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**中国大陆学者发表的结核病英文文章摘要**

**（29篇）**

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**1. RSC Adv. 2025 Jul 3;15(28):22745-22763. doi: 10.1039/d5ra01362c. eCollection**

**2025 Jun 30.**

Insights into anti-tuberculosis drug design on the scaffold of nitroimidazole

derivatives using structure-based computer-aided approaches.

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Z(1)(2), Zhao Y(1)(2), Lu S(1)(2), Wang F(8), Zhao Y(1)(2)(5)(6).

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Deazaflavin-dependent nitroreductase (Ddn) is a crucial enzyme involved in

mycolic acid biosynthesis, a vital component of the cell wall in Mycobacterium

tuberculosis (MTB)-the bacterial pathogen responsible for tuberculosis. Over the

past two decades, nitroimidazole oxazine scaffold (NOS) derivatives have been

investigated as potential therapeutic agents targeting Ddn in MTB, with a focus

on enhancing drug efficacy, minimizing toxicity, and combating drug resistance.

In this study, we performed an extensive theoretical investigation combining

three-dimensional quantitative structure-activity relationship (3D-QSAR)

studies, all-atom molecular docking, and atomic-level molecular dynamics (MD)

simulations. Additionally, we analyzed the binding free energies and their

decomposed terms between inhibitors and Ddn to elucidate the structure-activity

relationships (SARs) and mechanisms of a series of NOS derivatives developed for

MTB inhibition. The CoMFA and CoMSIA models demonstrated strong performance,

with cross-validation coefficients (R cv 2) of 0.591 and 0.629, respectively,

and prediction coefficients (R pred 2) of 0.7698 and 0.6848 for CoMFA and

CoMSIA, respectively. These models effectively predicted the minimum inhibitory

concentration (MIC) values of the compounds against MTB based on the NOS

scaffold. Molecular docking followed by MD simulations was employed to validate

the binding modes of these derivatives at the active site of Ddn, providing

detailed insights into their interaction patterns. Notably, our analysis

revealed that residues Tyr65, Ser78, Tyr130, Tyr133, and Tyr136 played critical

roles in determining the potency of the compounds by contributing significantly

to their binding energies. These findings provide valuable guidance for the

rational design of novel NOS inhibitors with enhanced potential as effective

anti-tuberculosis agents.

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**2. Eur J Clin Microbiol Infect Dis. 2025 Jul 3. doi: 10.1007/s10096-025-05170-0.**

**Online ahead of print.**

Effectiveness of centralized hospitalization treatment on transmission in

household contacts of pulmonary tuberculosis patients: a contact-traced study.

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**BACKGROUND:** Pulmonary tuberculosis (PTB) is a respiratory infectious disease

that seriously endangers people's health and incurs high treatment costs, which

quickly leads to catastrophic expenditure for patients and their families. A

centralized hospitalization treatment (CHT) strategy can be implemented to

mitigate the transmission of PTB. This study evaluates the effectiveness of a

CHT approach in reducing the magnitude of Mycobacterium tuberculosis (MTB)

transmission in household contacts (HHCs) of confirmed PTB cases and explores

potential risk factors for PTB.

**METHODS:** This retrospective cohort study used PTB cases from Guizhou, China,

between January 2022 and October 2023. The HHCs of PTB cases diagnosed

etiologically and treated with non-CHT were designated as the exposed group, and

the HHCs of those treated with CHT were the non-exposed group. The ratio of the

HHCs to index cases was 1:1-3. Face-to-face interviews were conducted for the

participants by medical staff at home. R software was used for data analysis.

Continuous variables were cut to create new categorical variables and were

analyzed using the Chi-square test or Fisher test according to the nature of the

data. The risk factors of PTB/LTBI and covariates were analyzed using a

multivariate logistic regression model evaluated by the Akaike information

criterion (AIC) and elucidated by a Directed Acyclic Graph (DAG). The alpha (α)

test level of all statistical tests was 0.05.

**RESULTS:** 1007 participants were investigated, including 559 HHCs of PTB index

cases from CHT settings and 448 HHCs of PTB index cases from non-CHT sites

(treated at home). Of the two groups, 46 HHCs tested positive for PTB/LTBI

(latent TB infections), with a 3.4% positive detection rate (19 cases) in the

HHCs of PTB index cases treated with CHT and 6.0% (27 cases) in the HHCs of

those treated with non-CHT, with positive detection of LTBI [17(3.0%) vs.

26(5.8%)] and [3(0.5%) vs. 5(1.1%)] of PTB in the former than that in the

latter. A statistically significant difference was found between the two LTBI

groups. In the univariate analysis, family caregivers, age, marital status, CHT,

eating the same food with the patient, sleeping in the same room with the

patient, and caring for the patient for more than or equal to 2 months were risk

factors for PTB/LTBI among HHCs. The treatment of PTB families with non-CHT was

an independent factor of PTB/LTBI in the HHCs through multivariate analysis and

AIC evaluation.

**CONCLUSIONS:** The transmission of PTB/LTBI to HHCs is lower in the HHCs of CHT

patients than in the HHCs of those treated with non-CHT after controlling for

the other factors including older age, abnormal marriage, and staying with PTB

patients equal to or more than two months.

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**3. Int J Surg. 2025 Jul 2. doi: 10.1097/JS9.0000000000002850. Online ahead of**

**print.**

Development and validation of a deep learning ultrasound radiomics model for

predicting drug resistance in lymph node tuberculosis a multicenter study.

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**BACKGROUND:** To develop and validate an ensemble machine learning ultrasound

radiomics model for predicting drug resistance in lymph node tuberculosis

(LNTB).

**MATERIALS AND METHODS:** This multicenter study retrospectively included 234

cervical LNTB patients from one center, randomly divided into training (70%) and

internal validation (30%) cohorts. Radiomic features were extracted from

ultrasound images, and an L1-based method was used for feature selection. A

predictive model combining ensemble machine learning and AdaBoost algorithms was

developed to predict drug resistance. Model performance was assessed using

independent external test sets (Test A and Test B) from two other centres, with

metrics including AUC, accuracy, precision, recall, F1 score, and decision curve

analysis.

**RESULTS:** Of the 851 radiometric features extracted, 161 were selected for the

model. The model achieved AUCs of 0.998 (95% CI: 0.996-0.999), 0.798 (95% CI:

0.692-0.904), 0.846 (95% CI: 0.700-0.992), and 0.831 (95% CI: 0.688-0.974) in

training, internal validation, and external test sets A and B, respectively. The

decision curve analysis showed a substantial net benefit across a threshold

probability range of 0.38 to 0.57.

**CONCLUSION:** The LNTB resistance prediction model developed demonstrated high

diagnostic efficacy in both internal and external validation. Radiomics, through

the application of ensemble machine learning algorithms, provides new insights

into drug resistance mechanisms and offers potential strategies for more

effective patient treatment.

KEY WORDS: Lymph node tuberculosis; Drug resistance; Ultrasound; Radiomics;

Machine learning.

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**4. Mycoses. 2025 Jul;68(7):e70084. doi: 10.1111/myc.70084.**

Deep Learning Models for CT Segmentation of Invasive Pulmonary Aspergillosis,

Mucormycosis, Bacterial Pneumonia and Tuberculosis: A Multicentre Study.

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C(2)(3), Ye F(1), Zheng J(1).

**Yun Li, Feifei Huang, Deyan Chen, Youwen Zhang, Xia Zhang, Lina Liang, Junnan Pan, Lunfang Tan, Shuyi Liu, Junfeng Lin, Zhengtu Li, Guodong Hu, Huai Chen, Chengbao Peng, Feng Ye\*, Jinping Zheng\***

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**BACKGROUND:** The differential diagnosis of invasive pulmonary aspergillosis

(IPA), pulmonary mucormycosis (PM), bacterial pneumonia (BP) and pulmonary

tuberculosis (PTB) are challenging due to overlapping clinical and imaging

features. Manual CT lesion segmentation is time-consuming, deep-learning

(DL)-based segmentation models offer a promising solution, yet disease-specific

models for these infections remain underexplored.

**OBJECTIVES:** We aimed to develop and validate dedicated CT segmentation models

for IPA, PM, BP and PTB to enhance diagnostic accuracy. Methods：Retrospective

multi-centre data (115 IPA, 53 PM, 130 BP, 125 PTB) were used for

training/internal validation, with 21 IPA, 8PM, 30 BP and 31 PTB cases for

external validation. Expert-annotated lesions served as ground truth. An

improved 3D U-Net architecture was employed for segmentation, with preprocessing

steps including normalisations, cropping and data augmentation. Performance was

evaluated using Dice coefficients. Results：Internal validation achieved Dice

scores of 78.83% (IPA), 93.38% (PM), 80.12% (BP) and 90.47% (PTB). External

validation showed slightly reduced but robust performance: 75.09% (IPA), 77.53%

(PM), 67.40% (BP) and 80.07% (PTB). The PM model demonstrated exceptional

generalisability, scoring 83.41% on IPA data. Cross-validation revealed mutual

applicability, with IPA/PTB models achieving > 75% Dice for each other's

lesions. BP segmentation showed lower but clinically acceptable performance (

＞72%), likely due to complex radiological patterns.

**CONCLUSIONS:** Disease-specific DL segmentation models exhibited high accuracy,

particularly for PM and PTB. While IPA and BP models require refinement, all

demonstrated cross-disease utility, suggesting immediate clinical value for

preliminary lesion annotation. Future efforts should enhance datasets and

optimise models for intricate cases.

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**5. Bioorg Med Chem. 2025 Jun 26;129:118294. doi: 10.1016/j.bmc.2025.118294. Online ahead of print.**

Jolkinolide B inhibits mycobacterial growth by down-regulating ribosomal

proteins and interfering with protein synthesis.

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The traditional Chinese medicine Euphorbia fischeriana Steud (E. fischeriana)

has been used for treating lymph node tuberculosis (TB) for a long time. This

study demonstrates that Jolkinolide B, a component of E. fischeriana, exhibits

antimycobacterial activity with a minimum inhibitory concentration (MIC) of

3 μg/mL against M. tuberculosis H37Ra. Additionally, it shows bactericidal

effect on RAW264.7 macrophages infected with M. tuberculosis at a concentration

of 2 × MIC. Mechanistic study via transcriptome revealed that Jolkinolide B

significantly reduced the transcription of 17 ribosomal proteins, thereby

inhibiting protein synthesis in M. tuberculosis. RT-qPCR confirmed that

Jolkinolide B decreased the expression of mycobacterial ribosomal proteins in a

concentration-dependent manner. Finally, morphological observations indicated

that Jolkinolide B caused the tubercle bacilli to become shorter and deformed.

This study highlights a natural compound from E. fischeriana and clarifies its

mechanism of action against TB, supporting the rational use of traditional

Chinese medicine (TCM) and antibiotics in TB treatment.

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**6. Front Immunol. 2025 Jun 18;16:1599667. doi: 10.3389/fimmu.2025.1599667.**

**eCollection 2025.**

Identification and validation of NETs-related biomarkers in active tuberculosis

through bioinformatics analysis and machine learning algorithms.

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**INTRODUCTION:** Diagnostic delays in tuberculosis (TB) threaten global control

efforts, necessitating early detection of active TB (ATB). This study explores

neutrophil extracellular traps (NETs) as key mediators of TB immunopathology to

identify NETs-related biomarkers for differentiating ATB from latent TB

infection (LTBI).

**METHODS:** We analyzed transcriptomic datasets (GSE19491, GSE62525, GSE28623)

using differential expression analysis (|log, FC| ≥ 0.585, adj. p < 0.05),

immune cell profiling (CIBERSORT), and machine learning (SVM-RFE, LASSO, Random

Forest). Regulatory networks and drug-target interactions were predicted using

NetworkAnalyst, Tarbase, and DGIdb.

**RESULTS:** We identified three hub genes (CD274, IRF1, HPSE) showing high

diagnostic accuracy (AUC 0.865-0.98, sensitivity/specificity >80%) validated

through ROC/precision-recall curves. IRF1 and HPSE correlated with neutrophil

infiltration (r > 0.6, p < 0.001), suggesting roles in NETosis. FOXC1, GATA2,

and hsa-miR-106a-5p emerged as core regulators, and 46 candidate drugs (e.g.,

PD-1 inhibitors, heparin) were prioritized for repurposing.

**DISCUSSION:** CD274, IRF1, and HPSE represent promising NETs-derived diagnostic

biomarkers for ATB. Their dual roles in neutrophil-mediated immunity highlight

therapeutic potential, though drug predictions require preclinical validation.

Future studies should leverage spatial omics and CRISPR screening to elucidate

mechanistic pathways.

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**7. Tuberculosis (Edinb). 2025 Jun 13;154:102667. doi: 10.1016/j.tube.2025.102667.**

**Online ahead of print.**

METTL3 contributes to M.tb-induced injury and inflammation in THP-1 macrophages

by mediating m6A methylation of IRF8 to activate TLR4/NF-kB pathway.

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China. Electronic address: 18274837689@163.com.

**BACKGROUND:** Macrophages play central roles in the immunity response to infection

of intracellular bacteria, including Mycobacterium tuberculosis (M.tb) in

tuberculosis (TB). Methyltransferase-like 3 (METTL3) has been implicated in the

macrophage regulation in TB, and this study intended to investigate the

molecular mechanism of METTL3 with interferon regulatory factor-8 (IRF8) in TB

using in vitro model established by M.tb-infected THP-1 macrophages.

**METHODS:** RT-qPCR and Western blot were utilized to analyze mRNA and protein

expression, respectively. Cell viability, proliferation, and apoptosis were

examined through cell counting kit-8 assay, EdU assay, and flow cytometry/TUNEL

assay. Inflammatory cytokines were detected via enzyme-linked immunosorbent

assay. Methylated RNA Immunoprecipitation (MeRIP), RIP and Co-IP were performed

to assess the interaction between genes.

**RESULTS:** IRF8 knockdown alleviated injury and inflammation in M.tb-infected

THP-1 macrophages. METTL3 enhanced IRF8 mRNA stability by inducing m6A

methylation. IGF2BP1 functioned as an m6A reader to affect m6A methylation of

IRF8. The function of METTL3 in M.tb-induced THP-1 macrophages was attributed to

the positive regulation of IRF8. IRF8 bound to TLR4 and METTL3 could regulate

TLR4 expression via targeting IRF8. IRF8/TLR4 axis promoted M.tb-induced

THP-1 cell injury and inflammation. TLR4/NF-kB pathway was activated by

METTL3-mediated IRF8.

**CONCLUSION:** These findings revealed that METTL3 expedited cell injury and

inflammatory reaction in M.tb-infected THP-1 macrophages by inducing m6A

methylation of IRF8 to activate TLR4/NF-kB pathway.

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**8. BMC Genom Data. 2025 Jul 12;26(1):48. doi: 10.1186/s12863-025-01338-x.**

Machine learning-based prediction of antimicrobial resistance and identification

of AMR-related SNPs in Mycobacterium tuberculosis.

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**BACKGROUND:** Mycobacterium tuberculosis (MTB) is a human-specific pathogen that

primarily infects humans, causing tuberculosis (TB). Antimicrobial resistance

(AMR) in MTB presents a formidable challenge to global health. The employment of

machine learning on whole-genome sequencing data (WGS) presents significant

potential for uncovering the genomic mechanisms underlying drug resistance in

MTB.

**METHODS:** We used 18 binary matrices, each consisting of genotypes and

antimicrobial susceptibility testing phenotypes from a specific

MTB-antimicrobial dataset. By constructing training and test datasets on all

SNPs, intersected SNPs, and randomly generated SNPs, we developed a Machine

learning (ML) framework using twelve different algorithms. Then, we compared the

performances of the various ML models and used the SHapley Additive exPlanations

(SHAP) framework to decipher why and how decisions are made within the optimal

algorithm. Lastly, we applied the models to predict the resistance phenotype to

rifampicin (RIF) and isoniazid (INH) in the additional independent MTB isolate

datasets from India and Israel.

**RESULTS:** In our study, the Gradient Boosting Classifier (GBC) model was the best

in terms of correctly identified percentages (97.28%, 96.06%, 94.19%, and 92.81%

for the four first-line drugs, RIF, INH, pyrazinamide, and ethambutol

respectively). By estimating the contributions of AMR-related SNPs by SHAP

values, we found that position 761,155 (rpoB\_p.Ser450), 2,155,168

(katG\_p.Ser315) rank top in RIF and INH, their higher values (1 for alternative

allele) tend to predict the resistance trait for these two drugs. In addition,

the best model GBC generalizes well in predicting the resistance phenotypes for

RIF and INH in the external independent MTB isolate datasets from India and

Israel.

**CONCLUSIONS:** This study integrates ML methods into antimicrobial resistance

research, develops a framework for predicting resistance phenotypes, and

explores AMR-related SNPs in MTB. Quantifying the important SNPs' contribution

to model decisions makes the ML algorithmic process more transparent,

interpretable enabling and enables clinical practice.

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**9. Microbiol Spectr. 2025 Jul 11:e0016925. doi: 10.1128/spectrum.00169-25. Online**

**ahead of print.**

High proportion of tuberculosis recent transmission in rural areas of

Northeastern China: a 3-year prospective population-based genotypic and spatial

analysis in Hinggan League, China.

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Tuberculosis (TB) remains a significant public health challenge in China,

particularly in rural areas like Hinggan League (HL), Inner Mongolia.

Understanding the genetic diversity and transmission dynamics of Mycobacterium

tuberculosis (MTB) strains is crucial for effective TB control. We conducted a

prospective study from 2021 to 2023, sequencing 221 MTB isolates from HL. After

quality control, 210 cases were analyzed. The genomic clustering rate was

calculated to evaluate the level of recent transmission. Risk factors were

identified by logistic regression analysis. Geospatial analysis was conducted

with kernel density estimation. The majority of strains belonged to sub-lineage

2.2.1 in lineage 2 (L2), also known as the Beijing family (89.0%, 187/210),

while the remainder belonged to lineage 4 (L4). L2 strains showed greater

genetic similarity and shorter branch lengths compared with L4 strains. The

overall drug resistance rate was 21.9%, with six multidrug-resistant TB (MDR-TB)

and five pre-extensively drug resistant TB (pre-XDR-TB) cases identified. Almost

half of the strains belonged to putative transmission clusters within 10 SNPs.

Logistic regression analysis identified living in Jalaid Banner and being

infected by L2 strains as significant risk factors for recent transmission.

Spatial analysis identified spatial aggregation of TB cases in the eastern

region of HL, with a hotspot for recent transmission in Jalaid Banner. The

temporal distribution of TB cases in HL exhibited seasonal fluctuations, with

diagnosis rates peaking in the first half of each year, and a notable increase

in clustered cases in 2022. This study provides insights into the molecular

epidemiology and transmission dynamics of TB in HL. Our results underscore the

ongoing problem of TB transmission in rural settings, indicating the need for

targeted interventions. These findings are vital for informing TB control

strategies in HL and similar settings.IMPORTANCETuberculosis (TB) remains a

major public health problem in China. This study provides insights into the

molecular epidemiology and transmission dynamics of TB in rural areas (Hinggan

League [HL], Inner Mongolia) in China. Nearly half of the enrolled TB cases were

attributed to recent transmission, a proportion higher than that observed in

other rural areas in China (31.4%), highlighting the significance of recent

transmission in driving the TB epidemic in this region. Only 19.6% of all

drug-resistant TB (DR-TB) cases were found within putative transmission

clusters, indicating a lower proportion compared with the previous studies,

which indicated that DR-TB is more associated with the de novo evolution of

resistance within patients. Spatial analysis showed that the TB epidemic was

concentrated in densely populated areas in eastern HL. The findings identified

epidemiological differences within HL, highlighting the importance of targeted

interventions and surveillance to control the spread of TB in HL.

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PMID: 40643231

**10. Ann Med. 2025 Dec;57(1):2527364. doi: 10.1080/07853890.2025.2527364. Epub 2025 Jul 9.**

Soluble programmed cell death ligand-1 as a predictive biomarker for severity

and poor prognosis in pulmonary tuberculosis.

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X(3), Yi L(1), Wang G(2).

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**BACKGROUND:** We aimed to assess whether soluble programmed death-ligand 1

(sPD-L1) could serve as a new biomarker for PTB.

**METHODS:** Plasma sPD-L1 levels in the discovery cohort were analyzed through flow

cytometry and validated by sandwich ELISA. Pleural effusion sPD-L1 levels were

measured using ELISA.

**RESULTS:** In the discovery cohort, sPD-L1 levels in the severe (SE, n = 44),

non-severe (non-SE, n = 34) and HC (n = 10) group were 67.41 (30.14-126.41),

26.75 (11.00-52.35) and 14.6 (10.78-21.91) pg/ml, respectively. The sPD-L1

levels in SE patients were significantly higher than those in both non-SE

patients and HCs (p < 0.0001). These findings were confirmed in the validation

cohort with sPD-L1 levels significantly higher in SE (n = 60,763.81 pg/ml)

compared to both non-SE patients (n = 80, 318.30 pg/ml) and HCs (n = 79,

202.33 pg/ml)(p < 0.0001). Receiver operating characteristic (ROC) analysis

demonstrated plasma sPD-L1 could distinguish SE from non-SE PTB with an AUC of

0.8058 (95% CI 0.7308-0.8808). sPD-L1 levels showed positive correlations with

inflammatory markers, such as neutrophil percentage (NEU%, r = 0.5743,

p < 0.0001), neutrophil-to-lymphocyte ratio (NLR, r = 0.5952, p < 0.0001).

Survival analysis revealed shorter survival times in groups with higher sPD-L1

(≥445.1 pg/ml, p = 0.0006). In addition, sPD-L1 levels in tuberculous pleural

effusion (TPE) were significantly higher than malignant pleural effusion (MPE)

(1964.72 versus 159.38 pg/ml, p < 0.001), showing diagnostic performance (AUC =

0.9837) similar to adenosine deaminase (AUC= 0.9859).

**CONCLUSION:** Elevated plasma sPD-L1 may be a predictive marker for both disease

severity and poor prognosis in PTB patients. Pleural effusion sPD-L1 levels

might potentially function as an adjunctive marker for differentiating TPE from

MPE.

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**11. J Orthop Surg Res. 2025 Jul 8;20(1):625. doi: 10.1186/s13018-025-06037-y.**

METTL14 mediates the m6A methylation of miR-29a-3p, thereby activating the

MAP2K6 signaling pathway and exacerbating the inflammatory response associated

with spinal tuberculosis.

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**BACKGROUND:** Spinal Tuberculosis (STB) constitutes a common form of tuberculosis

and is more widespread in developing countries. Not only is it one of the

principal causes of spinal deformity but also it may trigger severe neurological

impairments, thereby significantly influencing the quality of life of patients.

Additionally, microRNAs (miRNAs) participate in the signal transduction among

macrophages through multiple means. In the earlier work of our research group,

spinal tuberculosis tissues were subjected to miRNA differential analysis and

sequencing. The results indicated that miR-29a-3p was under-expressed in

patients with spinal tuberculosis relative to the normal population.

Nevertheless, it remains unknown at present how methyltransferase

14(METTL14)-mediated miR-29a-3p regulates the inflammatory response of spinal

tuberculosis via the Mitogen-Activated Protein Kinase Kinase 6(MAP2K6) signaling

pathway.

**OBJECTIVE:** This study aimed to validate the expression levels of METTL14 and

miR-29a-3p in spinal tuberculosis and explore the regulatory role of METTL14 in

mediating miR-29a-3p via the MAP2K6 signaling pathway during spinal

tuberculosis-associated inflammation.

**METHODS:** Twenty cases of peripheral blood samples from patients with spinal

tuberculosis and normal individuals were collected respectively. Through the

construction of a BCG-infected THP-1 macrophage model, the expression of METTL14

and miR-29a-3p in spinal tuberculosis was verified by means of clinical sample

analysis and cell experiments such as RT-qPCR, immunohistochemistry, and Western

blot. The regulation of METTL14-mediated miR-29a-3p through the MAP2K6 signaling

pathway in the inflammatory response of spinal tuberculosis was explored via

immunofluorescence, RT-qPCR, and ELISA.

**RESULT:** The expressions of METTL14 and miR-29a-3p were significantly

downregulated in patients with spinal tuberculosis, while the expression of

MAP2K6 was upregulated. METTL14 regulated the expression of miR-29a-3p through

m6A modification, thereby targeting and inhibiting the expression of MAP2K6.

Overexpression of METTL14 and miR-29a-3p could suppress the MAP2K6 signaling

pathway, alleviated inflammatory responses and spinal tissue damage; conversely,

inhibition of METTL14 and miR-29a-3p activated the MAP2K6 signaling pathway,

intensifying inflammatory responses and spinal tissue damage.

**CONCLUSION:** This research uncovers the crucial role of the METTL14/ miR-29a-3p/

MAP2K6 axis in spinal tuberculosis, providing experimental evidence for the

utilization of non-coding RNA as molecular targets in spinal tuberculosis,

providing references for the study of the pathogenesis of spinal tuberculosis,

and offering novel ideas and perspectives for the diagnosis and treatment of

spinal tuberculosis. This indicates that the treatment targeting METTL14 may

provide a new strategy for the treatment of STB and facilitate its early

clinical detection.

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The gut dysbiosis and plasma lipid metabolisms signatures in children with

active tuberculosis.

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**BACKGROUND:** The human gut microbiota is an important modulator of host immune

responses and has a crucial role in the development of tuberculosis (TB).

Evidences suggest that metabolites may function as a bridge between gut

microbiome and TB progression in children. However, the underlying interactive

mechanisms are not well explored. The results may provide useful insight into

the role played by the gut microbiome in pulmonary TB in children.

**METHODS:** To explore the gut bacterial features and its interaction with plasma

lipid metabolisms in children with TB. We enrolled children aged younger than 14

years old from Beijing Children’s Hospital and West China Second Hospital

between January 2020 and June 2021. We investigated the gut bacterial community

using 16S rRNA sequencing of 98 children with active TB, 37 other infectious

diseases, and 80 healthy children. The plasma lipids were further analyzed using

ultra-high-performance liquid chromatography coupled with mass spectrometry.

**RESULTS:** Children with TB showed decreased diversity and species richness

indices compared to healthy children. Significant increases in the abundance of

Firmicutes and Actinobacteriota combined with a decrease in the abundance of

Bacteroidetes and Proteobacteria were also observed in TB children when compared

with healthy controls. Among children with TB, gut bacterial composition

differed in subgroups with pulmonary and extrapulmonary TB, or subgroups with

different Mycobacterium tuberculosis (MTB) load. Children with TB had a higher

risk of fever (OR = 3.02, P = 0.005) and poor appetite (OR = 2.96, P = 0.02)

than the controls. Several bacterial genera were associated with severe illness

and clinical indices, such as aspartate aminotransferase levels and fever. The

plasma lipids showedc difference between TB patients and the children with other

infectious diseases. Eight genera with the highest relative abundance strongly

correlated with the plasma lipids.

**CONCLUSIONS:** The gut microbiome is compromised in TB children, with a

correlation with the plasma lipid metabolites and clinical presentations.

Integrating analysis of microbiome and metabolism may help improve precise

diagnosis, treatment, and mechanism study for TB in children.

SUPPLEMENTARY INFORMATION: The online version contains supplementary material

available at 10.1186/s12866-025-04141-x.

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PMID: 40629270

**13. BMJ Open. 2025 Jul 7;15(7):e101918. doi: 10.1136/bmjopen-2025-101918.**

Exploring tuberculosis patients' preferences for AI-assisted remote health

management services in China: a protocol for a discrete choice experiment.

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**INTRODUCTION:** Effective health management is critical for patients with

tuberculosis (TB), especially given the need for long-term treatment adherence

and continuous monitoring. Artificial intelligence (AI)-assisted remote health

management services offer a promising solution to increase patient engagement,

optimise follow-up and improve treatment outcomes. However, little research has

explored TB patients' preferences for these services, and no discrete choice

experiment (DCE) has systematically investigated how they make trade-offs

between different service attributes. This study aims to (1) identify key

attributes of AI-assisted remote health management services that influence TB

patients' choices, (2) assess how patients with TB evaluate trade-offs between

different service options using a DCE and (3) examine whether preferences vary

by sociodemographic characteristics and health system factors.

**METHODS AND ANALYSIS:** Six attributes were identified through a literature

review, focus group discussions and expert consultations. A fractional factorial

design was used to generate choice sets while maintaining statistical efficiency

and minimising respondent burden. The DCE will be analysed using a multinomial

logit model to estimate average preferences. A mixed logit model will be applied

to explore preference heterogeneity among participants, incorporating

interaction terms with sociodemographic and attitudinal variables. Stratified

and latent class analyses will also be considered to further investigate sources

of heterogeneity.

**ETHICS AND DISSEMINATION:** This study complies with the Declaration of Helsinki

and has been approved by the Ethics Committee of Wuhan Pulmonary Hospital. All

participant data will remain anonymous, and individuals may withdraw from the

study at any time. The findings will inform the development of patient-centred

AI-assisted TB management strategies and contribute to broader policy

discussions on AI integration in TB care. The results will be disseminated

through peer-reviewed journal publications, policy briefs, conferences and

online platforms.

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**14. Microbiol Spectr. 2025 Jul 7:e0009725. doi: 10.1128/spectrum.00097-25. Online**

**ahead of print.**

Real-world effectiveness and safety of prolonged bedaquiline course in the

treatment of drug-resistant tuberculosis-a multi-center retrospective cohort

study in a country with a high burden of drug-resistant tuberculosis.

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L(1), Qu Q(1), Wang L(1), Lu F(2), Chen H(2), Wang J(3), Sha W(1), Sun Q(1).

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Bedaquiline (BDQ) has gradually become a core drug in drug-resistant

tuberculosis (DR-TB) treatment, and the additional benefits of prolonging BDQ

use remain unclear. Patients with DR-TB who received a BDQ-containing regimen

from three Chinese clinical centers between 1 March 2018 and 31 December 2021

were retrospectively analyzed. Treatment outcomes and adverse drug reactions

were compared between 6-month and prolonged BDQ treatment group before and after

adjustment by propensity score matching (PSM). A total of 160 patients were

enrolled, 72 patients were treated with BDQ for 6 months, and 88 patients were

over 6 months, of which the median duration was 9 months (IQR: 8-11 months).

After PSM adjustment, there were no significant differences in treatment outcome

between the prolonged groups (7-9, 10-12, >12 months) and the 6-month group (all

P > 0.05). A total of 35 patients met the criteria for BDQ prolongation but did

not receive it, resulting in a success rate of 60%, significantly lower than the

prolonged group (78.4%, P = 0.038); however, after adjustment by PSM, there was

no statistically significance (P > 0.05). The median treatment duration (23

months, IQR: 18.50-25.00 months) was significantly longer than the prolonged

group (18 months, IQR: 15.00-20.25 months, P < 0.001). Additionally, two deaths

occurred in the prolonged group, and none in the 6-month group. The cause of

death in one patient was adjudicated as anti-TB treatment-related, while the

other one was considered not. There were no significant differences in the

effectiveness and safety between 6-month and prolonged group, it's still

recommended to prolong BDQ use under close monitoring when anti-TB drugs are

insufficient to form an effective treatment regimen. Prolonged use of BDQ

achieved similar treatment outcomes while potentially shortening the overall

anti-TB duration.IMPORTANCEThis real-world retrospective cohort study provides

critical evidence on the extended application of Bedaquiline (BDQ) in managing

drug-resistant tuberculosis (DR-TB). To date, the effectiveness and safety data

regarding prolonged BDQ treatment are still lacking, and the additional benefits

of prolonged BDQ use remain unclear. Our findings notably demonstrate that

prolonged use of BDQ can achieve similar treatment success rates while

potentially shortening the overall anti-TB treatment duration. We conclude that

when the anti-TB drugs are insufficient to form an effective treatment regimen,

prolonged BDQ use with rigorous safety monitoring is recommended. Our study

significantly advances the evidence base for prolonged use of BDQ in clinical

practice.

DOI: 10.1128/spectrum.00097-25

PMID: 40621913

**15. Diagn Microbiol Infect Dis. 2025 Jul 6;113(3):116966. doi:**

**10.1016/j.diagmicrobio.2025.116966. Online ahead of print.**

Recent transmission analysis of Mycobacterium tuberculosis isolated from rapidly

growing population region in Hangzhou china using 15-Locus MIRU-VNTR.

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**BACKGROUND:** Hangzhou, Zhejiang's capital, experienced rapid population growth

from 2013 to 2023, with significant increases in 2019 and 2020.Yuhang District

stood out with the most rapid population growth. The proportion of immigrant

tuberculosis patients in Yuhang District remained at a high level and the

prevalence of tuberculosis was severe.

**OBJECTIVE:** To explore the impact of the rapid growth of new permanent residents

in the region on tuberculosis transmission and whether there is transmission

between local residents and immigrants.

**METHODS:** We selected 91 Mycobacterium tuberculosis for MIRU-VNTR genotyping

isolated from Yuhang District in 2019-2020.

**RESULTS AND CONCLUSION:** The Beijing genotype was the prevalent strains in

circulation within this region. Nine transmission clusters were identified, with

five involving both local and immigrant populations, indicating transmission

between immigrant and native. The results also raised our concerns about TB

control and prevention in the Nanyuan Subdistrict of Yuhang District. The

minimum estimate of the proportion of TB cases related to recent transmission

was 9.89 % lower than that of previous study on 66 MDR - TB. This result

reiterated the heightened tendency of MDR-TB strains to cluster and suggested a

greater propensity for MDR - TB transmission than that of Non - MDR pulmonary

tuberculosis.

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**16. Front Public Health. 2025 Jun 25;13:1578658. doi: 10.3389/fpubh.2025.1578658.**

**eCollection 2025.**

Global burden and trend of tuberculosis in children and adolescents (under

15 years old) from 1990 to 2021, with projections to 2040.

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**BACKGROUND:** Tuberculosis (TB) remains a significant global health issue, but its

burden among children and adolescents under 15 years old is not well quantified.

This study evaluates TB trends in this age group from 1990 to 2021 and projects

future trends through 2040.

**METHODS:** We used data from the Global Burden of Disease Study (GBD) 2021 to

assess the incidence and mortality of TB in children and adolescents (under 15)

from 1990 to 2021. A Bayesian age-period-cohort model was employed to project

the TB burden.

**RESULTS:** In 2021, there were 799,047 new TB cases and 81,870 TB-related deaths

among children, with an age-standardized incidence rate (ASIR) of 40.01 per

100,000 population and an age-standardized mortality rate (ASMR) of 4.16 per

100,000 population. From 1990 to 2021, the ASIR declined by 2.4% annually, while

ASMR decreased by 4.19% per year. However, drug-resistant TB, especially

extensively drug-resistant TB, increased significantly. The burden was highest

in low-SDI regions, particularly among children under 5, who accounted for over

75% of TB-related deaths. Projections to 2040 indicate continued declines in

ASIR and ASMR for all TB forms, including drug-resistant and TB-HIV

co-infections.

**CONCLUSION:** Sustained investment in TB control programs, particularly in low-SDI

regions, is crucial. Addressing drug-resistant TB and TB-HIV co-infection should

be prioritized in global public health strategies.

Copyright © 2025 Liang, Wang, Yang, Liu and He.

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**17. Diabetes Metab Syndr Obes. 2025 Jul 5;18:2203-2212. doi: 10.2147/DMSO.S523027.**

**eCollection 2025.**

Inflammatory Markers as Predictors of Diabetes Mellitus in Patients with

Pulmonary Tuberculosis: A Retrospective Analysis of Hematological Parameters and

Clinical Features.

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**OBJECTIVE:** This study aimed to investigate whether pretreatment hematological

parameters and clinical features are associated with diabetes mellitus (DM) in

patients with pulmonary tuberculosis (PTB).

**METHODS:** A retrospective study was conducted at Meizhou People's Hospital from

April 2016 to December 2020, including 1106 PTB patients-326 PTB-DM patients as

the case group and 780 non-DM PTB patients as the control group. The clinical

manifestations were collected, and the level of the inflammation index was

measured. Receiver operating characteristic (ROC) curves were used to assess the

diagnosis and analysis of the selected indices.

**RESULTS:** There were no significant differences in the clinical manifestations

including gender and age distribution, fever, shortness of breath/difficulty in

breathing, expectoration, and extrapulmonary tuberculosis (all p>0.05). The

level of ESR was higher, while the levels of neutrophil-to-lymphocyte ratio

(NLR), platelet-to-lymphocyte ratio (PLR), and monocyte-to-lymphocyte ratio

(MLR), system immune inflammation index (SII), and system inflammation response

index (SIRI) were lower in PTB-DM patients than those in non-DM PTB patients

(all p<0.05). Regression analysis showed that erythrocyte sedimentation rate

(ESR) (p<0.001), MLR (p=0.021), and PLR (p=0.003) were found as the independent

risk factors for DM in PTB patients. The area under ROC curve (AUC) value of ESR

was 0.619 (95% CI: 0.590-0.648, cut-off value: 45.5), MLR was 0.600 (95% CI

0.570-0.629, cut-off value: 0.765), PLR was 0.584 (95% CI: 0.554-0.613, cut-off

value: 239.615), ESR+MLR was 0.689 (95% CI: 0.661-0.716), ESR+PLR was 0.694 (95%

CI: 0.666-0.721), MLR+PLR was 0.610 (95% CI: 0.574-0.645), and ESR+MLR+PLR was

0.712 (95% CI 0.685-0.739), respectively.

**CONCLUSION:** ESR, MLR, and PLR are associated with the risk of DM in patients

with PTB. In particular, the combined detection of ESR, MLR, and PLR showed

higher sensitivity and specificity for the diagnosis of DM among patients with

PTB.

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PMCID: PMC12239912

PMID: 40636751

**18. IDCases. 2025 Jun 23;41:e02302. doi: 10.1016/j.idcr.2025.e02302. eCollection**

**2025.**

Diagnostic and therapeutic strategies for solitary pulmonary nodules mimicking

malignancy: Insights from two cases of pulmonary tuberculosis.

Wang X(1)(2), Zhang Y(1)(2), Zhang H(1)(2), Zhang Z(1)(2), Xu W(1)(2).

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Pulmonary nodules present a diagnostic dilemma, particularly in differentiating

tuberculous nodules from malignant lesions. Misdiagnosis may lead to unnecessary

surgery or delayed treatment. We report two cases where solitary pulmonary

nodules were initially suspected as malignancies but were ultimately diagnosed

as pulmonary tuberculosis. In Case #1, a diabetic patient with a left lower lobe

nodule underwent resection, and postoperative pathology and molecular tests

confirmed tuberculosis. In Case #2, a patient with prior pulmonary surgery

developed a new right upper lobe nodule. Despite malignant imaging features,

CT-guided biopsy and GeneXpert plus nanopore sequencing confirmed Mycobacterium

tuberculosis, and anti-tuberculosis therapy led to lesion absorption without

repeat surgery. CT imaging alone is insufficient to distinguish tuberculosis

from malignancy. Integrating percutaneous biopsy with molecular diagnostics is

essential for accurate diagnosis. In high-risk patients, postoperative

anti-tuberculosis treatment should be considered. An individualized,

multidisciplinary approach is critical to avoid overtreatment and improve

outcomes.

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PMID: 40636746

**19. Front Cell Infect Microbiol. 2025 Jun 25;15:1582416. doi:**

**10.3389/fcimb.2025.1582416. eCollection 2025.**

Development and application of a curcumin-cinnamon essential oil nanoemulsion

agent against mycobacteria.

Lei Z(1)(2)(3), Ren Y(4), Wang J(2), Shi H(1), Lin H(5), Chen H(3), Bi L(3)(6),

Wang Y(2), Zhang H(1)(2)(4).

**Zhihui Lei, Yixuan Ren, Jinyao Wang, Haisu Shi, Hu Lin, Hong Chen, Lijun Bi\*, Yutang Wang\*, Hongtai Zhang\***

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With the increasing prevalence of drug-resistant Mycobacterium tuberculosis (M.

tuberculosis), the development of novel anti-mycobacterial agents has become

urgent. In this study, a curcumin-cinnamon essential oil (Cur-CEO) nanoemulsion

was developed with optimized preparation parameters, including a 10% CEO volume

fraction, 7.5 minutes of ultrasonic treatment, and 350 W ultrasound power,

yielding a particle size of 101.14 nm. The nanoemulsion demonstrated high

encapsulation efficiency (90.2%) and stability, with a stability coefficient of

0.984. Structural analysis revealed a dense network structure of the

nanoemulsion and amorphous forms of Cur and CEO, enhanced by hydrogen bonding

and electrostatic interactions, which improved solubility and bioavailability.

The Cur-CEO nanoemulsion exhibited potent antimicrobial activity against

mycobacteria, demonstrating MIC values of 2 µg/mL and 0.25 µg/mL against

Mycobacterium smegmatis and M. tuberculosis, respectively, representing a

fourfold reduction compared to the CEO solution alone, owing to its ability to

induce substantial damage to mycobacterial cell membranes and consequently

enhance nucleic acid and protein leakage. Furthermore, the aerosol form of the

nanoemulsion effectively inhibited both surface and airborne mycobacteria, with

no significant changes in structural properties post-atomization. Lung

deposition studies indicated that 75.6% of aerosol particles of the nanoemulsion

reached the alveolar region, suggesting its potential as an inhalation agent.

Additionally, the Cur-CEO nanoemulsion exhibited negligible effects on

macrophage viability, maintaining a survival rate exceeding 85% even at

concentrations up to 1250 ng/mL. These findings indicate that the Cur-CEO

nanoemulsion, formulated using natural ingredients, holds significant promise as

a food-grade antibacterial agent for the prevention and control of mycobacterial

infections.

Copyright © 2025 Lei, Ren, Wang, Shi, Lin, Chen, Bi, Wang and Zhang.

DOI: 10.3389/fcimb.2025.1582416

PMCID: PMC12238011

PMID: 40636263 [Indexed for MEDLINE]

**20. Infect Drug Resist. 2025 Jul 4;18:3307-3315. doi: 10.2147/IDR.S516991.**

**eCollection 2025.**

Safety and Tolerability of Contezolid Versus Linezolid for Short-Term Treatment

of Rifampicin-Resistant Pulmonary Tuberculosis: A Randomized Controlled Study.

Wang J(#)(1), Xue Y(#)(1), Nie W(1), Ma L(1), Chu N(1), Du Y(1).

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(#)Contributed equally

**PURPOSE:** Linezolid is a core drug used to treat rifampicin-resistant

tuberculosis (RR-TB) and multidrug-resistant tuberculosis (MDR-TB). However,

adverse events (AEs) have limited its clinical application. Safer alternatives

to linezolid are needed to address the safety concerns.

**PATIENTS AND METHODS:** A total of 27 patients with RR-TB (including MDR-TB) were

randomly assigned to receive either contezolid (n=14) or linezolid (n=13) in

combination with standardized background anti-TB regimens, that is,

linezolid-bedaquiline (pyrazinamide)-levofloxacin

(moxifloxacin)-cycloserine-clofazimine or contezolid-bedaquiline

(pyrazinamide)-levofloxacin (moxifloxacin)-cycloserine-clofazimine. The dosage

was 600 mg q12h for linezolid, and 800 mg q12h for contezolid. AE data were

collected during the 2-month treatment period to analyze the characteristics,

severity, onset time, duration, drug relatedness, management, and outcome of the

adverse drug reactions.

**RESULTS:** The median (range) age of contezolid- and linezolid-treated patients

was 40.9 (26-65) and 36.7 (18-65) years, respectively. The incidence of AEs was

14.3% (2/14) in contezolid-treated patients and 92.3% (12/13) in linezolid

group. All drug-related AEs in contezolid group were gastrointestinal reactions

(nausea and vomiting one case each). No peripheral neuropathy or

myelosuppression AEs were observed. The AEs in linezolid group included anemia

(30.8%, 4/13), peripheral neuropathy (53.8%, 7/13), and gastrointestinal

reactions (23.1%, 3/13). Dose reduction or discontinuation was required for

linezolid in 84.6% (11/13) of patients. The anti-TB efficacy of contezolid and

linezolid was comparable in terms of sputum culture conversion rate and

imaging-confirmed lesion absorption rate after treatment for 2 months.

**CONCLUSION:** Contezolid may be a safer alternative to linezolid based on AE

incidence in the treatment of multidrug-resistant tuberculosis for two months.

CLINICAL TRIAL REGISTRATION: This study was registered at

https://www.chictr.org.cn (identifier: ChiCTR2300074234).

© 2025 Wang et al.

DOI: 10.2147/IDR.S516991

PMCID: PMC12238134

PMID: 40635770

**21. ACS Omega. 2025 Jun 23;10(25):26551-26559. doi: 10.1021/acsomega.5c00610.**

**eCollection 2025 Jul 1.**

High-Level Primary Pretomanid-Resistant with ddn In-Frame Deletion of and Its

Association with Lineage 4.5 in China.

Pei S(1)(2), Yang W(3)(4), Ou X(5)(6), Zhao B(5)(6), Zhao Z(7), Wang Z(1), Song

Z(5)(6), Wang S(5)(6), Zhuang J(4), Li C(8), Zhao Y(5)(6).

**Shaojun Pei, Wei Yang, Xichao Ou, Bing Zhao, Zeyuan Zhao, Zekun Wang, Zexuan Song, Shengfen Wang, Jingyuan Zhuang, Chen Li, Yanlin Zhao\***

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Pretomanid (PMD) is a key antibiotic of the newest multidrug-resistant or

rifampicin-resistant tuberculosis treatment regimen "BPaL", but knowledge of its

resistance mutations is still limited, especially in China, as it was approved

only in late 2024. We analyzed a collection of (MTB) isolates from China

including the whole-genome sequencing and drug susceptibility testing data and

extended analysis to other 2165 isolates from lineage 4. We found in-frame

deletion variants in the ddn genome sequence in the isolates collected in

Xinjiang Uyghur Autonomous Region, China, with a high level of PMD resistance

without pre-exposure to PMD belonging to sublineage 4.5. The extended analysis

found that in-frame deletion variants occurred more frequently in sublineage

4.5. Some isolates contain multiple ancestral components after historical

evolution, which may cause in-frame deletion variants to spread in some

settings. Furthermore, molecular dynamics simulations and free energy

calculations of the key mutants indicated that the impaired mutant structures

result in unfavorable domination binding, which poses less probability for PMD

activation for targeting other critical MTB targets and also leads to

insufficient generation of NO (nitric oxide) to kill MTB. Currently, PMD

resistance is mainly due to ddn gene mutations, especially frameshift mutations.

However, our findings underscore the importance of surveillance for in-frame

deletions, especially in regions with a high prevalence of sublineage 4.5, and

the high level of PMD resistance conferred by deletions raises crucial concerns

about the future effectiveness of the BPaL regimen.

© 2025 The Authors. Published by American Chemical Society.

DOI: 10.1021/acsomega.5c00610

PMCID: PMC12235975

PMID: 40630726

**22. Front Nutr. 2025 Jun 24;12:1607507. doi: 10.3389/fnut.2025.1607507. eCollection 2025.**

Underweight was associated with increased mortality in adults with latent

tuberculosis infection.

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**OBJECTIVE:** Latent tuberculosis (TB) infection (LTBI) is a reservoir for active

TB. Although body mass index (BMI) predicts LTBI progression and influences

active TB outcomes, its association with mortality in LTBI patients remains

unclear. We therefore investigated this relationship in a US cohort.

**RESEARCH METHODS & PROCEDURES:** Data from the National Health and Nutrition

Examination Survey 2011-2012 was utilized. Survival differences across BMI

categories were assessed with Kaplan-Meier curves and multivariable Cox

regression. The Restricted Cubic Spline (RCS) analysis modeled the nonlinear

relationship between BMI and mortality risk.

**RESULTS:** Among 700 LTBI participants analyzed, multivariable Cox regression

identified underweight individuals as having higher mortality risk than

normalweight counterparts (adjusted HR = 2.77, 95% CI 1.06-7.22, p = 0.04). No

significant mortality associations were observed for obese or overweight

participants across both crude and adjusted models (all p > 0.05). RCS analysis

demonstrated a U-shaped pattern between BMI and mortality, with minimum

mortality risk at BMI 27.3 kg/m2 (p for nonlinearity = 0.0012).

**CONCLUSION:** In LTBI adults, underweight status independently predicted increased

mortality risk, while overweight or obesity showed no association. RCS analysis

confirmed a U-shaped BMI-mortality relationship with optimal survival at

27.3 kg/m2.

Copyright © 2025 Liao, Liu and Qi.

DOI: 10.3389/fnut.2025.1607507

PMCID: PMC12234320

PMID: 40630176

**23. Pak J Med Sci. 2025 Jun;41(6):1836-1844. doi: 10.12669/pjms.41.6.11722.**

Impact of body mass index on mortality rates in tuberculosis: A systematic

review and meta-analysis.

Li Y(1), Cheng J(2), Bai X(3), Zheng J(4), Mao P(5), Zhou X(6).

**Yichen Li, Jie Cheng, Xinxin Bai, Jie Zheng, Peifang Mao, Xiuzhi Zhou\***

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**OBJECTIVE:** To decipher the role of body mass index (BMI) measured at treatment

initiation on mortality rates in tuberculosis (TB).

**METHODS:** This PROSPERO-registered PRISMA compliant review searched PubMed,

Embase, CENTRAL, and Web of Science for studies from inception upto 10th June

2024. Studies on adult patients examining mortality rates in TB patients based

on BMI at treatment initiation were included. We analyzed crude and adjusted

mortality rates in a random-effects meta-analysis model. Data was pooled to

generate odds ratio (OR) and 95% confidence intervals (CI).

**RESULTS:** Ten studies were included. Both crude (OR: 2.54 95% CI: 2.13, 3.03

I2=56%) and adjusted (OR: 1.99 95% CI: 1.63, 2.44 I2=68%) data analysis showed

that low BMI (<18.5 kg/m2) at treatment initiation was a significant factor

increasing mortality rates of TB. Meta-analysis of crude data (OR: 1.07 95% CI:

0.68, 1.69 I2=76%) did not demonstrate a significant association between high

BMI and mortality, but adjusted data showed that high BMI was associated with

significantly reduced risk of mortality in TB patients (OR: 0.79 95% CI: 0.66,

0.95 I2=10%).

**CONCLUSIONS:** Low BMI is associated with a significantly increased risk of

mortality in TB patients. Scarce evidence also suggests that a high BMI may

offer better survival rates for TB.

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DOI: 10.12669/pjms.41.6.11722

PMCID: PMC12223727

PMID: 40621534

**24. China CDC Wkly. 2025 Jun 20;7(25):863-868. doi: 10.46234/ccdcw2025.142.**

Evaluation of the Immunogenicity of a Mycobacterium intracellulare Clinical

Isolate.

Duan H(1)(2), Xu D(1), Gu Y(1), Wang R(1), Li G(1), Liu H(1), Li M(1), Zhao

X(1), Wan K(1).

**Hongyang Duan, Da Xu, Yujie Gu, Ruihuan Wang, Guilian Li, Haican Liu, Machao Li, Xiuqin Zhao, Kanglin Wan\***

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**WHAT IS ALREADY KNOWN ABOUT THIS TOPIC?** Nontuberculous mycobacteria (NTM) and

Mycobacterium tuberculosis (MTB) share significant genomic similarity, enabling

NTM to induce protective immune responses against MTB infection. This

characteristic has led to their increasing application in tuberculosis (TB)

vaccine development.

**WHAT IS ADDED BY THIS REPORT?** This study found mice in the experimental group

developed high IgG antibody titers (1:921,600±446,351.3) and demonstrated a

Th1-type immune response. Post-immunization serum antibodies exhibited

cross-reactivity with MTB whole-cell proteins. Substantial neutrophil was

recruited following antigen challenge. Mycobacterium intracellulare (Mit)

whole-cell proteins demonstrate potent immunogenicity and cross-reactivity with

MTB whole-cell proteins.

**WHAT ARE THE IMPLICATIONS FOR PUBLIC HEALTH PRACTICE?** These findings suggest

that potential applications in the immunoprevention and treatment of

tuberculosis, and the Mit strain CHPC 1.5701 is identified as a promising

candidate for tuberculosis vaccine development.

Copyright © 2025 by Chinese Center for Disease Control and Prevention.

DOI: 10.46234/ccdcw2025.142

PMCID: PMC12228096

PMID: 40620661

**25. AIDS. 2025 Jul 15;39(9):1095-1105. doi: 10.1097/QAD.0000000000004216. Epub 2025 Jun 26.**

The impact and mechanism of HIV infection on tuberculous granuloma formation.

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The co-infection of Mycobacterium tuberculosis (MTB) and HIV continues to pose a

major challenge to healthcare systems. Currently, the effects of HIV infection

on tuberculous granulomas are not fully understood. This review discusses the

impact of HIV infection on the formation and function of tuberculous granulomas,

highlighting key immunological mechanisms and the interactions between HIV and

MTB infections. The co-infection results in atypical granulomas with weakened

immune defenses, which facilitate the dissemination of MTB and accelerate the

progression of tuberculosis. Additionally, this review explores current animal

models used for studying HIV/MTB co-infection, including nonhuman primates,

humanized mice, and zebrafish, and emphasizes their limitations in fully

replicating human pathological characteristics. This review further emphasizes

that the development of humanized animal models can enhance our understanding of

the cellular and molecular mechanisms underlying HIV/MTB co-infection.

Copyright © 2025 Wolters Kluwer Health, Inc. All rights reserved.

DOI: 10.1097/QAD.0000000000004216

PMID: 40568738 [Indexed for MEDLINE]

**26. Pak J Pharm Sci. 2025 May-Jun;38(3):751-758.**

Baseline keratin-18 level and risk of anti-tuberculosis drug-induced liver

injury: An individual matched case-control study.

Han B(1), Zhu M(1), He Y(1), Zhang M(2), Lu L(3), Pan H(4), He X(5), Yi H(1),

Tang S(1).

**Bing Han, Min Zhu, Yiwen He, Meiling Zhang, Lihuan Lu, Hongqiu Pan, Xiaomin He, Honggang Yi, Shaowen Tang\***

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China.

Anti-tuberculosis drug-induced liver injury (ATLI) presents a grand challenge to

the global control of tuberculosis. Serum keratin-18 may have a certain

predictive value for the occurrence of liver injury. The purpose of this study

is to examine the correlation between baseline serum keratin-18 levels and ATLI

risk among the eastern Chinese Han population. Employing a 1:2 individual

matched case-control approach, the study encompassed 88 ATLI cases and 176

controls. Univariate and multivariate conditional logistic regression analyses

were performed to evaluate the association between baseline keratin-18 levels

and ATLI risk. Furthermore, area under the curve (AUC) was used to assess

keratin-18's efficacy in distinguishing ATLI cases from controls. In ATLI cases,

baseline keratin-18 levels were significantly lower than controls (188.8 vs.

234.9 ng/L, P = 0.044), with higher levels associated with reduced ATLI risk (OR

= 0.995, 95% CI: 0.992-0.999, P = 0.005). Under the optimal keratin-18 cut-off

value of 191.6 ng/L, the AUCs were equal to 0.577 (95% CI: 0.513-0.640, P =

0.018) in univariate analysis and 0.597 (95% CI: 0.524-0.670, P = 0.010) in

multivariate analysis. The present study indicated that the higher the baseline

keratin-18 concentration in tuberculosis patients of eastern Chinese Han

population, the lower the risk of ATLI.

PMID: 40556280 [Indexed for MEDLINE]

**27. Chem Biodivers. 2025 Jul 5:e01274. doi: 10.1002/cbdv.202501274. Online ahead of print.**

Design, Synthesis, and Antibacterial Evaluation of Hybrid Product of

Benzimidazole and Isoxazole.

Bian X(1), Han M(2), Chen M(1), Zhu G(1), Wang J(1), Zhang Y(1), Lin F(2).

**Xingyu Bian, Mengliang Han, Mingyue Chen, Guangyuan Zhu, Jingjun Wang, Yumin Zhang\*, Feng Lin\***

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China.

A rapid and efficient method for synthesizing

1-[(3-aryl-5-isoxazolyl)methyl]-2-aryl-1H-benzimidazole was developed using

3-aryl-5-bromomethyl isoxazole and 2-substituted benzimidazoles as raw

materials, which could be expanded to a wide range of benzimidazoles in moderate

to excellent yields. Halo and hetero functional groups as well as alkyl groups

were tolerated in this transformation. The antimycobacterial activity of all

synthesized compounds were tested using rifampicin as a positive control. Some

compounds exhibited moderate to good tuberculostatic activities against

Mycobacteria smegmatis MC2155 with MIC values ranging from 64.00 to

128.00 µg/mL, providing lead compound for the subsequent development of

anti-tuberculosis drugs.

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DOI: 10.1002/cbdv.202501274

PMID: 40616832

**28. Microb Pathog. 2025 Jul 1:107861. doi: 10.1016/j.micpath.2025.107861. Online**

**ahead of print.**

Advances in the mechanisms of drug resistance of Mycobacterium tuberculosis.

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Mycobacterium tuberculosis (Mtb), the causative agent of tuberculosis (TB), has

developed different mechanism of action against antimicrobial drug therapies,

posing a significant threat to effective treatment against Mtb. This review

article provides an overview of the recent advancements in the mechanism of drug

resistance in Mtb and highlights how drugs target specific cellular processes.

Additionally, we also discuss the intrinsic resistance mechanisms employed by

Mtb and how alterations in drug target sites contribute to treatment failure.

Copyright © 2025. Published by Elsevier Ltd.

DOI: 10.1016/j.micpath.2025.107861

PMID: 40609770

**29. J Leukoc Biol. 2025 Jun 23:qiaf095. doi: 10.1093/jleuko/qiaf095. Online ahead of print.**

Berbamine promotes autophagy and GPX4 expression through inducing abundant ROS

to restrict HIV-1 and Mtb coinfection in macrophages.

Zhou X(1)(2), Zhang S(3), Ou M(3), Tao H(4), Cao T(3), Li L(5), Zhang G(3), Lu

H(1)(2)(3).

**Xuefeng Zhou, Su Zhang, Min Ou, Hong Tao, Tingzhi Cao, Lin Li\*, Guoliang Zhang\*, Hongzhou Lu\***

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China.

Human immunodeficiency virus type 1 (HIV-1) and Mycobacterium tuberculosis (Mtb)

co-infection poses a significant public health threat, characterized by a high

mortality rate due to impaired host immune responses. In this study, we

investigated the role of autophagy, primarily using macrophage cell models

co-infected with HIV-1 and Mtb. Our findings indicate that HIV-1 infection or

latency significantly suppresses autophagy in macrophages, thereby creating a

permissive environment for the survival and replication of intracellular Mtb.

Co-infection experiments demonstrated that Mtb exacerbates the autophagy

suppression induced by HIV-1, further promoting bacterial proliferation.

Notably, pharmacological activation of autophagy using berbamine (BBM), a

natural compound, significantly reduced HIV-1 latency reactivation and decreased

the intracellular Mtb burden. Colocalization of LC3 with the HIV-1 capsid

protein p24 and Mtb was observed using a confocal microscope. Mechanistic

investigations revealed that BBM-induced autophagy is mediated by elevated

levels of cytosolic reactive oxygen species (ROS), which trigger autophagosome

formation and lysosomal degradation.However, prolonged ROS elevation poses a

risk of cellular damage; thus, BBM concurrently upregulates the antioxidant

enzyme glutathione peroxidase 4 (GPX4) to alleviate oxidative stress and

maintain redox homeostasis. These findings underscore autophagy as a

dual-function mechanism that restricts both viral persistence and bacterial

survival during co-infection. This study highlights the therapeutic potential of

targeting the crosstalk between autophagy and ROS to manage HIV-1-Mtb

co-infection and suggests BBM as a promising candidate for further preclinical

evaluation. These insights may inform the development of host-directed therapies

aimed at improving clinical outcomes in co-infected patients.

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