UKRAINIAN JOURNAL OF VETERINARY SCIENCES

2025. Volume 16, No. 2. P. 63-75

Received: 12.01.2025 Revised: 31.03.2025 Accepted: 22.05.2025

DOI: 10.31548/veterinary2.2025.63

UDC: 59.611.591.4

Identification of methicillin-resistant *Staphylococcus aureus* from nasal carriage of goat and their antimicrobial resistance profiles

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Abstract. The methicillin-resistant *Staphylococcus aureus* (MRSA) is a global challenge in veterinary medicine due to its responsibility for nasal infection in goats. The present study was carried out to estimate the prevalence of this bacterium in goats and to detect their antimicrobial resistance profiles. A total of 153 nasal swab samples were collected from goats, and a questionnaire was used to collect necessary data related to this study. A standard laboratory analysis was done to recognise MRSA and to determine its antimicrobial sensitivity. Among 153 samples, 20.9% were

Suggested Citation:

Barua, B., Islam, S., Hasan, M.M., & Islam, Md.A. (2025). Identification of methicillin-resistant *Staphylococcus aureus* from nasal carriage of goat and their antimicrobial resistance profiles. *Ukrainian Journal of Veterinary Sciences*, 16(2), 63-75. doi: 10.31548/veterinary2.2025.63.

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found positive for *Staphylococcus aureus* based on results of cultural and biochemical properties. Overall, 4.58% of the samples were identified to be *mecA* gene positive. The prevalence of MRSA was higher in young goats aged below 1 year at 7.14%. In the case of female goats, the prevalence was 5.05%, which was greater than males at 3.70%. In Black Bengal goats, the prevalence was highest at 11.11%, and in the semi-intensive rearing system, the prevalence was 7.89%. Methicillin-resistant *Staphylococcus aureus* showed 100% resistance against Cefoxitin and Oxacillin. The organism also showed 42.86% resistance to Ampicillin, Erythromycin, and Oxytetracycline, followed by 14.29% to Ceftriaxone and Gentamicin, and 28.57% to Ciprofloxacin, respectively. The findings of 4.58% MRSA and multidrug-resistant MRSA in goats indicate a significant public and animal health concern. By identifying goats as potential carriers of MRSA, the findings emphasise the need for improved surveillance, biosecurity, and antibiotic stewardship in livestock farming. These results can guide veterinarians, farmers, and policymakers in developing effective strategies to control the spread of resistant bacteria from animals to humans, particularly in regions where close human-animal interactions are common

Keywords: prevalence; *mecA* gene; Antimicrobial Sensitivity Testing (AST); staphylococcal infection; risk factors

Introduction

The livestock sector has been playing a crucial role in the socio-economic development of Bangladesh. Bangladesh had a livestock population of more than 4,535.95 lakh, with 271.17 lakh goats and this livestock sector contribute about 1.80% in the GDP of Bangladesh (Bangladesh Bureau of Statistics, 2024). In livestock sector, the goat is called a poor man's cow. In developing countries like Bangladesh, small-income residents can easily rear goats with less investment in a minimum area. About 40.6% of the total population in Bangladesh may be directly or indirectly engaged with agriculture and its sub-sector as a source of income generation (Bangladesh National Portal, 2022). Goat farming plays an important and potential role in poverty reduction, income generation, contribution to food and nutrition security and employment (Barua *et al*., 2021). Goat farming provides employment opportunity which are associated with feed production, veterinary services, and marketing and play a great role for direct income generation of farmer through selling of meat, milk, skin, and live goat (FAO, 2018). As goat farming require less feed cost due to they mainly depend on tree leaves and green grass so net benefit is high 2,142.00 BDT per household (Haque *et al*., 2023), which is profitable. But this sector is challenging due to outbreak of many infectious, non-infectious, and production-related diseases in goat during rearing time.

For infectious diseases, many viruses and bacteria are responsible. Among different microbial pathogens, S. Piva *et al*. (2021) confirmed that *S. aureus* can cause many diseases such as abscesses, pneumonia, abortions, stillbirths and meningitis in goats and mammals. Y. Titouche *et al*. (2024) demonstrated that *S. aureus* is the main causative agent of mastitis in small ruminants such as goats. According to them, 15-25% of the goat population harbours this bacterium in the nasal cavity. A. Sakr *et al*. (2018) emphasised in their study that as a commensal organism, approximately 30% of the human population carries *S. aureus*

in their nasal passages. As A.F. Mechesso *et al*. (2021) argued, nasal carriage of *S. aureus* in livestock is a reservoir for human infection. *Staphylococcus aureus* poses a potential public health threat and the potential for zoonotic transmission of staphylococci among livestock and pets. According to E.O. Omoshaba *et al*. (2020), goats and sheep play an important role in the transmission of zoonotic staphylococcal infections and infections caused by other pathogens due to the close contact between the animals and their owners. Several risk factors contribute to *S. aureus* infections in goats, including those related to the animal, the environment, and farm management practices. *S. aureus* is one of the major carriers of new and re-emerging antibiotic resistance determinants represent a health risk for humans and animals (Abdullahi *et al*., 2023). As identified in their study by M. Pal *et al*. (2020), they are a major public health concern, especially given the rise in multidrug-resistant strains such as methicillin-resistant *Staphylococcus aureus* (MRSA). MRSA strains linked to livestock, which are classified as livestock-associated MRSA (LA-MRSA). There are few studies which were conducted to know the MRSA in goat. According to a study by M. Altaf (2019), methicillin-resistant *S. aureus* (MRSA) develops resistance by acquiring the *mecA* gene, which encodes the PBP2a protein, which aids in bacterial cell wall synthesis. Indiscriminate use of antibiotics in livestock management is a key factor in the rapid development and spread of AMR which has devastating effects in low and middle income countries. O. Herawati *et al*. (2023) wrote about this in their work. According to studies by K.M. Muwonge *et al*. (2025), *S. aureus* isolates from nasal swabs of goats were found to be resistant to several antibiotics.

As antimicrobial resistance is a burning issue, more attention is needed to control the infection and develop an effective treatment protocol against this infection. There are few studies which was conducted to know the MRSA in goat. So, the current research study aimed to estimate the prevalence of nasal carriage of *S. aureus* in goats, to detect the *mecA* gene containing methicillin-resistant *S. aureus* from goats and to know their resistance percentage against several antibiotics.

Materials and Methods

A cross-sectional study was conducted at the S.A. Quaderi Teaching Veterinary Hospital (SAQTVH), Chattogram Veterinary and Animal Sciences University (CVASU), from February to June 2023. The study population consisted of goats admitted to the clinic for treatment or routine examination. A total 153 swab sample were collected from the nostrils of 153 goats having respiratory problems. Samples were immediately inoculated into Mueller-Hinton broth supplemented with 6.5% NaCl (Oxoid, UK). Microbiological analyses were performed at the Poultry Research and Training Centre (PRTC) laboratory, CVASU. Data regarding the animals' age, sex, breed, and rearing system were systematically recorded using a structured questionnaire.

Isolation and identification of *Staphylococcus aureus*

The isolation of *S. aureus* organism involved placing swab samples into Mueller-Hinton broth supplemented with 6.5% NaCl, followed by incubation at 37°C overnight. Subsequently, the samples were streaked onto blood agar plates and incubated at 37°C for 24 hours to promote bacterial colony development. Colonies exhibiting typical features – such as hemolysis, round shape, smooth texture, and shiny surface – were subjected to Gram staining. Those identified as Gram-positive cocci underwent catalase testing according to standard protocols. Colonies that were both catalase-positive and Gram-positive

cocci were preliminarily classified as staphylococci. These suspected Staphylococcus colonies were further cultured on Mannitol Salt Agar and incubated at 37°C for an additional 24 hours to facilitate more precise identification and differentiation (Fig. 1).

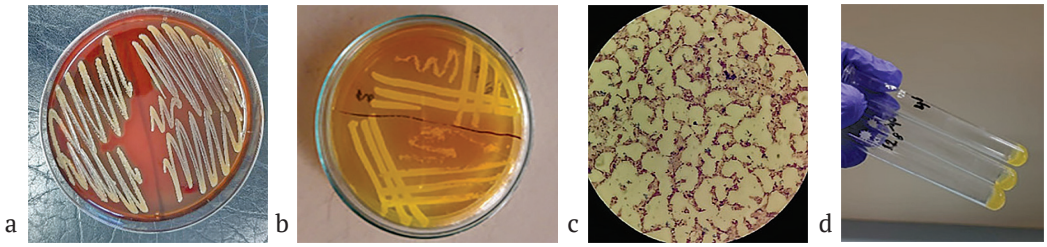

Figure 1. Isolation and identification of bacteria
***Note**: a – whitish and yellow colour colony on blood agar; b – golden yellow colour colony on mannitol salt agar; c – Gram's staining; d – coagulation in tube coagulase test*
***Source**: authors' original images from this experiment*

Colonies yielding a yellowish colour were suspected as *Staphylococcus aureus* species (Islam *et al.*, 2019). The presumptive *S. aureus* colonies on mannitol salt agar were then transferred onto blood agar for additional testing to confirm their identity by incubating at 37°C for 24 hours (Rahimi *et al.*, 2015). The positive samples were tested for coagulase using horse plasma.

Molecular identification of the *mecA* gene using polymerase chain reaction (PCR)

Staphylococcus aureus organisms that are resistant to specific antimicrobial drugs like oxacillin and cefoxitin were classified as MRSA and were tested in the laboratory (Broekema *et al.*, 2009). Initially identified MRSA were further examined by molecular diagnosis through PCR to detect the presence of the *mecA* gene as described by A.R. Larsen *et al.* (2008). Primers used were *mecA* P4 (Forward) 5'-TCCAGATTACAACTTCACCAGG-3' and *mecA* P7 (Reverse) 5'-CCACTTCATATCTTGTAACG-3'. The PCR amplification program was done by following the protocol of A.R. Larsen *et al.* (2008). The MRSA ATCC 33591 strain served as the positive control, while nuclease-free water was used as the negative control to ensure the accuracy and reliability of the PCR results (Fig. 2). The PCR products were visualised using gel electrophoresis.

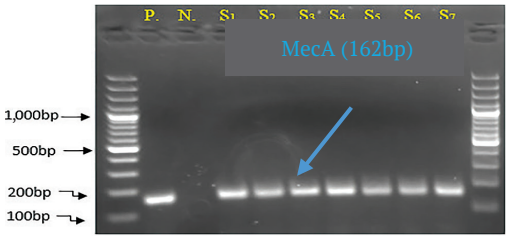

Figure 2. PCR products amplified using *mecA* gene-specific primers of MRSA
***Note:** P – positive control; N – negative control; S1-S7 – sample ID*
***Source**: authors' original images from this experiment*

The antimicrobial resistance test was performed by the disc diffusion method following the Clinical and Laboratory Standards Institute (CLSI) (2020) guidelines. The antibiotic resistance test results, based on the sizes of the zones of inhibition, are interpreted as resistant (R), intermediately resistant (I), or sensitive (S) to the antibiotics tested against the isolates shown in Table 1. Methicillin resistance was assessed by measuring the zone of inhibition around oxacillin and cefoxitin drugs. *S. aureus* isolates that demonstrated resistance to a minimum of three distinct classes of antimicrobial agents were considered to be multidrug-resistant (MDR) (Li *et al.*, 2014).

Table 1. The antimicrobials used, their concentrations, and Zone diameter interpretative standards for *Staphylococcus aureus*

Antimicrobial agent with disc code and Concentration (µg)	Diffusion zone breakpoint (mm)		
	S	I	R
Ampicillin (AMP_{10})	⩾29	27-28	⩽26
Oxacillin (OX_1)	⩾13	11-12	⩽10
Ceftriaxone (CRO_{30})	⩾23	20-22	⩽19
Cefoxitin (FOX_{30})	⩾22	–	⩽21
Gentamicin (CN_{10})	⩾15	13-14	⩽12
Ciprofloxacin (CIP_5)	⩾21	16-20	⩽15
Oxytetracyclines (TE_{30})	⩾15	12-14	⩽11
Erythromycin (E_5)	⩾23	14-22	⩽13
Sulfamethoxazole-trimethoprim (SXT_{25})	⩾16	11-15	⩽10

***Note**: S – sensitive; I – intermediate; R – resistance*
***Source**: created by the authors based on CLSI (2020)*

The collected data from goat-rearing farmers and the laboratory were then entered and tabulated into MS Excel 2010 spreadsheets. Data were analysed using the Statistical Package for Social Sciences 20 computer software package. This study was conducted by the ethical guidelines for animal research. The animals were kept and all manipulations were carried out by the European Convention for the Protection of Vertebrate Animals used for Experimental and Other Scientific Purposes (1986).

Results and Discussion

Prevalence of *Staphylococcus aureus* and *mecA* gene containing MRSA in the nasal carriage of goat

Among the total of 153 nasal swab samples collected from goats, 32 samples (20.9%) were identified as positive for *S. aureus* based on standard cultural characteristics and biochemical tests (coagulase test) while 79.08% sample were negative for S. aureus infection. These preliminary findings confirmed the presence of *S. aureus* colonisation in a notable proportion of the sampled goat population. To determine the presence of methicillin-resistant strains, all 32 *S. aureus* isolates were subjected to antimicrobial susceptibility testing specifically targeting resistance to Oxacillin and Cefoxitin, which are commonly used indicator antibiotics for the detection of MRSA. The antibiotic susceptibility testing was performed using the disc diffusion method following CLSI guidelines.

Out of these 32 isolates, 7 showed phenotypic resistance to both Oxacillin and Cefoxitin. These resistant isolates were then further confirmed through molecular analysis by polymerase chain reaction (PCR) targeting the *mecA* gene, a well-established genetic marker for methicillin resistance. All 7 isolates that exhibited phenotypic resistance were found to be mecA-positive, confirming them as MRSA. The findings (Fig. 3) indicate that MRSA was present in 7 out of 153 total goat nasal swab samples tested. Furthermore, when considering only the *S. aureus*-positive cases, the prevalence of MRSA was found to be 21.88% (7 out of 32).

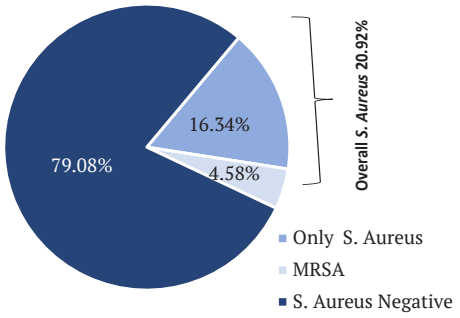

Figure 3. Prevalence of *S. Aureus* and MRSA in the Study location
***Source**: created by the authors*

In this study, various potential risk factors including age, sex, breed, and rearing system – were analysed to determine their association with Methicillin-resistant *S. aureus* positivity in the animal population (Table 2). Although differences in MRSA prevalence were observed across categories, statistical analysis showed that none of these factors were significantly associated with MRSA infection ($P > 0.05$). Age-wise distribution showed that animals under one year of age had the highest MRSA prevalence (7.14%), followed by those older than three years (4.05%) and those between one and two years (3.92%). The chi-square test ($\chi^2 = 0.519$, $P = 0.772$) indicated this variation was not statistically significant despite the slightly higher rate in younger animals. Similarly, the analysis of sex revealed that female animals had a higher prevalence (5.05%) compared to males (3.70%), but this difference was also not statistically meaningful ($\chi^2 = 0.145$, $P = 0.703$), suggesting that sex does not play a major role in determining susceptibility to MRSA.

Table 2. The risk factors for the presence of MRSA in goat

Risk factor		Number of MRSA-positive cases	Prevalence,%	χ^2 value	P value
Age	< 1 year	2 (28)	7.14	0.519	0.772
	1-2 year	2 (51)	3.92		
	> 3 year	3 (74)	4.05		
Sex	Male	2 (54)	3.70	0.145	0.703
	Female	5 (99)	5.05		
Breed	BB	1 (9)	11.11	1.883	0.597
	JP	1 (14)	7.14		
	JP Cross	3 (99)	3.03		
	Other cross	2 (31)	6.45		
Rearing system	Intensive	4 (115)	3.48	1.276	0.259
	Semi-intensive	3 (38)	7.89		

***Note**: BB – Black Bengal; JP – Jamunapari; P < 0.05 – significant at 5% level; P > 0.05 – non-significant; χ^2 – chi-square value*
***Source**: created by the authors*

Breed-wise analysis showed varying MRSA prevalence, with the highest in BB (Bangladeshi indigenous breed) animals (11.11%), followed by JP (Japanese breed) at 7.14%, other crossbreeds at 6.45%, and JP crossbreeds at 3.03%. However, despite these apparent differences, the chi-square value ($\chi^2 = 1.883$, $P = 0.597$) again indicated no significant association. Notably, the highest prevalence in BB animals might be influenced by the small sample size ($n = 9$), which limits the statistical power to detect a true effect. Regarding the rearing system, all animals in this study were reared under an intensive system, with an MRSA prevalence of 3.48%. The chi-square test ($\chi^2 = 1.276$, $P = 0.259$) showed no significant relationship between rearing system and MRSA status, which might also reflect limited variability in the rearing condition data.

Taken together, the findings indicate that none of the studied demographic or management factors had a significant influence on MRSA prevalence among the animals. These results suggest that MRSA infections may be more strongly associated with other factors not covered in this analysis, such as antibiotic

usage patterns, environmental contamination, farm-level biosecurity measures, or contact with human carriers. Further research with a larger sample size and more comprehensive data, including antimicrobial usage and hygiene practices, is needed to better understand the epidemiology and risk factors of MRSA in animal populations.

Antimicrobial resistance pattern of methicillin-resistant *Staphylococcus aureus*

The antimicrobial susceptibility testing conducted on the 7 MRSA isolates revealed important insights into the resistance patterns of these bacteria in goats (Fig. 4). Among the antibiotics tested, Sulphamethoxazole-trimethoprim showed the highest level of effectiveness, with 85.71% of the isolates being susceptible. This indicates that this combination of antibiotics remains a strong candidate for treating MRSA infections in goats. Its high susceptibility rate suggests that it could still reliably inhibit bacterial growth and thus be useful in clinical management. Following Sulphamethoxazole-trimethoprim, Ceftriaxone demonstrated considerable antimicrobial activity, with 71.43% of the MRSA isolates showing susceptibility. Ceftriaxone is a broad-spectrum third-generation cephalosporin commonly used in both human and veterinary medicine, and its relatively high effectiveness against MRSA in this study highlights its potential as an alternative therapeutic agent.

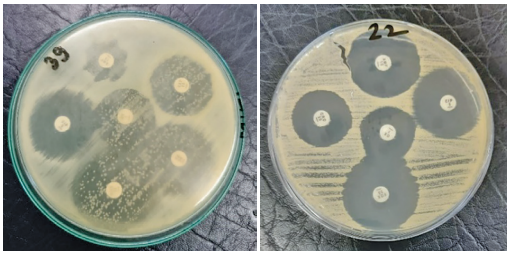

Figure 4. The sensitivity and resistance profile of MRSA against different antimicrobial drugs
***Source**: created by the authors*

In stark contrast, the isolates showed very low sensitivity to several other commonly used antibiotics. Ampicillin, Erythromycin, and Ciprofloxacin each exhibited only 14.29% susceptibility, indicating that these drugs are largely ineffective against the MRSA strains tested. This poor response reflects the widespread resistance mechanisms present in MRSA, making treatment with these antibiotics unreliable and likely to fail in clearing infections. Gentamicin and Oxytetracycline showed moderate susceptibility, each with 28.57% effectiveness against the isolates. While these drugs may still play a role in some treatment regimens, their lower susceptibility rates suggest that they should be used cautiously, preferably only after susceptibility testing confirms their efficacy for a specific case (Fig. 5).

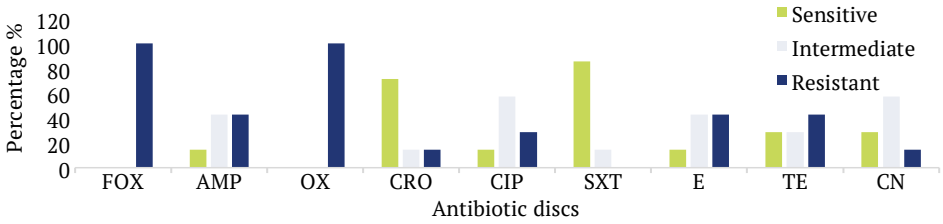

Figure 5. Antimicrobial susceptibility and resistance profile of MRSA in goat
***Note:** Cefoxitin (FOX); Ampicillin (AMP); Oxacillin (OX); Ceftriaxone (CRO); Ciprofloxacin (CIP); Sulfamethoxazole-trimethoprim (SXT); Erythromycin (E); Oxytetracycline (TE); Gentamicin (CN)*
***Source**: created by the authors*

The highest level of resistance was observed against Cefoxitin and Oxacillin, with 100% of the isolates resistant, confirming their methicillin-resistant status. Among the other antibiotics tested, the isolates showed 42.86% resistance to Ampicillin, 42.86% to Erythromycin, 42.86% to Oxytetracycline, 28.57% to Ciprofloxacin, and 14.29% to both Ceftriaxone and Gentamicin. In terms of intermediate resistance, the isolates displayed 57.14% intermediate resistance to both Ciprofloxacin and Gentamicin, 42.86% to Ampicillin and Erythromycin, 28.57% to Oxytetracycline, 14.29% to Sulphamethoxazole-trimethoprim, and Ceftriaxone (Fig. 5).

The observed resistance patterns raise significant concerns regarding the management of MRSA infections in goats. The limited effectiveness of several frontline antibiotics could lead to treatment failures, prolonged infections, and increased risk of transmission both within animal populations and potentially to humans. These findings emphasise the critical need for prudent use of antibiotics, guided by susceptibility testing, to slow down the emergence and spread of resistant strains. Overall, the data suggest that Sulphamethoxazole-trimethoprim and Ceftriaxone currently remain the most effective options for managing MRSA infections in goats in this study setting.

In the present study, 4.58% of nasal swab samples collected from goats tested positive for the presence of the *mecA* gene, confirming MRSA colonisation. This prevalence, although slightly lower than the 7.3% reported by A. Moroz *et al*. (2020), still indicates a noteworthy presence of MRSA in the sampled goat population. Conversely, a study from Tunisia by H. Gharsa *et al*. (2012) reported a lower MRSA prevalence, highlighting considerable variability in MRSA carriage rates globally. Such variations can be attributed to multiple factors, including geographic location, differences in animal husbandry practices, variation in the sampled animal populations, and differences in laboratory methodologies or sampling techniques. This variation underscores the importance of localised surveillance to better understand the epidemiology of MRSA in different regions and animal species.

To explore whether host factors or management systems influenced MRSA prevalence in this study, Chi-square (χ^2) tests were conducted on categorical variables such as age, sex, breed, and rearing system. The results showed no statistically significant associations ($P > 0.05$) between these variables and MRSA colonisation. This lack of significant correlation suggests that factors beyond the examined demographic and management variables might contribute more prominently to MRSA carriage in goats. These could include environmental contamination, farm hygiene practices, antibiotic usage patterns, or contact with humans and other animals, which were not assessed in the present study. Future research should consider incorporating these additional variables to better understand the dynamics of MRSA transmission and persistence in livestock.

Regarding antimicrobial susceptibility, the MRSA isolates demonstrated multidrug resistance but with varying degrees of sensitivity to different antibiotics. Most notably, Sulphamethoxazole-trimethoprim (SXT) was highly effective, with 85.71% of isolates showing susceptibility. This finding is in close agreement with the 87.23% susceptibility reported by C.A. Nsofor & O.O. Patience (2019), suggesting that SXT remains a promising option for treating MRSA infections in goats. The high susceptibility to SXT may be attributed to its mechanism of action and potentially limited misuse in veterinary settings compared to other antibiotics. Resistance patterns to other antibiotics revealed more concerning trends. Ampicillin resistance was observed in 42.86% of isolates,

closely matching the 40.43% resistance rate reported this authors. This highlights the persistent challenge of beta-lactam resistance among *S. aureus* strains. Similarly, Oxytetracycline resistance was found in 42.86% of isolates, consistent with the 44% tetracycline resistance rate documented by B. Egyir *et al*. (2020). These resistance levels indicate that both beta-lactam and tetracycline classes may have limited efficacy in treating MRSA infections in goats, possibly due to overuse or misuse in livestock.

Resistance to Ciprofloxacin was recorded at 28.57%, which is somewhat higher than rates reported by E.O. Omoshaba *et al*. (2020), but still signals emerging resistance to fluoroquinolones. Additionally, resistance to Ceftriaxone and Gentamicin was relatively low at 14.29% each, closely mirroring findings from M. Vitale *et al*. (2019). These moderate resistance levels suggest these antibiotics may still hold some therapeutic value but warrant cautious use and continued monitoring. The multidrug resistance observed among MRSA isolates in this study is a cause for concern. It reflects the growing global challenge posed by antimicrobial-resistant pathogens in veterinary medicine, which not only threaten animal health but also pose zoonotic risks. Resistant MRSA strains may be transmitted to humans through direct contact or via the food chain, complicating treatment of infections and increasing healthcare burdens.

These findings highlight the critical need for regular antimicrobial resistance surveillance, judicious antibiotic use, and enhanced biosecurity measures within livestock production systems. Furthermore, the consistency of resistance patterns across different geographic regions emphasises that antimicrobial resistance in MRSA is a global issue, influenced by local antibiotic usage practices and microbial ecology. Implementing One Health approaches that integrate human, animal, and environmental health perspectives is essential to controlling the spread of MRSA and safeguarding antibiotic efficacy for both veterinary and human medicine.

Conclusions

The occurrence and antimicrobial resistance profile of methicillin-resistant *Staphylococcus aureus* in goats, with a prevalence of 4.58% confirmed through PCR targeting the *mecA* gene. Although this prevalence is lower than some previous reports, the presence of MRSA in apparently healthy goats is significant. It indicates that goats may serve as asymptomatic carriers of MRSA, posing a potential zoonotic risk to individuals in close contact with livestock, such as farmers, veterinarians, and slaughterhouse workers. The detection of MRSA in livestock raises concerns regarding the potential transmission of resistant bacteria to humans and the environment. Antimicrobial susceptibility testing of the MRSA isolates revealed a worrying pattern of multidrug resistance. All seven isolates demonstrated 100% resistance to both Oxacillin and Cefoxitin, confirming their methicillin-resistant status. In addition, resistance was observed against commonly used antibiotics such as Ampicillin, Erythromycin, Oxytetracycline, and Ciprofloxacin, highlighting the risk of therapeutic failure in clinical cases. However, the isolates showed relatively high susceptibility to Sulphamethoxazole-trimethoprim and Ceftriaxone, indicating these antibiotics may still be effective treatment options against MRSA infections in goats. The study also investigated associations between MRSA occurrence and various host-related and management factors, including age, sex, breed, and rearing system. Chi-square analysis revealed no statistically significant association between MRSA prevalence and any of these variables ($P > 0.05$), suggesting that MRSA colonisation may be influenced by other unmeasured factors

such as antibiotic use history, farm hygiene, or environmental exposure.

Despite the valuable findings, the study was limited by a relatively small sample size (153 goats) and was conducted in a specific geographic area. As a result, the data may not fully represent the broader goat population in Bangladesh. Further studies with larger and more diverse samples are needed to better understand the epidemiology of MRSA in livestock. In conclusion, the detection of MRSA and its multidrug resistance in goats emphasises the need for routine surveillance, responsible antimicrobial use, and improved farm biosecurity. A One Health approach, integrating human, animal, and environmental health strategies, is essential to control the spread of antimicrobial-resistant pathogens and protect both public and animal health. Future research should also explore the molecular characterisation of resistance genes, whole-genome sequencing of MRSA isolates, and longitudinal studies to assess transmission dynamics between animals, humans, and the environment.

Acknowledgements

The author gratefully expresses his heartiest appreciation, deepest sense of gratitude, and best regards to the goat-rearing farmer and laboratory assistant of CVASU for their support in this research work. I sincerely acknowledge the contribution of Md. Mostain Billah (Scientific Officer), Bangladesh Livestock Research Institute, for his guidance during the data analysis.

Funding

The study was not funded.

Conflict of Interest

None.

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Виявлення носового носійства метицилін-резистентного *Staphylococcus aureus* у кіз та профілю стійкості збудника до антимікробних препаратів

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Анотація. Метицилін-резистентний *Staphylococcus aureus* (MRSA) є глобальною проблемою у ветеринарній медицині через його здатність викликати носові інфекції у кіз. Дослідження було проведено з метою оцінки поширеності цієї бактерії у кіз та визначення її профілю стійкості до антимікробних препаратів. Загалом було зібрано 153 зразки мазків з носа кіз, а також використано анкетування для збору необхідної супутньої інформації. Було проведено стандартний лабораторний аналіз для виявлення MRSA та визначення його чутливості до антибіотиків. Серед 153 зразків у 20,9 % було виявлено *Staphylococcus aureus* на основі культурних та біохімічних властивостей. Загалом, у 4,58 % зразків було виявлено наявність гена *mecA*. Поширеність MRSA була вищою серед молодих кіз віком до 1 року й становила 7,14 %. У самок поширеність становила 5,05 %, що більше, ніж у самців – 3,70 %. У кіз породи Black Bengal поширеність була найвищою – 11,11 %, а в умовах напівінтенсивного утримання – 7,89 %. Метицилін-резистентний *Staphylococcus aureus* виявив 100% стійкість до Цефокситину та Оксациліну. Також спостерігалася стійкість 42,86 % до ампіциліну, еритроміцину та окситетрацикліну, 14,29 % – до цефтріаксону та гентаміцину, та 28,57 % – до ципрофлоксацину. Виявлення MRSA у 4,58 % зразків та мультирезистентного MRSA у кіз свідчить про серйозну загрозу для громадського та ветеринарного здоров'я. Ідентифікація кіз як потенційних носіїв MRSA підкреслює необхідність посиленого епіднагляду, біобезпеки та відповідального використання антибіотиків у тваринництві. Ці результати можуть стати основою для ветеринарів, фермерів і політиків при розробці ефективних стратегій стримування поширення резистентних бактерій від тварин до людей, особливо в регіонах з тісними контактами між людиною і тваринами

Ключові слова: поширеність; ген *mecA*; тестування чутливості до антимікробних препаратів (AST); стафілококова інфекція; фактори ризику