**2025年第41周**

**中国大陆学者发表的结核病英文文章摘要**

**（37篇）**

**PubMed Publication date: 2025/10/6---2025/10/12**

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

**1. Microb Genom. 2025 Oct;11(10). doi: 10.1099/mgen.0.001460.**

Pan- and core genome analysis of Mycobacterium tuberculosis in high-resolution

transmission and genetic diversity studies.

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Y(6), Wu K(1), Wang X(1), Zhao Y(4).

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The application of pan-genomics in understanding Mycobacterium tuberculosis

complex (MTBC) transmission remains understudied, particularly in high-burden

settings such as China. We constructed an M. tuberculosis complex pan-genome

(MTB\_pan) using 307 complete genomes representing all eight lineages from the

National Center for Biotechnology Information (NCBI). Core and accessory genomes

were analysed, lineage-associated genes were identified and functional

annotations were assessed using Pfam domains. Transmission dynamics were

evaluated by comparing pan-genome- and H37Rv-based approaches for isolates

collected from China, focusing on alignment rates, clustering efficiency and SNP

distances. The MTB\_pan (5.75 Mb) consisted of 3,893 core and 958 accessory

genes, with 176 accessory genes significantly associated with specific lineages.

These genes were enriched in PE/PPE/PGRS families, mobile genetic elements (e.g.

IS6110) and pentapeptide repeats. The median alignment rate based on MTB\_pan

reached 99.8%, which was significantly higher than that based on H37Rv. The

clustering rate of isolates based on MTB\_pan (19.93%) was higher than that based

on H37Rv (18.90%). The pairwise SNP distances below 50 SNPs within lineage 2

decreased significantly, while those within lineage 4 showed no significant

differences. Compared to a single reference genome, clustering using the

pan-genome improved the identification of same-province transmission events.

Therefore, the pan-genomic analysis is a more powerful analytical tool that

enables the establishment of a high-resolution picture of tuberculosis

transmission in different epidemiological settings, which will enable more

precise outbreak mapping and support data-driven tuberculosis control

strategies.

DOI: 10.1099/mgen.0.001460

PMID: 41042591 [Indexed for MEDLINE]

**2. Inflamm Res. 2025 Oct 3;74(1):138. doi: 10.1007/s00011-025-02106-4.**

Lung epithelial injury impairs early host immune responses to Mycobacterium

tuberculosis.

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Q(5), Chen H(6)(7)(8).

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**OBJECTIVE:** Tuberculosis (TB), caused by Mycobacterium tuberculosis (Mtb),

remains a significant global health burden, characterized by complex

host-pathogen interactions that drive heterogeneous clinical outcomes. While

pulmonary epithelial cells are increasingly recognized as active participants in

innate immunity during Mtb infection, how host defense are altered when the

epithelial barrier is compromised remains unclear.

**METHODS:** In this study, we developed a murine model combining

naphthalene-induced pulmonary epithelial injury with Mtb infection and mapped

the pulmonary cells landscape through single-cell RNA sequencing (scRNA-seq),

followed by in vitro stimulation assays to validate macrophage functional

changes.

**RESULTS:** Notably, we found a pronounced impairment in pulmonary bacterial

clearance. Transcriptomic analysis revealed a widespread suppression of

epithelial immune functions and showed that macrophages transitioned from an

antimicrobial to an antigen-presenting phenotype, indicating waning pulmonary

innate defenses and heightened adaptive immune activation. In vitro experiments

further suggested that this macrophage transition may be linked to epithelial

cell alterations.

**CONCLUSIONS:** These findings indicate that pulmonary epithelial integrity may

influence early host immune responses to Mycobacterium tuberculosis and provide

a transcriptomic framework for exploring epithelial-immune crosstalk as a

potential therapeutic target.

© 2025. The Author(s).

DOI: 10.1007/s00011-025-02106-4

PMID: 41042276 [Indexed for MEDLINE]

**3. Sci Rep. 2025 Oct 2;15(1):34370. doi: 10.1038/s41598-025-17061-7.**

Determinants of treatment success and cost implications in MDR/RR-TB patients: a

prospective cohort study in China.

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Multidrug-resistant or rifampicin-resistant tuberculosis (MDR/RR-TB) remains a

critical global health threat. While novel regimens offer promise, the impact of

socioeconomic determinants and clinical factors on treatment success is

inadequately characterized, hindering targeted interventions. A prospective

cohort study was conducted across 13 TB-designated hospitals in Jiangsu

Province, China from 2021 to 2022. Binary logistic regression identified

predictors of treatment success, with model performance assessed via Receiver

Operating Characteristic (ROC) curves assessing predictive performance. The

overall treatment success rate for patients with MDR/RR-TB was 67.38%, with the

short-term regimen achieving a success rate of 74.4%, new long-term oral

regimens at 66.7%, new long-term injectable regimens at 71.0%, traditional

long-term regimens at 60.3%, though differences were not statistically

significant (P = 0.454). Patients educated at the junior and senior high school

levels (OR = 3.95, 95% CI: 1.70, 9.19, P = 0.001) and at the college level or

above (OR = 3.13, 95% CI: 1.03, 9.51, P = 0.044) exhibited significantly higher

success rates compared to those with primary school education or lower.

Moreover, it underscores the irrelevance of cost to treatment outcomes.

Additionally, urban workers (OR = 4.53, 95% CI: 1.22, 16.86, P = 0.024), urban

residents (OR = 4.61, 95% CI: 1.25, 17.04, P = 0.022), and individuals covered

by other medical insurance, including public medical insurance (OR = 8.82, 95%

CI: 1.50, 51.76, P = 0.016), demonstrated higher treatment success rates

compared to those without medical insurance. Conversely, hypokalemia (OR = 0.12,

95% CI: 0.02, 0.61, P = 0.010) was identified as a risk factor for successful

treatment. Treatment costs demonstrated no significant association with outcomes

(OR = 1.06, 95%CI: 0.96, 1.17, P = 0.284). Prioritizing health literacy

programs, insurance expansion, and hypokalemia monitoring is essential for

improving treatment success.

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DOI: 10.1038/s41598-025-17061-7

PMID: 41038881 [Indexed for MEDLINE]

**4. Int J Infect Dis. 2025 Sep 30:108085. doi: 10.1016/j.ijid.2025.108085. Online**

**ahead of print.**

Immune profiles of immune checkpoint molecules on peripheral T cells in

multidrug-resistant tuberculosis.

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**BACKGROUND:** T cell immunity is impaired due to T cell exhaustion during chronic

infection, including infections caused by Mycobacterium tuberculosis (M.tb).

However, the immunological characteristics of multidrug-resistant tuberculosis

(MDR-TB) patients remain unclear.

**METHOD:** Multiparametric flow cytometry was employed to measure the expression of

immune checkpoint molecules (CTLA-4, PD-1, TIM-3) and the proliferation marker

Ki67 in MDR-TB (n=27) and drug-sensitive TB (NR-TB) (n=51) samples.

**RESULT:** We showed that MDR-TB patients exhibited higher percentages of CTLA-4,

PD-1, and TIM-3 expressing T cells than NR-TB subjects before anti-TB treatment.

Additionally, significantly higher percentages of CTLA-4+ PD-1+ and CTLA-4+

TIM-3+ co-expressing T cells were observed in MDR-TB patients when compared to

NR-TB patients. Impaired cell proliferation of T cells was detected in MDR-TB

patients with more exhaustion status of T cells. Interestingly, In MDR-TB

patients, checkpoint-molecule expression on T cells declined during anti-TB

treatment and eventually matched NR-TB levels, whereas NR-TB patients showed no

significant change.

**CONCLUSION:** Our results thus indicate that T cells exhibit more exhausted status

in MDR-TB patients which could be reversed after the treatment, which suggests

that an additional host-directed treatment might improve the efficacy of anti-TB

drug regimens.

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DOI: 10.1016/j.ijid.2025.108085

PMID: 41038528

**5. J Infect. 2025 Sep 30:106621. doi: 10.1016/j.jinf.2025.106621. Online ahead of print.**

Detection of Pulmonary Tuberculosis and Drug Resistance in Sputum Samples Using

Targeted Next-Generation Sequencing.

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DOI: 10.1016/j.jinf.2025.106621

PMID: 41038518

**6. Mikrochim Acta. 2025 Sep 30;192(10):704. doi: 10.1007/s00604-025-07437-x.**

Enhanced cyclohexane resistive gas sensing using Mg-doped Bi(2)WO(6) hollow

microtubes derived from selective etching of MOF.

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The design of composition and morphology is a highly effective strategy for

transforming solid metal-organic frameworks (MOFs) into hollow structures. In

this study, we synthesized Mg-doped Bi2WO6 hollow tubes using bismuth

metal-organic frameworks (CAU-17) as templates. This process involves the

synthesis of solid CAU-17 microtubes, the etching of hollow tubes using

Mg2+/WO42- ions, and the formation of Mg/Bi2WO6 hollow microtubes through air

annealing. The unique hollow structure and complex composition of Mg/Bi2WO6

contribute to its exceptional resistive gas sensing performance for detecting

cyclohexane. The excellent cyclohexane sensing capabilities of Mg/Bi2WO6 are a

result of the cooperative enhancement from its hollow structure (high utility

factor) and Mg doping (optimized receptor and transducer functions), with its

high selectivity being fundamentally governed by the favorable adsorption

thermodynamics and kinetics of cyclohexane on its surface. The Mg/Bi2WO6

(ωMg = 0.2 wt.%) sensor exhibits remarkable sensitivity (50 ppm, Ra/Rg = 67),

detecting cyclohexane as low as 0.1 ppm at 275 °C (Ra/Rg = 1.2). Additionally,

it demonstrates excellent selectivity and outstanding stability for cyclohexane,

underscoring its potential for practical applications in the clinical diagnosis

of tuberculosis patients. This work presents a novel strategy for the rational

design of hollow tube metal oxides with superior resistive gas sensing

capabilities, paving the way for future advancements in multifunctional

materials.

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part of Springer Nature.

DOI: 10.1007/s00604-025-07437-x

PMID: 41028566

**7. J Clin Immunol. 2025 Sep 30;45(1):131. doi: 10.1007/s10875-025-01926-7.**

Five CGD-Linked CYBB Mutations in Chinese Patients: Insights Into Predicting

IFN-γ Treatment Efficacy.

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**BACKGROUND:** The CYBB gene encodes the gp91-phox protein, a critical component of

the NADPH oxidase complex involved in pathogen clearance. Mutations in CYBB are

associated with chronic granulomatous disease (CGD), leading to recurrent

bacterial infections.

**OBJECTIVE:** To understand the genetic causes of Chinese CGD patients.

**METHODS:** Exome sequencing was used to identify mutations in CGD patients' PBMCs,

confirmed by Sanger sequencing. Neutrophil respiratory burst capacity was

analyzed to correlate with clinical treatment efficacy.

**RESULTS:** We identified five CYBB mutations in six CGD patients from five

unrelated Chinese families, including two novel mutations (c.1507A > G:p.T503A,

c.1587\_1605del:p.529\_535del), two rare mutations without functional

characterization (c.43A > G:p.I15V, c.125C > A:p.T42K), and one recently

reported in a different ethnicity (c.252G > T:p.A84A). Our analysis revealed

that these mutations had varying effects on CYBB expression, demonstrating that

the synonymous c.252G > T mutation is indeed a splicing mutation, resulting in

exon 3 deletion and minimal protein expression. Neutrophils from all patients

exhibited defective mitogen-stimulated respiratory bursts. However, only

neutrophils with the I15V mutation responded to interferon-γ (IFN-γ) treatment,

significantly improving the respiratory capacity defect. Consistent with this,

the patient with the I15V mutation showed clinical improvement after two weeks

of IFN-γ and anti-bacterial co-treatment.

**CONCLUSION:** Our findings underscore the diverse effects of CYBB mutations on

protein expression and function. More importantly, they suggest that assessing

the IFN-γ-mediated potentiation of respiratory burst response in patient's

neutrophils is an effective way to predict the therapeutic efficacy of IFN-γ in

treating CGD cases, particularly those with non-tuberculous mycobacteria (NTM)

and Mycobacterium tuberculosis (TB).

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DOI: 10.1007/s10875-025-01926-7

PMCID: PMC12484266

PMID: 41026270 [Indexed for MEDLINE]

**8. Front Cell Infect Microbiol. 2025 Sep 11;15:1646194. doi:**

**10.3389/fcimb.2025.1646194. eCollection 2025.**

Optimization of decision thresholds for Mycobacterium tuberculosis can

effectively improve the performance of mNGS in tuberculosis diagnosis.

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**BACKGROUND:** Pulmonary tuberculosis (TB) diagnosis remains challenging due to

limitations in traditional methods. This study aimed to optimize the metagenomic

next-generation sequencing (mNGS) threshold for Mycobacterium tuberculosis

complex (MTBC) detection and evaluate its efficacy compared to standard

diagnostic approaches.

**METHODS:** A total of 264 bronchoalveolar lavage fluid (BALF) samples were

collected from patients with suspected pulmonary TB at Yongkang First People's

Hospital between January 2022 and June 2023. After excluding patients with

incomplete data, 59 clinically confirmed TB patients and 111 with

non-tuberculous conditions were enrolled. mNGS data were analyzed to calculate

reads per million (RPM) for MTBC, and thresholds of 0.02, 0.05, and 0.10 RPM

were evaluated for diagnostic efficacy using clinical diagnosis as the gold

standard.

**RESULTS:** The area under the receiver operating characteristic (ROC) curve (AUC)

for mNGS in diagnosing TB at RPM thresholds of ≥0.02, ≥0.05, and ≥0.10 were

0.881, 0.873, and 0.814, respectively. The optimal detection threshold was found

at RPM ≥ 0.05. Comparative analysis showed mNGS (AUC = 0.873) outperformed

routine culture (0.718), PCR (0.741), and Xpert (0.763). Combining mNGS with

these methods improved AUC values to 0.837, 0.868, and 0.873, respectively.

**CONCLUSION:** Optimizing the mNGS threshold to ≥0.05 significantly enhances MTBC

detection in pulmonary TB. Combining mNGS with traditional methods further

improves diagnostic efficacy, suggesting a potential role for mNGS in clinical

TB management.

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DOI: 10.3389/fcimb.2025.1646194

PMCID: PMC12485630

PMID: 41040987 [Indexed for MEDLINE]

**9. Front Cell Infect Microbiol. 2025 Sep 17;15:1653602. doi:**

**10.3389/fcimb.2025.1653602. eCollection 2025.**

Rapid identification of major Mycobacterium species by loop-mediated isothermal

amplification assay using novel species-specific genomic targets.

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**BACKGROUND:** Rapid and precise identification of Mycobacterium species is

critical for appropriate clinical management and epidemiological surveillance.

However, conventional methods often fail to differentiate closely related

nontuberculous mycobacteria (NTM) species, limiting their clinical utility.

**METHODS:** We developed a multiplex loop-mediated isothermal amplification (LAMP)

assay targeting newly identified species-specific genomic markers for

simultaneous detection of Mycobacterium tuberculosis complex (MTBC) and six

clinically important NTM species. Analytical performance was assessed using

serial dilutions of bacterial cultures and 36 reference strains. Clinical

validation was performed on 52 cultured isolates and 349 sputum samples,

compared to GeneXpert MTB/RIF and a commercial PCR-reverse dot blot assay.

**RESULTS:** The assay showed high analytical sensitivity, with limits of detection

ranging from 76.013 CFU/mL (95% CI: 60.329-113.924 CFU/mL) for MTBC to

166.602-690.629 CFU/mL for NTM species. All reference strains were correctly

identified with no cross-reactivity. Among the clinical isolates, all targeted

species were accurately detected. One isolate misidentified as M. abscessus by

an ITS-based assay was confirmed by sequencing to be M. massiliense,

demonstrating the assay's superior discriminatory capacity. For sputum samples,

the assay achieved 90.32% sensitivity and 97.55% specificity for MTBC, with an

overall agreement of 93.70% (κ = 0.8740).

**CONCLUSION:** This multiplex LAMP assay offers a rapid, accurate, and

field-deployable tool for species-level identification of MTBC and major NTM

pathogens. Its simplicity, stability, and compatibility with low-resource

settings support its application in routine diagnostics and decentralized

tuberculosis programs.

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DOI: 10.3389/fcimb.2025.1653602

PMCID: PMC12484021

PMID: 41040984 [Indexed for MEDLINE]

**10. Bioorg Chem. 2025 Sep 23;165:109016. doi: 10.1016/j.bioorg.2025.109016. Online ahead of print.**

Optimization of pyrrole-2-carboxamide to develop a potent antituberculosis agent

with improved physicochemical property and druggability.

Wu Y(1), Zhao H(1), Wang B(2), Chen X(2), Jin B(3), Zheng Y(1), Ma C(3), Sheng

L(3), Lu Y(4), Huang H(5), Zhang D(6).

**Yanan Wu, Hongyi Zhao, Bin Wang, Xi Chen, Bo Jin, Yixuan Zheng, Chen Ma, Li Sheng, Yu Lu\*, Haihong Huang\*, Dongfeng Zhang\***

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MmpL3, a mycobacterial membrane protein, is essential for the transport of

trehalose monomycolate, which is crucial for the formation of the M.

tuberculosis outer membrane and the survival of the bacterium. Herein, we

optimize our lead MmpL3 inhibitor bearing pyrrole-2-carboxamide scaffold to

develop antituberculosis agents with improved physicochemical properties.

Compound 27b, an optimized analog of our lead MmpL3 inhibitor, exhibited

enhanced antituberculosis activity along with reduced cytotoxicity, improved

microsomal stability, and high Caco-2 permeability. Significantly, the water

solubility and pharmacokinetic profile of compound 27b was markedly improved

compared to the lead compound 2. This compound demonstrated potent efficacy in

decreasing the intracellular M. tuberculosis load within mouse macrophages. The

results of this study indicated that incorporating an oxygen-containing group in

pyrrole-2-carboxamide scaffold can improve the compound's LogP value, thereby

achieving a balance between lipophilicity and antituberculosis activity.

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DOI: 10.1016/j.bioorg.2025.109016

PMID: 41037866

**11. Int Immunopharmacol. 2025 Sep 27;166:115582. doi: 10.1016/j.intimp.2025.115582. Online ahead of print.**

Synergistic elimination of bacillus Calmette-Guérin biofilm and tissue

restoration facilitated by ultrasound-mediated nanoparticles and antioxidants.

Zhang Y(1), Huang C(1), Qiu Y(1), Li R(1), Liu J(1), Du Y(2), Li D(3).

**Yuqing Zhang, Chaorong Huang, Yan Qiu, Ruicheng Li, Jialing Liu, Yonghong Du\*, Dairong Li\***

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Biofilm formation in Mycobacterium tuberculosis (MTB) enhances antibiotic

resistance by impeding drug penetration and evading host immunity. This poses a

significant challenge to conventional drug therapies, highlighting the urgent

need for novel treatment strategies to overcome MTB's biofilm-mediated

resistance. This study introduces the development of low-intensity

ultrasound-mediated levofloxacin (LEV) and catalase (CAT) -loaded PEG-PLGA

nanoparticles (LEV@CAT-NPs) for antimicrobial sonodynamic therapy (aSDT),

offering an innovative strategy to combat BCG biofilm infection, by utilizing

BCG as a model for MTB. N-acetylcysteine (NAC) was supplemented during the

latter stages of the treatment process of anti-infection therapy to facilitate

the transformation of macrophages to the M2 phenotype and to promote tissue

repair. Ultrasound-mediated LEV@CAT-NPs, along with the subsequent addition of

NAC not only enhanced repair at the infection site but also led to a progressive

resolution of the inflammatory response in tissues. The treatment regimen

induced a shift in macrophage polarization towards the M2 phenotype and

modulated cytokine expression, decreasing pro-inflammatory while increasing

anti-inflammatory cytokines, which contributed to the restoration of redox

balance in the infected tissues. This study proposes a novel therapeutic

strategy that not only targets drug-resistant MTB but also promotes tissue

repair, highlighting its dual role in infection management.

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DOI: 10.1016/j.intimp.2025.115582

PMID: 41016202

**12. Respiration. 2025 Sep 15:1-21. doi: 10.1159/000548355. Online ahead of print.**

Development and Validation of a Nomogram to Predict Airway Fibrostenosis in

Tracheobronchial Tuberculosis.

Zhao W, Fang W, Peng D, Feng Z, Wang M, Zhang H, Yuan Y, Wu D, Chen Z, Huang X,

Yang Z, Fan J, Xiao X, Kuang H.

**Wei Zhao, Weiming Fang, Dehu Peng, Zhiyu Feng, Min Wang, Hong Zhang, Yuan Yuan, Di Wu, Zeying Chen, Xianlin Huang, Zilong Yang, Jiahua Fan, Xincai Xiao, Haobin Kuang\***

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**BACKGROUND:**  Airway fibrostenosis, a severe complication of tracheobronchial

tuberculosis (TBTB), causes respiratory morbidity including atelectasis,

pneumonia, and respiratory failure. Early risk prediction remains challenging

due to the lack of validated assessment tools.

**METHODS:**  This retrospective cohort study analyzed TBTB patients undergoing

bronchoscopic interventions between January 2021 and June 2024 with 6-month

follow-up. A Cox regression model was developed in all 305 patients, internally

validated with 1,000 bootstrap resamples. Performance was evaluated via C-index,

ROC-AUC, calibration, and decision curve analysis. Kaplan-Meier analysis was

used to stratify groups, with log-rank tests assessing differences.

**RESULTS:**  Airway fibrostenosis incidence was 60.33% (184/305). Eight independent

predictors were identified: symptom duration, affected lung lobes, diabetes,

multiple TBTB types, bronchoscopic intervention frequency, initial sputum

acid-fast bacilli smear grade, neutrophil-to-lymphocyte ratio, and CD8+ T-cell

count. The nomogram demonstrated strong discrimination (C-index 0.77, 95%CI

0.75-0.81) with increasing predictive accuracy over time: 6-week AUC 0.773

(0.708-0.838), 8-week 0.792 (0.740-0.844), 12-week 0.830 (0.782-0.878), and

16-week 0.883 (0.842-0.923). High-risk patients exhibited a significantly higher

probability of developing airway fibrostenosis compared to low-risk patients

(P<0.001). Calibration and decision curve analyses confirmed clinical utility.

**CONCLUSIONS:**  This validated nomogram effectively predicts airway fibrostenosis

risk in TBTB patients, enabling early identification of high-risk individuals

for targeted interventions.

S. Karger AG, Basel.

DOI: 10.1159/000548355

PMID: 40947844

**13. bioRxiv [Preprint]. 2025 Apr 13:2025.04.11.648467. doi:**

**10.1101/2025.04.11.648467.**

Tissue-wide profiling of human lungs reveals spatial sequestration of

macrophages in tuberculosis.

Xiao W（1）（2）（3）, Sawyer AJ（1）（2）（4）, Mo S（5）, Bai X（1）（2）（6）, Yang Q（7）, Gao Y（7）, Fielder T（8）, Zhang Y（5）, Dai Y（5）, Yang

Q（9）, Cai Y（5）, Ding G（10）, Deng G（9）, Fu L（9）, Quek C（1）（2）（6）, Wilmott J（1）(2)(6), Palendira U(1)(2)(3)(4), Britton WJ(4)(11),

Barber DL(12), Ernst JD(13), Patrick E(14)(15)(16), Feng CG(1)(2)(3)(4), Chen X(5).

**Wei Xiao, Andrew J Sawyer, Siwei Mo, Xinyu Bai, Qinzhu Yang, Yi Gao, Timothy Fielder, Yue Zhang, Youchao Dai, Qianting Yang, Yi Cai, Guanggui Ding, Guofang Deng, Liang Fu, Camelia Quek, James Wilmott, Umaimainthan Palendira, Warwick J Britton, Daniel L Barber, Joel D Ernst, Ellis Patrick, Carl G Feng\*, Xinchun Chen\***

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The immune response to human tuberculosis (TB), particularly in the context of

complex lung pathology, remains incompletely understood. Here, we employed

whole-slide spatial proteomics to map immune cell organization in TB-affected

human lung tissues. Our analysis revealed pronounced spatial segregation of

major immune cell populations in non-necrotizing TB lesions. At the tissue

level, macrophages and lymphocytes formed distinct cellular communities

associated with specific pathological features. At the lesion level, macrophages

and B cells showed an inverse relationship in both abundance and spatial

distribution. Proinflammatory T cells preferentially accumulated in

macrophage-rich lesions but remained largely separated from macrophages.

Interestingly, lesions exhibiting clear segregation between T cells and

macrophages were more common in subclinical TB than in active disease. These

findings suggest that spatial isolation of macrophages from effector lymphocytes

may help temper inflammation and potentially prevent lesion progression to

necrosis, while also enabling immune evasion by Mycobacterium tuberculosis .

ONE SENTENCE SUMMARY: Xiao et al. reveal spatial segregation of immune cells in

TB-lung tissue and link the microenvironmental dynamics to disease states of

tuberculosis.

DOI: 10.1101/2025.04.11.648467

PMCID: PMC12478358

PMID: 41030999

**14. J Craniofac Surg. 2025 Oct 7. doi: 10.1097/SCS.0000000000012049. Online ahead of print.**

Intracranial Tuberculoma Mimicking Malignant Tumor in a Hemodialysis-Dependent

Patient With Multimorbidity: Diagnostic Challenges and Molecular Pathologic

Confirmation.

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Central nervous system tuberculomas are clinically rare (accounting for 1%-2% of

intracranial space-occupying lesions), and they are particularly prone to

misdiagnosis as malignant tumors when there is a lack of symptoms of

tuberculosis intoxication. This article reports a case of a 39-year-old female

who presented with generalized tonic-clonic seizures. Imaging suggested a

malignant invasive lesion in the frontal lobe with skull base destruction. The

patient had multiple high-risk factors including hemodialysis, diabetes, and

anticoagulation after coronary stent placement, and was ultimately diagnosed

with intracranial tuberculoma through molecular pathology. This case highlights

the insidious nature of extrapulmonary tuberculosis and the diagnostic

challenges under the coexistence of multiple diseases, providing a reference for

diagnosis in similar complex cases.

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DOI: 10.1097/SCS.0000000000012049

PMID: 41066634

**15. mSystems. 2025 Oct 9:e0097225. doi: 10.1128/msystems.00972-25. Online ahead of print.**

High-throughput cytological profiling uncovers genotype-phenotype associations

in Mycobacterium tuberculosis clinical isolates.

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NC(3), Gan M(1), Rubin EJ(3), Fortune SM(3), Zhu J(4).

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Understanding the functional impact of bacterial genetic diversity is crucial

for linking pathogen variants to clinical outcomes. Here, we introduce a

high-throughput cytological profiling pipeline optimized for Mycobacterium

tuberculosis (Mtb) clinical strains, integrating OD-calibrated feature analysis

and high-content microscopy. Our system quantifies single-bacterium

morphological and physiological traits related to DNA replication, redox state,

carbon metabolism, and cell envelope dynamics. Applied to 64 Mtb clinical

isolates from lineages 1, 2, and 4, the approach revealed that cytological

phenotypes recapitulate genetic relationships and exhibit both lineage- and

density-dependent dynamics. Notably, we identified a link between a convergent

"small cell" phenotype and a convergent ino1 mutation that is associated with

the presence of an antisense transcript, suggesting a potential non-canonical

regulatory mechanism under selection. In summary, we present a

resource-efficient approach for mapping Mtb's phenotypic landscape, uncovering

cellular traits that underlie its evolution and providing new insights into the

functional consequences of bacterial genetic diversity.

**IMPORTANCE:** Understanding how genetic variation in Mycobacterium tuberculosis

(Mtb) shapes its physical traits is essential to unraveling the evolution of

this global pathogen. Here, we introduce a systematically optimized,

high-throughput imaging platform for the comprehensive characterization of Mtb

clinical strains. We demonstrate that Mtb's phenotypic manifestation is shaped

by both genetic background and culture density. By accounting for these factors,

our analysis linked distinct cellular dynamics to specific lineages,

sublineages, and even single nucleotide variations. Notably, we linked a

recurring mutation to a unique cell-shortening phenotype, finding that it

potentially acts by creating a cryptic antisense transcript. This platform

provides a powerful framework for systematically dissecting the physiological

dynamics underlying Mtb evolution and identifying new therapeutic

vulnerabilities of this deadly pathogen.

DOI: 10.1128/msystems.00972-25

PMID: 41065399

**16. BMC Infect Dis. 2025 Oct 8;25(1):1251. doi: 10.1186/s12879-025-11664-1.**

Unveiling the crucial genomic players in pulmonary tuberculosis-associated

ferroptosis through bioinformatics scrutiny.

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**BACKGROUND:** Tuberculosis (TB) is a persistent infectious disease primarily

impacting the lungs. Despite its global prevalence, conventional diagnostic

methods suffer from prolonged detection times and low sensitivity, leading to

diagnostic challenges and suboptimal patient outcomes. Ferroptosis, which is

marked by an accumulation of iron-dependent lipid peroxides and subsequent lipid

peroxidation, has emerged as a promising prognostic indicator of various

maladies. This study aims to identify and pinpoint ferroptosis-related genes

pertinent to pulmonary tuberculosis (PTB), offering potential molecular

indicators for the early diagnosis, treatment, and prognosis of PTB.

**METHODS:** Employing bioinformatics analysis and transcriptome sequencing data of

tuberculosis patients, this research screened for differentially expressed

ferroptosis-related genes in tuberculosis sourced from FerrDb, with subsequent

identification of key genes. Whole blood samples collected from 10 tuberculosis

patients and 10 healthy volunteers were used for fluorescence-based real-time

quantitative polymerase chain reaction (qRT-PCR) to validate the expression

levels of identified genes, laying the groundwork for early tuberculosis

diagnosis and clinical intervention.

**RESULTS:** A total of 20 differentially expressed ferroptosis-related genes were

identified from the database. Gene Ontology functional enrichment analysis

highlighted their involvement in biological processes like hypoxia response,

enzyme activity, and autophagy. By constructing a protein-protein interaction

network via STRING and integrating it with enrichment analysis, key ferroptosis

genes in PTB, including HRAS, ATF3, MAPK8, ATM, IDH1, and HIF1A, were singled

out. The results of qRT-PCR demonstrate significantly elevated expression levels

of ATF3 and MAPK8 in PTB patients compared to those of healthy controls

(P < 0.05).

**CONCLUSION:** ATF3 and MAPK8 emerged as pivotal ferroptosis-related genes in PTB,

holding promise as molecular markers for PTB diagnosis and treatment.

SUPPLEMENTARY INFORMATION: The online version contains supplementary material

available at 10.1186/s12879-025-11664-1.

DOI: 10.1186/s12879-025-11664-1

PMCID: PMC12505692

PMID: 41063057

**17. Microbiol Spectr. 2025 Oct 8:e0225025. doi: 10.1128/spectrum.02250-25. Online**

**ahead of print.**

Lefamulin harbors promising anti-tuberculosis activity against

multidrug-resistant Mycobacterium tuberculosis isolates.

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Multidrug-resistant tuberculosis (MDR-TB) is often associated with poor clinical

outcomes. This study evaluated the in vitro activity of lefamulin (LEF) and

intracellular activities against Mycobacterium tuberculosis. In this study, we

evaluated the potential of LEF as a new drug candidate for treating M.

tuberculosis infections, including MDR-TB. The antimicrobial susceptibility

testing was performed to determine the minimum inhibitory concentrations (MICs)

of LEF against 132 clinical isolates of M. tuberculosis. The intracellular

activity of LEF and its interaction with other anti-tuberculosis drugs were also

evaluated using M. tuberculosis H37Rv. From the 132 M. tuberculosis clinical

isolates, the MIC50 and MIC90 were 0.5 µg/mL and 1 µg/mL, respectively. The

tentative epidemiological cut-off (ECOFF) against LEF was defined at 1 µg/mL.

After 5 days of incubation, LEF at 2 µg/mL inhibited 89.88% ± 1.73% of

intracellular bacterial growth, which was comparable with the inhibitory rate of

94.29% ± 1.32% achieved by INH at 2 µg/mL. In addition, a synergy between LEF

and bedaquiline (BDQ) was observed with a fractional inhibitory concentration

index = 0.5. Furthermore, LEF showed no correlation with resistance to 10

anti-tuberculosis drugs. The minimum bactericidal concentration/MIC of LEF

values suggested that it is a bacteriostatic drug against M. tuberculosis, and

the bactericidal activity is mainly characterized by a concentration-dependent

pattern. LEF has potent inhibitory activities against M. tuberculosis in vitro

as well as in macrophages. Furthermore, the synergistic effect with BDQ also

favors LEF as a promising drug candidate for tuberculosis treatment, especially

for MDR-TB.

**IMPORTANCE** Lefamulin (LEF), the first systemic pleuromutilin

antibiotic approved for human use, exhibits broad-spectrum activity against

Gram-positive bacteria. However, its in vitro activity against Mycobacterium

tuberculosis (Mtb) remains unexplored. This study evaluated the potential of LEF

for treating Mtb infections, including multidrug-resistant tuberculosis. Our

findings demonstrate that LEF possesses potent bacteriostatic activity against

Mtb in vitro and exhibits synergistic effects when combined with bedaquiline.

These results suggest LEF as a promising therapeutic candidate for tuberculosis

treatment.

DOI: 10.1128/spectrum.02250-25

PMID: 41059697

**18. BMC Infect Dis. 2025 Oct 7;25(1):1239. doi: 10.1186/s12879-025-11221-w.**

Whole genome sequencing for tuberculosis disease species identification, lineage

determination, and drug resistance detection in Kashgar prefecture, China.

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**BACKGROUND:** We aimed to use whole genome sequencing (WGS) to determine species

and lineage composition and drug resistance profile in a high tuberculosis

(TB)-burden region of China.

**METHODS:** We conducted WGS to 1791 acid-fast staining positive and

culture-positive isolates collected from Kashgar prefecture in 2020.

Bioinformatic analysis was applied to confirm species, lineage and drug

resistant-related mutations. The drug susceptibility testing was performed on

confirmed Mycobacterium tuberculosis complex (MTBC) isolates. We determined the

accuracy of WGS prediction by comparing with phenotypes.

**RESULTS:** 95.03% (1702/1791) were identified MTBC, 3.18% (57/1791) were

nontuberculous mycobacteria (NTM), 0.61% (11/1791) were nocardia, 0.89%

(16/1791) were gordonia and 0.056% (1/1791) were rhodococcus, the rest 4

isolations were identified as mixed infection. MTBC were composed of lineage 2

(45.83%, 780/1702), lineage 3 (462/1702, 27.14%), lineage 4 (455/1702, 26.73%),

lineage 1(1/1702, 0.06%) and M.bovis (La1, 4/1702, 0.24%). Resistance to

rifampicin, ethambutol, fluoroquinolones, aminoglycosides and ethionamide were

accurately predicted with sensitivity of 96.43%, 83.33%,100%, 100% and 94.74% by

WGS, while resistance to isoniazid with the sensitivity of 81.62%.

**CONCLUSIONS:** WGS can be an important approach in assessing TB control strategy

and for determining therapeutic schemes in high TB-burden regions. The drug

resistance TB of Kashgar prefecture is at low level and the application of WGS

may prevent the increase of resistance rate.

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DOI: 10.1186/s12879-025-11221-w

PMCID: PMC12502365

PMID: 41057789 [Indexed for MEDLINE]

**19. BMC Infect Dis. 2025 Oct 7;25(1):1246. doi: 10.1186/s12879-025-11689-6.**

Analysis of clinical and bronchoscopic features of multidrug-resistant

tracheobronchial tuberculosis.

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Z(1)(3), Ke X(1)(3), Wang X(1)(3), Gao W(2)(3), Li G(4)(5).

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**OBJECTIVE:** Investigate patients' clinical characteristics and bronchoscopic

features with multidrug-resistant tracheobronchial tuberculosis.

**METHODS:** A total of 118 patients with confirmed diagnosis of multidrug-resistant

tracheobronchial tuberculosis were selected retrospectively, and the demographic

data, clinical characteristics, and bronchoscopic manifestations were analyzed.

**RESULTS:** Among patients with multidrug-resistant tracheobronchial tuberculosis,

the main clinical features were cough (92.3%,109/118) and sputum (83.0%,98/118).

The primary infection sites of multidrug-resistant tuberculosis were the right

upper bronchus (39.8%,47/118) and the left upper bronchus (37.3%,44/118). The

main types of multidrug-resistant tracheobronchial tuberculosis lesions were

inflammatory infiltration type (46.6%,55/118) and necrosis type (32.2%,38/118).

**CONCLUSION:** The clinical manifestations of multidrug-resistant tracheobronchial

tuberculosis are non-specific. The main clinical features are cough and fever.

It often invades the right upper bronchus. The main bronchoscopic manifestation

is inflammatory infiltration.

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DOI: 10.1186/s12879-025-11689-6

PMCID: PMC12502215

PMID: 41057760 [Indexed for MEDLINE]

**20. Eur Spine J. 2025 Oct 8. doi: 10.1007/s00586-025-09434-3. Online ahead of print.**

Wasting phenotype for differentiating spinal tuberculosis from spinal pyogenic

infection.

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Z(2)(5), Gao Q(6)(7), Yi X(8)(9)(10), Chen BT(11).

**Zijun Wu, Fangxu Jia, Yiyan Chen, Yunran Wang, Haoling He, Ruixin Feng, Ziyang Zhu, Qile Gao\*, Xiaoping Yi\*, Bihong T Chen**

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**BACKGROUND:** Spinal tuberculosis (STB) and pyogenic spinal infection (PSI) often

present with overlapping clinical manifestations and imaging features, leading

to delayed diagnosis and suboptimal outcomes. Identifying reliable

laboratory-based markers may improve early differential diagnosis.

**PURPOSES:** To investigate wasting phenotype-related clinical and laboratory

indicators for differentiating STB from PSI and to establish a clinically

applicable diagnostic model.

**METHODS:** In this prospective study, 253 patients with confirmed spinal

infections were enrolled, including 159 with STB (62.85%) and 94 with PSI

(37.15%). Demographic, clinical, and routine laboratory data were collected.

Eight candidate metabolic and inflammatory variables were assessed using

univariate analyses and multivariable logistic regression. Model performance was

evaluated by receiver operating characteristic (ROC) analysis, calibration

testing, and Youden-derived optimal thresholds.

**RESULTS:** Three key variables-body temperature, high-density lipoprotein (HDL),

and blood glucose-were independently associated with STB. In the adjusted model,

each 1 °C increase in temperature reduced the odds of STB by approximately 69%

(OR = 0.318; 95% CI: 0.138-0.731; P = 0.009), each 1 mmol/L increase in HDL

increased the odds by 3.7-fold (OR = 3.692; 95% CI: 1.311-10.394; P = 0.011),

and each 1 mmol/L increase in blood glucose reduced the odds by 24% (OR = 0.764;

95% CI: 0.622-0.938; P = 0.014). The model demonstrated moderate discrimination

(AUC = 0.673, 95% CI: 0.604-0.740) but good calibration (P = 0.609). ROC-derived

optimal thresholds were T ≤ 36.7 °C, HDL ≥ 0.89 mmol/L, and blood glucose ≤ 5.85 mmol/L, providing practical reference points for clinical application.

**CONCLUSION:** A composite wasting phenotype defined by lower body temperature,

lower blood glucose, and elevated HDL significantly improves early

differentiation of STB from PSI. While individual thresholds show limited

standalone diagnostic value, the combined model provides a biologically

plausible, interpretable, and clinically useful tool to aid decision-making in

managing spinal infections.

**LEVELS OF EVIDENCE:** Level 3 (According to the Oxford CEBM 2016 criteria for

diagnostic studies).

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part of Springer Nature.

DOI: 10.1007/s00586-025-09434-3

PMID: 41057595

**21. Medicine (Baltimore). 2025 Oct 3;104(40):e44914. doi:**

**10.1097/MD.0000000000044914.**

Peripheral pulmonary tuberculoma diagnosed by targeted next-generation

sequencing with manual mapping navigation: A case report.

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Guangzhou, China.

**RATIONALE:** Pulmonary tuberculoma is a special type of tuberculosis, and

tuberculoma located in the peripheral part of the lung tend to be confused with

other pulmonary diseases such as peripheral lung cancer, so early diagnosis is

challenging. Manual mapping navigation defined as freehand sketching of

bronchial routes based on computed tomography (CT) images. Bronchoscopists use

this technique to assist in alveolar lavage and histological acquisition of

peripheral lung lesions. We report a case of a patient who was ultimately

diagnosed with peripheral tuberculoma of the lung after bronchoscopic tissue

biopsy and targeted next-generation sequencing (tNGS) by manual mapping

navigation.

**PATIENT CONCERNS:** A 29-year-old man was hospitalized for a solid nodule of about

27 mm × 20 mm subpleural in the basal segment of the right lower lobe detected

on CT screening.

**DIAGNOSES:** The patient's CT results suggest that the nature of the nodule is

undetermined.

**INTERVENTIONS: T**he patient underwent bronchoscopic biopsy, brushing, and

bronchoalveolar lavage fluid for tNGS testing guided by manual mapping

navigation, which was subsequently diagnosed as pulmonary tuberculoma.

**OUTCOMES**: Pathological results suggested lymphocytic infiltration, interstitial

fibrous tissue hyperplasia, and tuberculosis-causing mycobacterium complex was

detected in bronchoalveolar lavage fluid by tNGS. Finally, the patient was

transferred to a tuberculosis specialty hospital for \*\*\*antituberculosis

treatment, and the CT scan was repeated to show the nodule was smaller.

**LESSONS:** Diagnosis of peripheral pulmonary lesions is challenging, however, the

use of a manual mapping navigation system in combination with tNGS can help in

the diagnosis of most lung lesions in institutions that cannot provide advanced

bronchoscopy techniques.

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DOI: 10.1097/MD.0000000000044914

PMCID: PMC12499691

PMID: 41054132 [Indexed for MEDLINE]

**22. BMC Pediatr. 2025 Oct 6;25(1):768. doi: 10.1186/s12887-025-06127-0.**

Severe combined immunodeficiency with BCG-osis by salvage therapy with

allogeneic hematopoietic stem cell transplantation: cases report and literature

review.

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X(3), Li Z(3), Xiong H(4)(5).

**Yuqing Jiao, Quan Li, Zhi Chen, Li Yang, Zhuo Wang, Fang Tao, Yu Du, Xiuwen Xu, Zuofeng Li, Hao Xiong\***

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**BACKGROUND:** Severe combined immunodeficiency(SCID) combined with Bacillus

Calmette-Guérin(BCG) disease(BCG-osis) is a rare but life-threatening

complication in pediatric patients who received allogeneic hematopoietic stem

cell transplantation (allo-HSCT). Early recognition and intervention are

essential to prevent severe complications.

**CASE PRESENTATION:** We have described two pediatric cases of SCID combined with

BCG-osis in which the patients received salvage therapy with allo-HSCT. Data

were collected from two male infants who underwent allo-HSCT for SCID with

BCG-osis at Wuhan Children’s Hospital between January 2017 and December 2022.

The data of the two patients were retrospectively collected and analyzed to

summarize their clinical characteristics, treatment, and prognosis. Patient 1

presented with SCID combined with disseminated BCG-osis and underwent HSCT after

only 30 days of anti-tuberculosis therapy. The tuberculosis infection recurred

at 83 days after transplantation, and the patient eventually died of multi-organ

failure and disseminated intravascular coagulation. Patient 2 presented with

SCID combined with disseminated BCG-osis after HSCT. The patient responded well

to antituberculosis drugs and successfully completed a year and a half of

anti-tuberculosis treatment. On day 591 post-transplant, the anti-tuberculosis

regimen was discontinued in this patient.

**CONCLUSIONS:** Patients with SCID have severe defects in cellular and humoral

immunity. Genetic screening at birth would help identify such patients, and the

BCG vaccination should be delayed in such cases. The sole curative option for

SCID is HSCT, which can achieve immune reconstitution when performed early on

and can improve the survival rate.

SUPPLEMENTARY INFORMATION: The online version contains supplementary material

available at 10.1186/s12887-025-06127-0.

DOI: 10.1186/s12887-025-06127-0

PMCID: PMC12502436

PMID: 41053643

**23. BMC Microbiol. 2025 Oct 6;25(1):634. doi: 10.1186/s12866-025-04390-w.**

Characteristics of compensatory mutations in rifampicin-resistant tuberculosis

and their association with compensated transmission in Ningbo, China.

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**Yang Che, Xiangchen Li, Dongliang Zhang, Guoxin Sang, Junli Gao, Junshun Gao, Yewei Lu\*, Zhengwei Liu\***

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**BACKGROUND:** The global spread of rifampicin-resistant tuberculosis (RR-TB)

presents a significant challenge to tuberculosis control, with compensatory

mutations hypothesized to offset the fitness cost of drug resistance, thereby

facilitating transmission. However, the characteristics and epidemiological

impact of these mutations in coastal regions of Eastern China remain

inadequately understood. This study aimed to characterize the spectrum of

compensatory mutations in RR-TB isolates and to assess their association with

transmission dynamics in a well-developed coastal region of Eastern China.

**METHODS:** We collected RR-TB cases identified through drug-resistance

surveillance in Ningbo, China, from 2021 to 2024. Whole-genome sequencing (WGS)

was performed on 180 RR-TB isolates to identify resistance-conferring and

compensatory mutations, particularly in the rpoA, rpoB, and rpoC genes.

Transmission clusters were inferred using single nucleotide polymorphism (SNP)

analysis, and the association between compensatory mutations and the risk of

RR-TB clustering was evaluated using logistic regression.

**RESULTS**: Among the 180 RR-TB isolates analyzed, 28.9% harbored putative

compensatory mutations, predominantly in rpoC. Isolates with compensatory

mutations were significantly more likely to be part of genomic transmission

clusters than those without such mutations (odds ratio: 4.28, 95% CI:

2.07-8.85). No significant differences in demographic or clinical

characteristics were observed between clustered and non-clustered cases.

Phylogenetic analysis indicated ongoing local transmission of compensated RR-TB

strains.

**CONCLUSION:** Compensatory mutations are prevalent among RR-TB strains in coastal

Eastern China and are strongly associated with increased transmission,

underscoring their role in sustaining the RR-TB epidemic in this region.

Enhanced molecular surveillance and targeted interventions are warranted to curb

the spread of compensated RR-TB.

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DOI: 10.1186/s12866-025-04390-w

PMCID: PMC12502504

PMID: 41053587 [Indexed for MEDLINE]

**24. Commun Biol. 2025 Oct 6;8(1):1425. doi: 10.1038/s42003-025-08670-z.**

The acetyltransferase CysE modulates virulence and drug resistance of

Mycobacterium tuberculosis by interfering with oxidative stress responses.

Zhang LY(#)(1), Yin H(#)(2), Wang YC(#)(1), Yan MY(2), Wang CL(2), Shang XT(1),

Liu WY(1), Li ZH(1), Jia HY(1), Zhang ZD(1), Zhu CZ(3), Pan LP(4), Sun YC(5).

**Lan-Yue Zhang, Han Yin, Ying-Chao Wang, Mei-Yi Yan, Chun-Liang Wang, Xue-Tian Shang, Wei-Yi Liu, Zi-Hui Li, Hong-Yan Jia, Zong-De Zhang, Chuan-Zhi Zhu\*, Li-Ping Pan\*, Yi-Cheng Sun\***

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Acetyltransferases play a crucial role in biological processes by modifying a

variety of substrates. However, their roles in the virulence of Mycobacterium

tuberculosis (M. tb) are poorly understood. To systematically investigate the

roles of acetyltransferases in M. tb, we constructed an acetyltransferase mutant

library using CRISPR-assisted genome editing and screened for genes that are

essential for mouse infection. Seven acetyltransferases were identified as

essential for lung infection of M. tb. cysE, encoding a serine

acetyltransferase, was confirmed to be required for virulence of M. tb in mice

and its replication in macrophages. Further experiments revealed that mutation

of cysE or inhibition of CysE by small molecular chemical increased sensitivity

to clofazimine treatment. Finally, we demonstrated that cysE is involved in

mitigating oxidative stress, which modulates the virulence and drug resistance

of M. tb. Our study suggests that targeting cysE offers potential for the

development of anti-tuberculosis drugs, particularly for enhancing treatment

regimens for drug-resistant tuberculosis through the synergistic effect with

clofazimine.

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DOI: 10.1038/s42003-025-08670-z

PMCID: PMC12500854

PMID: 41053365 [Indexed for MEDLINE]

**25. Redox Rep. 2025 Dec;30(1):2565861. doi: 10.1080/13510002.2025.2565861. Epub 2025 Oct 6.**

Scutellarin suppresses Mycobacterium tuberculosis-induced pyroptosis in

macrophages by inhibiting the HIF-1α-mediated Warburg effect.

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Y(2)(3), Jiang X(1)(2).

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Medicine, Shanghai, 201203, People's Republic of China.

**BACKGROUND:** Mycobacterium tuberculosis (Mtb), the causative agent of

tuberculosis (TB), remains a major global health threat due to prolonged

treatment and drug-resistant strains. Host-directed therapy (HDT), which

modulates host-pathogen interactions, offers potential to shorten treatment and

limit resistance. This study investigates the effects of Scutellarin (SCU), a

flavonoid from Scutellaria baicalensis, on Mtb-infected macrophages within the

HDT framework.

**METHODS:** Anti-pyroptotic and anti-inflammatory effects of SCU were assessed in

Mtb-infected THP-1 and J774A.1 macrophages, and in a lipopolysaccharide

(LPS)-induced acute lung injury (ALI) mouse model. Mitochondrial function was

evaluated by oxygen consumption rate(OCR), membrane potential, and superoxide

levels; glycolytic activity was measured by proton efflux rate (GlycoPER).

Expression of inflammasome-related markers was analyzed by Western blot, qPCR,

ELISA, immunofluorescence, and flow cytometry. The role of hypoxia-inducible

factor 1-alpha (HIF-1α) was examined via siRNA knockdown.

**RESULTS:** SCU inhibited NLRP3 inflammasome activation, reduced IL-1β and IL-18

secretion, and attenuating pyroptosis. It restored mitochondrial integrity by

regulating p-DRP1, MFN2, and Cytochrome C expression, and suppressed

HIF-1α-mediated glycolytic reprogramming. Silencing of HIF-1α confirmed its role in SCU's mechanism. In vivo, SCU reduced pulmonary inflammation and cytokine

release in LPS-induced ALI.

**CONCLUSION:** SCU alleviates Mtb-induced pyroptosis and inflammation in

macrophages by inhibiting the HIF-1α-mediated Warburg effect.

DOI: 10.1080/13510002.2025.2565861

PMCID: PMC12502121

PMID: 41051976 [Indexed for MEDLINE]

**26. BMJ Open. 2025 Oct 5;15(10):e097912. doi: 10.1136/bmjopen-2024-097912.**

Comparative efficacy and safety of high-dose rifamycin regimens for tuberculosis

treatment: a Bayesian network meta-analysis.

Feng Z(#)(1), Wu H(#)(2)(3), Li Q(#)(4), Zhang X(#)(5), He Q(#)(6), Wang H(7),

Yu J(5), Ge S(1), Song L(1), Zhang Y(1), Zhou X(1), Sun F(1)(8), Zhang J(2)(3),

Li Y(9), Zhang W(1)(8).

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**OBJECTIVES:** High-dose rifamycin (HDR) regimens have demonstrated significant

potential in tuberculosis (TB) treatment. This study aims to evaluate the

efficacy and safety profile of different HDR regimens.

**DESIGN:** Using a systematic review and Bayesian network meta-analysis (NMA).

DATA SOURCES: PubMed, Web of Science, Cochrane Library and Embase were searched

up to 2 November 2024.

**ELIGIBILITY CRITERIA FOR SELECTING STUDIES:** Randomised controlled trials that

compared the efficacy and safety of HDR regimens (rifampin 15-30 mg/kg/day and

rifapentine 7.5-20 mg/kg/day) to standard-dose rifampin in patients with

pulmonary drug-susceptible TB were included.

**DATA EXTRACTION AND SYNTHESIS:** The risk of bias was assessed using Cochrane

tools. We conducted NMA with GEMTC in R. The simulation was performed using the

Markov Chain Monte Carlo technique set on four parallel chains, with 20 000

burn-in iterations, 50 000 inference iterations and a thinning factor of n=2.5.

To check for model convergence, Gelman and Rubin diagnostic plots and density

plots were applied. We assessed heterogeneity using the I² test, evaluated

transitivity by comparing effect modifiers across studies and examined

consistency via node-splitting analysis. The confidence in network meta-analysis

online tool and Cochrane Risk of Bias 2.0 Tool were used to assess evidence

certainty and risk of bias, respectively. Higher surface area under the

cumulative rank curve scores indicated a higher probability of top-ranking

treatments.

**RESULTS:** Out of 15 766 citations screened, 15 randomised controlled trials were

included, encompassing 6456 subjects. The risk of bias was low in 14 studies,

with some concerns in one. Patients receiving rifapentine 20 mg/kg/day (risk

ratio, 1.09; 95% credible interval, 1.03 to 1.17) had higher culture conversion

rates at 8 weeks in solid culture compared with the control. There was no

significant difference in primary efficacy within all HDR regimens. Rifapentine

20 mg/kg/day was ranked as the most effective intervention for primary efficacy.

No statistical difference in the incidence of serious adverse events was found

between all regimens.

**CONCLUSIONS:** Rifapentine 20 mg/kg/day may be the most effective for achieving

the strongest anti-TB activity. All HDR regimens demonstrated good safety.

PROSPERO REGISTRATION NUMBER: CRD42024504575.

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DOI: 10.1136/bmjopen-2024-097912

PMCID: PMC12506051

PMID: 41047272 [Indexed for MEDLINE]

**27. BMC Surg. 2025 Oct 3;25(1):444. doi: 10.1186/s12893-025-03200-4.**

One-stage posterior surgical treatment of the rare thoracolumbar spine process

and laminar nucleus with incomplete paralysis: a retrospective study.

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**BACKGROUND:** The study was to evaluate the results of the one-stage posterior

approach in treating patients with the rare thoracic and lumbar spinous process

and vertebral laminae tuberculosis of the spine with incomplete paralysis.

**MATERIALS AND METHODS:** 21 patients who were treated with bone graft fusion,

debridement, spinal canal decompression, and posterior transpedicle internal

fixation vie one-stage posterior approach were collected and analyzed. The data

was collected at perioperative period and at the final follow-up visit.

**RESULTS:** The follow up time was at an average of 21.62 ± 2.17 months. The mean

age of these patients was 44.81 ± 17.76 years. The intraoperative blood loss and

operative time were 538.09 ± 180.21 mL and170.95 ± 20.08 min, respectively. The C-reactive protein (CRP) level and erythrocyte sedimentation rate (ESR)

decreased to normal by the last follow-up evaluation. The Oswestry Disability

Index (ODI)and visual analogue scale (VAS) were substantially improved 4 weeks

postoperatively and at the last follow-up evaluation (P < 0.05). The incomplete

paralysis had improved significantly at the last follow-up evaluation based on

the American Spinal Injury Association (ASIA) grade (P < 0.05). All patients

achieved the bony fusion criteria. The average fusion time was 11.200 ± 2.16

months.

**CONCLUSIONS:** The one-stage posterior approach is an efficient and safe surgical

option for treating thoracic and lumbar spinous processes and vertebral laminae

tuberculosis of the spine with incomplete paralysis. Surgical decompression is

very necessary for the recovery of neurological function.

© 2025. The Author(s).

DOI: 10.1186/s12893-025-03200-4

PMCID: PMC12495794

PMID: 41044564 [Indexed for MEDLINE]

**28. BMC Public Health. 2025 Oct 3;25(1):3324. doi: 10.1186/s12889-025-24621-z.**

Impacts of the COVID-19 pandemic on tuberculosis patients' healthcare-seeking

behaviors and doctors' diagnosis delays.

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**INTRODUCTION:** Since the onset of the Corona Virus Disease 2019 (COVID-19)

pandemic, global healthcare systems have faced unprecedented challenges. To

control the spread of COVID-19, China implemented multiple nonpharmaceutical

interventions (NPIs). These measures have significantly altered people's

healthcare-seeking behaviors. This study aims to investigate the impact of the

COVID-19 pandemic on healthcare-seeking behaviors and doctor s' diagnostic

delays among pulmonary tuberculosis patients, providing systematic information

for future responses to pandemics of other "X diseases".

**METHODS:** We selected Changzhou and Suzhou as research sites in eastern China.

Pulmonary tuberculosis patients diagnosed from 2018 to 2022 were recruited as

study subjects. Based on the occurrence of the COVID-19 pandemic and the

measures implemented at the study sites from 2020 to 2022, the study period was

classified into the prepandemic, initial outbreak, regular management, strict

NPI implementation, regular management, and transition periods. Patient and

diagnosis delays were calculated. Hazard ratios (HRs) and 95% confidence

intervals (CIs) were calculated to estimate the risk of delay using Cox

regression models.

**RESULTS:** A total of 6,764 tuberculosis patients from Changzhou and 15,140

tuberculosis patients from Suzhou who were diagnosed from 2018 to 2022 were

included in the analysis. Compared with the prepandemic stage (2018-2020), the

risk of patient delay did not decrease significantly during the pandemic of

COVID-19 (P > 0.05), but the risk of diagnosis delay showed different trends at

different stages throughout the pandemic. The risk of diagnosis delay decreased

in Changzhou (HR: 1.18, 95% CI: 1.12-1.24), but it increased in Suzhou (HR:

0.92, 95% CI: 0.88-0.96).

**CONCLUSIONS:** The impact of the COVID-19 pandemic on tuberculosis varied by

region and population. It is necessary to respond in a timely and precise manner

according to the scope of the disease pandemic, accessibility of medical

resources, and population literacy to reduce the adverse impacts of other

disease epidemics on tuberculosis prevention and control.

© 2025. The Author(s).

DOI: 10.1186/s12889-025-24621-z

PMCID: PMC12495663

PMID: 41044522 [Indexed for MEDLINE]

**29. Case Rep Gastroenterol. 2025 Aug 19;19(1):581-589. doi: 10.1159/000547190.**

**eCollection 2025 Jan-Dec.**

Reactive Intravascular Plasmablastic/Immunoblastic Proliferation in a Patient

with Concurrent Gastric Mucosa-Associated Lymphoid Tissue Lymphoma and

Tuberculosis Potentially Mimicking Aggressive Intravascular Lymphoma: A Rare

Case Report.

Zhong LL(1)(2), Tang ZP(3), Zhang HP(1), Zhong S(4), Huang YW(4), Huang GX(1).

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**INTRODUCTION:** Reactive intravascular plasmablastic/immunoblastic proliferation

(RIVPIP) is rarely reported. RIVPIP may histologically mimic aggressive

intravascular lymphoma, especially in the context of an old patient presenting

with concurrent indolent lymphoma and tuberculosis, and easily lead to erroneous

diagnosis.

**CASE PRESENTATION:** A 79-year-old female presenting with upper abdominal

discomfort, weight loss, hypoproteinemia, and polyserosal effusions underwent a

gastric endoscopy examination. Biopsy revealed that the lamina propria was

infiltrated by a large number of uniformly small-sized lymphocytes (CD20+/PAX5+)

with lymphoepithelial lesions and epithelioid granuloma. Notably, vascular

lumens were filled and distended by abundant large-sized plasmablasts or

immunoblasts (CD79α+/MUM1+/CD20-/CD138-/PAX5-/CD30-/Bcl-2-/Bcl-6-/C-myc-). These intravascular large lymphoid cells demonstrated high proliferative activity

(Ki67 >80%) without immunoglobulin light chain restriction or EBV association

(EBER-ISH negative). Furthermore, PCR revealed monoclonal rearrangements in IgH,

IgK, and IgL genes. The patient had a history of endoscopic gastric biopsy 2

months ago. Retrospective analysis of a prior biopsy identified conspicuous

caseating necrosis, epithelioid granuloma, multinucleated giant cells with

suspicious positivity for acid-fast staining, highly suggestive of tuberculosis.

Based on two biopsy specimens and systemic symptoms, the case was finally

diagnosed as gastric MALT lymphoma and tuberculosis with extensive RIVPIP.

**CONCLUSION:** We present an unusual case of RIVPIP with severe systemic symptoms

due to concurrent gastric MALT lymphoma and tuberculosis, emphasizing a

potential diagnostic pitfall for clinical pathologists in distinguishing RIVPIP

from the aggressive intravascular lymphoma. A comprehensive evaluation of

clinical manifestations, pathological morphology, immunophenotype and gene

analysis is required to make the precise diagnosis.

© 2025 The Author(s). Published by S. Karger AG, Basel.

DOI: 10.1159/000547190

PMCID: PMC12503462

PMID: 41064544

**30. Case Rep Ophthalmol. 2025 Jul 24;16(1):597-603. doi: 10.1159/000547429.**

**eCollection 2025 Jan-Dec.**

Tuberculosis-Related Neuroretinitis and Central Retinal Vein Occlusion in a

Child, and a Literature Review.

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University, National Center for Children's Health, Beijing, China.

**INTRODUCTION:** Ocular tuberculosis (OTB) can occur in any part of the eye. We

present a rare case of an 11-year-old girl with tuberculosis-related

neuroretinitis and central retinal vein occlusion (CRVO).

**CASE PRESENTATION: T**he patient presented due to vision loss in the right eye. An

examination detected edema of the optic disc with peripapillary and scattered

retinal hemorrhages around the tortuous and dilated retinal veins in the right

eye. Optical coherence tomography showed macular edema and subretinal fluid in

the right eye. Fundus fluorescein angiography indicated hyper-fluorescence

staining of the optic disc and tortuous and dilated retinal veins with wall

staining and minor leakage in the right eye. Tuberculin skin test and

interferon-gamma release assay were positive. The patient's vision was improved

after anti-tuberculosis and systemic glucocorticoid therapy. A literature search

found reports on only 5 adult patients with a similar presentation.

**CONCLUSION:** Tuberculosis-related neuroretinitis and CRVO in children are rare.

Early diagnosis and treatment can somewhat restore the lost vision.

© 2025 The Author(s). Published by S. Karger AG, Basel.

DOI: 10.1159/000547429

PMCID: PMC12503614

PMID: 41063810

**31. J Infect Dev Ctries. 2025 Sep 30;19(9):1400-1406. doi: 10.3855/jidc.21028.**

Impact of drainage strategies on recovery in Stage III tuberculous empyema: a

retrospective study.

Xu J(1), Chen Y(2), Gong C(3), Liu H(1).

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(3)Department of Pathology, Nanjing Second Hospital, Nanjing Medical University,

Nanjing, China.

**INTRODUCTION:** Tuberculous empyema, a severe complication of pulmonary

tuberculosis, often requires surgical intervention in stage III to remove

fibrotic tissue and restore lung function.

**METHODOLOGY: T**his retrospective study enrolled 224 stage III tuberculous empyema

patients undergoing single-port thoracoscopic decortication and closed chest

drainage. Patients were divided into three groups: Single-Tube group (n = 42),

Double-Tube group (n = 51), and Double-Tube with Negative Pressure (Double-NP)

group (n = 131, with -8 to -10 cm H₂O negative pressure applied from

postoperative day 2). Primary outcomes included postoperative drainage volume,

chest tube duration, hospital stay, complications, and Visual Analog Scale (VAS)

pain scores. Data were analyzed using Analysis of Variance (ANOVA), chi-square

tests, and multivariate regression.

**RESULTS:** Baseline characteristics were comparable across groups. Postoperative

drainage volumes were similar, but chest tube duration and hospital stay were

significantly shorter in the Double-Tube and Double-NP groups compared to the

Single-Tube group (p < 0.05). The Double-NP group exhibited lower rates of

persistent air leak, pleural effusion, atelectasis, and reintubation (p < 0.05).

VAS scores were significantly lower in the Single-Tube group than in the

Double-Tube and Double-NP groups (p < 0.01).

**CONCLUSIONS:** While the double-tube with delayed low-negative-pressure drainage

strategy did not reduce postoperative pain, it significantly shortened chest

tube duration and hospital stay while reducing complications, thereby improving

overall prognosis in stage III tuberculous empyema patients.

Copyright (c) 2025 Jian Xu, Yuhua Chen, Cheng Gong, Hong Liu.

DOI: 10.3855/jidc.21028

PMID: 41060740 [Indexed for MEDLINE]

**32. Infect Drug Resist. 2025 Oct 2;18:5219-5222. doi: 10.2147/IDR.S540790.**

**eCollection 2025.**

Case Report: Rare Dupilumab-Associated Pulmonary and Extrapulmonary

Tuberculosis.

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China.

Dupilumab, a fully human monoclonal antibody targeting the interleukin-4

receptor alpha (IL-4Rα), has revolutionized the management of moderate-to-severe

atopic dermatitis (AD) by inhibiting signaling of interleukin-4 (IL-4) and

interleukin-13 (IL-13). Our case report is about a 71-year-old man with a

history of AD who developed pulmonary tuberculosis (PTB) and extrapulmonary

tuberculosis (EPTB) after treatment with dupilumab. The mechanism is unclear,

but it may be related to the fact that dupilumab inhibits the expression of

pro-inflammatory response-related genes and the innate immunity of macrophages,

thereby aggravating TB infection. This is the first report of PTB and EPTB

associated with dupilumab treatment, and it may be useful for clinicians to

enhance TB vigilance in patients receiving dupilumab therapy, particularly in

endemic regions.

© 2025 Xu and Zhong.

DOI: 10.2147/IDR.S540790

PMCID: PMC12499361

PMID: 41059397

**33. Front Cell Infect Microbiol. 2025 Sep 22;15:1629805. doi:**

**10.3389/fcimb.2025.1629805. eCollection 2025.**

Molecular mechanisms related to bone damage in spinal tuberculosis revealed by

4D-label-free proteomics analysis.

Xiao W(1), Yang G(2)(3), Xu S(1), Song S(3), Tang Y(1), Zhou T(2), Huang W(1),

Zhang L(1), Gu Y(2)(4).

**Wenxuan Xiao, Guangling Yang, Shuqin Xu, Shu Song, Yuting Tang, Tianyao Zhou, Weili Huang, Lu Zhang\*, Yutong Gu\***

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**AIMS:** Spinal tuberculosis (STB) is a common form of extrapulmonary tuberculosis

(ETB). However, the molecular mechanism of pathological injury in STB remains

unclear. The purpose of this study was to explore the pathogenic mechanism of

STB, and compare it with Escherichia coli (E.coli) bone infections and lumbar

degenerative disease (LDD) patients.

**MAIN METHODS:** In this study, the infected lumbar spine bone tissue of STB

patients was collected for the infection group. LDD patients and E.coli lumbar

spine infection (SEcoli) patients were collected for the non-M.TB infection

group. Proteins from the bone tissue were extracted for 4D-Label Free Proteomics

(4D-LFQ) analysis to compare the pathogenesis and immune mechanisms of STB and

SEcoli.

**KEY FINDINGS:** The osteoclast growth inhibitory factors tumor necrosis factor

receptor superfamily member 11B (TNFRSF11B) and semaphorin-3A (Sema3A) were

significantly down-regulated in STB, while the protein Wnt-5a (WNT5A) secreted

by osteoblasts was significantly up-regulated. These changes in STB bone

metabolism may lead to an increase in the number of osteoclasts and bone injury.

In addition, the significantly up-regulated expression of thymocyte

selection-related family member 2 (THEMIS2) suggests that THEMIS2 may be a

potential therapeutic target for STB that could control the Toll-like receptor

response of macrophages. Meanwhile, the PI3K-Atk anti-apoptotic pathway and the

ECM-receptor interaction pathway were inhibited during both infections.

**SIGNIFICANCE:** This study explored the pathogenic mechanism of STB based on

proteomics and compared its differences with E.coli bone infection, providing

new insight into the treatment of STB.

Copyright © 2025 Xiao, Yang, Xu, Song, Tang, Zhou, Huang, Zhang and Gu.

DOI: 10.3389/fcimb.2025.1629805

PMCID: PMC12497785

PMID: 41059041 [Indexed for MEDLINE]

**34. Front Cell Infect Microbiol. 2025 Sep 22;15:1666630. doi:**

**10.3389/fcimb.2025.1666630. eCollection 2025.**

Progress of single-cell sequencing technology in immunotherapy for tuberculosis.

Fan X(1), Chen M(1), Wu D(1), Lin Y(1), Chen X(1).

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According to the 2024 World Health Organization (WHO)Global Tuberculosis

(TB)Report, tuberculosis remains the leading cause of death from a single

infectious agent, with 10.8 million new cases and 1.25 million deaths in 2023.

Early and standardized treatment upon definitive diagnosis holds significant

importance for the prevention and prognosis of pulmonary tuberculosis patients.

However, the number of drug-resistant tuberculosis(DR-TB) cases is increasing,

while the interventions for tuberculosis are becoming increasingly limited.

There is an urgent need to develop new rapid diagnostic methods and effective

treatment drugs. Recent advances in tuberculosis immunotherapy have shown

promising results. Novel therapeutic vaccines like M72/AS01E demonstrate 54%

efficacy in preventing pulmonary TB, while host-directed therapies including

nano-based drug delivery systems offer enhanced treatment outcomes. The immune

system plays a vital role in the development and regulation of tuberculosis.

Single-cell sequencing(SCS) technology enables comprehensive analysis of immune

cells at the single-cell level, revealing the functions, states, distributions,

and communication behaviors among immune cell subpopulations. These insights

contribute to understanding the pathogenesis and discovering new diagnostic

markers and therapeutic targets in tuberculosis. This review provides a critical

overview of the immunological mechanisms underlying tuberculosis, immunotherapy

for tuberculosis, and single-cell sequencing technology, with specific focus on

key findings from recent studies and their clinical implications. It primarily

focuses on discussing the research progress of single-cell sequencing technology

in the context of tuberculosis immunotherapy and identifies current challenges

and future research priorities.

Copyright © 2025 Fan, Chen, Wu, Lin and Chen.

DOI: 10.3389/fcimb.2025.1666630

PMCID: PMC12497845

PMID: 41059038 [Indexed for MEDLINE]

**35. IJID Reg. 2025 Aug 7;16:100726. doi: 10.1016/j.ijregi.2025.100726. eCollection 2025 Sep.**

Clinical characteristics and prognostic outcomes of pediatric tuberculosis in a

tertiary care center in China: a 10-year retrospective cohort.

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**OBJECTIVES:** This study aims to investigate the clinical features and prognostic

outcomes of pediatric tuberculosis (TB) in Shenzhen.

**METHODS:** This retrospective study collected demographic, clinical, laboratory,

and prognostic data from pediatric patients diagnosed with TB between January

2013 and January 2023. Multivariable regression identified risk factors for loss

to follow-up and mortality.

**RESULTS:** A total of 358 children were included, and distinct age-related

patterns were observed. Younger children had more extrapulmonary TB, whereas

older children were more likely to develop pulmonary cavities. Nearly half

(47.6%) of the children aged 0-1 years were household contacts of patients with

TB, but none of the children had received TB preventive treatment before disease

onset. Infants showed the highest rates of drug-induced liver injury (31%) and

mortality (13.3%). Microbiological diagnosis was associated with reduced risk of

loss to follow-up before treatment completion (hazard ratio 0.463, 95%

confidence interval 0.248-0.863, P = 0.015). Tuberculous meningitis

significantly increased mortality risk (hazard ratio 10.830, 95% confidence

interval 1.214-96.645, P = 0.033).

**CONCLUSIONS:** Pediatric TB presents with diverse clinical features across age

groups. Early microbiological diagnosis and attention to high-risk populations,

especially infants and those with TB meningitis, are essential for improving

treatment outcomes. TB preventive treatment in exposed children remains

critically underused.

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DOI: 10.1016/j.ijregi.2025.100726

PMCID: PMC12490579

PMID: 41049170

**36. Front Public Health. 2025 Sep 19;13:1634772. doi: 10.3389/fpubh.2025.1634772.**

**eCollection 2025.**

Global, regional, and national burdens of MDR-TB attributable to smoking from

1990 to 2021 with a prediction from 2022 to 2050.

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**OBJECTIVE:** The aim was to offer a comprehensive epidemiological assessment of

the global prevalence and the smoking-related Multidrug-resistant tuberculosis

(MDR-TB) disease burden from 1990 to 2021 and to forecast the trends in smoking

burden over three decades.

**METHODS:** We compared the burden of smoking-related MDR-TB and temporal trends by

gender, age, socio-demographic index (SDI), region, and country. Forecasting

analyses of the changing trend in the burden of smoking-related MDR-TB up to

2050 was conducted based on the ARIMA model and ES models.

**RESULTS:** The global age-standardized rate (ASR) of smoking-related MDR-TB

increased from 1990 to 2021, highlighting a significant disease burden. In 2021,

the cumulative Disability adjusted life years (DALYs) attributed to MDR-TB

tallied up to 239,707 cases, with Lesotho, Uzbekistan, Kyrgyzstan, bearing the

brunt. The likelihood of developing MDR-TB rose as individuals advanced in

years, manifesting most acutely among men aged 35-39 in lower SDI and Low-middle

SDI regions. Predictive analysis suggests that by 2050, deaths and DALYs of

smoking-related MDR-TB, as well as their corresponding ASR, will continue to

decrease.

**CONCLUSION:** The burden of MDR-TB worldwide, adjusted for age, and related to

smoking, has shown a decline from 1990 to 2021. However, regional disparities

have been identified, with some areas experiencing an increase in this burden.

These regions with a higher burden emphasize the necessity for the

implementation of strong tobacco control measures.

Copyright © 2025 Dan, Lei, Xue and Ze-Xin.

DOI: 10.3389/fpubh.2025.1634772

PMCID: PMC12491277

PMID: 41048305 [Indexed for MEDLINE]

**37. Clin Radiol. 2025 Aug 23;90:107059. doi: 10.1016/j.crad.2025.107059. Online**

**ahead of print.**

A radiomics-clinical nomogram for predicting individualised treatment duration

in newly diagnosed pulmonary tuberculosis.

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**AIM:** The treatment duration for pulmonary tuberculosis (PTB) varies considerably

based on disease severity, pathogen characteristics, and host immune status.

This study aimed to develop predictive models for individualised treatment

duration in newly diagnosed PTB patients, thereby supporting personalised

therapeutic strategies.

**MATERIALS AND METHODS:** A retrospective cohort of 242 newly diagnosed PTB

patients was analysed and randomly divided into training and testing cohorts.

Radiomic features were selected via Least Absolute Shrinkage and Selection

Operator (LASSO)-Cox regression, while clinical indicators were identified

through univariate Cox regression. Three models-a radiomics model, clinical

model, and radiomics-clinical combined model-were constructed using Cox

proportional hazards regression. Model performance was assessed using the

C-index, with the optimal model visualised through a nomogram and forest plot.

The time-dependent area under the curve (AUC) was used to evaluate predictive

performance over time of the optimal model. Kaplan-Meier (K-M) survival analysis

was performed based on the Rad score to stratify patients into high- and

low-risk groups.

**RESULTS:** Two radiomic features and three clinical variables were incorporated

into the final models. The combined model outperformed the radiomics-only and

clinical-only models, achieving C-indices of 0.81 (training cohort) and 0.79

(testing cohort), with time-dependent AUCs consistently above 0.75. Calibration

curves demonstrated good agreement between predicted and observed outcomes, and

K-M analysis confirmed that the Rad score effectively stratified patients by

treatment duration (P<.05).

**CONCLUSION:** The radiomics-clinical model demonstrated superior predictive

performance, robustness, and clinical applicability compared to single-feature

models. This approach provides a practical tool for personalising treatment

duration and supports more precise management of PTB patients through effective

risk stratification.

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DOI: 10.1016/j.crad.2025.107059

PMID: 41045794