**2025年第27周**

**中国大陆学者发表的结核病英文文章摘要**

**（29篇）**

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

**1. J Infect Dis. 2025 Jun 25:jiaf332. doi: 10.1093/infdis/jiaf332. Online ahead of print.**

Safety and Diagnostic Performance of Recombinant Fusion Protein ESAT6-CPF10 Skin

Test in A Large Population: A Phase IV Clinical Trial.

Chen J(1), Zhao L(2), Zhou X(2), Mo Y(1), Kong L(2), Ma F(2), Wu L(3), Huang

D(4), Yang H(2), Gong L(2).

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Province, China.

**BACKGROUND:** This study aimed to evaluate the safety and diagnostic performance

of recombinant fusion protein ESAT6-CPF10 (EC) in a community-based population

aged ≥6 months.

**METHODS:** We conducted a two-stage trial in a community-based population. The

first stage used a randomized, double-blind, controlled design (n=500), while

the second stage used a non-randomized, open design (n=7000). Stage 1

participants underwent tuberculosis-specific enzyme-linked immunospot assay

(T-SPOT.TB), tuberculin skin test (TST) and EC skin test (ECST). Stage 2

participants only received the ECST. The purposes of the first and second stage

were to evaluate the diagnostic performance and safety of the ECST,

respectively.

**RESULTS:** At the first stage, the sensitivity of ECST and TST was 89.41% (95% CI:

80.85-95.04) and 85.88% (95% CI: 76.64-92.49), respectively. The specificity of

the ECST and TST was 96.98% (95% CI: 94.79-98.43%) and 61.06% (95% CI:

56.07-65.87%), respectively. The consistency between ECST and T-SPOT.TB was

higher than that between TST and T-SPOT.TB (Kappa=0.85 and 0.28, respectively).

At the second stage, the incidence of adverse drug reactions (ADRs) was 11.75%,

with 0.67% graded ≥3. The incidence of ADRs varied among age groups (<18 years:

2.89%, 18-64 years: 11.51%, ≥65 years: 16.98%) and was significantly higher in

individuals with pulmonary tuberculosis (TB) (46.58%), HIV infection (33.33%),

diabetes mellitus (15.56%), close contacts of TB patients (14.35%), and those

with allergic histories (11.93%).

**CONCLUSIONS:** EC has a satisfactory safety and diagnostic performance profile,

and it is suitable for screening Mycobacterium tuberculosis (MTB) infection in

the community-based population aged ≥6 months.

CLINICAL TRIALS REGISTRATION: NCT05746611.

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**2. Diagn Microbiol Infect Dis. 2025 Jun 3;113(3):116932. doi:**

**10.1016/j.diagmicrobio.2025.116932. Online ahead of print.**

Clinical indicators associated with tuberculous meningitis using multiple

correspondence analysis.

Zhu X(1), Li R(2), Zhang X(2), Wang D(2), Wang Y(2), Lin W(2), Zhang S(3), Chu

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**OBJECTIVES:** Tuberculous meningitis (TBM), the most severe extrapulmonary

manifestation of Mycobacterium tuberculosis (Mtb) infection, contributes to 5-10

% of global tuberculosis-related mortality. This study aimed to delineate

clinical indicators predictive of microbiologically confirmed TBM to facilitate

early diagnosis in resource-limited settings.

**METHODS:** A retrospective cohort analysis was conducted on 146 TBM cases admitted

to Shenzhen Third People's Hospital (2018-2020), undergoing cerebrospinal fluid

(CSF) culture and Xpert. Epidemiologic profiles and clinical outcomes were

systematically characterized. Multiple correspondence analysis (MCA) adjusted

for potential confounders was employed to identify clinical indicators

associated with microbiologically confirmed TBM.

**RESULTS:** Among 146 patients with defined or probable TBM, 80 cases were detected

for Mtb in CSF, with undetected in 66 cases. The increase in CSF white cell

count was more significant than that in blood. Serum sodium, serum chloride

(Cl), CSF glucose, CSF Cl, and CSF to blood glucose ratio in microbiologically

confirmed TBM were significantly lower than those in unconfirmed TBM, in

addition to having worse nutrition and lower blood lymphocytes. MCA identified

diagnostic indicators related to microbiologically confirmed TBM included neck

stiffness, decreased blood lymphocyte counts and serum sodium, elevated CSF

white cell count, decreased CSF glucose and Cl levels, HIV positivity, severe

pulmonary infection, and malnutrition. However, Hypertension and pulmonary

tuberculosis were associated with microbiologically unconfirmed TBM.

**CONCLUSIONS:** The clinical indicators identified in this study may assist

clinicians in high-tuberculosis-incidence-areas, particularly in regions with

limited capacity for CSF microbial culture, to empirically diagnose TBM. When

these indicators are abnormal, they may increase the likelihood of detecting

microbial evidence in CSF.

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PMID: 40561850

**3. Biomol Biomed. 2025 Jul 2. doi: 10.17305/bb.2025.12527. Online ahead of print.**

Vitamin D supplementation for tuberculosis prevention: A meta-analysis.

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Vitamin D plays an important role in immune regulation, prompting interest in

its potential for preventing tuberculosis. However, clinical findings regarding

its protective effects against tuberculosis infection and disease remain

inconsistent. We conducted a systematic review and meta-analysis of randomized

controlled trials (RCTs) to assess the impact of vitamin D supplementation on

the prevention of tuberculosis infection and the progression to active

tuberculosis. We searched PubMed, Embase, Cochrane Library, and Web of Science

databases through January 2025. Eligible studies involved participants without

active tuberculosis at baseline and reported outcomes related to tuberculosis.

Pooled odds ratios (ORs) and 95% confidence intervals (CIs) were calculated

using a random-effects model. Subgroup and sensitivity analyses were conducted,

and the certainty of evidence was evaluated using the GRADE approach. Six RCTs,

involving 15,677 participants, met our inclusion criteria. Compared to placebo,

vitamin D supplementation did not significantly reduce the risk of tuberculosis

infection (5 RCTs; OR: 0.95; 95% CI: 0.79-1.14; p = 0.55) or the development of

active tuberculosis (4 RCTs; OR: 0.77; 95% CI: 0.56-1.05; p = 0.10). The

certainty of evidence was moderate for both outcomes. Subgroup analyses based on

baseline vitamin D levels and duration of follow-up yielded consistent results.

The incidence of serious adverse events was comparable between the vitamin D and

placebo groups (OR: 1.02; 95% CI: 0.76-1.38; p = 0.87), and none of the serious

events were attributed to vitamin D supplementation. In conclusion, vitamin D

supplementation does not significantly reduce the risk of tuberculosis infection

or progression to active tuberculosis, although it is safe and well tolerated.

DOI: 10.17305/bb.2025.12527

PMID: 40613553

**4. Eur J Med Res. 2025 Jul 3;30(1):566. doi: 10.1186/s40001-025-02835-6.**

Plasma lipidomic analysis reveals distinct lipid alterations in patients with

pulmonary tuberculosis.

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**OBJECTIVE:** This study aimed to characterize the plasma lipidomic profile of

patients with pulmonary tuberculosis (PTB), identify lipid species with

potential diagnostic utility, and explore their associations with clinical

parameters to inform future biomarker development and mechanistic understanding.

**METHODS:** In a case-control study, 50 newly diagnosed PTB patients and 50 age-

and sex-matched healthy controls (HC) were enrolled between April and June 2021.

Plasma samples were analyzed using LC-MS/MS-based lipidomics. Multivariate

modeling and univariate statistical analyses were performed to identify

differential lipid species. Receiver-operating characteristic (ROC) curves

evaluated diagnostic performance, and correlation analyses assessed associations

with clinical indicators.

**RESULTS:** A total of 633 lipid species were profiled, with 61 showing significant

differential expression between PTB and HC groups. When compared with controls,

PTB patients exhibited significantly lower plasma levels of total cholesterol,

triglycerides, HDL, and LDL (all P < 0.05), as well as reduced triacylglycerol

(TAG), ceramide (CER), and hexosylceramide (HCER). In contrast,

phosphatidylethanolamine (PE) and phosphatidylcholine (PC) levels were elevated

in PTB. ROC analysis identified several lipid species-particularly CER(24:0) H,

HCER(d18:0/22:0) H, and PE(18:1/18:1)-with strong discriminative power

(AUC > 0.75). Correlation analysis revealed weak-to-moderate associations of

select lipids with age and glucose, but minimal or no correlation with BMI, sex,

or smoking, indicating that lipidomic alterations are primarily disease-driven.

**CONCLUSION:** PTB patients display a distinct plasma lipidomic signature, marked

by disrupted glycerolipid and sphingolipid metabolism. These findings support

the diagnostic value of lipidomic profiling and provide insights into

PTB-associated metabolic disturbances, laying a foundation for future biomarker

validation and therapeutic exploration.

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PMID: 40611333 [Indexed for MEDLINE]

**5. BMC Pulm Med. 2025 Jul 3;25(1):312. doi: 10.1186/s12890-025-03785-9.**

Association of dietary caffeine intake and metabolites in the urine of

individuals with latent tuberculosis infection: a cross-sectional study.

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**BACKGROUND:** Currently, there is insufficient evidence available regarding the

association between dietary caffeine intake and latent tuberculosis infection

(LTBI). The aim of this study was to elucidate the impact of dietary caffeine

intake and urinary caffeine metabolite levels on LTBI.

**METHODS:** We conducted a prospective cohort study using data from the National

Health and Nutrition Examination Survey (NHANES) from 2011 to 2012. We used

multivariate logistic regression to explore the relationship between dietary

caffeine intake and LTBI prevalence, and adjusted for confounding factors. At

the same time, we measured the level of caffeine metabolites in the urine.

**RESULTS:** The mean dietary caffeine intake was 94.0 mg (12.0–205.0 mg) in the

non-LTBI group and 71.0 mg (11.2–160.0 mg) in the LTBI group (P<0.05).

Multivariable-adjusted regression revealed that the participants with a dietary

caffeine intake of ≥ 150 mg/day have lower odds of LTBI compared with the

participants with a dietary caffeine intake<150 mg/day ( OR [odds ratio] 0.70,

95% confidence interval 0.54–0.91). In subgroup analysis, LTBI correlated

negatively with age < 65 years, the male sex, the Mexican American ethnicity, a

body mass index of 25 to < 30 kg/m2, and diabetes (Ps<0.05). Caffeine

metabolites such as 1-methyl-uric acid and 1,7-dimethyl-uric acid were

significantly lower in urine from the participants with LTBI (Ps<0.05).

**CONCLUSIONS:** A lower dietary caffeine intake was proportionally related to LTBI.

The findings presented in this study should be validated and investigated

further.

DOI: 10.1186/s12890-025-03785-9

PMCID: PMC12225470

PMID: 40611082

**6. Sci Rep. 2025 Jul 2;15(1):23633. doi: 10.1038/s41598-025-08078-z.**

Predictive modelling of air pollution affecting human tuberculosis risk on

Mainland China.

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Wu S(1), Chen J(1), Xue J(1), He K(3), Liu C(1), Ma J(4), Zhan X(5).

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In this study, we investigated the correlation between air pollution indicators

and pulmonary tuberculosis (TB) incidence and mortality rates across provincial

administrative regions of China from January 2013 to December 2020 to develop

predictive models using machine learning. Data on TB rates and six air pollution

indicators were collected and analyzed for correlations. Regression models were

built using six algorithms, among which the random forest (RF) model showed

superior performance. SHapley Additive exPlanations analysis helped interpret

the RF model's predictions. Seasonal and lag analyses identified a 10-month

optimal lag period. Seasonal autoregressive integrated moving average models

were used to predict 2020 TB incidence rates, which were validated by comparing

them with actual data. The results indicated significant correlations between

air pollution and TB rates, highlighting that air pollution data can predict TB

incidence and mortality; therefore, air pollution data can help develop public

health strategies. This study emphasized the importance of integrating

environmental factors into TB control efforts using artificial intelligence.

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DOI: 10.1038/s41598-025-08078-z

PMCID: PMC12223263

PMID: 40603496 [Indexed for MEDLINE]

**7. PLoS One. 2025 Jul 2;20(7):e0327767. doi: 10.1371/journal.pone.0327767.**

**eCollection 2025.**

Development and validation of a nomogram for predicting false negative IGRA

results in pulmonary tuberculosis patients using propensity score matching.

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**OBJECTIVE:** This study aims to explore factors influencing false-negative results

in Interferon-Gamma Release Assay (IGRA) for patients with Pulmonary

Tuberculosis (PTB), and develop a nomogram model to predict IGRA false

negatives, thereby optimizing clinical diagnosis and treatment decisions.

**METHODS:** Data were collected from January 2023 to September 2024 at the Second

People's Hospital of Fuyang City, involving 143 PTB patients. Among them, 63

patients who were IGRA negative but pathogen positive formed the observation

group, while 80 patients who were both IGRA and pathogen positive constituted

the control group. Propensity Score Matching (PSM) was used to balance potential

confounding factors between the two groups. Clinical characteristics and

laboratory indicators were compared, followed by logistic regression analysis to

identify independent risk factors affecting IGRA results. A nomogram model was

constructed based on these factors and its predictive performance evaluated.

**RESULTS:** After PSM, each group consisted of 55 patients. The observation group

showed significantly lower levels of white blood cell count (WBC), neutrophil

count (NEUT), lymphocyte count (LYM), red blood cell count (RBC), hemoglobin

(HGB), and albumin (ALB) compared to the control group (P < 0.05). Multivariate

analysis ultimately identified RBC, ALB and NLR as independent predictors of

IGRA false-negativity. The developed nomogram model demonstrated good

calibration (χ² = 4.482, P = 0.811), with an area under the receiver operating

characteristic curve (AUC) of 0.764 (95% CI: 0.675-0.853). Decision curve

analysis indicated that the net benefit of predicting false-negative IGRA

results using this nomogram model was greater than 0 when the threshold

probability ranged from 0.15 to 0.95.

**CONCLUSION:** Decreased RBC/ALB and elevated NLR may be pivotal factors

contributing to false-negative IGRA results in PTB patients. The three-variable

nomogram shows enhanced predictive performance, serving as a quantitative tool

to identify high-risk cases, particularly for patients with malnutrition or

pronounced inflammatory status.

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**8. BMC Med Imaging. 2025 Jul 1;25(1):212. doi: 10.1186/s12880-025-01753-7.**

Computed tomography imaging analysis of hematogenous disseminated pulmonary

tuberculosis cases combined with prostate tuberculosis.

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**OBJECTIVE:** The aim of this study is to enhance the understanding of prostate

tuberculosis by analyzing clinical data and prostate computed tomography (CT)

imaging of patients with hematogenous disseminated pulmonary tuberculosis and

prostate tuberculosis.

**METHODS:** Patients with hematogenous disseminated pulmonary tuberculosis and

prostate tuberculosis admitted to Kunming Third People's Hospital between

January 2018 and December 2024 were enrolled in the study. Their clinical and

imaging characteristics were retrospectively analyzed.

**RESULTS:** A cohort of 11 male patients were included in the study, with only 4

(36.4%) experiencing scrotal swelling and pain. All 11 patients (100.0%) had

positive γ-interferon release assay results. More than 90% exhibited a decreased

absolute value and percentage of peripheral blood lymphocytes, lower serum

albumin and prealbumin levels, elevated C-reactive protein, and an increased

erythrocyte sedimentation rate. CT images of prostate tuberculosis predominantly

revealed multiple hypodense shadows in the prostate, while contrast-enhanced

scans demonstrated annular enhancement or significant enhancement of prostate

tissue outside the lesion. Following effective anti-tuberculosis treatment,

follow-up CT scans showed lesion size reduction, decreased enhancement around

the hypodense lesion, and the emergence of punctate and sand-like

calcifications. If tuberculosis involved other organs of the male reproductive

system, corresponding CT findings were also observed.

**CONCLUSION:** Hematogenous disseminated pulmonary tuberculosis with concurrent

prostate tuberculosis is often associated with other extrapulmonary tuberculosis

and tuberculosis affecting organs of the reproductive system. Clinical symptoms

are generally mild. CT imaging plays a significant role in diagnosing and

monitoring this condition.

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**9. BMC Microbiol. 2025 Jul 1;25(1):373. doi: 10.1186/s12866-025-04091-4.**

Sputum microbiota profiles of patients with rifampicin-resistant tuberculosis

during the intensive-phase treatment.

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**BACKGROUND:** The respiratory microbiome plays a crucial role in respiratory

health and influences the onset and progression of tuberculosis (TB). However,

changes in the respiratory microbiota of patients with rifampicin-resistant TB

(RR-TB) during the intensive-phase treatment have not been assessed. This study

aimed to investigate the impact of a six-month intensive-phase treatment of

second-line anti-TB drugs on the respiratory microbiota of RR-TB patients.

**METHODS:** Sputum samples were collected from 14 RR-TB patients and 14 healthy

controls. Microbiota composition was analyzed using 16S rRNA gene sequencing,

and functional predictions were performed to assess metabolic pathway changes.

**RESULTS:** RR-TB patients exhibited significantly lower alpha diversity compared

to healthy controls, but no significant changes were observed after six months

of treatment. Beta diversity analysis revealed distinct clustering patterns

between RR-TB patients and healthy controls, with no significant differences

between pre- and post-treatment groups. Functional analysis showed reduced

microbial functions related to pyruvate fermentation and amino acid metabolism

in RR-TB patients.

**CONCLUSIONS:** These findings highlight the specific effects of second-line

anti-TB drugs on the respiratory microbiota and suggest potential roles of

respiratory ecological imbalance in RR-TB pathogenesis. Future studies could

explore microbiome-based diagnostic and therapeutic strategies for RR-TB.

SUPPLEMENTARY INFORMATION: The online version contains supplementary material

available at 10.1186/s12866-025-04091-4.

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PMCID: PMC12220151

PMID: 40597612

**10. BMC Infect Dis. 2025 Jul 1;25(1):861. doi: 10.1186/s12879-025-11227-4.**

Nanopore-based targeted sequencing (NTS) for drug-resistant tuberculosis: an

integrated tool for personalized treatment strategies and guidance for new drug

development.

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**BACKGROUND:** Drug-resistant tuberculosis has emerged as a major public health

issue that requires immediate attention. NTS is an innovative method that allows

for the direct detection of clinical samples without the need for culture. It

could provide more accurate, reliable, and comprehensive information on drug

resistance.

**METHODS**: We collected clinical data retrospectively from patients suspected of

having drug-resistant tuberculosis who visited the tuberculosis department at

the Second Hospital of Nanjing in Jiangsu Province, China, from December 2023 to

December 2024. The diagnostic efficiency of NTS for different types of

drug-resistant tuberculosis and antimicrobial resistance was calculated. The

relationship between resistance genes, mutated amino acids, and mutation sites

was demonstrated.

**RESULTS:** In this study, a total of 107 patients with drug-resistant tuberculosis

were included, comprising 43 cases of mono-drug resistant tuberculosis, 20

patients with poly-drug resistant tuberculosis, 22 cases of multidrug-resistant

tuberculosis, 21 cases of pre-extensively drug-resistant tuberculosis and 1 case

of extensively drug-resistant tuberculosis. The accuracy of NTS in diagnosing

drug-resistant tuberculosis ranged from 42.9 to 93.0%. Except for second-line

injectable drugs, NTS achieved a sensitivity of over 70% for other

anti-tuberculosis drugs. Serine was identified as the most frequently mutated

amino acid in both the rpoB gene (66.2%, 49/74) and the katG gene (86.3%,

44/51). Additionally, the most frequently mutated amino acids in the embB gene,

rpsL gene, and gyrA gene were methionine (94.7%, 44/51), lysine (100%, 28/28),

and aspartic acid (66.7%, 20/30), respectively.

**CONCLUSION:** NTS could effectively and precisely deliver comprehensive drug

resistance results, assisting medical professionals to create more personalized

treatment plans. Besides, it would encourage the development of new

anti-tuberculosis drugs to broaden clinical treatment options for drug-resistant

tuberculosis.

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**11. Sci Rep. 2025 Jul 1;15(1):21099. doi: 10.1038/s41598-025-08456-7.**

LASSO regression-based nomogram for distinguishing nontuberculous mycobacterial

pulmonary disease from pulmonary tuberculosis: a clinical risk prediction model.

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This study aims to identify predictive factors that can effectively distinguish

between non-tuberculous mycobacterial pulmonary disease (NTM-PD) and pulmonary

tuberculosis (PTB) by comparing their clinical characteristics and laboratory

indicators, and to construct a risk prediction model based on these factors to

improve the accuracy of clinical diagnosis, optimize treatment strategies, and

reduce the risks of misdiagnosis and drug resistance. Data from 150 hospitalized

patients treated at The Second People's Hospital of Fuyang City between January

2021 and December 2022 were collected, including 50 cases with NTM-PD and 100

cases with PTB. By gathering clinical data and laboratory inflammation markers

of the patients, key predictive factors were identified using LASSO regression.

These factors were further analyzed through univariate and multivariate logistic

regression analysis to determine the influencing factors of NTM-PD, thereby

constructing a nomogram prediction model. The accuracy of the model was

evaluated through calibration curves, ROC curves, and Hosmer-Lemeshow

goodness-of-fit tests, while its clinical utility was assessed using decision

curve analysis and clinical impact curves.The two groups showed significant

differences in age, BMI, bronchiectasis, and lung cavitation (P < 0.05). LASSO

regression analysis identified age, BMI, bronchiectasis, and lung cavitation as

four key variables. Multivariate logistic regression analysis revealed that old

age, bronchiectasis, and lung cavitation were risk factors for NTM-PD, while low

BMI acted as a protective factor. The nomogram model constructed based on these

four variables demonstrated excellent predictive performance. The

Hosmer-Lemeshow goodness-of-fit test indicated good model fit (P = 0.448), with

an area under the ROC curve (AUC) of 0.861 (95% CI: 0.798-0.923). Decision curve

and clinical impact curve analyses suggested that the model has the potential to

optimize clinical decision-making within a threshold probability range of 0.05

to 0.75. By analyzing the critical differential characteristics between NTM-PD

and PTB, we successfully developed a prediction model based on age, BMI,

bronchiectasis, and lung cavitation, which effectively assesses the risk of

NTM-PD occurrence, providing clinicians with a practical diagnostic aid.

© 2025. The Author(s).

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PMCID: PMC12216239

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**12. Sci Rep. 2025 Jul 1;15(1):21302. doi: 10.1038/s41598-025-06080-z.**

Treatment outcomes in cavitary multidrug-resistant/rifampicin-resistant

tuberculosis and risk factors for cavity closure: a retrospective cohort study

in Southwest China.

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Pulmonary cavities in patients with tuberculosis contribute to antibiotic

failure, transmission, morbidity, and mortality. We aimed to report the

treatment outcomes and risk factors for cavity closure in cavitary

multidrug-resistant/rifampicin-resistant tuberculosis in Southwest China. This

study was a retrospective cohort study which included adult patients with

multidrug-resistant /rifampicin-resistant tuberculosis in Southwest China from

January 2018 to January 2023. The patients were categorized into cavity and

non-cavity groups, and their clinical characteristics and treatment outcomes

were retrospectively compared. A logistic regression model was used to identify

potential risk factors associated with cavity closure. In this study, 305

patients were enrolled, with 223 cases in the cavity group and 82 cases in the

non-cavity group. The median age of patients in the cavity group was 31 (24, 44)

years, with a male to female sex ratio of 155/68. Within the cavity group, 8.1%

of patients had rifampicin-resistant tuberculosis, 49.8% had multidrug-resistant

tuberculosis, and 42.2% had pre-extensively-drug resistant tuberculosis. The

treatment outcomes of the cavitary group showed that 48.9% of patients were

cured, 28.3% completed treatment, 14.8% were lost to follow-up, and 6.7% could

not be evaluated, with one failure and two deaths. Various factors such as male

gender, smoking, drinking, tuberculosis treatment history, baseline AFB smear,

bilateral disease, and specific symptoms were more prevalent in the cavity group

compared to the non-cavity group. Sputum culture conversion rates at 2 and

6 months were lower in the cavity group (25.6% vs 37.8%; 63.7% vs 79.3% ,all

P < 0.05). Within patients with cavities, 40.6% experienced cavity closure after

treatment, with a median closure time of 9.00 months. Baseline CD3+ T cell

counts decreased was found to be an independent risk factor for cavity closure

(aOR = 2.278, 95% CI 1.109-4.680, P = 0.025), while the use of a

bedaquiline-containing regimen (aOR = 0.305, 95% CI 0.140-0.663, P = 0.003) and

a delamanid-containing regimen (aOR = 0.260, 95% CI 0.086-0.785, P = 0.017) were

protective factors. Cavities may influence the timing of culture conversion

rather than influencing the treatment outcomes in patients with MDR/RR-TB. The

use of bedaquiline and delamanid in treatment regimens for MDR/RR-TB patients

could promote cavity closure and may enhance the management of cavitary

MDR/RR-TB. Furthermore, the enhancement of immunotherapy could potentially

contribute to reducing the burden of cavitary MDR/RR-TB.

© 2025. The Author(s).

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**13. Front Cell Infect Microbiol. 2025 Jun 19;15:1592216. doi:**

**10.3389/fcimb.2025.1592216. eCollection 2025.**

Metagenomic sequencing for identification of nontuberculous mycobacteria and

other pathogens in patients with mixed infection of the lung.

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**BACKGROUND: I**t can be difficult to distinguish lung disease caused by

nontuberculous mycobacteria (NTM), Mycobacterium tuberculosis, and mixed

infections (MIs) that include NTM. Metagenomic next generation sequencing (mNGS)

is a highly sensitive method that can reliably identify lung pathogens. We

retrospectively analyzed the records of patients who had MIs of the lungs that

included NTM and received mNGS testing.

**METHODS:** The records of 36 patients who were diagnosed with NTM infection of the

lungs at the Second Hospital of Jilin University from Nov 2023 to Jun 2024 were

analyzed. Initial empirical treatments were ineffective in all patients, leading

to the application of mNGS of bronchoalveolar lavage fluid (BALF).

**RESULTS:** The average patient age was 62.4 years, 22 patients had one or more

underlying chronic disease, and all patients had at least one respiratory

symptom (cough, sputum production, fever, or dyspnea). Chest CT examinations

showed that patients had different degrees of pneumonia and pleural effusion.

Among tested patients, there were elevated levels of erythrocyte sedimentation

rate in 81.8% (18/22) and elevated C-reactive protein in 90.5% (19/21). There

were variable results from acid-fast staining of bronchoalveolar lavage fluid

(BALF; 3/36, 8.3%), and transbronchial lung biopsy (TBLB; 5/14, 35.7%). mNGS

identified seven NTM species. Treatment based on the mNGS results led to the

resolution of clinical symptoms and absorption of lung lesions in all patients.

**CONCLUSIONS**: Most of the 36 patients with MIs of the lungs that included NTM had

underlying diseases. The results of traditional tests, including sputum or BALF

culture and smear, acute phase markers, and TBLB pathological examination, were

problematic. mNGS provides rapid and reliable diagnosis, allowing the rapid

implementation of appropriate therapy in patients with MIs of the lungs that

include NTM.

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PMID: 40612390 [Indexed for MEDLINE]

**14. Sage Open Pediatr. 2025 Jun 20;12:30502225251346345. doi:**

**10.1177/30502225251346345. eCollection 2025 Jan-Dec.**

Clinical Characteristics and Outcomes of Severe Adverse Reactions to Bacille

Calmette-Guérin (BCG) Vaccination in China: A Single-Center Retrospective Study.

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**OBJECTIVES:** This study investigated the clinical features, treatment approaches,

and outcomes of severe Bacille Calmette-Guérin (BCG) vaccine complications in

Chinese children.

**INTRODUCTION:** BCG is the only available vaccine for tuberculosis (TB) prevention

but can cause serious complications such as local abscesses, lymphadenitis, and

disseminated BCG. Research on their management in China is limited.

**METHODS:** This observational study reviewed 95 children with severe BCG-related

complications treated at a tuberculosis-specialized hospital in Guangdong, China

(2016-2020). Of these, 33 (34.7%) had injection site reactions, 55 (57.9%)

developed lymphadenitis with 31 suppurative cases, and 7 (7.4%) had disseminated

BCG. All deep abscesses and suppurative lymphadenitis were successfully treated

with surgery and anti-tubercular therapy. Two disseminated BCG cases had primary

immunodeficiency, and 1 of them died.

**CONCLUSION:** Most local reactions respond to conservative treatment. Surgery

combined with anti-tubercular therapy is effective for suppurative

lymphadenitis. Early immunological evaluation is essential for disseminated

disease.

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DOI: 10.1177/30502225251346345

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PMID: 40612176

**15. Front Immunol. 2025 Jun 18;16:1605827. doi: 10.3389/fimmu.2025.1605827.**

**eCollection 2025.**

Single-cell analysis of peripheral blood and pleural effusion reveals functional

diversity of γδ T cells in tuberculosis infection.

Feng Y(#)(1), Chen Y(#)(2), Zhang W(#)(1), Shen X(1), Yan J(1), Yao L(1), Zhang

L(1), Niu Y(1), Zhang J(1), Tang P(1), Ling C(1).

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**INTRODUCTION:** Tuberculosis is a contagious airborne disease caused by the

Mycobacterium tuberculosis infection. γδ T cells are closely associated with TB

infection; however, the specific role of γδ T cells in the immune response to TB remains unclear, as does the differentiation and mechanism of γδ T cell subsets in TB patients.

**METHODS:** We analyzed the characteristics of γδ T subsets in the peripheral blood

(Peripheral Blood Mononuclear Cells,PBMC) and pleural effusions (Tuberculous

pleural effusion,TPE) and pleural effusions of TB patients using single-cell

sequencing to explore the distribution and characteristics of different γδ T

subpopulations.

**RESULTS:** Seven γδ Tcell subpopulations were identified. The highest percentage

of effector γδ2 cell cluster (C1) was found in PBMCs from TPE patients,

accounting for 36.1%, while the highest percentage of tissue-resident γδ2 cell

cluster (C0) was found in PFMCs, reaching 70.5%. Through in-depth analysis, we

identified a group of Vδ2 cells exhibiting strong effector function and high

expression of FCGR3A.

**DISCUSSION:** Therefore, exploring the mechanism of interaction between Vδ2 cells

and Mtb, as well as understanding host immune regulation during Mtb infection,

can not only enhance the understanding of the immune mechanism underlying TB but

also provide new theoretical ideas. This research may offer novel therapeutic

targets for TB and innovative strategies for treatment and prevention.

Copyright © 2025 Feng, Chen, Zhang, Shen, Yan, Yao, Zhang, Niu, Zhang, Tang and

Ling.

DOI: 10.3389/fimmu.2025.1605827

PMCID: PMC12213264

PMID: 40607390 [Indexed for MEDLINE]

**16. Int J Gen Med. 2025 Jun 28;18:3547-3556. doi: 10.2147/IJGM.S522251. eCollection 2025.**

Correlation Between Serum Inflammatory Factor Level Changes and Disease Severity

in Patients with Chronic Obstructive Pulmonary Disease Complicated by

Tuberculosis.

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**BACKGROUND:** The coexistence of chronic obstructive pulmonary disease (COPD) and

tuberculosis (TB) complicates diagnosis and treatment, increasing disease burden

and mortality. The correlation between serum inflammatory factors and disease

severity and prognosis in COPD patients with TB remains unclear.

**METHODS:** This retrospective study included 200 participants treated at the

Affiliated Hospital of Hebei University from December 2020 to December 2022: 80

patients with COPD and TB, 40 with COPD alone, 40 with TB alone, and 40 healthy

controls. Serum levels of tumor necrosis factor-α (TNF-α), interleukin-6 (IL-6), interferon-γ (IFN-γ), soluble IL-2 receptor (sIL-2R), and C-reactive protein

(CRP) were compared across groups and correlated with disease severity and

prognosis in COPD patients with TB.

**RESULTS:** Serum levels of TNF-α, IL-6, IFN-γ, sIL-2R, and CRP were significantly

higher in the COPD with TB group compared to all other groups (P<0.05). In this

group, elevated levels of these markers were associated with increased disease

severity and poorer prognosis (P<0.05). Correlation analysis showed positive

associations between inflammatory cytokine levels and disease severity, and

negative associations with prognosis (P<0.05).

**CONCLUSION:** Serum inflammatory markers may help assess disease severity and

prognosis in COPD patients with TB. However, due to the observational design,

causality cannot be inferred. Further prospective, multi-center studies are

required to validate these findings before clinical application.

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PMCID: PMC12219164

PMID: 40607012

**17. Front Cell Infect Microbiol. 2025 Jun 18;15:1573643. doi:**

**10.3389/fcimb.2025.1573643. eCollection 2025.**

Type VII secretion system gene mutations driving global mycobacterium

tuberculosis transmission revealed by whole genomic sequence.

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Pathogenic mycobacteria are able to transfer virulence factors across their

complex cell wall using a type VII secretion system (T7SS)/early secreted

antigenic target-6 of the kDa secretion system (ESX). Since the discovery of ESX

loci during the Mycobacterium tuberculosis H37Rv genome project, extensive

research in areas such as structural biology, cell biology, and evolutionary

analysis has improved our understanding of the role of these systems. However,

regulatory mechanisms for ESX in Mycobacterium tuberculosis remain elusive.

Despite extensive research, the effects of ESX gene mutations on the dynamics of

Mycobacterium tuberculosis transmission are not well understood. In this study,

we investigated the role of ESX mutations in TB transmission, assessing their

risk and characteristics. We analyzed 13582 whole genome sequences of

Mycobacterium tuberculosis isolates, of which 6130 (45.13%) were clustered

strains. Initially, Boruta algorithm was used to pinpoint SNPs that were

significant for TB transmission. These SNPs were then subjected to univariate

and multivariate logistic regression analysis to determine the significance of

each SNP. The intersection of these two independent methods was recognized as

the optimal set of risk mutations for TB transmission. Specifically, we

identified one risk mutation (espA(Rv3616c, 4055801)) in L1, four risk mutations

(espK(Rv3879c, 4357597), esxU(Rv3445c, 3863138), esxO(Rv2346c, 2626018), and

esxW(Rv3620c, 4060588)) in L2, and four risk mutations (eccE1(Rv3882c, 4362807),

espE(Rv3864, 4340330), espA(Rv3616c, 4055993), and eccC5(Rv1783, 2019942)) in

L4. These risk mutations were significantly associated with clustering,

potentially increasing TB transmission. Our findings suggest that mutations in

ESX genes play a crucial role in Mycobacterium tuberculosis transmission. These

results can be applied to the development of novel strategies for the treatment

and prevention of disease.

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PMID: 40606626 [Indexed for MEDLINE]

**18. Front Public Health. 2025 Jun 17;13:1599274. doi: 10.3389/fpubh.2025.1599274.**

**eCollection 2025.**

Spatiotemporal analysis of pulmonary tuberculosis in the central region of the

Zhejiang Province, China (2016-2024).

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Hangzhou, China.

**BACKGROUND:** In recent years, Shaoxing City, located in central Zhejiang

Province, has experienced a slow decline in the incidence of pulmonary

tuberculosis (PTB). Therefore, there is an urgent need to elucidate the

potential causes for this decline through spatiotemporal analyses to provide a

scientific basis for targeted prevention and control. We aimed to explore the

spatiotemporal distribution of PTB notification rates in Shaoxing City from 2016

to 2024 and identify high-incidence clusters, thereby offering data-driven

insights to optimize regional PTB control strategies.

**METHODS:** Statistical analyses were conducted using R and Excel on all reported

active PTB cases in Shaoxing City. Spatiotemporal analysis of case distribution

and regional clustering was conducted using ArcGIS and SatScan.

**RESULTS AND DISCUSSION:** In total, 17,298 active PTB cases were registered

between 2016 and 2024, including 9,749 laboratory-confirmed and 7,549 clinically

diagnosed cases. The male-to-female ratio was 2.34:1. Farmers represented 68.2%

of all cases. The PTB notification incidence showed a gradual decline. Spatial

autocorrelation results revealed 52 sub-districts with high-high clusters over

the nine-year period, primarily in Shengzhou and Xinchang counties.

Spatiotemporal scan analysis identified one primary cluster area (RR = 1.62,

LLR = 170.87, p < 0.001) and two secondary clusters between 2016 and 2024. The

incidence of PTB in Shaoxing City showed a downward trend, though the decline

was relatively slow. The southeastern region should be prioritized in efforts to

accelerate the End TB Strategy. Overall, comprehensive and intensive

interventions, such as large-scale chest X-ray screening and health education

programs, should be enhanced to effectively curb PTB transmission, especially

among males and farmers.

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PMCID: PMC12209324

PMID: 40600152 [Indexed for MEDLINE]

**19. Front Immunol. 2025 Jun 17;16:1606311. doi: 10.3389/fimmu.2025.1606311.**

**eCollection 2025.**

The PE/PPE family proteins of Mycobacterium tuberculosis: evolution, function,

and prospects for tuberculosis control.

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

global health threat, exacerbated by drug resistance and inadequate vaccine

efficacy. The PE/PPE protein family, unique to mycobacteria, constitutes ~10% of

the Mtb genome and plays critical roles in bacterial physiology, immune evasion,

and host-pathogen interactions. This review synthesizes advances in

understanding the evolutionary expansion, structural diversity, and functional

versatility of PE/PPE proteins, emphasizing their co-evolution with type VII

secretion systems (T7SS). We highlight their roles in nutrient acquisition,

immune modulation, and pathogenesis, alongside their potential as diagnostic and

vaccine targets. Clinical progress in PE/PPE-based vaccines, such as M72/AS01E

and ID93/GLA-SE, underscores their promise in combating TB, while challenges in

epitope variability and functional redundancy demand innovative strategies. By

integrating evolutionary, structural, and immunological insights, this review

provides a roadmap for leveraging PE/PPE biology to develop next-generation TB

interventions.

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**20. J Inflamm Res. 2025 Jun 27;18:8429-8445. doi: 10.2147/JIR.S517034. eCollection 2025.**

Host Immune Response to Mycobacterium tuberculosis Infection: Implications for

Vaccine Development.

Liu Q(1)(2), Que S(1)(2), Qiu Y(1)(2), Tang M(1)(2), Liu S(1)(2), Yang G(1)(2),

Wang Y(1)(2), Deng A(1)(2), Hu X(3), Lian X(#)(4), Gao Q(#)(1)(2).

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

(Mtb) infection, including pulmonary tuberculosis and extrapulmonary

tuberculosis. About a quarter of the people in the world are infected with TB,

but only 5-10% of them will progress to active TB, posing a major challenge to

the eradication of TB. The study of the host immune response to Mtb infection is

a key aspect of the development of effective vaccines and immunotherapies to

eradicate tuberculosis. In this review, we delve into the overview of animal

models of TB infection and the host's innate and adaptive immune responses to

Mtb infection. We discuss how Mtb is recognized and phagocytosed by macrophages,

how it evades immune responses, the recruitment and mobilization of neutrophils

and monocytes, the role of natural killer cells during the infection process,

how dendritic cells initiate adaptive immunity, the important roles of CD4+ T

cells and their subtypes in TB infection, how CD8+ T cells exert cytotoxic

functions, and how B cells produce antibodies and exhibit memory characteristics

to eliminate pathogens. Furthermore, we review the tuberculosis vaccines

currently entering clinical trials, emphasizing that studying the host's immune

responses following Mtb infection is crucial for the development of more

effective vaccines, providing a theoretical foundation and direction for the

treatment of tuberculosis.

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PMID: 40599694

**21. Nucleic Acids Res. 2025 Jun 20;53(12):gkaf622. doi: 10.1093/nar/gkaf622.**

CARF-dependent preferential RNA cleavage by Csm6 increases drug susceptibility

of mycobacteria.

Wei W(1), Gao CH(2), Jiang X(3), Qiao J(3), Zhang L(3), Yan Y(1), Zhao G(1),

Yang K(1), Yan J(1), Yang M(1).

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CRISPR-Cas systems are prokaryotic adaptive immune systems that defend against

invading mobile genetic elements. The type III-A CRISPR-Cas system has been

studied in the evolutionary and epidemiological context of Mycobacterium

tuberculosis, the causative agent of tuberculosis. However, its biological

function remains poorly understood. Here, we demonstrate that heterologous

expression of csm6, a single-stranded RNA ribonuclease of the CRISPR-Cas system,

exhibits preferential RNA cleavage activity targeting host transcripts. This

activity significantly downregulates ribosomal and mycolic acid biosynthesis

pathway genes, leading to a global reduction in translation levels and an

increased drug susceptibility of Mycobacterium smegmatis. Furthermore,

mutagenesis analysis revealed that Csm6's biological function critically depends

on its CARF domain rather than its HEPN domain. In conclusion, our study

elucidates the biological role of the Csm6 protein in the CRISPR-Cas system,

both in vitro and in vivo, highlighting how preferential RNA cleavage impacts

multiple mycobacterial processes. These findings provide novel insights into the

functional diversity of CRISPR-Cas systems in mycobacteria.

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Acids Research.

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**22. Infect Drug Resist. 2025 Jun 24;18:3087-3101. doi: 10.2147/IDR.S524300.**

**eCollection 2025.**

Epidemiology and Molecular Drug-Resistance Patterns of Tuberculosis in

Non-Elderly Patients in Luoyang, China, 2019-2023.

Wang Z(#)(1)(2), Xu L(#)(2)(3), Guo T(1), Liu J(1), Jin J(1), Zhang Q(1), Jiang

T(1), Zhao Z(4), Xue Y(2).

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(4)Animal Science and Technology, Henan University of Science and Technology,

Luoyang, Henan, People's Republic of China.

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**PURPOSE:** Existing data offer limited guidance on TB control strategies for the

non-elderly population, hampering effective epidemic management. This study

aimed to analyze TB transmission and molecular resistance profiles among

non-elderly patients (<60 years) in Luoyang City.

**PATIENTS AND METHODS:** From 2019-2023, 24,706 non-duplicate sputum samples from

10 TB-designated hospitals were tested for Mycobacterium tuberculosis complex

(MTBC) via IS6110-targeted real-time PCR. MTBC-positive specimens underwent

multicolor melting curve analysis (MMCA) to assess resistance to isoniazid

(INH), rifampin (RFP), streptomycin (SM), and ethambutol (EMB). Age-stratified

analyses were performed to compare drug-resistant TB (DR-TB) prevalence between

elderly and non-elderly groups, with multivariate regression identifying

resistance risk factors in non-elderly patients.

**RESULTS:** Non-elderly individuals exhibited significantly higher TB (17.54% vs

15.26%) and DR-TB (26.82% vs 21.62%) rates than the elderly (all, P < 0.001).

Among non-elderly patients, males, retreatment cases, main urban residents and

smear-positive groups had significantly elevated MTBC detection rates. The

predominant resistance patterns of multidrug-resistant tuberculosis (MDR-TB) and

poly-resistant tuberculosis (PDR-TB) were MDR4 (INH + RFP + EMB + SM) and PDR2

(INH + SM), with detection rates of 5.52% (142) and 2.33% (60), respectively.

MTBC positive rate peaked at 30-34 years (23.10%), while the resistance rate

peaked at 35-39 years. After adjusting for the effects of smear results and

diagnosis year, the multivariate regression analysis model indicated that male

sex, retreatment, and the main urban area were high-risk factors for TB

resistance in non-elderly cases.

**CONCLUSION:** The non-elderly population demonstrates a significantly higher

burden of both TB detection and resistance, particularly among males,

retreatment cases, and main urban patients. The emergence of complex drug

resistance patterns, combined with a distinct trend of younger age at infection,

highlights the critical need for targeted interventions tailored to specific

epidemiological and resistance profiles of MTBC-infected populations.

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**eCollection 2025.**

Transcriptomic and proteomic signatures of host NK cells delineate distinct

immune states across tuberculosis infection statuses.

Zhang H(#)(1), Liu L(#)(1), Hu J(1), Wu X(1), Zheng J(1), Xin H(1), Du J(1),

Yang J(1), Lv Z(2), Wu Z(2), Gao L(1), Liu R(2), Sun H(3), Zhang X(1), Jin Q(1).

**Han Zhang, Liguo Liu, Jie Hu, Xiaolin Wu, Jianhua Zheng, Henan Xin, Jiang Du, Jiarong Yang, Zizheng Lv, Zhuoran Wu, Lei Gao, Rongmei Liu, Haidan Sun, Xiaobing Zhang, Qi Jin**

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**INTRODUCTION:** Although natural killer (NK) cells play crucial roles in the

immune response to Mycobacterium tuberculosis (M.tb) infection, systematic

investigations delineating the immune characteristics of NK cells across the

tuberculosis (TB) disease spectrum are scarce.

**METHODS:** This multiomics study employed transcriptomic, proteomic, and RT-qPCR

analyses to characterize and validate CD56+ NK cells from 165 participants

stratified by TB infection status (active TB (ATB), latent TB infection (LTBI),

and healthy control (HC)). Peripheral blood samples from an independent cohort

of 85 participants were subjected to flow cytometry analysis and validation.

**RESULTS AND DISCUSSION:** Enrichment analyses of transcriptomic and proteomic data

revealed that the NK cell-mediated cytotoxicity and apoptosis pathways were

enriched in LTBI and ATB groups, whereas chemotaxis-related pathway enrichment

was specific to ATB. Further analysis revealed that the expression of genes

mediating the NK cell-mediated cytotoxicity signaling pathway through

perforin-granzyme was upregulated in the LTBI state, whereas that of those

associated with death receptors was elevated in ATB, potentially indicating a

transformation of NK cell function in different TB infection states. Moreover,

analysis of ATB-specific chemotaxis genes suggested that the migration of NK

cells was likely to occur in the ATB state. Flow cytometry revealed an increased

frequency of CD56dim NK cells and a decreased frequency of CD56bright NK cells

in individuals with LTBI versus that in HCs in an independent cohort. In

addition, RT-qPCR validation identified a four-biomarker combination (SLC7A5,

PDE4D, CXCR4, and SOCS3) distinguishing ATB from HCs, a three-biomarker

combination (SLC7A5, PER1, and PDE4D) differentiating LTBI from HC, and a

three-biomarker combination (SOCS3, GZMK, and HIST1H3B) differentiating ATB from

LTBI. These findings elucidate the immune clearance mechanism of NK cells in TB

and provide clinically actionable biomarkers for infection staging, advancing

our understanding of TB immunopathogenesis.

Copyright © 2025 Zhang, Liu, Hu, Wu, Zheng, Xin, Du, Yang, Lv, Wu, Gao, Liu,

Sun, Zhang and Jin.

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**24. Medicine (Baltimore). 2025 Jun 27;104(26):e43089. doi:**

**10.1097/MD.0000000000043089.**

Exploring the influencing factors of cavities persist in rifampicin-sensitive

pulmonary tuberculosis patients who have completed outpatient treatment based on

logistic regression forest plot.

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Tuberculosis Clinical Medical Research Center, Lishui, Zhejiang, China.

This study explores the factors influencing the persistence of cavities in

patients with rifampicin-sensitive pulmonary tuberculosis who have completed

outpatient follow-up treatment based on multiple regression analysis. A total of

218 rifampicin-sensitive pulmonary tuberculosis patients with pulmonary

cavities, who were followed up at our hospital from January 2022 to October

2023, were selected as the study subjects. General patient data were collected,

including gender, age, residence, smoking status, hemoptysis symptoms, presence

of diabetes, initial treatment/retreatment, number of outpatient visits,

duration of intensive treatment, presence of extrapulmonary tuberculosis, and

presence of chronic aspergillosis. Based on a reexamination of chest CT scans to

evaluate lung cavity absorption after completion of treatment, patients were

categorized into the cavity closure group or cavity persistence group.

Multivariate logistic regression analysis was conducted to identify factors

influencing cavity persistence, and a forest plot was generated. Among the 218

rifampicin-sensitive pulmonary tuberculosis patients, 55 (25.23%) had persistent

pulmonary cavities. Multivariate logistic regression analysis revealed that

smoking (OR = 2.209, 95% CI = 1.029-4.739, P = .042), diabetes (OR = 3.423, 95%

CI = 1.602-7.315, P = .001), retreatment (OR = 5.286, 95% CI = 1.983-14.087,

P < .001), and chronic pulmonary aspergillosis (OR = 5.684, 95%

CI = 2.459-13.138, P < .001) were significant factors influencing the

persistence of cavities (P < .05). Smoking, diabetes, retreatment of pulmonary

tuberculosis, and chronic pulmonary aspergillosis are all factors that influence

the persistence of cavities in patients with rifampicin-sensitive pulmonary

tuberculosis who have completed treatment in outpatient clinics. Early

intervention should be implemented in these cases.

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**25. Medicine (Baltimore). 2025 Jun 27;104(26):e42779. doi:**

**10.1097/MD.0000000000042779.**

Effect of combined clinical pathway and scenario simulation teaching on

psychological stress and anxiety among tuberculosis interns: A retrospective

cohort study.

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**Zhi Chen, Donglin Guo, Qian Shi, Zhong Zeng\***

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In the realm of medical education, clinical internship represents a pivotal

phase where theoretical knowledge must be practically applied amidst real-world

patient care, often leading to heightened stress and anxiety among interns. This

transitional challenge is particularly acute for tuberculosis (TB) clinical

interns, requiring innovative teaching methodologies. Therefore, we aim to

evaluate the efficacy of integrating clinical pathway instruction with

scenario-based simulation teaching in alleviating psychological stress and

anxiety among TB clinical trainees. Data extraction from electronic health and

educational evaluation records spanned September 2020 to September 2022,

focusing on TB clinical interns. The investigation centered on 2 principal

teaching methodologies used during training: the combination of clinical pathway

and scenario simulation approaches. Standardized instruments quantified

psychological stress and anxiety at 3 intervals - pre-teaching, post-teaching,

and a 6-month follow-up. The study encompassed 70 TB clinical interns,

allocating 34 to a combined teaching approach integrating clinical pathways and

scenario simulations, while 36 underwent conventional teaching methodologies.

Post-intervention assessments revealed significant reduction in psychological

stress levels among those subjected to the combined methods (t = 2.522,

P = .014). This difference was further magnified at the 6-month follow-up, with

the combined teaching method group demonstrating markedly lower psychological

stress levels (t = 3.54, P < .001). Also, immediately following the

intervention, the combined method group experienced significantly lesser anxiety

(t = 2.278, P = .026), and the beneficial effect endured through the 6-month

mark (t = 2.41, P = .019). Combining clinical pathway teaching method and

scenario simulation teaching method are associated with reduced psychological

stress and anxiety levels among TB clinical interns.

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**26. J Clin Tuberc Other Mycobact Dis. 2025 May 20;40:100535. doi:**

**10.1016/j.jctube.2025.100535. eCollection 2025 Aug.**

Characteristics of subclinical pulmonary tuberculosis compared to active

pulmonary tuberculosis: A retrospective cohort study.

Zhang A(1), Wang W(1), Wang Z(1), Sheng H(1), Yang J(1).

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College, Wuhu 241001 Anhui, PR China.

**BACKGROUND:** Little is known about subclinical pulmonary tuberculosis (SPTB), and

its diagnosis remains challenging. The aim is to analyze the results of

laboratory of SPTB and improve clinical understanding and help early diagnosis.

**METHOD:** This retrospective cohort study was conducted in patients with pulmonary

tuberculosis (TB) at a university hospital in China. 138 cases of SPTB were

compared with active pulmonary tuberculosis (APTB) (140 cases) and healthy

person (HC) (136 cases).

**RESULT:** The average age of the SPTB group (40.43 ± 19.85 years) was younger than that of the APTB group (50.01 ± 21.49 years) (p < 0.05). The WBC count was elevated in both pulmonary TB groups compared to the HC group(p < 0.05). CRP and CA-125 were higher in the APTB group than in SPTB and HC group (p < 0.05). The CD4+ T cells counts in SPTB group was lower than that in HC group (p < 0.05);

although the CD4+ T cells counts in SPTB group was lower than that in APTB

group, the difference was not statistically significant (p > 0.05). There were

statistically significant differences in CD8 + T cells counts between the three

groups (p < 0.05), and the CD8 + T cells counts in two pulmonary TB groups was lower than that in the HC group (p < 0.05), and there was no statistically

significant difference between SPTB and APTB group (p > 0.05). The T-SPOT.TB

value in SPTB were lower than those in the APTB group (p < 0.05).

**CONCLUSION:** Patients with SPTB tend to develop the condition at a younger age

and are predominantly male. Clinically, we can judge whether SPTB will develop

into APTB by monitoring WBC count, CA-125, CRP, T lymphocyte count and T-SPOT.TB

value level, in order to achieve the purpose of early diagnosis and treatment.

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**eCollection 2025.**

Clinical Mycobacterium tuberculosis isolates exhibit a molecular clock rate

below 1 SNP per genome per year.

Wang JL(1)(2)(3), Chen YL(4), Guan CP(4), Yu K(5)(6)(7), Wang MS(4).

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Australia.

**PURPOSE:** Tuberculosis (TB) remains a significant global health concern,

necessitating effective measures to control the epidemic. Understanding the

evolution of Mycobacterium tuberculosis (M. tb) through molecular clock analysis

is crucial for tracing outbreaks, managing transmission, and ultimately

improving TB management in practice.

**RESULTS:** A total of 27 studies were included for analysis. The pooled mutation

rate was estimated at 0.63 single nucleotide polymorphisms (SNPs) per genome per

year [95% confidence interval (CI): 0.51-0.75; 95% predictive interval (PI):

0.04-1.22], significant heterogeneity (I2 = 92.7%, p < 0.001) was observed.

Clinical strains had a mutation rate of 0.55 SNPs per year (95% CI: 0.45-0.65;

95% PI: 0.12-0.98), while model strains showed a higher rate of 1.14 SNPs per

year (95% CI: 0.68-1.60; 95% PI: -0.22-2.50; Meta-regression analysis,

p = 0.006). Mutation rates did not significantly differ between transmission

events and reactivation or single episodes (p = 0.497).

**CONCLUSION:** The mutation rate of clinical M. tb strains is below 1 SNP per

genome per year, indicating evolutionary stability in clinical settings. This

finding is important for TB outbreak reconstructions and public health

strategies. Future research should refine subgroup analyses based on infection

characteristics for more precise molecular clock estimates.

SYSTEMATIC REVIEW REGISTRATION: PROSPERO, identifier CRD42024595161.

Copyright © 2025 Wang, Chen, Guan, Yu and Wang.

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**28. Int J Infect Dis. 2025 Jun 26:107966. doi: 10.1016/j.ijid.2025.107966. Online**

**ahead of print.**

Global burden of tuberculosis among adults aged 60 years and older,1990-2021:

findings from the global burden of disease study 2021.

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Y(2), Li T(2), Jin L(2), Zhang L(1), Li Y(1), Wu L(1), Wang N(1), Liu Z(1), Liu

X(1), Wang Y(3), Wu Q(1), Liang L(4).

**Junping Liu, Yue Zhou, Juan Guan, Yaping Liu, Weijian Song, Wei Liu, Xinle Yin, Yuqin Liu, Ting Li, Long Jin, Lihan Zhang, Yunkai Li, Lin Wu, Nan Wang, Zhaoyue Liu, Xinru Liu, Yanfu Wang, Qunhong Wu, Libo Liang\***

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**OBJECTIVES:** Tuberculosis (TB) poses a significant threat to global public

health, particularly among the elderly. This study aim to provide a

comprehensive analysis of the pattern and temporal trends of the global disease

burden associated with HIV-negative TB in adults aged 60 years and older from

1990 to 2021.

**METHODS:** Data on incidence, deaths, and disability-adjusted-life-years (DALYs)

of TB, drug-susceptible tuberculosis (DS-TB), multidrug-resistant tuberculosis

(MDR-TB), and extensively drug-resistant tuberculosis (XDR-TB) were obtained

from the Global Burden of Disease (GBD) 2021. Frontier analysis was carried out

to pinpoint areas for enhancement and disparities among nations stratified by

development level. Bayesian age-period-cohort model (BAPC) was utilized to

forecast disease burden trends through 2035.

**RESULTS:** A decline trend in age-standardized incidence rate (ASIR),

age-standardized mortality rate (ASMR), and DALY rates for TB and DS-TB was

observed among the elderly population globally, whereas an upward trend was

noted of MDR-TB and XDR-TB. Frontier analyses revealed a potential for burden

alleviation among diverse nations and regions, with high SDI nations like the

Republic of Korea showing higher disease burden than expected for their

sociodemographic development. BAPC model revealed that by 2035, the MDR-TB and

XDR-TB burden will continue escalating in the elderly.

**CONCLUSIONS:** The increasing MDR-TB and XDR-TB burden in older individuals

underscores the need for tailored interventions to combat TB burden, such as

implementing active case finding (ACF) among adults aged 60 years and older.

Copyright © 2025. Published by Elsevier Ltd.

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PMID: 40581250

**29. Ann Med. 2025 Dec;57(1):2523557. doi: 10.1080/07853890.2025.2523557. Epub 2025 Jun 28.**

LncRNA C5orf64 polymorphisms (rs12518552 and rs2950218) decreases pulmonary

tuberculosis susceptibility.

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Diseases of Tibet Autonomous Region, School of Medicine, Xizang Minzu

University, Xianyang, China.

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

issue, with genetic factors playing a crucial role in susceptibility. Long

noncoding RNA (lncRNA) C5orf64 has been implicated in immune responses and

cancer, but its association with PTB risk has not been fully explored.

**METHODS:** Genomic DNA was extracted from peripheral blood samples of 955

participants (474 PTB cases and 481 controls). Rs12518552 and rs2950218 in

C5orf64 were genotyped using the Agena MassARRAY system. Logistic regression

analysis was performed to assess the association between these polymorphisms and

PTB risk. Stratified analysis was conducted to evaluate the influence of age,

gender, and smoking status.

**RESULTS:** Rs12518552-G (OR = 0.82, p = 0.034) and rs2950218-T (OR = 0.77, p =

0.012) were associated with a reduced PTB risk. Stratified analysis revealed

that rs12518552 was associated with a protective effect against PTB in

individuals over 40 years old (OR = 0.73, p = 0.024), females (OR = 0.77, p =

0.034), and non-smokers (OR = 0.78, p = 0.040), and rs2950218 was also

associated with a reduced PTB risk in individuals over 40 years old (OR = 0.73,

p = 0.040), females (OR = 0.72, p = 0.046), and non-smokers (OR = 0.72, p =

0.011).

**CONCLUSION:** C5orf64 polymorphisms, particularly rs12518552 and rs2950218, are

associated with a reduced risk of PTB. These findings suggest that C5orf64

polymorphisms contribute to genetic susceptibility to PTB, with implications for

PTB targeted screening and personalized therapeutic strategies.

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