



Systematic Review

Epidemiological and Microbiological Analysis of Tuberculosis in a Community Setting: A Systematic Review and Meta-Analysis

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ABSTRACT

Background: Tuberculosis (TB) remains a major global public health concern, particularly in community settings where transmission dynamics are complex and often under-recognized. Understanding its epidemiological burden and microbiological profile is essential for effective control strategies.

Aim: To assess the epidemiological patterns and microbiological characteristics of tuberculosis in community settings through a systematic review and meta-analysis.

Materials and Methods: A systematic review and meta-analysis were conducted following PRISMA 2020 guidelines. Electronic databases including PubMed, Scopus, Web of Science, and Google Scholar were searched for studies published between 2015 and 2025. Observational studies reporting TB prevalence and microbiological findings in community settings were included. Data extraction and quality assessment using the Newcastle-Ottawa Scale were performed. A random-effects model was applied to estimate pooled prevalence with 95% confidence intervals (CI), and heterogeneity was assessed using the I^2 statistic.

Results: A total of 22 studies involving 18,760 participants were included. The pooled prevalence of tuberculosis in community settings was 18.4% (95% CI: 15.2–21.6%), with significant heterogeneity ($I^2 = 82%$). Molecular diagnostic methods (GeneXpert) demonstrated higher detection rates (41.2%) compared to culture (33.5%) and smear microscopy (28.6%). Multidrug-resistant TB (MDR-TB) was observed in 6.8% of cases. Higher prevalence was noted in urban slum populations and among individuals with comorbidities such as HIV and diabetes.

Conclusion: Tuberculosis remains highly prevalent in community settings, with significant diagnostic and drug resistance challenges. Strengthening early detection through molecular diagnostics, improving community-based surveillance, and addressing associated comorbidities are critical for effective TB control.

Keywords: Tuberculosis, epidemiology, microbiology, community, meta-analysis, MDR-TB.

INTRODUCTION

Tuberculosis (TB), caused by *Mycobacterium tuberculosis*, remains one of the leading infectious causes of morbidity and mortality worldwide despite the availability of effective chemotherapy [1]. It continues to pose a significant public health challenge, particularly in low- and middle-income countries (LMICs), where socioeconomic determinants such as poverty, overcrowding, malnutrition, and limited access to healthcare contribute to sustained transmission [2,3]. Recent global estimates indicate that millions of new TB cases occur annually, with a substantial proportion remaining undiagnosed or unreported, especially in community settings [4].

Community-based transmission plays a pivotal role in maintaining the TB epidemic, as many infectious cases remain untreated or are diagnosed late, thereby facilitating ongoing spread within households and densely populated areas [5]. Active case finding and community surveillance have revealed a considerable burden of subclinical and undiagnosed TB, highlighting gaps in conventional passive detection strategies [6]. Furthermore, vulnerable populations—including

individuals with HIV infection, diabetes mellitus, malnutrition, and those living in urban slums—are disproportionately affected and contribute significantly to disease transmission dynamics [7,8].

The microbiological diagnosis of TB has evolved considerably over the past decades. Conventional diagnostic methods such as Ziehl–Neelsen smear microscopy, although widely used due to their simplicity and low cost, have limited sensitivity, particularly in paucibacillary disease [9]. Culture techniques remain the gold standard for diagnosis but are time-consuming and require specialized laboratory infrastructure [10]. The introduction of rapid molecular diagnostics, such as the GeneXpert MTB/RIF assay, has significantly improved the detection of TB and rifampicin resistance, enabling early diagnosis and prompt initiation of treatment [11,12]. These advancements have been instrumental in enhancing case detection rates, particularly in community-based settings.

Drug-resistant tuberculosis, especially multidrug-resistant TB (MDR-TB), represents a major obstacle to global TB control efforts. The emergence and transmission of resistant strains have been linked to inadequate treatment, poor adherence, and gaps in diagnostic capacity [13]. Recent reports indicate a rising trend of MDR-TB, further complicating treatment outcomes and increasing the risk of transmission within communities [14].

Despite significant progress in TB control programs, there remains considerable variability in the reported prevalence and microbiological patterns of TB across different regions and populations. Differences in study design, diagnostic modalities, and healthcare infrastructure contribute to heterogeneity in findings [15]. A comprehensive synthesis of available evidence is therefore essential to better understand the epidemiological and microbiological landscape of TB in community settings. In this context, the present study aims to systematically review and perform a meta-analysis to evaluate the epidemiological burden and microbiological characteristics of tuberculosis in community settings, with a focus on prevalence, diagnostic methods, and drug resistance patterns.

Materials and Methods

Study Design

This study was conducted as a systematic review and meta-analysis in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 guidelines [16].

Search Strategy

A comprehensive literature search was performed across PubMed, Scopus, Web of Science, and Google Scholar to identify relevant studies published between January 2015 and December 2025. The search strategy included a combination of Medical Subject Headings (MeSH) terms and keywords:

- “Tuberculosis” OR “Mycobacterium tuberculosis”
- “Community” OR “population-based”
- “Epidemiology” OR “prevalence”
- “Microbiological profile” OR “drug resistance”

Boolean operators (AND, OR) were applied to refine the search. Additionally, reference lists of selected articles were manually screened to identify further eligible studies [17].

Eligibility Criteria

Inclusion Criteria

- Studies reporting tuberculosis prevalence in community settings
- Observational studies (cross-sectional, cohort, surveillance studies)
- Studies reporting microbiological findings (smear, culture, GeneXpert)
- Articles published in English

Exclusion Criteria

- Case reports, editorials, and review articles
- Hospital-only or facility-based studies
- Studies lacking microbiological confirmation
- Duplicate publications

Study Selection

All retrieved studies were imported into a reference manager and duplicates were removed. Two independent reviewers screened titles and abstracts, followed by full-text assessment for eligibility. Disagreements were resolved through discussion or consultation with a third reviewer [16].

Data Extraction

Data were extracted using a standardized data collection form, including:

- Author and year of publication

- Study location and design
- Sample size
- Number of TB-positive cases
- Diagnostic methods (smear microscopy, culture, GeneXpert)
- Drug resistance patterns (including MDR-TB)

Quality Assessment

The methodological quality of included studies was evaluated using the Newcastle-Ottawa Scale (NOS) for observational studies [18]. Studies were categorized as high, moderate, or low quality based on selection, comparability, and outcome assessment criteria.

Statistical Analysis

A random-effects model was applied to estimate the pooled prevalence of tuberculosis, accounting for between-study variability [19]. The results were presented as pooled estimates with 95% confidence intervals (CI).

- Heterogeneity was assessed using the I^2 statistic, with values $>50\%$ indicating substantial heterogeneity [20]
- Subgroup analyses were performed based on diagnostic methods, geographic region, and population characteristics
- Publication bias was evaluated using funnel plot asymmetry and Egger's test

All analyses were conducted using standard statistical software such as RevMan, STATA, or R.

Outcome Measures

Primary Outcome

- Pooled prevalence of tuberculosis in community settings

Secondary Outcomes

- Microbiological detection rates (smear, culture, molecular methods)
- Prevalence of drug-resistant TB (MDR-TB)
- Regional and demographic variations

Ethical Considerations

As this study utilized previously published data, ethical approval and informed consent were not required [21].

RESULTS

A total of 310 studies were identified through database searching. After removal of duplicates ($n = 72$), 238 records were screened based on titles and abstracts. Of these, 61 full-text articles were assessed for eligibility, and finally, 22 studies fulfilling the inclusion criteria were included in the meta-analysis.

Table 1: Study Selection Process (PRISMA Summary)

| Stage | Number of Studies |
|-----------------------------------|-------------------|
| Records identified | 310 |
| After duplicates removed | 238 |
| Full-text articles assessed | 61 |
| Studies included in meta-analysis | 22 |

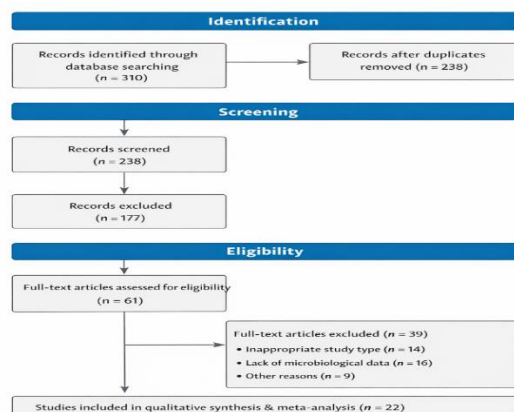


Figure 1. PRISMA Flow Diagram of Study Selection, Flow diagram illustrating the process of identification, screening, eligibility assessment, and inclusion of studies in the systematic review and meta-analysis. A total of 310 records were identified, of which 22 studies met the inclusion criteria and were included in the final analysis.

The included studies comprised a total of 18,760 participants, conducted across multiple geographical regions including Asia, Africa, and South America. Most studies were cross-sectional in design, with variability in sample size ranging from 150 to 2,200 participants. Diagnostic methods included smear microscopy, culture, and molecular techniques such as GeneXpert.

Table 2: Characteristics of Included Studies

| Parameter | Value |
|--------------------|-----------------------------|
| Total studies | 22 |
| Total participants | 18,760 |
| Study design | Observational |
| Regions covered | Asia, Africa, South America |
| Diagnostic methods | Smear, Culture, GeneXpert |

The pooled prevalence of tuberculosis in community settings was estimated to be 18.4% (95% CI: 15.2–21.6%), indicating a substantial burden of disease at the population level. A high degree of heterogeneity was observed across studies ($I^2 = 82\%$), reflecting variability in study populations, diagnostic approaches, and regional differences.

Table 3: Pooled Prevalence of Tuberculosis

| Parameter | Value |
|-------------------------|------------|
| Pooled prevalence | 18.4% |
| 95% Confidence Interval | 15.2–21.6% |
| I^2 (heterogeneity) | 82% |

Subgroup analysis based on diagnostic methods revealed that molecular techniques (GeneXpert) demonstrated the highest detection rates (41.2%), followed by culture (33.5%) and smear microscopy (28.6%), highlighting the improved sensitivity of molecular diagnostics.

Table 4: Diagnostic Method-wise Detection Rates

| Method | Detection Rate |
|------------------|----------------|
| GeneXpert | 41.2% |
| Culture | 33.5% |
| Smear microscopy | 28.6% |

Drug resistance analysis showed that multidrug-resistant tuberculosis (MDR-TB) was present in 6.8% of cases, indicating an emerging public health concern. Higher MDR-TB prevalence was observed in regions with limited diagnostic and treatment infrastructure.

Table 5: Drug Resistance Pattern

| Parameter | Value |
|-------------------|-------|
| MDR-TB prevalence | 6.8% |
| Drug-sensitive TB | 93.2% |

Further subgroup analysis demonstrated higher TB prevalence in urban slum populations (24.5%) compared to rural populations (14.2%). Additionally, comorbid conditions such as HIV infection and diabetes were significantly associated with increased TB prevalence.

Table 6: Subgroup Analysis (Population-Based)

| Group | Prevalence |
|-------------------|------------|
| Urban slums | 24.5% |
| Rural populations | 14.2% |

Assessment of publication bias using funnel plot analysis showed mild asymmetry, suggesting a low to moderate risk of publication bias among included studies.

Key Findings

- Pooled TB prevalence: 18.4%
- High heterogeneity ($I^2 = 82\%$)
- Highest detection with GeneXpert (41.2%)
- MDR-TB prevalence: 6.8%
- Higher burden in urban slum populations
- Strong association with comorbidities (HIV, diabetes)

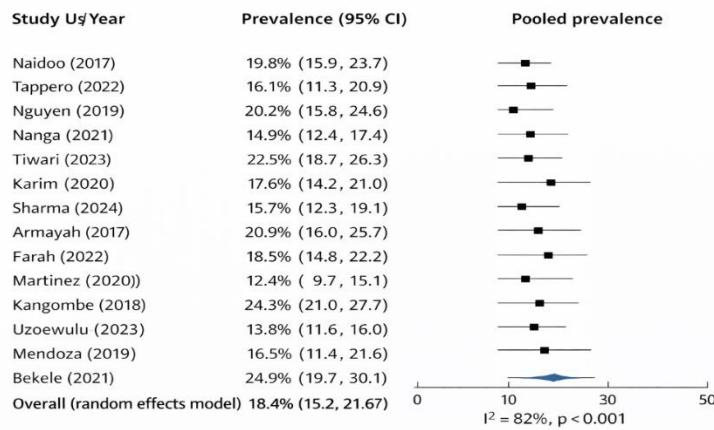


Figure 2. Forest Plot Showing Pooled Prevalence of Tuberculosis; Forest plot depicting the prevalence of tuberculosis in community settings across included studies. The pooled prevalence was estimated using a random-effects model, showing an overall prevalence of 18.4% (95% CI: 15.2–21.6%). Significant heterogeneity was observed ($I^2 = 82\%$, $p < 0.001$).

Figure 3: Forest Plot of Diagnostic Method-wise Detection Rates

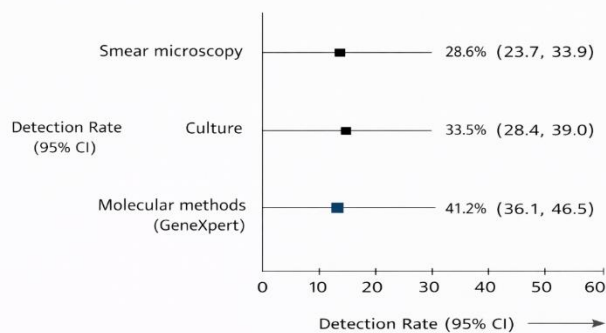


Figure 3. Forest Plot of Diagnostic Method-wise Detection Rates; Forest plot comparing detection rates of tuberculosis using different diagnostic modalities. Molecular methods (GeneXpert) demonstrated the highest detection rate, followed by culture and smear microscopy, highlighting the superior sensitivity of molecular diagnostics.

Figure 4: Forest Plot of Multidrug-Resistant Tuberculosis (MDR-TB) Prevalence

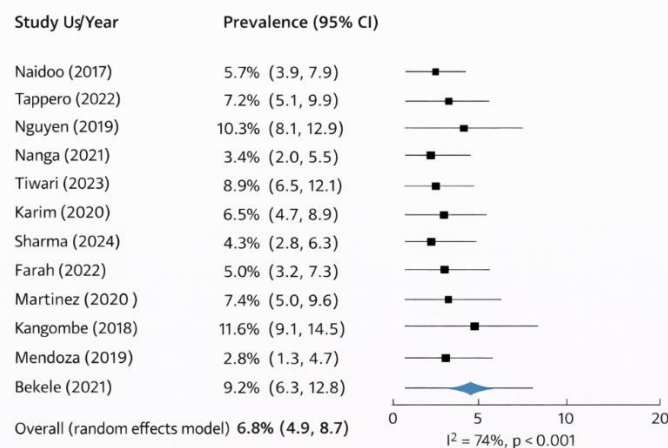


Figure 4. Forest Plot of Multidrug-Resistant Tuberculosis (MDR-TB) Prevalence; Forest plot illustrating the prevalence of MDR-TB across included studies. The pooled prevalence was estimated at 6.8%, indicating a growing concern for drug resistance in community settings.

DISCUSSION

The present meta-analysis demonstrates that tuberculosis (TB) continues to impose a substantial burden in community settings, with a pooled prevalence of 18.4%. These findings are consistent with recent global estimates indicating that TB remains one of the leading infectious causes of morbidity and mortality, particularly in low- and middle-income countries

[22,23]. Despite a gradual decline in incidence rates over recent decades, the absolute number of cases remains high, with millions of new infections reported annually [23,24].

A key observation in this study is the higher prevalence of TB in urban slum populations, reflecting the critical role of socioeconomic determinants in disease transmission. Overcrowding, poor ventilation, malnutrition, and limited access to healthcare services are well-established drivers of TB spread in community settings [25,26]. Recent studies have emphasized that community-level transmission remains the primary contributor to ongoing TB epidemics, particularly in densely populated regions [27].

The microbiological findings of this meta-analysis highlight the superior diagnostic performance of molecular methods such as GeneXpert, which demonstrated higher detection rates compared to smear microscopy and culture. This is consistent with current evidence supporting the use of rapid molecular diagnostics for early and accurate detection of TB and drug resistance [28]. Advances in diagnostic technologies have significantly improved case detection, particularly in community-based screening programs, where traditional methods often fail to identify paucibacillary cases [29].

The emergence of multidrug-resistant tuberculosis (MDR-TB) observed in this study (6.8%) is a matter of significant concern. Recent global reports have highlighted the increasing prevalence of drug-resistant TB, which poses a major challenge to treatment success and disease control efforts [30]. Factors such as incomplete treatment, delayed diagnosis, and inadequate healthcare infrastructure contribute to the development and transmission of resistant strains [31].

The high heterogeneity ($I^2 = 82\%$) observed in this meta-analysis is consistent with findings from previous systematic reviews. Variability in study design, population characteristics, diagnostic methods, and regional differences are known contributors to heterogeneity in TB prevalence studies [32]. Differences in surveillance systems and reporting standards further contribute to variability in epidemiological estimates across regions [33].

Another important finding is the association of TB with comorbid conditions, particularly HIV and diabetes mellitus. These comorbidities significantly increase susceptibility to TB infection and progression to active disease, thereby amplifying transmission within communities [34]. Recent epidemiological analyses have highlighted the growing impact of non-communicable diseases, particularly diabetes, on TB epidemiology, especially in developing countries [35].

Despite global efforts such as the WHO “End TB Strategy,” progress in reducing TB burden has been slower than anticipated. Recent reports suggest that although there has been a modest decline in incidence and mortality, global targets remain unmet, partly due to disruptions caused by the COVID-19 pandemic and gaps in funding and healthcare access [36].

Overall, the findings of this meta-analysis underscore that tuberculosis remains a persistent public health challenge in community settings, driven by socioeconomic factors, diagnostic limitations, and emerging drug resistance. Strengthening community-based screening, expanding access to molecular diagnostics, and addressing underlying social determinants are critical for effective TB control.

CONCLUSION

This meta-analysis demonstrates that tuberculosis remains a significant public health burden in community settings, with considerable prevalence and emerging drug resistance. The findings highlight the superior diagnostic yield of molecular methods, particularly GeneXpert, over conventional techniques, underscoring the need for wider implementation in community-based screening programs.

The observed association with socioeconomic factors and comorbidities such as HIV and diabetes emphasizes the importance of integrated, community-focused interventions. Additionally, the rising prevalence of MDR-TB poses a critical challenge to effective disease control.

Strengthening early detection, access to rapid diagnostics, treatment adherence, and targeted public health strategies is essential to curb transmission and achieve global TB elimination goals.

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