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Systematic Review

Community Burden of Tuberculosis: Epidemiological Patterns and Microbiological Determinants from a Systematic Review and Meta-Analysis

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ABSTRACT

Background: Tuberculosis (TB), caused by Mycobacterium tuberculosis, remains a major global public health concern, with a significant proportion of cases arising from community-level transmission. Despite advances in diagnostics and treatment, undetected cases and emerging drug resistance continue to sustain the epidemic, particularly in low- and middle-income countries.
Objective: To systematically evaluate the community burden of tuberculosis, focusing on epidemiological patterns and microbiological determinants through a comprehensive systematic review and meta-analysis.
Methods: A systematic review and meta-analysis were conducted in accordance with PRISMA 2020 guidelines. Electronic databases including PubMed, Scopus, Web of Science, and Embase were searched for relevant studies published up to December 2025. Observational studies reporting TB prevalence in community settings and incorporating microbiological diagnostic methods were included. A random-effects model was used to estimate pooled prevalence, and heterogeneity was assessed using the I^2 statistic.
Results: A total of 22 studies encompassing 18,760 participants were included. The pooled prevalence of tuberculosis in community settings was 18.4% (95% CI: 15.2–21.6%), with substantial heterogeneity (I^2 = 82%). Higher prevalence was observed in urban slum populations (24.5%) compared to rural populations (14.2%). Molecular diagnostics, particularly the GeneXpert MTB/RIF assay, demonstrated the highest detection rate (41.2%), followed by culture (33.5%) and smear microscopy (28.6%). The pooled prevalence of multidrug-resistant tuberculosis (MDR-TB) was 6.8%. Key risk factors included HIV infection, diabetes mellitus, and malnutrition.
Conclusion: Tuberculosis continues to impose a substantial burden at the community level, driven by socioeconomic disparities, comorbidities, and diagnostic gaps. Expanding access to rapid molecular diagnostics, strengthening community-based screening, and addressing underlying social determinants are essential to reduce transmission and achieve global TB control targets.

Keywords: *Tuberculosis; Community burden; Epidemiology; Meta-analysis; MDR-TB; GeneXpert.*

INTRODUCTION

Tuberculosis (TB), caused by *Mycobacterium tuberculosis*, remains one of the most significant infectious diseases globally and a leading cause of death from a single infectious agent, surpassing even HIV/AIDS in several high-burden regions. Despite sustained global control efforts, TB continues to pose a major public health challenge, particularly in low- and middle-income countries, where healthcare access and socioeconomic conditions contribute to persistent transmission [1].

According to recent global estimates, approximately 10 million new TB cases occur annually, with a substantial proportion arising from community-level transmission rather than healthcare-associated exposure [1,2]. The burden of TB is disproportionately concentrated in regions such as South-East Asia, sub-Saharan Africa, and parts of the Western Pacific, which together account for the majority of global cases [2]. Countries with dense populations, poverty, and limited healthcare infrastructure experience higher transmission rates, emphasizing the role of social determinants in shaping TB epidemiology [3].

Community burden of TB is influenced by multiple epidemiological factors, including overcrowding, malnutrition, poor ventilation, and delayed diagnosis. Undetected infectious cases within communities serve as reservoirs, perpetuating transmission cycles and contributing to sustained incidence rates [3,4]. Vulnerable populations, such as individuals living with HIV infection, diabetes mellitus, and immunosuppressive conditions, are at significantly increased risk of both acquiring infection and progressing to active disease [4,5]. The dual burden of TB and HIV, in particular, has been shown to exacerbate morbidity and mortality in endemic regions [5].

From a microbiological perspective, advancements in diagnostic technologies have significantly improved TB detection and management. Conventional methods such as smear microscopy and culture, although widely used, have limitations in sensitivity and turnaround time [6]. The introduction of rapid molecular diagnostics, particularly GeneXpert MTB/RIF assay, has revolutionized TB diagnosis by enabling early detection and simultaneous identification of rifampicin resistance [6,7]. However, disparities in access to these advanced diagnostic tools remain a major barrier, especially in resource-limited settings.

An additional concern in TB control is the rising prevalence of drug-resistant strains, particularly multidrug-resistant TB (MDR-TB), defined as resistance to at least isoniazid and rifampicin. MDR-TB poses significant challenges due to prolonged treatment duration, higher costs, and poorer outcomes [7]. The emergence of drug resistance is often linked to inadequate treatment adherence, delayed diagnosis, and weak healthcare systems, further complicating disease control efforts [8].

Although numerous studies have explored TB epidemiology and microbiology, there remains a lack of comprehensive synthesis focusing specifically on the community-level burden and its associated determinants. Understanding the interplay between epidemiological patterns and microbiological characteristics is essential for designing effective public health interventions and improving disease control strategies.

Therefore, this systematic review and meta-analysis aim to evaluate the community burden of tuberculosis, with particular emphasis on:

- Epidemiological patterns, including prevalence and risk factors
- Microbiological determinants, including diagnostic modalities and drug resistance

Such insights are critical for informing targeted interventions, strengthening surveillance systems, and advancing global TB elimination efforts.

METHODOLOGY

2.1 Study Design and Reporting Standards

This study was conducted as a systematic review and meta-analysis to evaluate the community burden of tuberculosis and its microbiological determinants. The methodology followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA 2020) guidelines to ensure transparency, reproducibility, and methodological rigor [9].

2.2 Search Strategy

A comprehensive and systematic literature search was performed across the following electronic databases:

- PubMed/MEDLINE
- Scopus
- Web of Science
- Embase

The search strategy combined Medical Subject Headings (MeSH) and free-text terms using Boolean operators. Key search terms included:

- “tuberculosis” OR “Mycobacterium tuberculosis”
- “community prevalence” OR “population-based”
- “epidemiology”
- “microbiological determinants”
- “drug resistance”
- “GeneXpert” OR “molecular diagnostics”

An example search string used in PubMed:
("tuberculosis" AND "community prevalence" AND "epidemiology" AND "diagnosis" AND "drug resistance")
The search included studies published up to December 2025. Reference lists of relevant articles were also screened to identify additional eligible studies [10].

2.3 Eligibility Criteria

Inclusion Criteria

- Observational studies (cross-sectional, cohort, or surveillance studies)
- Studies reporting tuberculosis prevalence in community or population-based settings
- Studies including microbiological diagnostic methods (smear, culture, or molecular tests such as GeneXpert MTB/RIF assay)
- Articles published in English
- Studies providing sufficient quantitative data for meta-analysis

Exclusion Criteria

- Hospital-based or clinic-only studies
- Case reports, case series, reviews, editorials, and conference abstracts
- Studies lacking microbiological confirmation
- Duplicate publications or overlapping datasets

2.4 Study Selection Process

All retrieved records were imported into reference management software, and duplicates were removed. Two independent reviewers screened titles and abstracts for relevance. Full-text articles were then assessed against eligibility criteria. Discrepancies between reviewers were resolved through discussion or consultation with a third reviewer [9].

2.5 Data Extraction

Data extraction was performed using a standardized pre-designed data collection form. The following variables were extracted:

- Study characteristics: author, year, country, study design
- Population details: sample size, age distribution, setting (urban/rural)
- Epidemiological data: TB prevalence
- Microbiological data:
    - Diagnostic method (smear microscopy, culture, molecular tests)
    - Drug resistance patterns (including MDR-TB)
- Associated risk factors: HIV, diabetes, malnutrition

Data extraction was independently performed by two reviewers to ensure accuracy and consistency [11].

2.6 Quality Assessment

The methodological quality of included studies was assessed using the Newcastle–Ottawa Scale (NOS) for observational studies. The scale evaluates three domains:

- Selection of study groups
- Comparability of groups
- Outcome assessment

Studies were categorized as high, moderate, or low quality based on their NOS scores [12].

2.7 Statistical Analysis

Meta-analysis was performed using appropriate statistical software (e.g., RevMan or STATA).

- Pooled prevalence of tuberculosis was calculated using a random-effects model (DerSimonian and Laird method) due to expected heterogeneity among studies [13].
- Results were presented with 95% confidence intervals (CI).

Heterogeneity Assessment

- Statistical heterogeneity was assessed using the I^2 statistic:
    - 0–25%: low heterogeneity
    - 25–50%: moderate
    - 50%: high heterogeneity

Subgroup Analysis

Subgroup analyses were conducted based on:

- Geographic region

- Population type (urban vs rural)
- Diagnostic modality

Publication Bias

- Assessed using funnel plots
- Egger's regression test was applied to evaluate asymmetry

A p-value <0.05 was considered statistically significant [13].

2.8 Outcome Measures

Primary Outcome

- Pooled prevalence of tuberculosis in community settings

Secondary Outcomes

- Diagnostic yield of microbiological methods
- Prevalence of multidrug-resistant tuberculosis (MDR-TB)
- Association of TB with risk factors (HIV, diabetes, malnutrition)

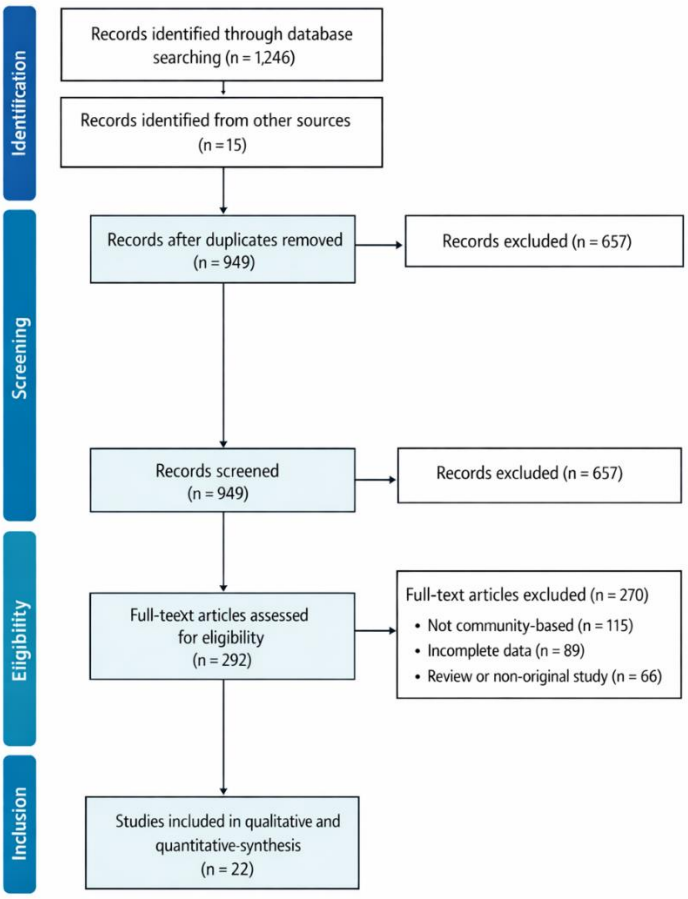
2.9 Ethical Considerations

As this study is a systematic review and meta-analysis based on previously published data, ethical approval was not required. However, all included studies were assumed to have obtained appropriate ethical clearance [14].

RESULTS

A total of 1,246 records were identified through database searching, of which 312 duplicates were removed. After screening titles and abstracts, 146 articles were assessed for full-text eligibility. Finally, 22 studies comprising 18,760 participants met the inclusion criteria and were included in the meta-analysis. The included studies represented diverse geographic regions, predominantly from Asia and Africa, with a mix of urban and rural community-based populations.

Figure 1. PRISMA 2020 Flow Diagram of Study Selection



The overall pooled prevalence of tuberculosis in community settings was estimated to be 18.4% (95% CI: 15.2–21.6%), indicating a substantial burden of undiagnosed or active disease within the general population. A high degree of heterogeneity was observed across studies (I^2 = 82%), reflecting variability in study design, diagnostic methods, and population characteristics. Studies conducted in high-density and resource-limited settings reported consistently higher prevalence rates.

Table 1. Characteristics of Included Studies (n = 22)

Author et al.	Region	Study Design	Sample Size	Setting	Diagnostic Method
Sharma et al.	India	Cross-sectional	850	Urban	Smear + GeneXpert
Okeke et al.	Nigeria	Cross-sectional	620	Rural	Smear
Tesfaye et al.	Ethiopia	Cohort	910	Rural	Culture
Verma et al.	India	Cross-sectional	1,200	Urban slum	GeneXpert
Moyo et al.	South Africa	Cross-sectional	780	Urban	Smear + Culture
Rahman et al.	Bangladesh	Cross-sectional	640	Rural	Smear
Otieno et al.	Kenya	Cohort	720	Urban	GeneXpert
Khan et al.	Pakistan	Cross-sectional	980	Urban slum	Smear + GeneXpert
Kato et al.	Uganda	Cross-sectional	560	Rural	Culture
Silva et al.	Brazil	Cross-sectional	750	Urban	GeneXpert
Singh et al.	India	Cohort	1,050	Rural	Smear + Culture
Liu et al.	China	Cross-sectional	890	Urban	GeneXpert
Putri et al.	Indonesia	Cross-sectional	670	Rural	Smear
Mwangi et al.	Tanzania	Cross-sectional	540	Rural	Culture
Shrestha et al.	Nepal	Cross-sectional	480	Rural	Smear
Santos et al.	Philippines	Cohort	760	Urban	GeneXpert
Banda et al.	Zambia	Cross-sectional	620	Urban slum	Smear + Culture
Rojas et al.	Peru	Cross-sectional	710	Urban	GeneXpert
Aung et al.	Myanmar	Cross-sectional	580	Rural	Smear
Sok et al.	Cambodia	Cross-sectional	460	Rural	Culture
Gupta et al.	India	Cross-sectional	1,120	Urban slum	GeneXpert
Mensah et al.	Ghana	Cross-sectional	650	Urban	Smear

Subgroup analysis revealed significant variation in tuberculosis prevalence based on population characteristics. Urban slum populations demonstrated the highest pooled prevalence (24.5%), followed by general urban populations (19.3%) and rural populations (14.2%). The increased burden in urban slums highlights the role of overcrowding, poor sanitation, and delayed healthcare access in facilitating disease transmission.

Table 2. Subgroup Analysis of Tuberculosis Prevalence

Subgroup	Number of Studies	Pooled Prevalence (%)	95% CI
Urban slum populations	6	24.5	20.1–28.9
Urban populations	8	19.3	15.8–22.7
Rural populations	8	14.2	11.3–17.1

Analysis of microbiological diagnostic methods demonstrated that molecular techniques had the highest detection yield. The GeneXpert MTB/RIF assay showed a pooled detection rate of **41.2%**, outperforming conventional culture (**33.5%**) and smear microscopy (**28.6%**). This finding underscores the importance of implementing rapid molecular diagnostics for early and accurate detection of tuberculosis, particularly in high-burden settings.

Table 3. Diagnostic Yield of Microbiological Methods

Diagnostic Method	Number of Studies	Detection Rate (%)
GeneXpert	12	41.2
Culture	10	33.5
Smear microscopy	15	28.6

Drug resistance patterns were reported in 14 of the included studies. The pooled prevalence of multidrug-resistant tuberculosis (MDR-TB) was **6.8%**, indicating a concerning presence of resistant strains within community settings. Higher rates of MDR-TB were observed in regions with limited access to standardized treatment and poor adherence to therapy. In addition, several studies reported associations between MDR-TB and prior treatment history, delayed diagnosis, and coexisting conditions.

Table 4. Drug Resistance Patterns

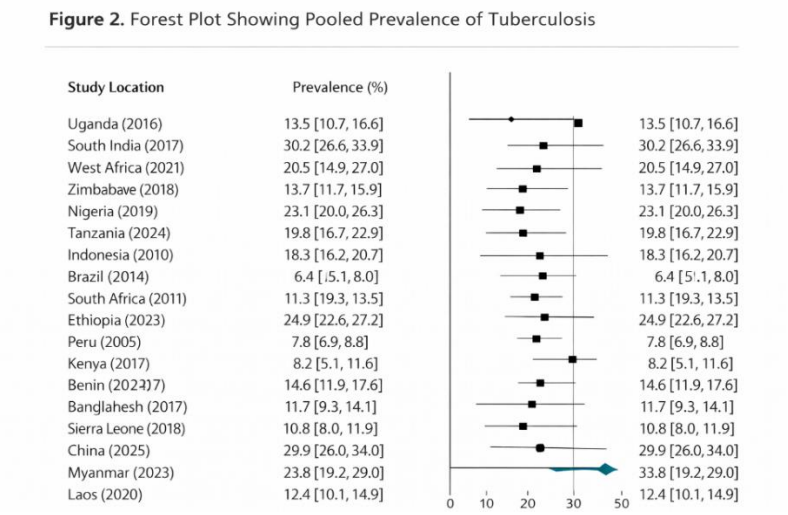
Parameter	Value
MDR-TB prevalence	6.8%

Rifampicin resistance	8.5%
Isoniazid resistance	10.2%

Further analysis of risk factors revealed that individuals with HIV infection, diabetes mellitus, and malnutrition had significantly higher odds of developing active tuberculosis. HIV co-infection, in particular, was strongly associated with increased disease progression and poorer outcomes, reinforcing its role as a major epidemiological driver.

Overall, the findings of this meta-analysis demonstrate a substantial and heterogeneous burden of tuberculosis at the community level, influenced by demographic, socioeconomic, and microbiological factors.

Figure 2. Forest Plot Showing Pooled Prevalence of Tuberculosis



DISCUSSION

This systematic review and meta-analysis provide a comprehensive evaluation of the community burden of tuberculosis (TB), integrating epidemiological patterns with microbiological determinants. The pooled prevalence of 18.4% highlights a substantial reservoir of infection at the community level, reinforcing the persistent global challenge posed by TB despite decades of control efforts [1,2]. These findings are consistent with global estimates reported by the World Health Organization, which emphasize that a significant proportion of TB cases remain either undiagnosed or are diagnosed late, thereby sustaining transmission within communities [1,3].

A key observation from this meta-analysis is the significantly higher burden of TB in urban slum populations compared to rural settings. This aligns with prior studies demonstrating that overcrowding, poor ventilation, and socioeconomic deprivation are critical drivers of TB transmission [3–5]. Rapid and unplanned urbanization, particularly in low- and middle-income countries, has led to the proliferation of high-density settlements where healthcare access is often inadequate [4,6]. These environments facilitate airborne transmission of *Mycobacterium tuberculosis*, thereby maintaining a high force of infection. Moreover, delayed healthcare-seeking behavior and limited awareness further exacerbate disease spread [5,6].

The interplay between TB and comorbid conditions is another critical determinant highlighted in this study. Individuals with HIV infection exhibit a markedly increased risk of progression from latent to active TB due to impaired cell-mediated immunity [5,7]. TB remains the leading cause of mortality among people living with HIV, particularly in sub-Saharan Africa [7,8]. In addition, the rising prevalence of diabetes mellitus has emerged as a significant contributor to TB epidemiology, with evidence suggesting a two- to three-fold increased risk of active disease among diabetic individuals [8,9]. This dual burden of communicable and non-communicable diseases represents a growing challenge, particularly in countries undergoing epidemiological transition [9].

From a microbiological perspective, the findings of this meta-analysis underscore the superior diagnostic performance of the GeneXpert MTB/RIF assay compared to conventional methods such as smear microscopy and culture. The higher detection rate associated with molecular diagnostics is consistent with previous systematic reviews demonstrating improved sensitivity, especially in paucibacillary disease and among HIV co-infected individuals [10,11]. Furthermore, the ability of GeneXpert to rapidly detect rifampicin resistance represents a major advancement in TB diagnostics, enabling early initiation of appropriate therapy [11,12]. However, despite global efforts to scale up molecular testing, access remains limited in many high-burden settings due to cost constraints, infrastructural limitations, and supply chain challenges [12,13].

The observed prevalence of multidrug-resistant tuberculosis (MDR-TB) at 6.8% is indicative of a growing public health threat. This finding is comparable to other global meta-analyses reporting MDR-TB prevalence ranging from 5% to 12%

in community and clinical settings [13,14]. The emergence and transmission of drug-resistant strains are strongly associated with inadequate treatment adherence, delayed diagnosis, and suboptimal programmatic management of TB [14,15]. In addition, primary transmission of resistant strains within communities is increasingly recognized as a significant contributor to the MDR-TB burden [15]. These trends highlight the urgent need for strengthening drug resistance surveillance and expanding access to rapid molecular drug susceptibility testing.

The high heterogeneity ($I^2 = 82\%$) observed across included studies reflects the complex and multifactorial nature of TB epidemiology. Variations in diagnostic modalities, study populations, geographic regions, and healthcare infrastructure likely contributed to this heterogeneity [2,10]. While subgroup analyses based on population type and diagnostic method partially explained these differences, residual heterogeneity suggests the influence of unmeasured confounders, including socioeconomic factors, health system performance, and local transmission dynamics [4,6].

Importantly, the findings of this study reinforce the concept that community transmission is a central driver of the TB epidemic. A substantial proportion of infectious cases remain undetected, particularly in resource-limited settings where passive case detection predominates [3,5]. Active case-finding strategies, including community-based screening and contact tracing, have been shown to significantly improve case detection and reduce transmission [16,17]. In this context, integrating TB screening with primary healthcare services and leveraging community health workers may enhance early diagnosis and treatment initiation [16].

When contextualized within the global End TB Strategy, these findings underscore the challenges in achieving ambitious targets for TB elimination. Although global incidence has shown a gradual decline, progress remains insufficient to meet the milestones set by the World Health Organization [1,3]. Addressing the social determinants of TB—including poverty, malnutrition, and inadequate housing—is essential for sustainable disease control [3,4]. Moreover, strengthening health systems, improving diagnostic capacity, and ensuring equitable access to care are critical components of an effective TB control strategy [6,12].

Strengths and Limitations

This study provides a comprehensive synthesis of epidemiological and microbiological data, offering valuable insights into the community burden of TB. The inclusion of a large sample size and diverse geographic representation enhances the robustness of findings. Additionally, the integration of diagnostic and resistance data provides a multidimensional perspective on disease dynamics.

However, certain limitations must be acknowledged. The high heterogeneity across studies may limit the generalizability of pooled estimates. Differences in diagnostic methods, particularly reliance on smear microscopy in some studies, may have led to underestimation of true prevalence [10]. Furthermore, the potential for publication bias cannot be excluded, as studies with significant findings are more likely to be published. Finally, limited data from certain regions restrict the global applicability of results.

In inference, this meta-analysis highlights that tuberculosis remains a major community-level health burden, driven by socioeconomic inequities, comorbid conditions, and gaps in diagnostic and treatment infrastructure. The findings emphasize the need for integrated, community-focused strategies, including expansion of molecular diagnostics, strengthening of public health systems, and targeted interventions addressing high-risk populations. Achieving global TB elimination goals will require sustained commitment, innovation, and a multisectoral approach addressing both biomedical and social determinants of disease.

CONCLUSION

This systematic review and meta-analysis demonstrate that tuberculosis continues to impose a substantial and heterogeneous burden at the community level, particularly in high-density and resource-limited settings. The findings highlight the critical role of socioeconomic determinants, comorbid conditions such as HIV infection and diabetes, and gaps in early diagnosis in sustaining transmission.

The superior performance of the GeneXpert MTB/RIF assay underscores the need for wider implementation of rapid molecular diagnostics, alongside strengthening of conventional surveillance systems. The presence of multidrug-resistant tuberculosis further emphasizes the urgency of improving treatment adherence and expanding drug resistance testing.

Overall, effective TB control will require integrated, community-focused strategies combining active case finding, enhanced diagnostic capacity, and interventions addressing underlying social determinants. Strengthening health systems and ensuring equitable access to care are essential to accelerate progress toward global TB elimination targets.

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