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**中国大陆学者发表的结核病英文文章摘要**

**（23篇）**

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

**1. Clin Infect Dis. 2025 Jun 18:ciaf313. doi: 10.1093/cid/ciaf313. Online ahead of print.**

Epidemiologic and Bacterial Factors Facilitating Long-Term Transmission of

Multidrug-Resistant Tuberculosis in Shanghai, China.

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Yang C(1)(5)(6).

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**BACKGROUND:** Long-term transmission of multidrug-resistant tuberculosis (MDR-TB)

challenges TB control by generating new cases and enabling the emergence of

extensively resistant strains. We investigated its epidemiologic and bacterial

drivers in Shanghai, China.

**METHODS:** We conducted a retrospective study of M. tuberculosis isolates and

associated epidemiological data from individuals diagnosed with

rifampicin-resistant TB in Shanghai over 14 years (2004-2018). Using

whole-genome sequencing, Bayesian reconstruction of transmission trees, and

multivariable regression analysis to identify epidemiological and bacterial

factors associated with the transmission of MDR-TB.

**RESULTS:** Between 2004 and 2018, 1,456 individuals in Shanghai were diagnosed

with MDR or rifampicin-resistant TB, with whole-genome sequences available for

1,100 isolates. The overall genomic clustering rate was 55.3%, with large

clusters (those containing ≥5 cases) accounting for 39.9% of the clustered

strains. Risk factors for clustered MDR-TB transmission included local residency

(aOR 2.28, 95% CI 1.67-3.11), diagnostic delays ≥2 months (aOR 1.75, 95% CI

1.24-2.47), specific M. tuberculosis sublineages (L2.3.3-L2.3.6), and the rpoB

S450L mutation with compensatory mutations (aOR 2.14, 95% CI 1.64-2.78). Large

MDR-TB clusters were significantly associated with long-term transmission (>5

years, p<0.001). Long-term transmission clusters correlated with same-street

residence, local residency, and MDR-TB strains carrying katG315T, rpoB450L and

compensatory mutations.

**CONCLUSIONS:** Despite ample healthcare resources, MDR-TB persists in urban areas

due to both epidemiological and bacterial factors. The rpoB S450 mutation with

compensatory mutations enhances transmission even in the absence of clear

epidemiologic links. Effective control measures must address both

epidemiological and bacterial factors.

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**2. Microb Pathog. 2025 Jun 19:107826. doi: 10.1016/j.micpath.2025.107826. Online**

**ahead of print.**

Advancements in the Identification and Utilization of Cerebrospinal Fluid

Immunological Biomarkers for the Diagnosis of Tuberculous Meningitis.

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Tuberculous meningitis (TBM), the most severe manifestation of tuberculosis,

poses a major global health challenge due to its high morbidity and mortality,

affecting over 100,000 individuals annually. Diagnosing TBM is challenging due

to its clinical resemblance to other forms of meningitis and the slow, often

inadequate, traditional diagnostic methods like CSF smear and culture. Despite

advancements such as the Xpert MTB/RIF assay, which has enhanced the speed and

sensitivity of diagnostics, significant challenges persist due to variability in

test performance and sample handling. This review explores the potential of CSF

immunological biomarkers to improve the diagnosis of TBM by reflecting the

complex immune responses to Mycobacterium tuberculosis. Focusing on

immune-related cytokines, chemokines, inflammatory mediators, and specific

immune cells, the review proposes these biomarkers as more precise and rapid

alternatives to conventional diagnostic methods. The review suggests that future

research should prioritize the development of a composite biomarker panel to

enhance diagnostic specificity and sensitivity. Additionally, integrating

biomarker data with clinical outcomes to create a reliable biomarker-based

diagnostic framework will ultimately improve patient management and outcomes in

TBM.

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**3. Diagn Microbiol Infect Dis. 2025 Jun 18;113(2):116960. doi:**

**10.1016/j.diagmicrobio.2025.116960. Online ahead of print.**

Metagenomic diagnosis of congenital tuberculosis with coinfections in an

extremely preterm infant conceived via in vitro fertilization.

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We describe a case of congenital tuberculosis in an extremely preterm infant (24

weeks' gestation, 800 g) conceived via in vitro fertilization, complicated by

cytomegalovirus and Klebsiella pneumoniae coinfections. Diagnosis was confirmed

by metagenomic next-generation sequencing after conventional tests were

inconclusive. Management included anti-tuberculosis, antiviral, and

antibacterial therapy, as well as surgical correction of a patent ductus

arteriosus. The infant demonstrated significant clinical recovery, with

resolution of pulmonary, splenic, and cardiac abnormalities. This case

underscores the value of advanced molecular diagnostics and multidisciplinary

care in managing life-threatening neonatal infections.

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**4. Int J Surg. 2025 Jun 20. doi: 10.1097/JS9.0000000000002720. Online ahead of**

**print.**

Comprehensive analysis of tuberculosis burden trends and attributable risk

factors in the BRICS countries from 1990 to 2021, with forecasts for the next 15

years.

Zhang X(1), Guo M(1), Song X(2), Abdalla AE(3), Wang G(4), Xie L(1).

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China.

**BACKGROUND:** The study was to elucidate a comprehensive view of the burden of TB

from different dimensions.

**METHODS:** Data were sourced from the GBD 2021. We provided a comprehensive

overview of all relevant measures and the associated age-standardized rates per

100,000 (ASR) across BRICS countries. And we analyzed risk factors contributed

to TB-related deaths and DALYs. Additionally, temporal trends in the disease

were delineated using a joinpoint regression model, while projections over the

subsequent 15 years were generated using the BAPC model.

**RESULTS:** The global ASIR was 103 per 100,000 in 2021, which represented a 40.5%

decrease since 1990. Notably, ASIR in China experienced a significant decline of

66.7%. Individuals aged 65 and above were high-risk group for TB. For the

Russian Federation, the percentages of deaths and DALYs caused by MDR-TB and

XDR-TB were approximately 30% and 14% respectively in 2021. Although DS-TB still

accounted for the highest proportion of about 55%, it was significantly lower in

contrast to other countries, where the rate reached over 80%. And the gradual

downward trends of ASIR and ASMR are expected to continue over the period from

2021 to 2036.

**CONCLUSIONS:** The results indicated that the burden of TB in BRICS countries has

decreased over the past 30 years. It highlights an urgent requirement to develop

and implement relevant strategies in the prevention and control of TB based on

country-specific development status.

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**5. Glob Health Res Policy. 2025 Jun 23;10(1):24. doi: 10.1186/s41256-025-00424-y.**

Prevalence of Tuberculosis among migrants under national screening programs: a

systematic review and meta-analysis.

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**BACKGROUND:** Tuberculosis (TB) continues to pose a significant global public

health threat, particularly among migrant populations. Screening policies exist

in many receiving countries but differ markedly, and there is limited pooled

evidence on TB and latent TB infection (LTBI) prevalence among migrants under

different screening frameworks. This systematic review and meta-analysis aims to

synthesize TB and LTBI prevalence among migrants and compared national screening

policies to inform evidence-based public health planning.

**METHODS:** PubMed, Embase, Web of Science and Cochrane Library were searched for

studies published 2016-2023. Random-effects models generated pooled prevalence

estimates with 95% CIs; subgroup analyses examined differences by screening

stage, migrant category, and country-of-origin incidence. Sensitivity analyses

tested robustness. Government and health-agency websites were systematically

examined and scored to table national TB-screening requirements.

**RESULTS:** 36 studies (26 TB, 21 LTBI) covering 40,738,331 migrants screened met

inclusion criteria. The Pooled TB prevalence was 214.52/100,000 (95% CI

112.18-349.66) and LTBI prevalence 14.9% (95% CI 9.91-20.60). Countries

employing both pre-entry screening and subsequent post-entry surveillance

achieved the lowest TB prevalence (94.09/100,000). The highest burdens occurred

among refugees/asylum seekers (439.25/100,000) and migrants from countries with

TB incidence 300-499/100,000 (491.96/100,000). LTBI was most common when

identified through post-entry screening (21.90%), those with multiple migrants

(18.11%), and among migrants originating from countries with ≥ 500/100,000 TB

incidence (30.90%). Policy comparison showed pre-entry screening is almost

universal; the United States is the only country mandating systematic LTBI

screening. Screening-scope scores were highest in traditional immigrant

countries (16-20), intermediate in middle-income destinations such as China and

Malaysia (10-14), and lowest in Nordic (4-8).

**CONCLUSIONS:** This study emphasizes the importance of targeted TB screening,

especially for migrants from high-prevalence regions and at-risk populations.

Comprehensive pre- and post-entry TB screening, along with strengthened latent

TB screening and surveillance for diverse migrant populations, is essential.

Meanwhile enhanced collaboration to update screening policies are key to

achieving the goal of TB eradication and provide practical insights for

effective TB control.

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**6. Microbiol Spectr. 2025 Jun 23:e0038025. doi: 10.1128/spectrum.00380-25. Online**

**ahead of print.**

Longitudinal phenotypic and genomic evidence revealing increased risk of drug

resistance accumulation in tuberculosis patients in the counties of central

China.

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Zhang Y-T(1), Chen S-Q(3), Wu X-J(3), Cao H-Y(3), Jiang Q(1).

**Fu-Lin Wang, Rong Chen, Qiao Xu, Xiao-Qin Wang, Feng-Xi Tao, Zi-Kang Huang, You-Tong Zhang, Shu-Qiong Chen, Xue-Jing Wu, Hong-Yuan Cao\*, Qi Jiang\***

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Drug-resistant tuberculosis (DR-TB) disproportionately affects rural China, yet

the molecular and epidemiological drivers of this disparity remain inadequately

explored. This study investigates resistance evolution and transmission dynamics

in Xianning, China, using longitudinal data from 3,865 culture-positive

pulmonary tuberculosis patients (2016-2023). Phenotypic drug susceptibility

testing for 14 commonly used anti-tuberculosis drugs showed a stable

multidrug-resistant tuberculosis (MDR-TB) rate of 6.6%, while mono-resistance

increased from 8.5% to 12.9% over the study period. Notably, 19.3% (53/275) of

patients with ≥2 months of culture positivity developed new phenotypic

resistance during treatment. Whole-genome sequencing of strains from the last

two years identified resistance accumulation through two additional mechanisms:

(i) acquisition of resistance via unfixed mutations in individuals and (ii)

transmitted strains harboring novel resistance-conferring mutations absent in

parental clones within genomic clusters. For the combined cases of resistance

accumulation, multivariable logistic regression revealed that baseline drug

resistance increased the risk more than threefold (aOR = 3.65-5.28, varying by

resistance type), while rural residence independently doubled the risk (aOR =

2.60, 95% confidence interval:1.11-6.49). Furthermore, three of five genomic

clusters with resistance accumulation exhibited urban-rural transmission,

highlighting risks linked to cross-district care-seeking. These findings

underscore how systemic healthcare barriers in rural China drive DR-TB through

both treatment failures and strain transmission. Urgent action is needed to

decentralize rapid resistance screening and implement tiered care models in

primary clinics to curb transmission and mitigate the expanding DR-TB

threat.**IMPORTANCE** The ongoing epidemic of drug-resistant tuberculosis (DR-TB) in

resource-poor settings poses a major public health challenge. This study sheds

light on the evolution of DR-TB and its community transmission dynamics in

central rural China, suggesting that unequal healthcare may exacerbate

resistance accumulation risks by driving acquired resistance through inadequate

treatment as well as facilitating strain transmission with escalating drug

resistance. These findings emphasize the critical need for decentralized, rapid

drug-resistance screening, and enhanced diagnosis and treatment strategies in

primary care settings, prioritizing vulnerable populations to curb this growing

threat.

DOI: 10.1128/spectrum.00380-25

PMID: 40548705

**7. Emerg Microbes Infect. 2025 Jun 23:2521842. doi: 10.1080/22221751.2025.2521842.**

**Online ahead of print.**

Genomic epidemiology analysis of extremely drug-resistant tuberculosis in

Shanghai, China.

Lu X(1), Jiang Y(2), Liu Y(1), Chen J(1), Lao Y(1), Li J(2), Zhang Y(2), Li

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Tuberculosis (TB), particularly extremely drug-resistant TB (EDR-TB), remains a

significant public health concern worldwide. Understanding the transmission

patterns and epidemiological characteristics of EDR-TB is vital for effective

disease control. Between January 1, 2006, and December 31, 2018, we collected

clinical M. tuberculosis strains in Shanghai, with whole-genome sequencing

performed on 58 identified clinical EDR-TB strains. We analyzed EDR-related

genetic mutations, conducted phylogenetic analyses, and examined bacterial and

epidemiological factors that influence their transmission. Among these 58 EDR

patients, 43.1% (25/58) were aged 45 to 64 years, with a median age of 51 years

(interquartile range, IQR, 29-59 years). About two-thirds of the EDR-TB patients

were residents. We observed a clustering rate of 44.8% (26/58) among EDR

strains. Logistic regression analysis indicated a higher risk of recent EDR-TB

transmission among the strains with the drug-resistant compensatory mutations.

The primary mode of EDR-TB transmission in the study setting was recent, direct

person-to-person spread of drug-resistant strains, as evidenced by high

clustering rates and the presence of identical resistance mutations among

clustered cases.

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PMID: 40548454

**8. Front Med (Lausanne). 2025 Jun 12;12:1519216. doi: 10.3389/fmed.2025.1519216.**

**eCollection 2025.**

Investigation of the relationship between chronic hepatitis B and tuberculosis

using bioinformatics and systems biology approaches.

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**BACKGROUND:** Hepatitis B virus (HBV) is a globally prevalent pathogen that poses

significant public health challenges. Active HBV replication can trigger immune

responses that result in liver damage. Tuberculosis (TB), caused by

Mycobacterium tuberculosis (Mtb), remains one of the leading causes of death

from a single infectious agent worldwide. Notably, in TB patients with HBV

infection and, the incidence of adverse events is six times higher than in those

with TB alone, and HBV infection increases the risk of latent TB. However, the

relationship between HBV and TB have not been thoroughly investigated.

**METHODS:** To elucidate the relationship between HBV and TB, we performed an

integrated bioinformatics analysis using expression profiling and RNA sequencing

data from the GSE83148 and GSE126614 datasets. We identified differentially

expressed genes (DEGs) associated with both diseases and analyzed shared

biological pathways, key genes, transcriptional regulatory networks, and

gene-disease associations. Furthermore, we predicted potential therapeutic

agents targeting these shared molecular features.

**RESULTS:** A total of 35 overlapping DEGs were identified for in-depth analysis.

Functional enrichment revealed that these genes are involved in both

immune-related pathways and cellular metabolic regulation, underscoring their

potential role in the progression of HBV and TB. Protein-protein interaction

(PPI) network analysis highlighted four hub genes: CCL2, CD69, EGR2, and CCL20.

Additionally, 35 transcription factors (TFs) were predicted to regulate these

hub genes. Several candidate drugs, including etoposide, 8-azaguanine,

menaquinone, emetine and N-acetyl-L-cysteine, were identified as potential

therapeutic options. The DEGs were also significantly associated with other

conditions such as pneumonia.

**CONCLUSION:** This study provides novel insights into the relationship between HBV

and TB, offering potential targets for diagnosis and treatment. Our findings may

contribute to the development of integrated strategies to manage HBV infection

and TB more effectively.

Copyright © 2025 He, Zhou, Zhang, Cai, Pan, Huang and He.

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PMID: 40575568

**9. Front Cell Infect Microbiol. 2025 Jun 12;15:1586938. doi:**

**10.3389/fcimb.2025.1586938. eCollection 2025.**

Prevalence and molecular characterization of drug-resistant Mycobacterium

tuberculosis in Heyuan City in China.

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**PURPOSE:** Tuberculosis (TB) represents a significant global public health

challenge, with China identified as a high-burden country. Data on the

prevalence of drug resistance is crucial for informing the selection of

appropriate pharmacological interventions for the treatment of drug-resistant

tuberculosis (DR-TB).To evaluate the prevalence and drug resistance patterns

among patients with DR-TB in Heyuan City, China.

**METHODS:** All 291 patients registered between April 2021 and March 2023 were

tested for drug resistance, and information about their medical history and

demographics was collected directly from the hospital's computer database. Eight

genes were analyzed for mutations associated with resistance to five

antituberculosis drugs: the katG, ahpC, and inhA promoters for isoniazid (INH);

rpoB for rifampicin (RIF); embB for ethambutol (EMB); gyrA for fluoroquinolones

(FQs); and rrs and rpsL for streptomycin (STR). All strains were genotyped using

fluorescence melting curve analysis.

**RESULTS:** In Heyuan, 24.4% (71/291) of patients with treatment-resistant TB were

resistant to at least one drug. Following are the rates of general resistance to

each drug: RIF (28/272, 10.29%), INH (38/274, 13.87%), FQs (10/259, 3.86%), EMB

(20/248, 8.06%), and STR (15/150, 10.00%). Age or gender had no statistically

significant impact on the likelihood of developing drug resistance.

Nevertheless, a statistically significant difference was observed between the

three strategies of drug resistance testing, AFB testing, and MTB antibody

testing. There were 48 cases of single-drug resistance and 23 cases of

multiple-drug resistance among the 71 drug-resistant patients. Eight genes had

127 altered nucleotide sequences, with KatG315 (20.47%) having the most

significant incidence of mutations. The top three mutated genes were rpoB

(32.28%), katG (23.62%), and embB (15.75%).

**CONCLUSION:** These findings may be helpful in Heyuan City for the quick molecular

identification of DR-TB isolates in clinical samples.

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**10. Vaccines (Basel). 2025 May 30;13(6):597. doi: 10.3390/vaccines13060597.**

Assessment of the Adjuvant Effects of Lentinan on the Tuberculosis Subunit

Vaccine BG.

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**Objectives:** This study aims to assess the adjuvant effects of lentinan and its

combination with Mn(J), a manganese-based colloidal adjuvant, on the BG (fusion

protein BfrB-GrpE of Mycobacterium tuberculosis) subunit vaccine. **Methods:** A

rabbit skin infection model was established to evaluate the immune protection

conferred by the BG-lentinan vaccine, the BG-lentinan/Mn(J) vaccine, and the

Bacillus Calmette-Guérin (BCG) vaccine against tuberculosis. Rabbits were

vaccinated at weeks 0, 2, and 4. Six weeks post-vaccination, antigen-specific

IgG levels were measured, followed by a BCG skin challenge. **Results:** Both the

BG-lentinan and BG-lentinan/Mn(J) vaccines significantly increased

antigen-specific IgG levels against BfrB and GrpE in rabbits (p < 0.05).

Furthermore, these vaccines accelerated the pathological process following BCG

infection. The bacterial load in nodules was notably reduced, with the

BG-lentinan vaccine group exhibiting the lowest levels (p < 0.01). **Conclusions:**

Lentinan and its combined adjuvant, lentinan/Mn(J), significantly enhance the

immune response elicited by the BG tuberculosis subunit vaccine, providing

effective protection.

DOI: 10.3390/vaccines13060597

PMID: 40573928

**11. Microorganisms. 2025 Jun 16;13(6):1401. doi: 10.3390/microorganisms13061401.**

The Identification of Novel Mutations in ATP-Dependent Protease ClpC1 Assists in

the Molecular Diagnosis of Obscured Pyrazinamide-Resistant Tuberculosis Clinical

Isolates.

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S(1)(2)(3)(4), Chen X(5), Zhong N(5)(6), Aung HL(2)(7), Hu J(1), Zhang

T(1)(2)(3)(4)(5).

**H M Adnan Hameed, Cuiting Fang, Zhiyong Liu, Yamin Gao, Shuai Wang, Xinwen Chen, Nanshan Zhong, Htin Lin Aung, Jinxing Hu\*, Tianyu Zhang\***

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Pyrazinamide (PZA) is a key component of tuberculosis treatment, with drug

resistance (PZAR) primarily related to pncA mutations. However, discordance

between phenotypic resistance and conventional pncA-based molecular diagnostics

challenges diagnostic accuracy. This study investigates discrepancies between

phenotypic and genotypic resistance profiles among Mycobacterium tuberculosis

(Mtb) clinical isolates. Fifty-three Mtb isolates from Guangzhou Chest Hospital

were tested for PZA resistance using the BACTEC MGIT 960 system and PZase

activity assay. Thirty-one phenotypically PZAR strains were genetically assessed

by Sanger sequencing of PZAR-associated customary genes. Five pncA-wild-type

PZAR strains were investigated through whole-genome sequencing. ClpC1P1P2

activity was evaluated by proteolytic degradation assay. Notably, 26/31 of the

PZAR strains harbored mutations in pncA and/or its upstream region, aligning

PZase activity and phenotypic profiles. However, five PZAR strains lacked pncA

mutations. The WGS of five discordant strains revealed four novel mutations

(Gly58Ser, Val63Ala, Ala567Val, and Pro796Leu) across ClpC1 domains.

Incorporating clpC1 mutations improved molecular diagnostic sensitivity and

accuracy from 48.3% and 69.8% (pncA alone) to 100%. This is the first report

from southern China that identifies novel clpC1 mutations in wild-type pncA PZAR

Mtb isolates. Our findings underscore the limitations of pncA-targeted

diagnostics and support the integration of WGS and clpC1 analysis in molecular

diagnostics to prevent false-negative diagnoses and improve clinical outcomes.

DOI: 10.3390/microorganisms13061401

PMCID: PMC12196252

PMID: 40572289

**12. Front Cell Infect Microbiol. 2025 Jun 11;15:1571291. doi:**

**10.3389/fcimb.2025.1571291. eCollection 2025.**

Prevalence and related factors of TB/HIV co-infection among hospitalized

children with tuberculosis in Southwest China.

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**OBJECTIVES:** This study aimed to investigate the prevalence of TB/HIV

co-infection in pediatric TB patients in southwest China and its associated

variables.

**METHODS:** Pediatric TB patients were recruited from January 2014 to September

2024 in southwest China, based on etiology or clinical confirmation.

Hospitalization records were extracted for each patient.

**RESULTS:** Among 2,607 pediatric TB patients with an average age of 9.58 ± 4.08

years, 39 (1.5%) were HIV-positive. The TB/HIV co-infection group male-to-female

ratio was 2:1, higher than the TB-only group 1.19:1. The highest proportion of

TB/HIV co-infection was in the 5-9 years age group (43.6%), while the 10-14

years age group accounted for the highest proportion of TB-alone cases (57.5%).

In terms of population distribution, the Yi ethnic group had the highest

proportion of TB/HIV co-infection cases (43.6%), while the Tibetan group had the

highest proportion of TB-alone cases (51.1%). Extrapulmonary TB in the TB/HIV

co-infection group primarily involved abdominal and pericardial sites, whereas

the TB-alone infection group had more cases of lymphadenitis and pleural TB. The

length of hospitalization (>14 days) in the TB/HIV co-infection group (74.4%)

was significantly longer than in the TB-alone infection group (51.7%). Over the

past 11 years, most pediatric TB/HIV co-infection cases were from the

eastern-central and southern-central regions of Sichuan, particularly the

southern Liangshan Yi Autonomous Prefecture. The number of children with

TB-alone infections increased gradually during this period. No significant

difference in the number of pediatric TB/HIV co-infection cases was observed

over the 11 years.

**CONCLUSION:** Pediatric TB/HIV co-infection in southwest China predominantly

affects middle-aged and young boys, with a higher co-infection rate than the

national average. The central and southern regions of Sichuan have a relatively

high proportion of cases. Public health efforts should focus on strengthening

awareness, screening, and early diagnosis of TB and HIV in children in high-risk

areas to prevent further infections.

Copyright © 2025 Wang, An, Yang and Liao.

DOI: 10.3389/fcimb.2025.1571291

PMCID: PMC12187718

PMID: 40568707 [Indexed for MEDLINE]

**13. Trop Med Infect Dis. 2025 Jun 1;10(6):154. doi: 10.3390/tropicalmed10060154.**

A Blood and Biochemical Indicator-Based Prognostic Model Predicting Latent

Tuberculosis Infection: A Retrospective Study.

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**BACKGROUND AND OBJECTIVES:** Abnormal blood and biochemical indicators could

increase the risk of infectious diseases. However, the association between blood

together with biochemical indicators and latent tuberculosis infection (LTBI)

has not been well confirmed.

**MATERIALS AND METHODS:** Our aim was to assess the role of blood and biochemical

indicators in the risk of LTBI. We enrolled 965 freshmen who were originating

from tuberculosis key areas of a college in Nanjing. We used logistic regression

models, restricted cubic spline (RCS), and nomograms to evaluate the association

between blood and biochemical indicators and LTBI. In addition, calibration

curves were performed to evaluate the quality of the model.

**RESULTS:** Among these 965 participants, 311 were diagnosed as LTBI according to

TST. Multivariate models showed that the population with an eosinophils

percentage around <0.5% (OR: 2.82, 95% CI: 1.39-5.74, p = 0.004) and 0.5-5% (OR:

2.78, 95% CI: 1.07-7.23, p = 0.036) were positively associated with LTBI.

Elevated uric acid levels (OR: 1.01, 95% CI: 1.00-1.02, p = 0.047) were

significantly associated with LTBI. In addition, participants with a history of

tuberculosis exposure (OR: 3.26, 95% CI: 1.39-7.66) and a history of

tuberculosis (OR: 10.92, 95% CI: 1.24-96.08) were also positively correlated

with LTBI.

**CONCLUSIONS:** Eosinophils percentage and uric acid are associated with LTBIs.

Participants who have tuberculosis exposure history and tuberculosis history are

the critical target population.

DOI: 10.3390/tropicalmed10060154

PMCID: PMC12197490

PMID: 40559721

**14. Diseases. 2025 Jun 11;13(6):184. doi: 10.3390/diseases13060184.**

Integration of AI and ML in Tuberculosis (TB) Management: From Diagnosis to Drug

Discovery.

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Tuberculosis (TB) is an infectious disease caused by Mycobacterium tuberculosis.

Despite the improvements in diagnostic techniques, the accuracy of TB diagnosis

is still low. In recent years, the development of artificial intelligence (AI)

has opened up new possibilities in diagnosing and treating TB with high accuracy

compared to traditional methods. Traditional diagnostic techniques, such as

sputum smear microscopy, culture tests, and chest X-rays, are time-consuming,

with less sensitivity for the detection of TB in patients. Due to the new

developments in AI, advanced diagnostic and treatment techniques have been

developed with high accessibility, speed, and accuracy. AI, including various

specific methodologies, is becoming vital in managing TB. Machine learning (ML)

methodologies, such as support vector machines (SVMs) and random forests (RF),

alongside deep learning (DL) technologies, particularly convolutional neural

networks (CNNs) for image analysis, are employed to analyze diverse patient

data, including medical images and biomarkers, to enhance the accuracy and speed

of tuberculosis diagnosis. This study summarized the benefits and drawbacks of

both traditional and AI-driven TB diagnosis, highlighting how AI can support

traditional techniques to increase early detection, lower misdiagnosis, and

strengthen international TB control initiatives.

DOI: 10.3390/diseases13060184

PMCID: PMC12192536

PMID: 40558595

**15. Cells. 2025 Jun 9;14(12):867. doi: 10.3390/cells14120867.**

The Antibiotic-Resistant Protein MfpA Modulates Host Cell Apoptosis and Promotes

Mycobacterial Survival by Targeting Mitochondria and Regulating the NF-κB

Signaling Pathway.

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Mycobacterium tuberculosis (Mtb) is a major global health threat, exacerbated by

the emergence of antibiotic-resistant strains. This study investigated

fluoroquinolone resistance protein A (MfpA), which enhances mycobacterial

survival by targeting host mitochondria and regulating apoptosis. Wild-type (WT)

and knockout (KO) Mycobacterium bovis Bacillus Calmette-Guérin (BCG) strains, a

common model for Mtb, were utilized to examine host cell responses. Compared to

WT strains, KO strains showed reduced colony-forming units (CFUs), elevated

TNF-α and IL-6 levels, and increased apoptosis. MfpA was found to localize to

mitochondria, increasing ROS production and disrupting mitochondrial membrane

potential. Transcriptomic analysis revealed that MfpA modulated the NF-κB

signaling pathway, regulating the expression of gadd45β. These results suggest

that MfpA drives both antibiotic resistance and virulence by suppressing

apoptosis via the mitochondrial and NF-κB pathways, promoting mycobacterial

persistence. Studies using BCG provide valuable insight into Mtb's survival

mechanisms, highlighting MfpA's dual role in resistance and pathogenesis.

DOI: 10.3390/cells14120867

PMCID: PMC12190985

PMID: 40558494 [Indexed for MEDLINE]

**16. Front Cell Infect Microbiol. 2025 Jun 9;15:1584237. doi:**

**10.3389/fcimb.2025.1584237. eCollection 2025.**

A comprehensive evaluation of a novel targeted-sequencing workflow for

Mycobacterium species identification and anti-tuberculosis drug-resistance

detection.

Ou X(#)(1), Pei S(#)(1)(2), Li H(#)(3), Qin Z(#)(4), Anthony R(5), Wang J(6),

Song Z(1), Xing R(1), Zhang L(4), Teng C(7), Xia H(1), Zhou Y(1), Song Y(1),

Zheng Y(1), Wang S(1), Zhao B(1), Zhao Y(1).

**Xichao Ou, Shaojun Pei, Hongru Li, Zhonghua Qin, Richard Anthony, Jichun Wang, Zexuan Song, Ruida Xing, Lixia Zhang, Chong Teng, Hui Xia, Yang Zhou, Yuanyuan Song, Yang Zheng, Shengfen Wang, Bing Zhao\*, Yanlin Zhao\***

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(#)Contributed equally

**BACKGROUND:** Although several World Health Organization-endorsed targeted

next-generation sequencing (tNGS) assays exist for tuberculosis (TB)

drug-resistance detection, their target selection and diagnostic accuracy vary

widely. In this study, we developed a novel tNGS workflow (the TB Pro assay) and

evaluated its performance in identifying Mycobacterium species and predicting

drug resistance.

**METHODS:** The TB Pro assay was validated for identifying 10 Mycobacterium

tuberculosis complex (MTBC) and 39 nontuberculous mycobacterial (NTM) species,

as well as predicting resistance to 4 first-line and 13 second-line anti-TB

drugs. The limit of detection (LOD) was determined using 11 reference strains

spiked in sputum. The prediction of resistance to anti-tuberculous drugs/drug

classes was compared with phenotypic drug susceptibility testing (pDST) and

whole-genome sequencing (WGS) using 435 clinical isolates.

**RESULTS:** The assay demonstrated high sensitivity with a calculated LOD of 3.0

CFU/ml for MTB and 1.4-16.2 CFU/ml for most NTMs, except for Mycobacterium

intracellulare with 117.9 CFU/ml. Using pDST as the reference standard, the

sensitivity of the TB Pro assay for the detection of resistance ranged from

74.3% (ethambutol) to 94.4% (rifampicin), with specificity values >98% for all

drugs. Compared with WGS, the sensitivity of the TB Pro assay was over 98.0% for

all drugs except pyrazinamide (66.7%), and the specificity values were all

nearly 100.0%. Directly on sputum, the TB Pro assay showed 100% agreement with

smear- and culture-positive sputum specimens.

**CONCLUSIONS:** The TB Pro assay represents a sensitive and specific solution for

simultaneous mycobacterial identification and comprehensive drug-resistance

profiling, performing robustly on both cultured isolates and direct clinical

specimens.

Copyright © 2025 Ou, Pei, Li, Qin, Anthony, Wang, Song, Xing, Zhang, Teng, Xia,

Zhou, Song, Zheng, Wang, Zhao and Zhao.

DOI: 10.3389/fcimb.2025.1584237

PMCID: PMC12183266

PMID: 40552123 [Indexed for MEDLINE]

**17. Int J Gen Med. 2025 Jun 19;18:3267-3276. doi: 10.2147/IJGM.S516998. eCollection 2025.**

Advances in the Treatment and Clinical Management Strategies of Tuberculous

Meningitis.

Li R(1)(2), Yin R(2), Li Y(2), Wei Y(2), Zhao B(2), Ge C(1).

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Tuberculous meningitis (TBM), a central nervous system infection caused by

Mycobacterium tuberculosis, is a rapidly progressing, insidious disease with an

exceptionally high disability and mortality rate. Its significant global burden

has become a critical focus in public health. The clinical diagnosis of TBM

faces challenges due to the lack of specific symptoms and imaging

characteristics, making early detection difficult. Combined with the shielding

effect of the blood-brain barrier against anti-tuberculosis drugs and the issue

of drug resistance, treatment outcomes are often suboptimal. Furthermore,

current early sensitive diagnostic tools are inadequate, leading to delayed

treatment for many patients and adversely affecting their prognosis. This paper

reviews the pathophysiological mechanisms of TBM, the types and mechanisms of

action of therapeutic drugs, and the common drug selection issues and safety

challenges encountered in clinical practice. The aim is to provide comprehensive

guidance and references for clinical diagnosis and treatment to improve the

therapeutic outcomes and quality of life for TBM patients.

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DOI: 10.2147/IJGM.S516998

PMCID: PMC12184685

PMID: 40551753

**18. JB JS Open Access. 2025 Jun 20;10(2):e24.00249. doi: 10.2106/JBJS.OA.24.00249.**

**eCollection 2025 Apr-Jun.**

Long-Segment Ventral Spinal Epidural Abscesses Caused by Mycobacterium

Tuberculosis: A Report of 2 Cases and Review.

Le S(1), Tang J(1), Zhang J(1), Fu J(2), Zhang W(1), He M(1), Dai M(1), Wang

L(1).

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» Abscesses caused by spinal tuberculosis typically occur in the anterior and

lateral regions of the vertebral bodies, often extending to the paraspinal

muscles as cold abscesses. Although intraspinal abscesses due to spinal

tuberculosis are very common, cases with longitudinally extensive abscesses in

the ventral epidural space of the spinal cord are not well-documented. The

disease is characterized by insidious onset, rapid progression, and a high risk

of irreversible neurological damage, highlighting the necessity for early

diagnosis and prompt treatment. » This review presents 2 rare cases of

long-segment tuberculous spinal epidural abscesses, with both patients achieving

significant symptom improvement after precise surgical intervention and

standardized antituberculosis therapy. A long-segment tuberculous spinal

epidural abscess (SEA) is an extremely rare complication that may cause severe

neurological impairment, and magnetic resonance imaging revealed extensive

spinal epidural abscesses. Clinical manifestations, such as neck stiffness, can

easily be mistaken for tuberculous encephalopathy; therefore, contrast-enhanced

MRI is recommended to differentiate a SEA from tuberculous encephalopathy. »

Local decompression with catheter drainage can help preserve neurological

function, establish a definitive etiological diagnosis, and guide subsequent

treatment. Early, adequate, and comprehensive antituberculosis therapy is

crucial for successful management.

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Surgery, Incorporated. All rights reserved.

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PMCID: PMC12178294

PMID: 40547101

**19. iScience. 2025 May 23;28(6):112743. doi: 10.1016/j.isci.2025.112743. eCollection 2025 Jun 20.**

Habitat radiomics and transformer fusion model to evaluate treatment

effectiveness of cavitary MDR-TB patients.

Lv X(1), Wang Y(2), Ding C(3), Qin L(3), Xu X(1), Li Y(4), Hou D(1).

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First Medical University, Shandong Provincial Hospital, Jinan, China.

Promptly identification of multidrug-resistant tuberculosis (MDR-TB) patients at

high risk of treatment failure is essential for improving cure rates. This study

aimed to develop a habitat radiomics based transformer fusion model to assess

treatment effectiveness of MDR-TB. Independent patient cohorts from two

hospitals were included. Radiomics features were extracted from the habitat and

peripheral regions of cavities to construct predictive models. Then, a

transformer-based fusion model integrating features from all regions was

established. The areas under the receiver operating characteristic curves (AUCs)

were used to evaluate the performance. The transformer fusion model combining

two subregions and peripheral area achieved remarkable performance, with AUC

values of 1.000, 0.959, and 0.879 in the training, validation, and test cohort,

respectively. The finding highlights the efficacy of our model in predicting

treatment effectiveness of MDR-TB patients and its potential to guide

individualized therapy.

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PMCID: PMC12178788

PMID: 40546963

**20. J Multidiscip Healthc. 2025 Jun 17;18:3519-3530. doi: 10.2147/JMDH.S516019.**

**eCollection 2025.**

Association Between 10 Autoimmune Diseases and Risk of Pulmonary Tuberculosis: A

Mendelian Randomization Study.

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(#)Contributed equally

**BACKGROUND:** Pulmonary tuberculosis (PTB) may have an autoimmune component.

However, the cause of autoimmune diseases associated with PTB remains unclear.

We performed a Mendelian randomization (MR) study to determine the causal

genetic connections between liability to autoimmune diseases (AIDs) and PTB.

**METHODS:** After rigorous assessment, potential candidate SNPs for 10 AIDs and PTB

were extracted from GWAS datasets. Three common MR approaches-inverse variance

weighted (IVW), weighted median, and MR-Egger-were employed to assess causal

relationships. To ensure the robustness of the findings, sensitivity analyses

were performed to evaluate the stability of the results by estimating the

heterogeneity and pleiotropy.

**RESULTS:** Our MR analysis indicated no discernible causal genetic connections

between the seven AIDs, including rheumatoid arthritis (RA), asthma, Crohn's

disease (CD), systemic lupus erythematosus (SLE), psoriasis (PsO), multiple

sclerosis (MS), ankylosing spondylitis (AS), and PTB (all P>0.05).

Interestingly, inflammatory bowel disease (IBD; OR, 0.967; 95% CI: 0.941-0.994,

P=0.015), celiac disease (CeD; OR, 0.944; 95% CI: 0.917-0.972, P<0.001), and

primary sclerosing cholangitis (PSC; OR, 0.935; 95% CI: 0.877-0.997, P=0.041)

were significantly associated with a decreased risk of PTB. The sensitivity

analyses confirmed the robustness of the results.

**CONCLUSION:** Our MR observations collectively highlight that genetically

predicted IBD, CeD, and PSC may be protective factors against PTB. However,

there was no evidence of causal ramifications between the other seven AIDs (RA,

asthma, CD, SLE, PsO, MS, and AS) and PTB, implying that unmeasured confounders

or shared genetic structures may be the cause of the reported epidemiological

associations.

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DOI: 10.2147/JMDH.S516019

PMCID: PMC12182061

PMID: 40546289

**21. Acta Otolaryngol. 2025 Jun 27:1-9. doi: 10.1080/00016489.2025.2522899. Online**

**ahead of print.**

Clinical characteristics of tuberculous otitis media: when to sound the alarm?

Zhang N(1)(2), Wang D(1)(2), Zou Q(1)(2), Ma X(1)(2), Li Y(1)(2), Piao Y(3),

Zhao S(1)(2).

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University, Beijing, China.

**BACKGROUND:** Tuberculous otitis media (TOM) is a rare form of chronic otitis

media, which presents diagnostic challenges due to nonspecific symptoms.

AIMS/OBJECTIVES: To characterize the clinical features and identify strategies

for early diagnosis.

**MATERIALS AND METHODS:** A retrospective analysis was conducted on 32 patients (40

ears) diagnosed with TOM between 2002 and 2024. Clinical, audiologic,

radiologic, and laboratory findings were reviewed.

**RESULTS:** Mean diagnostic delay was 28.9 months. Persistent otorrhea (90%) and

hearing loss (HL) (100%) were predominant. Tympanic membrane findings varied:

single perforation (70%), multiple (12.5%), and intact (17.5%). Granulations

were universal. Age stratification revealed conductive HL and pneumatized

mastoids predominated in patients <40 years, while mixed HL and mixed-type

mastoid were more common in patients >40 years (p = 0.016, p = 0.005). Bone

destruction was evident in 25% of the cases. Mastoid type correlated with HL

patterns in non-destructive cases (p = 0.040). Interferon-gamma release assay

(IGRA) and polymerase chain reaction (PCR) showed relatively high detection

rates.

**CONCLUSIONS AND SIGNIFICANCE:** Early suspicion of TOM in refractory/recurrent

otitis media, combined with IGRA/PCR screening, prompt imaging, and

consideration of age-specific patterns, facilitates timely diagnosis. Surgical

biopsy remains critical for confirmation. Integration of age-stratified

clinical, laboratory, and radiological findings improves detection accuracy and

patient outcomes.

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Abdominal tuberculosis with pancreatic head involvement mimicking pancreatic

malignancy in a young man: A case report.

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**BACKGROUND:** Pancreatic tuberculosis (PTB) is a rare disease, even in

immunocompetent hosts. Abdominal tuberculosis involving the pancreatic head and

peripancreatic areas may simulate pancreatic head carcinoma.

**CASE SUMMARY:** We present the case of a 32-year-old man who was admitted to our

hospital for intermittent epigastric pain and weight loss. A computed tomography

scan and magnetic resonance imaging revealed a mass in the head of the pancreas.

The lesion was initially diagnosed as pancreatic head carcinoma on abdominal

imaging. Laparotomy confirmed the diagnosis of PTB and the patient received

antituberculosis therapy.

**CONCLUSION:** The present case is reported to emphasize the importance of

including PTB in the differential diagnosis of pancreatic lesions.

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Multifocal bone tuberculosis with adrenal involvement mimicking malignant tumors

with multiple metastases on PET/CT.

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