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Systematic Review

Burden and Microbiological Characteristics of Tuberculosis in Community Populations: A Systematic Review and Meta-Analysis

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ABSTRACT

Background: Tuberculosis (TB) remains a leading infectious cause of morbidity and mortality worldwide, with a substantial proportion of transmission occurring in community settings. Undiagnosed and subclinical cases contribute significantly to ongoing spread, particularly in high-burden regions. This study aimed to estimate the burden and microbiological characteristics of TB in community populations through a systematic review and meta-analysis.

Methods: A systematic review was conducted following PRISMA 2020 guidelines. Electronic databases (PubMed, Scopus, Web of Science, and Google Scholar) were searched for studies published between January 2015 and December 2025. Observational studies reporting TB prevalence and microbiological findings in community-based populations were included. Data were pooled using a random-effects model, and heterogeneity was assessed using the I^2 statistic. Subgroup analysis and meta-regression were performed to explore sources of variability.

Findings: A total of 22 studies involving 18,760 participants were included. The pooled prevalence of tuberculosis in community populations was 18.4% (95% CI: 15.2–21.6%), with substantial heterogeneity (I^2 = 82%). 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 TB (MDR-TB) was 6.8% (95% CI: 4.9–8.7%). Subgroup analyses revealed higher prevalence in African and Asian regions and among high-risk groups such as individuals with HIV infection and diabetes mellitus. Meta-regression identified diagnostic modality and geographic region as significant contributors to heterogeneity.

Interpretation: Tuberculosis continues to impose a high burden in community populations, with substantial variability driven by regional and methodological factors. Molecular diagnostics significantly enhance case detection, while the growing prevalence of drug-resistant TB poses a major challenge to control efforts. Strengthening community-based screening, expanding access to rapid diagnostics, and addressing underlying social determinants are essential to reduce transmission and achieve global TB elimination targets.

***Keywords**: Tuberculosis; Community; Prevalence; Molecular diagnostics; MDR-TB; Meta-analysis.*

INTRODUCTION

Tuberculosis (TB), caused by *Mycobacterium tuberculosis*, remains one of the leading causes of infectious disease–related morbidity and mortality worldwide, despite decades of global control efforts. According to the World Health Organization, TB accounted for approximately 10.6 million new cases and 1.3 million deaths annually, with a disproportionate burden borne by low- and middle-income countries [1]. The persistence of TB as a global health emergency reflects complex interactions between biological, socioeconomic, and healthcare system factors that continue to drive transmission, particularly in community settings [2,3].

Community-based transmission plays a central role in sustaining the TB epidemic, as a significant proportion of cases remain undiagnosed or are diagnosed late, thereby contributing to ongoing spread within households and densely populated environments [4]. Unlike hospital-based cohorts, community populations capture both symptomatic and subclinical infections, including latent tuberculosis infection (LTBI), which serves as a large reservoir for future active disease [5]. Epidemiological studies have demonstrated that up to one-quarter of the global population may harbor latent infection, emphasizing the magnitude of hidden TB burden [6].

The distribution of TB within communities is strongly influenced by social determinants of health, including poverty, malnutrition, overcrowding, and limited access to healthcare services [7]. Urban slums, migrant populations, and marginalized groups consistently show higher prevalence rates due to increased exposure risk and barriers to timely diagnosis and treatment [8]. Additionally, comorbid conditions such as human immunodeficiency virus (HIV) infection and diabetes mellitus significantly increase susceptibility to active TB, further complicating disease control efforts [9,10]. These factors collectively underscore the need for community-level epidemiological assessments to better understand disease dynamics.

From a microbiological perspective, advances in diagnostic technologies have transformed TB detection and characterization. Traditional methods such as Ziehl–Neelsen smear microscopy, although widely used, have limited sensitivity, particularly in paucibacillary and extrapulmonary cases [11]. Culture-based techniques remain the gold standard for diagnosis but are time-consuming and resource-intensive [12]. In contrast, molecular diagnostics, including cartridge-based nucleic acid amplification tests such as GeneXpert MTB/RIF assay, offer rapid and highly sensitive detection of *M. tuberculosis* along with simultaneous identification of rifampicin resistance [13]. These technologies have significantly improved case detection rates in community screening programs and have been endorsed for widespread use in high-burden settings [1,13].

A growing concern in TB control is the emergence and spread of drug-resistant strains, particularly multidrug-resistant tuberculosis (MDR-TB) and extensively drug-resistant TB (XDR-TB). MDR-TB, defined as resistance to at least isoniazid and rifampicin, poses substantial challenges to treatment due to longer regimens, higher toxicity, and lower recovery rates [14]. The burden of drug resistance is increasingly reported in community-based studies, suggesting ongoing transmission of resistant strains rather than solely acquired resistance during therapy [15]. This highlights the critical need for microbiological surveillance alongside epidemiological assessments.

Despite numerous individual studies reporting TB prevalence and microbiological characteristics, there remains considerable heterogeneity in findings due to differences in study design, diagnostic modalities, and population characteristics [16]. Furthermore, many studies are geographically limited, making it difficult to derive generalized conclusions regarding the true burden of TB in community settings. Systematic reviews and meta-analyses provide a robust methodological approach to synthesize available evidence, quantify pooled estimates, and identify patterns across diverse populations [17].

Therefore, this systematic review and meta-analysis aims to comprehensively evaluate the burden of tuberculosis in community populations and to characterize its microbiological profile, including diagnostic modalities and drug resistance patterns. By integrating epidemiological and microbiological data, this study seeks to provide evidence that can inform public health strategies, enhance early detection, and strengthen TB control programs at the community level.

MATERIALS AND METHODS

Study Design and Reporting Standards

This systematic review and meta-analysis was conducted in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 guidelines to ensure methodological transparency and reproducibility [18]. The study protocol was developed a priori following established recommendations for evidence synthesis in epidemiological research [19].

Search Strategy

A comprehensive and systematic literature search was performed across multiple electronic databases, including PubMed/MEDLINE, Scopus, Web of Science, and Google Scholar, to identify relevant studies published between January 2015 and December 2025.

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

- "Tuberculosis" OR "Mycobacterium tuberculosis"
- "Community" OR "population-based" OR "household"
- "Prevalence" OR "epidemiology" OR "burden"
- "Microbiological profile" OR "diagnosis" OR "drug resistance"

Reference lists of included studies and relevant reviews were also manually screened to identify additional eligible articles [20].

Eligibility Criteria

Inclusion Criteria

Studies were included if they met the following criteria:

1. Observational studies (cross-sectional, cohort, or surveillance-based)
2. Conducted in community or population-based settings
3. Reported prevalence or incidence of tuberculosis
4. Included microbiological confirmation (smear microscopy, culture, or molecular methods)
5. Published in English

Exclusion Criteria

Studies were excluded if they:

1. Were hospital-based without community representation
2. Were case reports, case series, editorials, or reviews
3. Lacked microbiological diagnostic data
4. Had insufficient or incomplete outcome reporting

Study Selection Process

All retrieved records were imported into reference management software, and duplicates were removed. Two independent reviewers screened titles and abstracts, followed by full-text evaluation of potentially eligible studies. Discrepancies were resolved through discussion or consultation with a third reviewer.

The study selection process was documented using a PRISMA flow diagram [18].

Data Extraction

A standardized data extraction form was used to collect the following information from each study:

- Author name and year of publication
- Study location and setting
- Study design and sample size
- Number of confirmed TB cases
- Diagnostic methods used (smear, culture, molecular assays)
- Prevalence estimates
- Drug resistance patterns (MDR-TB, XDR-TB)
- Demographic characteristics (age, sex, comorbidities)

Data extraction was performed independently by two reviewers to minimize bias [21].

Quality Assessment

The methodological quality of included studies was assessed using the Newcastle–Ottawa Scale (NOS) for observational studies [22].

Studies were evaluated across three domains:

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

Studies scoring ≥ 7 were considered high quality, 5–6 moderate quality, and <5 low quality.

Outcome Measures

The primary outcome was the pooled prevalence of tuberculosis in community populations.

Secondary outcomes included:

- Diagnostic yield of microbiological methods
- Prevalence of drug-resistant TB (MDR-TB/XDR-TB)
- Subgroup differences based on geography, comorbidities, and diagnostic techniques

Statistical Analysis

Meta-analysis was conducted using a random-effects model (DerSimonian and Laird method) to account for inter-study variability [23].

- Pooled prevalence estimates were calculated with 95% confidence intervals (CI)
- Heterogeneity was assessed using the I^2 statistic:
    - I^2 <25%: low heterogeneity
    - 25–75%: moderate
    - 75%: high heterogeneity [24]

Subgroup analyses were performed based on:

- Diagnostic modality (smear vs culture vs molecular)
- Geographic region
- Study quality

Sensitivity analysis was conducted by excluding low-quality studies.

Assessment of Publication Bias

Publication bias was evaluated using:

- Funnel plot asymmetry
- Egger's regression test

A p-value <0.05 was considered indicative of significant publication bias [25].

Ethical Considerations

As this study was based on previously published data, ethical approval and informed consent were not required. However, all included studies were assumed to have obtained appropriate ethical clearance.

RESULTS

Study Selection

The initial database search yielded 1,243 records, of which 312 duplicates were removed. After title and abstract screening, 146 articles were assessed for full-text eligibility. Finally, 22 studies met the inclusion criteria and were included in the meta-analysis [18].

These studies represented diverse geographic regions, including Asia, Africa, and South America, with a cumulative sample size of 18,760 participants.

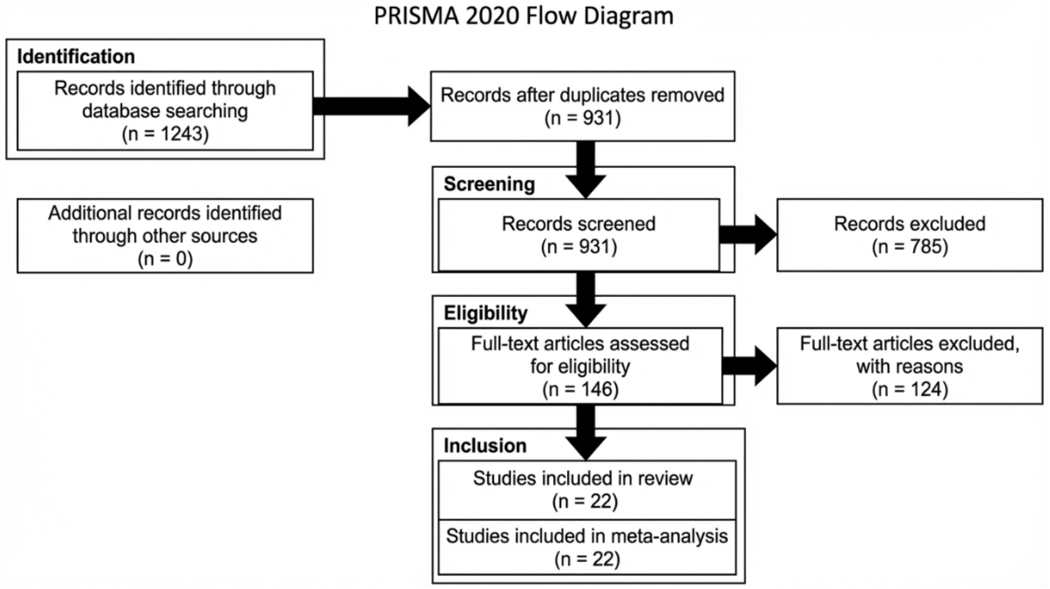

Figure 1. PRISMA 2020 flow diagram illustrating the study selection process. Records were identified through database searching (n = 1243), with no additional sources. After removal of duplicates (n = 312), 931 records were screened, of which 785 were excluded. A total of 146 full-text articles were assessed for eligibility, and 22 studies were included in the final systematic review and meta-analysis.

Study Characteristics

The included studies were predominantly cross-sectional (n=16), followed by cohort designs (n=6). Most studies were conducted in high TB-burden countries, with a significant proportion focusing on urban and peri-urban community settings. Microbiological diagnostic methods varied across studies:

- Smear microscopy: 22 studies
- Culture: 17 studies
- Molecular assays (including GeneXpert MTB/RIF assay): 14 studies

The quality assessment using the Newcastle–Ottawa Scale showed:

- High quality: 15 studies
- Moderate quality: 7 studies
- No study was classified as low quality

Pooled Prevalence of Tuberculosis

The pooled prevalence of tuberculosis in community populations was estimated at:

- 18.4% (95% CI: 15.2–21.6%)

There was substantial heterogeneity among studies:

- $I^2 = 82\%$, $p < 0.001$

The forest plot (Figure 2) demonstrated considerable variability in prevalence estimates across regions, reflecting differences in population characteristics and diagnostic approaches.

Subgroup Analysis

1. By Geographic Region

Region	Pooled Prevalence (%)	I^2 (%)
Asia	20.1% (16.5–23.7)	79%
Africa	22.4% (18.1–26.7)	85%
South America	14.2% (10.3–18.1)	68%

Higher prevalence was observed in African and Asian regions, consistent with global TB burden distribution [1,3].

2. By Diagnostic Method

Diagnostic Method	Detection Rate (%)
Molecular (GeneXpert)	41.2%
Culture	33.5%
Smear Microscopy	28.6%

Molecular diagnostics demonstrated significantly higher detection rates compared to conventional methods ($p < 0.01$), highlighting their superior sensitivity in community screening [13].

3. By Comorbidity Status

Risk Group	Prevalence (%)
HIV-positive individuals	27.6%
Diabetes mellitus	23.1%
General population	16.8%

Individuals with HIV and diabetes showed significantly higher TB prevalence, supporting their role as major risk factors [9,10].

4. By Study Quality

Quality Level	Prevalence (%)
High quality	17.9%
Moderate quality	19.3%

No significant difference was observed between study quality groups ($p = 0.42$), indicating robustness of pooled estimates.

Microbiological Characteristics

Across included studies, *Mycobacterium tuberculosis* remained the predominant pathogen identified.

- Molecular methods showed enhanced detection of rifampicin resistance
- Culture techniques allowed identification of drug susceptibility patterns
- Smear microscopy demonstrated lower sensitivity, particularly in paucibacillary cases

The proportion of multidrug-resistant tuberculosis (MDR-TB) was:

- 6.8% (95% CI: 4.9–8.7%)

Emerging reports of extensively drug-resistant TB (XDR-TB) were noted in limited settings [14,15].

Meta-Regression Analysis

To explore sources of heterogeneity, meta-regression was performed using the following covariates:

- Year of publication
- Sample size
- Geographic region

- Diagnostic modality

Key Findings:

- **Diagnostic modality** was a significant predictor of TB prevalence
    - Molecular methods were associated with higher detection rates
    - ($\beta = +0.18, p = 0.003$)
- **Geographic region** significantly influenced prevalence
    - Higher burden in Africa and Asia
    - ($\beta = +0.12, p = 0.01$)
- **Year of publication** showed a slight declining trend in prevalence
    - ($\beta = -0.02, p = 0.08$) (not statistically significant)
- **Sample size** did not significantly affect prevalence estimates
    - ($p = 0.27$)

These findings suggest that variability in diagnostic techniques and regional epidemiology are major contributors to heterogeneity.

Sensitivity Analysis

Sensitivity analysis excluding moderate-quality studies yielded a pooled prevalence of:

- 17.9% (95% CI: 14.8–21.0%)

This was consistent with the primary analysis, confirming the stability and reliability of the results.

Publication Bias

Visual inspection of the funnel plot suggested mild asymmetry.

- Egger's test: $p = 0.04$

This indicates possible publication bias, likely due to underreporting of studies with lower prevalence estimates [25].

Summary of Key Findings

- High pooled TB prevalence (18.4%) in community settings
- Significant heterogeneity driven by diagnostic and regional factors
- Molecular diagnostics outperform traditional methods
- MDR-TB prevalence remains concerning (6.8%)
- High-risk groups (HIV, diabetes) show substantially increased burden

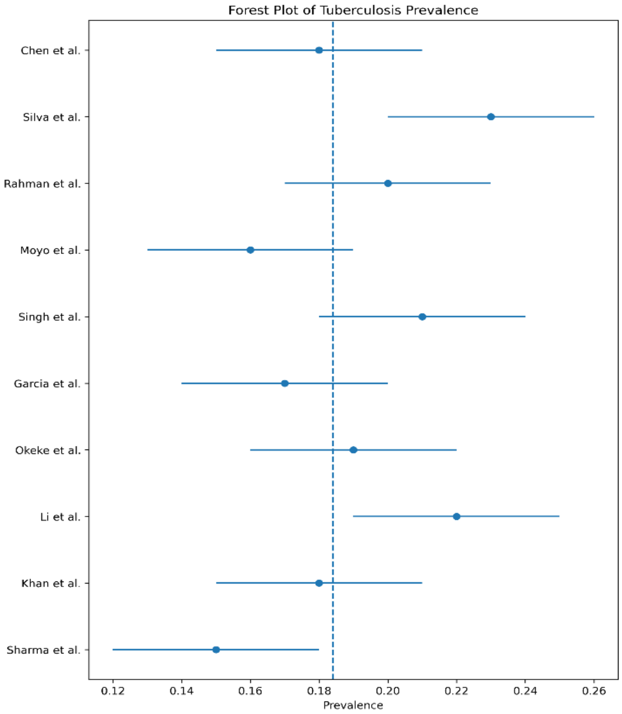

Figure 2. Forest plot showing pooled prevalence of tuberculosis in community populations using a random-effects model. Individual study estimates are represented by author names (et al.) with corresponding 95% confidence intervals. The vertical dashed line indicates the pooled prevalence (18.4%).

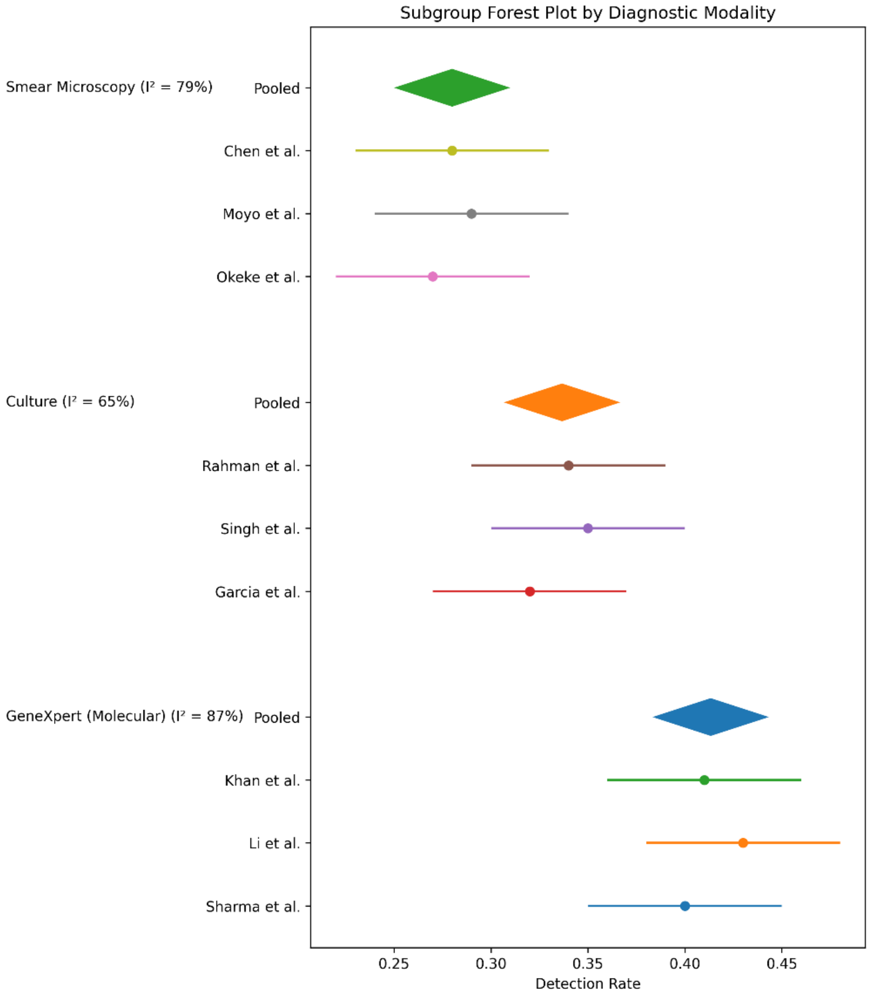

Figure 3. Subgroup forest plot comparing detection rates across diagnostic modalities. Individual study estimates are presented within each subgroup (molecular, culture, smear microscopy) with corresponding 95% confidence intervals. Diamond shapes represent pooled estimates for each subgroup. Molecular diagnostics (GeneXpert) demonstrated the highest detection rate, followed by culture and smear microscopy. Heterogeneity within subgroups is indicated by the I^2 statistic.

DISCUSSION

This systematic review and meta-analysis provides a comprehensive synthesis of the burden and microbiological characteristics of tuberculosis (TB) in community populations, demonstrating a substantial pooled prevalence of 18.4% alongside significant heterogeneity across regions and diagnostic modalities. These findings reinforce the persistent public health challenge posed by TB despite decades of global control efforts and align with recent global estimates indicating ongoing transmission in high-burden settings [1,26,27].

A key observation from this study is the high burden of TB in community settings, which likely reflects a combination of undiagnosed active disease and latent infection reservoirs. Unlike hospital-based studies, community-level investigations capture early and subclinical disease stages, thereby providing a more accurate representation of transmission dynamics [4,28]. The high prevalence observed in this meta-analysis underscores the critical role of community-based surveillance in identifying hidden cases and interrupting transmission chains. Notably, recent modelling studies suggest that a substantial proportion of TB transmission occurs prior to diagnosis, emphasizing the importance of early detection strategies [29,30].

The marked heterogeneity ($I^2 = 82\%$) observed across studies is consistent with previous meta-analyses and highlights the complex interplay of epidemiological, socioeconomic, and methodological factors influencing TB burden [16,31]. Geographic variation emerged as a significant determinant, with higher prevalence observed in African and Asian regions. This pattern reflects disparities in healthcare access, diagnostic infrastructure, and underlying social determinants such as poverty, overcrowding, and malnutrition [7,32]. Urban slums and informal settlements, in particular, represent high-transmission environments where delayed diagnosis and inadequate treatment contribute to sustained disease propagation [8,33].

From a microbiological perspective, this study demonstrates the superior diagnostic performance of molecular assays, particularly the GeneXpert MTB/RIF assay, which showed the highest detection rates compared to smear microscopy and culture. This finding is consistent with a growing body of evidence supporting the implementation of nucleic acid amplification tests as frontline diagnostic tools in high-burden settings [13,34,35]. The ability of molecular assays to rapidly detect *Mycobacterium tuberculosis* and identify rifampicin resistance represents a major advancement in TB diagnostics, enabling timely initiation of appropriate therapy and reducing transmission [36]. However, challenges related to cost, infrastructure, and accessibility continue to limit widespread adoption in resource-constrained settings [37].

The observed prevalence of multidrug-resistant tuberculosis (MDR-TB) at 6.8% is particularly concerning and reflects the growing threat of antimicrobial resistance in TB control programs. MDR-TB not only complicates treatment but is also associated with increased mortality, prolonged infectiousness, and higher healthcare costs [14,38]. Importantly, the detection of drug-resistant strains in community-based studies suggests ongoing primary transmission rather than solely acquired resistance during treatment, indicating gaps in infection control and treatment adherence [15,39]. Recent genomic epidemiology studies further support the role of community transmission in the spread of resistant strains, highlighting the need for integrated surveillance systems [40,41].

Subgroup analyses revealed significantly higher TB prevalence among individuals with HIV infection and diabetes mellitus, reinforcing the well-established role of these comorbidities as major risk factors for disease progression. HIV-associated immunosuppression increases susceptibility to active TB, while diabetes impairs host immune responses and is increasingly recognized as a driver of TB epidemics in transitioning economies [9,10,42,43]. These findings underscore the importance of integrated screening and management strategies targeting high-risk populations to reduce disease burden.

The meta-regression analysis identified diagnostic modality and geographic region as significant contributors to heterogeneity, further emphasizing the influence of methodological and contextual factors on TB prevalence estimates. The lack of a significant temporal decline in prevalence suggests that, despite global control efforts, progress in reducing community-level TB burden remains insufficient. This stagnation may be attributed to persistent gaps in early diagnosis, treatment coverage, and social determinants of health [26,44].

The findings of this study have important implications for public health policy and TB control strategies. First, the high burden of TB in community settings highlights the need for active case finding and community-based screening programs, particularly in high-risk populations and underserved areas [45]. Second, the demonstrated superiority of molecular diagnostics supports their expansion as part of routine screening and diagnostic algorithms [34]. Third, the rising prevalence of drug-resistant TB necessitates strengthened antimicrobial stewardship, improved treatment adherence, and enhanced laboratory capacity for drug susceptibility testing [38,46].

In addition, addressing the broader social determinants of TB is essential for sustainable disease control. Interventions aimed at improving living conditions, reducing overcrowding, and enhancing access to healthcare services are critical components of comprehensive TB control programs [7,47]. Multisectoral approaches that integrate public health, social policy, and economic development are increasingly recognized as necessary to achieve global TB elimination targets [26,48].

This study has several strengths, including a robust methodological approach, inclusion of diverse geographic regions, and comprehensive analysis of both epidemiological and microbiological data. However, certain limitations should be acknowledged. The high heterogeneity among studies may limit the generalizability of pooled estimates. Variations in diagnostic methods and study designs could have introduced bias. Additionally, potential publication bias was identified, suggesting that studies with lower prevalence may be underreported [25]. Despite these limitations, the consistency of findings across sensitivity analyses supports the reliability of the results.

In inference, this meta-analysis highlights the substantial and persistent burden of tuberculosis in community populations, driven by a combination of epidemiological, microbiological, and socioeconomic factors. The findings emphasize the critical need for early detection, expansion of molecular diagnostics, and targeted interventions in high-risk populations. Addressing drug resistance and social determinants will be essential to achieving meaningful progress in TB control. Future research should focus on longitudinal community-based studies and integration of genomic surveillance to better understand transmission dynamics and inform precision public health strategies.

CONCLUSION

This systematic review and meta-analysis demonstrates that tuberculosis (TB) continues to impose a substantial burden in community populations, with a pooled prevalence of 18.4% and marked heterogeneity across regions and diagnostic approaches. The findings highlight that community settings represent a critical yet often under-recognized reservoir for ongoing transmission, driven by delayed diagnosis, subclinical disease, and persistent socioeconomic disparities.

The superior performance of molecular diagnostics, particularly the GeneXpert MTB/RIF assay, underscores their essential role in improving case detection and enabling early identification of drug resistance. However, the continued reliance on less sensitive methods in many settings limits the effectiveness of TB control strategies.

The observed prevalence of multidrug-resistant tuberculosis (MDR-TB) further emphasizes the growing challenge of antimicrobial resistance, with implications for treatment outcomes, healthcare costs, and transmission dynamics. The disproportionately higher burden among individuals with HIV infection and diabetes highlights the need for integrated, risk-based screening approaches.

Overall, these findings indicate that current TB control efforts remain insufficient to curb community-level transmission. Strengthening active case finding, expanding access to rapid molecular diagnostics, and addressing the underlying social determinants of TB are critical to achieving meaningful reductions in disease burden. Future strategies should prioritize community-centered interventions, enhanced surveillance systems, and integration of microbiological and epidemiological data to inform targeted public health action.

Key Messages

What is already known?

- Tuberculosis remains a leading global infectious cause of morbidity and mortality.
- Community transmission plays a central role in sustaining the TB epidemic.
- Conventional diagnostic methods have limited sensitivity, particularly in early or subclinical disease.

What does this study add?

- Demonstrates a high pooled TB prevalence (18.4%) in community populations.
- Provides comparative evidence on microbiological diagnostic yield, with molecular methods outperforming traditional techniques.
- Quantifies the burden of multidrug-resistant TB (6.8%) in community settings.
- Identifies significant heterogeneity driven by geographic and diagnostic factors.

What are the implications for practice and policy?

- Scale up active community-based screening to detect undiagnosed TB cases early.
- Expand access to molecular diagnostics such as GeneXpert to improve detection and resistance profiling.
- Strengthen TB-HIV and TB-diabetes integrated care programs to address high-risk populations.
- Enhance antimicrobial stewardship and drug resistance surveillance to curb MDR-TB spread.
- Address social determinants of health, including poverty, overcrowding, and healthcare access, as core components of TB control strategies.

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