isolation from poultry with septicemia, endocarditis, and ocular infections, thereby indicating that poultry may also constitute a susceptible host (McDougall et al., 2014; Watanabe et al., 2016; Idalan et al., 2026). The increasing detection of *S. dysgalactiae* in poultry and farms underscores its growing significance in veterinary medicine and highlights the need to understand its epidemiology, pathogenic potential, and antimicrobial resistance in poultry production systems (Watanabe et al., 2016; Glambek et al., 2024). The infections can have significant economic impacts, especially in developing countries where poultry farming is vital for food security and rural livelihoods (FAO, 2019).



The pathogenicity of *S. dysgalactiae* is associated with different virulence factors, including adhesins, hemolysins, and immune-evasion mechanisms that facilitate colonization and persistence within the host (Fulde and Valentin-Weigand, 2013; Walker et al., 2014). In addition, antimicrobial-resistant strains have increasingly been reported worldwide (Glajzner et al., 2023; López de Egea et al., 2023). Mobile genetic elements, such as plasmids, transposons, and integrative conjugative elements, contribute to the dissemination of antimicrobial resistance genes among streptococci and other bacteria. The pattern raises concerns about potential treatment failures and resistance distribution in animal production systems (Glajzner et al., 2023; López de Egea et al., 2023) and underscores the importance of integrated surveillance from a One Health perspective (Glambeek et al., 2024).

Poultry production systems can also serve as reservoirs for antimicrobial-resistant bacteria. Continuous or improper antibiotic use in poultry farming can exert selective pressure, promoting the emergence and persistence of resistant bacterial populations (WOAH, 2023). Farm environments, such as drinking water, feed, litter, and equipment, can support bacterial survival and transmission among chickens, contributing to the maintenance of antimicrobial resistance in poultry systems and potentially increasing the risk of resistant bacteria spreading to other populations via environmental routes (Hossain et al., 2020; Glambeek et al., 2024).

In Bangladesh, the irrational use of antimicrobials in food-producing animals significantly contributed to antimicrobial resistance, underscoring the need for antimicrobial stewardship and coordinated One Health interventions (Islam et al., 2026). Previous studies have primarily focused on antimicrobial-resistant bacteria such as *Escherichia coli*, *Salmonella* spp., and *Staphylococcus* spp. found in different environmental settings (Hossain et al., 2020). Different factors in the coastal region of Barishal, Bangladesh, including elevated humidity, seasonal flooding, saline intrusion associated with climate change, and intensive poultry production with different biosecurity practices, may collectively facilitate bacterial persistence (Islam et al., 2026). However, information specifically describing the occurrence and antimicrobial resistance of *S. dysgalactiae* in poultry and associated farm environments remains limited, particularly in the coastal region of Barishal, Bangladesh. Consequently, the epidemiological distribution and antimicrobial susceptibility characteristics of *S. dysgalactiae* in poultry production systems remain poorly understood. Therefore, monitoring bacterial occurrence and antimicrobial resistance in this region is important for supporting disease control strategies and antimicrobial stewardship (WOAH, 2023; Glambeek et al., 2024). The present study aimed to investigate the prevalence and antimicrobial resistance patterns of *S. dysgalactiae* isolated from poultry tissue and farm environmental samples in coastal Barishal, Bangladesh.

MATERIALS AND METHODS

Ethical approval

The study used samples from broiler chickens collected during routine farm management and slaughter processes. No live animals were specifically handled for the experiment. Sample collection was carried out with farm owners' permission, following proper biosafety and animal welfare protocols.

Study location

A cross-sectional study was carried out from July 2024 to June 2025 in selected commercial broiler chicken farms within specific areas of Barishal, Bangladesh (Figure 1).

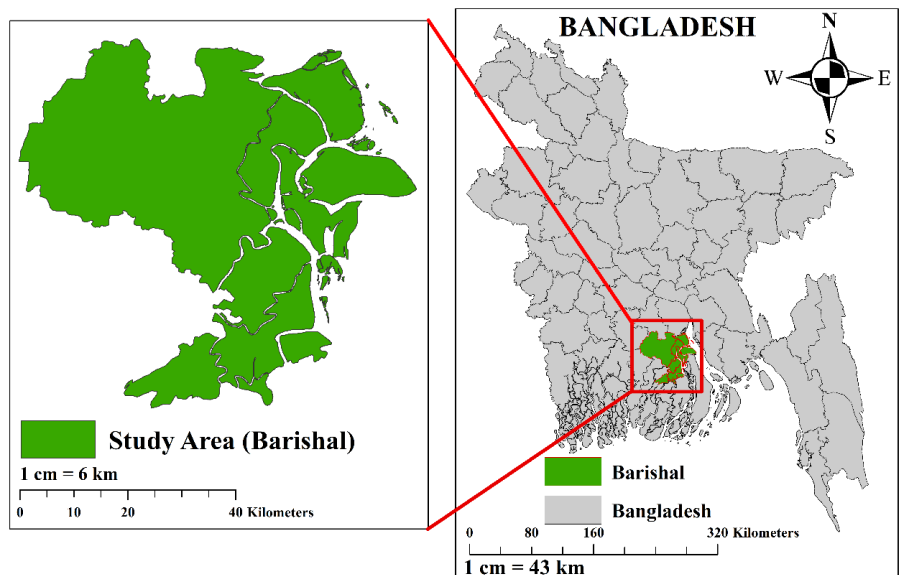


Figure 1. Location of the selected commercial broiler chicken farms in specific areas of Barishal, Bangladesh. The figure was designed using ArcGIS Software version 8

Sample collection

A total of 64 samples were collected from 10 commercial broiler chicken farms using a simple random sampling approach, consisting of 38 poultry-derived samples from heart (n = 8), intestine (n = 18), and feces (n = 12), and 26 farm-environment samples, including 14 samples collected from drinking water and 12 from poultry feed. All poultry flocks were fed commercially formulated, balanced broiler feeds obtained from established local commercial feed suppliers, according to the recommended nutritional requirements of the respective broiler breeds and growth stages.

Certified veterinarians conducted routine clinical examinations of the broiler chicken flocks at all participating farms to assess flock health and identify any clinical signs suggestive of infectious diseases. Samples collected from farms were included in the present study because they presented possible sources of bacterial exposure and transmission within the poultry production system. The samples were used to examine the presence and antimicrobial resistance patterns of *S. dysgalactiae*. To prevent selection bias, samples were collected from randomly selected poultry farms during the sampling period. As a result, not every chicken contributed all three sample types, yielding 38 independent poultry samples rather than matched tissue samples from the same chicken. Heart and intestinal samples were aseptically collected immediately after slaughter using sterile scissors and forceps. Approximately 5-10 g of intestinal tissue and heart tissue were placed separately into sterile sample containers. Fresh fecal samples (approximately 5 g) were collected directly from poultry house floors immediately after defecation using sterile spatulas. For farm-associated sampling, approximately 100 mL of drinking water was aseptically collected into sterile, screw-capped bottles from the drinking system of each poultry house. Feed samples (approximately 50 g) were collected individually from feeders using sterile gloves and transferred into sterile polyethylene bags. Each sample was analyzed individually; no pooled samples were included. Immediately after collection, all samples were transported to the laboratory under refrigerated conditions (4-8°C) and processed within 6 hours of collection. Isolation and presumptive identification of *S. dysgalactiae*. Due to financial constraints, molecular confirmation was not performed; bacterial identification was carried out using traditional phenotypic methods, including colony morphology, hemolytic features, Gram staining, and catalase testing.

Isolation and identification of *Streptococcus dysgalactiae*

Approximately 1 g of tissue or fecal sample was homogenized in 9 mL of sterile physiological saline. Water samples were mixed thoroughly before processing, while feed samples were homogenized in sterile saline at a 1:10 dilution. Sterile cotton swabs soaked in the prepared suspensions were streaked onto 5% sheep blood agar (HiMedia, India) and incubated aerobically at 37°C for 24-48 hours. Presumptive streptococcal colonies were selected based on α - and β -hemolysis, colony morphology, Gram staining (Gram-positive cocci arranged in chains), and a catalase-negative reaction (Quinn et al., 2011; Markey et al., 2013). Selected isolates were inoculated onto Mannitol salt agar (MSA; HiMedia, India) to assess growth in high-salt conditions and to exclude salt-tolerant *Staphylococcus* species. The MSA results were used only as supportive observations and were not considered a definitive criterion for identifying *S. dysgalactiae* (Vieira et al., 1998; Quinn et al., 2011).

Antibiogram profiling of *Streptococcus dysgalactiae*

Antimicrobial susceptibility testing was performed using the Kirby-Bauer disk diffusion method according to the recommendations of the Clinical and Laboratory Standards Institute (CLSI VET01S). Fresh bacterial colonies were inoculated into sterile nutrient broth and incubated overnight. The suspension was uniformly spread onto Mueller-Hinton agar supplemented with 5% sheep blood using sterile cotton swabs. Plates were incubated at $35 \pm 2^\circ\text{C}$ for 18-24 hours. The diameter of inhibition zones was measured in millimeters using a digital caliper and interpreted according to CLSI guidelines (CLSI, 2023). The commercially available discs (Himedia, India) were used, including ampicillin (10 µg), penicillin G (10 units), amoxicillin (25 µg), vancomycin (30 µg), oxytetracycline (30 µg), azithromycin (15 µg), doxycycline (30 µg), gentamycin (10 µg), streptomycin (10 µg), ciprofloxacin (5 µg), and levofloxacin (5 µg). For antimicrobials without an established resistance breakpoint for *Streptococcus* spp., resistance was interpreted using breakpoints for either another antimicrobial in the same drug class or another pathogen group (Zhang et al., 2018).

Statistical analysis

Data were entered into Microsoft Excel and analyzed using IBM SPSS Statistics version 26.0 (IBM Corp., USA). The prevalence of presumptive *S. dysgalactiae* was calculated as the percentage of positive samples among the total samples examined. Categorical variables were expressed as frequencies and percentages. Differences in prevalence between poultry and farm-associated samples were evaluated using the Chi-square test or Fisher's exact test, depending on the expected cell frequencies. Differences among poultry sample types (heart, intestine, and feces) and farm-associated sample types (water and feed) were similarly assessed using Fisher's exact test where appropriate. All statistical tests were two-tailed, and p-values less than 0.05 were considered statistically significant.

RESULTS

Streptococcus dysgalactiae isolation and identification

A total of 64 poultry and farm-associated samples were examined for the presence of presumptive *S. dysgalactiae*. Identification of *S. dysgalactiae* was based on conventional phenotypic characteristics, including colony morphology, hemolytic activity on blood agar, Gram staining, and catalase testing. The presumptive isolates demonstrated α -hemolytic colonies on 5% sheep blood agar, no or minimal growth on MSA, Gram-positive cocci arranged in chains, and catalase-negative reactions (Figures 2 and 3). Based on these phenotypic characteristics, the isolates were identified as *S. dysgalactiae*.



Figure 2. *Streptococcus dysgalactiae* isolated from broiler chicken fecal samples from July 2024 to June 2025 in Barishal, Bangladesh. **A:** Growth of *Streptococcus dysgalactiae* on 5% sheep blood agar with α -hemolysis, **B:** Poor or no growth on Mannitol salt agar without mannitol fermentation, consistent with *Streptococcus dysgalactiae* growth, **C:** Growth with mannitol fermentation characteristic of *Staphylococcus* spp., indicated by a yellow color change on Mannitol salt agar.

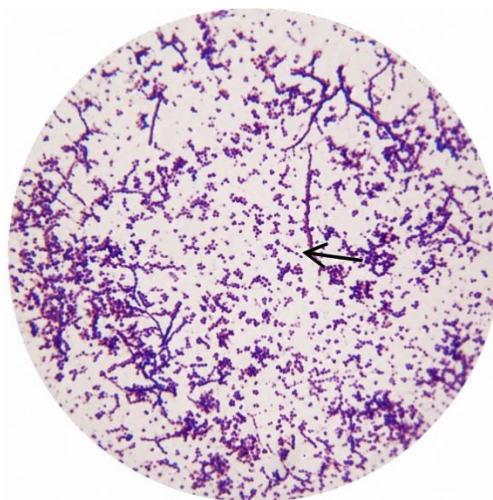


Figure 3. Gram staining characteristics of *Streptococcus dysgalactiae* showing Gram-positive cocci arranged in chains

Prevalence of *Streptococcus dysgalactiae* across different sample sources

Among the 64 samples examined, 26 were positive for *S. dysgalactiae*, resulting in an overall prevalence of 40.62%. The prevalence of *S. dysgalactiae* differed between poultry and farm-associated samples (Table 1). Among poultry-derived samples, 20 of 38 samples (52.63%) tested positive, while 6 of 26 farm-associated samples (23.08%) were positive for *S. dysgalactiae*. The difference between poultry and farm-associated samples was statistically significant ($p < 0.05$), indicating that poultry samples were more frequently positive than farm-associated samples during the present study.

Prevalence of *Streptococcus dysgalactiae* among poultry sample types

The prevalence of *S. dysgalactiae* among different poultry sample types is presented in Table 2. Isolates of *S. dysgalactiae* were identified in 4 out of 8 heart samples (50.00%), 10 out of 18 intestinal samples (55.55%), and 6 out of 12 fecal samples (50.00%). No statistically significant differences were observed among the three poultry sample types ($p > 0.05$), suggesting similar prevalence across the sampled tissues. Because different sample types were collected from

randomly selected poultry rather than the same individuals, the current findings confirmed the presence of *S. dysgalactiae* in multiple poultry samples but did not indicate systemic colonization or dissemination within individual chickens.

Prevalence of *Streptococcus dysgalactiae* in farm-associated samples

The prevalence of *S. dysgalactiae* among farm-associated samples is presented in Table 3. *S. dysgalactiae* was found in 4 out of 14 water samples (28.57%) and 2 out of 12 feed samples (16.66%). While the prevalence was greater in water samples, this difference was not statistically significant ($p > 0.05$).

Table 1. Prevalence of *Streptococcus dysgalactiae* among poultry-derived and farm-associated samples collected from July 2024 to June 2025 in Barishal, Bangladesh

Sample source	Sample type	Total samples (n)	Positive samples	Prevalence (%)	95% CI (%)	Statistical comparison
Heart, intestine, and feces	Poultry	38	20	52.63	36.50 - 68.30	$p = 0.018^*$
Water and feed	Farm-associated samples	26	6	23.08	9.00 - 43.00	

n: Number of samples, *: Significantly lower than poultry

Table 2. Prevalence of *Streptococcus dysgalactiae* among different poultry tissue samples

Sample type	Total samples (n)	Positive samples	Prevalence (%)	95% CI (%)	Statistical comparison
Heart	8	4	50.00	15.70 - 84.30	$p = 0.943^*$
Intestine	18	10	55.55	30.80 - 78.50	
Feces	12	6	50.00	21.10 - 78.90	

n: Number of samples, *: P-value versus Heart/Feces

Table 3. Prevalence of *Streptococcus dysgalactiae* among farm-associated samples from July 2024 to June 2025 in Barishal, Bangladesh

Farm-associated source	Total samples (n)	Positive samples	Prevalence (%)	95% CI (%)	Statistical comparison
Water	14	4	28.57	8.40 - 58.10	$p = 0.473^*$
Feed	12	2	16.66	2.10 - 48.40	

n: Number of samples, *: P-value versus Water

Antimicrobial resistance patterns of *Streptococcus dysgalactiae*

The antimicrobial resistance profiles of *S. dysgalactiae* isolates recovered from poultry and farm-associated samples are presented in Table 4. Resistance to β -lactam antibiotics was widespread, with all isolates resistant to ampicillin and penicillin. Different resistance rates were observed for amoxicillin, azithromycin, doxycycline, oxytetracycline, and streptomycin, whereas resistance to ciprofloxacin, levofloxacin, and gentamicin remained relatively low. Although resistance percentages differed among sample types, no statistically significant differences were detected between poultry and farm-associated isolates for any of the antimicrobial agents tested ($p > 0.05$).

Poultry isolates multidrug resistance patterns

Among poultry-derived *S. dysgalactiae* isolates, antimicrobial resistance patterns differed by sample type. All heart isolates (100%) were resistant to ampicillin, penicillin, and amoxicillin, whereas no resistance was detected to ciprofloxacin, levofloxacin, or gentamicin. Resistance to azithromycin, doxycycline, oxytetracycline, vancomycin, and streptomycin was observed in 50% of heart isolates. Similarly, all intestinal isolates (100%) were resistant to ampicillin and penicillin. Resistance was also observed to azithromycin (60%), doxycycline (60%), amoxicillin (60%), and vancomycin (40%), while lower resistance rates were detected for ciprofloxacin (20%), levofloxacin (20%), gentamicin (20%), and streptomycin (20%). Among fecal isolates, resistance was highest to ampicillin and penicillin (100%), followed by amoxicillin (83.3%). Resistance to azithromycin, doxycycline, oxytetracycline, vancomycin, and streptomycin ranged from 50.0% to 66.7%, whereas resistance to ciprofloxacin was comparatively low (16.7%). No gentamicin resistance was detected among heart isolates, while intestinal (20.0%) and fecal (33.3%) isolates exhibited low resistance rates. Although resistance percentages differed numerically among heart, intestinal, and fecal isolates, antimicrobial resistance patterns did not differ significantly among poultry sample types ($p > 0.05$). This result indicated a generally similar distribution of resistance patterns across the different tissues sampled.

Among the farm-associated *S. dysgalactiae* isolates, all isolates collected from water samples (100%) were resistant to ampicillin and penicillin, with high resistance observed to amoxicillin (75.00%) and streptomycin (75.00%). Resistance to azithromycin, doxycycline, oxytetracycline, vancomycin, gentamicin, ciprofloxacin, and levofloxacin ranged from 25.00% to 50.00%. Similarly, all feed isolates (100%) were resistant to ampicillin, penicillin, and amoxicillin. No resistance was detected to ciprofloxacin or levofloxacin, whereas 50.0% of feed sample isolates were resistant to azithromycin, doxycycline, oxytetracycline, vancomycin, gentamicin, and streptomycin.

Table 4. Antibiotic resistance patterns of *Streptococcus dysgalactiae* isolated from poultry tissues and farm-associated samples from July 2024 to June 2025 in Barishal, Bangladesh

Source	Sample type	Antibiotic resistance against <i>Streptococcus dysgalactiae</i> (%)										
		CIP	AZM	DOX	OXY	VAN	LEV	AMP	CN	P	S	AMX
Poultry	Heart	0	50	50	50	50	0	100	0	100	50	100
	Intestine	20	60	60	40	40	20	100	20	100	20	60
	Feces	16.7	50	50	33.3	16.7	33.3	100	33.3	100	66.7	83.3
Farm-associated samples	Water	25	25	50	50	25	25	100	25	100	75	75
	Feed	0	50	50	50	50	0	100	0	100	50	100

AMX: Amoxicillin, AMP: Ampicillin, AZM: Azithromycin, CIP: Ciprofloxacin, DOX: Doxycycline, CN: Gentamicin, LEV: Levofloxacin, P: Penicillin, OXY: Oxytetracycline, S: Streptomycin, VAN: Vancomycin

Poultry and farm-associated multidrug resistance patterns

Streptococcus dysgalactiae isolates derived from poultry and farm-associated samples demonstrated resistance to multiple antimicrobial agents. Resistance was particularly frequent against β -lactam antimicrobials, while different resistance patterns were observed to macrolides, tetracyclines, aminoglycosides, glycopeptides, and fluoroquinolones. Among isolates derived from heart samples, multidrug resistance (MDR) profiles exhibited resistance to multiple antibiotic classes, including β -lactams (ampicillin, penicillin, amoxicillin), macrolides (azithromycin), tetracyclines (doxycycline, oxytetracycline), glycopeptides (vancomycin), and aminoglycosides (streptomycin). Isolates from intestinal samples demonstrated broader MDR profiles, with resistance to β -lactams, macrolides, tetracyclines, glycopeptides, and aminoglycosides. Additionally, some isolates were resistant to fluoroquinolones (ciprofloxacin and levofloxacin) and gentamicin. Similarly, isolates derived from fecal samples were resistant to β -lactams, macrolides, tetracyclines, glycopeptides, and aminoglycosides, whereas resistance to fluoroquinolones and gentamicin was less frequent. Furthermore, isolates from farm-associated samples exhibited MDR patterns. Water-derived isolates demonstrated concurrent resistance to β -lactams, tetracyclines, macrolides, glycopeptides, and aminoglycosides. Feed-derived isolates were resistant to β -lactams, macrolides, tetracyclines, glycopeptides, and aminoglycosides; however, no resistance to fluoroquinolones was observed.

DISCUSSION

Detection of presumptive *Streptococcus dysgalactiae* in poultry-derived and farm-associated samples indicates its possible occurrence in commercial broiler chicken production systems in coastal Barishal, Bangladesh. The higher detection rate in poultry-derived samples (52.63%) than in farm-associated samples (23.08%) suggests a greater association with poultry-derived materials, while detection in drinking water and feed indicates possible persistence or dissemination within farm systems. However, as the isolates were identified presumptively based on phenotypic characteristics without molecular confirmation, the findings should be interpreted cautiously and do not establish definitive species-level occurrence or reservoir status. Previous studies have reported *Streptococcus* spp. in livestock production systems in Bangladesh (Hassan et al., 2023), including molecularly confirmed *S. dysgalactiae* from bovine mastitis in southern Bangladesh (Farzana et al., 2023). *S. dysgalactiae* has also been molecularly characterized in bovine mastitis in China (Xu et al., 2021) and in slaughtered pigs in India, where antimicrobial resistance was reported (Patel et al., 2024). Differences in host, sample type, geographical setting, and diagnostic methods limit direct comparison among these studies.

The high level of antimicrobial resistance observed in the present study indicated that antimicrobial-resistant *S. dysgalactiae* was circulating within commercial poultry production systems in Barishal, Bangladesh. Similar resistance patterns of *S. dysgalactiae* have been identified in isolates collected from food-producing animals in China (Zhang et al., 2018). The widespread and frequently inappropriate use of antimicrobial agents in livestock production is a well-recognized major contributor to antimicrobial resistance. The extensive use of antimicrobials can create selective pressure that promotes the emergence and persistence of resistant bacteria (WHO, 2019). No statistically notable differences in antimicrobial resistance were found between poultry and farm-associated isolates, suggesting that similar resistance profiles circulated within the farm ecosystem, likely due to shared antimicrobial exposure and bacterial exchange between chickens and their environment. Although the present study did not investigate transmission routes of *S. dysgalactiae*, it highlighted the necessity of careful antimicrobial use, enhanced farm biosecurity measures, and comprehensive One Health surveillance to prevent the development and dissemination of antimicrobial-resistant *S. dysgalactiae* within poultry production systems (Glambek et al., 2024; Hossain et al., 2020).

Poultry-derived and environmental samples were MDR, indicating that resistant *S. dysgalactiae* strains were present within poultry production systems. Similar findings have been reported in food-producing animals regarding livestock-associated streptococci, highlighting the growing challenge of antimicrobial resistance (FAO, 2019).

CONCLUSION

The present study demonstrated the occurrence of *S. dysgalactiae* in poultry and environmental samples collected from commercial broiler chicken farms in the coastal region of Barishal, Bangladesh. Isolates from poultry samples exhibited a significantly higher *S. dysgalactiae* prevalence than farm-associated samples. Antimicrobial susceptibility results demonstrated high resistance to β -lactam antibiotics, especially ampicillin and penicillin, and revealed MDR patterns among the isolates derived from poultry- and farm-associated samples. Although bacterial identification was based solely on conventional phenotypic methods without molecular confirmation, the present study provided valuable baseline information on the occurrence and antimicrobial resistance patterns of *S. dysgalactiae* in coastal poultry farms in Barishal, Bangladesh. In addition, the relatively small sample size and descriptive analysis might have limited the generalizability of the current findings. Future investigations incorporating molecular identification, antimicrobial resistance gene characterization, and larger sample sizes are recommended to comprehensively understand the epidemiology and public health significance of *S. dysgalactiae* in Bangladesh.

DECLARATIONS

Acknowledgement

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Authors' contributions

Farzana Islam Rume conceptualized, supervised the study, and revised the final draft. Md. Yeasin Arafat and Arobi Jahan Disha conducted the experiments and documented the results. Md. Yeasin Arafat, Wahedul Karim Ansari, Md. Kamruzzaman Akimul, and Nasrin Akter Sumona performed the formal analysis, drafted the manuscript, generated figures, and created the maps. Farzana Islam Rume provided critical reviews and contributed to the final edition of the manuscript. All authors read and approved the final edition of the manuscript.

Availability of data and materials

All data generated and analyzed during the present study are included in this published article. No supplementary materials are associated with this manuscript. Requests for additional information or data related to this study should be directed to the corresponding author.

Competing interests

The authors have no competing interests to declare.

Ethical considerations

The authors confirmed that the present study is original, has not been previously submitted for publication or under review elsewhere, and adheres to ethical standards regarding data integrity and the avoidance of plagiarism. During the

preparation of this manuscript, the authors utilized ChatGPT (version 4.0) for linguistic improvements. The authors carefully reviewed and revised the AI-edited language content to ensure accuracy, completeness, and adherence to the journal's requirements, and take full responsibility for the final content of the published article. The authors assume full responsibility for the originality of the data prior to the submission of the article, throughout the peer review process, and subsequent to acceptance.

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