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**中国大陆学者发表的结核病英文文章摘要**

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Evaluation of the diagnostic efficacy of CRISPR-based tuberculosis diagnostics,

GeneXpert MTB/RIF, and innowave DX MTB/RIF across diverse tuberculosis patient

populations.

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**PURPOSE:** This study aimed to evaluate the diagnostic efficacy of CRISPR

(Clustered Regularly Interspaced Short Palindromic Repeats)-based tuberculosis

(TB) diagnostics, GeneXpert MTB/RIF, and Innowave DX MTB/RIF assays across

diverse tuberculosis patient populations.

**METHODS:** A case-control study was conducted on hospitalized patients with

suspected tuberculosis from June 2023 to September 2023. The study population

was stratified by age, gender, and comorbidity status. Participants underwent

testing with CRISPR-based diagnostics, GeneXpert MTB/RIF, and Innowave DX

MTB/RIF assays. Mycobacterial culture served as the reference standard.

Sensitivity, specificity, accuracy, false positive rate, and false negative rate

were calculated for each test across strata. Diagnostic performance was compared

using Chi-square tests.

**RESULTS:** Our study included 187 patients, with 114 testing positive for TB.

CRISPR diagnostics exhibited the highest sensitivity (0.660) across all tests,

while GeneXpert MTB/RIF demonstrated perfect specificity (0.986). Innowave DX

MTB/RIF assays showed sensitivity and specificity of 0.576 and 0.984. Notably,

CRISPR diagnostics outperformed other tests in accuracy (0.798) among elderly

patients, while maintaining robust diagnostic efficacy across gender and

comorbidity groups. Statistical analysis indicated no significant differences in

sensitivity and specificity among age groups (all P > 0.8), nor any significant

effect of gender or comorbid conditions on diagnostic performance (all P > 0.7).

**CONCLUSION:** CRISPR-based diagnostics, GeneXpert MTB/RIF, and Innowave DX MTB/RIF

assays demonstrate high diagnostic utility across diverse TB patient

populations. CRISPR diagnostics show promising sensitivity and accuracy,

suggesting significant potential for TB diagnosis. Their performance remains

consistent regardless of age, gender, or comorbidities, supporting broad

clinical applicability.

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Silver-loaded hollow copper sulfide particles for antibacterial therapy.

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The misuse of antibiotics has accelerated the spread of antibiotic resistance

(AR), making it a major global health threat. Drug-resistant bacteria, such as

Mycobacterium tuberculosis (M. tb), Staphylococcus aureus (S. aureus),

Escherichia coli (E. coli), and Pseudomonas aeruginosa (P. aeruginosa), continue

to cause severe infections worldwide. This underscores the need for alternative

antibacterial strategies. Photothermal therapy (PTT) is an appealing

antibacterial approach with excellent biocompatibility and the ability to

overcome AR; however, its effectiveness is often limited by the heat resistance

of bacteria. In this study, a stepwise preparation method was employed, where a

hollow copper sulfide (CuS) structure was first synthesized using a templating

method, followed by the reduction of silver nanoparticles (Ag NPs) on its

surface to obtain the CuS@Ag hybrid nanostructure. In vitro, Bacillus

Calmette-Guérin (BCG) was selected as a model for M. tb in the antibacterial

activity testing. Briefly, BCG was treated with 0.02 mg mL-1 CuS@Ag, followed by

exposure to 808 nm laser irradiation for 6 minutes, and then incubated at 37 °C

for 24 hours, achieving an antibacterial rate of 94.8%. Additionally, E. coli

and S. aureus were subjected to the same conditions and incubated at 37 °C for 1 hour, achieving antibacterial rates of 33.5% and 49.4%, respectively. At a high

1.02 mg mL-1 concentration, CuS@Ag exhibited 100% antibacterial efficacy against

BCG, E. coli, S. aureus, and P. aeruginosa. Overall, our results demonstrate

that CuS@Ag effectively combines the controllable photothermal therapeutic

properties of CuS with the antibacterial activity of Ag nanoparticles, resulting

in potent antimycobacterial and broad-spectrum antibacterial effects.

DOI: 10.1039/d5dt01646k

PMID: 40814737

**3. BMC Public Health. 2025 Aug 14;25(1):2758. doi: 10.1186/s12889-025-23620-4.**

Spatiotemporal distribution and detection of spatial clusters of tuberculosis in

Hubei Province, China using FleXScan (2017-2023).

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**BACKGROUND:** This study investigates the spatiotemporal distribution and spatial

clustering of tuberculosis(TB) in 103 counties of Hubei Province, China, using

spatial scan statistics. By identifying high-risk areas and temporal trends, the

findings will provide a scientific foundation for targeted TB prevention and

control strategies.

**METHODS:** This study employed the FleXScan method to detect spatial clusters of

pulmonary tuberculosis cases in Hubei Province and identify statistically

significant high-risk areas. Combined with Geographic Information System (GIS)

spatial analysis techniques, we visualized the spatiotemporal distribution

patterns and dynamic changes of these high-risk tuberculosis clusters.

**RESULTS:** Between 2017 and 2023, the incidence rate of Hubei Province decreased

from 68.28 to 54.54 per 100,000 population. Using the FleXScan method,

significant spatial clustering of TB cases was identified. The most likely

clusters (MLCs) were primarily located in the western and southwestern regions,

including Enshi Prefecture, the Shennongjia Forestry District, and parts of

Yichang City. Notably, Enshi Prefecture maintained a persistently high average

annual incidence of 110.78 per 100,000 with no significant temporal decline,

highlighting the urgent need for targeted prevention and control measures.

**CONCLUSION:** TB in Hubei Province exhibits significant spatiotemporal

heterogeneity. Its epidemiology is influenced by multiple factors, including

economic conditions, geographical environment, healthcare access, and social

determinants. Control strategies should take into account differences both

between regions and within individual regions to accurately identify high-risk

areas.

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**4. Infection. 2025 Aug 13. doi: 10.1007/s15010-025-02620-x. Online ahead of print.**

Predictors of therapeutic exposure and pharmacokinetic variability of

second-line anti-TB drugs in MDR-TB patients: a retrospective study.

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**BACKGROUND:** Therapeutic drug monitoring (TDM) is increasingly recommended for

managing multidrug-resistant tuberculosis (MDR-TB) due to significant

interindividual pharmacokinetic variability. However, data on plasma

concentration variability and associated patient factors for second-line anti-TB

drugs remain limited.

**METHODS:** We conducted a retrospective observational study including 74 patients

with MDR-TB at West China Hospital, Sichuan University, from January 2022 to

December 2024. Plasma concentrations of second-line drugs (levofloxacin,

cycloserine, clofazimine, bedaquiline, and linezolid) were measured at

steady-state. We analyzed therapeutic target attainment rates, evaluated

correlations between drug concentrations and patient baseline characteristics,

and explored predictors of drug exposure using multivariable linear regression.

**RESULTS:** Significant interindividual variability in drug exposure was observed

across the studied second-line anti-TB drugs. Clofazimine demonstrated the

highest therapeutic target attainment (72.7%), while bedaquiline had the lowest

(21.1%). For levofloxacin, 29.8% of patients achieved therapeutic

concentrations, whereas cycloserine reached target levels in 43.2% of cases. Age

was positively correlated with cycloserine concentrations (ρ = 0.328,

p = 0.030). Multivariable regression identified age and liver enzymes (ALT and

AST) as independent predictors of levofloxacin exposure. Specifically, elevated

ALT was associated with lower levofloxacin levels (B = -0.191, 95% CI: -0.337 to

-0.045), while elevated AST was linked to higher levels (B = 0.292, 95% CI:

0.080 to 0.503). Linezolid trough concentrations showed a negative correlation

with RBC count, and peak concentrations were positively associated with ESR.

Additionally, bedaquiline concentrations correlated positively with CRP levels.

**CONCLUSION:** Our findings highlight substantial pharmacokinetic variability among

second-line anti-TB drugs, influenced by patient age, liver function, and

systemic inflammation. These results underscore the potential importance of

individualized dosing and routine TDM in optimizing drug exposure and minimizing

toxicity in patients with MDR-TB.

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**5. Tuberculosis (Edinb). 2025 Jul 25;154:102676. doi: 10.1016/j.tube.2025.102676.**

**Online ahead of print.**

Biomarkers for diagnosing pulmonary tuberculosis in adolescents: Peripheral

blood monocyte myotubularin-related protein 4 and oncostatin M genes.

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**BACKGROUND/OBJECTIVES:** Although research has increasingly been focused on

pulmonary tuberculosis (PTB) in adolescents, its diagnosis remains complex and

challenging. Thus, the use of host transcription markers in the diagnosis of

adolescent PTB was evaluated in this study.

**METHODS:** The study cohort comprised 40 adolescents (aged 14-18 years) with PTB

who had received their first PTB diagnosis at Anhui Provincial Chest Hospital,

China, between January and December 2023 (case group) and 32 healthy adolescents

who had undergone physical examinations at The First Affiliated Hospital of the

University of Science and Technology of China during the same period (control

group). Peripheral blood samples were collected from both groups, and isolated

monocytes were subjected to transcriptome sequencing and bioinformatic analysis.

The relevant genes were confirmed through quantitative polymerase chain

reaction. The diagnostic value of these genes in adolescent PTB patients was

analysed using receiver operating characteristic curves. Furthermore, an in

vitro model was constructed by infecting THP-1 cells with the Mycobacterium

tuberculosis strain H37Ra to assess whether the in vitro expression levels of

the identified genes were consistent with those of the genes in the peripheral

blood monocytes of adolescents with PTB. The specific mechanisms were explored

using methods such as lentiviral infection, flow cytometry, immunofluorescence,

Western blotting, and qRT‒PCR.

**RESULTS:** The results revealed that the expression level of the

myotubularin-related protein 4 gene (MTMR4) was lower in the case group than in

the control group (P < 0.0001; area under the curve: 0.946; 95 % confidence

interval: 0.893-0.999; cut-off value: 0.844; sensitivity: 0.875; specificity:

0.969). The expression level of the oncostatin M gene (OSM) was greater in the

case group than in the control group (P = 0.014; area under the curve: 0.962;

95 % confidence interval: 0.914-1.000; cut-off value: 0.919; sensitivity: 0.950;

specificity: 0.969). However, no significant between-group difference was

detected in the expression level of the complement component 1q subcomponent A

gene. The results from the in vitro experiment indicated that the expression

levels of MTMR4 and OSM were consistent between the H37Ra-infected cells and the

case group samples. Bioinformatics analysis revealed that cytokine-cytokine

receptor interactions, JAK/STAT signalling and PI3K/cell survival-related

pathways play key roles in the pathogenesis of adolescent PTB. Additionally, we

found that H37Ra infection affected tuberculosis progression via the

OSM/PI3K/GPX4 pathway.

**CONCLUSIONS:** Peripheral blood monocyte OSM and MTMR4 may serve as biomarkers of

adolescent PTB. We speculate that targeting the OSM signalling pathway by

knocking down OSM expression or inhibiting its ligand/receptor might be a

strategy to reduce pulmonary tuberculosis-related tissue damage.

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Integrating WGCNA and machine learning to distinguish active pulmonary

tuberculosis from latent tuberculosis infection based on neutrophil

extracellular trap-related genes.

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**BACKGROUND:** Pulmonary tuberculosis (PTB) remains a major global public health

challenge, with diagnostic delays being a key factor contributing to its high

morbidity and mortality. Growing evidence suggests that neutrophil extracellular

traps (NETs) are closely associated with PTB pathogenesis. This study focuses on

elucidating the role of NETs in PTB and identifying critical diagnostic methods

and potential biomarkers.

**METHODS:** Weighted gene co-expression network analysis (WGCNA) was employed to

identify the three modules most strongly correlated with NETs. Differentially

expressed genes (DEGs) from GSE39939 dataset were intersected with module genes

to obtain NET-related DEGs. Four machine learning algorithms (LASSO, random

forest, RFE, and Boruta) were applied to select feature genes and develop a PTB

diagnostic model. Model's performance was evaluated using support vector machine

(SVM)-based receiver operating characteristic (ROC) and precision-recall (PR)

curves, with validation in the GSE39940 dataset. The optimal algorithm was

selected to refine feature genes and construct a miRNA-gene regulatory network.

**RESULTS:** ROC and PR curve analyses revealed that RFE and Boruta algorithms

exhibited superior diagnostic efficacy in distinguishing active PTB from latent

TB infection (LTBI). Further analysis identified five overlapping high-ranking

feature genes (GPR84, SIGLEC10, CCR2, TMEM167A, and GYG1) between the RFE and

Boruta algorithms. hsa-miR-1264, hsa-miR-664a-3p, hsa-miR-548e-5p, hsa-miR-4775,

and hsa-miR-5056 were predicted to potentially target these genes.

**CONCLUSION:** RFE algorithm achieves high diagnostic accuracy for PTB and

identifies five potential biomarkers (GPR84, SIGLEC10, CCR2, TMEM167A, and

GYG1). These findings may provide valuable tools for PTB diagnosis and

treatment.

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**7. J Orthop Surg Res. 2025 Aug 20;20(1):779. doi: 10.1186/s13018-025-06204-1.**

ALKBH5 suppresses miR-29a-3p expression, thereby exacerbating the inflammatory

response associated with spinal tuberculosis.

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**BACKGROUND:** N6-methyladenosine (m6A) is the most common and abundant internal

modification in RNA. However, the role of m6A in spinal tuberculosis (STB)

remains incompletely elucidated. In our previous study, miRNA-seq was performed

on peripheral blood and tissues from STB patients, and miR-29a-3p was identified

as differentially expressed in STB patients through screening. In this study, we

mainly explored the regulation of miR-29a-3p by ALKB homolog 5 (ALKBH5) in STB.

**METHODS:** Tissue specimens were obtained from 20 patients with lumbar

degenerative disease and 20 patients with STB. The expression levels of ALKBH5

and miR-29a-3p in STB were assessed using qRT-PCR, immunohistochemistry, and

immunofluorescence assays. MeRIP analyses were performed to investigate the role

of ALKBH5 in regulating the m6A modification of miR-29a-3p. Additionally,

Western blot, ELISA, and qRT-PCR techniques were employed to validate the

regulatory mechanism of ALKBH5-mediated miR-29a-3p in the inflammatory response

associated with STB.

**RESULTS:** ALKBH5 was upregulated in both spinal tuberculosis tissues and cellular

models, whereas miR-29a-3p exhibited marked downregulation. Inhibition of

miR-29a-3p expression led to increased levels of tumor necrosis factor-α

(TNF-α), interleukin-1β (IL-1β), and interleukin-17 A (IL-17 A). Conversely,

overexpression of miR-29a-3p effectively suppressed the production of

inflammatory factors. Furthermore, ALKBH5 was found to directly target

miR-29a-3p and regulate its methylation modification, thereby inhibiting the

maturation of miR-29a-3p. Additionally, ALKBH5 suppressed the expression of

miR-29a-3p, which in turn promoted the release of inflammatory factors

associated with spinal tuberculosis.

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**8. BMC Infect Dis. 2025 Aug 19;25(1):1043. doi: 10.1186/s12879-025-11316-4.**

Epidemiology of tuberculosis and HIV coinfection among inpatients in chengdu,

china, 2018-2022.

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**BACKGROUND:** Tuberculosis (TB) and human immunodeficiency virus (HIV) infection

are infectious diseases that pose serious threats to human health. TB and HIV

can interact to promote the progression of diseases. This study aims to provide

basic evidence for the formulation of disease prevention and control strategies.

**METHOD:** A retrospective study was conducted to analyze the characteristics of

demographics and comorbidity, in an attempt to identify factors associated with

HIV and TB coinfection among TB inpatients at Public Health Clinical Center of

Chengdu, China from January 2018 to December 2022.

**RESULTS:** Among 37,587 TB inpatients, HIV-positive and HIV-negative TB cases

accounted for 6.1% (2,301) and 93.9% (35,286), respectively.11.9% (4,468) were

extrapulmonary tuberculosis (EPTB), of which 6.2%(278) were HIV-positive EPTB.

Among TB, the most common types of HIV-positive TB were pulmonary tuberculosis

(PTB) (87.9% [2,023]), tuberculous pleurisy (34.4% [791]), and lymph node

tuberculosis (33.1% [762]). The proportion of HIV-positive TB decreased from

7.0% in 2018 to 5.1% in 2022 (P < 0.001), showing a downward trend. Factors

associated with HIV-positive TB included being 18–59 years of age, male sex,

divorced or widowed status, and urban residence. The comorbidity factors

associated with HIV-positive TB included hepatitis C infection and syphilis.

Those with HIV-positive TB were more likely to be complicated with opportunistic

infections, including cryptococcal infection, toxoplasma infection,

cytomegalovirus (CMV) infection, and Pneumocystis jirovecii pneumonia (PjP).

**CONCLUSION:** Early screening for HIV in TB with associated factors, comprehensive

management, and control of comorbidities may significantly contribute to

achieving the WHO End TB Strategy targets.

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**Online ahead of print.**

Microbiological evidence for the trisubstituted benzimidazoles targeting MmpL3

in Mycobacterium tuberculosis.

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New anti-tuberculosis (TB) drugs with novel modes of action are in great demand

due to the complex treatment regimens as well as the rising number of

multidrug-resistant TB cases. We recently re-evaluated a few

2,5,6-trisubstituted benzimidazole derivatives (SBZ) previously demonstrated to

have potent antitubercular activity. These compounds displayed favorable MICs

and significantly reduced bacterial counts in an acute mouse infection model.

Although this antitubercular lead series was initially reported to inhibit

mycobacterial cell division, our findings suggest that its primary activity

likely involves other cellular targets. By using bacterial cytological

profiling, we observed that SBZ-treated Mycobacterium tuberculosis cells exhibit

cell wall-damaging phenotypes resembling those caused by known cell wall

biosynthesis inhibitors, such as AU1235 and SQ109, that mostly target the

membrane protein large 3 (MmpL3). Whole-cell assays further supported the

findings by showing activation of the iniBAC operon and accumulation of

intracellular ATP. The antitubercular activity of SBZs was tested against

engineered mycobacterial strains that have the transcriptionally regulated mmpL3

gene expression, confirming that SBZs engage the MmpL3 target in the cell.

Strains with mutations in mmpL3 exhibited either low- or high-level resistance

to the SBZs. A molecule docking model is proposed, based on a high-resolution

crystal structure of MmpL3, which could be useful in reconciling the inhibition

mechanism and suggesting a further development of MmpL3 inhibitor starting with

the SBZ scaffold.

DOI: 10.1128/aac.00368-25

PMID: 40827962

**10. Virulence. 2025 Dec;16(1):2542466. doi: 10.1080/21505594.2025.2542466. Epub 2025 Aug 18.**

Cytotoxic granules and effector molecules from immune cells in tuberculosis:

Mechanisms of host defense and therapeutic potential.

Qin Y(1), Xu J(2), Wang Q(3), Shi J(4).

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Tuberculosis (TB), a disease caused by Mycobacterium tuberculosis (Mtb), remains

one of the most formidable infectious diseases globally. The immune system

orchestrates a complex response including, but not limited to, T lymphocytes,

natural killer (NK) cells, macrophages, and dendritic cells (DCs) to control and

eliminate Mtb. While these cells are well-recognized for their roles in

anti-tumor immunity, their contributions to the defense against Mtb are equally

critical. This review delves into the specific mechanisms by which these immune

cells release cytotoxic enzymes and effector molecules, offering new insights

into their pivotal roles in Mtb clearance. A deeper understanding of these

mechanisms is essential for developing more effective strategies to combat

tuberculosis.

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PMCID: PMC12363531

PMID: 40825006

**11. China CDC Wkly. 2025 Aug 15;7(33):1073-1078. doi: 10.46234/ccdcw2025.181.**

Genotypic Characteristics of Mycobacterium Tuberculosis Based on Whole Genome

Sequencing - Southern Xinjiang Uygur Autonomous Region, China, 2021-2023.

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Ma X(1), Wang X(2).

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**WHAT IS ALREADY KNOWN ABOUT THIS TOPIC?** Currently, Mycobacterium tuberculosis is

classified into 9 major lineages, each exhibiting distinct geographical

distribution patterns and transmission characteristics. In China, Lineage 2

predominates, while Lineage 3 is primarily distributed in the Xinjiang region.

**WHAT IS ADDED BY THIS REPORT?** This study integrated multidimensional analyses

incorporating patient characteristics, strain lineages, drug resistance

profiles, and transmission networks, providing a comprehensive elucidation of

Mycobacterium tuberculosis molecular epidemiology.

**WHAT ARE THE IMPLICATIONS FOR PUBLIC HEALTH PRACTICE?** Molecular epidemiological

insights into Mycobacterium tuberculosis transmission in Southern Xinjiang

enable precision tuberculosis control.

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DOI: 10.46234/ccdcw2025.181

PMCID: PMC12365654

PMID: 40843139

**12. China CDC Wkly. 2025 Aug 15;7(33):1079-1086. doi: 10.46234/ccdcw2025.180.**

Epidemiological Characteristics of Tuberculosis Among Interprovincial Migrants -

China, 2019-2023.

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**INTRODUCTION:** Tuberculosis (TB) represents one of China's most significant

infectious disease, with inter-provincial population migration posing a

challenge to controlling its spread. This study examined TB cases among

inter-provincial migrants across China from 2019 to 2023.

**METHODS:** TB surveillance data were extracted from China's Tuberculosis

Information Management System and analyzed using R software (version 4.4.0).

After information desensitization, the relevant information of TB patients with

differing current and permanent address codes was extracted.

**RESULTS:** Between 2019 and 2023, we identified 123,945 TB cases among

inter-provincial migrants, representing 4.03% (123,945/3,077,951) of all

reported TB cases. The primary destination provincial-level administrative

divisions (PLADs) for TB patients were Guangdong (48,183 cases, 38.9%), Zhejiang

(27,383 cases, 22.1%), Fujian (8,582 cases, 6.9%), Beijing (7,959 cases, 6.4%),

and Shanghai (7,403 cases, 5.9%), collectively accounting for 80.3% of all

inter-provincial migrant TB cases. The PLADs with the highest outflow of TB

migrants were Sichuan (15,155 cases, 12.23%), Hunan (14,707 cases, 11.87%),

Guizhou (13,927 cases, 11.24%), Jiangxi (8,892 cases, 7.17%), and Hubei (8,441

cases, 6.81%). Among these migrant cases, 66.2% were male, 93.0% were newly

diagnosed, 2.4% exhibited drug resistance. The proportion of individuals aged

45-64, aged ≥65 and re-treated exhibited a significant annual increase

(P<0.001). The overall successful treatment rate was 89.5%, while 5.3%

experienced adverse treatment outcomes. Throughout the study period, the lowest

proportion of TB cases among inter-provincial migrants occurred in February.

**CONCLUSION:** From 2019 to 2023, the characteristics of TB among inter-PLADs

migrant patients have undergone certain changes. The migration of TB primarily

flows from economically weaker regions to more developed areas, with the main

destination PLADs relatively stable. Effective TB control among inter-PLADs

migrants requires targeted screening programs focusing on individuals from major

source and destination PLADs. Tailored strategies should be developed based on

the migration patterns of different PLADs.

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

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PMID: 40843138

**13. China CDC Wkly. 2025 Aug 15;7(33):1087-1092. doi: 10.46234/ccdcw2025.183.**

An Outbreak of Isoniazid-Resistant Tuberculosis in a School Originating from

Household Transmission - Guigang City, Guangxi Zhuang Autonomous Region, China,

November 2024.

Xu D(#)(1)(2)(3), Liang X(#)(1), Zhou L(#)(1), Chen W(3)(4), Ye J(1), Li J(1),

Yao W(5), Zhu J(6), Cui Z(1).

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**WHAT IS ALREADY KNOWN ABOUT THIS TOPIC?** Tuberculosis (TB) represents one of the

world's most significant infectious diseases, caused by Mycobacterium

tuberculosis (M. tuberculosis). The pathogen spreads readily among students due

to crowded environments and prolonged close contact during school activities.

**WHAT IS ADDED BY THIS REPORT?** This outbreak investigation identified 18 TB cases

(15 students, 1 teacher, and 2 staff members), including 5 cases with

isoniazid-resistant TB. Sixteen pulmonary TB cases demonstrated clear

epidemiological linkage, indicating a clustered outbreak spanning multiple

households, school grades, and both junior and senior high schools.

**WHAT ARE THE IMPLICATIONS FOR PUBLIC HEALTH PRACTICE?** This outbreak underscores

the critical importance of comprehensive household contact screening. When

tuberculosis emerges within a family unit, school contacts - particularly

students and teachers - require immediate and thorough screening. Additionally,

the outbreak reveals significant gaps in the effectiveness and quality of

entrance physical examinations that demand urgent improvement.

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Association of tuberculosis infection with the development of active

tuberculosis and comorbidities in rural China: a 10-year follow-up results of a

population-based, multicentre, prospective study.

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Feng B(1)(2), He Y(1)(2), Shen L(1)(2), Huang J(1)(2), Liu Z(3), Liu F(4), Yang

S(4), Xu Z(5), Chen C(6), Zhang B(3), Yan J(3), Liang Y(7), Liu R(8), Zhu T(9),

Li H(10), Shen F(10), Guo T(1)(2), Di Y(1)(2), Li Z(1)(2), Liang J(1)(2), Zhao

Y(1)(2), Bai L(5), Lu W(6), Jin Q(1)(2), Gao L(1)(2).

**Henan Xin, Jiang Du, Xuefang Cao, Weitao Duan, Aiwei He, Jun Liang, Limei Zhu, Boxuan Feng, Yijun He, Lingyu Shen, Juanjuan Huang, Zisen Liu, Fang Liu, Shumin Yang, Zuhui Xu, Cheng Chen, Bin Zhang, Jiaoxia Yan, Yanchun Liang, Rong Liu, Tao Zhu, Hongzhi Li, Fei Shen, Tonglei Guo, Yuanzhi Di, Zihan Li, Jianguo Liang, Yaqi Zhao, Liqiong Bai, Wei Lu, Qi Jin, and Lei Gao∗**

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**BACKGROUND:** In China, there is limited research on the role of recent and

long-term infection of Mycobacterium tuberculosis in relation to the incidence

of pulmonary tuberculosis (PTB), as well as the impact of tuberculosis infection

(TBI) on other diseases. A population-based, multicenter prospective study

(LATENTTB-NSTM) was implemented since 2013 to assess the prevalence of TBI and

to track the development of active disease in rural China. This cohort study

provides an opportunity to address these gaps in knowledge.

**METHODS:** In October 2023, all 21,832 participants from rural China who initially

participated in the baseline survey of the LATENTTB-NSTM study were invited to

take part in the 10-year follow-up survey. The data on the incident PTB and

other health concerns including type 2 diabetes mellitus (T2DM), cancers,

cardiovascular and cerebrovascular diseases were acquired from medical record or

self-reported. The proportion of baseline TBI and newly acquired infection to

the incident PTB and the association of baseline TBI status with the incidence

of other diseases were analyzed.

**FINDINGS:** Overall, 21,211 study participants with a sum of 170,152 person-years

were included in final analysis. During the 10-year period, a total of 181

incident PTB patients were identified, including 134 patients developed from TBI

defined at baseline and 47 patients developed from newly acquired infection

during follow-up. The proportion of newly acquired infection during follow-up

was statistically pronounced in incident PTB cases diagnosed in the latter 5

years as compared to in the first 5 years of the follow-up period (38·30%

(18/47) vs. 21·64% (29/134), p = 0·031). The proportion of baseline TBI was

statistically higher in incident PTB cases aged ≥60 years than in those aged <60

years (85·19% (69/81) vs. 65·00% (65/100), p = 0·002). In addition, baseline TBI status was found to be significantly associated with increased risk of incident

T2DM, cancers and chronic bronchitis with adjusted hazard ratio of 1·22 (95%

confidence interval (CI): 1·04-1·42), 1·81 (95% CI: 1·20-2·72), and 2·94 (95% CI: 1·06-8·15), respectively. The risk of incident T2DM slightly increased along with the increasing intensity of the immune response in TBI testing at baseline.

**INTERPRETATION:** As compared to recent infection, TBI remains the dominating

contributor of incident PTB in rural China. Alongside efforts to systematically

manage infectious cases and close contacts, preventive treatment targeting

individuals under high risk of developing active diseases from TBI is crucial

for achieving rapid declining of PTB incidence. Moreover, the possible influence

of TBI on the other health conditions further underscores the importance of TBI

management from a new perspective.

**FUNDING:** The CAMS Innovation Fund for Medical Sciences and the National Natural

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**15. Front Public Health. 2025 Aug 4;13:1467509. doi: 10.3389/fpubh.2025.1467509.**

**eCollection 2025.**

Decadal trends and regional disparities in tuberculosis burden: a comprehensive

analysis of global, African, and Southeast Asian data from the GBD 1990-2021.

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Medical University, Kunming, Yunnan, China.

**BACKGROUND:** Tuberculosis (TB), an infectious disease caused by Mycobacterium

tuberculosis, remains a major global public health challenge, particularly in

developing countries. Despite a global reduction in TB incidence from 2015 to

2020, the disease continues to be prevalent, with 9.4 million new cases and 1.35

million deaths reported in 2021. This study aims to assess the global, regional,

and national burden of TB, with a specific focus on Africa and Southeast Asia,

using data from the Global Burden of Disease Study.

**METHODS:** Data from the Global Burden of Disease 2021 (GBD 2021) study were used

to evaluate TB incidence, prevalence, mortality, and disability-adjusted life

years (DALYs) from 1990 to 2021. Statistical analyses were conducted using R

software and Joinpoint Regression Program to identify trends in age-standardized

incidence rate (ASIR), age-standardized mortality rate (ASMR), and

age-standardized DALY rate (ASDR). The annual percentage change (APC) was

calculated to assess the significance of temporal trends.

**RESULTS:** From 1990 to 2021, global age-standardized rates of TB declined

markedly, with ASIR decreasing from 173.0 to 103.0 per 100,000, ASMR from 40.0

to 14.0, and ASDR from 1,650.6 to 580.3. Although incident case numbers slightly

declined globally, absolute numbers increased in Africa and Southeast Asia,

despite reductions in standardized rates. The disease burden has shifted from

younger to older age groups, reflecting population aging. Males consistently

exhibited a higher burden than females, though sex disparities narrowed over

time. Joinpoint regression confirmed sustained declines in all indicators,

particularly in Africa and Southeast Asia. Projections to 2040 suggest continued

reductions and convergence in burden across regions. Spatial analyses identified

persistent high-burden clusters in sub-Saharan Africa and Southeast Asia,

despite overall global improvement.

**CONCLUSION:** TB remains a significant public health issue, especially in Africa

and Southeast Asia. While global incidence and mortality have decreased,

persistent regional disparities call for more targeted interventions. Ongoing

global efforts are essential to further reduce TB-related morbidity and

mortality.

Copyright © 2025 Xie, Xiao, Xu, Zhang and Luo.

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**16. Infect Drug Resist. 2025 Aug 13;18:4087-4099. doi: 10.2147/IDR.S538824.**

**eCollection 2025.**

Distinctive Immuno-Inflammatory Pattern in Tuberculous Lymphadenitis: A

Retrospective Cohort Study with Propensity Score Matching.

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**PURPOSE:** Tuberculous lymphadenitis (TBL) represents a common form of

extrapulmonary tuberculosis (EPTB), yet its immunological characteristics

compared to other EPTB forms remain poorly characterized. We aimed to compare

immunological parameters between TBL and non-TBL patients to elucidate

site-specific immune phenotypes.

**PATIENTS AND METHODS:** We conducted a retrospective single-center study at Fuzhou

Pulmonary Hospital, China (April 2018-April 2024). From 1,408 EPTB patients

screened, 862 met inclusion criteria after excluding immunocompromised patients,

those with incomplete data, or age <18 years. Patients were stratified into TBL

(n=337) and non-TBL EPTB (n=525) groups. To mitigate confounding, we implemented

1:1 propensity score matching based on demographic factors (age, sex) and

nutritional status (BMI, hemoglobin, albumin), yielding 323 matched pairs. We

compared inflammatory markers (neutrophil count, neutrophil-to-lymphocyte ratio

[NLR]) and immunological parameters (lymphocyte count and T lymphocyte subsets:

CD3+, CD4+, CD8+, CD45+) between groups using Mann-Whitney U-tests and Spearman

correlation analyses.

**RESULTS:** In matched cohorts, TBL patients demonstrated markedly higher

lymphocyte counts than non-TBL patients (1.27 vs 1.04×109/L, P<0.001) despite

comparable neutrophil counts (4.45 vs 4.49×109/L, P=0.724), resulting in

significantly lower NLR (3.58 vs 4.38, P=0.001). T lymphocyte subset analysis

revealed substantially elevated absolute counts in TBL patients: CD3+ (1000.00

vs 829.00 cells/μL, P<0.001), CD4+ (555.00 vs 474.00 cells/μL, P=0.007), CD8+

(372.00 vs 305.00 cells/μL, P<0.001), and CD45+ (1393.00 vs 1196.00 cells/μL,

P<0.001). Lymphocyte counts strongly positively correlated with all T cell

subsets (CD3+: r=0.72, CD4+: r=0.72, CD8+: r=0.55; all P<0.001), while higher

NLR values were associated with lower T cell subset counts.

**CONCLUSION:** TBL patients exhibit distinctive immunological characteristics,

including lower NLR values and elevated T lymphocyte subset counts compared to

other EPTB forms. These findings provide novel insights into site-specific

immune responses to Mycobacterium tuberculosis infection, enhancing our

understanding of the pathophysiological mechanisms underlying different

manifestations of tuberculosis.

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**17. Medicine (Baltimore). 2025 Aug 15;104(33):e43947. doi:**

**10.1097/MD.0000000000043947.**

Mycobacterium tuberculosis infection following polyacrylamide hydrogel

(Amazingel) breast augmentation: A case report and literature review.

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Province, China.

**RATIONALE:** Polyacrylamide hydrogel (PAAG) injection for breast augmentation is

linked to long-term complications like inflammation and infection, with

bacterial infections being well-documented. However, mycobacterial infections

following such procedures are extremely rare, making this case clinically

significant for enhancing awareness of unusual pathogens in post-PAAG

complications.

**PATIENT CONCERNS:** A 42-year-old female reported persistent right breast pain,

and the wound failed to heal for a long time after surgery to remove the

injected material, 15 years after undergoing PAAG injection for breast

augmentation. These symptoms persisted despite prior interventions, causing

significant discomfort and prompting further medical evaluation.

**DIAGNOSES:** The initial assessment misdiagnosed the condition as a bacterial

infection. However, subsequent acid-fast bacilli staining of wound secretions

and TBseq Ultra-gene sequencing confirmed the presence of Mycobacterium

tuberculosis, leading to a definitive diagnosis of mycobacterial infection.

**INTERVENTIONS:** The patient received a 2-month intensive anti-tuberculosis

regimen consisting of rifampicin, isoniazid, ethambutol, and pyrazinamide. This

targeted therapy was initiated following the confirmation of M tuberculosis

infection.

**OUTCOMES:** After completing the 2-month anti-tuberculosis treatment, the patient

achieved complete wound healing. A 3-month follow-up period showed no recurrence

of symptoms, indicating successful resolution of the infection.

**LESSONS:** This case emphasizes that M tuberculosis should be considered a

potential pathogen in refractory soft tissue infections following PAAG

injection. Clinicians must maintain a high index of suspicion for mycobacterial

infections when wounds fail to respond to standard therapies. Early use of

acid-fast staining and molecular diagnostics (e.g., gene sequencing) is critical

for timely and accurate diagnosis, enabling targeted treatment to improve

patient outcomes.

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**18. J Inflamm Res. 2025 Aug 9;18:10723-10740. doi: 10.2147/JIR.S533116. eCollection 2025.**

Host Circulating Immunometabolism-Associated Biomarkers for Early Diagnosis of

Active Tuberculosis: Multi-Omics Screening with Experimental Validation.

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**BACKGROUND:** Accurate diagnosis of active tuberculosis (TB) remains challenging

when facing with no clinical symptom and negative pathogen tests. Metabolic

reprogramming is the main characteristic of Mycobacterium tuberculosis (Mtb)

infection and has the potential to be used as a diagnostic biomarker for active

TB.

**METHODS:** Datasets including healthy donors (HCs) and active TB patients were

obtained from the Gene Expression Omnibus database. Machine learning methods

were used to identify the metabolism-related hub genes. Correlation analysis

between gene expression and immune cell infiltration was performed using the

CIBERSORT algorithm. Single-cell RNA-seq analysis was performed to explore the

expression of hub genes in the different immune cells.

**RESULTS:** In this study, we first obtained 41 differentially expressed

metabolism-related genes in active TB patients compared to HCs through bulk

transcriptomic analysis. Four metabolism-related hub genes (GCH1, GK, MTHFD2,

and SLC7A6) were identified using machine learning algorithms for the diagnosis

of active TB with high accuracy and verified using external datasets. A nomogram

was constructed to comprehensively predict the risk of active TB.

Mechanistically, protein-protein interactions and gene set enrichment analysis

revealed that four hub genes affected pteridine and lipid metabolism and were

associated with the innate immune pathways. Immune cell infiltration and

single-cell sequencing analyses showed that GCH1, GK, and MTHFD2 were mainly

expressed in M1 macrophages and were significantly upregulated after Mtb

infection, suggesting that they might participate in macrophage-mediated

anti-Mtb immune responses. Furthermore, the expression levels of GCH1, GK, and

MTHFD2 in macrophages showed a strong correlation with the course and efficacy

of antituberculosis therapy. Changes in the expression of these hub genes were

validated in active TB samples and Mtb-infected mouse models.

**CONCLUSION:** Our results demonstrate that changes in immunometabolism-related

genes are associated with TB pathogenesis and could serve as biomarkers for the

evaluation of active TB.

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**19. J Res Med Sci. 2025 Jul 15;30:34. doi: 10.4103/jrms.jrms\_446\_23. eCollection**

**2025.**

Status and outlook of pulmonary tuberculosis coinfection.

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Coinfections with pulmonary tuberculosis (TB) occur in people with damaged lung

structures, chronic malnutrition, and those with compromised immunity. Moreover,

it is a common clinical challenge that leads to poor clinical outcomes and

contributes to increased morbidity and mortality in patients with TB.

Coinfection in the lungs can prolong hospital stay and increase the cost of

treatment for TB patients, which imposes a heavy burden on families and society.

Therefore, pulmonary TB (PTB) combined with pulmonary infections should be

diagnosed and treated promptly. This review describes trends in epidemiology and

other factors that influence the incidence of PTB coinfection. Current and

emerging diagnoses well as infection treatments are discussed.

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Synergistic antibacterial photodynamic therapy of lysine-porphyrin conjugate and

metal ions combination against Candida albicans and Mycobacterium tuberculosis.

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**INTRODUCTION:** In previous research, antibacterial photodynamic therapy using

lysine-porphyrin conjugate LD4 effectively inactivated methicillin-resistant

Staphylococcus aureus, Pseudomonas aeruginosa, and Escherichia coli; however, it

exhibited limited activity against Candida albicans and Mycobacterium

tuberculosis.

**METHODS:** To address this limitation, we developed a synergistic antibacterial

strategy by combining LD4 with Cu2+ or Zn2+.

**RESULTS:** Synergy was confirmed via minimum inhibitory concentration and

fractional inhibitory concentration index analyses, demonstrating 16- to 64-fold

enhanced antibacterial efficacy compared to LD4 alone. Mechanistic studies

revealed divergent pathways for LD4 + Cu2+ and LD4 + Zn2+: Zn2+ increased the

reactive oxygen species yield and promoted LD4 uptake by pathogens, while LD4 +

Cu2+ induced oxidative damage to cell walls and membranes in darkness, with

light exposure exacerbating structural damage. Cytotoxicity assessments

confirmed low toxicity, with >90% survival of normal cells at bactericidal

concentrations. Fluorescence and infrared spectroscopy characterized metal-LD4

complexes, showing stabilization through interactions between amino and pyrrolic

imino groups of LD4 and metal ions, which promoted non-radiative transitions and

fluorescence quenching. Both combinations caused significant bacterial membrane

disruption and growth suppression. Notably, cytotoxicity exhibited a biphasic

dose-response linked to metal-LD4 complexation-dependent particle size changes.

**DISCUSSION:** This study elucidated the enhanced antimicrobial mechanisms and

safety of LD4-metal ion combinations. The findings resolve the limitations of

LD4 while providing a theoretical framework for developing novel therapies

against fungal and mycobacterial infections.

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**21. Biomed Environ Sci. 2025 Jul 20;38(7):867-872. doi: 10.3967/bes2025.083.**

Spatial-temporal Dynamics of Tuberculosis and Its Association with

Meteorological Factors and Air Pollution in Shaanxi Province, China.

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HW(5), Xu YY(1), Zhang WY(1).

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PMID: 40820253

**22. Biomed Environ Sci. 2025 Jul 20;38(7):781-791. doi: 10.3967/bes2025.078.**

Comparative Transcriptomic and Metabolomic Analyses Reveal the Mechanism by

Which Foam Macrophages Restrict Survival of Intracellular Mycobacterium

Tuberculosis.

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Jia AN(1), Yu YB(1), Guo YL(1), Lu J(1).

**Xiao Peng, Yuan Yuan Liu, Li Yao Chen, Hui Yang, Yan Chang, Ye Ran Yang, Xuan Zhang, An Na Jia, Yong Bo Yu, Yong Li Guo\*, Jie Lu\***

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**OBJECTIVES:** This study aimed to investigate the impact of foam macrophages (FMs)

on the intracellular survival of Mycobacterium tuberculosis (MTB) and identify

the molecular mechanisms influencing MTB survival.

**METHODS:** An in vitro FM model was established using oleic acid induction.

Transcriptomic and metabolomic analyses were conducted to identify the key

molecular pathways involved in FM-mediated MTB survival.

**RESULTS:** Induced FMs effectively restricted MTB survival. Transcriptomic and

metabolomic profiling revealed distinct changes in gene and metabolite

expression in FMs during MTB infection compared with normal macrophages.

Integrated analyses identified significant alterations in the cyclic adenosine

monophosphate (cAMP) signaling pathway, indicating that its activation

contributes to the FM-mediated restriction of MTB survival.

**CONCLUSIONS:** FMs inhibit MTB survival. The cAMP signaling pathway is a key

contributor. These findings enhance the understanding of the role of FMs in

tuberculosis progression, suggest potential targets for host-directed therapies,

and offer new directions for developing diagnostic and therapeutic strategies

against tuberculosis.

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A multilevel analysis on spatiotemporal and individual-level determinants of

tuberculosis treatment failure in China.

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By exploring the factors that influence treatment failure in tuberculosis, the

study aimed to provide references for the treatment and management of

tuberculosis. The study data were derived from the National Tuberculosis

Specialized Reporting System. Univariate analysis was used to test individual

characteristic variables related to tuberculosis treatment failure. A

three-level model was conducted to estimate the risk of tuberculosis treatment

failure from both temporal and spatial levels, as well as from the individual

level. Analysis revealed that demographic characteristics, such as older age (50

years and above) and male sex, were independent risk factors for tuberculosis

treatment failure. Among diagnostic and treatment factors, the type of

tuberculosis diagnosis contributed the most to treatment failure, followed by

positive result for Mycobacterium tuberculosis detection, a history of previous

drug therapy and treatment delays of more than one month. After excluding the

effects of individual factors, there was also a spatiotemporal effect of

treatment failure. Besides the effect of the individual factors, macro factors

such as the socioeconomic development level and the quality of tuberculosis

management might also play an important role in treatment failure. The study on

the spatiotemporal effect provided a reference for objectively evaluating the

quality of work in different regions.

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Prior appendectomy attenuates the immune protective efficacy of BCG vaccination

against Mycobacterium tuberculosis infection.

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Cecal appendix is a unique niche for commensal bacteria, and has been considered

the primary site for immunoglobulin A production. Yet its immune function in

anti-infection immunity has not been fully understood. In order to elucidate

whether cecal patch (CeP), the murine version of appendix, would influence the

immune response induced by Mycobacterium tuberculosis (M. tb) and the vaccine

effect of Bacillus Calmette-Guérin (BCG), BALB/c mice at 4 weeks of age received

appendectomy or sham operation and recovered for 2 weeks before intranasal

infection with 2 × 107 CFU Mycobacterium tuberculosis H37Ra. Appendectomy of

mice led to a reduction in lung macrophage numbers 7 days post infection (p.

i.), and aggravated lung immunohistopathology 4 weeks p. i.. Appendectomized

mice vaccinated with 5 × 106 CFU BCG exhibited attenuated BCG-specific serum

IgG, reduced lung/splenic IFN-γ+ T response, and weakened T proliferation and

cytotoxicity, and eventually worsened lung pathology compared to sham operated

mice. Mechanistically, we found that appendectomized mice at a young age

(4 weeks) had an attenuated maturation of mesenteric lymph node (MLN)

conventional dendritic cells (cDCs), which accounted for the impaired systemic

IFN-γ+ T response and cytotoxicity against M. tb. Our data suggest that intact

appendix maintain intestinal DC maturation and systemic Th1 induction against M.

tb and has an assistant role in increasing immune efficiency of BCG vaccine.

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Inflammation-nutrition biomarker model for survival prediction in lung cancer

patients with concurrent tuberculosis.

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**OBJECTIVES:** To explore the prognostic value of eight inflammation-nutrition

biomarkers in patients with lung cancer and tuberculosis as no multidimensional

prognostic models for this comorbid population are available currently.

**METHODOLOGY:** A retrospective study included 100 patients with lung cancer and

tuberculosis admitted to a tertiary hospital from October 2019 to October 2024.

Eight inflammation-nutrition markers (NLR, PLR, SII, LMR, PNI, HALP, HRR,

ALB/GLB) were chosen as predictors while overall survival (OS) was the major

event. Feature selection was implemented by LASSO regression; a Cox proportional

hazards model was established afterwards. The nomogram's performance was

assessed by ROC curve and C-index as well as the calibration using bootstrap

resampling. The statistical power was calculated by PowerSurvEpi and sensitivity

analyses were implemented to test the robustness of the model.

**RESULTS:** There were six predictors remaining in the final model including

diabetes, ECOG PS, NLR, PNI, HRR and RDW. Among them, ECOG PS was an independent

prognostic factor (HR = 1.76, p = 0.04). The nomogram achieved a good

performance (C-index = 0.71), an AUC of 0.693 for 3-year OS as well as an

excellent calibration (Bootstrap P > 0.05). In the high-risk subgroup with ECOG

PS ≥ 2 and NLR>8, the 5-year survival rate was close to zero. The model achieved

an adequate statistical power (83%, α = 0.05). Sensitivity analysis revealed an

significant interaction between ECOG PS and NLR (p = 0.032) and NLR>8 was the

most robust threshold for this interaction.

**CONCLUSION:** This is the first study to establish and validate a combined

inflammation-nutrition prognostic model for patients with lung cancer and

tuberculosis. Our model provides a quantitative tool to stratify individual risk

and offers evidence for the usage of nutritional interventions in high-risk

patients.

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Tang and Li.

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Enhanced Targeted NGS Assay for Comprehensive Diagnosis in Tuberculosis and

Drug-Resistant Tuberculosis Patients.

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Sun J(5), Yang X(6), Tang J(7), Li L(8), Chen Y(9).

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**BACKGROUND:** Accurate and timely diagnosis of tuberculosis (TB) and

drug-resistant TB is crucial; however, current methods have limitations in

sensitivity and scope, especially for detecting drug resistance and

differentiating other respiratory pathogens.

**METHODS:** We developed a multiplex PCR-based targeted next-generation sequencing

(tNGS) assay and validated its analytical performance, including limit of

detection (LoD), precision, and resistance to interference. A single-centre

prospective study was conducted with 181 suspected TB patients to evaluate the

assay's clinical performance using bronchoalveolar lavage or sputum samples,

compared against microbiological culture and Xpert MTB/RIF.

**RESULTS:** The tNGS assay demonstrated a low LoD of 10 copies/mL for TB and other

respiratory pathogens, with high precision and resistance to interference. In

clinical validation, it achieved 94.94% sensitivity in confirmed TB cases and

showed a 92.86% positive percent agreement with Xpert MTB/RIF for rifampicin

resistance, while also identifying additional mutations. The assay accurately

detected nontuberculous mycobacteria (NTM) and other respiratory pathogens,

aiding differential diagnosis.

**CONCLUSION:** The tNGS assay provides reliable detection of TB, drug-resistant

mutations, and respiratory pathogens, including NTM, thereby enhancing

differential diagnosis and supporting effective treatment strategies in the

management of patients with suspected TB.

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