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Original Article

Antibiotic resistance patterns of bacterial isolates from raw milk sold in coolers in Kawuku, Entebbe, Wakiso district.

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ABSTRACT

Background:
Milk is an essential animal-derived food that provides proteins, vitamins, and minerals vital for human growth and metabolism. However, raw milk is a major vehicle for foodborne pathogens. This study aimed to determine the resistance patterns of pathogenic bacterial species in raw milk sold in coolers in Kawuku Entebbe Wakiso District.

Methodology:
This laboratory-based cross-sectional study aimed to determine the prevalence of bacterial pathogens and their antimicrobial resistance patterns in raw milk sold from coolers in Kawuku. A total of 20 raw milk samples were aseptically collected from selected milk stalls between January and February 2025 and analyzed using standard microbiological techniques. Bacterial identification was carried out through culture, Gram staining, and biochemical tests, while antimicrobial susceptibility testing was performed using the Kirby–Bauer disc diffusion method in accordance with CLSI guidelines.

Results:
Staphylococcus saprophyticus (23.3%) and *Escherichia coli* (16.7%) were the most prevalent pathogens, followed by *Klebsiella pneumoniae* and *Proteus mirabilis* (10.0% each). Other bacteria, including *S. aureus*, *E. faecalis*, and *Citrobacter freundii*, were also detected in varying proportions. Antimicrobial susceptibility testing demonstrated high resistance to Cefoxitin (CX5), Tetracycline (TE30), and Penicillin G (P10), while Ciprofloxacin (CIP5), Vancomycin (VA30), and Levofloxacin (LEV15) exhibited higher efficacy. Resistance patterns varied significantly across organisms and media types, with Gram-negative isolates showing more resistance to commonly used antibiotics.

Conclusion:
Raw milk sold in Kawuku is contaminated with multiple pathogenic bacteria exhibiting significant antimicrobial resistance.

Recommendation:
Further molecular-level studies are recommended to understand the genetic mechanisms driving resistance.

Keywords*: Raw milk, antimicrobial resistance, bacterial pathogens, Kawuku, Uganda, public health*
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Background of the study

Milk, as a product of animal origin, constitutes a valuable source of macronutrients and micronutrients, including proteins, energy, vitamins, and minerals, all of which are fundamental for tissue development and structural maintenance (Aliyo et al., 2022). The presence of bioactive constituents, particularly casein and whey proteins, has been shown to play a pivotal role in diverse physiological and biochemical processes, thereby exerting a significant influence on human metabolic activity and overall health outcomes (Algammal et al., 2020).

Over the last decade, dairy farming has expanded considerably within East African nations. Among the six leading milk-producing countries in Africa, two are located in East Africa Kenya and Ethiopia with reported annual outputs of 5,528,900 and 3,644,000 metric tonnes, respectively (Bleasdale et al., 2021). Despite this increase in production, corresponding shifts in cultural practices and traditional attitudes toward milk consumption have remained limited (Prakashbabu et al., 2020).

Microbial contamination of unprocessed milk remains a principal contributor to foodborne illnesses, representing a major threat to public health worldwide. The consequences of milk-related infections, including morbidity, mortality, and associated complications, continue to escalate, placing substantial pressure on healthcare systems (Aliyo et al., 2022). The global burden of foodborne diseases constitutes a significant public health concern, with pathogens such as *Salmonella* ranking among the most prevalent. Food poisoning of this nature is estimated to account for approximately 1.3 billion cases of gastroenteritis and nearly 3 million deaths annually across the globe (Mohamed et al., 2018)

The organisms often found in milk are bacteria, and many bacterial organisms have a tendency to develop resistance and are much less treatable with one or more antimicrobial medicines previously used to treat or prevent contamination (Mailafia et al., 2017).

Antimicrobial resistance contributes to higher rates of illness, death, and treatment costs, particularly in infections associated with ESBL-producing bacteria (Mpatswenumugabo et al., 2023). Routine microbiological testing plays a crucial role in the dairy sector by safeguarding public health and minimizing potential economic losses (Chengat et al., 2020).

Methodology

Study design

The research is a laboratory-based cross-sectional study that was carried out in raw milk collected from coolers in conveniently selected sites in Kawuku, Entebbe, Wakiso District.

Study area

The study was conducted in a few conveniently selected milk stalls located within Kawuku, Entebbe, Wakiso District. It ran from January to February 2025.

Sampling technique and sample space

Twenty (20) raw milk samples were conveniently sampled during the selection of the raw milk from the stalls. This sampling technique was chosen because of the limited number of stalls available at the study site. The research selected stalls and samples of raw milk are presumed to represent the entire population since there are selection criteria.

Study selection criteria

Inclusion criteria

All commercial milk sellers with milk coolers were included in the study, with a limit of twenty (20) samples.

Exclusion criteria

All commercial milk sellers without milk coolers were excluded from the study.

Quality assurance and quality control

Data quality was ensured through carrying out analysis following standardized analytical techniques and Standard Operating procedures on sample collection, transportation, and analysis. The data collected was thoroughly checked, verified, and validated for completeness and consistency. All the steps and equipment calibrations were guided and done by a qualified laboratory technologist and the Institution Supervisor. Other quality controls that were observed were:

Pre-Examination

- Ensuring proper sample collection with minimized contamination – sterilizing of sample bags, double packaging, and disinfection of hands before sample handling.
- Use a cool box during sample transportation to the laboratory.
- Properly labeling samples for easy identification and avoiding sample swapping.
- Precautions for storing samples in the refrigerator at 4 to 8°C.

Examination

- Sample preparation was done on arrival at the laboratory or within a time span of 24 hours.
- Sample verification was done before examination.
- Aseptic microbiological techniques were carefully observed during analysis.
- Ensuring proper care and maintenance of equipment, e.g., incubator temperature maintenance log charts, was carefully observed.
- Following and adhering to protocol SOPs.

Post Examination

- Constantly verifying the microbiological test results.
- Recording results.
- Analysis, interpretation, and inference of results.
- Writing reports and documentation.

Materials

A sterile normal saline solution to immerse the samples was prepared. Primary media, i.e., MAC, MSA, and BEA, onto which the samples were cultured, peptone water, and NA for sub-culturing. Coagulase, Catalase, Citrate, TSI, SIM, and Kovac's reagent for biochemicals, followed by MHA or NA, and antibiotic discs for AST (Antimicrobial Susceptibility Testing) were used.

Sample Collection

Twenty (20) raw milk samples were collected directly from the storage containers used by the corresponding milk sellers. Approximately 50mls were aseptically collected and put into sterile polythene bags.

Generally, sample collection involved the following steps:

- Sterile polythene bags were bought from shops and surface sterilized using 70% ethanol to prevent possible external contaminants.
- The bags were double-packaged and transported to the sample collection site.
- The hands were always disinfected using 70% ethanol, and were constantly disinfected before handling the specimen that was aseptically double packaged in the sterile polythene bags.
- The samples were then transported back to the laboratory in a cool box at 4 0C to 8 0C.

Laboratory analysis

Sample preparation

During sample preparation for analysis:

- Gram staining was performed on the raw milk samples.
- After inoculation on primary cultures, sub-culturing on NA, Gram staining, then biochemical tests, and finally AST was done, based on the zone diameter of inhibition around the disc, and isolates were classified under Susceptible (S), Intermediate (I), or Resistant (R) based on the Clinical Laboratory Standard Institute (CLSI) standards.

Actual bacteria isolation

- The isolation followed these steps: Different Gram staining forms, NA sub-cultures, and different biochemical tests were carried out to identify the bacterium isolate to the species hierarchy. District Laboratory Practices will be used to identify the different bacteria isolated according to their biochemical tests.

Antimicrobial Susceptibility Patterns of the isolates

During this process, NA/MHA was prepared, and the Kirby-Bauer disc diffusion method of AST was used to determine the antimicrobial susceptibility patterns of the different isolates.

- The AST chart was used to interpret the zones of clearance. The different antibiotics, which include Cefoxitin (CX5), Tetracycline (TE30), Vancomycin (VA30), Ciprofloxacin (CIP5), Levofloxacin (LEV15), Clindamycin (DA15), and Penicillin G (P10), were classified into Susceptible (S), Intermediate (I), or Resistant (R) based on the CLSI standards.

Data management and analysis

Data was entered, organized, and cleaned using Microsoft Excel 2021, and the analysis was done using the Python programming language in the Jupyter Notebook.

RESULTS

Prevalence of Pathogens in the Raw Milk Sample

The overall prevalence of pathogens in raw milk samples shows that S. saprophyticus is the most prevalent pathogen, found in 23.33% of the samples, followed by E. coli at 16.67%, Klebsiella pneumoniae 10.0%, and Proteus mirabilis 10.0% were also commonly detected, S. aureus and E. faecalis in mid proportions at 6.67%, and several other pathogens appear less frequently at 1.67% but may still pose health risks, as shown in the table 1.

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Table 1: Pathogen frequency in the raw milk samples

Organism	Frequency	Percentage (%)
S. SAPROPHYTICUS	14	23.33
E. COLI	10	16.67
KLEBSIELLA PNEUMONIAE	6	10
PROTEUS MIRABILIS	6	10
CITROBACTER FREUNDII	5	8.33
E. FAECALIS	4	6.67
S. AUREUS	4	6.67
S. EPIDERMIDIS	2	3.33
B. SUBTILIS	2	3.33
PROTEUS VULGARIS	1	1.67
STREPTOCOCCUS GALACTIAE	1	1.67
S. HAEMOLYTICUS	1	1.67
S. XYLOSUS	1	1.67
MORGANELLA MORGANII	1	1.67
CITROBACTER KOSERI	1	1.67
SERRATIA MARCESCENS	1	1.67

Resistance Patterns of the pathogenic bacterial species in the raw milk samples

The boxplots below visualize the distribution of the diameters of the grouped antibiotics across the three (3) media types used.

BROAD-SPECTRUM AND RESISTANT PATHOGEN AGENT (BS)

- In this group, antibiotics like **CIP5** and **VA30** show higher mean zone diameters, suggesting stronger susceptibility; C**X5** and **TE30** have lower means and wider ranges, indicating variable resistance across organisms and media.
- The BEA and MAC media show wider variability, indicating differential growth and resistance expression, while MSA shows tighter distributions, suggesting more consistent resistance.

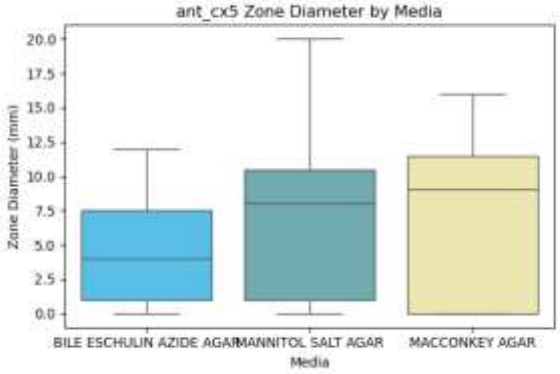

Figure 1: Zone diameter for CX5

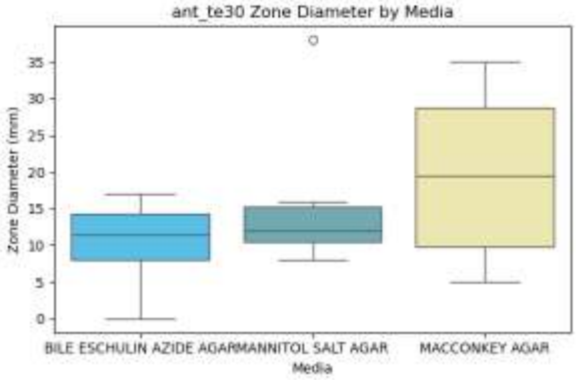

Figure 2: Zone diameter for TE30

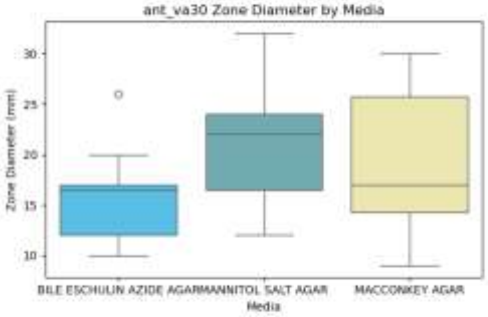

Figure 3: Zone diameter for VA30

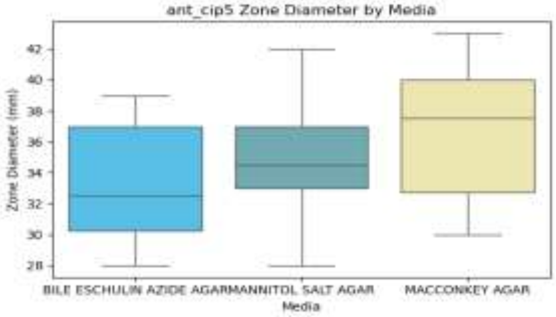

Figure 4: Zone diameter for CIP5

COMMUNITY-ACQUIRED INFECTION AGENTS (CB)

LEV15 and **DA15** show moderate to high zone diameters, suggesting partial susceptibility, and **P10** consistently shows low zone diameters, indicating high resistance.

The BEA and MAC media show lower median resistance scores, indicating higher resistance, whilst MSA shows higher medians for TE30 and LEV15.

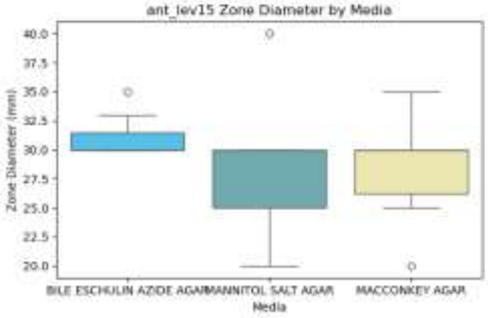

Figure 5: Zone diameter for LEV15

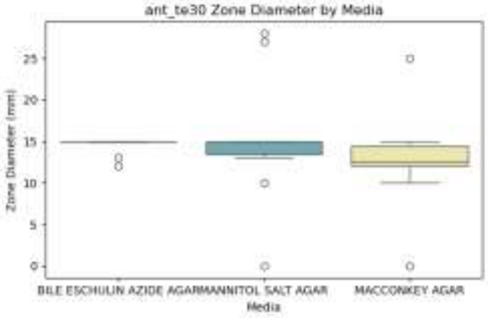

Figure 6: Zone diameter for TE30

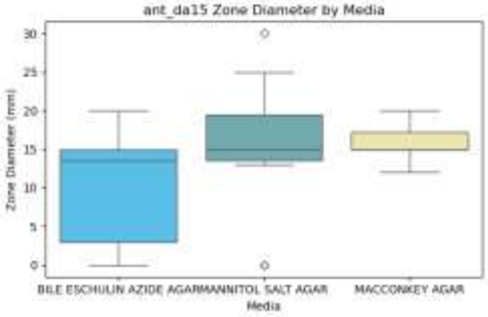

Figure 7: Zone diameter for DA15

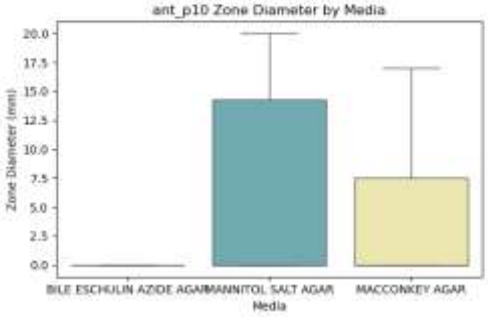

Figure 8: Zone diameter for P10

Average resistance per organism stratified by media.

BROAD-SPECTRUM AND RESISTANT PATHOGEN AGENT (BS)

Figure 9: Organism-Antibiotic Resistance in the first 10 samples under BEA

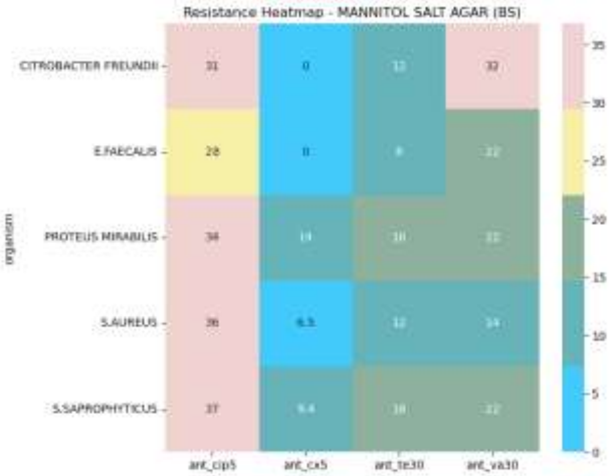

Figure 10: Organism-Antibiotic Resistance in the first 10 samples under MSA

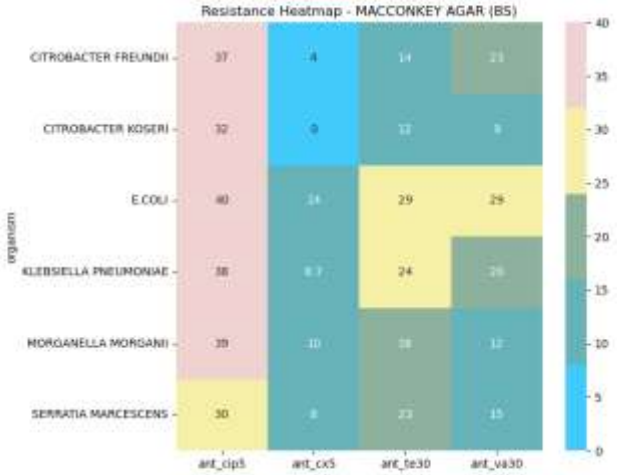

Figure 11: Organism-Antibiotic Resistance in the first 10 samples under MAC

Among organisms in this group, S. aureus and E. faecalis show high resistance across most antibiotics, B. subtilis and S. saprophyticus show moderate susceptibility.

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COMMUNITY-ACQUIRED INFECTION AGENTS (CB)

Figure 12: Organism-Antibiotic Resistance in the last 10 samples under BEA

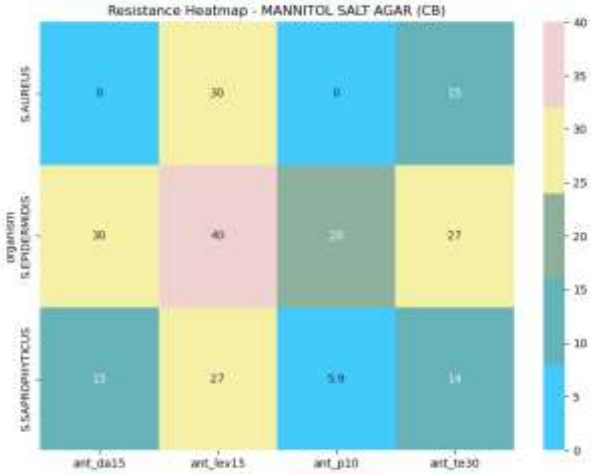

Figure 13: Organism-Antibiotic Resistance in the last 10 samples under MSA

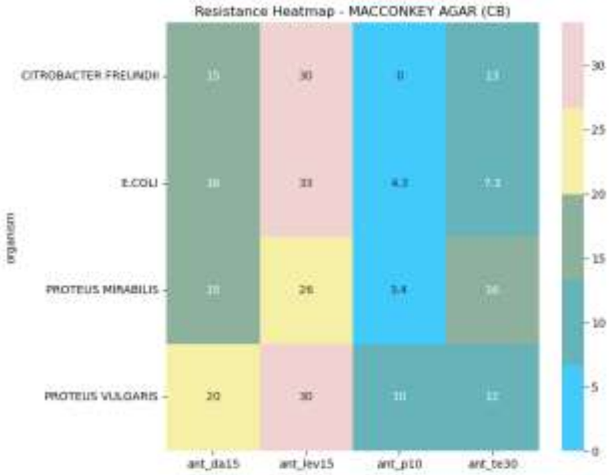

Figure 14: Organism-Antibiotic Resistance in the last 10 samples under MAC

E. coli and K. pneumoniae show high resistance to P10 and DA15, and S. saprophyticus shows variable resistance across media.

Relationships between the resistance levels to the different antibiotics

Correlation matrices in the correlation heatmaps below reveal relationships of resistance levels between the different antibiotics.

BROAD-SPECTRUM AND RESISTANT PATHOGEN AGENT (BS)

CX5 ↔ TE30 (0.76) shows a strong positive correlation in that, when results for Cefoxitin are high (more susceptible), Tetracycline results tend to be high too. This could hint at shared resistance patterns or linked resistance mechanisms in these isolates.

CX5 ↔ VA30 (0.33) shows moderate positive correlation, indicating some tendency for these two to move together, but with notable variability. Thus, it may suggest partial overlaps in resistance mechanisms or selective pressures.

CX5 ↔ CIP5 (0.26) shows a weak positive correlation with a slight association, but has many exceptions.

TE30 ↔ VA30 (0.44) shows moderate positive correlation — more relationship than either has with ciprofloxacin, but not as strong as CX5–TE30.

TE30 ↔ CIP5 (0.26) shows Weak positive correlation — little predictive value.

VA30 ↔ CIP5 (0.23), very weak correlation — essentially, vancomycin and ciprofloxacin susceptibilities behave quite independently here.

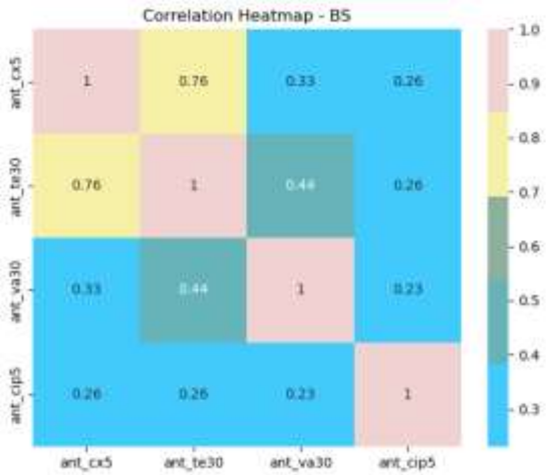

Figure 15: Correlation of the different antibiotics in the first group of samples

COMMUNITY-ACQUIRED INFECTION AGENTS (CB)

TE30 ↔ LEV15 (0.21) has a weak correlation – results for tetracycline and levofloxacin barely trend together, indicating largely independent resistance profiles.

TE30 ↔ DA15 (0.11), very weak – almost no meaningful relationship; resistance to one informs little about the other.

TE30 ↔ P10 (0.25), weak – small positive tendency but lots of variability.

LEV15 ↔ DA15 (0.11), very weak – suggests these two have unrelated resistance mechanisms.

LEV15 ↔ P10 (0.39), moderate – some shared pattern; perhaps partial linkage in resistance genes or co-selection in certain strains.

DA15 ↔ P10 (0.44), moderate – the strongest relationship here, hinting at a possible common pathway or frequent co-resistance in your dataset.

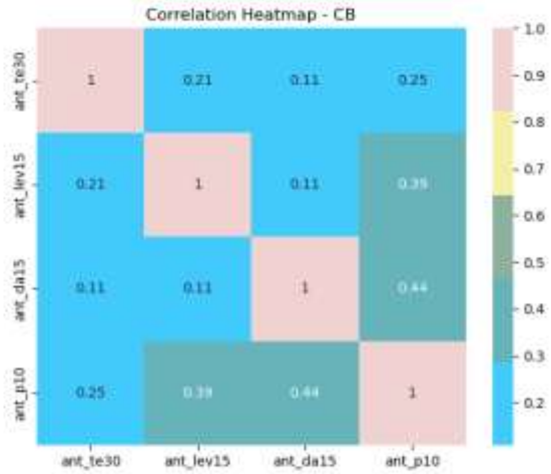

Figure 16: Correlation of the different antibiotics in the second group of samples

AST Classification Summaries

Each antibiotic was classified as Susceptible (S), Intermediate (I), or Resistant (R) based on zone diameter thresholds.

BROAD-SPECTRUM AND RESISTANT PATHOGEN AGENT (BS)

In this group, most organisms were Resistant to CX5 and TE30, and VA30 and CIP5 had more Susceptible classifications.

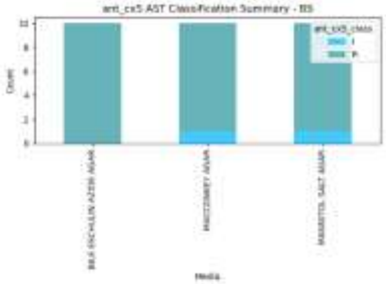

Figure 17: CX5 AST Classification Summary per media

Bile Esculin Azide Agar:

R: High count (10), indicating all isolates tested on this medium were resistant

MacConkey Agar:

R: High count (9). Also shows a high count, like Bile Esculin.
I: Low count (1), suggesting few intermediate isolates.

Mannitol Salt Agar:

R: High count (9). Also shows a high count, like Bile Esculin.

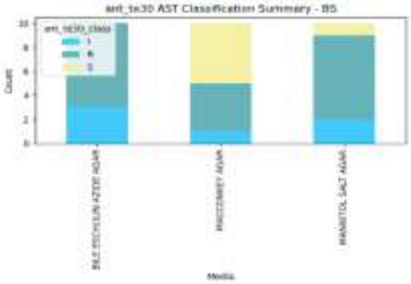

Figure 18: TE30 AST Classification Summary per media

Bile Esculin Azide Agar:

Has only **R**: High count (7), indicating all isolates tested on this medium were resistant, and **I** (3), which indicates a few isolates had intermediate rates.

MacConkey Agar:

R: medium count (4), **I**: Low count (1), suggesting few intermediate isolates, and **S** (5), thus a variable susceptibility rate

Mannitol Salt Agar:

I: Low count (1), suggesting few intermediate isolates.

Overall Insights

- This group generally shows a significant resistance rate across all three media types.

R: High count (7) also shows a high count, **I**: Low count (2) and **S** (1), suggesting some sort of resistance in this medium.

Overall Insights

- This group generally shows a significant resistance rate across all three media types.

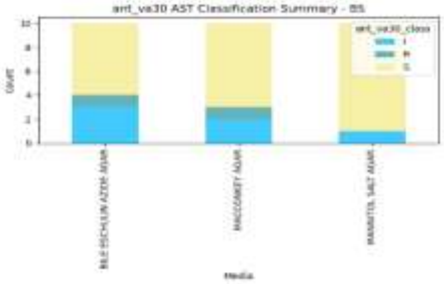

Figure 19: VA30 AST Classification Summary per media

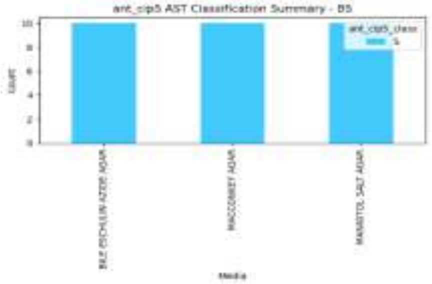

Figure 20: CIP5 AST Classification Summary per media

Bile Esculin Azide Agar:

It has a mixture of R: low count (1), indicating all isolates tested on this medium were not very resistant, and I (3), which indicates a few isolates had intermediate rates, and S (6), which indicates very high susceptibility rates.

MacConkey Agar:

Almost having the same profile as Bile Esculin Azide Agar, only that the S (7) count increased slightly, showing there were susceptible isolates generally.

Mannitol Salt Agar:

S (9) count increased even higher, showing there were susceptible isolates generally.

Overall Insights

- This group generally shows a significant susceptibility rate across all three media types.

In all three (3) media, there is significant susceptibility.

COMMUNITY-ACQUIRED INFECTION AGENTS (CB)

In this group of antibiotics, LEV15 showed a mix of S and I, while P10 was predominantly Resistant, DA15 had a balanced distribution across S/I/R.

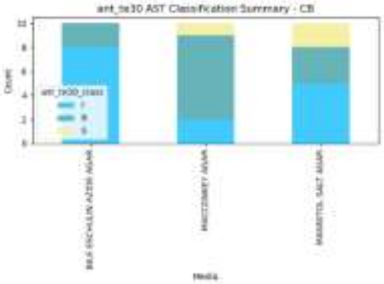

Figure 21: TE30 AST Classification Summary per media

Bile Esculin Azide Agar:

Class I: High count (8), indicating most isolates tested on this medium were intermediate.

Class R: Low count (2), suggesting few resistant isolates.

MacConkey Agar:

I: Also shows a high count, like Bile Esculin.

R: Higher (7) than Bile Esculin but still significantly lower than Class I.

S: Shows a low count (1) of susceptibility.

Mannitol Salt Agar:

I: Again, a high count (5), consistent with the other media.

R: Slightly higher (3) than Bile Esculin but still lower than Class I.

S: Slightly higher (2) than MacConkey Agar susceptibility count.

Overall Insights

- Across all three media, **I and R isolates dominate**, suggesting that most bacterial samples tested fell in the intermediate and resistant rates.

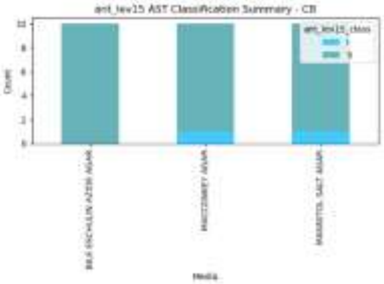

Figure 22: LEV15 AST Classification Summary per media

Bile Esculin Azide Agar:

Class S: High count (10), indicating all isolates tested on this medium were susceptible

MacConkey Agar:

S: High count (9). Also shows a high count, like Bile Esculin.

I: Low count (1), suggesting few intermediate isolates.

Mannitol Salt Agar:

S: High count (9). Also shows a high count, like Bile Esculin.

I: Low count (1), suggesting few intermediate isolates.

Overall Insights

- This group shows **full representation (10 isolates)** across all three media types.
- The presence of both **Class I and Class S** suggests a **diverse susceptibility profile**

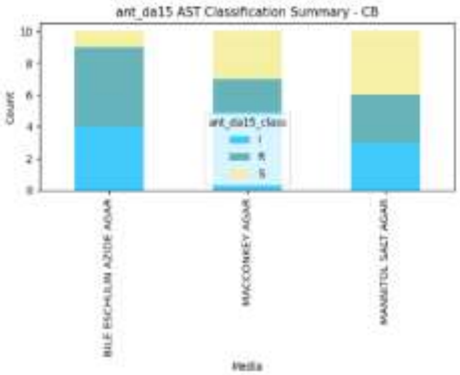

Figure 23: DA15 AST Classification Summary per media

Bile Esculin Azide Agar:

Contains a mix of **I** (4), **R** (5), and **S** (1), **R** being dominant here

The presence of all three classes suggests a diverse susceptibility profile.

Generally, **I** appear dominant, indicating most isolates are Intermediate.

MacConkey Agar:

Also, it shows all three classifications.

It is more prominent here than in Bile Esculin, suggesting an intermediate resistance rate.

R (2) and **S** (3) segments are present but smaller.

Mannitol Salt Agar:

Displays a relatively balanced distribution of **I, R**, and **S**.

R and **I** have the same counts (3) each, indicating a balance in Intermediate and Resistant rates.

S (4) indicates there were susceptibility rates.

Overall Insights

The sample tested with ant_da15 shows a mixed susceptibility profile across all media.

Susceptible isolates (S) are present in all media, but Intermediate (I) and Resistant (R) are more significant, indicating a variable intermediate-resistant rate.

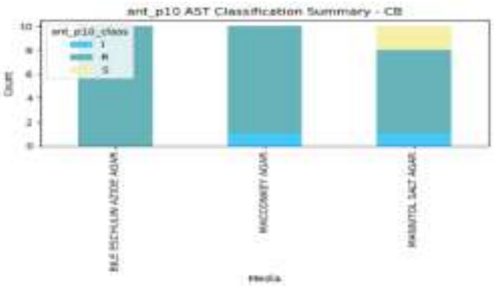

Figure 24: P10 AST Classification Summary per media

Bile Esculin Azide Agar:

Contains only **R** (10), which shows significant isolate resistance.

MacConkey Agar:

Shows **R** (9) and **I** (1), still indicating how resistant the isolates are to the antibiotic.

Mannitol Salt Agar:

R (7) is still dominant here, followed by **S** (2) and **I** (1), thus deeming the organisms resistant.

Overall Insights

Generally, the organisms are resistant to this antibiotic.

Table 2: Comparing and contrasting the two groups

Feature	BS group (Y1–Y10)	CB group (Y11–Y20)
Antibiotics Tested	CX5, TE30, VA30, CIP5	TE30, LEV15, DA15, P10
Resistance Profile	More resistant overall	Mixed susceptibility
Media Impact	Strong influence on TE30, CX5	Strong influence on P10, LEV15
Organism Variability	High (S. aureus, E. faecalis)	Moderate (E. coli, K. pneumoniae)

DISCUSSION

Prevalence of Pathogens in Raw Milk

The study revealed that *Staphylococcus saprophyticus* was the most prevalent pathogen, detected in 23.3% of the raw milk samples, followed by *Escherichia coli* (16.7%), *Klebsiella pneumoniae* (10%), and *Proteus mirabilis* (10%). Mid-level prevalence was observed for *S. aureus* and *E. faecalis* (6.7%), while less frequent organisms such as *S. haemolyticus*, *Streptococcus galactiae*, and *Morganella morganii (1.7%)* were also detected.

The high prevalence of *S. saprophyticus* may reflect poor milking hygiene and environmental contamination, as this organism is commonly found on human skin and in the environment. The detection of *E. coli* and *K. pneumoniae* further suggests fecal contamination, possibly due to unclean milking equipment, contaminated water, or improper handling practices. These findings align with previous studies in Uganda and Tanzania, which reported coliform bacteria, including *E. coli*, as frequent contaminants of raw milk (Nathan et al., 2022; Hassani et al., 2022). While pathogens with low prevalence may seem less concerning, they can still pose a risk to consumers, particularly the immunocompromised, as even a small number of organisms like *Serratia marcescens* can cause severe infections (Wai et al., 2020).

This prevalence pattern highlights the critical role of farm hygiene, animal health, and proper milk handling in preventing milk-borne infections. The presence of multiple pathogenic species in the same milk samples emphasizes the complex microbial ecology of raw milk, consistent with findings from Michira et al. (2023), who reported co-existence of various Staphylococcus spp. and coliforms in Kenyan raw milk.

Antimicrobial Susceptibility Patterns

Antimicrobial susceptibility testing (AST) revealed high resistance to Cefoxitin (CX5) and Tetracycline (TE30) among the broad-spectrum pathogens, while Vancomycin (VA30) and Ciprofloxacin (CIP5) showed higher susceptibility. Among community-acquired pathogens, *E. coli* and *K. pneumoniae* demonstrated high resistance to Penicillin (P10) and Daptomycin (DA15), whereas *S. saprophyticus* displayed variable susceptibility across different media.

The high resistance to commonly used antibiotics like tetracycline and beta-lactams can be attributed to their frequent and sometimes unregulated use in livestock, a phenomenon widely reported in developing countries (Tang et al., 2017; Ababu et al., 2020). Conversely, the retained susceptibility to vancomycin and ciprofloxacin is consistent with previous reports where these antibiotics remain effective due to limited use in agricultural settings (Mugenyi et al., 2023; Zafar et al., 2020).

Importantly, the study observed media-dependent resistance patterns. Broad-spectrum pathogens showed higher resistance in Bile Esculin Azide (BEA) and MacConkey (MAC) agar compared to Mannitol Salt Agar (MSA), while community-acquired pathogens showed notable resistance in BEA and MAC for P10 and LEV15. This suggests that growth environment influences the expression of resistance genes, highlighting the importance of using multiple media for comprehensive AST (Chengat et al., 2020).

Correlation Between Antibiotics

Correlation analysis revealed a strong positive correlation between Cefoxitin and Tetracycline (0.76) among broad-spectrum pathogens, suggesting possible co-selection of resistance genes. Moderate correlations such as DA15 ↔ P10 (0.44) indicate partial overlap in resistance mechanisms, possibly due to plasmid-mediated gene transfer or selective pressure from repeated antibiotic exposure. Weak correlations between other antibiotics suggest independent resistance pathways, echoing findings by Liu et al. (2022) in China and Kumar et al. (2018) in India.

These correlations have practical implications: the co-resistance observed may limit treatment options in humans consuming raw milk, making infections harder to treat and increasing reliance on last-resort antibiotics.

Public Health and Socio-Economic Implications

The presence of multidrug-resistant bacteria in raw milk has serious implications for both public health and the local dairy economy. Consumers are at risk of infections that are difficult to treat, particularly children, the elderly, and immunocompromised individuals. Resistance patterns suggest that first-line antibiotics may be ineffective against common pathogens such as *E. coli, S. aureus, and K. pneumoniae*, consistent with global concerns regarding antimicrobial resistance in foodborne pathogens (Mpatswenumugabo et al., 2023; Abolghait et al., 2020).

Conclusion

Generally, S. saprophyticus and E. coli are the most prevalent pathogens in raw milk samples. Gram-negative rods dominate the bacterial profile. High resistance to CX5, P10, and TE30 suggests these antibiotics may be less effective. CIP5 and LEV15 show strong efficacy across isolates, and Significant variation in resistance patterns among organisms for LEV15.

This analysis provides robust evidence of antimicrobial resistance patterns in raw milk bacteria; it implores strategic public health interventions that monitor and control the hygiene, handling, and distribution of raw milk in communities with numerous raw milk service points, thus advocating for targeted therapy, improved AST protocols, and informed public health interventions in Kawuku Entebbe Wakiso District.

Recommendations

Avoid empirical use of CX5, TE30, and P10 due to high resistance; prioritize effective antibiotics like CIP5, VA30, and LEV15 due to their demonstrated susceptibility rates. Use multiple media for AST to capture the full resistance spectrum, implement organism-specific therapy based on AST results, and monitor resistance trends in milk supply chains to guide policy and treatment protocols.

Policy makers should strengthen Public Health through targeted interventions of reinforcing milk hygiene practices and enforcing pasteurization to reduce pathogen transmission, and implement regular surveillance of antimicrobial resistance in dairy products. Similarly, it should regulate antibiotic use in dairy farming to curb resistance.

In veterinary practice, overuse of CX5, TE30, and P10 should be avoided; rather, consider CIP5 and LEV15 for empirical treatment.

Further molecular-level studies to understand resistance mechanisms, especially for LEV15.

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Abbreviations

%	_	Percentage
AST	–	Antimicrobial Susceptibility Testing
AMR	-	Antimicrobial Resistance
BEA	–	Bile Esculin Agar
E. coli	–	Escherichia coli
e.g.	–	for example
etc.	–	Et cetera
MAC	–	MacConkey Agar
MHA	–	Muller Hinton Agar
MSA	–	Mannitol Salt Agar
NA	–	Nutrient Agar
SIM	–	Sulphur Indole Motility
SOPs	–	Standard Operating Procedures
S. aureus	–	Staphylococcus aureus
Spp	–	Species

TSI - Triple Sugar Iron Agar
CX5 – Cefoxitin
TE30 – Tetracycline
VA30 – Vancomycin
CIP5 – Ciprofloxacin
LEV15 – Levofloxacin
DA15 – Clindamycin
P10 – Penicillin G

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Conflict of interest

The authors declare no conflict of interest

Data availability

Data is available upon request from the author

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Egidio Mubangizi, a student pursuing a bachelor's Degree in Biomedical Laboratory Technology at the University of Kisubi

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