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**中国大陆学者发表的结核病英文文章摘要**

**（27篇）**

**PubMed Publication date: 2025/9/22---2025/9/28**

**(tuberculosis[Title/Abstract]) AND (English[Language]) AND (China[Affiliation])**

**1. J Infect Dis. 2025 Sep 17:jiaf484. doi: 10.1093/infdis/jiaf484. Online ahead of print.**

Mycobacterium tuberculosis PE\_PGRS62 protein inhibits type I IFN responses to

promote HIV-2 replication by directly interacting with IRF3.

Pan C(1), Xu H(1), Huang M(1), He J(1), Li S(1), Tao X(1), Cao T(1), Zhang G(1).

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Co-infection with Mycobacterium tuberculosis (Mtb) and HIV-2 increased the viral

load of HIV-2. Type I interferons (IFNs) are essential for limiting HIV-2

progression. However, it is unclear whether and how Mtb affects HIV-2

co-infection by regulating type I IFNs. Here, Mtb PE\_PGRS62 protein was

identified as an inhibitor of cGAS-STING-mediated type I IFN expression by

performing functional screens. Ectopic expression of PE\_PGRS62 impaired type I

IFN expression stimulated by cytosolic DNA, while knockout of pe\_pgrs62

potentiated Mtb-induced type I IFN and downstream IFN-stimulated gene. PE\_PGRS62

interacts directly with IRF3 and inhibits the interaction of IRF3 with TBK1 as

well as the binding of IRF3 to the IFNβ promoter. Furthermore, reduced HIV viral

load was observed in pe\_pgrs62 knockout Mtb-infected macrophages compared with

wild type Mtb. These findings reveal an important mechanism by which Mtb

infection promotes HIV-2 immune evasion.

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Infectious Diseases Society of America.

DOI: 10.1093/infdis/jiaf484

PMID: 40974064

**2. J Clin Microbiol. 2025 Sep 19:e0053725. doi: 10.1128/jcm.00537-25. Online ahead of print.**

Transforming tuberculosis diagnosis with clinical metagenomics: progress and

roadblocks.

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Tuberculosis (TB) remains a leading global infectious killer, yet traditional

diagnostic methods are inadequate. Acid-fast staining suffers from low

sensitivity, and mycobacterial culture requires prolonged incubation because of

the slow growth of Mycobacterium tuberculosis. PCR-based molecular assays allow

rapid detection, but their capacity for resistance profiling is limited to a

narrow set of mutations. Metagenomic next-generation sequencing (mNGS) has

emerged as a promising culture-independent tool for TB detection, enabling

broad-spectrum pathogen identification and offering added value in complex

scenarios including extra-pulmonary disease, mixed infections, and infections in

immunocompromised or pediatric populations. Clinical studies indicate that mNGS

achieves moderate to high sensitivity and excellent specificity in the diagnosis

of tuberculosis. However, its diagnostic performance is often constrained by low

mycobacterial read counts, interference from abundant host nucleic acids, and

the inability to distinguish active from latent infection. In addition, the

accuracy of drug resistance prediction using mNGS remains limited, and the World

Health Organization currently endorses targeted NGS as the preferred

sequencing-based approach for resistance profiling. Despite these challenges,

mNGS has facilitated novel diagnostic strategies that combine pathogen detection

with host-response data, thereby broadening its potential clinical utility.

Nevertheless, practical barriers such as high cost, complex laboratory

workflows, and difficulties in data interpretation continue to restrict

widespread adoption in routine practice. Future efforts should prioritize

technical optimization, standardized protocols, and integration with

conventional diagnostics to establish cost-effective and clinically meaningful

roles for mNGS in TB diagnosis and management.

DOI: 10.1128/jcm.00537-25

PMID: 40970697

**3. Arch Microbiol. 2025 Sep 15;207(10):262. doi: 10.1007/s00203-025-04463-4.**

Comparative immunogenicity study of two different types of tuberculosis vaccines

based on a heterologous boosting strategy.

Wang X(1)(2), Wang R(2), Wang J(3), Zhang Z(4), Kong L(2), Xia L(2), Qi Z(2),

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BCG, one of the oldest vaccines in clinical use, has demonstrated

well-documented safety, quality, and efficacy in preventing severe forms of

tuberculosis (TB) in neonates. However, its protective efficacy declines

significantly in adulthood, failing to prevent pulmonary the TB -a major driver

of global TB transmission. To address this limitation, this study systematically

evaluated two novel BCG-boosting strategies: a recombinant subunit protein

vaccine targeting the Rv2074 antigen and a DNA vaccine encoding the same

antigen, both evaluated in murine immunization. Antigen-specific cytokine levels

in splenocyte supernatants and serum antibody titers were quantified by ELISA

after euthanizing mice at 8 weeks (8w) and 16 weeks (16w) post-immunization. The

results indicated that both vaccine types induced robust Th1-type immune

responses in mice. Additionally, antigen-specific T cell cytokine secretion was

analyzed using flow cytometry combined with intracellular cytokine staining.

Experimental data revealed that the BCG + P group exhibited a significant

increase in CD4+ T cells, while the BCG + D group showed a higher proportion of

CD8+ T cells.Long-term immune effects surpassing short-term outcomes in both

groups. These findings suggest that both vaccine types show promise as BCG-based

booster vaccines.

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**4. Bioorg Chem. 2025 Sep 10;165:108981. doi: 10.1016/j.bioorg.2025.108981. Online**

**ahead of print.**

Identification of a potential anti-nontuberculous mycobacterial drug candidate

targeting a mycothiol disulfide reductase.

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The resistance of nontuberculous mycobacteria (NTM) to conventional

anti-tuberculosis drugs and its growing infection rate year by year urgently

require new treatment strategies. Structure-based virtual screening, which can

greatly improve efficiency and reduce costs in the early stage of drug

development, is an indispensable part of modern drug discovery. In this study,

the crystal structure of the mycothiol disulfide reductase from Mycobacterium

abscessus (MabMtr) was determined. Through virtual screening, compound

AK-968/11492032 was identified as a promising candidate capable of fitting well

into the potential MSSM-binding pocket of MabMtr. It was discovered that

AK-968/11492032 and its derivatives (Y6B and Y6C) could produce antimicrobial

effects on the Mycobacterial type strain Mycobacterium smegmatis. Moreover,

microscale thermophoresis analysis was employed to evaluate the high binding

affinity of the compounds to MabMtr. Furthermore, the key residues (S14, I47,

H451) of MabMtr involved in the interaction with AK-968/11492032 were predicted

and confirmed through molecular docking and mutational analysis, MabMtr was

verified as the target for it to exert antibacterial effects through in vitro

enzyme activity and in vivo gene knockout, complementation, and overexpression.

These findings provide a potential development target to develop effective and

specific anti-NTM drugs.

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**5. Microorganisms. 2025 Sep 22;13(9):2216. doi: 10.3390/microorganisms13092216.**

In Vitro Antimicrobial Activity of Contezolid Against Mycobacterium tuberculosis

and Absence of Cross-Resistance with Linezolid.

Wang L(1)(2), Chen J(3), He Y(1)(2), Zheng R(4), Wang J(4), Huang X(4), Sha

W(1)(2)(4), Qin L(4).

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Tuberculosis (TB) persists as a formidable global health threat, especially with

the rising incidence of multidrug-resistant strains. This study aimed to

evaluate the in vitro activity of contezolid, a novel oxazolidinone antibiotic,

against Mycobacterium tuberculosis (Mtb) and assess potential cross-resistance

with linezolid. Thirty-one Mtb clinical isolates (5 susceptible, 8

multidrug-resistant [MDR], 18 pre-extensively drug-resistant [pre-XDR]) were

tested. Minimum inhibitory concentrations (MICs) of contezolid and linezolid

were determined, along with mutation resistance frequencies. Intracellular

replication inhibition in macrophages and whole-genome sequencing of resistant

colonies were assessed. Cytotoxicity was evaluated via luciferase-coupled ATP

assay. The MIC50 and MIC90 values of contezolid were comparable to those of

linezolid. Contezolid induced higher mutation frequencies in 7 isolates. At 12

mg/L, both drugs similarly inhibited intracellular Mtb replication. Whole-genome

sequencing revealed that the mce3R gene was linked to contezolid resistance,

with no cross-resistance observed between two drugs. No significant cytotoxicity

was observed in contezolid-treated mouse peritoneal macrophages (p > 0.05).

Contezolid exhibits anti-Mtb activity, with mce3R potentially associated with

resistance. No cross-resistance with linezolid was found.

DOI: 10.3390/microorganisms13092216

PMID: 41011547

**6. Microorganisms. 2025 Sep 22;13(9):2214. doi: 10.3390/microorganisms13092214.**

Development of a Chemiluminescence Immunoassay for the Serological Diagnosis of

Sheep and Bovine Brucellosis.

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Brucellosis, a zoonotic infection caused by the intracellular pathogen Brucella,

leads to chronic multi-organ damage. Currently, rapid, accurate, and sensitive

diagnostic technologies are crucial for the prevention and control of

brucellosis. This study describes the development of a chemiluminescent

immunoassay (Bru-CLIA) for sheep and bovine brucellosis antibody detection,

utilizing Brucella abortus strain A19 lipopolysaccharide-coated magnetic

particles (LPS-MPs) as the serum antigen and acridinium ester-labeled

recombinant streptococcal protein G (AE-SPG) for signal generation. After

optimizing the assay's parameters, the Bru-CLIA demonstrated a sensitivity of

approximately 1 IU/mL and 2 IU/mL for detecting sheep and bovine brucellosis,

respectively. No cross-reactivity was observed with sera from animals immunized

with Escherichia coli O157:H7, Mycobacterium tuberculosis, Vibrio cholerae,

Legionella, Salmonella, Foot and Mouth Disease virus types O and A, Bovine viral

diarrhea virus, Sheep contagious pleuropneumonia, Goat pox virus, or Peste des

Petits Ruminants virus, indicating strong specificity. The testing of 81 sheep

serum samples and 96 bovine serum samples revealed that Bru-CLIA showed 87.65%

and 93.75% concordance with the ID-VET commercial kits for sheep and bovine

brucellosis detection, respectively. These results demonstrate that Bru-CLIA

offers high specificity, sensitivity, repeatability, and reliability, making it

a viable rapid diagnostic tool for the epidemiological surveillance of

brucellosis.

DOI: 10.3390/microorganisms13092214

PMID: 41011545

**7. J Med Internet Res. 2025 Sep 26;27:e77491. doi: 10.2196/77491.**

Preferences of Patients With Tuberculosis for AI-Assisted Remote Health

Management: Discrete Choice Experiment.

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**BACKGROUND:** Tuberculosis remains a major global public health challenge,

especially in low-resource settings where long-term treatment adherence and

regular follow-up are critical. The integration of artificial intelligence (AI)

into remote health management has the potential to improve care delivery and

patient outcomes. However, evidence on the preferences of patients with

tuberculosis regarding AI-assisted services remains limited.

**OBJECTIVE:** This study aimed to examine the preferences of patients with

tuberculosis for AI-assisted remote health management services in China,

identifying key service characteristics that influence their choices.

**METHODS:** A discrete choice experiment was conducted among 203 patients with

tuberculosis in Hubei province, China. Attributes and levels were identified

through a systematic literature review, qualitative interviews, and expert panel

consultations. The final design included 6 attributes: interaction method,

service provider, service frequency, service content, out-of-pocket cost, and

service integration. Each participant completed 8 choice tasks comparing

hypothetical service options constructed based on these attributes. Preferences

were analyzed using a mixed logit model to account for preference heterogeneity.

Additional subgroup analyses were performed to explore variations in preferences

across sociodemographic characteristics.

**RESULTS:** All 6 attributes significantly influenced patients' preferences (all P

values <.05). Participants strongly favored services involving physician

oversight (P<.001), video-based interactions (P<.001), and comprehensive content

(P<.001), while higher costs were associated with lower acceptance (P<.001).

Subgroup analyses indicated that higher-income patients demonstrated both a

greater willingness to pay and a stronger preference for physician involvement.

Female participants expressed a lower preference for AI-assisted physician-led

services compared to AI-only configurations. Patients with higher educational

attainment also reported lower preferences for physician-involved services.

Age-related differences were not statistically significant. Across all

subgroups, cost remained a critical determinant of service acceptance.

**CONCLUSIONS:** Patients with tuberculosis expressed a clear preference for

high-quality, human-integrated remote health management services, emphasizing

the importance of physician involvement and personalized, interactive care.

These findings suggest that fully AI-driven models may face resistance and that

hybrid models combining AI efficiency with professional oversight are more

acceptable. Policymakers and service designers should prioritize affordability,

provide targeted financial support for populations considered vulnerable, and

invest in digital literacy initiatives to enhance equitable access. This study

provides critical evidence to support the development of AI-assisted

tuberculosis management strategies that align with patient preferences and

improve treatment adherence in low-resource settings.

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Internet Research (https://www.jmir.org), 26.09.2025.

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**8. Ital J Pediatr. 2025 Sep 24;51(1):271. doi: 10.1186/s13052-025-02118-0.**

A clinical prediction model for rapidly differentiating pulmonary tuberculosis

from community acquired pneumonia in children.

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**BACKGROUND:** Due to the non-specific symptoms of pulmonary tuberculosis (PTB) in

children, the diagnosis of PTB in children is a major challenge for clinicians

in the absence of microbiological confirmation. This study aims to construct a

simple clinical prediction model for empiric diagnosis of PTB through careful

clinical symptoms and medical history.

**METHODS:** Retrospective analysis of clinical data and laboratory data of children

with PTB and community acquired pneumonia (CAP) diagnosed at Tianjin Children's

Hospital from January 2018 to October 2023. All patients were randomly divided

into a 7:3 ratio into a modeling group and a validation group. The modeling

group was used to perform logistic analysis to identify independent risk factors

and construct a clinical prediction model for PTB in children. The validation

group was used to further assess the clinical efficacy of the model.

**RESULTS:** A total of 434 children were included in this study. The modeling group

included 305 patients (125 with PTB, 180 with CAP) and validation group included

129 patients (53 with PTB, 76 with CAP). Four variables including basic disease,

tuberculosis contact history, maximum body temperature and weight loss were

identified as potential predictors used for developing a nomogram. The nomogram

showed a good diagnostic performance in the modeling group [area under the curve

(AUC) (95% confidence interval (CI)), 0.810(0.759 ~ 0.860)]. The decision curve

analysis (DCA) and calibration curve indicated that the clinical prediction

model for pediatric PTB has good clinical practicality and accuracy. The

validation group also showed good clinical efficacy [AUC (95%CI),

0.864(0.794 ~ 0.934)], indicating that the model is feasible and reproducible.

**CONCLUSIONS:** This study developed and validated a nomogram for predicting PTB in

children. This nomogram represents good clinical performance and might be

utilized clinically in the empirical diagnosis of PTB in children.

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**9. BMC Public Health. 2025 Sep 24;25(1):3102. doi: 10.1186/s12889-025-24421-5.**

Beyond additive effects: examining the combined impact of air pollutant

interactions on pulmonary tuberculosis in China.

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**BACKGROUND:** Various ambient air pollutants within a mixture may interact with

each other and amplify or reduce the cumulative effects of individual air

pollutants on health outcomes. However, health-related studies on the

interactive effects of air pollutant mixtures remain limited. Additionally, the

influence of greenness on health outcomes in the context of air pollutant

mixtures has seldom been explored.

**OBJECTIVE:** To develop a joint analysis framework that focuses on the interactive

effects among pollutants to evaluate the combined effects of ambient air

pollutant mixtures on pulmonary tuberculosis (PTB) risks, taking into account

greenness as a moderating factor.

**METHODS:** In this case-control study conducted in Lanxi, China, 1128 newly

diagnosed PTB cases from 2019 to 2021 were matched with 2256 controls by sex and

age. To evaluate exposure, the 24-month average values of particulate matter

with aerodynamic diameters of ≤ 2.5 µm (PM2.5), sulfur dioxide (SO2), ozone

(O3), nitrogen dioxide (NO2), and the Normalized Difference Vegetation Index

before diagnosis or study entry were assessed using a high-resolution dataset. A

quantile-based g-computation model was then used to estimate the additive and

interactive effects of air pollutants on PTB risks and identify the moderating

influence of greenness on these relationships.

**RESULTS:** Additive effect models showed that a one quartile increase in exposure

to the air pollutant mixture was associated with elevated PTB risks (mixture

odds ratio: 1.17, 95% confidence intervals: 1.07, 1.36), with NO2 contributing

the most significant positive effect. Interactive effect models showed that

incorporating interaction terms for O3 and other pollutants resulted in PTB

risks that exceeded those estimated using the additive effects of various

pollutants. Furthermore, areas with higher levels of greenness exhibited lower

PTB risks associated with air pollutant mixture than areas with lower levels of

greenness.

**CONCLUSIONS:** To reduce biases in air pollution control policies and maximize

their health benefits, it is essential to assess both the additive and

interactive effects when evaluating the health impacts of air pollutant

mixtures. Furthermore, the influence of greenness should be considered in the

context of these air pollutant mixtures.

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**10. BMC Infect Dis. 2025 Sep 24;25(1):1121. doi: 10.1186/s12879-025-11331-5.**

Diagnostic accuracy of T-SPOT.TB and TST in detecting active tuberculosis in

patients with rheumatic immune diseases: a fully matched comparative study.

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**BACKGROUND AND OBJECTIVES:** Patients with rheumatic immune diseases (RD) are

considered a high-risk population for developing active tuberculosis (ATB).

Timely and accurate diagnosis of ATB in RD patients is critical for optimizing

treatment outcomes and improving prognosis. Both interferon-gamma release assays

(IGRA) and the tuberculin skin test (TST) are immunological methods employed in

the diagnosis of tuberculosis. However, the diagnostic accuracy of these tests

in RD patients, who often experience immune dysfunction, remains underexplored.

This study aims to compare the diagnostic accuracy of TST and T-SPOT.TB in RD

patients with suspected tuberculosis symptoms.

**METHODS:** This prospective study included RD patients presenting with any of the

following symptoms-fever, cough, night sweats, or unexplained weight loss (all

symptoms recommended by the World Health Organization for tuberculosis

screening)-from September 2014 to September 2015. Both T-SPOT.TB and TST were

performed, and patients were categorized into ATB and non-ATB groups based on

clinical diagnosis (including microbiologically confirmed and clinically

diagnosed cases). Receiver operating characteristic (ROC) curves were

constructed to compare the diagnostic accuracy of T-SPOT.TB and TST for ATB and

to determine the optimal cutoff values. Sensitivity, specificity, predictive

values, and likelihood ratios were calculated, along with 95% confidence

intervals (CIs). The concordance between T-SPOT.TB and TST in diagnosing ATB was

also evaluated.

**RESULTS:** A total of 300 RD patients were enrolled in the study. Of these, 35

(11.7%) were diagnosed with ATB, 258 (86.0%) were excluded from ATB, and 7

(2.3%) had an unclear diagnosis. Among the RD patients, the ATB group exhibited

significantly higher frequencies of night sweats (34.3% vs. 14.0%, p=0.002) and

unexplained weight loss (17.1% vs. 3.1%, p<0.001) compared to the non-ATB group,

while no significant differences were observed between the groups for fever and

cough. The area under the ROC curve (AUROC) for T-SPOT.TB was 0.89 (95% CI

0.82-0.95), while the AUROC for TST was 0.74 (95% CI 0.63-0.84), with T-SPOT.TB

demonstrating significantly superior diagnostic accuracy (AUROC difference 0.15,

95% CI 0.06-0.24, p=0.001) (Figure). The optimal cutoff for T-SPOT.TB in

diagnosing ATB was 24 spot-forming cells (SFCs) per 10^6 peripheral blood

mononuclear cells (PBMCs), with sensitivity, specificity, positive likelihood

ratio, negative likelihood ratio, positive predictive value, and negative

predictive value of 88.6%, 84.9%, 5.86, 0.13, 44.3%, and 98.2%, respectively.

The optimal cutoff for TST was a 5mm induration diameter, yielding diagnostic

metrics of 57.1%, 88.8%, 5.08, 0.48, 40.8%, and 93.9%, respectively. The

sensitivity of T-SPOT.TB was significantly higher than that of TST (p=0.003),

while no significant difference in specificity was observed (p=0.193). As the

T-SPOT.TB spot count and TST induration diameter increased, the likelihood

ratios for diagnosing ATB also increased. The agreement between T-SPOT.TB and

TST in diagnosing ATB in RD patients was moderate (kappa=0.466, p<0.001), and

parallel testing with TST did not improve the sensitivity of T-SPOT.TB.

**CONCLUSION:** In RD patients with suspected ATB symptoms, both T-SPOT.TB and TST

offer valuable diagnostic assistance. T-SPOT.TB demonstrates superior diagnostic

accuracy, particularly in terms of sensitivity. Higher spot counts on T-SPOT.TB

or larger induration diameters on TST should raise clinical suspicion for the

presence of concurrent ATB.

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**11. Int J Surg. 2025 Sep 24. doi: 10.1097/JS9.0000000000003412. Online ahead of**

**print.**

Global, regional, and national burden of tuberculosis, 1990-2050: a systematic

comparative analysis based on retrospective cross-sectional of GBD 2021 and WHO

surveillance systems.

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S(1)(5)(6), Li Y(1)(5)(6), Ni R(1)(5), An Y(1)(5), Liu Y(1), Zhang L(1), Gong

W(1).

**Fan Jiang, Xuemei Li, Qing Qiao, Mingming Zhang, Yuan Tian, Shuang Zhou, Yufeng Li, Ruizi Ni, Yajing An, Yanhua Liu\*, Lingxia Zhang\*, Wenping Gong\***

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Beijing, China.

**BACKGROUND:** Tuberculosis (TB) persists as a leading global health threat.

Current surveillance is fragmented, and the surgical burden of drug-resistant

forms remains poorly quantified.

**METHODS:** Using GBD 2021 (1990-2050) and WHO-GHO (2000-2021), we estimated

mortality, incidence, prevalence and disability-adjusted life years (DALYs) for

204 countries by age, sex and four TB subtypes: latent tuberculosis infection

(LTBI), drug-susceptible tuberculosis (DS-TB), multidrug-resistant tu-berculosis

(MDR-TB), and extensively drug-resistant tuberculosis (XDR-TB). We compared WHO

and GBD figures in eight high-burden countries, applied joinpoint regression to

project trends, and quantified risk-factor contributions.

**RESULTS:** In 2021, global TB rates per 100,000 were: prevalence 236.14 (95 % UI

214.51-260.20), incidence 103.00 (92.21-114.91), deaths 13.96 (12.61-15.72) and

DALYs 580.26 (522.37-649.82). Socio-demographic index (SDI) gradients were

steepest for XDR-TB. Smoking, high alcohol use and elevated fasting glucose

explained >0.1 % of DS-TB DALYs each. WHO-GBD mortality diverged in Bangladesh,

Nigeria and the Democratic Republic of the Congo; incidence differed markedly in

Indonesia and the Philippines. Projections indicate rising mortality after 2030

in Indonesia and the Western Pacific under high-risk scenarios.

**CONCLUSIONS:** XDR-TB is emerging as the fastest-growing threat. Discrepancies

between WHO and GBD compromise resource allocation; harmonisation is urgently

needed, especially for surgical services planning in Indonesia and the Western

Pacific.

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PMID: 40990501

**12. J Med Internet Res. 2025 Sep 22;27:e69998. doi: 10.2196/69998.**

Using Machine Learning Methods to Predict Early Treatment Outcomes for

Multidrug-Resistant or Rifampicin-Resistant Tuberculosis to Enhance Patient Cure

Rates: Development and Validation of Multiple Models.

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Shang Y(1), Ren W(1), Liu R(1), Kuang H(4), Li L(#)(1)(2), Pang Y(#)(1).

**Fuzhen Zhang, Zilong Yang, Xiaonan Geng, Yu Dong, Shanshan Li, Cong Yao, Yuanyuan Shang, Weicong Ren, Ruichao Liu, Haobin Kuang, Liang Li, Yu Pang\***

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**BACKGROUND:** Early prediction of treatment outcomes for patients with

multidrug-resistant or rifampicin-resistant tuberculosis (MDR/RR-TB) undergoing

extended therapy is crucial for enhancing clinical prognoses and preventing the

transmission of this deadly disease. However, the absence of validated

predictive models remains a significant challenge.

**OBJECTIVE:** This study compared a conventional logistic regression model with

machine learning (ML) models using demographic and clinical data to predict

outcomes at 2 and 6 months of treatment for MDR/RR-TB. The goal was to advance

model applications, refine control strategies, and boost MDR/RR-TB cure rates.

**METHODS:** This retrospective study encompassed an internal cohort of 744 patients

with MDR/RR-TB examined between January 2017 and June 2023, as well as an

external cohort comprising 137 patients with MDR/RR-TB examined between March

2021 and June 2022. Data on culture conversion were collected at 2 and 6 months,

and culture conversion was tracked in the external cohort at the same time

points. The internal cohort was assigned as the training set, whereas the

external cohort was used as the validation set. Logistic regression and 7 ML

models were developed to predict the culture conversion of patients with

MDR/RR-TB at 2 and 6 months of treatment. Model performance was evaluated using

the area under the curve, accuracy, sensitivity, and specificity.

**RESULTS:** In the internal cohort, culture conversion rates for MDR/RR-TB were

81.9% (485/592) at 2 months and 87.1% (406/466) at 6 months. The odds ratio for

treatment success was 8.55 (95% CI 3.31-22.08) at 2 months and 20.33 (95% CI

6.90-59.86) at 6 months after conversion, with sensitivities of 86.5% and 92.2%

and specificities of 57.1% and 63.2%, respectively. The artificial neural

network model was the best for culture conversion at both 2 and 6 months of

treatment, with areas under the curve of 0.82 (95% CI 0.77-0.86) and 0.90 (95%

CI 0.86-0.93), respectively. The accuracy, sensitivity, and specificity of the

model were 0.74, 0.74, and 0.75 at 2 months of treatment and 0.80, 0.79, and

0.87 at 6 months of treatment, respectively.

**CONCLUSIONS: T**he ML models based on 2- and 6-month culture conversion could

accurately predict treatment outcomes for patients with MDR/RR-TB. ML models,

particularly the artificial neural network model, outperformed the logistic

regression model in both stability and generalizability and offer a rapid and

effective tool for evaluating therapeutic efficacy in the early stages of

MDR/RR-TB treatment.

©Fuzhen Zhang, Zilong Yang, Xiaonan Geng, Yu Dong, Shanshan Li, Cong Yao,

Yuanyuan Shang, Weicong Ren, Ruichao Liu, Haobin Kuang, Liang Li, Yu Pang.

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PMID: 40982802 [Indexed for MEDLINE]

**13. Vaccines (Basel). 2025 Sep 10;13(9):959. doi: 10.3390/vaccines13090959.**

Recent Advances in Clinical Research of Prophylactic Vaccines Against

Tuberculosis.

Xu B(1)(2), Yuan M(1)(2), Yang L(1)(2), Huang L(1)(3), Li J(1)(2), Tan Z(1)(2).

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Tuberculosis (TB), caused by Mycobacterium tuberculosis (MTB), is one of the

leading infectious causes of adult mortality worldwide. The Bacillus

Calmette-Guérin (BCG) vaccine is currently the only approved vaccine for TB

prevention, but its protective efficacy against adult pulmonary TB is limited,

and it lacks effective protection against primary or latent TB infection. There

is an urgent need to develop more effective preventive TB vaccines. Currently,

preventive TB vaccines under clinical investigation globally include live

attenuated vaccines, recombinant subunit vaccines, viral vector vaccines, and

mRNA vaccines. This article reviews and summarizes recent progress in the

clinical development of preventive TB vaccines, analyzing and comparing their

safety, immunogenicity, and protective efficacy. It also explores novel

strategies for next-generation TB vaccine development, aiming to provide

insights and directions for future research.

DOI: 10.3390/vaccines13090959

PMID: 41012162

**14. Pharmaceuticals (Basel). 2025 Sep 18;18(9):1408. doi: 10.3390/ph18091408.**

Immunoregulation by ESAT-6: From Pathogenesis of Tuberculosis to Potential

Anti-Inflammatory and Anti-Rejection Application.

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The early secreted antigenic target of 6 kDa (ESAT-6), a main effector molecule

of the ESX-1 secretion system, is identified as a virulence determinant and

immunoregulatory protein of Mycobacterium tuberculosis (Mtb), affecting the

interaction between host immune cells and pathogens. ESAT-6 facilitates the

survival of mycobacteria and their cell-to-cell spreading through

membrane-permeabilizing activity and the regulation of host immune cell

functions. In this review, we first summarize the recent knowledge of the roles

of ESAT-6 in the survival of bacteria, phagosomal escape, and pathogenicity

during Mtb infection. Then, we focused on its complex immunomodulatory effects

on different immune cells, such as macrophages, dendritic cells, neutrophils,

and T cells, accentuating its capability to either facilitate or inhibit immune

responses through different signaling pathways. While our review has summarized

its main roles in immunopathology in the context of tuberculosis, we

additionally search for emerging evidence indicating that ESAT-6 has

anti-inflammatory and immunosuppressive properties. Particularly, we discuss

recent preclinical studies showing its capability to suppress transplant

rejection and alloimmunity, probably via the induction of regulatory T cells.

Nevertheless, the potential clinical use of ESAT-6 remains uncertain and needs

further verification by comprehensive preclinical and clinical studies. Thus, we

propose that ESAT-6 may be exploited to ameliorate immunopathology in TB

infection and to suppress immune-mediated inflammation or transplant rejection

as well.

DOI: 10.3390/ph18091408

PMID: 41011275

**15. Biomedicines. 2025 Aug 26;13(9):2076. doi: 10.3390/biomedicines13092076.**

The Evolving Landscape of Host Biomarkers for Diagnosis and Monitoring of

Tuberculosis.

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Tuberculosis (TB) remains a formidable global public health challenge. The

rising prevalence of drug-resistant TB and increased human immunodeficiency

virus(HIV) co-infection further exacerbate TB control efforts. Mycobacterium

tuberculosis (Mtb) achieves highly heterogeneous infection outcomes (active

disease, latency, or clearance) through immune evasion and host metabolic

reprogramming. While conventional diagnostic techniques offer cost-effectiveness

and accessibility without complex infrastructure, they are constrained by low

sensitivity, prolonged turnaround times, and an inability to distinguish latent

TB infection (LTBI) from active TB disease (ATB). Recent research into

host-derived biomarkers provides a promising strategy to overcome diagnostic

bottlenecks by deciphering characteristic molecular changes in host-pathogen

interactions. This review systematically reviews advances in host-derived

biomarkers for TB diagnosis, critically discussing the clinical potential,

translational challenges, and future research directions of integrated

multi-omics biomarker panels to enhance diagnostic sensitivity and specificity,

differentiate ATB from LTBI, and guide precision therapy.

DOI: 10.3390/biomedicines13092076

PMID: 41007639

**16. Biology (Basel). 2025 Sep 5;14(9):1196. doi: 10.3390/biology14091196.**

CP91110P: A Computationally Designed Multi-Epitope Vaccine Candidate for

Tuberculosis via TLR-2/4 Synergistic Immunomodulation.

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Tian Y(2), Jiang L(5), Gong W(1)(2).

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**Background:** Tuberculosis (TB) remains a global health priority, with current

interventions like the Bacille Calmette-Guérin (BCG) vaccine lacking efficacy

against latent infection and drug-resistant strains. Novel vaccines targeting

both latent and active TB are urgently needed. **Objective:** This study aims to

design a multi-epitope vaccine (MEV) and evaluate its immunogenicity, structural

stability, and interactions with toll-like receptor 2/4 (TLR-2/4) via

computational biology approaches. **Methods:** We designed MEV using bioinformatics

tools, prioritizing immunodominant epitopes from Mycobacterium tuberculosis

antigens. Structural stability was optimized through disulfide engineering, and

molecular docking/dynamics simulations were used to analyze interactions and

conformational dynamics with TLR-2/4. Antigenicity, immunogenicity, population

coverage, and immune responses were computationally assessed. **Results:** The MEV

candidate, CP91110P, exhibited 86.18% predicted global human leukocyte antigen

(HLA)-I/II coverage, high antigenicity (VaxiJen: 0.8789), and immunogenicity

(IEDB: 4.40091), with favorable stability (instability index: 33.48) and

solubility (0.485). Tertiary structure analysis indicated that 98.34% residues

were located in favored regions. Molecular docking suggested strong TLR-2

(-1535.9 kcal/mol) and TLR-4 (-1672.5 kcal/mol) binding. Molecular dynamics

simulations indicated stable TLR-2 interactions (RMSD: 6-8 Å; Rg: 38.50-39.50 Å)

and flexible TLR-4 binding (RMSD: 2-6 Å; Rg: 33-36 Å). Principal component

analysis, free energy landscapes, and dynamic cross-correlation matrix analyses

highlighted TLR-2's structural coherence versus TLR-4's adaptive flexibility.

Immune simulations predicted potential robust natural killer cell activation, T

helper 1 polarization (interferon-gamma/interleukin-2 dominance), and elevated

IgM/IgG levels**. Conclusions:** CP91110P is predicted to stably bind to TLR-2 and

flexibly interact with TLR-4, with prediction of its high antigenicity and broad

coverage across immune populations. However, this conclusion requires

confirmation through experimental validation. Therefore, it may provide a

promising candidate for experimental validation in the development of

tuberculosis vaccines.

DOI: 10.3390/biology14091196

PMID: 41007341

**17. Front Public Health. 2025 Sep 10;13:1614339. doi: 10.3389/fpubh.2025.1614339.**

**eCollection 2025.**

Feasibility of ending tuberculosis in Shangrao City through active intervention

measures: a mathematical study.

Xu M(#)(1), He Y(#)(2), Liu Q(#)(2), Chen Q(2)(3)(4), Zhao Z(2), Xu Z(1), Shu

C(1), Xia J(1), Yang Y(1), Gavotte L(5), Frutos R(3), Ye H(6), Su Y(2), Wang

X(7), Liu Z(1).

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**OBJECTIVE:** China faces significant challenges in ending tuberculosis (TB).

Active case finding (ACF) and TB preventive therapy (TPT) have proven to be

critical measures in reducing TB incidence. This study uses a transmission

dynamics model to identify the optimal intervention strategies for achieving

WHO's TB elimination targets in Shangrao City. The findings guide targeted TB

control efforts in similar settings.

**METHODS:** To account for COVID-19 pandemic disruptions, we first used a seasonal

autoregressive integrated moving average (SARIMA) model to predict and

substitute the reported TB incidence during 2020-2023. Subsequently, we

developed an age-stratified dynamic transmission model using surveillance data

from Shangrao City's Infectious Diseases Reporting System (IDRS) between 2008

and 2023 to evaluate tuberculosis transmission patterns across age groups. The

model assessed the effectiveness of key interventions including active case

finding (ACF), latent tuberculosis infection (LTBI) screening, and tuberculosis

preventive treatment (TPT).

**RESULTS:** The model fit well with the reported data (R2 = 0.53, p < 0.001).

Preventive treatment measures can fully achieve the goal of reducing incidence.

All five TPT regimens showed potential to meet the TB elimination targets, with

the 3HP regimen (weekly rifapentine + isoniazid for 3 months) performing the

best. With the proportion of post-detection consent to TPT of 0.6 and rate of

LTBI screening of 0.5, the 3HP regimen met the 2030 and 2035 incidence targets,

with projected rates of 15.27/100,000 and 7.98/100,000, respectively.

**CONCLUSION:** The current TB control efforts face significant challenges, with a

considerable gap remaining in achieving TB elimination targets. Combining ACF

with TPT presents a promising strategy to reach these goals. Older tuberculosis

(TB) patients constitute a high-risk population, and effective prevention and

treatment in this group are critical to achieving future TB elimination goals.

To reduce the risk of recurrence and reinfection, enhanced follow-up monitoring

of older patients should be prioritised alongside targeted health education

interventions tailored to high-risk groups.

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Ye, Su, Wang and Liu.

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PMID: 41000308 [Indexed for MEDLINE]

**18. Age Ageing. 2025 Aug 29;54(9):afaf268. doi: 10.1093/ageing/afaf268.**

Prevalence of latent tuberculosis infection in older adults: a systematic review

and meta-analysis.

Ling Y(1), Wang M(2), Chen S(3)(4), Wu Q(3)(4), Zhang Y(3)(4), Liu K(3)(4), Yang

K(3), Wang L(5), Wang W(3)(4), Chen B(3)(4), Jiang J(3)(4).

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**BACKGROUND:** The burden of tuberculosis (TB) is increasingly borne by older

adults. Several studies have investigated the prevalence of latent tuberculosis

infection (LTBI) in special populations. However, the global estimates of the

prevalence of LTBI in older adults are unclear. This study aimed to assess the

prevalence of LTBI amongst older adults.

**METHODS:** We conducted a systematic search of PubMed, Web of Science, Scopus and

Embase databases. A systematic review and meta-analysis of relevant research

articles published between 1 January 2000 and 28 February 2025 was performed.

The I2 and Cochran's Q statistical tests were used to assess heterogeneity.

Funnel plots and Egger's test were used to examine publication bias.

Meta-regression and subgroup analyses were performed to assess the sources of

heterogeneity.

**RESULTS:** A total of 20 studies were finally included in this study after

screening the articles. The overall pooled prevalence of LTBI in older adults

was 31.1% [95% confidence intervals (CIs): 22.8%-39.3%]. Subgroup meta-analyses

revealed significant differences in the prevalence of LTBI between countries

when categorised by WHO regions and WHO TB incidence intervals. Besides, the

prevalence of LTBI was 30.9% (95% CI: 23.9%-37.9%) and 33.4% (95% CI:

25.9%-40.8%) based on studies that utilized interferon-gamma release assay and

tuberculin skin test, respectively.

**CONCLUSIONS:** The prevalence of LTBI is relatively high amongst older adults,

emphasising the high burden of undetected infection in this population. Future

research integrating cost-effectiveness analyses and intervention studies is

needed to further explore the feasibility of population-based screening and

prevention strategies to promote TB prevention and control.

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**19. Front Cell Infect Microbiol. 2025 Sep 9;15:1662518. doi:**

**10.3389/fcimb.2025.1662518. eCollection 2025.**

Pathological subtypes and sampling strategies determine diagnostic sensitivity

in cervical lymph node tuberculosis: a retrospective study.

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**OBJECTIVE:** To investigate how pathological types and sampling methods affect

positivity rates of five diagnostic techniques in cervical lymph node

tuberculosis.

**METHODS:** We retrospectively analyzed 198 surgically confirmed cervical lymph

node tuberculosis patients from Wuhan Pulmonary Hospital. Cases were stratified

by pathological subtypes and collection methods. The specimens were tested using

acid-fast bacillus smear microscopy, mycobacterium tuberculosis culture,

quantitative polymerase chain reaction for tuberculosis DNA, simultaneous

amplification and testing for tuberculosis, or GeneXpert.

**RESULTS:** All 198 cases showed granulomatous inflammation. Liquefactive necrosis

occurred in 91.92% (182/198) of cases, with caseous necrosis in 87.88%

(174/198), adjacent soft-tissue necrosis in 57.07% (113/198), and suppurative

inflammation in 20.20% (40/198). Solid alterations without liquefactive necrosis

(coagulative necrosis/non-necrotizing lymphadenitis) comprised 8.08% (16/198).

The overall etiological positivity rate was 90.40% (179/198). GeneXpert showed

highest sensitivity (90.36%), followed by tuberculosis DNA (74.24%),

simultaneous amplification and testing (40.22%), Mycobacterium tuberculosis

culture (16.67%), and acid-fast bacillus smear (14.72%). Among 33

culture-positive cases, 32 (96.97%) were GeneXpert positive. Rifampicin

resistance detected by GeneXpert was 5.62% (10/178). In specimens with caseous

necrosis, soft-tissue necrosis, or liquefactive necrosis, GeneXpert positivity

significantly exceeded tuberculosis DNA (all P < 0.01). Liquefactive necrosis

samples showed higher positivity than solid-change specimens for all techniques

except culture (all P < 0.001). Drainage specimens yielded higher tuberculosis

DNA and GeneXpert positivity than surgical resection specimens. Combining

surgical and drainage specimens increased culture positivity to 26.09%.

**CONCLUSION:** Etiological positivity rates in cervical lymph node tuberculosis

correlate with pathological features. Maximizing liquefactive necrosis sampling

for the GeneXpert assay and combining different sampling techniques (such as,

surgical resection, incision and drainage, needle biopsy) for etiological

detection enhances diagnostic accuracy.

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**20. iScience. 2025 Aug 26;28(9):113444. doi: 10.1016/j.isci.2025.113444. eCollection 2025 Sep 19.**

International multicenter development of ensemble machine learning driven host

response based diagnosis for tuberculosis.

Zheng S(1)(2)(3)(4), Qu W(1)(2)(3), Zhang D(1)(2)(3), Zhou J(1)(2)(3), Xu Y(1),

Wu W(4), Liu C(1), Huang M(1), Shen E(5), Chen X(1)(2)(3)(4), Timko MP(6), Fan

L(5), Yu F(1)(2)(3), Han D(1)(2)(3), Shen Y(1)(2)(3).

**Shufa Zheng, Wenxin Qu, Dan Zhang, Jieting Zhou, Yifan Xu, Wei Wu, Chang Liu, Mingzhu Huang, Enhui Shen, Xiao Chen, Michael P Timko, Longjiang Fan, Fei Yu\*, Dongsheng Han\*, Yifei Shen\***

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Active pulmonary tuberculosis (TB) is challenging to diagnose, and monitoring

treatment response effectively remains difficult. To address these challenges,

we developed TB-Scope, a host-gene-expression-based ensemble machine learning

classification model. Using large-scale microarray datasets (N = 1,258) from

three retrospective transcriptomic studies, we selected 143 feature genes

(biomarkers) based on their expression ranks to predict ATB. The Top Scoring

Pairs (TSP) ensemble classifier for ATB diagnosis was optimized using

multi-cohort training samples. We then combined the ATB/Health, ATB/LTBI, and

ATB/ODs classifiers to construct an ATB diagnosis decision model (TB-Scope

decision). To assess the performance of the TB-Scope algorithm and decision

model, we analyzed 12 independent microarray and RNA-seq validation datasets (N

= 1,786) comprising both children and adults from seven countries. Thus, our

data demonstrates that TB-Scope provides a powerful and reliable tool for

accurately diagnosing ATB across diverse data platforms.

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**eCollection 2025.**

ULK1 gene polymorphisms and severe tuberculosis in the Chinese Han population: a

case-control study.

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**OBJECTIVES:** Polymorphisms in the uncoordinated 51-like kinase 1 (ULK1) gene are

associated with susceptibility to multiple diseases, including neurodegenerative

disorders and specific cancer types. In tuberculosis (TB) research, autophagy is

recognized as an essential host mechanism against Mycobacterium tuberculosis

(Mtb) infection. Consequently, functional variations in the ULK1 gene may affect

autophagic efficiency, influencing the host immune response to Mtb and altering

the severity of TB. This study aimed to investigate the association between ULK1

gene polymorphisms and severe TB within a Chinese Han population using a

case-control study design.

**METHODS:** A case-control study was conducted, with patients diagnosed with mild

TB as controls and those diagnosed with severe TB as cases. Peripheral blood

samples were collected from all participants for genomic DNA extraction. Four

tag single nucleotide polymorphisms (SNPs) within the ULK1 gene (rs9481,

rs7138581, rs11616018, and rs1134574) were selected based on genotype data from

the Han Chinese population in Beijing. The association between these SNPs and TB

severity was analyzed. Additionally, clinical phenotype analysis was conducted

for the loci associated with TB severity.

**RESULTS:** The minor allele G of the ULK1 gene SNP rs1134574 (A > G) was

significantly associated with an increased risk of severe TB (ORa = 23.499, 95%

CI = 7.339-75.249, Pa < 0.0001). However, no statistically significant

difference was observed in genotype frequencies or genetic models at this locus

between severe and mild TB groups. Clinical phenotype analysis identified 995

patients with the AA genotype, 136 patients with the AG genotype, and 6 patients

with the GG genotype at rs1134574. Significant differences were observed among

these genotypes regarding the proportion of patients experiencing night sweats

(p = 0.045) and the percentage of neutrophils (p = 0.046).

**CONCLUSION:** The polymorphism rs1134574 of the ULK1 gene is significantly

associated with severe TB, and clinical phenotype variations exist among

different genotypes at this locus. These findings suggest a potential

correlation between ULK1 gene polymorphisms and the incidence of severe TB

within the Chinese Han population.

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**22. Front Public Health. 2025 Sep 9;13:1658814. doi: 10.3389/fpubh.2025.1658814.**

**eCollection 2025.**

Disparities in the burden of tuberculosis associated with urbanization across

178 countries and territories: an observational study.

Wang Y(1)(2), Liu Q(1)(2), Chen Z(3), Liu M(1)(2), Chen B(4), Zhao Y(5), Liu

J(1)(2)(6)(7).

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**BACKGROUND:** Tuberculosis (TB) remains the leading cause of death from a single

infectious agent. However, there is limited quantitative evidence on the impact

of urbanization on TB burden. We aimed to assess the relationship between

urbanization and the global TB burden.

**METHODS:** Using multi-source data, we developed a composite index of urbanization

across 178 countries and territories from 2012 to 2019, incorporating the

proportion of urban population, the proportion of population using improved

sanitation, nighttime light intensity, normalized difference vegetation index,

and per capita gross domestic product. Fixed-effects linear models were applied

to estimate the rate ratios (RRs) and 95% confidence intervals (CIs) for the

association between urbanization and the incidence, prevalence, and mortality of

total TB and three subtypes: drug-susceptible TB (DS-TB), multidrug-resistant TB

(MDR-TB), and extensively drug-resistant TB (XDR-TB).

**RESULTS:** Overall, higher urbanization scores were associated with significant

reductions in the burden of MDR-TB and XDR-TB but showed no effect on total TB

or DS-TB. For MDR-TB, each additional urbanization score was associated with a

1.0% decrease in incidence (RR = 0.990; 95% CI: 0.985-0.996), a 1.1% decrease in

prevalence (0.989; 0.984-0.994), and a 0.7% decrease in mortality (0.993;

0.988-0.998). For XDR-TB, the corresponding reductions were 0.9% in incidence

(0.991; 0.986-0.996), 1.0% in prevalence (0.990; 0.985-0.995), and 0.7% in

mortality (0.993; 0.988-0.998). These relationships persisted when considering a

one-year lag in urbanization. In subgroup analyses, however, urbanization was

associated with increased MDR-TB and XDR-TB burdens in upper-middle-income

countries.

**CONCLUSION:** Urbanization was linked to reduced MDR-TB and XDR-TB burdens

globally, but to increased burdens in upper-middle-income countries. Building

well-managed and healthy cities is essential not only for sustainable

urbanization but also for strengthening TB prevention and control, especially in

rapidly transitioning upper-middle-income countries.

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**23. Front Microbiol. 2025 Sep 5;16:1637254. doi: 10.3389/fmicb.2025.1637254.**

**eCollection 2025.**

Progress of anti-tuberculosis drug targets and novel therapeutic strategies.

Zhang Y(1), Wu R(1), Sun M(1), Li X(1), Fang R(1), Xing J(1), Li Z(2), Wen Y(3),

Song N(1).

**Yang Zhang, Ruiying Wu, Mingrui Sun, Xiaotian Li, Ren Fang, Jiayin Xing, Zhaoli Li, Yurong Wen, Ningning Song**

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Tuberculosis, a chronic infectious disease caused by Mycobacterium tuberculosis

complex, has re-emerged as the leading cause of death worldwide as a single

infectious agent. The increasing prevalence of multidrug-resistant tuberculosis

and extensively drug-resistant tuberculosis poses a severe and growing threat to

global health. Therefore, it is urgent to find new drug targets. Recently,

significant advancements have been made in the research of drug targets and

novel therapeutic strategies for tuberculosis. This review summarizes recent

processes on anti-tuberculosis drug targets, such as cell wall synthesis,

nucleic acid replication and transcription, energy metabolism, and ferroptosis.

Furthermore, this review summarizes the research progress of three innovative

tuberculosis treatment strategies, including antimicrobial peptides,

host-directed therapies, and nanoparticle-based drug delivery systems, aiming to

provide a theoretical foundation and new research perspectives for the clinical

development of new drugs.

Copyright © 2025 Zhang, Wu, Sun, Li, Fang, Xing, Li, Wen and Song.

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**24. Front Pediatr. 2025 Sep 5;13:1626146. doi: 10.3389/fped.2025.1626146.**

**eCollection 2025.**

Disseminated BCG infection in a child with multifocal osteomyelitis due to STAT1

LOF variant and primary immunodeficiency disease was significantly improved

after anti-tuberculosis treatment: a case report.

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**BACKGROUND:** This was a rare case where the diagnosis was not obvious during

treatment, but the treatment was effective after diagnosis. An infant with

recurrent fever was considered for systemic multiple osteomyelitis after two

surgical biopsies. After a third operation to take a lymph node biopsy, the

patient was finally diagnosed as having disseminated Bacille

Calmette-Guerin(BCG) disease caused by BCG vaccination. After diagnosis, the

child was effectively treated with anti-tuberculosis therapy.

**CASE DESCRIPTION:** A 2-month-old female patient was hospitalized twice for fever

and surface mass. The patient underwent a puncture biopsy of the right tibia and

a puncture biopsy of the lesion of the right leg respectively. The patient was

diagnosed with systemic multiple osteomyelitis. The patient still had recurrent

fever after antibiotic treatment. At outpatient follow-up, the patient was found

to have primary immunodeficiency disease with STAT1 LOF mutation. When the child

was one year and one month old, she was hospitalized again with a fever. The

patient underwent a third operation, a biopsy of the left axillary lymph node.

The pathological results suggested granulomatous inflammation, which was

considered tuberculosis. The child was diagnosed with disseminated BCG vaccine

disease. After 16 months of oral treatment with isoniazid, rifampicin,

ethambutol,and levofloxacin, the child's condition was significantly improved.

**CONCLUSIONS:** The performance of multiple surgical biopsies is crucial in cases

of infants presenting with recurrent fever and widespread bone destruction, as

well as in children diagnosed with primary immunodeficiency disease,

particularly when the available etiological tests offer limited diagnostic

evidence.

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**25. Infect Drug Resist. 2025 Sep 16;18:4953-4964. doi: 10.2147/IDR.S540446.**

**eCollection 2025.**

Identification of Specific LncRNA Markers in Severe Tuberculosis for Early

Diagnosis.

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**BACKGROUND:** The progression of tuberculosis to severe disease is the main cause

of death of tuberculosis patients. Early identification of severe tuberculosis

is very important. LncRNA can be used as a potential marker in the diagnosis of

tuberculosis, but there is a lack of research on lncRNA in the field of severe

tuberculosis.

**METHODS:** Peripheral blood samples of severe pulmonary tuberculosis patients,

mild pulmonary tuberculosis patients and healthy controls were collected to

extract peripheral blood monocytes. The RNA was then extracted and sent to the

SBC human ceRNA V1.0 analysis. The results were verified by qPCR and analyzed by

KEGG and GO analyses. Differentially expressed lncRNAs were measured by ROC

curves.

**RESULTS:** Four lncRNAs exhibited statistically distinct expression patterns in

STB versus MTB groups (NR\_033909: p=0.0097; lnc-MYCBPAP-2:4: p=0.0053;

lnc-PRDM7-1:2: p<0.0001; NR\_033841: p=0.0279). The areas under the curve (AUC)

value are respectively 0.7280(lnc-PRDM7-1:2), 0.7288(lnc-MYCBPAP-2:4),

0.6647(NR\_033909) and 0.6615(NR\_033841).

**CONCLUSION:** LncRNAs NR\_033909, lnc-MYCBPAP-2:4, lnc-PRDM7-1:2 and NR\_033841 may

demonstrate diagnostic potential for differentiating severe from mild pulmonary

tuberculosis cases. These results create a platform for monitoring TB

progression and open new avenues for studying disease pathogenesis.

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**26. Front Oncol. 2025 Sep 4;15:1564686. doi: 10.3389/fonc.2025.1564686. eCollection 2025.**

Concurrent active pulmonary tuberculosis and small cell lung cancer: diagnostic

challenges and therapeutic insights from a case report.

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The coexistence of active pulmonary tuberculosis (TB) and small cell lung cancer

(SCLC) is an exceptionally rare clinical phenomenon, presenting significant

diagnostic and therapeutic challenges due to overlapping symptoms, radiological

findings, and drug interactions. We report the case of a 68-year-old male with a

four-month diagnostic journey, involving persistent cough, exertional chest

tightness, and multiple inconclusive bronchoscopic examinations. Active TB was

confirmed via sputum smear tests identifying acid-fast bacilli, while SCLC was

diagnosed later through a third bronchoscopy, supported by elevated

progastrin-releasing peptide (ProGRP, 127.28 pg/mL). The patient received a

two-month course of anti-TB therapy before initiating four cycles of

etoposide-cisplatin chemotherapy, followed by chest radiotherapy. Anti-TB

treatment was intermittently paused during chemotherapy cycles to minimize drug

interactions, and the patient completed 11 months of therapy. Follow-up imaging

showed partial resolution of the left upper lung lesion, with normalized tumor

markers (ProGRP: 66.20 pg/mL). However, at 17 months, disease progression was

noted with a metastatic lesion in the right lower lobe. This case underscores

the complex interplay between TB-induced chronic inflammation and tumor

progression, highlighting the need for early tumor marker testing, advanced

imaging modalities such as PET-CT, and tailored therapeutic strategies.

Multidisciplinary collaboration is critical for optimizing outcomes in such rare

and challenging scenarios. Further research into the mechanistic links between

TB and SCLC could improve early diagnosis, guide therapeutic decisions, and

inform preventive strategies.

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**27. Front Public Health. 2025 Sep 4;13:1655711. doi: 10.3389/fpubh.2025.1655711.**

**eCollection 2025.**

The role of expanded close contact screening in the tuberculosis outbreak at a

school in China.

Peng L(#)(1), Mei J(#)(1), Hu F(1), Xie M(1), Liu Z(1), Guo Y(1), Yang C(2),

Wang Y(1).

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**BACKGROUND:** Tuberculosis (TB) outbreaks in confined settings such as schools

pose significant public health challenges due to the potential for rapid

transmission among closely interacting individuals. In December 2018, a senior

high school student in Shenzhen City, China, was diagnosed with etiological

positive TB, prompting an investigation that extended until November 2024. This

study aimed to analyze the outbreak's characteristics, identify its causes, and

provide insights for timely identification and management of similar clusters.

**METHODS:** The confirmed, clinically diagnosed, and suspected cases of TB were

identified according to the "Tuberculosis diagnosis WS288-2017" criteria.

Epidemiological investigations of TB cases included close contact screening via

symptom assessment, TST, and chest radiography. Moderately TST-positive contacts

underwent IGRA confirmation for preventive therapy eligibility, while MIRU-VNTR

genotyping of culture-positive isolates delineated transmission networks. The

Chi-square test or Fisher's exact test was employed to analyze changes in TST

positivity rates and differences in TB incidence rates.

**RESULTS:** A total of six TB cases were detected in the high school, with five

screenings conducted over the study period. Misdiagnosis caused a

near-three-month delay from symptom onset to confirmed TB in the index case.

Among the five newly diagnosed patients, four were in the same class as the

index case, and one was in an adjacent class. These two classes are located on

the middle horizontal line of the "B"-shaped teaching building. For the

indicated case's class, the positive rate of TST in the second screening (35.85,

95% CI: 23.49-19.25%) was significantly higher than in the first screening

(8.93, 95% CI: 3.33-20.37%) (χ2 = 11.493, p < 0.001). MIRU-VNTR genotyping of

four clinical isolates identified concordant non-Beijing strains with matching

profiles at 11/12 loci (excluding VNTR3232), demonstrating a single transmission

chain.

**CONCLUSION:** This outbreak was a cluster epidemic driven by misdiagnosis, poor

ventilation, and insufficient routine prevention measures. Establishing

long-term close-contact monitoring and secondary screening is crucial for

identifying infections missed during the initial window period, thereby

mitigating the spread of TB in similar settings and improving outbreak

management strategies.

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