Detection of Methicillin-Resistant *Staphylococcus aureus* (MRSA) in Poultry and Cattle Farms from Urban and Rural Farms of Bangladesh

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Introduction

Methicillin-Resistant *Staphylococcus aureus* (MRSA) poses a significant health risk in both humans and animals. The presence of MRSA on animal farms could lead to higher rates of colonisation and infection among animals and the farmers. The presence of MRSA in livestock and farm environments poses significant challenges for infection control and requires ongoing surveillance to reduce its impact on public health.

Objective

Our cross-sectional study aimed to evaluate MRSA prevalence on poultry and cattle farms in Bangladesh and to compare prevalence between urban and rural settings.

Methods

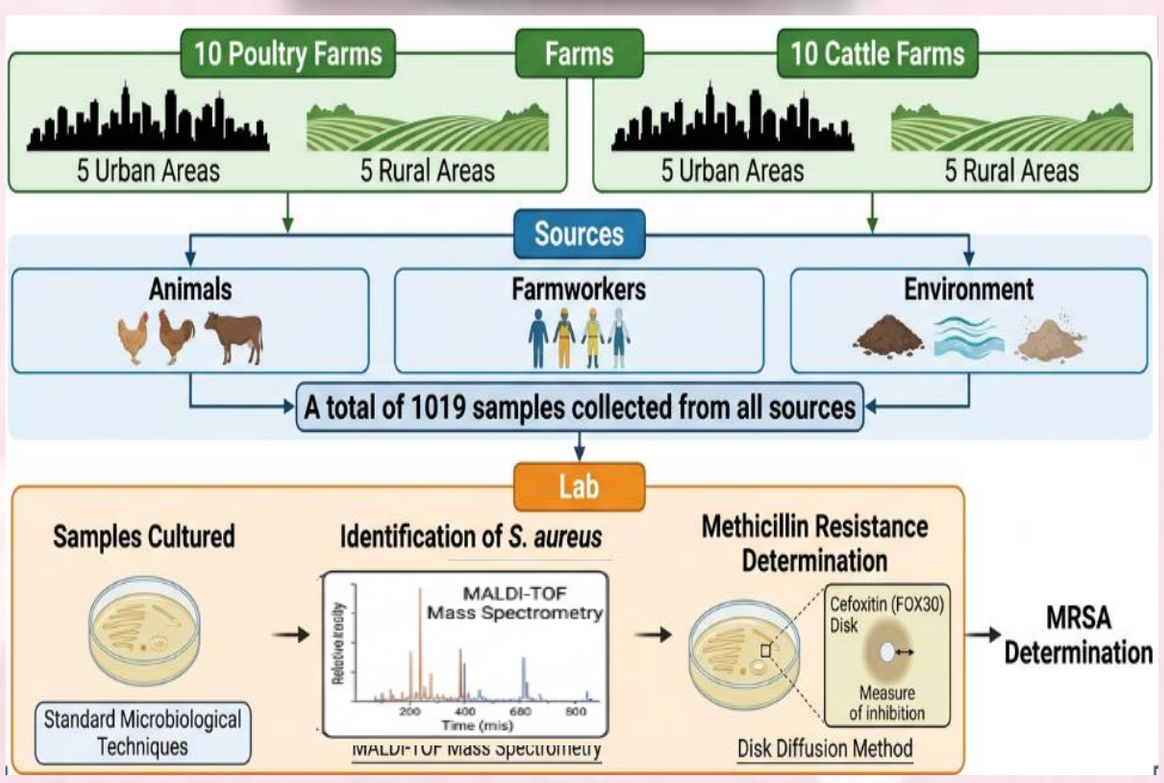

Figure 1. *S. aureus* sampling and MRSA identification workflow

Results & Discussion

Table 1:MRSA prevalence across sample types

Category	MRSA positives	Prevalence
Total samples	13 / 1019	1.3%
Total S. aureus	67 / 1019	6.6%

Table 2: MRSA by farm-related subgroup (poultry and cattle)

Farm type	Subgroup	MRSA positives	Total (n)	Prevalence
Poultry	Poultry samples	5	217	2.3%
Poultry	Poultry farm workers	6	93	6.5%
Poultry	Poultry farm environment	0	203	0%
Cattle	Cattle farmworkers	1	105	1.0%
Cattle	Cattle farm environment	1	197	0.5%
Cattle	Cattle (overall—no MRSA)	0	204	0%

Table 3: MRSA prevalence at the farm level

Farm type	Farms tested	MRSA-positive farms	Prevalence of farms
Poultry	10	6	60%
Cattle	10	2	20%

Table 4: Rural vs urban farms (MRSA-positive farms)

Location	MRSA-positive farms / total farms	Prevalence
Rural	5 / 10	50%
Urban	3 / 10	30%

Among the 1019 collected samples, 6.6% were identified as *S. aureus* and 1.3% as MRSA strains.
MRSA prevalence is higher across poultry subgroups compared to cattle subgroups, with poultry farm workers exhibiting the highest overall prevalence at 6.5%.
Both the poultry farm environment and cattle subgroups overall had zero MRSA isolates.
MRSA-positive farms are more prevalent in rural locations (50%) compared to urban locations (30%).

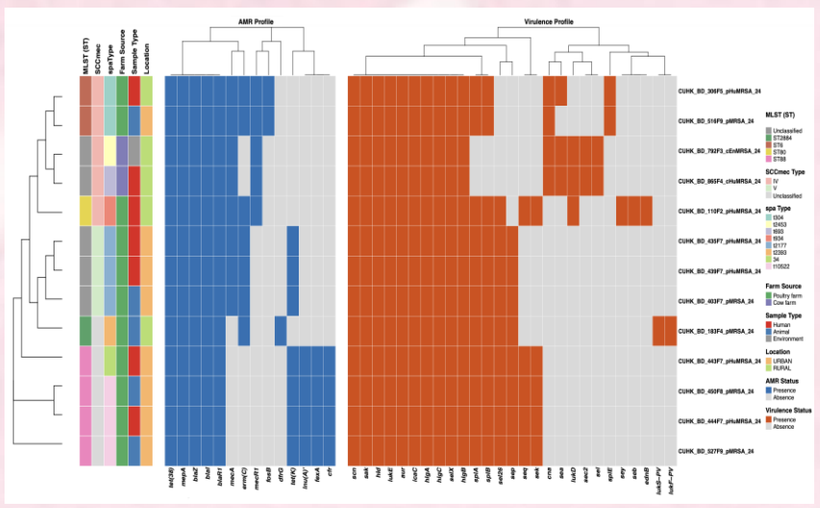

Figure 2. Distribution of AMR and virulence genes among MRSA isolates. The presence of genes is represented through colored patterns.

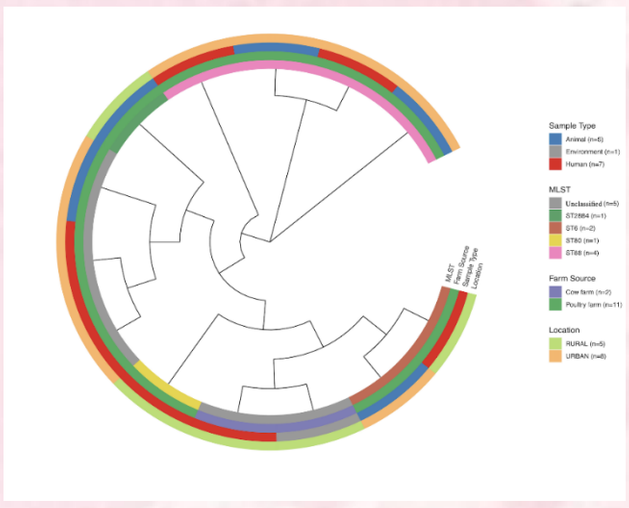

Figure 3: Circular phylogenetic tree visualisation. Sample types, MLST, Farm source and locations are colour-coded in the rings

A single PVL-positive MRSA strain was identified from a poultry farm, isolated from a worker associated with that farm.
The presence of *mecA* gene was confirmed in 8 MRSA strains. No *mecC* gene was identified.
Phenotypic resistance to cefoxitin was observed in five isolates despite the genetic absence of the *mecA* or *mecC* gene.
The ST88 type and the unclassified ST types are exclusively associated with poultry farm sources. The remaining sequence types include ST2884, ST6, and ST80.

Conclusion

Our study shows the presence of MRSA in livestock (cattle and poultry), farm environments, and farm workers. Phenotypic resistance to cefoxitin was observed in five isolates despite the absence of the classic *mecA* gene. While the inhibition zone of two isolates is 21 mm, which sits exactly on the clinical resistance breakpoint, the inhibition zone of the remaining three isolates was 17mm, 10mm, and 9mm, respectively. The observed resistance in these *mec*-negative strains likely stems from alternative mechanisms, such as mutations in specific core cell-wall proteins or the hyper-expression and upregulation of *bla* regulatory genes. Future work would focus on utilising whole-genome sequencing and transcriptomic analysis to precisely map point mutations in native penicillin-binding proteins and quantify the expression of *bla* regulatory genes in these *mec*-negative isolates. Understanding the dynamics of MRSA in animal farms and responsible use of antimicrobials in agriculture are critical for mitigating public health risks and ensuring food safety.

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