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The Role of Epidemiologic Surveillance in the Control of Drug-Resistant Tuberculosis (TB): A Literature Review

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Abstract: Drug-resistant tuberculosis (DR-TB) poses a serious threat to global public health and is a major barrier to achieving TB elimination targets. Epidemiological surveillance plays a central role in its control, yet its implementation faces various challenges, leading to gaps in detection and response. This literature review aims to synthesize the latest scientific evidence on the role, methods, and challenges of DR-TB surveillance to formulate a comprehensive overview as a basis for program improvement recommendations. A systematic literature search was conducted in PubMed and Google Scholar for articles published between 2015 and 2025. From an initial 347 articles, 6 relevant studies from various countries were selected based on inclusion and exclusion criteria for narrative analysis. The analysis reveals a significant gap between the estimated disease burden and detected cases, with the sensitivity of surveillance systems in some countries (e.g., Brazil) reported as low (~46.4%) and massive diagnostic failures (59% in Madagascar). Strong evidence indicates that active community transmission is a key driver of the epidemic, demonstrated by high primary resistance rates (9% in Bhutan) and the presence of genetic transmission clusters (37% of cases in Pará, Brazil). The studies also highlight the potential of innovative methods such as statistical correction to improve estimation accuracy and genomic surveillance for detecting new drug resistance and mapping transmission. Conventional DR-TB surveillance is no longer adequate to address the current complexity of the epidemic. Future effective control demands a dual approach: strengthening fundamental health systems (diagnostics and logistics) integrated with the adoption of innovative, data-driven surveillance methods such as statistical modeling and genomics for a more accurate, timely, and precise response.

Keywords: Epidemiological Surveillance; Drug-Resistant Tuberculosis; MDR-TB; Disease Control; Literature Review.

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1. Introduction

Tuberculosis (TB) continues to be one of the most persistent global health threats in the modern era. As an infectious disease that ranks among the top causes of death worldwide, TB claimed an estimated 1.3 million lives in 2022 alone, out of 10.6 million people who fell ill. The global commitment to end the epidemic is enshrined in the World Health Organization's "End TB Strategy", which targets a 90% reduction in incidence and 95% reduction in mortality by 2035 [1]. However, achieving these ambitious targets is significantly hampered by an increasingly complex challenge: the emergence and spread of Drug Resistant Tuberculosis (DR-TB).

The threat of DR-TB, particularly in the form of multidrug-resistant (MDR-TB) and extensively drug-resistant (XDR-TB), has fundamentally altered the TB control landscape[2]. MDR-TB, defined as resistance to the two most effective first-line drugs, isoniazid and rifampicin, is not only a clinical problem but also a public health crisis[3]. Treatment requires longer (up to 24 months), more toxic and much more expensive regimens, with global success rates still below 65% (Baum et al., 2024). With an estimated 410,000 new cases of MDR/RR-TB by 2022, DR-TB is a major barrier that could reverse the progress of TB programs and threaten global health security [4].

Epidemiological surveillance serves as a key navigation system for national TB control programs, especially in the face of such a crisis. Its role cannot be underestimated, as an effective surveillance system is the foundation of any measured and targeted public health

response [5]. Fundamentally, the function of epidemiologic surveillance in DR-TB control covers four critical domains: (1) Detection and Monitoring, to measure the magnitude of the problem, monitor resistance trends over time, and detect the emergence of new strains; (2) Resource Allocation and Policy, to direct investments to high-risk geographic areas and populations; (3) Program Evaluation, to assess the impact of interventions such as the use of new drug regimens or changes in diagnostic strategies; and (4) Understanding Transmission, to distinguish between cases of acquired resistance (due to inadequate treatment) and cases of primary resistance (due to direct transmission in the community) [6]. However, despite this ideal framework, the implementation of DR-TB surveillance in various countries shows a significant disconnect between objectives and capabilities in the field. An evaluative study in Brazil, for example, revealed that the national system was only able to detect less than half (46.4%) of estimated MDR-TB cases, indicating a massive hidden burden [7]. Meanwhile, a cascade of care analysis in Madagascar clearly shows that the biggest failure point is at the diagnosis stage, where 59% of MDR-TB patients who have accessed health services failed to be diagnosed correctly, exacerbated by extreme logistical delays [8]. On the other hand, studies in Bhutan and Pará, Brazil, highlighted that high primary transmission in the community is the main driver of the epidemic, a dynamic that is often missed by conventional surveillance systems [9]. This gap, coupled with methodological variations from passive systems to state-of-the-art genomic surveillance creates uncertainty in disease burden estimates and hinders the formulation of effective public health responses.

Given this complex landscape, this literature review was developed to systematically review and synthesize the current scientific evidence on the role, methods, challenges, and innovations in epidemiological surveillance for drug-resistant TB control. By deeply analyzing various surveillance approaches and their findings across different countries, this study aims to formulate a conceptual framework that can guide future improvements in DR-TB control program policies and practices.

2. Proposed Method

This study used a literature review method to review and synthesize information from various scientific sources on the role of epidemiological surveillance in drug-resistant tuberculosis (TB) control efforts. This approach allowed for an in-depth analysis of existing studies to gain a comprehensive overview of the topic.

Article Search and Selection Strategy

A systematic literature search was conducted in June 2025 through two major electronic databases, PubMed and Google Scholar. The search process used a combination of specific keywords with the formula: ("epidemiological surveillance" OR "disease surveillance") AND ("drug-resistant tuberculosis" OR "MDR-TB" OR "XDR-TB") AND ("control" OR "prevention"). The article selection process followed the steps adapted from the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) flow chart. In the identification stage, an initial search of the PubMed and Google Scholar databases yielded 19 and 328 articles, respectively, for a total of 347 articles. Next, at the screening stage, the articles were evaluated based on title, abstract, and duplication. Articles that were not relevant to the topic or were duplicates were excluded. Next, at the eligibility stage, the remaining articles were examined in their entirety (full text) based on predefined inclusion and exclusion criteria. Inclusion criteria included original research or review articles that addressed the role of epidemiologic surveillance in controlling drug-resistant TB, published between 2015-2025, and available in full-text format. After going through all these selection stages, at the final stage (included), 6 articles were obtained that were considered to meet the criteria for further analysis.

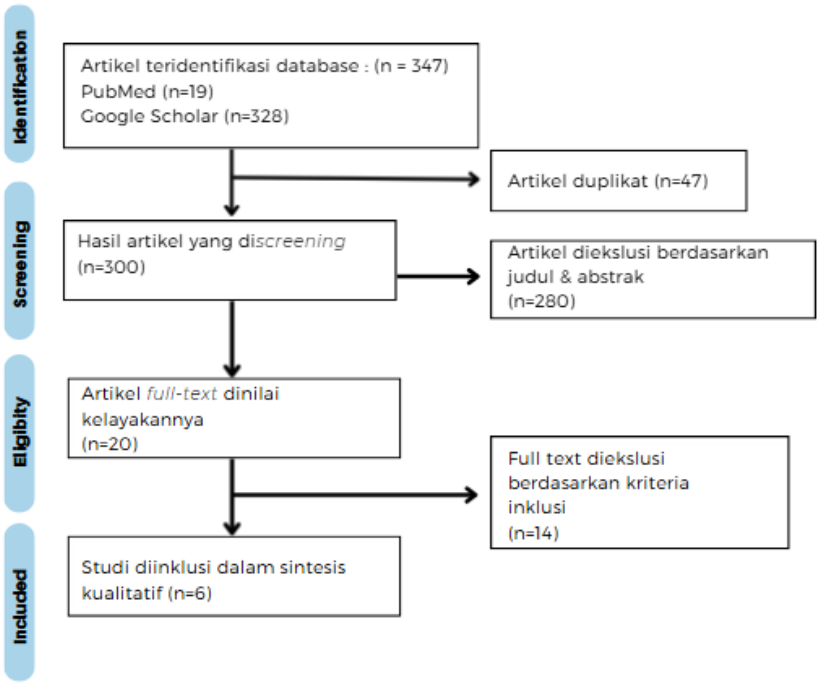

Figure 1. Flowchart of Search

Data Extraction and Analysis

From the six selected articles, a systematic data extraction process was carried out, which included the author's name, year of publication, study design, research location, and main findings. The collected data were then synthesized and analyzed descriptively to answer the research objectives.

3. Results and Discussion

Table 1. Summary of Epidemiologic Surveillance Studies on Drug-Resistant TB (2015-2025)

No.	Author (Year)	Study Title	Study Design	Location & Population	Surveillance Method	Main Findings	Conclusion & Relevance
1	Sarah E. Baum, *et al.* (2024) [4]	*Surveillance For TB Drug Resistance Using Routine Rapid Diagnostic Testing Data: Methodological Development and Application in Brazil*	Methodological development study applying a statistical correction model (*hierarchical generalized additive regression model*) to individual-level TB case data in Brazil from 2017-2023.	Brazil; more than 800,000 reported TB cases, categorized into new and treated cases.	Propose a new surveillance method that uses routine rapid diagnostic test (RDT) data that is not universal in coverage. This method corrects for selection bias by: (1) modeling the probability of resistance in tested patients, and (2) using the model results to impute (estimate) the resistance	The corrected prevalence estimates of rifampicin resistance were statistically higher (28-44% for new cases, 2-17% for old cases) than the naive estimates (directly from RDT data), suggesting that RDT testing is more common in populations with lower risk of resistance, so the naive estimates underestimate the true burden of resistance; This method produces estimates with narrower *uncertainty*	This statistical correction method can be generally used to utilize routine RDT data to produce more accurate and timely estimates of drug-resistant TB prevalence. It is particularly relevant for countries where drug resistance testing coverage is not yet universal, allowing them to get a better picture of the epidemiology without having to wait for expensive and infrequent national prevalence surveys.

					status in untested patients.	*intervals* than the WHO estimates ; There was a downward trend in rifampicin-resistant cases between 2017-2023 for both new and treated cases.	
2	Mei-Hua Wu, *et al.* (2022) [10]	*Surveillance Of Multidrug-Resistant Tuberculosis In Taiwan, 2008-2019*	Population-based retrospective study analyzing reported MDR-TB case data from 2008 to 2019.	Taiwan; 1,511 MDR-TB cases, consisting of 941 new cases and 485 previously treated cases.	Population-based continuous surveillance system. Includes universal Drug Sensitization Testing (DST) for almost all culture-positive TB cases (98.5%), with confirmation by the *National Reference Laboratory* (NRL). Data were collected from various national registry systems.	There was a significant decline in total MDR-TB cases from 2008-2019, with an annualized rate of decline (APC) of -4.17%; the steepest decline was in previously treated cases (APC -9.18%), while the decline in new cases was slower (APC -1.41%); among MDR-TB patients, resistance to other drugs remains high: Ethambutol (47.2%), Streptomycin (42.4%), and Pyrazinamide (28.9%); There is a downward trend in resistance to some second-line drugs, especially to injectable drugs (SLIDs) in new cases and fluoroquinolones in previously treated cases; The XDR-TB rate is relatively low (1.9%).	The MDR-TB management program in Taiwan is considered effective, as indicated by the overall downward trend in cases. However, the slow decline in new cases remains a challenge. It shows the success of structured program interventions (such as DOTS-Plus and universal DST). These surveillance results are important for guiding drug procurement policies, updating treatment regimens, and designing diagnostic algorithms to achieve TB elimination.
3	Knoblauch, A.M., Grandjean Lapierre, S., Randriamanana, D., *et al.* (2020) [7]	*Multidrug-Resistant Tuberculosis Surveillance And Cascade Of Care In*	This study was a retrospective review that analyzed data from the	Madagascar; The main population in this study were "*presumptive*	Passive & active surveillance; national NTP & lab data.	59% of MDR-TB patients who reached health centers failed to be accurately diagnosed; in 2017, only	The study concludes that it is urgent to expand coverage and strengthen diagnostic and management capacity for MDR-TB

		Madagascar: A Five-Year (2012-2017) Retrospective Study	tuberculosis (TB) control program in Madagascar over a five-year period, from September 2012 to December 2017. We collected and analyzed notification data from the national TB control program, clinical management data, and data from the national reference laboratory.	*MDR-TB cases*". A total of 2,391 samples from presumptive MDR-TB patients referred to the national reference laboratory between 2012-2017 were analyzed in this study.		about one-third (32.7%) of cases that should have been screened were actually referred; Only 75% of diagnosed patients successfully started treatment, and in the end, only 33% achieved a long-term relapse-free cure; Among the high-risk groups tested, the MDR-TB rate was relatively stable, ranging from 3.9% to 4.4% during the study period.	throughout Madagascar. Current surveillance data likely underestimates the true burden of MDR-TB in the country, so the implementation of a new national drug resistance survey is highly recommended to obtain accurate prevalence data. Relevantly, this study provides clear evidence of weaknesses in the health system that directly impact disease control. Using a cascade of care approach and GIS, the study effectively identified critical points that require intervention, such as increased access to rapid diagnosis (e.g. GeneXpert), improved logistical referral systems, and strengthened treatment monitoring. These findings are not only important for Madagascar but can also serve as lessons for other resource-limited countries facing similar challenges in MDR-TB control.
4	Tourinho *et al.* (2020) [9]	*Evaluation of the Drug-Resistant Tuberculosis Surveillance System, Brazil, 2013-2017*	Descriptive evaluative study based on data for the period 2013-2017, using guidelines from the *Centers for Disease Control and Prevention* (CDC).	Brazil; 6,078 Drug-Resistant Tuberculosis (DRTB) cases reported to the SITETB information system.	A passive and universal surveillance system that uses two information systems: SINAN (for initial notification of all TB cases) and SITETB (an *online*	The data quality of the systems was rated as very good (average completeness of 95%); The sensitivity of the system was low, detecting only about 46.4% of the WHO estimated MDR-TB cases; The flexibility,	While the system is useful, its low sensitivity suggests significant gaps in case detection. Improved access to DRTB diagnosis is urgently needed. The results of this evaluation provide strong evidence for health program managers in Brazil to improve *case*

					system specialized for cases diagnosed as drug-resistant).	acceptability, timeliness, and stability of the system were rated as "moderate"; Compliance for follow-up sputum culture testing declined dramatically with time on treatment (from 94.8% on the first culture to 43.6% on the fourth culture).	*detection,* strengthen laboratory networks, and simplify surveillance system workflows.
5	Thinley Dorji, *et al.* (2024) [5]	*High Incidence Of Multidrug-Resistant Tuberculosis In Bhutan: A Cohort Study Based On National TB Surveillance Data*	Retrospective cohort study using national surveillance data from 2018-2021 to analyze resistance patterns and identify risk factors using logistic regression.	Location : Bhutan, Population: 2,290 samples from TB cases tested for drug resistance between 2018-2021.	Based on data from the national surveillance system (TBISS). Initial diagnosis using microscopy and Xpert MTB/RIF. Samples were then sent centrally to the *National Tuberculosis Reference Laboratory* (NTRL) for genotypic (MTBDRplus) and phenotypic (pDST) testing.	The incidence of MDR-TB was high (10.6%), while Isoniazid resistance (HR-TB) was lower (3.5%), in contrast to patterns in neighboring countries; Significant risk factors for MDR/pre-XDR-TB were age 18-39 years, female gender, and previous TB treatment history; Distribution of cases was uneven, with the highest incidence in Thimphu, Samtse, and Sarpang districts; The proportion of primary MDR-TB (9%) was higher than the global average, suggesting the possibility of active transmission in the community; There was a significant diagnostic gap, with only about half of the samples successfully tested for resistance due to logistical challenges.	Bhutan has a high and uneven incidence of MDR-TB. There is a need to decentralize diagnostic facilities to areas with high case load to expedite diagnosis and close monitoring of at-risk groups. This study has the relevance of providing the first comprehensive national data on the burden and risk factors of DR-TB in Bhutan, which is crucial for policy making, intervention planning, and strengthening the national TB control program.

6	Davi Josué Marcon, *et al.* [8]	*Comprehensive Genomic Surveillance Reveals Transmission Profiles of Extensively Drug-resistant Tuberculosis Cases in Para, Brazil*	Retrospective *cross-sectional* observational study using *Whole-Genome Sequencing* (WGS) for genomic analysis	Location: Pará state, Brazil. Population: 103 patients treated for Drug Resistant TB (DR-TB) between October 2021 - December 2022, with 40 isolates randomly selected for WGS analysis.	Using genomic surveillance by performing *Whole-Genome Sequencing* (WGS) on bacterial isolates from DR-TB patients. WGS results were compared with existing *Standard of Care* (SOC) diagnostic results (such as Xpert and pDST) for resistance and transmission analysis.	First report on detection and transmission of XDR-TB in Pará, Brazil, based on 2021 WHO definition; WGS identified a complex resistance profile: MDR (52%), pre-XDR (20%), and XDR (7%); Evidence of active transmission was found (37% of cases were in genetic clusters), including clusters of pre-XDR and XDR strains; WGS successfully detected mutations related to resistance to a new drug (Bedaquiline), which were not detected by standard methods; There was a significant discrepancy (41%) between WGS results and standard diagnostic methods, largely due to not testing for second-line drugs.	Genomic surveillance (WGS) is essential to detect and monitor the emergence and transmission of DR-TB strains, including XDR-TB. There are critical gaps in existing standardized diagnostic protocols. This has prompted the implementation of WGS as a routine tool in TB surveillance in Brazil to speed up diagnosis, understand transmission patterns, detect resistance to new drugs, and guide more effective public health interventions.

Discussion

A comparative analysis of six drug-resistant tuberculosis (DR-TB) surveillance studies from different countries highlights a complex and challenging picture of global TB control efforts. The review systematically revealed significant gaps between estimated disease burden and detected cases, the importance of understanding local transmission patterns, and the urgency to adopt more sophisticated and integrated surveillance methods. Despite programmatic successes in some regions such as Taiwan, studies from Brazil, Madagascar, and Bhutan collectively demonstrate that surveillance systems in many high TB burden countries still struggle to achieve adequate sensitivity and timeliness.

One of the most consistent and alarming findings of this review is the low sensitivity of conventional surveillance systems in detecting DR-TB cases. An evaluative study in Brazil by Tourinho et al. (2020) quantitatively showed that the national surveillance system was only able to detect about 46.4% of the estimated MDR-TB cases estimated by WHO. This low sensitivity indicates that a large proportion of drug-resistant cases in the population are likely to go undiagnosed, untreated, and potentially continue to transmit the disease [9]. This problem was further detailed by a case study from Madagascar, Knoblauch et al. (2020), which used a cascade of care approach. The study identified that the biggest "gap" in the flow of care occurred at the diagnosis stage, where 59% of MDR-TB patients who had reached a

health facility failed to be accurately diagnosed. Logistical delays, with an average of 28 days from sample collection to testing, further exacerbated this situation and contributed to poor treatment outcomes, with only 33% of patients achieving a long-term cure [7].

Facing the challenge of bias due to non-universal test coverage, a methodological study by Baum et al. (2024) in Brazil offers an innovative solution. By applying a statistical correction model, they showed that the true estimated prevalence of rifampicin resistance was 28-44% higher in new cases and 2-17% higher in previously treated cases compared to naive estimates from existing rapid diagnostic test (RDT) data. These findings unequivocally confirm that the current system underestimates the burden of DR-TB due to test selection bias more often in populations with lower risk of resistance. This underscores the importance of not only expanding test coverage but also applying sophisticated analytical methods to interpret incomplete surveillance data, an approach that is particularly relevant for many low- and middle-income countries [4].

Understanding the source of DR-TB cases whether due to treatment failure (secondary resistance) or direct transmission in the community (primary resistance) is key to designing effective interventions. A cohort study from Bhutan by Dorji et al. (2024) provides worrying evidence, where the proportion of primary MDR-TB (in new cases) reached 9%, which is much higher than the global average. This indicates that active transmission of MDR-TB strains in the community is a major driver of the epidemic in Bhutan, not just individual treatment failure. This high proportion of primary MDR-TB also makes the epidemic pattern in Bhutan (10.6% MDR-TB vs 3.5% HR-TB) unique when compared to neighboring countries such as India and Thailand, where Isoniazid resistance (HR-TB) is predominant [5]. This suspicion of community transmission was further confirmed by a genomic surveillance study in Pará, Brazil Marcon et al., (2024) using Whole-Genome Sequencing (WGS), this study definitively identified that 37% of the analyzed cases were part of a genetic transmission cluster, including the spread of pre-XDR and XDR-TB strains. WGS not only proved the existence of active transmission but also revealed the evolution of a locally endemic strain (SIT 2517) that had evolved into pre-XDR. These findings provide strong molecular evidence that DR-TB control must shift from a reactive approach (treating the resistant) to a proactive one (breaking the chain of transmission) [8].

The evolution of surveillance methods is another important theme in this review. Wu et al. (2023), Taiwan, represents the gold standard with a continuous surveillance system that includes universal Drug Sensitization Testing (DST) for 98.5% of culture-positive cases, which has proven effective in significantly reducing MDR-TB cases. However, in countries where resources are limited, innovative approaches are crucial. The study by Marcon et al. (2024) demonstrated the power of WGS as a superior surveillance tool, which was able to detect resistance to new drugs such as Bedaquiline missed by standard methods, as well as identify diagnostic discrepancies of up to 41%. Meanwhile, the statistical correction method by Baum et al. (2024) shows how existing RDT data can be utilized to produce more accurate estimates, even when test coverage is not ideal. This suggests that there is a spectrum of solutions that can be applied, ranging from basic system strengthening to the adoption of cutting-edge genomic technologies.

The implications of these findings for public health policy are clear. First, closing diagnostic gaps is a top priority. Recommendations from the study in Madagascar to strengthen capacity and the study in Bhutan to decentralize diagnostic facilities to high-burden areas should be addressed. Second, the adoption of more advanced technologies should no longer be considered a luxury, but rather a necessity. WGS, as demonstrated in Pará, provides insights that cannot be obtained from other methods and is crucial for dealing with XDR strains and resistance to new drugs. Third, the focus of control programs must expand to include breaking the chain of transmission in communities, given the strong evidence of primary resistance transmission in Bhutan and Brazil. This means more aggressive contact investigations and possibly active screening in high-risk populations. Fourth, integration of information systems, as successfully implemented in Taiwan and a challenge in Brazil, is the foundation for effective surveillance and accurate program evaluation.

This review certainly has limitations. The studies analyzed come from different geographical contexts and timescales, with varying health systems and disease burdens, so direct comparisons should be made with caution. The diverse methodologies ranging from retrospective cohort studies, system evaluations, to the development of statistical methods and genomic surveillance present different puzzle pieces of the same problem, rather than a single complete picture. Reliance on routine surveillance data also carries inherent risks regarding data quality and completeness, a limitation recognized in some of the studies themselves.

Taken together, these six studies collectively confirm that DR-TB surveillance is at a crossroads. On the one hand, there are mature systems that are successfully curbing the epidemic. On the other hand, many countries still face a hidden burden of disease that continues to spread in communities. Future progress will not come from a single solution, but rather from a dual approach: strengthening the foundations of conventional surveillance systems as outlined in the Madagascar study and the Brazil evaluation, while strategically adopting innovations such as genomic surveillance and advanced statistical methods to make TB control programs more sensitive, accurate, and responsive to the evolving DR-TB threat.

4. Conclusions

A comprehensive review of various drug-resistant tuberculosis (DR-TB) surveillance systems around the world confirms a crucial paradigm shift. DR-TB control can no longer rely solely on passive approaches and treatment of detected cases. Evidence from Brazil, Madagascar, and Bhutan consistently suggests a much larger disease burden than reported with massive diagnostic gaps and low system sensitivity being major barriers. Furthermore, genomic and epidemiologic analyses in Pará (Brazil) and Bhutan revealed that active transmission in the community rather than treatment failure is the main driver of the DR-TB epidemic, including for pre-XDR and XDR strains. Therefore, the future of effective DR-TB surveillance lies in the integration of two main pillars. First, fundamental strengthening of public health systems, including decentralization of diagnostics, accelerated sample logistics, and enhanced contact investigation capacity, as is urgently needed in Madagascar and Bhutan. Second, the adoption of smarter and more accurate innovative surveillance methods. The use of statistical correction models for incomplete data, as applied in Brazil, and the implementation of genomic surveillance as a routine tool not just for research have proven to be able to provide a truer picture of epidemiology, detect new drug resistance, and map the chain of transmission with precision. Only by marrying conventional system strengthening with data-driven innovation can TB control programs move from merely managing the epidemic to actually having a chance to eliminate it according to global targets.

Based on the synthesis of findings from various TB control program contexts, several strategic suggestions and recommendations can be formulated to strengthen DR-TB surveillance systems and accelerate global elimination efforts. These recommendations are designed to address identified gaps, ranging from the fundamental level to the application of cutting-edge technologies.

1. Strengthening Diagnostic Capacity at the Primary Care Level.
   Expanding access to rapid diagnostic tests (RDTs) such as GeneXpert and decentralizing culture and Drug Sensitivity Testing (DST) facilities to regional or district levels should be a priority. This is crucial to address massive diagnostic gaps such as those identified in Madagascar (59% of MDR-TB cases missed) and Bhutan, where logistical challenges impede timely testing.
2. Adoption of Statistical Correction Methods for Disease Burden Estimation.
   For countries with non-universal coverage of drug resistance testing, National TB Programs (NTPs) are recommended to adopt statistical correction models on existing routine RDT data to generate more accurate DR-TB prevalence estimates. As demonstrated in Brazil, this method corrects for selection bias and reveals a higher disease burden than initially estimated, allowing for more targeted resource allocation without having to wait for a national survey.
3. Programmatic Implementation of Genomic Surveillance.
   Genomic surveillance (Whole-Genome Sequencing/WGS) should begin to be integrated as a routine public health tool, especially in DR-TB hotspot areas or in high-risk cases. Utilization of WGS has proven to be very effective for: (a) map transmission clusters in real-time, (b) detect early resistance to new drugs (such as Bedaquiline) not covered by standard tests, and (c) identify diagnostic discrepancies for continuous improvement of laboratory workflows, as clearly demonstrated in the study in Pará, Brazil.
4. Increased Focus on Contact Investigation and Breaking the Chain of Transmission. Given the strong evidence of active transmission of DR-TB in communities, as demonstrated by the high incidence of primary resistance in Bhutan and the presence of genetic clusters in Brazil, programs should improve the capacity and quality of contact investigations. Interventions should not only focus on treatment, but also proactively find source cases and break the chain of transmission, a crucial step to reduce the rate of new MDR-TB cases.

5. Development of Integrated Information Systems and Program Evaluation.
Investing in the development of an integrated and digitized health information system is necessary to ensure that patient, laboratory, and treatment data are seamlessly linked. A solid system, as implemented in Taiwan, provides the backbone for accurate data analysis, standardized program performance evaluation, and evidence-based decision-making essential for effective disease control.

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