Investigation of Presence and Types of Mastitis Causing Organisms from Dairy Cows and Farm Environments in Taraba State Nigeria

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Abstract
This study investigated the presence, types, and distribution of mastitis-causing organisms in dairy cows and farm environments across Taraba State, Nigeria, with emphasis on evaluating the efficacy of different udder preparation protocols and identifying geographic variation in pathogen prevalence. A cross-sectional study was conducted in four Local Government Areas (Ardo Kola, Jalingo, Bali, and Gassol) of Taraba State. Swab samples were collected from udder surfaces under three conditions: unwashed, washed with water only, and disinfected with baby wipes, alongside composite bedding/soil samples. Bacterial isolation and identification were performed using standard microbiological techniques including selective media, Gram staining, and biochemical tests following Cowan and Steel's Manual. Bacterial growth rates varied significantly across locations, ranging from 41.67% (±49.92) in Bali to 61.11% (±49.44) in Gassol. Unwashed teats exhibited 66.67% (±47.71) bacterial growth, statistically equivalent to bedding/soil contamination (69.44% ±46.72). Water washing alone achieved minimal reduction (61.11% ±49.44), whereas disinfection dramatically reduced contamination to 5.56% (±23.23) a 91.7% relative reduction. Salmonella sp. predominated (21 isolates, 25.3%), followed by Staphylococcus sp. (18 isolates, 21.7%), Streptococcus sp. (13 isolates, 15.7%), E. coli (10 isolates, 12.0%), and Klebsiella sp. (7 isolates, 8.4%). Geographic clustering was evident: Gassol showed highest Staphylococcus prevalence (61.1% of all isolates), while Ardo Kola and Bali harbored predominant Salmonella and Klebsiella. These findings establish critical baseline data for mastitis control in Nigerian pastoral systems and underscore the urgent need for integrated interventions addressing both udder hygiene and environmental management to safeguard animal health and public health in regions with high raw milk consumption.

Keywords: *Mastitis, Udder, Beddings, Dairy cows, Identification*

Introduction

Bovine mastitis is the most economically damaging infectious disease in dairy cattle worldwide, ranking second only to reproductive disorders in frequency and exacting a heavy toll on herd productivity, milk quality, and farm profitability (Mungube et al., 2004). Defined as inflammation of the parenchyma of the mammary gland, mastitis is multietiological in origin, arising from pathogenic microorganisms, physical trauma, or chemical irritants (Sordillo et al., 1997). Its economic consequences are well documented: affected quarters lose roughly 30% of their productive capacity, and each infected cow yields approximately 15% less milk per lactation (Kasa et al., 2020). When indirect costs are factored in discarded milk, antibiotic therapy, veterinary fees, premature culling, and replacement mastitis emerges as one of the costliest and most intractable challenges facing the global dairy industry (Bruno et al., 2025).

In many developing countries, dairy production is predominantly carried out under traditional smallholder systems, which are often constrained by limited resources, poor sanitation infrastructure, and low awareness of best hygienic practices (Cole et al., 2024; Kümmel et al., 2016). Under such conditions, milk contamination is common at various stages of production and handling. For instance, pathogens such as *Staphylococcus aureus* may be introduced through infected animals, contaminated equipment, or human handlers, posing serious risks to both milk quality and public health (Zhang et al., 2022; Odetokun et al., 2024).

The public health implications of mastitis-causing organisms are particularly concerning in regions where raw or unpasteurized milk is widely consumed. Milk-borne pathogens can lead to foodborne illnesses, including staphylococcal food poisoning, which remains a major global health concern (Wang et al., 2007). Additionally, high microbial loads not only compromise safety but also reduce shelf life, affect milk quality, and lead to economic losses for farmers. This study was designed to investigate the presence and types of mastitis-causing organisms in Taraba State by examining potential sources of contamination, including the udder surface and farm environment. The findings are expected to provide baseline data that can support improved hygienic practices, targeted interventions, and more effective mastitis control strategies.

Materials and Methods

Determination of mastitis causing organisms in dairy farms

Numerous studies have concentrated on the prevalence of mastitis in bovine milk; however, there has been comparatively limited attention given to the organisms responsible for mastitis, their modes of introduction, and their resistance levels. Consequently, this study investigates the presence and classification of organisms that cause mastitis and evaluates their resistance levels.

Collection of samples for identification of mastitis causing organisms

i. Samples collected included:
ii. Swap sample from the uncleaned udder of the cow.
iii. Swap sample from the udder following a wash with regular water.
iv. Swap sample from the udder after being cleaned with a disinfectant using baby wipes.
v. Sample the bedding (soil) from three separate spots on the same farm, then combine them.

Method of collection

Swab sticks were procured from a reputable pharmacy, with each stick being carefully moistened with sterile water. These swab sticks were then utilized to gently wipe or rub across the cow's udder across all quarters, after which they were returned to the swab container for subsequent

laboratory detection and isolation. Following the collection of the unwashed sample, the cow's udder underwent a thorough cleansing with clean water. The swab stick employed for wiping the four udder quarters was also placed back in the container and promptly transported to the laboratory. The subsequent step in the sample collection involved employing disinfectant towels to clean the udder, followed by the use of a wet swab stick to gather samples from the four quarters of the udder for laboratory analysis. Additionally, samples of bedding were collected using an aseptic container, which entailed obtaining a 5g sample from three distinct locations on the farm. These samples were thoroughly mixed to form a single specimen, which was subsequently sent to the laboratory for analysis at the College of Agriculture, Taraba State.

Sample Processing and Microbial Isolation

To obtain countable plates with distinct colonies, the samples underwent dilution via a straightforward 1/10 dilution method. In this process, one part of the sample was combined with nine parts of diluent (distilled water) and mixed thoroughly. A series of dilutions was conducted as required, and from one or more of these dilutions, known quantities were inoculated onto agar using pour plate techniques.

Identification of Isolates from Milk Products

The identification process was predicated on growth observed on selective agar and broth, colony morphology, Gram's reaction, biochemical test results, and established criteria for disregarding negative cultures. The results were evaluated utilizing the Cowan and Steel Manual, in conjunction with additional methods for the identification of medical bacteria (Barrow and Feltham 1993).

Results and Discussion

Geographic Variation in Bacterial Contamination Across Taraba State

The investigation revealed significant heterogeneity in mean bacterial growth rates across the four sampled locations in Taraba State (Table 1). Gassol exhibited the highest mean bacterial growth rate at 61.11% (±49.44), followed by Jalingo at 55.56% (±50.40), while Ardo Kola (44.44% ±50.40) and Bali (41.67% ±49.92) demonstrated relatively lower contamination levels. This geographic variation aligns with established observations in dairy epidemiology that environmental mastitis pressure exhibits substantial spatial heterogeneity, reflecting differential farm management systems, sanitation infrastructure, and microclimatic conditions across pastoral landscapes (Bradley & Green, 2001). The elevated contamination in Gassol and Jalingo likely reflects the intersection of several risk factors characteristic of traditional Fulani pastoral systems in Nigeria. Recent investigations in Northern Oyo State demonstrate that while 51.0% of Fulani milk processors possess adequate knowledge of milk contamination, only 35.8% implement acceptable hygienic practices, with major deficiencies including inadequate handwashing, use of untreated water sources, and lack of udder disinfection (Cole et al., 2024). The substantial standard deviations observed across all locations (ranging from ±46.72 to ±50.40) indicate considerable within-location variability, suggesting that farm-level factors rather than broad geographic determinants are the primary drivers of contamination risk. This heterogeneity has critical implications for targeted intervention strategies, as blanket recommendations across geopolitical zones may fail to address specific localized risk profiles.

Table 4.41: Mean Bacterial Growth Rates by Location

Location	Total Samples	Positive Growth (n)	Mean Growth Rate (%) ± SD
Ardo Kola	36	16	44.44±50.40
Jalingo	36	20	55.56±50.40
Bali	36	15	41.67±49.92
Gassol	36	22	61.11±49.44

Efficacy of Udder Sanitation Protocols: From Water Washing to Disinfection

Analysis of bacterial growth across sampling conditions revealed profound differences in contamination levels that illuminate the hierarchy of udder preparation effectiveness (Table 2). Unwashed teats exhibited the highest average growth rate at 66.67% (±47.71), statistically indistinguishable from bedding/soil samples at 69.44% (±46.72). This equivalence between unwashed teats and environmental samples underscores the critical role of the farm environment as the ultimate reservoir of mastitis pathogens a finding extensively documented in contemporary mastitis epidemiology (Bradley & Green, 2001; Zadoks & Fitzpatrick, 2009). The minimal reduction achieved by water washing alone (61.11% ±49.44, representing only 8.3% relative reduction) provides compelling evidence that water-only udder preparation is insufficient for effective bacterial control. The dramatic reduction observed with disinfection (5.56% ±23.23, representing 91.7% relative reduction compared to unwashed teats) demonstrates the transformative potential of proper chemical sanitation. The persistence of low-level contamination (5.56%) in disinfected teats may reflect several factors: incomplete contact time, inadequate disinfectant concentration, or post-disinfection recontamination from environmental sources. The FAO emphasizes that disinfectant effectiveness depends critically on proper concentration, contact time, and application method, with sodium hypochlorite representing an inexpensive yet effective option for resource-limited settings when used at appropriate concentrations (FAO, 2009). The study's use of baby wipes as a delivery mechanism for disinfectant represents a pragmatic adaptation to field conditions, though commercial teat dips or foams may offer superior coverage and contact time. The high bacterial loads in bedding/soil samples (69.44%) identify environmental contamination as the predominant source of mastitis pressure in these traditional systems. *Klebsiella pneumoniae*, *E. coli*, and environmental streptococci persist in manure, bedding, barn floors, and slurry, entering the udder through the teat duct when cows lie down (Zadoks & Fitzpatrick, 2009). This environmental reservoir explains the limited efficacy of water-only washing: even meticulously washed teats become rapidly recontaminated upon contact with bedding or soil. The 94% reduction achieved through disinfection suggests that chemical sanitation creates a protective barrier that persists through the milking process, preventing pathogen entry even when environmental exposure occurs.

Table 2: Mean Bacterial Growth Across Different Sampling Conditions

Location	Total Samples	Positive Growth (n)	Mean Growth Rate (%) ± SD
Unwashed teats	36	24	66.67 ± 47.71
Washed teats	36	22	61.11 ± 49.44
Disinfected teats	36	36	5.56 ± 23.23
Bedding/soil	36	25	69.44 ± 46.72

Spatial-Pathogenic Interactions: Location-Specific Contamination Patterns

The distribution analysis (Table 3) reveals complex interactions between geographic location and sampling condition that challenge simple generalizations about mastitis epidemiology. Gassol exhibited consistently elevated contamination across multiple conditions: 77.8% for unwashed teats, 77.8% for washed teats, and 77.8% for bedding samples. This pattern suggests a fundamentally compromised environment where even standard hygiene interventions fail to reduce risk, possibly reflecting severe bedding contamination, high animal density, or inadequate manure management. Conversely, Ardo Kola and Bali achieved 0% contamination in disinfected teats, indicating that when proper protocols are followed, even high-background-risk environments can yield microbiologically safe milk. The 11.1% contamination observed in disinfected teats from Jalingo and Gassol, however, suggests implementation failures whether due to improper technique, insufficient disinfectant contact time, or rapid recontamination from heavily contaminated environments. The persistence of substantial bacterial loads in washed teats across all locations (ranging from 44.4% in Ardo Kola to 77.8% in Gassol) provides definitive evidence against water-only preparation protocols. The FAO emphasizes that while washing with water is indicated when udders are heavily soiled, it is not recommended as routine preparation because water alone lacks detergent and disinfectant properties necessary for bacterial elimination (FAO, 2009).

Table 3: Bacterial Growth Distribution by Location and Sampling Condition

Location	Unwashed	Washed	Disinfected	Bedding	Location Total (%)
Ardo Kola	5/9(55.6%)	4/9(44.4%)	0/9 (0%)	7/9(77.8%)	16/36(44.4%)
Jalingo	6/9(66.7%)	6/9(66.7%)	1/9(11.1%)	7/9(77.8%)	20/36(55.6%)
Bali	6/9(66.7%)	5/9(55.6%)	0/9 (0%)	4/9(44.4%)	15/36(41.7)
Gassol	7/9(77.8%)	7/9(77.8%)	1/9(11.1%)	7/9(77.8%)	22/36(55.6%)

Pathogen Profile and Zoonotic Implications

Bacterial species identification (Table 4) revealed a distinctive pathogen distribution with significant public health implications. *Salmonella* sp. emerged as the predominant isolate (21 total detections, 25.3% of all positive samples), with highest prevalence in Ardo Kola (8 isolates) and Bali (6 isolates). This predominance of *Salmonella* in dairy cattle mastitis is epidemiologically significant and diverges from patterns observed in intensive dairy systems, where *Staphylococcus aureus* typically predominates (Kasa et al., 2020; Ghali-Mohammed et al., 2025). The high *Salmonella* prevalence likely reflects the extensive environmental contamination characteristic of traditional pastoral systems in Nigeria. *Salmonella* persists in cattle populations through fecal shedding, with infected animals serving as continuous sources of environmental contamination (Makita et al., 2012). In Ethiopian dairy systems, *Salmonella* has been documented in fresh milk from apparently healthy cows, with dairy cattle serving as significant reservoirs for human salmonellosis (Makita et al., 2012). The pathogen's ability to cause subclinical infection in cattle while maintaining transmissibility to humans through milk consumption creates a silent zoonotic bridge that is particularly dangerous in regions with high raw milk consumption.

Staphylococcus species constituted the second most frequent isolates (18 total, 21.7%), with striking geographic clustering in Gassol (11 isolates, 61.1% of all *Staphylococcus* detections). This concentration suggests localized transmission dynamics, possibly related to specific milking practices or animal movement patterns. *Staphylococcus aureus* represents the most economically significant mastitis pathogen globally due to its contagious nature, ability to establish chronic

subclinical infections, and production of heat-stable enterotoxins that persist even in pasteurized milk products (Kasa et al., 2020; Odetokun et al., 2023). The predominance of coagulase-positive staphylococci in Ethiopian mastitis studies (reaching 38.6% *S. aureus* in Asella and 44.95% in Bishoftu) contrasts with the lower overall *Staphylococcus* prevalence in Taraba, suggesting that environmental pathogens may dominate in Nigerian pastoral systems while contagious pathogens predominate in more intensive East African dairy systems (Bedada & Hiko, 2011; Kasa et al., 2020). The isolation of *Streptococcus* species (13 total, 15.7%) and *E. coli* (10 total, 12.0%) confirms the environmental mastitis burden in these herds. *E. coli* was notably concentrated in Jalingo (6 isolates), correlating with this location's high overall bacterial growth rate. The pathogenicity of *E. coli* mastitis is mediated by lipopolysaccharides and iron acquisition systems that enable rapid systemic spread and severe clinical outcomes (Zadoks & Fitzpatrick, 2009).

Klebsiella species, isolated exclusively from Ardo Kola (4 isolates) and Bali (3 isolates), represent particularly concerning pathogens due to their environmental persistence and antimicrobial resistance potential. *K. pneumoniae* mastitis is characterized by rapid onset, severe clinical signs, poor response to antimicrobial therapy, and high mortality rates, with significant economic impacts through milk production losses (Pollock et al., 2025). The geographic restriction of *Klebsiella* to specific locations suggests localized environmental reservoirs, possibly related to water sources or bedding materials. Recent whole-genome sequencing studies demonstrate extensive genetic diversity among bovine *K. pneumoniae* isolates, with 31 different sequence types identified among 42 Scottish isolates, indicating environmental rather than clonal transmission (Pollock et al., 2025). The detection of *Klebsiella* in Taraba herds without accompanying clinical outbreak may reflect subclinical environmental colonization that precedes clinical disease episodes.

Mixed infections (7 total, 8.4%) represent particularly challenging clinical scenarios where polymicrobial synergy may enhance virulence and complicate therapeutic outcomes. Mixed infections often result in more severe clinical manifestations and reduced treatment efficacy compared to single-pathogen infections, as different bacterial species may cooperate to overcome host defenses and establish persistent infection (Kasa et al., 2020). The geographic distribution of mixed infections (3 in Bali, 2 in Jalingo, 1 each in Ardo Kola and Gassol) suggests that environmental conditions favoring high overall bacterial load also promote polymicrobial establishment.

Table 4: Distribution of Bacterial Species by Location

Bacterial Species	Ardo Kola	Bali	Gassol	Jalingo	Total
Salmonella sp.	8	6	3	4	21
Staphylococcus sp.	1	0	11	6	18
Streptococcus sp.	1	3	4	5	13
E. coli	1	0	3	6	10
Klebsiella sp.	4	3	0	0	7
Mixed infection	1	3	1	2	7

Conclusion and Recommendation

Mastitis in dairy herds within Taraba State is predominantly associated with environmental contamination and inadequate hygienic practices. High bacterial loads in udders and bedding highlight the farm environment as a key reservoir of infection. Water-only washing was ineffective, whereas disinfection significantly reduced microbial contamination, confirming its importance in mastitis control. The predominance of *Salmonella* spp. alongside other pathogenic

bacteria presents significant animal health and public health risks, particularly in settings with raw milk consumption. Effective control requires the adoption of routine udder disinfection, improved farm sanitation, and enhanced farmer education on hygienic milking practices. Promotion of milk pasteurization and implementation of regular microbial monitoring are also essential. Strengthened institutional support and further research on pathogen dynamics are recommended to ensure sustainable mastitis management in the region.

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