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# Bovine mastitis-associated bacterial pathogens: a systematic review based on some African dairy systems

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Mastitis occurs when microbes invade the teat through the teat canal. Most microbes can cause opportunistic infections of the udder. However, fatal infections are due to various species of Streptococci, Staphylococci, and coliforms. Notable economic effects of bovine mastitis include reduced milk yield, increased treatment costs, and premature culling of affected animals. This systematic review collates published reports of bacterial pathogens isolated from mastitis-positive bovine milk samples in African dairy systems from 2013 to 2023. The search was conducted using Google Scholar, PubMed, Web of Science, and ScienceDirect, and assessed using a modified ROBIS tool. The search terms were: "bovine mastitis", "bacterial pathogens", and "African dairy systems". Findings indicate that *Staphylococcus aureus* (80%) and *Escherichia coli* (63%) were among the most frequently reported pathogens. Other frequently reported bacterial species included *Streptococcus* spp. (37%) and *Streptococcus agalactiae* (37%). A greater proportion of the studies were based on Ethiopian dairy farming systems. Overall, the results show that mastitis-causing pathogens are common isolates in milk from smallholder African farming systems. Therefore, milk bacterial isolation and testing should be adopted as a standard practice to inform decision-making on mastitis treatment and control programmes.

## KEYWORDS

bacterial isolation, *Escherichia coli*, *Staphylococcus* species, *Streptococcus* species, udder infections

## Introduction

Mastitis results in reduced milk yield and quality, compromises animal welfare, and increases the rate of premature culling of cows, and increases the running costs incurred by farmers when treating infected animals. The disease limits farmer income in production systems that are often small-scale and subsistence-based (Ajose et al., 2022; Crippa et al., 2024). Zoonotic pathogens such as *S. aureus* and *E. coli* remain problematic, especially in informal milk markets where surveillance systems to detect and monitor the emergence of pathogens at the human-animal interface are weak or absent (Garcia et al., 2019). In addition, the misuse of antimicrobials when managing mastitis-positive cases contributes to drug residues and resistant bacteria that enter the environment through milk waste, sustaining reservoirs of infection that may yield

mixed infections (van Zyl et al., 2023; Lyimo and Sonola, 2025). Environmental pathogens include *Escherichia coli* and *Klebsiella* species, which are typically derived from the cow's surroundings (Phiri et al., 2022; van Zyl et al., 2023; Khasaphane et al., 2023). Hota et al. (2020); Yusuf-Isleged (2022); and Ramuada et al. (2024) highlighted the type of production system, dairy cattle breed, seasonal changes, and hygiene practices during milking among the various factors that can influence the prevalence of bovine mastitis as well as the microbiota of the udder. Additionally, the scarcity of water around the animal production facilities, as well as the lack of awareness among farmers, were reported to play a significant role. Previous studies emphasised the importance of understanding breed susceptibility, production systems, and seasonal influences on mastitis prevalence and pathogen diversity (Moosavi et al., 2014; Cremonesi et al., 2018). In the African dairy farming systems, particularly the smallholder farming sector, mastitis has a high incidence rate and therefore is a significant economic burden to the farmers. Therefore, the study systematically collates literature on the bacterial pathogens that were isolated from milk samples of mastitis-positive cows raised in diverse African production systems.

## Materials and methods

### Eligibility criteria

Identification of Population, Exposure, and Outcomes (PEO) components was performed for this systematic review. PEO ensures clarity in defining the research question (Capili, 2020). The “dairy cows” were defined as the population of the study, with “mastitis-causing bacterial pathogens” as the exposure and “reported prevalence and diversity of pathogens in African dairy systems” as the outcomes. Before conducting the review, an initial search of the PEO elements was performed on Google Scholar, PubMed, Science Direct, and Web of Science.

### Search strategy

Two authors independently conducted a systematic review of articles in the databases Google Scholar, PubMed, Science Direct, and Web of Science, using combinations of the following key terms: ‘bovine mastitis’, ‘bacterial pathogens’, and ‘African dairy systems’. Search terms were combined using Boolean operators (AND, OR) and adapted for each database. The manual search yielded 113 full research articles from the databases.

### Inclusion criteria

This systematic review was conducted following the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) guidelines (Moher et al., 2009). Following these guidelines ensures that all pertinent information is incorporated into the analysis. After screening, 83 articles were eliminated, resulting in the inclusion of 30 studies in this systematic review based on the following criteria: (i) Focus on bovine mastitis, (ii) Availability of total sample size data, (iii) Access to full-text articles, (iv) Peer-reviewed status, (v) Publication

date between 1 January 2013 until 31st December 2023, (vi) Conducted within Africa, (vii) Addressing mastitis pathogens. Quality assessment was performed using a simplified ROBIS tool applied to all 30 included studies (Whiting et al., 2016). Five domains were evaluated: (i) clarity of inclusion criteria, (ii) description of diagnostic methods, (iii) appropriateness of sampling, (iv) clarity of pathogen reporting, and (v) consideration of confounding factors. Each domain was scored as low or high risk of bias. A total score out of 5 was used to categorise each study as low (4–5), moderate (3), or high (0–2) risk of bias.

### Exclusion criteria

Studies were excluded if they (i) were not published in English, (ii) were review articles, (iii) were theses or dissertations, (iv) were studied with no clearly defined number of samples screened, (v) the study area was not mentioned, (vi) had no isolates, or (vii) had no number of isolates. (viii) outside the year range 2013 to 2023.

### Data extraction

Two authors independently extracted data and resolved discrepancies by consensus. Extracted data included author names, publication year, location, total number of isolates, frequency percentages, and pathogens isolated. Data were compiled into an Excel spreadsheet (Microsoft Corporation, 2024). Text, tables, and figures were used for data extraction and presentation.

### Data analysis

Pathogen detection was synthesised at the study level and computed pathogen-specific pooled prevalence as a sample size-weighted proportion across studies. Pooled prevalence for mastitis positive samples was calculated as:

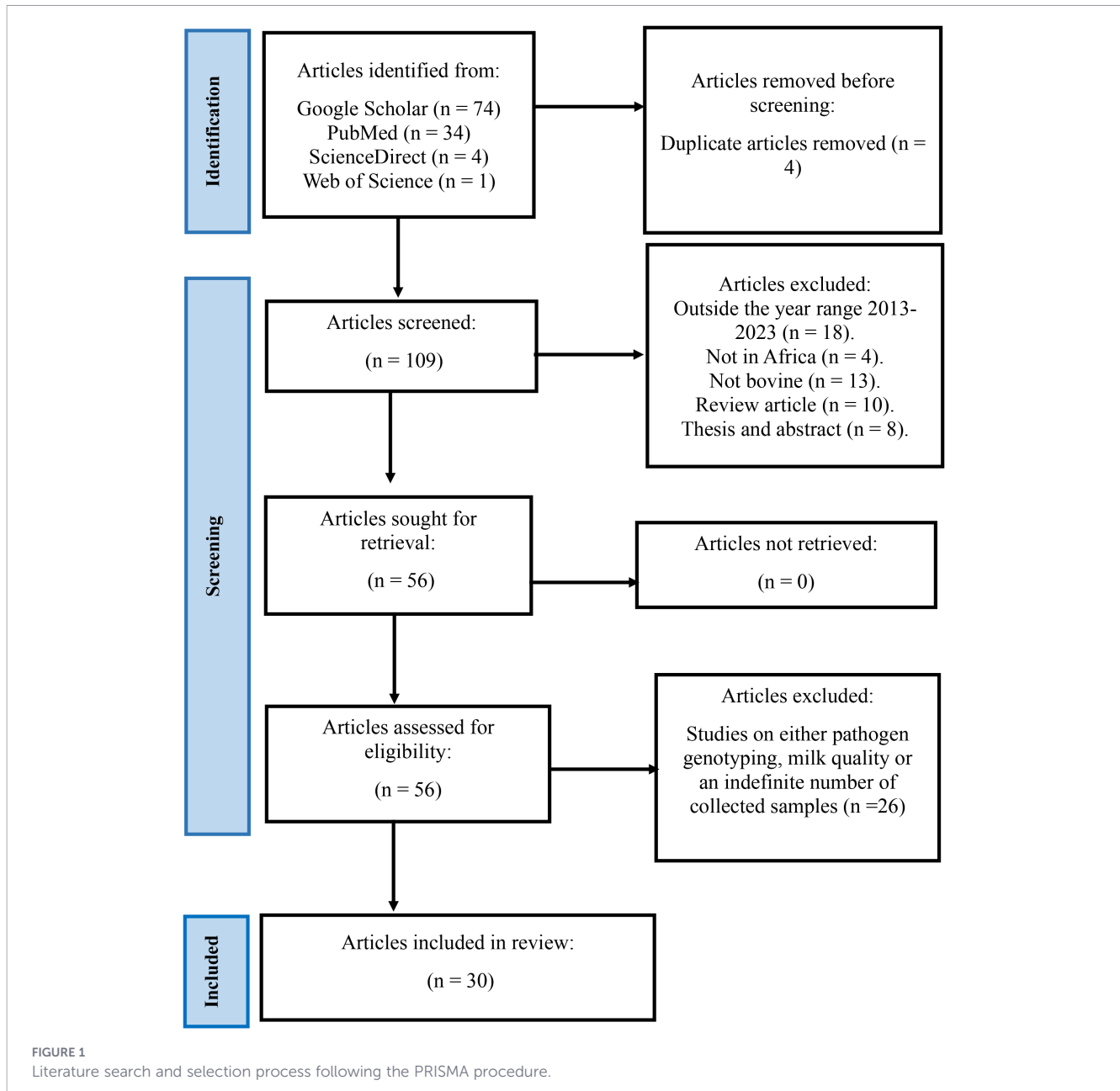
$$\text{Pooled prevalence \%} = \frac{\sum \text{positive samples}}{\sum \text{total samples}} * 100$$

To address heterogeneity, season was harmonised as either wet, dry, or wet-to-dry or not reported. Some studies collected data across both seasons; classification was derived based on the month reported in the study, and seasonal variations were noted per country and classified. Production system was harmonised as intensive, semi-intensive or extensive or not reported; and breed as exotic, crossbred, indigenous or not reported. Missing data were retained as not reported for consistency. Sensitivity analyses were performed by (i) excluding studies at high risk of bias and (ii) excluding the largest denominator study to assess the effect of outlier sample size on pooled estimates.

## Results

### Searched results

Figure 1 characterises the flowchart of the identification and selection of studies for the systematic review. The search yielded 113



full-text articles. After removing duplicates and applying eligibility criteria, 30 studies were included in the systematic review. Reasons for exclusion included: studies outside the 2013–2023 range, non-African regions, non-bovine species, review articles, theses, and studies lacking isolate data.

## Characteristics of included studies

A total of 30 included studies represented diverse African systems. Using a ROBIS-style 5 domain assessment applied to the 30 included studies, 17 studies were judged to have low overall risk of bias, 9 had moderate risk, and 4 were classified as high risk. High-risk studies commonly exhibited failure to account for potential confounding factors such as production system, breed, season, or outlying sample size. Diagnostic methods were generally robust

across the studies, with all investigations using conventional bacteriological culture for pathogen identification. Screening approaches varied between California Mastitis Test (n = 26), Electric conductivity (n = 1), Somatic Cell Count (n = 1), pH testing (n = 1), and physical examinations (n = 1). Therefore, all studies were rated low risk in the diagnostic methods domain across the included studies.

The combined sample size of mastitis-positive cases across the 30 studies was 35672, and the sample population was 101877. The pooled prevalence was based on the positive milk samples across all studies, indicating a pooled mastitis prevalence of 35%. Data analysis based on [Table 1](#) showed that crossbreeds were the most frequently reported bovine breed (n = 12). Regarding production systems, intensive systems were the most studied (n = 11), whereas extensive systems were the least represented (n = 5). Crossbred

TABLE 1 Characterisation of the included studies.

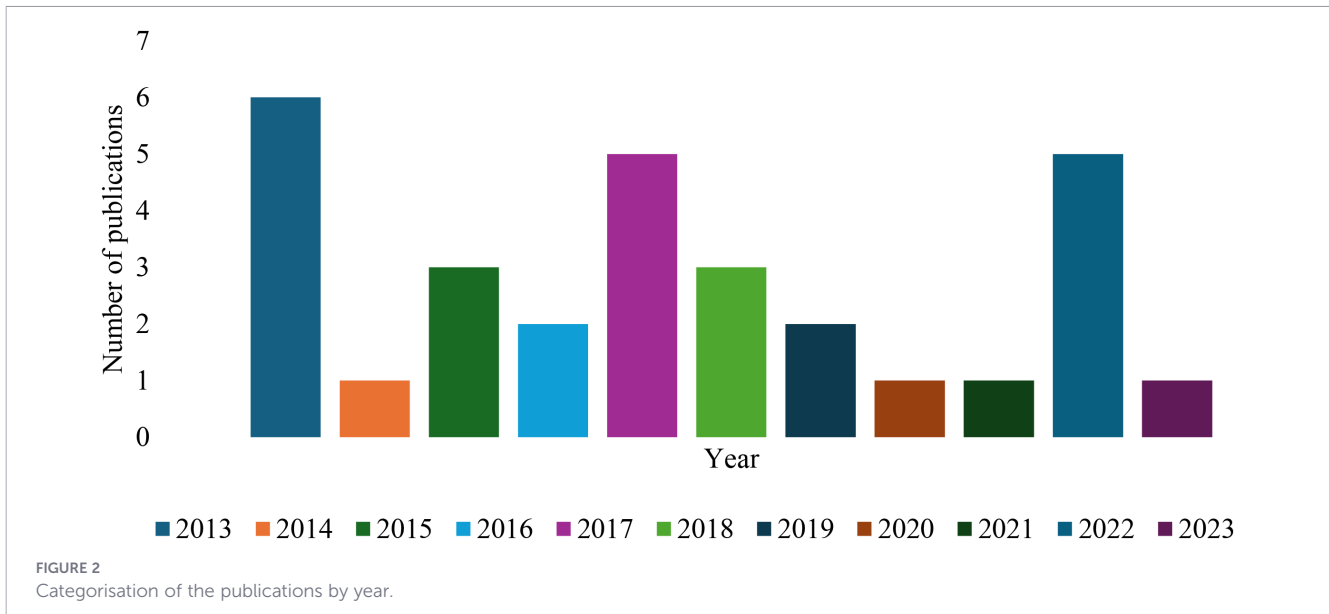
Author	Production system	Breed	Season	Country	Positive samples	Culture positive
Kateete et al. (2013)	Semi-intensive	Exotic	Wet-Dry	Uganda	97	82
Zeryehun et al. (2013)	Intensive	Crossbreed	Wet	Ethiopia	499	80
Gelgelu et al. (2023)	Semi-intensive	Crossbreed	Wet-Dry	Ethiopia	344	302
Kashoma et al. (2015)	Intensive	Not mentioned*	Dry	Tanzania	100	49
Salih (2015)	Semi-intensive	Not mentioned*	Dry	Sudan	500	100
Seid et al. (2015)	Semi-intensive	Crossbreed	Dry	Ethiopia	101	83
Ssajjakambwe et al. (2017)	Intensive	Crossbreed	Not mentioned*	Uganda	71	65
Amdhun et al. (2016)	Extensive	Indigenous	Dry	Ethiopia	1536	119
Adane et al. (2017)	Intensive	Crossbreed	Dry	Ethiopia	384	35
Yohannes and Alemu (2018)	Not mentioned*	Exotic breed	Dry	Ethiopia	173	51
Ngwa et al. (2018)	Semi-intensive	Crossbreed	Wet-Dry	Cameroon	164	68
Kaki et al. (2019)	Intensive	Not mentioned*	Dry	Algeria	100	26
Belay et al. (2022)	Intensive & Semi-intensive	Cross breed	Wet-Dry	Ethiopia	72	64
Abegewi et al. (2022)	Intensive	Cross breed	Wet-Dry	Cameroon	205	132
Ngotho et al. (2022)	Intensive	Exotic breed	Wet-Dry	Kenya	140	101
Byaruhanga et al. (2022)	Extensive	Indigenous breed	Dry	Uganda	1152	253
Fosgate et al. (2013)	Not mentioned*	Not mentioned*	Not mentioned*	South Africa	484	477
Gitau et al. (2013)	Intensive & Semi-intensive	Not mentioned*	Dry	Kenya	269	241
Abrahmsén et al. (2014)	Extensive	Exotic breed	Wet	Uganda	195	168
Beyene et al. (2017)	Not mentioned*	Not mentioned*	Dry	Ethiopia	92	24
Mekonnen et al. (2017)	Intensive	Cross breed	Not mentioned*	Ethiopia	1543	633
Birhanu et al. (2017)	Intensive	Cross breed	Dry	Ethiopia	170	153
Petzer et al. (2017)	Not mentioned*	Not mentioned*	Wet-Dry	South Africa	89635	30399
Saidi et al. (2013)	Semi extensive	Not mentioned*	Wet-Dry	Algeria	428	48
Suleiman et al. (2018)	Not mentioned*	Not mentioned*	Dry-Wet	Tanzania	1648	831
Ndahetuye et al. (2019)	Not mentioned*	Exotic breed	Wet-Dry	Rwanda	418	291
Ndahetuye et al. (2020)	Extensive	Exotic breed	Wet-Dry	Rwanda	664	457
Kitila et al. (2021)	Extensive	Indigenous breed	Dry	Ethiopia	210	153
Demil et al. (2022)	Intensive	Cross breed	Dry	Ethiopia	419	128
Abebe et al. (2023)	Intensive	Cross breed	Dry-Wet	Ethiopia	64	59

\*Not mentioned: information was not provided in the primary article.

cattle were the most studied ( $n = 12$ ), followed by exotic cattle ( $n = 6$ ), while indigenous cattle were the least reported (Amdhun et al., 2016; Kitila et al., 2021; Byaruhanga et al., 2022). Nine studies did not specify the breed of cattle. Most studies were conducted during the dry season ( $n = 13$ ), followed by the wet-to-dry transition ( $n = 12$ ); the fewest number of studies were conducted during the wet season (Zeryehun et al., 2013; Abrahmsén et al., 2014). Figure 2 shows that the highest number of articles was published in 2013 ( $n = 6$ ), followed by 2017 (Adane et al., 2017; Beyene et al., 2017; Birhanu et al., 2017; Mekonnen et al., 2017; Petzer et al., 2017). Figure 3 depicts the geographical distribution of the 30 reviewed studies. Ethiopia had the highest number of studies ( $n = 13$ ), followed by Uganda (Kateete et al., 2013; Ssajjakambwe et al., 2017; Byaruhanga et al., 2022). While Sudan had the lowest (Salih, 2015).

## Bovine mastitis isolated pathogens

Table 2 shows a total of 74 unique mastitis pathogens, including co-infections and coliforms, which were identified across the 30 reviewed articles. *Staphylococcus aureus* was the most frequently isolated pathogen ( $n = 24$ ), accounting for 80% of the total studies reviewed. *Staphylococcus aureus* was commonly reported during the dry season ( $n = 10$ ) and during the wet-to-dry seasons ( $n = 10$ ), with the wet season being the least reported (Zeryehun et al., 2013). Fosgate et al. (2013); Mekonnen et al. (2017) did not mention the seasonal variations of the study site. Among the 30 reviewed studies, crossbred cattle were the most frequently reported as susceptible to *S. aureus* ( $n = 10$ ), followed by exotic cattle ( $n = 6$ ), while indigenous cattle were the least reported (Amdhun et al., 2016; Byaruhanga et al., 2022). Eight studies did not specify the breed of



cattle. Most studies reported on *S. aureus* and co-infections involving *S. aureus* isolations were in intensive and semi-intensive production systems ( $n = 7$ ;  $n = 7$ ), with the fewest reports from extensive systems (Abrahmsén et al., 2014; Amdhun et al., 2016; Ndahetuye et al., 2020; Byaruhanga et al., 2022). However, some studies ( $n = 6$ ) did not specify the type of production system in which *S. aureus* was reported.

*Escherichia coli* (*E. coli*) was the second most frequently reported pathogen ( $n = 20$ ), accounting for 63% of the total studies. *E. coli* and co-infections involving *E. coli* were commonly reported in intensive production systems ( $n = 8$ ), followed by semi-intensive systems ( $n = 6$ ), with the lowest occurrence in extensive systems (Abrahmsén et al., 2014; Amdhun et al., 2016). Four studies that reported on *E. coli* did not specify the type of production system (Fosgate et al., 2013; Petzer

et al., 2017; Suleiman et al., 2018; Yohannes and Alemu, 2018). *E. coli* isolates were most frequently reported in cross breeds ( $n = 10$ ), followed by exotic breeds (Kateete et al., 2013; Abrahmsén et al., 2014; Yohannes and Alemu, 2018; Ngotho et al., 2022), with indigenous breeds being the least reported (Amdhun et al., 2016). Several studies reported on *E. coli* without specifying the breed (Fosgate et al., 2013; Saidi et al., 2013; Petzer et al., 2017; Suleiman et al., 2018; Kaki et al., 2019). Studies reporting *E. coli* and co-infections involving *E. coli* were most frequently conducted across both the dry and wet seasons ( $n = 10$ ), followed by the dry season ( $n = 6$ ). Only two studies were conducted during the wet season (Zeryehun et al., 2013; Abrahmsén et al., 2014), while two studies did not specify the season (Fosgate et al., 2013; Ssajakambwe et al., 2017).

*Streptococcus agalactiae* (*S. agalactiae*) ( $n = 11$ ) and other unspecified *Streptococcus* spp. were the third most reported isolates ( $n = 11$ ), accounting for 37% of the total reviewed studies. Studies that reported *S. agalactiae* isolates during the dry season were most common (Gitau et al., 2013; Seid et al., 2015; Amdhun et al., 2016; Yohannes and Alemu, 2018; Demil et al., 2022), followed by studies conducted during both the dry and wet seasons (Petzer et al., 2017; Ndahetuye et al., 2019; Ngwa et al., 2018). This pathogen was least reported during the wet season (Zeryehun et al., 2013), whilst two studies did not mention the seasonal variations (Fosgate et al., 2013; Mekonnen et al., 2017). *Streptococcus agalactiae* isolates were common in crossbreeds (Zeryehun et al., 2013; Seid et al., 2015; Mekonnen et al., 2017; Ngwa et al., 2018; Demil et al., 2022). Indigenous breed was mentioned once in all the reviewed studies (Amdhun et al., 2016), and exotic breeds were mentioned twice (Yohannes and Alemu, 2018; Ndahetuye et al., 2019). Fosgate et al. (2013); Gitau et al. (2013), and Petzer et al. (2017) did not mention breeds that were included in the studies. *Streptococcus agalactiae* was mostly prevalent in the intensive production system (Zeryehun et al., 2013; Mekonnen et al., 2017; Demil et al., 2022), followed by the semi-intensive (Gitau et al., 2013; Seid et al., 2015; Ngwa et al., 2018), with the least prevalence being in the extensive system

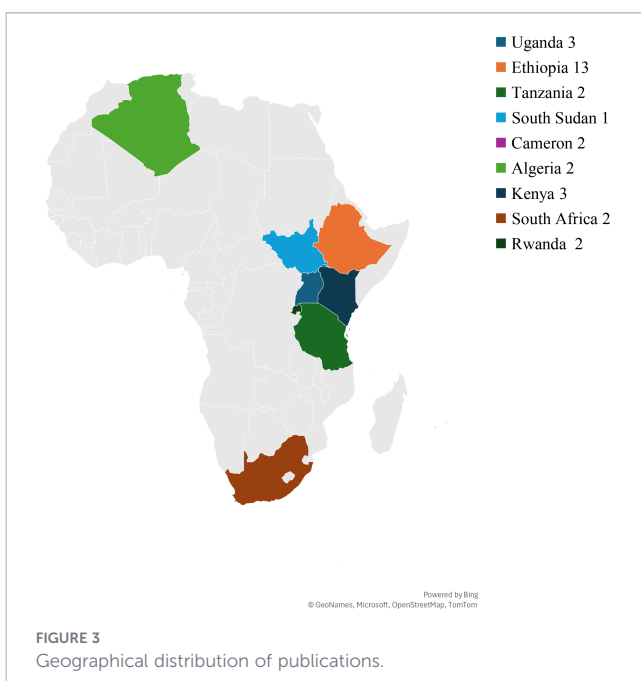


TABLE 2 Bovine mastitis-isolated pathogens.

ISOLATE	AUTHOR	ISOLATE	AUTHOR	ISOLATE	AUTHOR
1. <i>Staphylococcus aureus</i>	Fosgate et al. (2013); Gitau et al. (2013); Kateete et al. (2013); Saidi et al. (2013); Zeryehun et al. (2013); Abrahmsén et al. (2014); Kashoma et al. (2015); Seid et al. (2015); Amdhun et al. (2016); Beyene et al. (2017); Birhanu et al. (2017); Mekonnen et al. (2017); Petzer et al. (2017); Ngwa et al. (2018); Suleiman et al. (2018); Yohannes and Alemu (2018); Kaki et al. (2019); Ndahetuye et al. (2019); Ndahetuye et al. (2020); Belay et al. (2022); Byaruhanga et al. (2022); Demil et al. (2022); Abebe et al. (2023); Gelgelu et al. (2023)	2. <i>Escherichia coli</i>	Fosgate et al. (2013); Kateete et al. (2013); Saidi et al. (2013); Zeryehun et al. (2013); Abrahmsén et al. (2014); Seid et al. (2015); Amdhun et al. (2016); Adane et al. (2017); Birhanu et al. (2017); Petzer et al. (2017); Ssajjakambwe et al. (2017); Ngwa et al. (2018); Suleiman et al. (2018); Yohannes and Alemu (2018); Kaki et al. (2019); Abegewi et al. (2022); Belay et al. (2022); Ngotho et al. (2022); Abebe et al. (2023); Gelgelu et al. (2023)	3. Other <i>Streptococcus</i> spp.	Gitau et al. (2013); Kateete et al. (2013); Saidi et al. (2013); Abrahmsén et al. (2014); Seid et al. (2015); Adane et al. (2017); Birhanu et al. (2017); Kaki et al. (2019); Abebe et al. (2023); Belay et al. (2022); Byaruhanga et al. (2022)
4. <i>Streptococcus agalactiae</i>	Fosgate et al. (2013); Gitau et al. (2013); Zeryehun et al. (2013); Seid et al. (2015); Amdhun et al. (2016); Mekonnen et al. (2017); Petzer et al. (2017); Ngwa et al. (2018); Ndahetuye et al. (2019); Demil et al. (2022)	5. <i>coagulase-negative Staphylococcus</i>	Fosgate et al. (2013); Gitau et al. (2013); Abrahmsén et al. (2014); Mekonnen et al. (2017); Petzer et al. (2017); Ngwa et al. (2018); Byaruhanga et al. (2022); Abebe et al. (2023)	6. <i>Micrococcus</i> spp.	Fosgate et al. (2013); Zeryehun et al. (2013); Mekonnen et al. (2017); Petzer et al. (2017); Suleiman et al. (2018); Yohannes and Alemu (2018); Kitila et al. (2021); Gelgelu et al. (2023)
7. Other <i>Klebsiella</i> spp.	Gitau et al. (2013); Salih (2015); Ssajjakambwe et al. (2017); Suleiman et al. (2018); Ngotho et al. (2022); Abebe et al. (2023); Gelgelu et al. (2023)	8. Other <i>Staphylococcus</i> spp.	Gitau et al. (2013); Salih (2015); Adane et al. (2017); Birhanu et al. (2017); Ssajjakambwe et al. (2017); Kitila et al. (2021); Ngotho et al. (2022)	9. <i>Bacillus</i> spp.	Salih (2015); Mekonnen et al. (2017); Ssajjakambwe et al. (2017); Suleiman et al. (2018); Abebe et al. (2023); Gelgelu et al. (2023)
10. <i>Corynebacterium bovis</i>	Gitau et al. (2013); Mekonnen et al. (2017); Yohannes and Alemu (2018); Ngwa et al. (2018); Byaruhanga et al. (2022)	11. <i>Streptococcus dysgalactiae</i>	Fosgate et al. (2013); Mekonnen et al. (2017); Petzer et al. (2017); Ngwa et al. (2018); Yohannes and Alemu (2018)	12. Other <i>Corynebacterium</i> spp.	Salih (2015); Ssajjakambwe et al. (2017); Suleiman et al. (2018); Abebe et al. (2023); Gelgelu et al. (2023)
13. <i>Klebsiella pneumoniae</i>	Seid et al. (2015); Petzer et al. (2017); Yohannes and Alemu (2018); Abegewi et al. (2022); Belay et al. (2022)	14. Mixed growth	Fosgate et al. (2013); Gitau et al. (2013); Saidi et al. (2013); Abrahmsén et al. (2014); Kaki et al. (2019)	15. <i>Streptococcus uberis</i>	Fosgate et al. (2013); Mekonnen et al. (2017); Petzer et al. (2017); Ndahetuye et al. (2019); Ndahetuye et al. (2020)
16. non- <i>aureus Staphylococci</i>	Ndahetuye et al. (2019); Ndahetuye et al. (2020); Belay et al. (2022); Abebe et al. (2023)	17. <i>Klebsiella oxytoca</i>	Kateete et al. (2013); Saidi et al. (2013); Ndahetuye et al. (2019); Abegewi et al. (2022)	18. Other <i>Proteus</i> spp.	Ssajjakambwe et al. (2017); Suleiman et al. (2018); Abebe et al. (2023); Gelgelu et al. (2023)
19. Other <i>Pseudomonas</i> spp.	Saidi et al. (2013); Ssajjakambwe et al. (2017); Kaki et al. (2019); Ngotho et al. (2022)	20. <i>Pseudomonas aeruginosa</i>	Zeryehun et al. (2013); Seid et al. (2015); Suleiman et al. (2018); Byaruhanga et al. (2022)	21. <i>Staphylococcus intermedius</i>	Beyene et al. (2017); Birhanu et al. (2017); Yohannes and Alemu (2018); Gelgelu et al. (2023)
22. Other <i>Enterobacteriae</i> spp.	Fosgate et al. (2013); Kaki et al. (2019); Kitila et al. (2021)	23. Other <i>Enterobacter</i> spp.	Amdhun et al. (2016); Suleiman et al. (2018); Abebe et al. (2023)	24. <i>Enterococcus faecalis</i>	Fosgate et al. (2013); Petzer et al. (2017); Ngwa et al. (2018)
25. Other <i>Serratia</i> spp.	Petzer et al. (2017); Ssajjakambwe et al. (2017); Suleiman et al. (2018)	26. <i>Staphylococcus epidermidis</i>	Amdhun et al. (2016); Suleiman et al. (2018); Yohannes and Alemu (2018)	27. <i>Staphylococcus hyicus</i>	Beyene et al. (2017); Birhanu et al. (2017); Yohannes and Alemu (2018)

(Continued)

TABLE 2 Continued

ISOLATE	AUTHOR	ISOLATE	AUTHOR	ISOLATE	AUTHOR
28. Coliforms	Mekonnen et al. (2017); Byaruhanga et al. (2022)	29. <i>Trueperella pyogenes</i>	Petzer et al. (2017); Ngwa et al. (2018); Suleiman et al. (2018)	30. <i>Citrobacter freundii</i>	Kateete et al. (2013); Abegewi et al. (2022)
31. <i>Clostridium</i> spp.	Mekonnen et al. (2017); Suleiman et al. (2018)	32. <i>Enterobacter cloacae</i>	Saidi et al. (2013); Abegewi et al. (2022)	33. <i>Klebsiella variicola</i>	Ndahetuye et al. (2019); Ndahetuye et al. (2020)
34. <i>Pasteurella</i> spp.	Suleiman et al. (2018); Gelgelu et al. (2023)	35. <i>Lactococcus</i> spp.	Kateete et al. (2013); Ndahetuye et al. (2020)	36. <i>Pseudomonas fluorescens</i>	Suleiman et al. (2018); Ndahetuye et al. (2019)
37. <i>Serratia odorifera</i>	Saidi et al. (2013); Abegewi et al. (2022)	38. <i>Arcanobacterium</i>	Kateete et al. (2013)	39. <i>Acinetobacter iwofii</i>	Ndahetuye et al. (2019)
40. <i>Cedecea davisae</i>	Kateete et al. (2013)	41. <i>Campylobacter</i> spp.	Suleiman et al. (2018)	42. <i>Chromobacterium violaceum</i>	Suleiman et al. (2018)
43. <i>Enterobacter asburiae</i>	Ndahetuye et al. (2020)	44. <i>Enterobacter sakazakii</i>	Abegewi et al. (2022)	45. <i>Enterococcus canis</i>	Petzer et al. (2017)
46. <i>Lactobacillus</i> spp.	Ssajakambwe et al. (2017)	47. <i>Enterococcus faecium</i>	Ndahetuye et al. (2019)	48. <i>Leclercia adecarboxylata</i>	Kateete et al. (2013)
49. Negative growth	Abrahmsén et al. (2014)	50. <i>Neisseria</i> spp.	Suleiman et al. (2018)	51. Other <i>Enterococcus</i> spp.	Mekonnen et al. (2017)
52. <i>Proteus vulgaris</i>	Kateete et al. (2013)	53. <i>Pneumotropica haemolytica</i>	Saidi et al. (2013)	54. <i>Providencia alcalifaciens</i>	Saidi et al. (2013)
55. <i>Providencia stuartii</i>	Saidi et al. (2013)	56. <i>Pseudomonas rhodesiae</i>	Ndahetuye et al. (2019)	57. <i>Rhodococcus equi</i>	Kitila et al. (2021)
58. <i>Salmonella</i> spp.	Belay et al. (2022)	59. <i>Serratia ficaria</i>	Abegewi et al. (2022)	60. <i>Serratia liquefaciens</i>	Abegewi et al. (2022)
61. <i>Serratia marcescens</i>	Kateete et al. (2013)	62. <i>Staphylococcus haemolyticus</i>	Suleiman et al. (2018)	63. <i>Staphylococcus pseudintermedius</i>	Petzer et al. (2017)
64. <i>Staphylococcus warneri</i>	Saidi et al. (2013)	65. <i>Staphylococcus xylosus</i>	Saidi et al. (2013)	66. <i>Streptococcus faecalis</i>	Zeryehun et al. (2013)
67. <i>Streptococcus pyogenes</i>	Petzer et al. (2017)	68. <i>Staphylococci</i> + <i>Streptococcus</i> spp.	Gitau et al. (2013); Kaki et al. (2019)	69. <i>Streptococcus</i> spp.+ <i>Staphylococcus aureus</i> + <i>Escherichia coli</i>	Kaki et al. (2019)
70. <i>Staphylococcus aureus</i> + <i>Escherichia coli</i>	Kaki et al. (2019)	71. <i>Staphylococcus aureus</i> + <i>Mycoplasma</i> spp.	Kaki et al. (2019)	72. <i>Staphylococcus aureus</i> + <i>Streptococcus</i> spp.	Kaki et al. (2019)
73. <i>Staphylococcus lentus</i> + <i>Klebsiella ornithinolytica</i>	Saidi et al. (2013)	74. <i>Streptococcus</i> spp. + <i>Escherichia coli</i>	Kaki et al. (2019)		

(Amdhun et al., 2016). However, Fosgate et al. (2013); Mekonnen et al. (2017); Petzer et al. (2017), and Ndahetuye et al. (2019) did not mention the production system type.

The distribution of key mastitis pathogens is highlighted in Figure 4. *S. aureus* and *E. coli* were the most frequently detected pathogens across all strata, while *S. agalactiae* and other unspecified *Streptococcus* spp. was less common. Detection of *S. aureus* and *E. coli* was highest in intensive and semi-intensive systems and in crossbred cattle. Seasonal analysis showed that *S. aureus* and *E. coli* were most often reported in studies conducted during transition periods of wet and dry seasons, whereas *S. agalactiae* was more frequently detected in dry seasons. Ethiopia accounted for the largest number of detections overall, while Sudan reported none of the four key pathogens of the

systematic review and is shown for completeness of the countries involved in the systematic review. Detection counts reflect study-level presence or absence, not isolate counts. Among the key pathogens, *S. aureus* had the highest pooled prevalence of 21%, followed by *S. agalactiae* at 6%. *E. coli* accounted for 1% while other unspecified *Streptococcus* spp. contributed only 0.4%. Excluding high-risk studies did not change the direction of detection patterns; *S. aureus* and *E. coli* remained dominant in the intensive systems, and *S. agalactiae* remained more frequent in the dry season studies.

Co-infections, defined as the isolation of two or more mastitis pathogens from the same sample, were reported in 5 of the 30 reviewed studies and were isolated in 9 of the 74 identified isolates (Gitau et al., 2013; Saidi et al., 2013; Fosgate et al., 2013; Abrahmsen



FIGURE 4 Detection of four key mastitis pathogens (*S. aureus*, *E. coli*, *S. agalactiae*, *Streptococcus* spp.) across: (a) Season, (b) Production system, (c) Breed, (d) Country. Bars represent the number of studies reporting each pathogen within each category.

et al., 2014; Kaki et al., 2019). Among these mixed infections, *S. aureus* was present in four isolates, and *E. coli* in three isolates (Kaki et al., 2019), and *Streptococci* were present in four isolates (Gitau et al., 2013; Kaki et al., 2019). The pathogens involved in two identified mixed isolates were not specified (Fosgate et al., 2013; Abrahmsén et al., 2014). Mixed infections were common in both semi-intensive and intensive production systems (Gitau et al., 2013; Saidi et al., 2013; Kaki et al., 2019) and least in the extensive system (Abrahmsén et al., 2014). Most studies that isolated mixed infections did not specify the breed (Fosgate et al., 2013; Gitau et al., 2013; Saidi et al., 2013; Kaki et al., 2019), and one study reported on exotic cattle (Abrahmsén et al., 2014). Two studies reported mixed infections during the dry season (Gitau et al., 2013; Kaki et al., 2019). One study took place during the wet season (Abrahmsén et al., 2014) and one throughout the wet and dry season (Saidi et al., 2013). One study did not mention the seasonal variations (Fosgate et al., 2013). This critical synthesis evaluates the distribution and determinants of bovine mastitis pathogens across 30 studies encompassing 74 unique isolates. The review reveals a consistent dominance of *Staphylococcus aureus*, *Escherichia coli*, and *Streptococcus agalactiae*, with clear associations to production intensity, cattle breed, and seasonal variation. Beyond prevalence, methodological inconsistencies such as incomplete reporting of seasons, production systems, and breeds limit the comparability of findings and highlight key evidence gaps in mastitis epidemiology across sub-Saharan Africa.

## Discussion

The current review showed that the evidence on the geographical distribution of 30 reviewed studies revealed significant regional disparities in mastitis research across African countries. The findings of the study showed that the highest number of reviewed articles were based on milk samples collected from Ethiopian dairy farming systems. This observation could be attributed to the country's relatively large dairy cattle population and its emerging smallholder-based dairy industry (Dekebo and Kebede, 2023). The concentration of studies in East Africa, contrasted with limited data from regions such as North and Southern Africa, this observation emphasises the urgent need for broader surveillance and more comprehensive research across diverse production systems. Addressing these gaps is crucial for developing effective, evidence-based mastitis control strategies that can reduce economic losses, enhance animal health and productivity, and provide a more comprehensive understanding of mastitis epidemiology across the continent (Mitsunaga et al., 2024).

Over the review period, milk testing and isolation of bacterial pathogens associated with bovine mastitis were performed using various screening methods paired with conventional methods. Although a detailed review of mastitis diagnostic methods falls outside the primary scope of this manuscript, fundamental information on diagnostic approaches used in each included study was extracted only to assess methodological comparability, study quality, and potential sources of heterogeneity in pathogen detection. Sensitivity testing confirmed that major patterns persisted after excluding high-risk studies and outlier denominators, supporting the

robustness of directional findings. Although isolation methods were uniform, heterogeneity arose from differences in preliminary screening, sampling frames, and reporting granularity. Harmonisation of season, breed, and production system reduced variability but cannot fully reconcile non-comparable designs; and retaining the Not reported category avoids biased omission, however, it may dilute contrasts.

The dominance of *S. aureus* confirms its high prevalence in smallholder African dairy farming systems and hence its significant role in contagious mastitis. Sarba and Tola (2017) and Dagnaw et al. (2024) reported that production systems that promote increased animal densities and repeated milking procedures are among the common risk factors for the transmission of contagious pathogens. Azevedo et al. (2016) highlighted that dry seasonal conditions lead to compromised hygiene standards, such as irregular cleaning of the udders, which favours the persistence and spread of contagious pathogens. The ability of *S. aureus* to form biofilms, produce toxins, and resist common antibiotic therapies enhances the pathogenicity (Wang et al., 2025).

The findings of the study revealed a high occurrence of the *E. coli* species. However, due to geographical imbalances, one large dataset with a very low *E. coli* percentage explains the discrepancies between detection frequency and pooled prevalence. Excluding the largest dataset (Petzer et al., 2017) increased *E. coli* prevalence to 4%, demonstrating the influence of large denominators on weighted estimates. Naranjo-Lucena et al. (2025) indicated that intensive systems and wet-to-dry transition periods are among the factors that promote a high occurrence of *E. coli* species in milk. The authors further explained that drought-induced hygiene stress and wet-season bacterial proliferation contribute to a high incidence through increased contamination of milking utensils, milking parlour floors, feed, and water, particularly in production facilities where biosecurity and sanitation are suboptimal. Singh (2022) reported the effects of seasonal fluctuations on the prevalence of *E. coli* species in dairy farming systems. Kitila et al. (2021) and Byaruhanga et al. (2022) highlighted the issue of genetic susceptibility, with some exotic dairy cattle breeds being reported as highly predisposed to mastitis due to their higher milk yield and associated metabolic stress. Ayalew et al. (2023) and Slayi et al. (2024) indicated that the dairy cattle breeds that are indigenous to Africa have developed resilience to mastitis due to their genetic adaptation to African environmental conditions, including resistance to heat stress and endemic pathogens. These findings underscore the need for selecting breeding programs that strike a balance between productivity and disease resistance, potentially integrating genetic traits from indigenous breeds to enhance mastitis resilience in crossbred cattle. However, differences in management practices and access to veterinary care are also critical factors that determine the occurrence and diversity of bacterial pathogens associated with bovine mastitis.

The study revealed *Streptococcus* species as the third most common bacterial pathogens that were isolated from mastitis-positive milk samples. Blignaut et al. (2018) stated that the control of *Streptococcus* bacterial species is a challenge, especially in more commercially oriented dairy setups. *Streptococci* are highly contagious pathogens that are commonly spread during milking and may persist in the mammary gland without showing any clinical signs and thus leading to chronic clinical mastitis, making detection and eradication difficult (Morales-Ubaldo et al., 2023).

Previous research has shown that *Streptococcus* species, particularly *S. agalactiae*, are mostly reported during the dry seasons, which relates to its subclinical persistence nature, with increased cases likely under more stressful or poor sanitation conditions.

The dominance of *S. aureus* and *Streptococcus* spp and *S. agalactiae* in the reviewed studies confirms their role as primary gram-positive pathogens associated with contagious mastitis. In contrast, *E. coli* represents a major Gram-negative pathogen commonly linked to environmental mastitis. Mastitis pathogens may be classified as either Gram-positive or Gram-negative bacteria based on their cell wall structures. Classification of mastitis pathogens assists in a more appropriate intervention approach because Gram-negative bacteria are resistant to broad-spectrum antibiotic therapy (Steele et al., 2020). Understanding these differences is essential for designing effective control programs, as treatment protocols targeting gram-positive pathogens may fail against gram-negative pathogens, leading to therapeutic failures and contributing to antimicrobial resistance, which poses a significant one-health risk. Resistant bacteria and drug residues can enter the food chain through contaminated milk and spread to humans, while environmental contamination from discarded milk and manure sustains reservoir organisms. This highlights the need for routine pathogen identification and antimicrobial sensitivity testing before initiating treatment, particularly in resource-limited African dairy systems where empirical therapy is common to safeguard public health and reduce environmental contamination (Marbach et al., 2019; Perdomo et al., 2024).

Multiple bacterial species were isolated from the same milk samples. The occurrence of mixed infections, particularly involving *S. aureus*, *Streptococcus* spp., and *E. coli*, highlights the complexity of mastitis infections and the potential for synergistic pathogen interactions. Shum et al. (2009) stated that the co-isolation of *S. aureus* and *E. coli* in mixed infections reinforces the need for differential diagnosis, rather than solely relying on clinical or somatic cell counts, as co-infections may introduce new pathogens and complicate mastitis management. Poor hygiene practices, high stocking densities, and increased cow-to-cow contact in intensive systems may facilitate pathogen transmission and co-infections (Abed et al., 2021). Gitau et al. (2013) and Kaki et al. (2019) indicated that most cases of co-infections are documented during the dry season, suggesting that environmental stressors such as heat, limited water availability, and increased pathogen load in bedding and milking equipment may contribute to higher infection rates. On the other hand, multiple occurrences of milk bacteria could be attributed to improper sampling procedures or contamination (Dyson et al., 2022).

## Conclusion and recommendations

Bovine mastitis is a major challenge in African dairy systems. The systematic collation of potentially zoonotic pathogens in the reviewed studies, such as *S. aureus* and *E. coli*, presents a threat to the One Health initiative, especially in informal milk markets, where surveillance systems to detect and monitor the emergence of pathogens at the human-animal interface are weak or absent. There is an urgent need for the responsible use of antimicrobials in mastitis management to curb drug residues and bacterial resistance. The study

concludes that effectively addressing mastitis in African dairy systems demands coordinated strategies that integrate animal health, human health, and environmental health within the One Health framework. Such an approach not only improves disease control but also promotes sustainable dairy production and public health resilience.

## Author contributions

TC: Writing – original draft, Writing – review & editing.  
 LG: Writing – original draft, Writing – review & editing.  
 MR: Writing – original draft, Writing – review & editing.  
 TLT: Writing – original draft, Writing – review & editing.

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## Conflict of interest

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