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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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**1. Eur J Pharmacol. 2025 Aug 28:178102. doi: 10.1016/j.ejphar.2025.178102. Online**

**ahead of print.**

Tioconazole Exerts Anti-TB activity By Destroying Cell Integrity.

Chen Z(1), Wang X(1), Zhang H(1), Kong X(1), Chen J(1), Wang Q(2), Meng J(3), Lu

S(4).

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The increasing prevalence of drug-resistant tuberculosis (TB), coupled with the

lengthy and toxic nature of conventional treatments and the complicating factor

of Human Immunodeficiency Virus (HIV) co-infection, underscores the urgent need

for the development of effective anti-TB drugs and robust stockpiles to combat

this global health crisis. In this study, the anti-tubercular activity and

potential antibacterial mechanisms of tioconazole were investigated. Tioconazole

exhibited remarkable antibacterial activity against Mtb H37Ra and H37Rv, with

minimum inhibitory concentrations (MICs) of 4 μg/mL and 1μg/mL respectively.

While cholesterol or palmitic acid was utilized as a solo carbon source, its MIC

against Mtb H37Ra decreased to 2 μg/mL. Mtb H37Ra CYP121 conditional mutant was

more sensitive to tioconazole in comparison with Mtb H37Ra in the presence of

the pristinamycin (0.1μg/mL and 0.001μg/mL). Further experiments demonstrated

that treatment with 0.5 × MIC of tioconazole (2μg/mL) for five days resulted in

the formation of invagination and bulge on the surfaces of Mtb cells.

Concurrently, intracellular ATP levels decreased by nearly 50%, likely due to

the inhibition of lipid metabolism by tioconazole, which compromises the

integrity of the cell wall and cell membrane. Taken together, these findings

suggest that tioconazole may serve as a novel anti-TB agent, exerting anti-TB

activities by disrupting the structural integrity of the pathogen's cells.

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**2. J Immunol Methods. 2025 Aug 28:113969. doi: 10.1016/j.jim.2025.113969. Online**

**ahead of print.**

Immunogenicity, biodistribution, and toxicology evaluation of Mycobacterium

tuberculosis ag85a plasmid DNA in cynomolgus monkeys, mice and guinea pigs.

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**BACKGROUND:** Mycobacterium tuberculosis (MTB) Ag85A has become a component of

multiple new tuberculosis vaccines. It is necessary to evaluate the

immunogenicity, biological distribution, and safety of ag85a plasmid DNA (pDNA)

to lay the foundation for the design of new vaccines.

**METHOD:** Chronic toxicity test: cynomolgus monkeys were injected intramuscularly

with different doses of ag85a pDNA, and the vaccine absorption kinetics, tissue

distribution, and toxicity were observed. Their immune function was evaluated.

Acute toxicity test: Mice were injected intramuscularly 0.5 ml saline, and

injected intramuscularly and intravenously 0.5 mg/0.5 ml ag85a pDNAs,

respectively. The toxicity and death of the mice were observed continuously for

14 days. Allergic test: Guinea pigs were intraperitoneally injected with

different doses of ag85a pDNA. After stimulation, the allergic reaction and its

severity were observed.

**RESULTS:** Chronic and acute toxicity tests demonstrated that ag85a pDNA

injections caused no clinical symptoms or tissue damage. Repeated intramuscular

injections in cynomolgus monkeys enhanced specific Th1 immune responses, with

pDNA rapidly entering the bloodstream and its concentration positively

correlating with dosage. After 8 weeks, ag85a gene was detected only in muscles,

myocardium, iliac lymph nodes, and blood. Guinea pig allergy tests showed no

weight changes or allergic reactions, even after multiple sensitizations.

**CONCLUSIONS:** The ag85a pDNA showed good safety in cynomolgus monkeys, mice, and

guinea pigs, and induced high levels of antibodies and T-cell responses, making

it a candidate antigen for the construction of a new tuberculosis vaccine.

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**3. Exp Clin Transplant. 2025 Jul;23(7):501-504. doi: 10.6002/ect.2024.0315.**

Can Tuberculosis Infection After Liver Transplant Induce Lung Squamous Cell

Carcinoma from Squamous Metaplasia of Alveolar Epithelium?

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This case report describes a 65-year-old male patient with hepatocellular

carcinoma who received an orthotopic liver transplant. One month after surgery,

the patient was treated for tuberculosis due to the fever. At 16 months after

the operation, a chest computed tomography scan revealed a mixed ground-glass

nodule at the apex of the right upper lobe, which gradually grew from 5 mm to 10

mm and then was removed via thoracoscopy. Pathology examination revealed

extensive squamous metaplasia of the alveolar lumen, with focal areas of

malignant transformation of the squamous epithelium into moderately

differentiated squamous cell carcinoma. This study highlighted the increased

risks of tuber-culosis infection and lung cancer in liver transplant recipients

because of use of immunosuppressive drugs, which presented as a rare case of

carcino-genesis based on alveolar epithelial squamous metaplasia.

DOI: 10.6002/ect.2024.0315

PMID: 40878143 [Indexed for MEDLINE]

**4. Clin Chim Acta. 2025 Aug 22;578:120565. doi: 10.1016/j.cca.2025.120565. Online ahead of print.**

The diagnostic value of combined detection of GBP1, IFN-γ and IL-2 in

differentiating NTM from TB infection.

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**BACKGROUND:** Early differentiation between Mycobacterium tuberculosis (MTB) and

non-tuberculous mycobacteria (NTM) is critical due to distinct treatment

protocols. Traditional diagnostic methods, including acid-fast staining,

bacterial culture, and nucleic acid assays, often face challenges. This study

evaluated the diagnostic value of Guanylate-Binding Protein 1 (GBP1),

interferon-gamma (IFN-γ), and interleukin-2 (IL-2) in peripheral blood for

distinguishing active TB, NTM infections, and cured TB.

**METHODS:** We recruited patients with active TB (n = 50), NTM disease (n = 46),

cured TB (n = 37), and healthy controls (HC, n = 20). GBP1 mRNA in peripheral

blood mononuclear cells was quantified by qPCR. MTB-specific IFN-γ and IL-2

levels were measured by ELISA.

**RESULTS:** The relative expression of GBP1 was significantly higher in active TB

(2.764 ± 1.774) and in NTM patients (2.099 ± 0.665) compared to healthy control group (-0.001 ± 1.844; P < 0.0001 and P < 0.01, respectively). Additionally, IL-2 showed prognostic value, as levels in cured TB patients (135.7 ± 332.9) were significantly lower than in active TB patients (362.7 ± 530.7, P < 0.01). For differentiating active TB from healthy controls, the area under the receiver operating characteristic curve (AUC) for GBP1 was 0.899, outperforming IFN-γ (0.846) and IL-2 (0.786). Crucially, a combined three-marker panel demonstrated superior diagnostic performance in all comparisons, notably achieving an AUC of 0.990 for distinguishing active TB from NTM disease, significantly higher than any single marker.

**CONCLUSIONS:** GBP1 is a robust marker for identifying mycobacterial infections

(both MTB and NTM). While IL-2 shows potential for monitoring treatment

response, the combined detection of GBP1, IFN-γ, and IL-2 provides the highest

diagnostic accuracy, effectively differentiating between NTM and MTB infections.

This panel offers a promising tool for improving clinical diagnosis and patient

management.

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**5. J Med Chem. 2025 Sep 6. doi: 10.1021/acs.jmedchem.5c01856. Online ahead of**

**print.**

Synthesis and Biological Evaluation of Platensimycin Analogues with Improved

Antimycobacterial Activity.

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KasA and KasB are promising drug targets against Mycobacterium tuberculosis and

infectious nontuberculous mycobacteria, while most lead compounds are in the

preclinical development stage. Herein, a platensimycin (PTM) analogue library

consisting of 340 members was first screened to identify 46 PTM thioethers with

superior activity compared to that of PTM against Mycobacterium smegmatis. Next,

19 PTM thioethers were chosen and semisynthesized from PTM oxirane (7), together

with seven PTM ether derivatives and 6-ido, 6-bromo-, and 6-thiocyanato PTM.

Most of them showed stronger antimycobacterial activity than PTM. In particular,

one thioether Ec42 exhibited superior antimycobacterial activity to INH in M.

smegmatis-infected mouse model. Molecular docking analysis revealed that Ec42

may bind to the active sites of KasA and KasB. Our study revealed that these PTM

derivatives significantly expand dual inhibitors for KasA and KasB, and suggest

that late-stage functionalization of natural antibiotics targeting mycolic acid

biosynthesis remains fruitful for antimycobacterial drug discovery.

DOI: 10.1021/acs.jmedchem.5c01856

PMID: 40913570

**6. J Antimicrob Chemother. 2025 Sep 4:dkaf321. doi: 10.1093/jac/dkaf321. Online**

**ahead of print.**

Novel mutations associated with clofazimine resistance in Mycobacterium

intracellulare.

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**BACKGROUND**: Clofazimine is a promising repurposed drug for treating

Mycobacterium avium-intracellulare complex pulmonary disease, but its resistance

mechanisms in Mycobacterium intracellulare remain poorly understood.

**OBJECTIVE:** This study aims to elucidate the resistance mechanisms of M.

intracellulare to clofazimine.

**METHODS:** We isolated 36 clofazimine-resistant M. intracellulare mutants in vitro

and performed whole-genome sequencing to identify resistance-associated

mutations. Gene complementation was used to validate the role of the identified

mutations.

**RESULTS:** We identified various mutations in the marR gene (WP\_009952290.1) in

61% of clofazimine-resistant mutants by whole-genome sequencing. Mutations were

identified in additional genes encoding ssuD (flavin-dependent oxidoreductase,

C67A), lppI (membrane lipoprotein, C207 deletion), GMC oxidoreductase

(glucose-methanol-choline oxidoreductase, G157 deletion), MASE1

domain-containing protein (C62G) and PPE family protein (222C deletion). Gene

complementation experiments demonstrated that introducing the wild-type marR in

clofazimine-resistant strain (L72) with marR mutations reduced clofazimine MIC

from 1 mg/L to susceptible baseline (0.25 mg/L), confirming its critical role in

clofazimine resistance. Notably, the M. intracellulare MarR lacks homology to

Mycobacterium tuberculosis MarR family protein Rv0678 (MmpR) involved in

clofazimine and bedaquiline resistance but is flanked by non-efflux pump genes

(dhmA and doxX), and unlike M. tuberculosis, its mutation does not cause

bedaquiline cross-resistance, indicating a different MarR and distinct

regulatory mechanism for clofazimine resistance in M. intracellulare.

**CONCLUSIONS:** This work highlights marR as a key determinant of clofazimine

resistance in M. intracellulare and underscores the need for further mechanistic

studies with implications for rapid molecular detection and effective treatment.

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**7. Infect Dis Ther. 2025 Sep 3. doi: 10.1007/s40121-025-01221-3. Online ahead of**

**print.**

A New Era in Tuberculosis Prevention and Treatment: Breakthroughs in Drug

Development and Future Prospects.

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Tuberculosis (TB) remains a significant global public health challenge, despite

recent advances in drug development. However, a comprehensive and systematic

overview of the current clinical trial landscape in TB prevention and treatment

is still lacking. This study aims to systematically review recent breakthroughs

in TB drug development, assess their scientific value and global impact, and

provide valuable insights for clinicians and policymakers involved in TB control

efforts. We systematically searched the INFORMA pharmaceutical database to

identify 1041 clinical trial projects related to TB. Two independent researchers

screened and extracted the data, and discrepancies were resolved through

consultation with a third researcher. Inclusion criteria were: (1) trials

explicitly focused on TB drug development, (2) studies containing detailed

descriptions of drug mechanisms or therapeutic targets, and (3) interventional

studies. Exclusion criteria were the absence of key information, incomplete

datasets, or non-interventional study designs. Descriptive statistical analyses

were employed to systematically summarize trial characteristics, and data

distribution features were visualized accordingly. Between 1990 and 2025, the

number of TB-related clinical trials increased significantly, with a notable

peak observed between 2018 and 2023. China and South Africa emerged as leading

contributors to research activity, while the United States and the United

Kingdom accounted for the majority of "Completed" trials. Despite the emergence

of novel agents, traditional cornerstone drugs continued to dominate the

development pipeline. Bedaquiline, in particular, demonstrated rapid, largely

driven by supportive health policies. Academic institutions were the primary

funding of TB trials, and regional analysis revealed heightened research

activity in Asia and Africa. However, the global distribution of research

resources remained uneven, highlighting the need for improved collaboration

mechanisms to promote both health equity and innovation. This study

systematically offers a comprehensive review of recent breakthroughs in TB drug

development, revealing the current status and persistent challenges facing

global clinical trials. Realizing the goal of ending TB will require sustained

investment in scientific innovation, equitable resource allocation, and

steadfast political commitment. Through coordinated global efforts, a new era in

TB prevention and treatment is within reach.

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**8. Microbiol Spectr. 2025 Sep 3:e0016525. doi: 10.1128/spectrum.00165-25. Online**

**ahead of print.**

Application of engineered CRISPR/Cas12a variants with altered protospacer

adjacent motif specificities for the detection of isoniazid resistance mutations

in Mycobacterium tuberculosis.

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Drug-resistant tuberculosis (TB) is a major global public health concern.

Although isoniazid is currently considered one of the most effective first-line

drugs for TB treatment, its efficacy is limited by the emergence of resistance.

Therefore, it is imperative to develop new methods for detecting drug-resistant

TB. In this study, we developed a nucleic acid detection system based on the

clustered regularly interspaced short palindromic repeat (CRISPR) Cas12a\_RR

protein. The system combines recombinase polymerase amplification with an

engineered CRISPR/Cas12a\_RR protein to enable rapid and specific detection of

the katG G944C mutation in isoniazid-resistant Mycobacterium tuberculosis (Mtb).

It could detect the target DNA at concentrations as low as 1% in a mixed sample.

Compared with TaqMan quantitative polymerase chain reaction and DNA sequencing,

the CRISPR/Cas12a\_RR system demonstrated superior detection performance in terms

of sensitivity, specificity, and cost-effectiveness. Furthermore, it effectively

differentiated between drug-resistant Mtb strains from wild-type Mtb strains in

clinically isolated samples, with the entire detection process completed in 60

min. In conclusion, the CRISPR/Cas12a\_RR detection system offers a novel, rapid,

simple, sensitive, and specific approach for identifying isoniazid-resistant

Mtb, with significant potential for clinical application, particularly in

resource-limited settings.

**IMPORTANCE:** This study presents a novel method for detecting isoniazid-resistant

Mycobacterium tuberculosis (Mtb) using clustered regularly interspaced short

palindromic repeat (CRISPR)/Cas12a mutants, offering rapid detection,

cost-effectiveness, and high specificity, and thereby providing a promising new

avenue for detecting isoniazid-resistant Mtb.

DOI: 10.1128/spectrum.00165-25

PMID: 40899880

**9. Microbiol Spectr. 2025 Sep 3:e0137025. doi: 10.1128/spectrum.01370-25. Online**

**ahead of print.**

Prevalence and distribution patterns of drug resistance in Mycobacterium

tuberculosis to first-line antituberculosis drugs in Urumqi, China.

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This study aimed to investigate the epidemic status and distribution

characteristics of drug-resistant Mycobacterium tuberculosis in Urumqi. From

January 2019 to July 2024, all sputum culture-positive Mycobacterium

tuberculosis strains were collected in Urumqi. Using the traditional solid-state

proportion method for drug-sensitivity testing, we determined the resistance of

Mycobacterium tuberculosis to first-line antituberculosis (TB) drugs. The

epidemic status and distribution characteristics of first-line antituberculosis

drug-resistant Mycobacterium tuberculosis were analyzed using R statistical

software (version 3.6.1). Among the 1,241 culture-positive Mycobacterium

tuberculosis strains included in this analysis, 973 (78.40%) were smear

positive. The overall proportion of non-tuberculous mycobacteria was 2.5%. The

overall prevalence of drug-resistant tuberculosis (DR-TB) was 18.93%, with a

prevalence of 17.78% in new cases and 24.40% in retreatment cases, respectively.

In this survey, the overall prevalence was 10.91% (132 out of 1,210) for

mono-drug-resistant tuberculosis, 3.72% (45 out of 1,210) for polydrug-resistant

tuberculosis, and 4.30% (52 out of 1,210) for multidrug-resistant tuberculosis.

Moreover, the patterns of resistance to first-line anti-TB drugs were highly

diverse. The drug-resistance rate among retreatment tuberculosis patients in

Urumqi remains notably high. Thus, enhancing drug-resistance surveillance in

these patients is critical for effective tuberculosis prevention and control in

the region.

**IMPORTANCE:** The result of this study indicated that DR-TB is a serious public

health problem in Urumqi. Resistance drugs distributed type to first-line

anti-TB drugs are very broad in Urumqi. Any resistance to anti-TB drugs in new

cases is more than in retreatment cases.

DOI: 10.1128/spectrum.01370-25

PMID: 40899878

**10. BMC Infect Dis. 2025 Sep 2;25(1):1094. doi: 10.1186/s12879-025-11460-x.**

Risk factors and prevalence of latent tuberculosis infection in rheumatic

patients: a meta-analysis.

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**OBJECTIVE:** This study aims to evaluate the risk factors and prevalence of latent

tuberculosis infection (LTBI) in patients with rheumatic diseases.

**METHODS:** Databases including PubMed, EMBASE, Web of Science, Cochrane Library,

CNKI, Vip, and Wanfang were searched. Data extraction was performed

independently by two authors. The Newcastle-Ottawa Scale (NOS) was utilized to

assess study quality. Heterogeneity was evaluated using I2 statistics and the

chi-square test. The relative risk (RR), odds ratio (OR) with 95% confidence

intervals (95% CI), and prevalence rate were calculated. Sensitivity analysis

was conducted using the leave-one-out method. Publication bias was assessed

using either the Begg rank correlation or Egger’s linear regression.

**RESULTS:** Eighteen studies (13 cross-sectional and 5 cohort studies) involving

12,167 rheumatic patients were included. Increased risk of LTBI was associated

with current smoking (OR = 1.50, 95%CI: 1.28–1.78), Golimumab treatment

(OR = 2.90, 95% CI: 1.08–7.78), Chloroquine treatment ( OR = 1.27, 95%

CI:1.01–1.61), age > 40 (OR = 1.84, 95% CI: 1.51–2.24) and a history of

tuberculosis (TB) ( OR = 3.26, 95% CI: 1.87–5.68). Additionally, male rheumatic

patients had a higher risk of LTBI compared to females (OR = 1.72, 95% CI: 1.46–

2.02). However, no significant associations were found between LTBI risk and

history of smoking, duration of disease, history of Bacillus Calmette-Guérin,

positive rheumatoid factor, corticosteroid use, diabetes history, TB exposure,

Adalimumab or Etanercept use. The pooled prevalence rate of LTBI in rheumatic

patients was 22% (95% CI: 18–27%).

**CONCLUSIONS:** Current smoking, Golimumab treatment, Chloroquine treatment, age

>40 and a history of TB are identified as risk factors for LTBI in rheumatic

patients. Male patients are more prone to developing LTBI. The overall LTBI

prevalence in rheumatic patients is high.

SUPPLEMENTARY INFORMATION: The online version contains supplementary material

available at 10.1186/s12879-025-11460-x.

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PMID: 40898127

**11. BMJ Open. 2025 Sep 2;15(9):e103676. doi: 10.1136/bmjopen-2025-103676.**

Diagnostic accuracy of nanopore sequencing for the rapid diagnosis of

extrapulmonary tuberculosis: a protocol for a systematic review and

meta-analysis.

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**BACKGROUND:** Extrapulmonary tuberculosis (EPTB) is a serious type of tuberculosis

(TB) which can cause systemic clinical manifestations. Rapid diagnosis of EPTB

for intervention is of great importance. Nanopore sequencing as a

third-generation gene sequencing method is a new kind of rapid TB detection.

Previous studies have shown that nanopore sequencing has higher diagnostic

sensitivity and specificity for TB diagnosis compared with other diagnostic

methods. The aim of this research is to develop a systematic review and

meta-analysis protocol for assessing the accuracy of nanopore sequencing in

diagnosing EPTB.

**METHODS AND ANALYSIS:** This protocol was conducted in strict adherence to the

Preferred Reporting Items for Systematic Reviews and Meta-analysis Protocols

guidelines. The study protocol has been prospectively registered with the

International Prospective Register of Systematic Reviews under the unique

identifier CRD42024608415. We will search Chinese databases and English

databases in June 2026. Chinese databases will include Wanfang database, China

National Knowledge Infrastructure. English databases will include PubMed, EMBASE

and the Cochrane Library. Adhering strictly to the reference standard outlined

in this protocol, we will screen the literature. The Quality Assessment of

Diagnostic Accuracy Studies will be used by us to assess the methodological

quality of the included studies. The statistical tools used are Stata with midas

commands and RevMan, and we will perform meta-analysis, generate forest plots

and Summary Receiver Operating Characteristic curves. A p value of less than

0.05 will be considered statistically significant. If significant heterogeneity

exists and there is a sufficient number of studies, we will investigate its

source through subgroup analysis and meta-regression.

**ETHICS AND DISSEMINATION:** This investigation uses publicly accessible data

repositories, exempting it from ethical review board approval requirements. On

finalisation of the analysis, findings will be prepared for dissemination

through submission to a reputable medical journal employing rigorous peer review

processes. The study methodology adheres to established protocols for systematic

review and meta-analysis.

PROSPERO REGISTRATION NUMBER: CRD42024608415.

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**12. BMC Infect Dis. 2025 Sep 1;25(1):1086. doi: 10.1186/s12879-025-11491-4.**

Treatment outcomes and associated influencing factors among elderly patients

with rifampicin-resistant tuberculosis: a multicenter, retrospective, cohort

study in China.

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J(1), Chen Q(2), Shi Z(2), Tang X(2), Liang L(2), Tang P(6), Pan Q(7), Guo C(8),

Du J(9), Chang Z(10), Guo Z(2), Wu G(11), Tang S(12).

**Huicong Liu, Liping Zou, JiaJia Yu, Qingdong Zhu, Song Yang, Wanli Kang, Jiaojie Ma, Qing Chen, Zhengyu Shi, Xianzhen Tang, Li Liang, Peijun Tang, Qing Pan, Chunhui Guo, Juan Du, Zhanlin Chang, Zhouli Guo, Guihui Wu\*, Shenjie Tang\***

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**BACKGROUND:** Rifampicin-resistant tuberculosis (RR-TB) remains a significant

global public health concern. The elderly population is not only at high risk

and among the primary victims of RR-TB but also plays a crucial role in the

transmission chain of RR-TB. Their biological particularities, treatment

complexities, and social vulnerabilities collectively present substantial

challenges to global tuberculosis control. This study aimed to evaluate

treatment outcomes and identify predictors of unfavorable outcomes among elderly

patients with RR-TB in China.

**METHODS:** A multicenter retrospective cohort study was conducted, including 248

elderly RR-TB patients treated across eight tertiary hospitals in China from May

2018 to April 2020. Multivariate logistic regression and Propensity Score

Matching (PSM) analyses were performed to identify factors associated with

unfavorable outcomes. Statistical analyses were performed using SPSS.

**RESULTS:** Among 248 patients, 65.7% (163/248) achieved treatment success (cured

or completed treatment), while 34.3% (85/248) experienced unfavorable outcomes,

including treatment failure (10.5%), death (2.4%), loss to follow-up (15.7%),

and non-evaluation (5.6%). Adverse events (AEs) were reported in 56.0% (139/248)

of patients, among which anemia was the most common (25.8%). And the use of

bedaquiline and linezolid was significantly associated with the occurrence of QT

interval prolongation and optic neuritis (p < 0.05). Multivariate analysis

revealed that BMI < 18.5 kg/m²(aOR: 3.66, 95% CI: 1.89-7.08, p < 0.01), advanced

drug resistance (aOR: 2.25, 95% CI: 1.14-4.45, p = 0.020), pre-treatment anemia

(aOR: 4.16, 95% CI: 2.01-8.61, p < 0.001) were independent predictors of

unfavorable outcomes. Adjunctive immunotherapy was associated with favorable

outcomes (aOR: 0.23, 95% CI: 0.09-0.55, p < 0.001). After PSM, pre-treatment

anemia remained significantly correlated with unfavorable outcomes (aOR: 3.5;

95% CI: 1.41-8.67, p = 0.007).

**CONCLUSION:** A relatively low rates of treatment success were achieved for RR-TB

patients in the elderly at tertiary tuberculosis hospitals in China. Low BMI,

advanced drug resistance, and pre-treatment anemia were independent prognostic

factors for unfavorable treatment outcomes. Adjunctive immunotherapy was

prognostic factors for unfavorable treatment outcomes of elderly RR-TB patients.

In tuberculosis management, special consideration should be given to elderly

patients.

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**13. BMC Musculoskelet Disord. 2025 Sep 1;26(1):830. doi: 10.1186/s12891-025-09053-5.**

Clinical and epidemiological analysis of 893 patients with spinal tuberculosis:

an 11-Year investigation of a general hospital in East China.

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**BACKGROUND:** The burden of spinal tuberculosis (STB) in China remains

substantial, with the country ranking third in the number of tuberculosis cases

globally in 2022, among the 30 countries with a high tuberculosis burden. In

East China, few large-scale studies have been conducted on STB.

**METHODS:** This retrospective study analyzed 893 confirmed STB cases (2010-2020).

Demographic, clinical, and diagnostic data were statistically characterized

using χ²/t-tests for categorical/continuous variables (significance at

P < 0.05).

**RESULTS:** The annual number of confirmed STB cases of spinal TB showed a

sustained upward trend. Among 893 STB patients (male: female = 1.4:1; median age

56 years), rural populations exhibited higher prevalence (P = 0.264 for delayed

hospitalization vs. urban). Farmers/laborers predominated (84.7%), with

hypertension (32.4%), diabetes (18.5%) and osteoporosis (12.9%) as major

comorbidities. Concurrent pulmonary TB occurred in 435 cases (48.7%) and other

extrapulmonary TB in 71 (8.0%). Diagnostic evaluations revealed TSPOT (82.7%),

histopathology (75.9%) and Xpert-MTB/RIF (71.8%) as most sensitive methods.

Compared with histopathological gold standard, Xpert demonstrated 81.5%

sensitivity, 58.8% specificity, 87.0% PPV and 48.3% NPV (kappa = 0.374).

Combining histopathology with Xpert achieved 86.6% diagnostic accuracy,

significantly surpassing individual methods (P < 0.001). Lesion distribution

showed lumbar (44.3%) and thoracic (42.3%) predominance, mostly involving ≥ 2

contiguous vertebrae (91.3% continuous vs. 8.7% skip lesions). Chemotherapy

remained primary treatment, with 6.5% drug resistance rate showing annual

escalation (mainly monoresistance). Surgical intervention achieved favorable

outcomes in 648 cases (72.6%).

**CONCLUSION:** Over the course of the study period, the overall diagnosis rate of

spinal tuberculosis exhibited an upward trend. Despite East China's relatively

advanced socioeconomic and healthcare systems, spinal tuberculosis remains a

substantial public health challenge, primarily due to the region's complex

population composition and high population mobility. The prevention and

management of spinal tuberculosis continue to present considerable challenges.

Early diagnosis, combined with an appropriate treatment course, ensures that

both chemotherapy and surgical interventions yield satisfactory outcomes.

Increasing the allocation and investment of medical resources for tuberculosis,

enhancing health management for migrant populations, and raising public health

awareness are essential.

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PMID: 40890663 [Indexed for MEDLINE]

**14. Front Microbiol. 2025 Aug 20;16:1653031. doi: 10.3389/fmicb.2025.1653031.**

**eCollection 2025.**

Value of urinary lipoarabinomannan levels for tuberculosis diagnosis and

monitoring of therapy.

Xiong Y(#)(1), Shen Z(#)(1), Dong B(1), Wang Y(1), Zhu Y(1), Wei H(2), Zhang

D(3), Che Y(3).

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**BACKGROUND:** The urinary lipoarabinomannan (LAM) assay has emerged as a promising

tool for tuberculosis (TB) diagnosis and treatment monitoring. This study aimed

to evaluate the diagnostic and monitoring performance of LAM compared to

Acid-fast bacilli (AFB), Mycobacteria Growth Indicator Tube (MGIT), and

GeneXpert, and to establish its clinical utility in a stratified TB population.

**METHODS:** A prospective cohort study included TB patients stratified by AFB/MGIT

status into three groups. Diagnostic accuracy was tested against composite

reference standard (CRS). Early monitoring performance was assessed via serial

LAM measurements during 12-week treatment. ROC/KM/Cox analyses determined

optimal thresholds and predictors of LAM conversion.

**RESULTS:** Against CRS, LAM demonstrated a sensitivity of 58.75%, which was

numerically higher than AFB smear (45.00%, p = 0.082) and comparable to MGIT

culture (58.75%, p = 1.00), but numerically lower than GeneXpert (61.25%,

p = 0.205). In the early monitoring phase, LAM showed sustained positivity in

11.54-51.72% at week 12, compared to <15% for other methods. The

diagnostic-monitoring quadrant analysis revealed LAM's optimal positioning for

monitoring (mean conversion time 4.63-11.49 weeks), compared to 0-8.25 weeks for

other methods. A combined model incorporating baseline PreLAM and week 4 change

(ΔLAM) showed the highest predictive value for 12 weeks conversion

(AUC = 0.871-0.943). Multivariate cox analysis identified ΔLAM as independent

predictors in total cohort (HR = 0.013, p = 0.001) and double positive group

(HR = 0.020, p = 0.002).

**CONCLUSION:** Urinary LAM serves as a dual-role biomarker, providing moderate

diagnostic sensitivity and dynamic monitoring signals reflecting early bacillary

response to therapy. The PreLAM+ΔLAM model enables early treatment response

assessment for personalized therapy.

Copyright © 2025 Xiong, Shen, Dong, Wang, Zhu, Wei, Zhang and Che.

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PMID: 40909925

**15. Medicine (Baltimore). 2025 Aug 29;104(35):e44078. doi:**

**10.1097/MD.0000000000044078.**

Influence of metabolic dysfunction-associated steatotic liver disease on

antituberculosis drug-induced liver injury.

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The risk of antituberculosis drug-induced liver injury (AT-DILI) in patients

with metabolic dysfunction-associated steatotic liver disease (MASLD) is not

clear. The aim of this study was to investigate incidence and risk factors

associated with AT-DILI in MASLD patients. Retrospectively, a total of 120 MASLD

patients who received antituberculosis medication from December 2017 to March

2023 were reviewed, including 91 males and 29 females. The participants were

categorized into 2 cohorts based on the presence or absence of liver injury.

Risk factors for AT-DILI were analyzed using logistic regression analysis. Among

the 120 patients with treatment of tuberculosis complicated with MASLD, 28

(23.3%) patients developed AT-DILI. The remaining 92 (76.7%) patients did not

develop AT-DILI. In the group of patients with liver injury, there were 26 cases

of mild liver injury, one case of moderate liver injury, and one case of acute

liver failure. Additionally, there were 23 cases of hepatocellular injury, 3

cases of cholestasis, and 2 cases of mixed liver injury. AT-DILI was observed

during antituberculosis treatment 30.4 ± 17.6 days after the treatment began.

There were significant differences in age, body mass index (BMI), platelet

count, total bilirubin, fibrosis-4 (FIB-4) between the liver injury group, and

the non-liver injury group (P < .05 in all). There were no significant

differences in gender, hemoglobin, albumin, alanine aminotransferase, aspartate

aminotransferase, alkaline phosphatase, γ-glutamyltransferase, total

cholesterol, triglyceride, combined hypertension, and combined diabetes mellitus

between the liver injury group, and the non-liver injury group (P > .05 in all).

By logistic regression analysis, low BMI and FIB-4 were a high-risk factor for

liver injury. The incidence of AT-DILI was high in patients with pulmonary

tuberculosis complicated with MASLD. Clinicians should focus on the risk of

AT-DILI in patients with low BMI and elevated FIB-4 scores.

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**16. Front Endocrinol (Lausanne). 2025 Aug 14;16:1630603. doi:**

**10.3389/fendo.2025.1630603. eCollection 2025.**

Recent advances in biomarkers for diabetes mellitus and tuberculosis

comorbidity: a comprehensive review.

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Diabetes mellitus (DM) and tuberculosis (TB) are significant global health

challenges that complicate diagnosis, treatment, and management due to their

interrelated nature. DM increases TB risk and worsens outcomes, highlighting the

need for early detection and effective management. This review summarizes recent

advancements in biomarkers for DM-TB comorbidity, including microbial,

metabolic, immunological, inflammatory, clinical, and genetic markers. We

identified 30 relevant studies, through a literature search using keywords

related to DM, TB, and biomarkers. Key findings include specific gut microbiota

genera and lipid mediators that show promise for early diagnosis and treatment.

Immunological biomarkers like altered CD8+ T cells and NK cells provide insights

into disease severity and treatment monitoring. Inflammatory markers such as

elevated CRP, ferritin, and IL-6 reflect heightened inflammation and could guide

treatment strategies. Clinical biomarkers, including serum CA-125 (sensitivity

88.14%, specificity 95.83%) and AUC/MIC ratios of anti-TB drugs (e.g.,

moxifloxacin ≥67; sensitivity 97.3%, specificity 90.0%), demonstrate high

diagnostic accuracy. Future research should focus on validating these biomarkers

across diverse populations and integrating them into clinical practice to

enhance DM-TB management and contribute to global disease control efforts.

Copyright © 2025 Fang, Wu, Fang and Ning.

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PMCID: PMC12390818

PMID: 40895633 [Indexed for MEDLINE]

**17. Front Immunol. 2025 Aug 14;16:1624923. doi: 10.3389/fimmu.2025.1624923.**

**eCollection 2025.**

Therapeutic vaccination with the Ag85B-Rv2660c-MPT70 fusion protein enhances

Mycobacterium tuberculosis H37Ra clearance in post-exposure mice.

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Latent tuberculosis infection (LTBI), affecting nearly one-quarter of the global

population, represents a major barrier to Tuberculosis (TB) eradication and a

paradigm of chronic infectious disease. Current chemotherapeutic regimens for

TB, although effective, are limited by drug resistance, toxicity, and poor

adherence, underscoring the urgent need for alternative strategies. In this

study, we investigated ARM-a recombinant fusion protein comprising Ag85B,

Rv2660c, and MPT70-as a therapeutic vaccine in a murine model of post-exposure

Mycobacterium tuberculosis (Mtb) infection. ARM immunization elicited robust

CD4+ T cell responses, with a higher frequency of polyfunctional T cells

producing IFN-γ, and TNF-α compared to the classical BCG vaccine. Critically,

ARM also induced strong humoral immunity, marked by elevated Mtb- and

ARM-specific IgG levels that enhanced FcγR-dependent phagocytosis,

phagosome-lysosome fusion, and intracellular bacterial clearance. ARM-treated

mice exhibited reduced pulmonary pathology, improved weight recovery, and

superior control of bacterial burden. These findings demonstrate the potential

of therapeutic vaccination to mobilize both cellular and antibody-mediated

immunity in controlling Mtb infection and offer a broader immunological strategy

for managing chronic infectious diseases. ARM represents a promising candidate

for post-exposure TB vaccination, with potential to enhance bacterial clearance

and reduce disease progression in high-burden populations.

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PMID: 40895571 [Indexed for MEDLINE]

**18. Front Public Health. 2025 Aug 15;13:1600214. doi: 10.3389/fpubh.2025.1600214.**

**eCollection 2025.**

Prevalence and epidemiological pattern of drug-resistant tuberculosis among

migrant populations in Wenzhou City, China, 2014-2023: implications for public

health strategies.

Wu L(1)(2), Cai X(3), Xu S(4), Lin X(5), Wu S(1), Xu X(1)(6).

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**OBJECTIVE:** This study aimed to analyze the epidemiological characteristics and

trends of notified multidrug-resistant tuberculosis (MDR-TB) in Wenzhou City,

China, from 2014 to 2023, with a focus on differences between migrant and local

populations among reported TB cases.

**METHODS:** This was a facility-based retrospective cohort study that included all

bacteriologically confirmed TB cases notified between 1 January 2014 and 31

December 2023 in the Tuberculosis Information Management System (TBIMS) of the

Chinese Center for Disease Control and Prevention and the hospital's laboratory

information system, provided they had available phenotypic drug-susceptibility

testing (pDST) results. Pearson's chi-square test was used to compare

drug-resistance rates between groups, the trend chi-square test was applied to

assess temporal changes, and a Sankey diagram was employed to illustrate the

origins and intra-city distribution of MDR-TB among the migrant population.

**RESULTS:** Among 10,993 notified TB patients, 734 (6.68%) were classified as

MDR-TB. The proportion of MDR-TB among notified cases declined over the study

period (p < 0.001). Nearly half (352/734; 47.96%) of the notified MDR-TB

patients were migrants; 226 (64.21%) originated from elsewhere in Zhejiang

Province, and 126 (35.79%) came from outside the province. Guizhou, Jiangxi and

Sichuan were the leading external contributors. Within Wenzhou, Yueqing City,

Yongjia County and Ouhai District reported the highest numbers of migrant MDR-TB

notifications.

**CONCLUSION:** The proportion of MDR-TB among notified TB cases in Wenzhou City has

steadily decreased. Migrants account for almost half of these notified MDR-TB

cases. Surveillance-driven and migrant-targeted interventions should be

prioritized to further reduce MDR-TB transmission.

Copyright © 2025 Wu, Cai, Xu, Lin, Wu and Xu.

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**19. Ann Clin Microbiol Antimicrob. 2025 Aug 31;24(1):48. doi:**

**10.1186/s12941-025-00816-5.**

Efflux pumps positively contribute to rifampin resistance in rpoB mutant

Mycobacterium tuberculosis.

Meng F(#)(1), Chen Y(#)(1), Wei Z(1), Liu Z(1), Lai X(1)(2), Lei J(1), Wu L(1),

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J(1), Wang N(3)(4), Hu J(5).

**Fanrong Meng, Yuanjin Chen, Zeyou Wei, Zhihui Liu, Xiaomin Lai, Jie Lei, Ling Wu, Li Deng, Qi Wang, Yu Yang, Hua Li, Bei Xie, Lan Gong, Qun Niu, Junwen Gao, Nan Wang\*, Jinxing Hu\***

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**BACKGROUND:** While several recent studies have documented the importance of

efflux pumps as mediators of rifampin (RIF) resistance, it remains uncertain

which efflux pumps play major roles in rifampin-resistant Mycobacterium

tuberculosis strains harboring rpoB gene mutations.

**METHODS:** In this study, minimum inhibitory concentration (MIC) values for RIF

were calculated and the expression of 13 efflux pump genes was evaluated across

35 clinical rifampicin-resistant M. tuberculosis isolates carrying the rpoB

mutation before and after efflux pump inhibitor treatment.

**RESULTS:** Rv0677c and Rv0191 were identified as the efflux pump genes that were

most frequently overexpressed, and treatment with the inhibitor verapamil was

sufficient to synergistically enhance the antibacterial effects of RIF and

downregulate efflux pump gene expression. Greater numbers of overexpressed

efflux pump genes were associated with a more significant decrease in the MIC

value for RIF following verapamil treatment. Levels of RIF resistance for

clinical isolates with the rpoB codon 445 mutation were also found to be

significantly less susceptible to the effects of verapamil as compared to the

resistance of strains with the codon 450 and 170 mutations.

**CONCLUSIONS:** These results suggest that levels of RIF resistance in clinical

RIF-resistant M. tuberculosis isolates are ultimately determined by a

combination of efflux pump activity and rpoB gene mutations.

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The real-world performance of a novel interferon gamma release assay based on

fluorescence immunochromatography in detecting Mycobacterium tuberculosis

infection in South China.

Tian N(1), Li P(2), Ju D(2), Lai S(1), Hu J(2), Tan Y(1), Zhu J(3).

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