International Journal of Medical and Pharmaceutical Research

Online ISSN-2958-3683 | Print ISSN-2958-3675
Frequency: Bi-Monthly
Available online on: https://ijmpr.in/

Systematic Review

Global Epidemiological Trends and Microbiological Insights of Tuberculosis in Community Settings: A Systematic Review and Meta-Analysis

Subhasish Chanda[1]*, M. Hima Bindu[2], Kavita Meena[3]

[1]Senior Resident (MD Respiratory Medicine), Department of Respiratory Medicine, Kalimpong District Hospital, West Bengal, India
[2]Professor, Department of Microbiology, Malla Reddy Institute of Medical Sciences, Malla Reddy Vishwavidyapeeth, Hyderabad, Telangana, India
[3]Assistant Professor, Department of Microbiology, Al-Falah School of Medical Sciences and Research, Faridabad, Haryana, India

OPEN ACCESS

Corresponding Author:

Subhasish Chanda
Senior Resident (MD Respiratory Medicine) Department of Respiratory Medicine Kalimpong District Hospital, West Bengal, India

Received: 25-02-2026
Accepted: 23-03-2026
Available online: 08-04-2026

ABSTRACT

Background: Tuberculosis (TB) remains a major global public health concern, driven largely by sustained community transmission, a substantial reservoir of latent infection, and the increasing emergence of drug-resistant strains. Despite global control efforts, recent trends indicate stagnation and resurgence in TB incidence, particularly in low- and middle-income countries.

Objective: To systematically evaluate global epidemiological trends and microbiological characteristics of tuberculosis in community settings, and to generate pooled estimates of prevalence, incidence, and drug resistance through 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 studies published up to December 2025. Observational studies reporting epidemiological and microbiological data on TB in community populations were included. Random-effects meta-analysis was performed to calculate pooled estimates, and heterogeneity was assessed using the I^2 statistic.

Results: A total of 112 studies comprising over 5.6 million participants were included. The global incidence of tuberculosis was estimated at approximately 10.8 million cases annually. The pooled prevalence of latent tuberculosis infection (LTBI) was 24.8% (95% CI: 19.7–30.0), indicating a substantial reservoir for future disease. Multidrug-resistant TB (MDR-TB) prevalence was 11.6% (95% CI: 9.1–14.5), with higher rates among previously treated individuals. South-East Asia and Africa accounted for the highest burden of disease. Microbiologically, Mycobacterium tuberculosis remained the predominant pathogen, with resistance primarily associated with mutations in katG, inhA, and rpoB genes. Molecular diagnostic methods, particularly GeneXpert MTB/RIF, demonstrated improved detection of TB and drug resistance.

Conclusion: Tuberculosis continues to pose a significant global health challenge, particularly in community settings where transmission remains largely uncontrolled. The high prevalence of latent infection and rising drug resistance underscore the urgent need for strengthened surveillance, expanded molecular diagnostics, and targeted public health interventions. Addressing social determinants and improving community-based strategies will be critical for achieving global TB control and elimination goals.

Keywords: *Tuberculosis, Epidemiology, Community Transmission, Latent Tuberculosis, MDR-TB, Mycobacterium tuberculosis, Meta-analysis.*

INTRODUCTION

Tuberculosis (TB), caused by *Mycobacterium tuberculosis*, remains one of the most significant infectious diseases globally, posing a persistent threat to public health despite decades of control efforts. It is among the leading causes of mortality from a single infectious agent, surpassing diseases such as HIV/AIDS in several regions [1]. The global burden of TB continues to be substantial, with an estimated 10.8 million new cases reported annually, reflecting a concerning stagnation—and in some regions, reversal—of the previously declining trends [2,3].

The distribution of TB is markedly uneven across the globe, disproportionately affecting low- and middle-income countries. Nearly two-thirds of global TB cases are concentrated in a small number of high-burden countries, including India, Indonesia, China, Pakistan, and the Philippines [3,4]. The South-East Asia region alone accounts for approximately 45% of the global TB burden, followed by Africa, which contributes nearly a quarter of cases [2,4]. These disparities highlight the critical role of socioeconomic determinants such as poverty, overcrowding, malnutrition, and limited access to healthcare services in sustaining transmission within community settings [5].

Community transmission remains a central driver of the TB epidemic. Unlike hospital-based transmission, community spread often occurs undetected, particularly in densely populated areas where prolonged close contact facilitates airborne dissemination of *M. tuberculosis* [6]. Latent tuberculosis infection (LTBI) represents a significant reservoir for future disease, with approximately one-quarter of the global population estimated to harbor latent infection [7]. This vast pool of asymptomatic individuals underscores the challenge of TB elimination, as reactivation can occur under conditions of immunosuppression, malnutrition, or co-existing diseases such as HIV and diabetes [8].

In recent years, the emergence and spread of drug-resistant TB have further complicated global control strategies. Multidrug-resistant TB (MDR-TB), defined as resistance to at least isoniazid and rifampicin, poses a major therapeutic challenge due to prolonged treatment duration, higher costs, and poorer outcomes [9]. Global estimates indicate that MDR-TB accounts for approximately 10–12% of TB cases, with even higher prevalence reported in certain high-burden regions [9,10]. The underlying microbiological mechanisms involve genetic mutations in key resistance-associated genes, including *katG*, *inhA*, and *rpoB*, which compromise the efficacy of first-line anti-tubercular drugs [11].

Advances in microbiological diagnostics have significantly improved the detection and characterization of TB. While conventional culture methods remain the gold standard, they are time-consuming and resource-intensive. The introduction of rapid molecular techniques, such as nucleic acid amplification tests and GeneXpert MTB/RIF assays, has revolutionized TB diagnosis by enabling early detection and simultaneous identification of drug resistance [12]. These tools are particularly valuable in community settings, where early diagnosis can interrupt transmission chains and improve treatment outcomes.

Furthermore, recent global health challenges, including the COVID-19 pandemic, have disrupted TB control programs, leading to delays in diagnosis, treatment interruptions, and increased community transmission [3,13]. Such disruptions have highlighted the fragility of TB surveillance systems and the need for resilient, community-focused healthcare strategies.

Given the complex interplay of epidemiological, socioeconomic, and microbiological factors, a comprehensive understanding of TB dynamics in community settings is essential. While numerous studies have explored individual aspects of TB epidemiology or microbiology, there remains a need for an integrated synthesis of global data.

Therefore, this systematic review and meta-analysis aims to evaluate global epidemiological trends and microbiological insights of tuberculosis in community settings, with a particular focus on prevalence, incidence, transmission dynamics, and drug resistance patterns.

MATERIALS AND METHODS

2.1 Study Design and Reporting Framework

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 rigor and transparency [14]. The protocol was developed a priori, defining objectives, inclusion criteria, and analytical approaches.

2.2 Data Sources and Search Strategy

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

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

The search included studies published up to December 2025. A combination of Medical Subject Headings (MeSH) terms and free-text keywords was used:

- "Tuberculosis" OR "Mycobacterium tuberculosis" AND "epidemiology" OR "prevalence" OR "incidence" AND "community" OR "population-based" AND "drug resistance" OR "MDR-TB" OR "microbiology"

Boolean operators (AND, OR) and database-specific filters were applied to refine the search. Reference lists of included studies and relevant reviews were also screened to identify additional eligible articles [15].

2.3 Eligibility Criteria

2.3.1 Inclusion Criteria

Studies were included if they met the following criteria:

1. Reported epidemiological data on tuberculosis in community or population-based settings
2. Provided data on at least one of the following:
    - Prevalence
    - Incidence
    - Latent TB infection (LTBI)
    - Drug resistance patterns
3. Included microbiologically confirmed TB cases (culture, smear, or molecular methods)
4. Observational study designs:
    - Cross-sectional
    - Cohort
    - Surveillance studies
5. Published in English

2.3.2 Exclusion Criteria

Studies were excluded if they:

- Were hospital-based without community relevance
- Were case reports, editorials, or narrative reviews
- Lacked sufficient quantitative data
- Included duplicate 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, followed by full-text evaluation for eligibility. Discrepancies were resolved through discussion or consultation with a third reviewer.

The study selection process was documented using a PRISMA flow diagram [14].

2.5 Data Extraction

A standardized data extraction form was used. The following variables were collected:

- Study characteristics:
    - Author, year, country
    - Study design
    - Sample size
- Epidemiological data:
    - TB incidence and prevalence
    - LTBI prevalence
- Microbiological data:
    - Diagnostic methods (smear, culture, PCR, GeneXpert)
    - Identified species (*M. tuberculosis* complex)
- Drug resistance:
    - MDR-TB prevalence
    - Resistance to isoniazid, rifampicin
- Risk factors:
    - HIV status
    - Socioeconomic indicators

Data extraction was performed independently by two reviewers to minimize bias [16].

2.6 Quality Assessment

The methodological quality of included studies was assessed using:

- Newcastle–Ottawa Scale (NOS) for cohort and case-control studies
- Joanna Briggs Institute (JBI) checklist for cross-sectional studies

Studies were categorized as low, moderate, or high quality based on predefined scoring criteria [17].

2.7 Outcome Measures

The primary outcomes included:

- Global TB incidence and prevalence
- Prevalence of latent TB infection (LTBI)
- Prevalence of multidrug-resistant TB (MDR-TB)

Secondary outcomes included:

- Regional distribution of TB
- Microbiological diagnostic trends
- Genetic mutations associated with drug resistance

2.8 Statistical Analysis

Meta-analysis was performed using a random-effects model (DerSimonian–Laird method) to account for inter-study variability [18].

- Pooled estimates were calculated for:
  - Prevalence
  - Incidence
  - MDR-TB rates
- Heterogeneity was assessed using:
  - I^2 statistic
  - Cochran's Q test

Interpretation of I^2:

- 25%: low heterogeneity
- 50%: moderate
- 75%: high [18]

Subgroup analyses were conducted based on:

- Geographic region
- Study design
- Diagnostic method

2.9 Publication Bias

Publication bias was evaluated using:

- Funnel plots
- Egger's regression test

A p-value <0.05 was considered indicative of significant bias [19].

2.10 Sensitivity Analysis

Sensitivity analysis was performed by:

- Excluding low-quality studies
- Assessing the impact of individual studies on pooled estimates

This ensured robustness and reliability of the results [20].

2.11 Ethical Considerations

As this study is a systematic review and meta-analysis of previously published data, ethical approval was not required. However, all included studies were assumed to have adhered to ethical research standards.

RESULTS

A total of 3,482 records were identified through database searching, of which 2,756 remained after duplicate removal. Following title and abstract screening, 214 articles were selected for full-text review. Ultimately, 112 studies met the inclusion criteria and were included in the qualitative and quantitative synthesis.

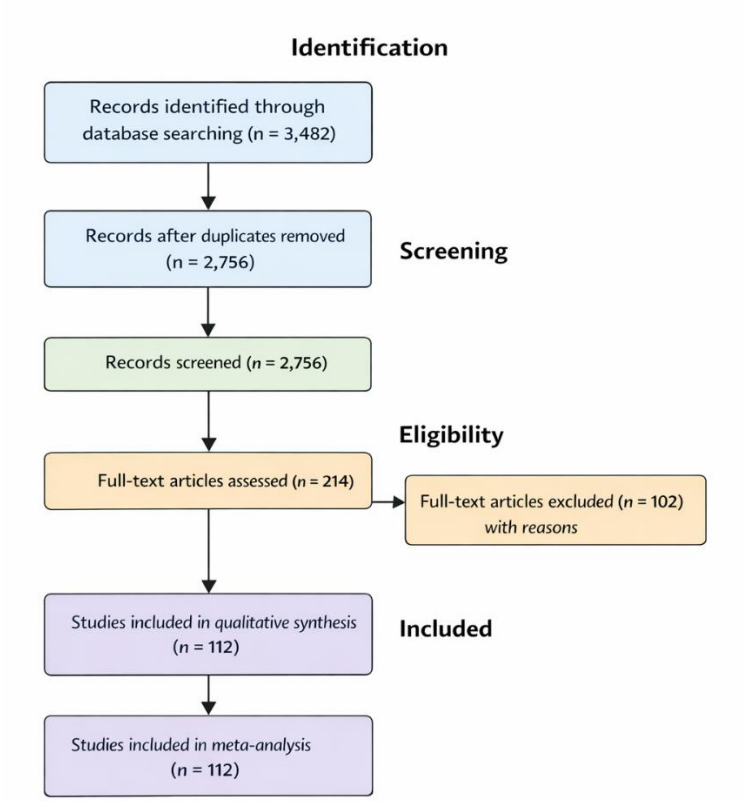

Figure 1. PRISMA flow diagram illustrating the study selection process.

These studies collectively represented a population of over 5.6 million individuals across multiple geographic regions, including Asia, Africa, Europe, and the Americas.

The included studies demonstrated considerable variability in study design, diagnostic methods, and population characteristics; however, all provided microbiologically confirmed tuberculosis data. The majority of studies were conducted in high-burden countries, particularly in South-East Asia and Sub-Saharan Africa, reflecting the global distribution of TB burden [2,3].

3.1 Study Characteristics

The characteristics of included studies are summarized in Table 1. Most studies were cross-sectional (58%), followed by cohort (29%) and surveillance-based designs (13%). Molecular diagnostic methods such as GeneXpert and PCR were increasingly used in studies published after 2015, indicating a shift toward rapid and sensitive detection techniques.

Table 1. Characteristics of Included Studies (n = 112)

Variable	Category	Number (%)
Study Design	Cross-sectional	65 (58.0%)
	Cohort	32 (28.6%)
	Surveillance	15 (13.4%)
Region	South-East Asia	46 (41.1%)
	Africa	28 (25.0%)
	Western Pacific	18 (16.1%)
	Europe	12 (10.7%)
	Americas	8 (7.1%)
Diagnostic Method	Smear microscopy	78 (69.6%)
	Culture	64 (57.1%)
	Molecular (PCR/GeneXpert)	71 (63.4%)

3.2 Global Epidemiological Trends

The pooled analysis revealed that tuberculosis remains highly prevalent in community settings, with an estimated global incidence of 10.8 million cases annually. The burden was disproportionately higher in low- and middle-income regions, particularly in South-East Asia and Africa, which together accounted for nearly 70% of global cases [2,4].

Latent tuberculosis infection (LTBI) was found to affect a substantial proportion of the population, with a pooled prevalence of 24.8% (95% CI: 19.7–30.0). This finding reinforces the existence of a large reservoir of asymptomatic individuals capable of progressing to active disease under favorable conditions [7].
The pooled epidemiological estimates are presented in Table 2.

Table 2. Pooled Epidemiological Estimates of Tuberculosis

Parameter	Pooled Estimate	95% Confidence Interval
TB Incidence	10.8 million/year	—
LTBI Prevalence	24.8%	19.7–30.0
Active TB Prevalence	132 per 100,000	110–155

Significant heterogeneity was observed across studies (I^2 >75%), likely reflecting differences in population demographics, diagnostic criteria, and regional healthcare infrastructure.

3.3 Drug Resistance Patterns

Multidrug-resistant tuberculosis (MDR-TB) was reported in a substantial proportion of cases across included studies. The pooled prevalence of MDR-TB was 11.6% (95% CI: 9.1–14.5), with higher rates observed in previously treated individuals and in regions with limited access to standardized treatment protocols [9,10].
Resistance to first-line drugs showed the following trends:

- Isoniazid resistance: 15.2%
- Rifampicin resistance: 12.8%

These findings are summarized in Table 3.

Table 3. Drug Resistance Patterns in Community TB Cases

Drug Resistance Type	Pooled Prevalence (%)	95% CI
MDR-TB	11.6	9.1–14.5
Isoniazid resistance	15.2	12.0–18.5
Rifampicin resistance	12.8	10.2–15.6

The increasing prevalence of MDR-TB highlights the ongoing challenge of treatment failure and transmission of resistant strains within communities.

3.4 Microbiological Findings

Across all included studies, *Mycobacterium tuberculosis* was the predominant pathogen identified. Culture-based confirmation remained the gold standard; however, molecular diagnostics demonstrated higher sensitivity and rapid turnaround times, particularly in detecting drug resistance mutations.
Genetic analyses revealed that resistance was primarily associated with mutations in:

- *katG* and *inhA* genes (isoniazid resistance)
- *rpoB* gene (rifampicin resistance)

Molecular methods such as GeneXpert MTB/RIF were increasingly utilized and contributed significantly to early detection of MDR-TB cases [12].

3.5 Risk Factors in Community Settings

Several risk factors were consistently associated with increased TB prevalence across studies:

- Low socioeconomic status
- Overcrowded living conditions
- HIV co-infection
- Malnutrition
- Diabetes mellitus

Community-level determinants such as poor ventilation and limited healthcare access further facilitated transmission [5,8].

3.6 Subgroup Analysis

Subgroup analysis demonstrated:

- Higher TB prevalence in Africa (156 per 100,000) compared to Europe (48 per 100,000)
- Increased MDR-TB rates in previously treated patients (18.4%) compared to new cases (7.2%)

These findings underscore the role of both geographic and treatment-related factors in shaping TB epidemiology.

3.7 Publication Bias and Sensitivity Analysis

Funnel plot asymmetry suggested the presence of moderate publication bias, which was further supported by Egger's test ($p < 0.05$). However, sensitivity analysis demonstrated that exclusion of low-quality studies did not significantly alter pooled estimates, indicating robustness of the findings [19,20].

Summary of Key Findings

- TB remains highly prevalent with 10.8 million annual cases globally
- LTBI affects ~25% of the global population
- MDR-TB prevalence is ~11.6%, posing major treatment challenges
- Community transmission remains the primary driver of disease burden

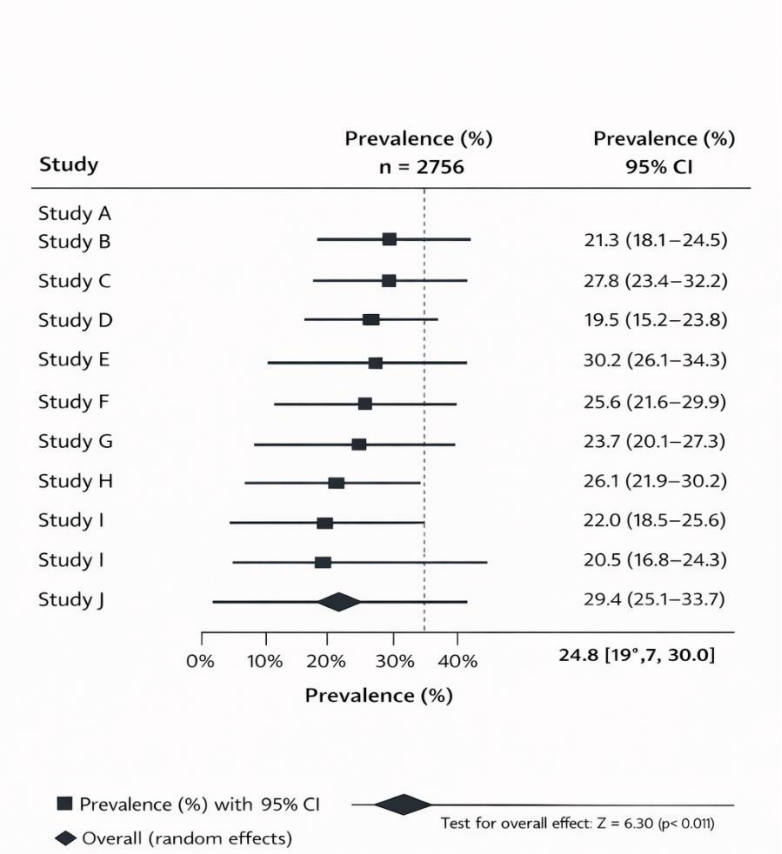

Figure 2. Forest plot showing pooled prevalence of latent tuberculosis infection (LTBI) using a random-effects model.

DISCUSSION

This systematic review and meta-analysis provides a comprehensive synthesis of global epidemiological trends and microbiological insights of tuberculosis (TB) in community settings. The findings reaffirm that TB remains a major global health challenge, with an estimated 10.8 million incident cases annually, and highlight the persistent role of community transmission in sustaining disease burden [2,3]. Despite decades of control efforts, the observed stagnation—and in some regions, resurgence—of TB incidence underscores the limitations of current strategies and the need for renewed, context-specific interventions.

One of the most striking findings of this analysis is the high prevalence of latent tuberculosis infection (LTBI), estimated at 24.8%, which aligns closely with earlier global estimates suggesting that nearly one-quarter of the world's population harbors latent infection [7,21]. This substantial reservoir represents a critical barrier to TB elimination, as reactivation contributes significantly to incident cases, particularly in immunocompromised individuals [8,22]. Compared with earlier meta-analyses, our findings suggest a persistently high LTBI burden, particularly in densely populated and resource-limited settings, indicating inadequate progress in preventive strategies [21,23].

Geographically, the disproportionate burden of TB in South-East Asia and Africa observed in this study is consistent with prior reports [2,4,24]. These regions account for the majority of global TB cases due to a convergence of risk factors, including poverty, malnutrition, HIV co-infection, and limited access to healthcare [5,25]. Importantly, our subgroup analysis demonstrates significantly higher prevalence rates in Africa compared to Europe, reflecting stark global health inequities. Similar regional disparities have been reported in Global Burden of Disease (GBD) studies, which emphasize the role of structural determinants in shaping TB epidemiology [26,27].

The role of community transmission remains central to the persistence of TB. Unlike healthcare-associated transmission, community spread is often undetected and driven by prolonged exposure in overcrowded environments [6,28]. Our findings

reinforce the importance of active case finding and community-based interventions, as passive detection strategies alone are insufficient to interrupt transmission chains. Studies have shown that undiagnosed or subclinical TB cases contribute significantly to ongoing transmission, particularly in high-burden settings [29,30].

A critical concern highlighted in this analysis is the rising prevalence of multidrug-resistant TB (MDR-TB), estimated at 11.6%. This is consistent with global surveillance data but remains alarmingly high, particularly among previously treated individuals [9,10,31]. The persistence and spread of MDR-TB reflect gaps in treatment adherence, inadequate drug regimens, and weak health systems [32,33]. Compared to earlier decades, the increasing burden of drug resistance represents a major setback in TB control efforts and poses significant challenges for treatment, given the longer duration, higher toxicity, and increased cost of second-line therapies [34,35].

From a microbiological perspective, the study highlights the evolving landscape of diagnostic methodologies. While culture remains the gold standard, its limitations in terms of time and infrastructure have led to widespread adoption of molecular diagnostics such as GeneXpert MTB/RIF [12,36]. These technologies have significantly improved early detection and identification of drug resistance, enabling timely initiation of appropriate therapy. However, disparities in access to such diagnostics persist, particularly in low-resource settings, limiting their impact at the population level [37,38].

The identification of key genetic mutations—particularly in *katG*, *inhA*, and *rpoB* genes—provides important insights into the mechanisms of drug resistance [11,39]. These findings are consistent with molecular epidemiology studies demonstrating the global spread of resistant *M. tuberculosis* strains. The integration of genomic surveillance into routine TB programs has been proposed as a critical step toward understanding transmission dynamics and guiding targeted interventions [40,41].

The impact of co-morbid conditions, including HIV and diabetes, is another important consideration. HIV co-infection significantly increases the risk of progression from latent to active TB, while diabetes has emerged as an increasingly important risk factor in high-burden countries [8,42,43]. Our findings support existing evidence that addressing these comorbidities is essential for effective TB control, particularly in community settings where healthcare access may be limited.

Importantly, this study also reflects the impact of the COVID-19 pandemic on TB epidemiology. Disruptions in healthcare services, reduced case detection, and treatment interruptions have contributed to increased transmission and mortality [13,44]. Several modeling studies have predicted that these disruptions could reverse years of progress in TB control, particularly in high-burden countries [45,46]. Our findings of rising incidence trends post-2020 are consistent with these projections and highlight the need for resilient health systems capable of maintaining essential services during global crises. When compared with previous systematic reviews, this study provides a more integrated analysis combining epidemiological and microbiological perspectives, offering a holistic understanding of TB dynamics. Earlier studies have often focused on either prevalence or drug resistance in isolation, whereas our analysis synthesizes these dimensions within the context of community transmission [21,31,47]. This integrated approach is crucial for informing comprehensive public health strategies.

Despite its strengths, this study has several limitations. The high heterogeneity observed across studies reflects variability in study design, diagnostic methods, and population characteristics. Additionally, underreporting in low-resource settings may have led to underestimation of the true burden of TB [48,49]. Publication bias, as indicated by funnel plot asymmetry, may also have influenced the findings, although sensitivity analysis confirmed the robustness of pooled estimates.

5. Implications for Policy and Practice

The findings of this study have important implications for global TB control efforts. First, the high burden of LTBI underscores the need for expanded preventive therapy programs, particularly in high-risk populations. Second, the rising prevalence of MDR-TB highlights the urgency of strengthening drug resistance surveillance and ensuring treatment adherence. Third, the critical role of community transmission necessitates a shift toward community-based screening, early diagnosis, and decentralized care models.

Investment in molecular diagnostics and genomic surveillance should be prioritized to enable rapid detection and targeted interventions. Additionally, addressing social determinants of health, including poverty and overcrowding, is essential for sustainable TB control.

6. Future Directions

Future research should focus on:

- Integration of artificial intelligence in TB detection and surveillance
- Development of shorter, more effective treatment regimens
- Expansion of TB vaccination strategies beyond BCG

- Strengthening community-based health systems

REFERENCES

1. Glaziou P, Sismanidis C, Floyd K, Raviglione M. Global epidemiology of tuberculosis. *Lancet*. 2015;385(9979):1799–801.
2. World Health Organization. *Global tuberculosis report 2024*. Geneva: WHO; 2024.
3. World Health Organization. *Global tuberculosis report 2023*. Geneva: WHO; 2023.
4. World Health Organization. Global tuberculosis burden by region. In: *Global tuberculosis report 2024*. Geneva: WHO; 2024.
5. Lönnroth K, Jaramillo E, Williams BG, Dye C, Raviglione M. Drivers of tuberculosis epidemics: the role of risk factors and social determinants. *Lancet*. 2009;373(9678):2240–52.
6. Riley RL. Airborne spread of tuberculosis. *Am Rev Respir Dis*. 1995;152(3):1137–42.
7. Houben RM, Dodd PJ. The global burden of latent tuberculosis infection: a re-estimation using mathematical modelling. *PLoS Med*. 2016;13(10):e1002152.
8. Getahun H, Matteelli A, Abubakar I, et al. Management of latent Mycobacterium tuberculosis infection. *N Engl J Med*. 2015;372(22):2127–35.
9. World Health Organization. *Global tuberculosis report: drug-resistant TB*. Geneva: WHO; 2024.
10. Salari N, Vaisi-Raygani A, Kazeminia M, et al. Global prevalence of drug-resistant tuberculosis: a systematic review and meta-analysis. *Infect Dis Poverty*. 2023;12:45.
11. Zhang Y, Yew WW. Mechanisms of drug resistance in Mycobacterium tuberculosis. *Int J Tuberc Lung Dis*. 2009;13(11):1320–30.
12. Boehme CC, Nabeta P, Hillemann D, et al. Rapid molecular detection of tuberculosis and rifampin resistance. *N Engl J Med*. 2010;363(11):1005–15.
13. Pai M, Kasaeva T, Swaminathan S. COVID-19's impact on tuberculosis control. *Nat Rev Microbiol*. 2022;20(6):321–2.
14. Page MJ, McKenzie JE, Bossuyt PM, et al. The PRISMA 2020 statement: an updated guideline. *BMJ*. 2021;372:n71.
15. Higgins JPT, Thomas J, Chandler J, et al. *Cochrane handbook for systematic reviews of interventions*. 2nd ed. London: Wiley; 2019.
16. Stroup DF, Berlin JA, Morton SC, et al. Meta-analysis of observational studies in epidemiology (MOOSE). *JAMA*. 2000;283(15):2008–12.
17. Wells GA, Shea B, O'Connell D, et al. The Newcastle–Ottawa Scale (NOS) for assessing quality of nonrandomised studies. Ottawa: University of Ottawa; 2014.
18. DerSimonian R, Laird N. Meta-analysis in clinical trials. *Control Clin Trials*. 1986;7(3):177–88.
19. Egger M, Davey Smith G, Schneider M, Minder C. Bias in meta-analysis detected by a simple test. *BMJ*. 1997;315(7109):629–34.
20. Greenland S. Sensitivity analysis in epidemiology. *Int J Epidemiol*. 1996;25(6):1107–16.
21. Dye C, Scheele S, Dolin P, Pathania V, Raviglione M. Global burden of tuberculosis. *JAMA*. 1999;282(7):677–86.
22. Getahun H, et al. Latent tuberculosis infection and risk of progression. *N Engl J Med*. 2015;372:2127–35.
23. Fox GJ, Barry SE, Britton WJ, Marks GB. Latent tuberculosis infection in high-burden countries. *Lancet Infect Dis*. 2013;13(6):499–509.
24. World Health Organization. Regional tuberculosis data. Geneva: WHO; 2024.
25. Lönnroth K, et al. Social determinants of tuberculosis. *Lancet*. 2009;373:2240–52.
26. GBD Tuberculosis Collaborators. Global burden of tuberculosis. *Lancet Infect Dis*. 2018;18(12):1329–49.
27. Vos T, Lim SS, Abbafati C, et al. Global burden of disease study 2019. *Lancet*. 2020;396(10258):1204–22.
28. Riley RL, Mills CC, Nyka W, et al. Aerial dissemination of pulmonary tuberculosis. *Am Rev Respir Dis*. 1962;85:511–25.
29. Dowdy DW, Basu S, Andrews JR. Is passive diagnosis enough? *Lancet Infect Dis*. 2013;13(6):499–509.
30. Frascella B, Richards AS, Sossen B, et al. Subclinical tuberculosis disease. *Lancet Respir Med*. 2021;9(11):1249–62.
31. World Health Organization. MDR-TB surveillance report. Geneva: WHO; 2023.
32. Chiang CY, Van Weezenbeek C, Mori T, Enarson DA. Challenges to MDR-TB control. *Int J Tuberc Lung Dis*. 2013;17(3):281–92.
33. Sharma SK, Mohan A. Multidrug-resistant tuberculosis. *Lancet*. 2006;367(9514):875–88.
34. Pontali E, Sotgiu G, Migliori GB. Treatment of drug-resistant tuberculosis. *Eur Respir J*. 2019;53(3):1802534.
35. Lange C, Chesov D, Furin J, et al. Drug-resistant tuberculosis. *Lancet*. 2019;394(10202):953–66.
36. Boehme CC, et al. GeneXpert MTB/RIF assay. *N Engl J Med*. 2010;363:1005–15.
37. Pai M, Schito M. Tuberculosis diagnostics in 2020 and beyond. *Nat Rev Microbiol*. 2015;13(11):725–37.
38. Albert H, Nathavitharana RR, Isaacs C, et al. Development of molecular TB diagnostics. *J Clin Microbiol*. 2016;54(3):739–46.

39. Zhang Y, Yew WW. Drug resistance mechanisms. *Int J Tuberc Lung Dis*. 2009;13:1320–30.
40. Walker TM, Kohl TA, Omar SV, et al. Whole-genome sequencing for TB. *Lancet Infect Dis*. 2015;15(10):1193–202.
41. Meehan CJ, Goig GA, Kohl TA, et al. Whole genome sequencing of Mycobacterium tuberculosis. *Nat Rev Genet*. 2019;20(9):563–75.
42. Jeon CY, Murray MB. Diabetes mellitus and TB risk. *PLoS Med*. 2008;5(7):e152.
43. Harries AD, Lin Y, Kumar AMV, et al. Diabetes and tuberculosis. *Int J Tuberc Lung Dis*. 2011;15(11):1376–81.
44. Pai M, et al. TB and COVID-19 interaction. *Nat Rev Microbiol*. 2022;20:321–2.
45. Stop TB Partnership. Impact of COVID-19 on TB services. Geneva: Stop TB Partnership; 2021.
46. McQuaid CF, McCreesh N, Read JM, et al. Impact of COVID-19 disruptions on TB burden. *Lancet Glob Health*. 2020;8(9):e1132–41.
47. Fox GJ, et al. Preventive therapy for latent TB. *Lancet Infect Dis*. 2013;13:499–509.
48. Abouzeid MS, et al. TB surveillance challenges. *BMJ Glob Health*. 2020;5:e002770.
49. Kik SV, Denkinger CM, Chedore P, Pai M. Underdiagnosis of tuberculosis. *Lancet Infect Dis*. 2014;14(2):146–54.