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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. Microb Pathog. 2025 Aug 4:107948. doi: 10.1016/j.micpath.2025.107948. Online**

**ahead of print.**

The Role of Methylglyoxal Detoxification in Mycobacterium tuberculosis Fitness

and Pathogenesis.

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Tuberculosis (TB), caused by Mycobacterium tuberculosis (Mtb), constitutes a

major global health challenge. The pathogenesis of Mtb can be largely attributed

to its sophisticated survival strategies within host macrophages. Methylglyoxal

(MGO), a ubiquitous reactive dicarbonyl metabolite that spontaneously reacts

with biopolymers forming advanced glycation end products (AGEs), togethers with

reactive oxygen species (ROS) damage cellular events. The glyoxalase system

serves as the primary metabolic pathway for MGO detoxification, mitigating

carbonyl stress induced by excess MGO. The mycobacterial glyoxalase system

likely functions as a vital defense mechanism against glycation and oxidative

stress generated during pathogenic infection. Although extensive research has

been conducted on the host glyoxalase system against diabetes, little is known

about the mechanisms behind MGO detoxification in Mtb. This review aims at

exploring the impact of MGO and its product AGEs on TB treatment and discussing

the key molecular components, functions, and regulatory roles of the glyoxalase

system in Mtb. Finally, we propose the utilization of mycobacterial glyoxalases

as therapeutic targets for the development of anti-tuberculosis drugs.

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**2. Int J Biol Macromol. 2025 Aug 3:146294. doi: 10.1016/j.ijbiomac.2025.146294.**

**Online ahead of print.**

Mycobacterium tuberculosis Rv2521 promotes ferroptosis-dependent pathogenicity

by inhibiting NF-κB activation.

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Mycobacterium tuberculosis (M.tb) manipulates host ferroptosis, a novel form of

programmed cell necrosis, to enhance its pathogenicity. However, the precise

molecular mechanisms remain poorly be understood. A key feature of M.tb

evolution is the set of eukaryotic-like secreted proteins that can modulate host

immunological system. This study aimed to identify such proteins involved in

host ferroptosis and their regulatory mechanisms. Our results showed that

Rv2521, one of the secreted proteins, significantly promotes ferroptosis by

modulating glutathione peroxidase 4 (GPX4) expression in M.tb-infected

macrophages. Rv2521 downregulates GPX4 by binding to NF-κB, inhibiting NF-κB/p65

phosphorylation, thereby blocking the NF-κB signaling pathway activation and

reducing NF-κB/p65 occupancy at the GPX4 promoter. Importantly, these regulatory

effects can be reversed using ferroptosis or NF-κB inhibitors. Additionally, our

results found that Rv2521 directly interacts with NF-κB. Compared to wild-type

and complemented strains, the Rv2521 knockout strain exhibited reduced survival

and dissemination in macrophages due to the suppression of ferroptosis and the

enhanced immune evasion. Collectively, our results identify a novel M.tb

eukaryotic-like secreted protein involved in ferroptosis and provide new

insights into M.tb-host interactions, offering potential host-directed therapy

strategies for tuberculosis.

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**3. J Infect Public Health. 2025 Jul 24;18(11):102914. doi:**

**10.1016/j.jiph.2025.102914. Online ahead of print.**

Anti-tuberculosis therapy combined with ventriculoperitoneal shunt for

tuberculous meningitis combined with hydrocephalus: A case report.

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Tuberculous meningitis is a severe and potentially life-threatening form of

central nervous system tuberculosis. Hydrocephalus is a critical complication

and risk factor for the high mortality of tuberculous meningitis, exacerbating

neurological damage and intensifying treatment. We reported a critical case of

an elderly male patient with altered consciousness of consciousness who was

diagnosed as tuberculous meningitis with hydrocephalus. The patient was treated

with multi-drug anti-tuberculosis therapy, intracranial hypertension control,

and surgical intervention consisting of external ventricular drainage and

ventriculoperitoneal shunt, which successfully cured the patient.

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**4. J Orthop Surg Res. 2025 Aug 14;20(1):768. doi: 10.1186/s13018-025-05957-z.**

Mid- to short-term efficacy of Uniportal Video-Assisted Thoracoscopic Surgery in

the treatment of thoracic spinal tuberculosis.

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**BACKGROUND:** Surgical treatment of thoracic spine tuberculosis using traditional

procedures is often challenged by high trauma and slow recovery. This study

aimed to investigate the short- and medium-term efficacy and safety of Uniportal

Video-Assisted Thoracoscopic Surgery, a minimally invasive single-port

thoracoscopy combined with posterior internal fixation for the treatment of

thoracic spinal tuberculosis.

**METHODS:** Nineteen patients with thoracic spinal tuberculosis (15 men and four

women, mean age of 52 years) were retrospectively included. All patients

underwent single-port thoracoscopic lesion removal and intervertebral implant

fusion combined with posterior internal fixation. Surgical time, intraoperative

bleeding volume, hospitalization time, and complications were recorded, and the

rate of bone fusion and correction of the kyphosis angle were assessed using

imaging, with a follow-up period of 6-12 months.

**RESULTS:** All patients achieved postoperative bone fusion without serious

complications. The average operative time was 149.58 min (75-212 min), the

average intraoperative bleeding volume was 210.53 mL (50-600 mL), and the

average hospital stay was 15.58 d (2-29 d). The mean thoracic kyphosis angle

improved from 23.33° preoperatively to 19.00° at the final follow-up.

**CONCLUSIONS:** Single-port thoracoscopic technique combined with posterior

internal fixation can effectively remove thoracic tuberculosis foci and correct

kyphosis deformity. Moreover, it has the advantages of less trauma, quicker

recovery, and significant short- and medium-term efficacy, making it a feasible,

minimally invasive surgical procedure for treating thoracic spinal tuberculosis.

However, further optimizing the instrumentation design and expanding the sample

size in the future is necessary to validate its long-term effects.

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PMID: 40814110

**5. J Am Chem Soc. 2025 Aug 13. doi: 10.1021/jacs.5c08704. Online ahead of print.**

Photocontrolled Programmable Enzymatic Cascade for Robust CRISPR Diagnostics.

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CRISPR-Cas12a-based diagnostic technologies have revolutionized nucleic acid

detection, but their broader application remains constrained by the protospacer

adjacent motif (PAM) requirement and limited multiplexing capabilities due to

reliance on trans-cleavage. Here, we present a photocontrolled programmable

enzymatic cascade strategy that enables temporal regulation of three sequential

reactions─nucleic acid amplification, photoactivated lambda exonuclease

(λ-exon)-mediated single-stranded DNA (ssDNA) generation, and PAM-independent

Cas12a detection─all within a one-pot system, effectively overcoming the PAM

constraint. We further exploit the orthogonal trans-cleavage activity of Cas12a

and Cas13a to enable simultaneous dual-gene detection within the one-pot system,

thereby circumventing multiplexing limitations. Applied to clinical

Mycobacterium tuberculosis (MTB) samples, the method allows detection of both

the IS6110 gene of MTB and the human ACTB (β-actin) internal control gene. This

photocontrolled one-pot CRISPR diagnostic technology enhances flexibility in

target site selection and overcomes the limitations of conventional CRISPR

diagnostics, which cannot simultaneously detect both target genes and internal

controls. This approach holds promise for advancing the clinical application of

CRISPR-based diagnostics.

DOI: 10.1021/jacs.5c08704

PMID: 40802893

**6. Eur J Med Res. 2025 Aug 12;30(1):737. doi: 10.1186/s40001-025-03011-6.**

Adverse effects of linezolid in the treatment of drug-resistant tuberculosis

combined with diabetic peripheral neuropathy.

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**OBJECTIVE:** This aimed to observe the adverse effects of linezolid on nerve

conduction velocity in patients with drug-resistant tuberculosis combined with

diabetic peripheral neuropathy.

**METHODS:** Patients hospitalized in our hospital from March 2018 to March 2022

were divided into the drug-resistant tuberculosis (DRTB) group, type 2 diabetes

peripheral neuropathy (DPN) group, and type 2 diabetic peripheral neuropathy

combined with drug-resistant tuberculosis (DM-DRTB) group. The drug-resistant TB

treatment regimen used linezolid with antituberculous drugs. Neurophysiological

examinations were performed on the patients before and 2 months after treatment,

the conduction velocities of the superficial peroneal nerve and peroneal nerve

of the lower limbs of the three groups were recorded, and the conduction

velocities of the deep peroneal nerve, superficial peroneal nerve, common

peroneal nerve, tibial nerve, and femoral nerve of the lower limb motor nerves

of the three groups were compared and statistically analyzed.

**RESULTS:** After 2 months of linezolid treatment, the sensory nerve conduction

velocities of the superficial peroneal nerve and sural nerve of the lower limb

in the DRTB group and the DM-DRTB group significantly decreased, and the

difference was statistically significant (p < 0.05). There was no significant

decrease in the motor nerve conduction velocities of the deep peroneal nerve,

superficial peroneal nerve, common peroneal nerve, tibial nerve, or femoral

nerve of the lower limb in the DRTB and the DM-DRTB groups, and the differences

were not statistically significant (p > 0.05).

**CONCLUSION:** Linezolid can slow lower limb sensory nerve conduction velocity in

patients with DRTB and DM-DRTB; however, the effect on lower limb motor nerves

was not significant.

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PMID: 40797354

**7. BMC Public Health. 2025 Aug 12;25(1):2739. doi: 10.1186/s12889-025-23750-9.**

Impact of detection rate and preventive treatment of latent tuberculosis

infection on the future burden of tuberculosis among students in shanghai: a

predictive study using Markov modeling.

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**BACKGROUND:** Students represent a key demographic for tuberculosis (TB) control

in China. This study utilizes a dynamic Markov model to forecast the

epidemiological trends of active tuberculosis (ATB) among students in Shanghai

through 2035 and evaluate the effectiveness of different control strategies.

**METHODS:** A Markov model incorporating six distinct states of TB transmission was

utilized to simulate disease dynamics within a hypothetical cohort of 100,000

individuals. The model assessed the prevalence of latent tuberculosis infection

(LTBI) and ATB, categorizing the cases based on whether they received the

recommended treatment regimen.

**RESULTS:** Under the current measures without any additional interventions, the

model projected a marginal decline in ATB prevalence. Specifically, ATB

prevalence is predicted to decrease to 14.80 per 100,000 by 2035. With an

increase in tuberculosis preventive treatment (TPT) coverage to 20%, 50%, or

80%, the reductions in ATB prevalence were modest. When the detection rate of

LTBI was fixed at 12% and combined with TPT coverage levels of 20%, 50%, and

80%, the reductions in ATB prevalence were 17.01%, 36.56%, and 50.68%

respectively. Increasing the detection rate of LTBI to 35% alongside TPT

coverages of 20%, 50%, and 80% led to more pronounced declines in ATB

prevalence, at 40.95%, 69.36%, and 80.46% respectively.

**CONCLUSIONS:** Under the current TB control measures, the prevalence of ATB among

students would result in only marginal decline trajectories through 2035,

falling substantially short of achieving the strategic goal of ending TB.

Enhanced strategies that simultaneously increase detection rates and coverage of

TPT are likely to significantly reduce ATB prevalence in this population.

SUPPLEMENTARY INFORMATION: The online version contains supplementary material

available at 10.1186/s12889-025-23750-9.

DOI: 10.1186/s12889-025-23750-9

PMCID: PMC12341062

PMID: 40797252

**8. Microbiol Spectr. 2025 Aug 12:e0109625. doi: 10.1128/spectrum.01096-25. Online**

**ahead of print.**

Genetic determinants of Mycobacterium tuberculosis adaptation and drug efficacy

during stationary phase growth.

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The adaptation of Mycobacterium tuberculosis (Mtb) to a slowly growing or

nongrowing state in growth-limited conditions plays a crucial role for drug

tolerance. Although the mechanisms of Mtb adaptation under growth-limited

conditions have been extensively studied, it remains unclear to what extent the

cellular processes necessary to sustain nongrowing state affect drug efficacy.

To investigate this, we performed a genome-wide transposon mutant screen, which

allowed parallel identification of the genes that influence bacterial fitness

and drug efficacy during the stationary phase. Our analysis revealed that genes

encoding the SOS response, membrane phospholipid biosynthesis, proteasomal

protein degradation, and cell wall remodeling critically determine Mtb fitness

in both stationary-phase condition and antibiotic exposure. Surprisingly, we

found that many mutants that compromise stationary-phase adaptation result in

increased fitness during antibiotic treatment, including the recently identified

genetic markers associated with poor clinical outcomes. Furthermore, genes

involved in cell envelope biosynthesis and remodeling, antibiotic efflux, and

phosphate transport are significantly enriched in the mutants sensitized to

antibiotics, indicating that reduced drug entry is a critical factor that limits

antibiotic efficacy in nonreplicating Mtb. We demonstrated that mutants

deficient in utilization of lipids, the primary carbon sources for Mtb during

infection, became tolerant to killing by rifampicin. We provided genetic and

metabolic evidence that the activities of lipid metabolism are associated with

rifampicin efficacy. These findings provide the detailed assessment of Mtb genes

necessary for adaptation to the stationary phase and drug treatment and new

insights into the mechanisms of antibiotic tolerance in nongrowing

Mtb. **IMPORTANCE** It has long been known that antibiotic efficacy is generally

proportional to the bacterial growth rate. Yet it remains unclear how and to

what extent the growth arrest-induced physiological and metabolic changes affect

drug efficacy. Using the genome-wide transposon mutant screen, we identified the

mutants that influence Mycobacterium tuberculosis adaptation and drug efficacy

during the stationary phase of growth. We revealed both positive and negative

correlations between stationary phase adaptation and drug sensitivity and

identified many mutants that compromise stationary phase adaptation and result

in increased fitness during antibiotic treatment, including the identified

genetic markers associated with poor clinical outcomes. These results provide

new insights into the mechanisms of antibiotic tolerance in nongrowing Mtb and

suggest potential targets for drug development.

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PMID: 40793863

**9. ACS Infect Dis. 2025 Aug 12. doi: 10.1021/acsinfecdis.4c00891. Online ahead of print.**

Dynamic Proteomic and PTMomic Characterization of Mycobacteria after Clinical

Pharmaceutical Intervention.

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Song Y(2)(10), Tan L(1), Xu JY(5)(7)(8).

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Tuberculosis, a major global health threat, necessitates understanding the

pharmacological mechanisms of current drugs to combat multidrug resistance. In

addition to alterations at the proteome level, the dynamic changes occurring at

various levels of post-translational modifications (PTMs) following

pharmacological intervention remain unclear. In our current study, we employed a

quantitative proteomic approach to systematically analyze the dynamic molecular

alterations at both the proteome and PTM levels in response to clinical drugs,

including ethambutol, bedaquiline, moxifloxacin, and streptomycin. Our findings

revealed enriched bioprocesses beyond known functions, phosphorylation-level

changes in kinases and phosphatases, and increased acetylation levels with all

four drugs. Overexpression of CobB in Mycobacterium smegmatis significantly

increased its susceptibility to ethambutol, indicating enhanced drug

sensitivity. Our study provides integrated multiomics resources for

understanding the dynamic molecular characteristics and drug resistance

associated with clinical drug interventions and proposes novel therapeutic

strategies targeting the PTM levels.

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PMID: 40791120

**10. Eur J Med Res. 2025 Aug 11;30(1):732. doi: 10.1186/s40001-025-02895-8.**

Analysis of the clinical value and influencing factors of combined detection of

tuberculosis-specific cytokines IFN-γ and IL-2 in the diagnosis of active

tuberculosis in children and adolescents.

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**OBJECTIVE:** This study aimed to conduct a combined detection of Mycobacterium

tuberculosis (MTB) infection using the tuberculosis (TB)-specific cytokine

interferon-γ (IFN-γ) and interleukin-2 (IL-2) release assays in hospitalized

children and adolescents with TB, evaluate the clinical value of this technique

in the diagnosis of active TB in children and adolescents, and to analyze the

related influencing factors.

**METHOD**: A retrospective study was conducted to collect data from suspected

pediatric and adolescent TB patients hospitalized at Chengdu Public Health

Clinical Medical Center between April 2022 and December 2024. The combined

detection of MTB infection using IFN-γ and IL-2 release assays (referred to as

"dual-factor detection of TB infection") was carried out. Microbiological or

molecular biological test results of MTB were also obtained. A total of 904

patients diagnosed with TB and 176 non-TB patients were included in the analysis

of the effectiveness of dual-factor TB infection testing and related influencing

factors.

**RESULTS:** The combined detection of IFN-γ and/or IL-2 demonstrated improved

diagnostic performance for active tuberculosis (ATB), with a sensitivity of

91.04% and specificity of 65.34% (AUC = 0.782, 95% CI 0.745-0.818). While IFN-γ

and IL-2 levels showed no significant differences between MTB-positive and

MTB-negative subgroups within the TB cohort (IFN-γ: 365.52 vs. 382.11 pg/ml;

IL-2: 241.56 vs. 213.12 pg/ml), both cytokines were markedly elevated in the TB

group compared to non-TB controls (IFN-γ: 68.1 pg/ml; IL-2: 41.68 pg/ml).

Age-related variations were observed in IFN-γ (P < 0.05) but not IL-2

concentrations. Untreated patients exhibited higher median levels of IFN-γ

(397.9 vs. 306.0 pg/ml) and IL-2 (239.2 vs. 173.3 pg/ml) than treated

individuals. Among 904 ATB cases, 8.96% (81/904) were false-negative for both

cytokines. Multivariate analysis identified advanced age, retreatment TB,

pleural effusion, and TST positivity as independent risk factors for

dual-negative results (all P < 0.05).

**CONCLUSION:** In pediatric and adolescent patients, the combined detection of

IFN-γ and IL-2 exhibits high sensitivity and specificity in diagnosing ATB. The

test is convenient, stable, and highly accurate, making it of great significance

for the early diagnosis of TB and the evaluation of treatment effects. Age, a

positive TST result, retreatment TB, and the presence of pleural effusion may

all influence the results of IFN-γ and/or IL-2.

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**11. BMC Microbiol. 2025 Aug 12;25(1):499. doi: 10.1186/s12866-025-04206-x.**

Dysbiosis associated with enhanced microbial mobility across the respiratory

tract in pulmonary tuberculosis patients.

Qin M(1)(2), Ding W(3), Qin L(3), Liang R(4), Guo Y(3), Zhao Y(3), Xu H(3), Wen

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**BACKGROUND:** The microbiota is actively engaged in interaction networks both with

the host and among its own constituent members. However, comprehensive studies

examining the microbiome profiles across various respiratory sites in pulmonary

tuberculosis (PTB) are lacking. Here, we explored the diversity of the

microbiome in PTB patients across multiple respiratory sites and investigated

potential interactions between the microbiomes of these sites.

**METHODS:** A total of 130 respiratory tract samples were collected from multiple

sites of 22 patients with PTB and 14 healthy individuals, including the oral

cavity, trachea, and both the healthy and affected sides of the lungs. These

samples were subjected to metagenomic sequencing to analyze the characteristics

and diversity of the respiratory microbiome.

**RESULTS:** We found that the respiratory tract of PTB patients had higher

microbial diversity than seen in the healthy individuals (8,182 vs 6,465). Among

them, Rothia, Prevotella and Actinomyces exhibited higher proportions in PTB.

The characteristics of high diversity features in the oral site were more

prominent with PTB, especially the notable difference of Rothia mucilaginosa.

Additionally, Streptococcus, Neisseria, Prevotella and Fusobacterium have strong

interactions with other species at present at various sites of PTB patients, as

well as frequent communication between these species during migration in the

upper and lower respiratory tract.

**CONCLUSIONS:** The diversity and translocation of microbiota across the

respiratory tract in PTB patients are associated with increased susceptibility

of microbiome. The predominance of Rothia, Prevotella, and Actinomyces may

represent progression-associated microbial signatures, warranting mechanistic

studies on their pathogenic potential through host-microbe interactions to guide

therapeutic targeting.

SUPPLEMENTARY INFORMATION: The online version contains supplementary material

available at 10.1186/s12866-025-04206-x.

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**12. Arch Microbiol. 2025 Aug 11;207(9):218. doi: 10.1007/s00203-025-04422-z.**

Bactericidal activity of gallic acid against multidrug-resistant Mycobacterium

tuberculosis.

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The persistent rise of multidrug-resistant (MDR) bacteria represents a

significant public health challenge, necessitating the exploration of

alternative therapeutic options. The slow pace of approval for new

anti-tuberculosis (TB) medications underscores the urgent need to identify

potential alternative agents. Gallic acid (GA) possesses numerous biological

properties, including antibacterial and antiseptic effects. In this study, both

standard and MDR strains of M. tuberculosis were utilized to assess the

antibacterial efficacy of GA and related mechanisms. GA achieved minimum

inhibitory and minimum bactericidal concentrations comparable to those of the

examined antibiotics with significantly lower cytotoxicity in the THLE-3 cell

line (p-value < 0.05). Furthermore, GA displayed bactericidal properties,

enhanced the effectiveness of moxifloxacin and levofloxacin against MDR M.

tuberculosis, and modulated the expression of efflux pump genes, specifically

Rv1410c and Rv1258c (p-value < 0.001). These results contribute to a deeper

understanding of GA's antibacterial potential and suggest a novel alternative

approach for managing MDR bacterial infections.

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**13. BMC Anesthesiol. 2025 Aug 9;25(1):403. doi: 10.1186/s12871-025-03292-8.**

Remimazolam is more suitable for general anesthesia bronchoscopy in tuberculosis

patients treated with isoniazid: a retrospective cohort analysis.

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**OBJECTIVE:** The objective of this study was to assess the suitability of

remimazolam compared to propofol for general anesthesia during tracheoscopic

procedures in patients with tuberculosis undergoing treatment with isoniazid.

**PATIENTS AND METHODS:** A retrospective analysis was conducted on 1,098 patients

diagnosed with pulmonary tuberculosis who underwent bronchoscopic general

anesthesia at our institution between January and June 2023 (Protocol No.

2022LY0416). The patients were categorized into remimazolam and propofol groups

based on the primary anesthetic agent administered. The primary outcomes

assessed included the time from the conclusion of anesthesia to patient

awakening, as well as hemodynamic changes during the anesthesia period.

**RESULTS:** The time from drug withdrawal to awakening was significantly shorter in

the remimazolam group compared to the propofol group (38.0 s vs. 100.0 s,

P < 0.001). Additionally, the time to extubation was reduced in the remimazolam

group (88.5 s vs. 181.0 s, P < 0.001), although the time to induction of

anesthesia was longer, and the post-anesthesia Aldrete score was higher in the

remimazolam group than in the propofol group (P < 0.001). These findings were

consistently observed in subgroup analyses. During anesthesia maintenance, the

amount of intraoperative vasoactive drugs (dopamine and nicardipine)

administered to patients in the remimazolam group was lower than that in the

propofol group (P = 0.014 and P = 0.031, respectively). Furthermore, during

anesthesia, blood pressure in the remimazolam group was higher and more stable,

exhibiting smaller fluctuations compared to the propofol group. Specifically,

changes in systolic blood pressure were 38.2 ± 15.9 mmHg in the remimazolam

group compared to 46.7 ± 19.0 mmHg in the propofol group (P < 0.001), while

changes in diastolic blood pressure were 6.4 ± 16.4 mmHg in the remimazolam

group versus 12.7 ± 18.7 mmHg in the propofol group (P = 0.002).

**CONCLUSION:** In patients with tuberculosis undergoing treatment with isoniazid,

general anesthesia with remimazolam was associated with a shorter time from the

cessation of anesthesia to recovery, a reduced requirement for vasoactive

agents, and improved hemodynamic stability, without an increase in postoperative

complications, when compared to propofol.

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PMID: 40783679 [Indexed for MEDLINE]

**14. BMC Infect Dis. 2025 Aug 8;25(1):1002. doi: 10.1186/s12879-025-11408-1.**

Drug resistance among students with pulmonary tuberculosis: a study based on

screening in Henan, China.

Xu J(#)(1)(2), Zhang Y(#)(3), Wang G(4), Jiang J(3), Du W(3), Chen S(5), Meng

D(3), Suo W(3), Zhuang Y(3), Wang K(3), Wang W(3), Zhao D(6)(7).

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**BACKGROUND:** Tuberculosis (TB) can easily spread among students and can lead to

an outbreak once there is an infection in a school. Outbreaks of drug-resistant

TB (DR-TB) in schools have occasionally been reported, but the profile of DR-TB

in students in a province has rarely been described. This study was conducted to

determine the prevalence of DR-TB and factors associated with it in students in

Henan Province, China.

**METHODS:** We retrospectively reviewed the data of 3527 pulmonary TB patients

among students with culture-confirmed Mycobacterium tuberculosis (M.tb) isolates

collected from the Tuberculosis Information Management System of the China

Disease Prevention and Control Information System from 2015 to 2021. Prevalence

of DR-TB was analyzed. Comparisons between categorical variables were analyzed

using the chi-square test or Fisher's exact test as appropriate. Logistic

regression models were used to identify the factors associated with DR-TB.

**RESULTS:** Any DR-, RR (rifampin resistance)- and MDR (multi-drug resistance) -TB

rates in students were 10.46%, 7.91% and 6.10%, respectively. And they all

showed a downward trend from 2015 to 2021 (p < 0.001). Previously treated cases

were 7.30 (95% CI: 5.30, 10.05), 8.60 (95% CI: 6.14,12.14) and 9.43 (95% CI:

6.64,13.40) times more likely than the new cases to be diagnosed with Any DR-TB,

RR-TB and MDR-TB, respectively. Patients from schools in the western region of

Henan had greater odds of having Any DR- (AOR = 2.06, 95% CI: 1.31, 3.24), RR-

(AOR = 2.81, 95% CI: 1.66, 4.76) and MDR-TB (AOR = 2.07, 95% CI: 1.13, 3.80)

than those from schools in the northern region. Males had a 1.40-fold (95% CI:

1.11, 1.78), 1.34-fold (95% CI: 1.02, 1.75) greater likelihood of being

diagnosed with Any DR- and RR-TB, respectively. The risk of being diagnosed with

MDR-TB was 1.42 (95% CI: 1.00, 2.02) times greater in students migrant between

prefectures of the province than in the locals.

**CONCLUSION:** The prevalence of DR-TB among students with PTB in Henan, China,

significantly decreased from 2015 to 2021. Previous treated cases and those in

west-region schools in Henan were at greater risk of being diagnosed with Any

DR-, RR- and MDR-TB. In addition, males were more likely to be diagnosed with

Any DR- and RR-TB. It requires further study that whether those who migrated

between prefectures of the province were more likely to be diagnosed with

MDR-TB.

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**15. Front Public Health. 2025 Jul 30;13:1609990. doi: 10.3389/fpubh.2025.1609990.**

**eCollection 2025.**

Study on the 1990-2021 trend of global childhood respiratory infection and

tuberculosis disease burden and related risk factors.

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**BACKGROUND:** Respiratory tract infections (RTIs) and tuberculosis (TB) impose a

critical global health burden on children, serving as leading causes of

morbidity and mortality. Lower respiratory tract infections (LRIs) remain the

primary cause of death in under-5 s, though mortality has declined recently.

**OBJECTIVE:** This study aims to analyze trends in RTIs and TB among 0-14-year-olds

using Global Burden of Disease (GBD) data from 1990 to 2021.

**METHODS:** Global data on childhood RTIs and TB were collected from GBD, with

standardized methods used to assess disease burden trends, age/sex/SDI

differences, and the contribution of 11 risk factors.

**RESULTS:** From 1990 to 2021, incidences of upper RTIs, otitis media, and TB

decreased, but overall RTIs increased. Neonatal LRI had the highest mortality

(1,560.6/100 k). Male children showed higher TB incidence/mortality. Low-SDI

areas had the highest burden (mortality 2.036/100 k), while high-SDI areas saw

the largest TB mortality drop (95.7%). Underweight remained the main risk

factor, with DALY rate falling 80.3%, though household air pollution, low birth

weight, short gestation, and high temperature rose in rank.

**CONCLUSION:** Global childhood respiratory disease burden faces challenges,

requiring strengthened international cooperation and targeted interventions,

especially in low-SDI regions, to improve public health and nutrition.

Copyright © 2025 Chen, Fang, Lu, Wu and Zhang.

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**16. Front Med (Lausanne). 2025 Jul 30;12:1615302. doi: 10.3389/fmed.2025.1615302.**

**eCollection 2025.**

Association between systemic immune-inflammation index and latent tuberculosis

infection: a cross-sectional study.

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**BACKGROUND:** The systemic immune-inflammation index (SII) has been associated

with various diseases, but its relationship with latent tuberculosis infection

(LTBI) remains unclear. This study aimed to evaluate the association between SII

and LTBI in United States adults.

**METHODS:** Data were obtained from the National Health and Nutrition Examination

Survey (NHANES) 1999-2000 and 2011-2012 cycles. LTBI was defined as a positive

result on either the QuantiFERON®-TB Gold In-Tube (QFT-GIT) assay or the

tuberculin skin test (TST). SII was calculated based on neutrophil, platelet,

and lymphocyte counts. All analyses were performed using complex survey design

and sampling weights. Multivariable logistic regression models were applied to

evaluate the association between SII and LTBI. SII was also analyzed in

quartiles to assess trends. Restricted cubic spline (RCS) was employed to

explore the potential non-linear associations. Subgroup analyses were conducted

to assess whether the association varied across demographic and clinical strata.

**RESULTS:** A total of 9,489 participants were included, among whom 1,068 were

identified with LTBI. Multivariable logistic regression demonstrated that SII

was inversely associated with LTBI. For each 100-unit increase in SII, the odds

of LTBI decreased by 6% (adjusted OR = 0.94, 95% CI: 0.90-0.97). When analyzed

by quartiles, participants in the highest quartile had significantly lower odds

of LTBI compared to those in the lowest quartile (adjusted OR = 0.58, 95% CI:

0.41-0.81), with a significant trend across quartiles (P for trend = 0.003). RCS

showed a linear relationship between SII/100 and LTBI (P for non-linearity

>0.05). The results of further subgroups analysis were consistent, with a

significant interaction observed only for HIV status (P for interaction =

0.034).

**CONCLUSION:** SII was inversely associated with LTBI and may serve as a readily

accessible marker for LTBI risk stratification. Given its non-specific nature,

further longitudinal studies are needed to validate its clinical and public

health utility.

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PMID: 40809440

**17. J Clin Tuberc Other Mycobact Dis. 2025 Jul 29;41:100555. doi:**

**10.1016/j.jctube.2025.100555. eCollection 2025 Dec.**

Tuberculosis infection control in MDR-TB designated hospitals in Jiangsu

Province, China.

Song H(1), Li G(1), Xu Z(2), Wang F(3), Wang X(4), Dai B(5), Zhang X(6), Li

J(7), Li Y(1), Zhu L(1).

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**BACKGROUND:** Hospital-acquired Tuberculosis (TB) infections among healthcare

workers (HCWs) and patients present a significant challenge due to the increased

risk of TB infection within healthcare settings.

**METHODS:** A standardized assessment tool was applied for the evaluation, which

involved direct observation, document review, and interviews with facility

heads. A baseline evaluation of TB infection control (TBIC) measures in TB

outpatient and inpatient departments, as well as laboratories, was completed by

January 2019. Based on the results, a comprehensive intervention package was

implemented, incorporating a three-tiered hierarchy of controls: administrative

control (AC), environmental control (EC), and respiratory protection (RP).

Subsequent monitoring was conducted quarterly, with corrective actions

accordingly. More than two years of follow-up data were collected, with the

collaboration of local hospitals, the municipality Centers for Disease Control

and Prevention (CDC), and the Jiangsu Provincial CDC, concluding on August 31,

2021.

**RESULTS:** At baseline, the average implementation rates of AC, EC and RP were

57.3 %, 59.2 %, and 66.6 %, respectively. After the intervention, significant

improvements were observed in key infection control measures. A triage process

for cough patients was established, mechanical ventilation systems were

installed, and the use of masks was improved. In addition, ultraviolet (UV) and

upper-room ultraviolet germicidal irradiation (UVGI) systems were installed

where required. As a result, the average implementation rates of AC, EC and RP

significantly increased to 86.3 %, 87.4 %, and 98.4 % (P < 0.05), respectively. However, at the study's conclusion, Suzhou Fifth People's Hospital reported a lower AC implementation rate of 70.7 %, while Changzhou Third People's Hospital had an EC implementation rate of 68.1 %. These discrepancies were primarily attributed to suboptimal architectural designs that hindered proper ventilation in the wards.

**CONCLUSIONS:** This study demonstrates that designated hospitals still face

persistent gaps in tuberculosis infection control (TBIC). However, over the

course of one and a half years of targeted and standardized interventions,

substantial improvements in TBIC practices were achieved across most

participating institutions. Despite the suboptimal availability of dedicated TB

wards, strengthening TBIC measures remains crucial to reducing TB transmission

among healthcare workers and non-TB patients. This approach is both practical

and scalable, particularly in high-burden TB settings. Nevertheless, the

long-term efficacy and sustainability of these TBIC practices warrant ongoing

evaluation.

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**eCollection 2025.**

Experimental validation of cuproptosis-associated molecular signatures and their

immunological implications in pulmonary tuberculosis.

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Liu Y(1), Liang Y(#)(1), Liang J(#)(3), Wu X(#)(1).

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**BACKGROUND:** The pathogenic mechanism underlying Mycobacterium tuberculosis (MTB)

remains elusive, posing challenges to its diagnosis and treatment. Cuproptosis

is a newly identified mechanism of cell death. This study explores the role of

cuproptosis-related genes (CRGs) in pulmonary tuberculosis (PTB) to uncover

potential diagnostic biomarkers and therapeutic targets.

**METHODS:** Differentially expressed gene (DEG) analysis and weighted gene

co-expression network analysis (WGCNA) were carried out using the GSE83456

dataset. PTB-associated DEGs were intersected with CRGs to identify PTB-related

CRGs. Subsequent analyses included functional enrichment, gene interaction, and

protein-protein interaction (PPI) network construction. Hub CRGs were screened

out via least absolute shrinkage and selection operator (LASSO) regression and

random forest (RF) algorithms. Diagnostic models were subsequently constructed

and validated. The associations of immune cell infiltration and pathway with the

identified hub genes were evaluated through single-sample gene set enrichment

analysis (ssGSEA) and CIBERSORT. Hub gene expressions were validated in the

GSE42834 and GSE89403 datasets, as well as by RT-qPCR and Western blot (WB) in

PTB and extrapulmonary tuberculosis (EPTB) patients. The GSE89403 dataset and

gene expression profiling were leveraged to analyze the differential expression

of hub genes and their dynamic changes during treatment.

**RESULTS**: Seven PTB-related CRGs were significantly upregulated, were

significantly upregulated, among which ASPHD2, GK, and GCH1 were identified as

hub genes. These genes exhibited high expression levels in patients with PTB and

EPTB, with marked reductions observed following treatment. Notable alterations

in immune cell infiltration and immune function in PTB patients were closely

related to these hub genes, suggesting activation of innate immune responses and

suppression of adaptive immune function.

**CONCLUSION:** The cuproptosis hub genes ASPHD2, GK, and GCH1 influence the

pathogenesis of PTB, and possibly serve as novel diagnostic biomarkers and

therapeutic targets.

Copyright © 2025 Liu, Ma, Li, Xue, Mi, Li, Bai, Guo, Liu, Liang, Liang and Wu.

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**19. IDCases. 2025 Jul 27;41:e02335. doi: 10.1016/j.idcr.2025.e02335. eCollection**

**2025.**

An elderly couple suffers from tuberculosis of the reproductive system.

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**INTRODUCTION:** Genitourinary tuberculosis is often secondary to tuberculosis in

other parts of the body, and transmits through blood, direct spread, and

lymphatic pathway. Female primary infection through sexual intercourse with an

active reproductive tuberculosis spouse in an upward transmission way is rare.

**CASE REPORT:** There is an elderly couple with testicular tuberculosis in the male

and endometrial tuberculosis in the female. The onset of male patients precedes

female patients, and there is no protected sexual intercourse. The possibility

of direct sexual transmission and primary infection of genitourinary

tuberculosis is considered.

**CONCLUSIONS:** Our findings raise awareness of the transmission route of

reproductive system tuberculosis, attach importance to prevention and reduce

damage, which is of great significance to reducing infertility and the resulting

family problems.

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**10.1093/gpbjnl/qzaf065. Online ahead of print.**

Macrophage Response to Avirulent and Virulent Mycobacterium tuberculosis and

Anti-TB Effects of Exosome Treatment.

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Wang X(1)(2), Xu S(8), Sheng Y(9), Jiang C(9), Wang J(10), Hu X(10), Bahetibieke

T(10), Zhang Z(6), Chen F(1)(2)(3)(10)(11)(12).

**Li Yang****,****Lingna Lyu****,****Cuidan Li****,****Xiuli Zhang****,****Yingjiao Ju****,** **Ju Zhang****,****Jie Liu****,****Liya Yue****,****Nan Ding****,****Xiangli Zhang****,****Dandan Lu****,****Tingting Yang****,****Peihan Wang****,****Jie Wang****,****Xiaotong Wang****,****Sihong Xu****,****Yongjie Sheng****,****Chunlai Jiang****,****Jing Wang****,****Xin Hu****,****Tuohetaerbaike· Bahetibieke****,****Zongde Zhang****\*,****Fei Chen****\***

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Tuberculosis (TB) returned as the leading cause of death from a single

infectious agent in 2023. Human-macrophages and their secreted exosomes play

important roles in combating invading Mycobacterium tuberculosis (Mtb). However,

panoramic analysis of the underlying immune mechanism for infected macrophages,

package mechanism and anti-TB effect of Mtb treated exosomes remain understood.

Here we conducted comprehensive analyses of the macrophages infected with

avirulent and virulent Mtb (H37Ra & H37Rv) and their exosomes through omics and

phenotypic analyses. The results showed that H37Ra stimulated strong immune

responses and apoptosis in macrophages to eliminate the invading Mtb, while

H37Rv induced severe necrosis and immune escape for survival. Interestingly, our

results suggest that macrophages kill Mtb in an interferon-gamma (IFN-γ)

independent but simulative way, highlighting the central role of IFN signaling

pathway in anti-TB response. Moreover, we observed selective transport of host

and Mtb RNAs from macrophages to exosomes. Notably, H37Ra-treated exosomes

displayed a higher anti-TB effect than H37Rv-treated exosomes due to some

enriched pro-inflammation and immune escape related Mtb proteins in these two

exosomes, respectively. Conclusively, our findings shed new light on the immune

mechanism of macrophages in response to Mtb infection, offering a new TB

treatment strategy and promising vaccine candidates.

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Global, regional, and national burden of tuberculosis due to smoking, 1990-2021:

analysis for the Global Burden of Disease study.

Zhao G(#)(1), Wu Y(#)(2), Song C(1), Sun Y(1), Zang S(1), Tian F(1), Gao

Z(1)(3), Zhang C(1)(4), Wang X(1).

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

tuberculosis invading the lungs and other organs, which is a serious threat to

human life and health. Recent studies have shown that smoking is an important

risk factor for the development of TB and advances the progression of TB through

multiple mechanisms that affect the body's immune function.

**METHODS:** A multidimensional analytical approach was taken to gain a

comprehensive understanding of the burden of disease. First, the burden of TB

due to smoking (Deaths, DALYs, YLDs, and YLLs) from 1990-2021 was conducted. And

then, differences in the burden of disease in 2021 were explored across gender,

age, SDI regions, GBD regions and countries. In addition, decomposition analysis

was performed to understand the influencing factors of disease burden. Finally,

ARIMA and ES models were used to predict trends in disease burden from

2022-2050.

**RESULTS:** Globally, the number of cases and ASR of TB due to smoking have

decreased over time. The burden of disease is heaviest in the middle-aged male

population and is much higher than in women. The burden is higher in regions

with lower levels of SDI than in those with higher levels of SDI. Australasia

has the lowest burden, while India is the country with the highest burden.

Projections show a general downward trend in the number of disease burdens from

2022 to 2050, but there is still a need to develop the right strategies to meet

the challenges of disease.

**CONCLUSIONS:** Smoking as an independent risk factor for several chronic diseases,

this study focuses on the burden of TB due to smoking. Although the results show

that the burden situation is decreasing year by year, the state and society

still need to increase the publicity of science, raise the awareness of the

disease among the public, and develop public health programs to deal with the

disease.

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Efficacy of Belimumab for Active Lupus Nephritis in a Young Asian Man with

Latent Pulmonary Tuberculosis: A Case Report.

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**INTRODUCTION:** Managing active lupus nephritis (LN) in the presence of latent

tuberculosis (TB) presents a significant treatment challenge. Traditional

treatment with glucocorticoids combined with mycophenolic acid carries a high

risk of triggering pulmonary TB infection in LN patients. In this report, we

discuss a novel approach using belimumab in combination with rapidly tapering

corticosteroids to treat a patient with active class IV and V LN and latent TB.

**CASE PRESENTATION:** A 24-year-old Chinese male was diagnosed with active class IV

and V LN and latent TB. He underwent induction therapy with a combination of

belimumab, rapidly tapering methylprednisolone and mycophenolate mofetil. After

18 months of belimumab therapy, the patient's blood albumin levels and kidney

function normalized, with 24-h urinary protein levels stabilizing between 500 mg

and 725 mg. Notably, there was no recurrence of TB.

**CONCLUSION: T**his case demonstrates that the combination of belimumab and rapid

corticosteroid tapering effectively reduced the duration of high-dose

glucocorticoid therapy, highlighting the efficacy and safety of belimumab in

managing LN with latent TB.

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The impact of IGRA positivity in untreated inactive pulmonary tuberculosis on

IVF-ET outcomes in infertile women: an ambispective cohort study.

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**BACKGROUND:** Tuberculosis can negatively impact both overall health and female

reproductive function. This study investigated the relationship between the

interferon-gamma release assay (IGRA) status and pregnancy outcomes in infertile

women, with untreated "inactive" tuberculosis lesions observed on chest

radiography, who are undergoing in vitro fertilization and embryo transfer

(IVF-ET).

**METHODS:** This ambispective cohort study, which includes retrospective

(2012-2019) and prospective (2020-2024) cohorts, enrolled infertile women with

untreated inactive tuberculosis lesions visible on chest imaging who are

planning to undergo IVF-ET. All patients underwent IGRA testing. Baseline

characteristics, such as age, body mass index (BMI), infertility factors,

ultrasound follicle count, and hormone levels, were collected. Pregnancy

outcomes, including live birth rates, oocyte retrieval numbers, embryo quality,

clinical pregnancy, miscarriage, and preterm birth rates, were followed and

compared between the IGRA-positive and IGRA-negative groups.

**RESULTS:** Among 836 patients, the IGRA positivity rate was 42.5%. The cumulative

miscarriage rate was higher in the IGRA-positive group than in the IGRA-negative

group (21.5% vs. 15.0%, p = 0.047). No significant differences were found in

clinical pregnancy or live birth rates. Age, BMI, and endometrial thickness were

independent risk factors influencing clinical pregnancy and live birth rates,

while the IGRA status was not.

**CONCLUSION:** In infertile women with untreated inactive tuberculosis lesions on

chest radiography, IGRA positivity is associated with higher cumulative

miscarriage rates following IVF-ET. Early IGRA screening and intervention may

help improve pregnancy outcomes.

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Zhou, Liu, Sun, Li and Qiao.

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Balancing nitrogen metabolism to efficiently drive anti-tuberculosis ilamycins

biosynthesis in Streptomyces atratus.

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The deep-sea-derived Streptomyces atratus SCSIO ZH16 is a promising host for

producing nanomole-level anti-tuberculosis ilamycins. However, limited research

on regulating the ilamycins biosynthetic gene cluster (BGC) has hindered

industrial production. Our previous study found that nitrogen metabolism-related

genes were upregulated in strains with enhanced ilamycins production. Since

amino acids from nitrogen metabolism are key precursors, we aimed to optimize

ilamycins production by balancing BGC expression and nitrogen metabolism. Using

RNA-seq and hierarchical clustering, we identified the native promoter P20605

and its modified version P20605-400, which regulate the positive regulator IlaB

in ilamycins BGC. To synchronously boost ilamycins synthesis and precursor

supply, we analyzed P20605's function via bioinformatics and validated it using

an indigoidine biosynthetic model. The engineered strain

ΔilaR::P20605-400-ilaB::PermE\*-phoP achieved over a dozen-fold increase in

ilamycins yield. Fermentation was successfully scaled up in 5-L and 500-L

bioreactors, reaching titers of 2,546.4 mg/L and 1,993.9 mg/L, respectively,

significantly surpassing previously reported yields. This study highlights the

industrial potential of ilamycins and provides insights into enhancing peptide

compound production in Streptomyces.

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Anti-Mycobacterium tuberculosis activity of 17-hydroxy-jolkinolide B by

interacting with RNA polymerase.

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Euphorbia fischeriana has been traditionally used in Chinese medicine for

tuberculosis (TB) treatment since ancient times. In this study, we first report

the identification of an abietane-type diterpenoid, 17-hydroxy-jolkinolide B

(HJKB), from E. fischeriana, which exhibits potent antimycobacterial activity

against both Mycobacterium tuberculosis H37Ra strain and clinical isolates. The

minimum inhibitory concentrations (MICs) of HJKB against diverse M. tuberculosis

strains range from 1 to 12 μg/mL. Notably, HJKB demonstrates significant

bactericidal activity against intracellular M. tuberculosis H37Ra in macrophage

models, accompanied by anti-inflammatory effects at concentrations of 2-5 μg/mL.

Using a combination of chemoproteomic analysis and pull-down assays, we explored

the preliminary antimycobacterial mechanism of HJKB. Results indicate that HJKB

interacts with the target proteins RpoB and RpoC in M. tuberculosis H37Ra, a

finding further corroborated by molecular docking studies. RpoB and RpoC are

essential subunits of the DNA-directed RNA polymerase holoenzyme, which is

critical for bacterial ribosomal transcription regulation. In summary, HJKB

represents a bioactive constituent of E. fischeriana with anti-TB efficacy,

acting as a transcription inhibitor against M. tuberculosis. This study not only

elucidates its antimycobacterial mechanism but also provides a preclinical

foundation for the development of natural product-based TB therapeutics.

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