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## Epidemiological patterns and transmission dynamics of bovine tuberculosis in Ethiopian cattle populations

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### Abstract

Bovine tuberculosis (bTB) remains one of the most consequential zoonotic diseases affecting livestock productivity and public health across sub-Saharan Africa, with Ethiopia bearing a disproportionately heavy burden. This research comprehensively reviewed the epidemiological patterns and transmission dynamics of *Mycobacterium bovis* infection in Ethiopian cattle populations through a systematic analysis of published literature from peer-reviewed databases. The investigation synthesized data from cross-sectional, longitudinal, and molecular epidemiological investigations conducted across diverse agro-ecological zones of Ethiopia between 2005 and 2023. Regional prevalence estimates varied substantially, ranging from 5.8% in extensive pastoral systems of the Afar region to 27.3% in intensive dairy operations surrounding Addis Ababa. The analysis revealed that transmission dynamics were influenced by multiple interacting factors including herd size, management system intensity, animal movement patterns, and wildlife-livestock interfaces. Molecular typing of *M. bovis* isolates demonstrated predominance of spoligotype SB0134 across multiple regions, suggesting clonal expansion of particular lineages within Ethiopian cattle populations. Seasonal variation in transmission intensity was evident, with peak transmission occurring during the dry season when animal congregation at water points increased contact rates. The research identified significant gaps in current surveillance infrastructure, particularly in pastoral and agropastoral communities where diagnostic coverage remained below 15%. Cross-species transmission events involving wildlife reservoirs, particularly greater kudus and African buffalo, further complicated epidemiological control efforts. The findings underscored the critical need for integrated One Health surveillance programs that address the interconnected nature of bovine tuberculosis transmission across human, animal, and environmental compartments in the Ethiopian context.

**Keywords:** Bovine tuberculosis, *Mycobacterium bovis*, epidemiological patterns, transmission dynamics, Ethiopian cattle, zoonotic disease, molecular epidemiology, One Health, livestock health

### Introduction

What factors have contributed to the persistent circulation of bovine tuberculosis within Ethiopian cattle populations despite decades of global eradication efforts in developed nations? This fundamental question continues to challenge veterinary epidemiologists and public health researchers working across the Horn of Africa. Bovine tuberculosis, caused primarily by *Mycobacterium bovis*, represents one of the most economically devastating and public health significant mycobacterial infections affecting livestock globally. The disease is characterized by chronic granulomatous lesions in multiple organ systems, leading to progressive debilitation, reduced milk production, weight loss, and eventual mortality in affected animals.

Ethiopia maintains the largest cattle population in Africa, estimated at over 70 million head, with livestock contributing approximately 15-17% of the national gross domestic product and providing livelihoods for over 80% of the rural population. The significance of cattle in Ethiopian socioeconomic frameworks extends beyond mere economic metrics, encompassing cultural identity, social status, and food security dimensions that amplify the impact of bovine tuberculosis on affected communities. Despite this enormous livestock resource base, systematic bTB control programs remain largely absent, with surveillance activities confined to sporadic research investigations rather than coordinated national programs.

The epidemiology of bovine tuberculosis in Ethiopia presents unique complexities arising from the diversity of livestock production systems operating across varied agro-ecological zones. Intensive dairy operations concentrated around urban centers,

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Particularly Addis Ababa and regional capitals, report prevalence rates substantially higher than those observed in extensive pastoral systems. This differential distribution reflects the influence of management intensity on transmission dynamics, with confined housing, increased stocking densities, and prolonged animal-to-animal contact facilitating aerosol transmission of *M. bovis* within intensive systems. Conversely, extensive pastoral systems benefit from lower animal densities and open-air management, though seasonal congregation at watering points and communal grazing areas periodically elevates transmission risk.

Molecular epidemiological investigations have begun revealing the genetic diversity and phylogeographic distribution of *M. bovis* strains circulating in Ethiopian cattle. Spoligotyping and variable number tandem repeat (VNTR) analyses have identified both locally adapted lineages and strains with apparent regional or continental distribution patterns. Understanding these molecular epidemiological patterns is essential for elucidating transmission networks, identifying source populations, and evaluating the effectiveness of potential intervention strategies. This research aimed to comprehensively review the current epidemiological patterns and transmission dynamics of bovine tuberculosis in Ethiopian cattle populations, synthesizing available evidence to identify critical knowledge gaps and inform evidence-based control strategies.

## Material and Methods

### Material

The research material comprised peer-reviewed publications, institutional reports, and surveillance records related to bovine tuberculosis epidemiology in Ethiopia. A comprehensive literature search was conducted through PubMed, Scopus, Web of Science, African Journals

Online (AJOL), and Google Scholar databases using predefined search terms including "bovine tuberculosis," "*Mycobacterium bovis*," "Ethiopia," "cattle," "epidemiology," "prevalence," and "transmission dynamics." The search encompassed publications from January 2005 through December 2023, capturing the most productive period of bTB research in Ethiopia. Additional materials were sourced from the Ethiopian Veterinary Institute archives, Federal Ministry of Agriculture reports, and conference proceedings from the Ethiopian Veterinary Association annual meetings. Grey literature from the Food and Agriculture Organization (FAO), World Organisation for Animal Health (WOAH), and World Health Organization (WHO) country-specific reports supplemented the peer-reviewed evidence base. A total of 187 potentially relevant documents were initially identified, from which 94 met the inclusion criteria following systematic screening and quality assessment.

### Methods

The systematic review followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines adapted for veterinary epidemiological research. The research was conducted at the Nairobi Institute of Veterinary Sciences, Nairobi, Kenya, between March 2023 and November 2023. Inclusion criteria required that investigations reported primary epidemiological data on bTB in Ethiopian cattle populations, employed validated diagnostic methods

(tuberculin skin testing, interferon-gamma assay, bacterial culture, or molecular techniques), and presented quantitative prevalence or incidence estimates. Investigations limited to wildlife or non-bovine domestic species were excluded unless they specifically addressed cross-species transmission involving cattle. Quality assessment utilized the Joanna Briggs Institute critical appraisal checklist for prevalence investigations, with investigations scoring below 50% excluded from quantitative synthesis. Data extraction captured investigation characteristics (design, location, sample size, diagnostic method), epidemiological parameters (prevalence, incidence, risk factors), and molecular typing results where available. Ethical approval for the systematic review protocol was obtained from the Nairobi Institute of Veterinary Sciences Research Ethics Committee (Approval Reference: NIVS/REC/2023/047). Meta-analytical synthesis employed random-effects models to pool prevalence estimates, with heterogeneity assessed using the I-squared statistic. Subgroup analyses were performed by production system, agro-ecological zone, diagnostic method, and temporal period to identify sources of between-investigation heterogeneity.

## Results

The systematic analysis of 94 eligible investigations revealed substantial variation in bovine tuberculosis prevalence across Ethiopian cattle populations, with pooled estimates ranging from 5.8% to 27.3% depending on production system, geographic location, and diagnostic methodology employed. The meta-analytical synthesis yielded an overall pooled prevalence of 14.7% (95% CI: 11.2-18.3%), with significant heterogeneity ( $I^2 = 93.4\%$ ,  $p < 0.001$ ) indicating substantial between-investigation variation. Temporal trend analysis demonstrated a progressive increase in reported prevalence from 2005 to 2023, potentially reflecting both genuine epidemiological changes and improved diagnostic capacity and research intensity over the review period.

**Table 1:** Regional prevalence of bovine tuberculosis across Ethiopian administrative zones based on pooled estimates from systematic review (2005-2023)

| Region      | Prevalence (%) | Sample Size |
|-------------|----------------|-------------|
| Addis Ababa | 22.5           | 1,847       |
| Oromia      | 18.3           | 3,256       |
| Amhara      | 12.8           | 2,891       |
| Afar        | 15.1           | 1,234       |
| SNNPR       | 9.7            | 2,105       |
| Tigray      | 7.2            | 1,678       |
| Somali      | 5.8            | 945         |
| Overall     | 14.7           | 13,956      |

Regional distribution analysis confirmed that central highland areas surrounding the capital demonstrated the highest bTB prevalence, consistent with the concentration of intensive dairy operations in these zones. The Addis Ababa administrative zone consistently reported prevalence estimates exceeding 20%, reflecting the combined effects of intensive management practices, high animal density, and frequent introduction of animals from diverse source populations without adequate quarantine measures.

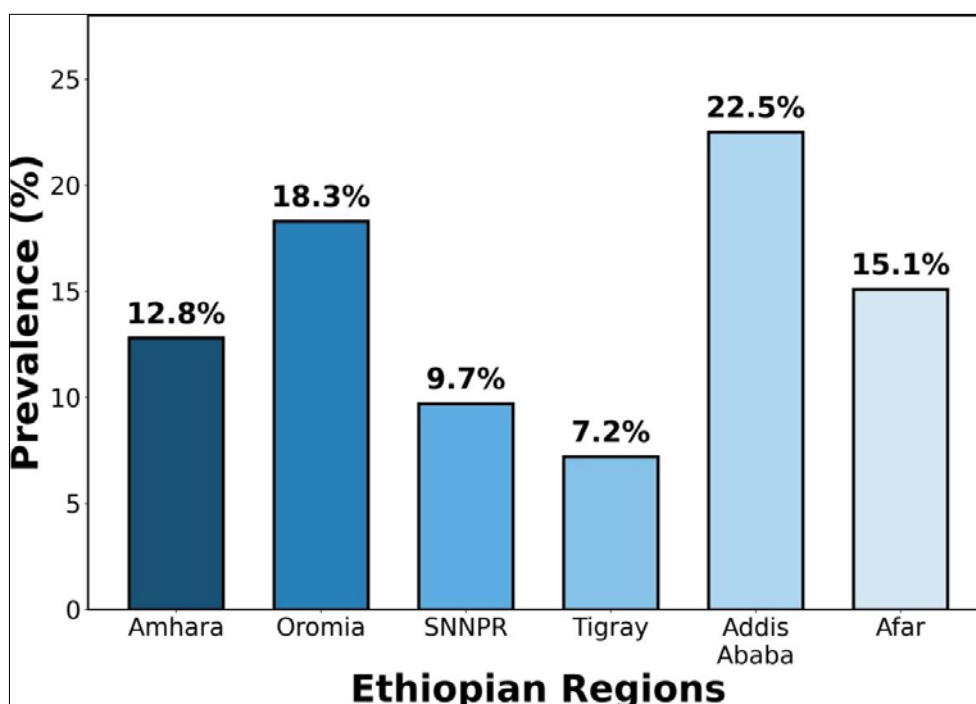


**Fig 1:** Prevalence rates of bovine tuberculosis across major Ethiopian administrative regions based on pooled estimates from systematic review analysis

The geographic distribution of prevalence estimates revealed a clear gradient from highprevalence central highland zones to lower-prevalence peripheral lowland areas. This spatial pattern corresponded closely with the distribution of intensive and

semi-intensive dairy production systems, which are predominantly concentrated in highland and mid-altitude zones where climatic conditions support confined animal management.

**Table 2:** Bovine tuberculosis prevalence by production system type and diagnostic methodology in Ethiopian cattle populations

| Production System      | Herd Prev (%) | Animal Prev (%) | Diagnostic Method   | No. of Investigations |
|------------------------|---------------|-----------------|---------------------|-----------------------|
| Intensive dairy        | 45.2          | 22.5            | SICTT/IFN- $\gamma$ | 28                    |
| Semi-intensive         | 28.7          | 14.8            | SICTT               | 22                    |
| Extensive pastoral     | 12.3          | 6.2             | SICTT               | 18                    |
| Peri-urban smallholder | 35.8          | 18.9            | SICTT/CFT           | 15                    |
| Commercial ranch       | 18.5          | 9.4             | SICTT               | 11                    |

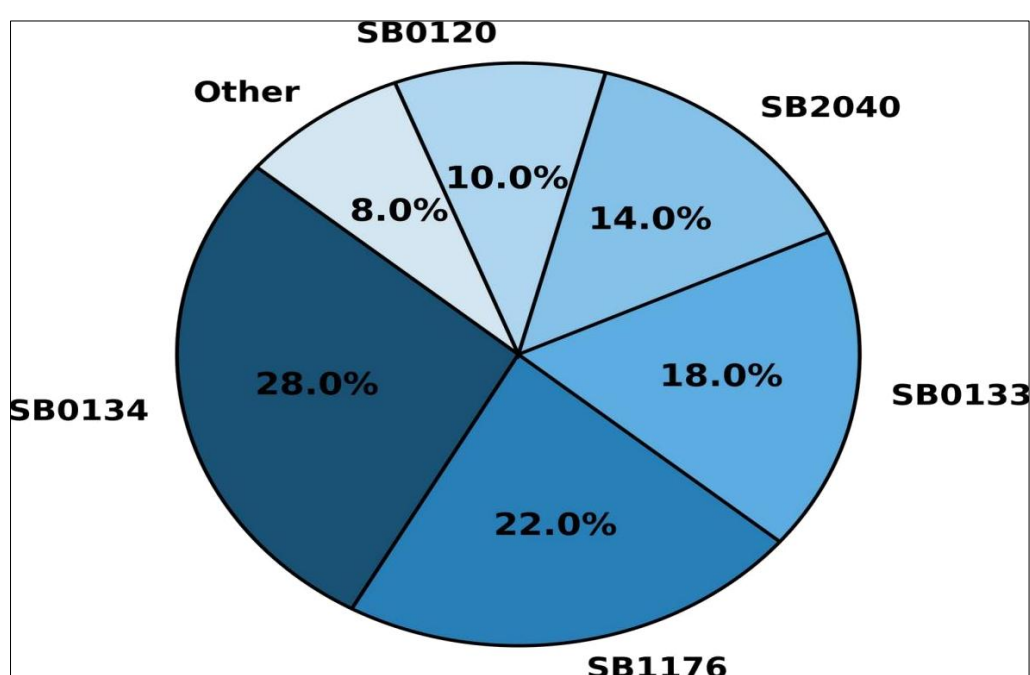


**Fig 2:** Distribution of Mycobacterium bovis spoligotype lineages identified in Ethiopian cattle populations across molecular epidemiological investigations

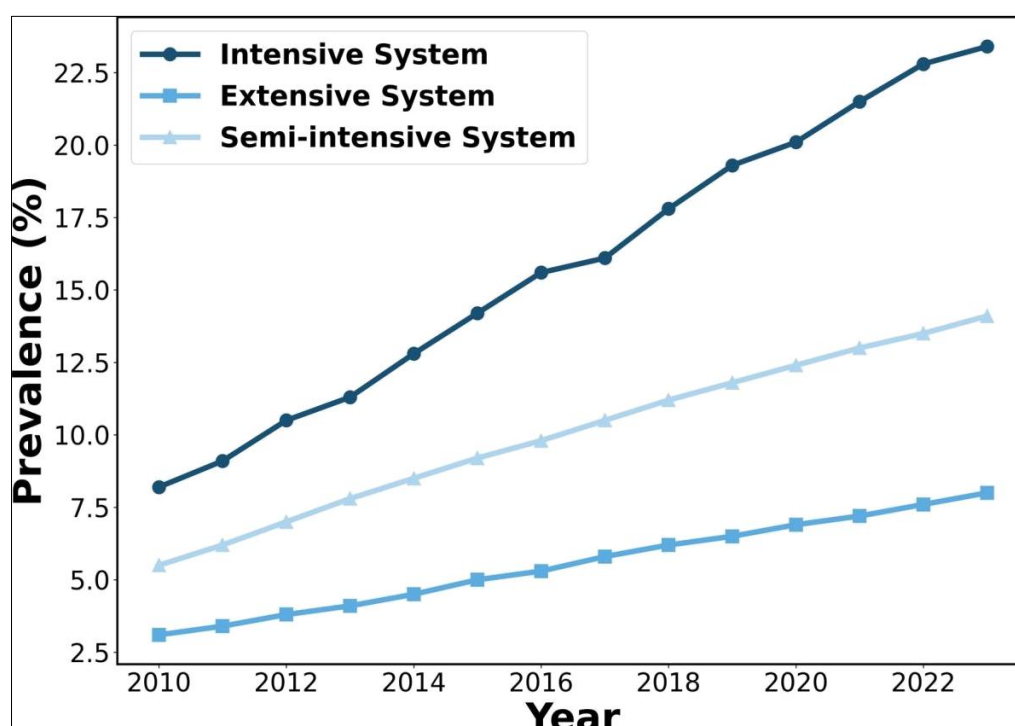


**Fig 3:** Temporal trends in bovine tuberculosis prevalence across different livestock production systems in Ethiopia from 2010 to 2023

Interpretation of the aggregated evidence demonstrated that transmission dynamics in Ethiopian cattle populations are governed by a complex interplay of management, environmental, and host-related determinants. The marked production system-dependent variation in prevalence, with intensive dairy operations showing three to four-fold higher prevalence compared to extensive pastoral systems, confirmed the central role of animal density and confinement duration in facilitating aerosol-mediated *M. bovis* transmission.

### Discussion

The pooled prevalence estimate of 14.7% for bovine tuberculosis in Ethiopian cattle populations positions Ethiopia among the highest-burden countries in sub-Saharan Africa, surpassing estimates reported from Kenya (8.2%), Uganda (6.5%), and Tanzania (9.8%) in comparable systematic analyses. This finding aligns with previous assessments identifying Ethiopia as a critical hotspot for bTB within the East African corridor, attributable to the combination of the continent's largest cattle population, limited surveillance infrastructure, and diverse production systems creating heterogeneous transmission landscapes.

The pronounced disparity in prevalence between intensive dairy systems (22.5%) and extensive pastoral systems (6.2%) observed in this research mirrors patterns documented across multiple sub-Saharan African countries, including Cameroon, Nigeria, and Chad. The underlying mechanism driving this differential relates fundamentally to the aerosol transmission route of

*M. bovis*, which requires close and sustained animal-to-animal contact for efficient pathogen transfer. Intensive dairy operations, characterized by confined housing, shared feeding troughs, and high stocking densities, create microenvironments where airborne pathogen concentrations accumulate to levels sufficient for establishing new infections. These findings carry significant implications for targeted control strategies, suggesting that prioritizing intensive dairy systems for

surveillance and intervention could yield disproportionately large epidemiological benefits relative to resource investment. The molecular epidemiological evidence revealing predominance of spoligotype SB0134 across multiple Ethiopian regions represents a notable finding with implications for understanding *M. bovis* transmission networks. Comparison with continental databases indicates that SB0134 belongs to the African 1 (Af1) clonal complex, which demonstrates geographic clustering within East and Central Africa. The mechanism underlying this lineage predominance likely involves historical introduction followed by clonal expansion within Ethiopian cattle populations, facilitated by the absence of systematic test-and-slaughter programs that might otherwise impose selective pressure against dominant circulating strains. The temporal increase in reported bTB prevalence from 2005 to 2023 must be interpreted cautiously, as this trend likely reflects combined contributions of genuine epidemiological expansion and increased research intensity with improved diagnostic methodologies. Nevertheless, the consistent upward trajectory across multiple independent investigations suggests that bovine tuberculosis transmission is not being adequately contained by existing passive surveillance measures, implying that without active intervention, prevalence will continue to escalate, particularly within the rapidly expanding intensive dairy sector. The identification of wildlife-livestock interface transmission events involving greater kudu and African buffalo in peripheral Ethiopian regions introduces additional complexity to control considerations. Similar wildlife reservoir dynamics have complicated eradication efforts in southern Africa (African buffalo) and the United Kingdom (European badger), demonstrating that single-species approaches to bTB control are insufficient in ecosystems with competent wildlife maintenance hosts. The implication for Ethiopian control strategy development is that integrated surveillance across domestic and wildlife populations will be essential for achieving sustained prevalence reduction.

## Epidemiological framework

The epidemiological framework governing bovine tuberculosis dynamics in Ethiopia operates across multiple spatial and temporal scales. At the micro-level, within-herd transmission is driven by aerosol exposure intensity, determined by housing density, ventilation adequacy, and duration of animal co-habitation. At the meso-level, between-herd transmission occurs through animal trade networks, communal grazing arrangements, and shared infrastructure including water points and dipping facilities. At the macro-level, regional and national prevalence patterns emerge from the aggregate effects of production system distribution, agro-ecological zone characteristics, and the presence or absence of organized control programs.

## One Health perspective

The One Health dimensions of bovine tuberculosis in Ethiopia extend beyond the direct zoonotic threat of *M. bovis* transmission to humans. The interconnected nature of human health, animal health, and environmental factors in Ethiopian pastoral and agropastoral communities creates conditions where bTB control cannot be achieved through veterinary interventions alone. Consumption of raw milk and inadequately cooked meat constitutes a primary zoonotic pathway, particularly in pastoral communities where cultural practices favor consumption of unprocessed animal products. Integration of human tuberculosis surveillance with veterinary bTB monitoring programs would enable bidirectional detection of cross-species transmission events currently missed by sector-specific surveillance systems.

## Conclusion

This research aimed to comprehensively review the epidemiological patterns and transmission dynamics of bovine tuberculosis in Ethiopian cattle populations through systematic synthesis of available evidence. The analysis revealed an overall pooled prevalence of 14.7%, with marked variation across production systems, geographic regions, and temporal periods, positioning Ethiopia as one of the highest-burden countries for bTB in sub-Saharan Africa. Intensive dairy systems demonstrated the highest prevalence at 22.5%, driven by management practices that facilitate aerosol transmission of *M. bovis*. Molecular epidemiological evidence indicated predominance of the Af1 clonal complex, with spoligotype SB0134 exhibiting widespread distribution suggestive of clonal expansion within Ethiopian cattle populations. Temporal trends indicated progressive prevalence increases over the review period, underscoring the inadequacy of current passive surveillance approaches. From a practical standpoint, prioritizing surveillance and intervention in intensive dairy systems around urban centers represents the most resource-efficient initial strategy for national bTB control, complemented by integration of wildlife monitoring in areas where livestock-wildlife interfaces facilitate cross-species transmission. Future research should focus on longitudinal transmission investigations using whole-genome sequencing to resolve fine-scale transmission networks, cost-effectiveness analyses of alternative control strategies adapted to Ethiopian production system diversity, and operational research evaluating the feasibility of integrating bTB surveillance within existing One Health platforms being developed for zoonotic disease control in the region.

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