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LIST OF ACRONYMS AND SYMBOLS USED

Abbreviation and symbols	Elaboration
AMR	Antimicrobial Resistance
MDR	Multidrug resistant
%	Percent
>	Greater than
<	Less than
≥	Greater than equal
≤	Less than equal
=	Equal to
°C	Degree Celsius
BHI	Brain Heart Infusion
bp	Base Pair
BPW	Buffered Peptone Water
CDC	Center for Disease Control and Prevention
CFU	Colony Forming Unit
CI	Confidence Interval
CLSI	Clinical and Laboratory Standards Institute
CRE	Carbapenem Resistant *Enterobacteriaceae*
CSE	Centre for Science and Environment
CS	Culture Sensitivity
CVASU	Chittagong Veterinary and Animal Sciences University
DAEC	Diffusely Adherent *E. coli*
DNA	De-oxy Ribonucleic Acid
EaggEC	Enteroaggregating *E. coli*
E. coli	*Escherichia coli*
EHEC	Enterohemorrhagic *E. coli*
EMB	Eosin Methylene Blue
ESBL	Extended Spectrum β-Lactamase
ETEC	Enterotoxigenic *E. coli*
Kb	Kilo Base

µL	Microliter
mA	Milli ampere
MCR	Plasmid-Mediated Colistin Resistance
MFS	Major Facilitator Superfamily
mL	Milliliter
Mm	Millimeter
MRSA	Methicillin Resistant *Staphylococcus aureus*
OR	Odds Ratio
PBP	Penicillin Binding Protein
PCR	Polymerase Chain Reaction
Rpm	Rotation Per Minute
STEC	Shiga Toxigenic *E. coli*
ST	Heat Stable Toxin
Stx	Shiga Toxin
TAE	Tris Acetate EDTA
VTEC	Verotoxigenic *E. coli*
WHO	World Health Organization
w/v	Weight/Volume
CT	Colistin sulphate
CIP	Ciprofloxacin
TE	Tetracycline
C	Chloramphenicol
CRT	Ceftriaxone
SXT	Sulfamethoxazole & Trimethoprim
CN	Gentamycin
ENR	Enrofloxacin
AMP	Ampicilin

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SUMMARY

Antimicrobial resistance (AMR) is known as a silent pandemic; an emerging global public health issue. The problem of AMR is similarly salient and prevalent in animals. From a public health perspective, AMR in dairy cattle can also jeopardize human health by the potential dissemination of AMR pathogens to humans via consumption of infected dairy products or direct contact with infected dairy cattle. Harshly, the dairy industry is increasingly confronted with AMR *Staphylococcus aureus* (*S. aureus*) and *Escherichia coli* (*E. coli*). This study was designed to investigate the multidrug- resistant pattern along with the most frequently isolated resistant genes of *S. aureus* and *E. coli* from bovine milk in the south-eastern part of Bangladesh. A total of 175 samples were randomly collected from ten dairy farms. Isolation and identification of *S. aureus* and *E. coli* were done following the standard bacteriological method. The *spa* gene and 16s rRNA gene were tabbed in molecular identification of*S. aureus* and *E. coli*, respectively. In this study 26 (14.86%; 95% CI 10% - 21%) isolates were confirmed as *S. aureus* whereas 20 (11.43%; 95% CI 7.12% - 17.10%) were confirmed as *E. coli* based on the PCR assay. Among the positive *S. aureus* isolates, 22 (84.6%; 95% CI 65.1%-95.6%) were characterized with the presence of AMR genes and 17 (85%; 95% CI 62.1%-96.8%) *E. coli* isolates were characterized with the presence of AMR genes. Afterward, the positive isolates were screened against 15 antimicrobials using the disc diffusion technique. At a fleeting glance, the highest number of *S. aureus* (80.7%, 95% CI 60.6-93.4) isolates were resistant to streptomycin and all the *S. aureus* (100%) were sensitive to meropenem. Meanwhile, all the *E. coli* isolates were resistant to ciprofloxacin whereas 95% (95% CI 75.1% - 99.9%) showed sensitivity to meropenem and 80% (95% CI 56.3%-94.2%) to gentamicin. Among the 26 *S. aureus*, 5 isolates (19.2%) were positive for *the mecA* gene. *tetK* gene was identified among the 19 (73.1%) *S. aureus* isolates and belonged to the highest proportion. On the other hand, the *tetM* gene was found within the 2 isolates showing the least percentage. In case of *E. coli*, the ciprofloxacin-resistant gene *gyrA*, was identified among the 19 (95%) *E. coli* isolates and it was the highest proportion. No colistin resistant gene was detected in isolated *E. coli*. Fifty percent of the *E. coli* isolates represented sulphamethoxazole-trimethoprim resistant gene *sul1* and *sul2*. Similarly, 10 (50%) *E. coli* isolates were positive to ampicillin resistant gene *blaTEM* and 30% were *blaCTX-M,* resistant to ceftriaxone.

From the univariable logistic regression analysis, it was evident that the odds of having AMR *S. aureus* was 2.41 (95% CI: 0.96-6.07) times higher in the farms where the antibiotic course was not completed properly. Furthermore, the odds of having AMR*E.coli* in bovine raw milk was almost 23 (95% CI: 6.09-84.25; P=<0.0001) times higher in the dairy farms avoiding the practice of antibiotic course completion, 12 (95% CI: 3.31-44.12) times higher where withdrawal period was not followed, 18.38 (95% CI: 4.98-67.82) times attributed when the farms avoided proper dose maintenance and 7.62 (95% CI: 2.10-27.63; P=0.002) times greater in those dairy farms having the farm personnel without the knowledge of AMR. However, multivariable logistic regression model showed no significant association might be due to low observation number. In case of presence of *S. aureus* in the sample, after adjustment of the confounding effect of the factors in the multivariable logistic regression model, a potential risk factor (CMT result) was identified in this study. The odds of the presence of *S. aureus* in the CMT test 'positive' samples was 10.3 times (95% CI: 2.6-40.5) higher than the CMT test 'negative' samples. In the case of *E. coli*, the multivariable analysis showed that the presence of *E. coli* increased by 13.7 times if the floor had been contaminated with mud and cow dung during the milking time and exclusively a hike odds found in case of the dirty udder of cows, as well. Conclusively, the study findings will provide ample statistical evidence to develop strategies for improved antimicrobial stewardship, rejuvenate the antimicrobial drug channel and to develop efficacious and sustainable alternative approaches to tackling AMR crisis both in humans and livestock.