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**中国大陆学者发表的结核病英文文章摘要**

**（23篇）**

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

**1. Clin Infect Dis. 2025 Jul 8:ciaf351. doi: 10.1093/cid/ciaf351. Online ahead of print.**

A Short, All-Oral Regimen for Pre-Extensively Drug-Resistant Tuberculosis: A

Multicenter Open-label Single-arm Study.

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Qian Y(7), Yu H(8), Lan Y(9), Shi J(10), Huang Y(11), Zhang Y(12), Feng S(13),

Xiao M(14), Wang J(15), Li Y(16), Wang H(17), He Z(18), Liu H(19), Zhang Y(20),

Zhou Y(21), Wu Y(22), Sun F(1)(2), Zhang W(1)(2).

**Yang Li, Yilin Zhang, Lingyun Song, Cui Cai, Yuanyuan Chen, Hengzhong Yi, Qianhong Wu, Yuan Qian, Hongying Yu, Yuanbo Lan, Jichan Shi, Ya Huang, Yungui Zhang, Shun Feng, Mingying Xiao, Jing Wang, Yiming Li, Hua Wang, Zebao He, Haiqing Liu,** **Yena Zhang, Yong Zhou, Yuqing Wu, Feng Sun\*, Wenhong Zhang**

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**BACKGROUND:** Pre-extensively drug-resistant tuberculosis (pre-XDR-TB) remains a

critical public health threat due to limited treatment options and significant

disease burden. Existing regimens have shown high success rates but are often

inaccessible globally, necessitating alternative options.

**METHODS:** This study was an open-label, multicenter, single-arm study conducted

in China to evaluate the efficacy and safety of a 6- to 9-month oral regimen.

Eligible participants, aged 18-70 with pulmonary pre-XDR-TB received a regimen

of bedaquiline, linezolid, cycloserine, pyrazinamide and/or clofazimine.

Pyrazinamide was either replaced with clofazimine or retained without

clofazimine based on molecular susceptibility results. The primary efficacy

endpoint was the percentage of participants with a favorable outcome at 84 weeks

after treatment initiation in the modified intention-to-treat population.

**RESULTS:** A total of 89 patients with pre-XDR-TB were enrolled. At 84 weeks after

treatment initiation in the modified intention-to-treat analysis, 62 of 80

participants (77.5%; 95% confidence interval, 67.2% to 85.3%) had favorable

outcomes. The 18 unfavorable outcomes were 5 regimen discontinuations or changes

(6.3%, 4 due to adverse events and 1 decided by the local investigator), 4

bacteriological failures (5.0%), 4 withdrawals of consent (5.0%), 3 deaths

(3.8%), and 2 losses to follow-up (2.5%). No relapse was reported after the end

of treatment. Adverse events of grade 3 or higher were observed in 59.1% of

participants, with QTc prolongation being the most frequently reported.

**CONCLUSIONS:** This study demonstrated that an all-oral, bedaquiline-based regimen

provides a viable treatment option for patients with pre-XDR-TB, achieving

acceptable efficacy and manageable safety profiles.

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**2. Chem Sci. 2025 Jun 25. doi: 10.1039/d5sc03865k. Online ahead of print.**

Catalytic enantioselective total synthesis of antitubercular agents

(-)-bedaquiline and (-)-sudapyridine enabled by dynamic kinetic

resolution-asymmetric transfer hydrogenation.

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(-)-Bedaquiline [(-)-BDQ] is considered to be one of the most promising new

therapeutic agents for tuberculosis for over 50 years. However, there are

limited general and highly stereocontrolled asymmetric synthetic methods

available for (-)-BDQ and its analogues due to the challenge of forging their

vicinal stereocenters. Herein, we report a concise and stereocontrolled

synthetic route to (-)-BDQ in six steps with an overall yield of 34%,

integrating a Rh-catalyzed dynamic kinetic resolution-asymmetric transfer

hydrogenation (DKR-ATH) with TADDOL-mediated diastereoselective allylation. The

reactivity and stereoselectivity of DKR-ATH were systematically investigated

using a range of sterically hindered N-hetero-1,2,2-triarylethanones. This

approach offers a robust and reliable method for synthesizing

N-hetero-1,2,2-triarylethanols featuring two continuous stereocenters, which

serve as crucial chiral building blocks for pharmaceutical applications.

Furthermore, the aforementioned two-stage protocol has been successfully applied

to the synthesis of (-)-sudapyridine, a tuberculosis drug candidate currently in

phase III clinical trials. This study presents a versatile and generalizable

strategy for the synthesis of BDQ-type architectures, which hold significant

interest for both medicinal and process chemists.

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**3. Tuberculosis (Edinb). 2025 Jul 3;154:102671. doi: 10.1016/j.tube.2025.102671.**

**Online ahead of print.**

Identification of monocyte-associated genes MSRB2, CLEC4D, and ASGR2 as

potential biomarkers for tuberculosis via machine learning and mendelian

randomization.

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**OBJECTIVE:** This study explores the link between immune cells and tuberculosis

(TB) pathogenesis and progression, proposing diagnostic strategies based on

immune microenvironment changes.

**METHODS:** The CIBERSORT algorithm assessed immune cell infiltration in TB

tissues, validated by routine blood tests. Differential expression analysis and

WGCNA identified key genes and modules. GO and KEGG analyses elucidated

biological functions. Machine learning pinpointed diagnostic biomarkers and

built a predictive model. Further validation included GSVA, single-cell data,

Mendelian randomization, and RT-qPCR.

**RESULTS:** Analysis of the immune microenvironment in TB patients and healthy

controls revealed monocytes as the predominant immune cell type. A total of 90

overlapping genes were identified through differential expression analysis and

WGCNA. A diagnostic model incorporating MSRB2, CLEC4D, and ASGR2 was constructed

using three distinct machine learning algorithms and logistic regression.

Single-cell data analysis demonstrated that these three genes were predominantly

expressed in mononuclear cells of TB patients. MR analysis further established a

causal relationship between CLEC4D and an elevated risk of TB.

**CONCLUSION:** We established a monocyte-based diagnostic model demonstrating

robust predictive accuracy. MSRB2, CLEC4D, and ASGR2 represent promising

therapeutic targets for TB immunotherapy, providing potential breakthroughs in

diagnostic precision and treatment efficacy.

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**4. J Cardiothorac Surg. 2025 Jul 19;20(1):308. doi: 10.1186/s13019-025-03544-1.**

Potential auxiliary diagnostic role of pentraxin 3 in plasma and bronchoalveolar

lavage fluid for pulmonary tuberculosis.

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**OBJECTIVE:** This study aimed to assess the auxiliary diagnostic efficacy of

Pentraxin 3 (PTX3) as a biomarker for pulmonary tuberculosis (TB) by analyzing

its levels in plasma and bronchoalveolar lavage fluid (BALF) in TB patients.

Given the limitations of current TB diagnostic methods, the investigation also

sought to evaluate the possible auxiliary help of PTX3 in distinguishing TB from

other pulmonary conditions.

**METHODS:** The bioinformatic analysis utilized the Gene Expression Omnibus (GEO)

dataset (GSE34608), including peripheral blood samples from individuals with TB,

sarcoidosis, and healthy controls. Clinical specimens were obtained from

hospitalized patients between January 2020 and March 2022, comprising 126

peripheral blood samples and 68 BALF samples. PTX3 levels were measured via

enzyme-linked immunosorbent assays (ELISA), with subsequent statistical analyses

conducted to assess the auxiliary diagnostic efficacy of PTX3 through ROC curve

analysis.

**RESULTS:** The analysis of the GEO dataset revealed a notable increase in PTX3

levels in the peripheral blood of TB patients compared to controls, with an area

under the curve (AUC) of 0.889. However, no significant differences in plasma

PTX3 levels were observed among TB, community-acquired pneumonia (CAP), and lung

cancer patients in clinical samples (AUC: 0.472). Conversely, PTX3 levels in

BALF were significantly elevated in TB patients compared to individuals with CAP

and lung cancer (P < 0.001), with an AUC of 0.806, along with a sensitivity of

0.800 and specificity of 0.810, suggesting its potential auxiliary diagnostic

utility.

**CONCLUSION:** Plasma PTX3 levels have limited diagnostic utility in distinguishing

tuberculosis from other pulmonary conditions, whereas BALF PTX3 levels exhibit

more possible auxiliary diagnosis ability as an auxiliary diagnostic indicator,

offering a localized assessment of lung inflammation. BALF PTX3 could be a

helpful adjunct in diagnosing TB, particularly in cases where conventional

sputum-based tests are inconclusive. Further research is needed to validate

these findings.

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**5. BMJ Open. 2025 Jul 18;15(7):e098692. doi: 10.1136/bmjopen-2024-098692.**

Effect of prior anti-tuberculosis treatment on assisted reproductive outcomes in

infertile women: a retrospective cohort study.

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**PURPOSE:** Tuberculosis (TB) is a significant factor contributing to infertility.

For some infertile patients, chest radiography (CXR) screenings prior to

assisted reproductive treatment (ART) reveal old/inactive TB lesions. However,

the pregnancy outcomes after ART for such patients who had a history of prior

anti-TB treatment remain unclear.

**DESIGN:** Retrospective cohort study.

**SETTING:** Peking University Third Hospital, a tertiary care centre.

PARTICIPANTS: This study analysed and focused on infertile patients aged 20-50

years with prior TB lesions on CXR (treated/untreated) and normal CXR. Active TB

cases were excluded from this study. Patients were categorised into three groups

based on CXR findings and prior anti-TB treatment: treated prior-pulmonary TB

(PTB) group, untreated prior-PTB group and a non-PTB control group with normal

CXR.

**PRIMARY AND SECONDARY OUTCOME MEASURES:** ART outcomes, including clinical

pregnancy rate, miscarriage rate and live birth rate, were compared among the

groups.

**FINDINGS TO DATE:** Among 8769 patients analysed, including treated prior-PTB

group (n=171), untreated prior-PTB group (n=791) and non-PTB group (n=7807). The

treated prior-PTB group showed a similar clinical pregnancy rate (41.5% vs

38.1%, p=0.360) and live birth rate (35.3% vs 30.6%, p=0.187) compared with the

non-PTB group. The miscarriage rate was slightly lower in the treated prior-PTB

group than in the non-PTB group (11.3% vs 15.5%, p=0.325), although the

discrepancy was not statistically significant. Compared with the untreated

prior-PTB group, the treated prior-PTB group exhibited significantly higher live

birth rate (35.3% vs 23.8%, p<0.05), clinical pregnancy rate (41.5% vs 31.7%,

p<0.05) and with a lower miscarriage rate (11.3% vs 19.1%, p=0.123), although

the latter was not statistically significant. Multivariable regression confirmed

significantly higher live birth rates in the treated prior-PTB group versus

untreated prior-PTB group (aOR: 1.69, 95% CI: 1.01 to 2.83, p=0.045).

**CONCLUSIONS AND FUTURE PLANS:** Anti-TB treatment in infertile women with prior

PTB lesions was associated with improved ART outcomes, comparable to those in

patients without TB lesions. This suggests a potential clinical benefit of

anti-TB treatment in improving reproductive outcomes in this population. Further

research is warranted to explore ART outcomes in patients with untreated prior

TB lesions.

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**6. PLoS One. 2025 Jul 17;20(7):e0328255. doi: 10.1371/journal.pone.0328255.**

**eCollection 2025.**

Long-term trends and future projections of the burden of tuberculosis among

children and adolescents in China.

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**BACKGROUND:** China ranks third in estimated TB incidence in 2023, accounting for

6.8% of the global cases. TB in children and adolescents is a public health

issue that today warrants priority attention in China.

**OBJECTIVE:** The purpose of this study was to investigate the burden of TB among

Chinese children and adolescents aged 0-19 years from 1990 to 2021 and to

estimate the incidence rate, mortality rate, and disability-adjusted life years

(DALYs) rate from 2022 to 2031.

**METHODS:** The Joinpoint regression analysis was used to identify periods of

significant change and autoregressive Integrated Moving Average (ARIMA) modeling

was employed to predict the TB burden for 2022-2031.

**RESULTS:** The study indicated that China has significantly reduced the TB burden

among children and adolescents over the past 32 years, the most pronounced

reductions in incidence occurred during the periods 2010-2015 (APC = -8.64%,

P < 0.05) and 2019-2021 (APC = -6.09%, P < 0.05). Meanwhile, death and DALYs

rates showed a consistently rapid decline across the entire 32-year span.

Adolescents aged 15-19 years have the highest incidence rates, and children

under 5 continue to face high mortality and DALYs rates. Additionally, females

experienced a more significant decline compared to males across all age groups.

Despite minor fluctuations in some age groups, a downward trend in incidence,

death, and DALYs rates was anticipated to continue until 2031, with persistent

gender differences in future projections.

**CONCLUSIONS:** Our findings demonstrate a persistent downward trajectory in TB

burden among Chinese children and adolescents from 1990 to 2021, with

significant gender disparities favoring females across all age groups. Notably,

children younger than 5 years and adolescents aged 15-19 years are at higher

risk, which emphasizes the importance of tailored interventions to ensure

continued progress towards comprehensive TB control goals.

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**7. Sci Rep. 2025 Jul 15;15(1):25594. doi: 10.1038/s41598-025-11465-1.**

Short- and long-term exposure to ambient air pollution and greenness in relation

to pulmonary tuberculosis incidence.

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Epidemiological studies have found inconsistent relationships between air

pollutants and the risk of pulmonary tuberculosis (PTB), possibly due to

variations in exposure windows and limited attention to environmental modifiers

such as greenness. However, few studies has systematically examined how short-

and long-term exposure to air pollution may differentially impact PTB risk, and

how greenness may modify these associations. We utilized comprehensive data,

including daily PTB incidence, air pollutants, meteorological data, and the

normalized difference vegetation index (NDVI) from Zhejiang Province, China,

spanning from 2013 to 2019. A distributed lag nonlinear model (DLNM) was

employed to examine the relationships between air pollution and PTB incidence by

county, and a meta-analysis was conducted to aggregate county-specific

estimates. In the single-pollutant model, the lag-specific excess risk (ER) of

PTB was 0.7% (95% CI 0.05%, 1.4%, 13-week lag) for each 0.1 mg/m3 increase in

carbon monoxide (CO). For each 10 µg/m3 increase in the combined oxidant

capacity (OX), the lowest risk was a 0.9% decrease (95% CI -1.5%, -0.3%, 16-week

lag). For each 10 µg/m3 increase in particulate matter 2.5 (PM2.5), the highest

risk was a 1.7% increase (95% CI 0.8%, 2.6%, 19-week lag). Conversely, each

10 µg/m3 increase in sulfur dioxide (SO2) showed a dual association with PTB

incidence, encompassing a short-term negative correlation and a long-term

positive correlation. Furthermore, the associations between CO and PM2.5 and PTB

incidence were more pronounced in the male and working-age subgroups, whereas

the associations with SO2 were more significant in the female and elderly

subgroups. Additionally, we observed that greenness negatively modified the

relationship between short- and long-term exposure to OX and PTB incidence. Our

findings revealed significant long-term lagged effects of CO, OX, and PM2.5 on

PTB incidence, as well as short- and long-term lagged effects of SO2.

Furthermore, greenness was identified as a modifier of the association between

OX and PTB incidence at various lag times.

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**8. Nat Commun. 2025 Jul 16;16(1):6538. doi: 10.1038/s41467-025-61824-9.**

Mycobacterium bovis frd operon phase variation hijacks succinate signaling to

drive immunometabolic rewiring and pathogenicity.

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Tuberculosis (TB), caused by Mycobacterium tuberculosis complex (MTBC)

pathogens, remains a global health threat. While bacterial genetic adaptations

during host infection are poorly understood, phase variation in genomic

homopolymeric tracts (HT) may drive pathogenicity evolution. Here, we

demonstrate that M. bovis exploits HT insertion mutations in the fumarate

reductase-encoding frd operon to subvert host immunometabolism. In macrophages,

wild-type M. bovis secretes FRD-catalyzed succinate, stabilizing

hypoxia-inducible factor-1α (HIF-1α) to drive glycolytic reprogramming and IL-1β production. This activates IL-1R-dependent Th1 immunity, restraining bacterial

replication. Conversely, M. bovis frd HT insertion mutants impair succinate

secretion, suppressing HIF-1α/IL-1β signaling and redirecting immunity toward

pathogenic Th17 responses that promote neutrophil infiltration and tissue

necrosis. Mice infection models reveal that M. bovis frd mutants exhibit

enhanced pathogenicity, with higher pulmonary bacterial burdens. IL-1R blockade

phenocopies frd HT insertion mutation effects, exacerbating lung pathology.

Crucially, conserved frd HT polymorphisms in clinical M. tb isolates suggest

shared immune evasion strategies across MTBC pathogens. Our work uncovers the

bacterial gene phase variation mechanism of hijacking the succinate/HIF-1α/IL-1β axis to operate host immunity, providing a framework for targeting host

metabolic checkpoints in TB therapy.

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**9. Gut Microbes. 2025 Dec;17(1):2531201. doi: 10.1080/19490976.2025.2531201. Epub 2025 Jul 14.**

Gut microbiota and tuberculosis infection: interaction and therapeutic

potential.

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Pulmonary tuberculosis (PTB), caused by Mycobacterium tuberculosis (MTB), is a

serious chronic infectious disease. Although significant progress has been made

in the prevention and treatment of MTB, current anti-tuberculosis therapies

still face numerous challenges. The human gut microbiota, a complex ecosystem,

plays a role in host metabolism, immune regulation, and health maintenance.

Recent studies have increasingly highlighted a close relationship between gut

microbiota and PTB. The gut microbiota, through the gut-lung axis, mediates the

immune processes of PTB, while MTB infection can disrupt the ecological balance

of the gut microbiome. This review aims to summarize the changes in gut

microbiota among PTB patients and their relationship with clinical

manifestations, explore the role of gut microbiota in PTB immunity, and further

analyze the potential application of gut microbiota therapy in PTB treatment.

The goal is to provide clear direction for future research on gut microbiota and

lung diseases and propose new strategies for MTB treatment.

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PMCID: PMC12269669

PMID: 40654283 [Indexed for MEDLINE]

**10. Front Public Health. 2025 Jul 3;13:1621695. doi: 10.3389/fpubh.2025.1621695.**

**eCollection 2025.**

Analysis of the epidemiological characteristics of pulmonary tuberculosis in

Shijiazhuang, China 2010-2023.

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**BACKGROUND: S**patio-temporal analysis is a key epidemiological tool for

monitoring disease transmission and identifying outbreak hotspots. However, the

patterns of pulmonary tuberculosis (PTB) spread over time and space in

Shijiazhuang remain poorly understood. This study aims to clarify the

spatio-temporal dynamics of PTB transmission in this region.

**METHODS:** We conducted a retrospective study using PTB surveillance data from

2010 to 2023, extracted from the national Tuberculosis Information Management

System. Descriptive epidemiological analysis was conducted to assess the

severity and distribution characteristics of PTB in Shijiazhuang. The Joinpoint

regression model was employed to analyze the annual temporal trends. Spatial

autocorrelation analysis and Space-time scan analysis were utilized to explore

the spatio-temporal clustering characteristics.

**RESULTS:** From 2010 to 2023, a total of 54,855 PTB cases were reported, with an

average annual incidence of 38.97 per 100,000 population. Males, older adults,

and farmers were disproportionately affected. The overall incidence declined

significantly (AAPC = -7.65%, p < 0.05), with a steeper drop between 2010 to

2013 and a more gradual decline thereafter. Spatial analysis revealed persistent

high-high clusters in rural counties such as Lingshou county and Pingshan

county, and low-low clusters in central urban districts. The phased space-time

scan analysis results identified 19 clusters.

**CONCLUSION:** This study reveals a declining PTB incidence in Shijiazhuang, with a

higher burden among males, older adults, and farmers, alongside persistent

spatial clusters in rural areas, particularly in the north. These findings

emphasize the need for targeted interventions and strengthened rural

surveillance to achieve tuberculosis elimination goals.

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**11. Front Microbiol. 2025 Jul 2;16:1609146. doi: 10.3389/fmicb.2025.1609146.**

**eCollection 2025.**

Epidemiology of drug-resistant tuberculosis among hospitalized children with

tuberculosis in southwest China, 2017-2024.

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**BACKGROUND:** To describe the demographic and clinical characteristics of

pediatric tuberculosis (TB) inpatients diagnosed with resistance to any

anti-tuberculosis drug [drug-resistant tuberculosis (DR-TB)] in southwest China.

**METHODS:** Patients aged ≤14 years with clinically diagnosed pediatric TB were

recruited from January 2017 to December 2024 at specialty hospitals in southwest

China based on either etiology or clinical confirmation. Hospitalization records

were extracted for each patient.

**RESULTS:** Among 2,208 pediatric TB patients, 90 (4.08%) had DR-TB. DR-TB cases

had an average age of 10.94 ± 3.52 years, with a male-to-female ratio of 0.76:1.

The highest proportion was in the 10-14-year age group (72.2%), and prevalence

was significantly higher in girls than boys. By disease type, 13.33% had

pulmonary tuberculosis, 5.56% had extrapulmonary tuberculosis (EPTB), and 81.11%

had combined TB. The most common form of EPTB was lymph node TB (30.00%),

followed by pleural TB (20.71%), abdominal TB (19.29%), and TB meningitis

(14.29%). Among the 90 pediatric DR-TB cases, 74.4% were primary patients (with

rifampicin-resistant TB and multidrug-resistant TB accounting for 36.7 and

30.0%, respectively). The Tibetan ethnic group had the highest proportion of

DR-TB cases (63.3%). Over the 8-year period, most pediatric DR-TB cases were

from western Sichuan (including Ganzi, Aba, and Liangshan minority areas), with

the highest number in the Ganzi Tibetan Autonomous Prefecture.

**CONCLUSION:** Pediatric DR-TB in southwest China predominantly affects older

girls, with primary cases representing a high proportion. The western regions of

Sichuan bear a relatively high burden. Public health efforts should prioritize

awareness, screening, and early diagnosis of pediatric DR-TB in high-risk areas

to prevent transmission.

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**12. Transl Lung Cancer Res. 2025 Jun 30;14(6):2272-2280. doi:**

**10.21037/tlcr-2025-450. Epub 2025 Jun 24.**

Research progress on lung cancer complicated with pulmonary tuberculosis: a

narrative review.

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**BACKGROUND AND OBJECTIVE:** Pulmonary tuberculosis (PTB) and lung cancer (LC) are

both serious health threats and have a complex relationship. Research has shown

that tuberculosis (TB) may induce LC through chronic inflammation. TB infection

is also more common in LC patients than in the general population. Patients with

LC and TB have a higher rate of misdiagnosis, missed diagnosis, and a worse

prognosis. Thus, the diagnosis and treatment of patients with LC and TB are

highly challenging. This narrative review aims to provide some information for

clarification on the relationship between LC and TB.

**METHODS:** We searched for retrospective cohort studies, observational studies,

systematic reviews, and meta-analyses published between the database's inception

and 2024 to retrieve relevant articles on TB and LC from the PubMed/MEDLINE

database.

**KEY CONTENT AND FINDINGS:** We outline the latest research on the relationship

between pulmonary TB and LC, potential biological mechanisms, as well as the

co-treatment of TB and the tumor.

**CONCLUSIONS:** Chronic inflammatory stimulation, scar formation, DNA damage,

immune dysfunction, and other mechanisms caused by TB are associated with the

development and progression of LC. LC may also reactivate TB. Currently, there

is no standard diagnosis and treatment plan for co-existent TB and LC. The

fundamental principle of patient management is to balance anti-tumor and anti-TB

treatments based on the patient's physical condition and make comprehensive

intervention decisions.

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**13. Gland Surg. 2025 Jun 30;14(6):1154-1160. doi: 10.21037/gs-2025-19. Epub 2025 Jun 26.**

Thyroid tuberculosis misdiagnosed as papillary thyroid carcinoma under

ultrasound-guided fine-needle aspiration cytology: a case report and literature

review.

Gan L(1), Sun L(2), Zhao J(3), Feng Q(1), Li J(1), Wan Q(1), Meng Q(1), Liu

J(1).

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Medical University, Baoji, China.

**BACKGROUND:** Thyroid tuberculosis is very rare, making diagnosis challenging

without fine-needle aspiration cytology (FNAC) because of its atypical features.

We report a case of thyroid tuberculosis that was misdiagnosed as papillary

thyroid carcinoma (PTC).

**CASE DESCRIPTION:** A 68-year-old woman visited Baoji Central Hospital following

ultrasound (US) performed at another hospital indicated a suspicious malignant

nodule in her thyroid. Physical examination and thyroid US revealed a hard mass

and irregular hypoechoic area in the right lobe, suggesting a possible malignant

lesion. Ultrasound-guided FNAC (US-FNAC) was suspicious for PTC. The patient

subsequently underwent right thyroid lobectomy and isthmusectomy, and

postoperative histopathology revealed an epithelioid granulomatous lesion

without tumor tissue. Meanwhile, postoperative serum testing revealed elevated

TB-γ interferon concentration, and a specific T lymphocyte testing was positive,

indicating a tuberculosis infection. Primary thyroid tuberculosis was ultimately

confirmed. Postoperatively, the patient recovered well after surgery and

received anti-tuberculosis therapy in a tuberculosis hospital for 1 year.

**CONCLUSIONS:** This case reminds us that although thyroid tuberculosis is very

rare, especially when imaging features and FNAC results resemble those of PTC,

the diagnosis of primary thyroid tuberculosis should still be considered, and

serum TB-related indicator testing can aid in diagnosis.

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**14. Infect Drug Resist. 2025 Jul 12;18:3459-3470. doi: 10.2147/IDR.S530067.**

**eCollection 2025.**

Trends in Drug Resistance and Epidemiological Patterns of Tuberculosis in

Elderly Patients in Wenzhou, China (2014-2023).

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

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**PURPOSE:** This study aimed to elucidate the epidemiological features, drug

resistance patterns, and temporal trends among elderly tuberculosis (TB)

patients in Wenzhou, China, from 2014 to 2023, providing insights for targeted

TB control strategies.

**PATIENTS AND METHODS:** Data were extracted from 10,993 TB patients registered in

the Laboratory Information System of Wenzhou Central Hospital and the

Tuberculosis Information Management System of the Chinese Center for Disease

Control and Prevention. Patients were divided into elderly (≥60 years, n=2,727)

and non-elderly (<60 years, n=8,266) groups. Sociodemographic, clinical, and

phenotypic drug susceptibility testing data were analyzed using chi-square

tests. Temporal trends in drug resistance were assessed via Joinpoint regression

to estimate annual percentage changes (APC).

**RESULTS:** The elderly group had higher proportions of males (79.65% vs 69.66%),

Han ethnicity (99.63% vs 96.35%), and lesions involving ≥3 lung fields (42.35%

vs 32.62%), but lower proportions of migrants (20.32% vs 51.20%), urban

residents (41.03% vs 53.41%), employed individuals (8.98% vs 32.91%), and

pulmonary cavitation (46.75% vs 53.54%). The overall drug-resistant tuberculosis

(DR-TB) rate was similar between the elderly and non-elderly groups (20.76% vs

20.30%). However, the elderly group had lower rates of streptomycin (SM)

resistance (11.07% vs 12.62%), rifampicin (RFP) resistance (6.20% vs 8.06%), and

multidrug-resistant tuberculosis (MDR-TB) (5.39% vs 7.10%). From 2014 to 2023,

the overall DR-TB rate among elderly patients decreased from 31.58% to 20.64%

(-34.63%), with a significant decline in MDR-TB (APC of -9.9%). Resistance to

isoniazid (INH) decreased from 2016 to 2023 (APC -4.0%), and RFP resistance

decreased from 2014 to 2021 (APC -10.7%). Significant decreases were also

observed among migrant populations (APC -10.1%, 2014-2020), urban residents (APC

-8.7%, 2014-2021), and unemployed individuals (APC -4.3%, 2014-2023).

**CONCLUSION:** Our study revealed that drug resistance among elderly TB patients in

Wenzhou has decreased over the past decade, particularly for MDR-TB and key

first-line drugs. However, the elderly group still exhibited distinct

epidemiological and drug resistance profiles compared to younger patients. These

findings offer clear suggestions for public health policy-making and clinical

practice, which can help further reduce the burden of tuberculosis and drug

resistance in the elderly population.

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**15. Infect Drug Resist. 2025 Jul 11;18:3505-3509. doi: 10.2147/IDR.S528414.**

**eCollection 2025.**

A Case Report of Pediatric Abdominal Tuberculosis with Intestinal Perforation

Misdiagnosed as Malignancy.

Tong M(1), Ding W(1), Wu H(1), Yuan L(1), Ma X(1), Yang X(1), Wang Y(1), Luo

Y(1)(2).

**Mengyue Tong, Wenrui Ding, Hao Wu, Lijiao Yuan, Xin Ma, Xiaotao Yang, Yanchun Wang\*, Yonghan Luo\***

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**BACKGROUND:** Abdominal tuberculosis (TB) in pediatric patients is a rare but

serious condition that can often be misdiagnosed as malignancy or other

abdominal disorders. Intestinal perforation is a rare and life-threatening

complication that presents significant diagnostic and therapeutic challenges.

**CASE REPORT:** We report a case of a 13-year-old girl from a TB-endemic region who

presented with abdominal distension, weight loss, and vomiting. Initial imaging

revealed a multilocular cystic mass in the abdominal cavity, raising suspicion

of malignancy. Despite negative results from the tuberculin skin test (TST) and

interferon-gamma release assay (IGRA), diagnostic laparoscopy identified severe

intestinal adhesions and multiple perforations. Histopathological examination

confirmed abdominal TB, and Mycobacterium tuberculosis was detected in

peritoneal fluid using Xpert TB-DNA testing. The patient underwent emergency

small bowel ostomy and received intravenous antitubercular therapy along with

broad-spectrum antibiotics due to concurrent bacterial infection. After clinical

improvement, oral anti-TB therapy was initiated, leading to significant

resolution of abdominal pathology.

**CONCLUSION:** This case highlights the diagnostic complexity of pediatric

abdominal TB, particularly when presenting with an abdominal mass complicated by

intestinal perforation. Misleading clinical and imaging findings, along with

negative immunological tests, may delay diagnosis. Clinicians in TB-endemic

regions should maintain a high index of suspicion for TB in cases of unexplained

abdominal masses, especially when routine tests fail to provide a clear

diagnosis.

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**16. Infect Drug Resist. 2025 Jul 11;18:3471-3479. doi: 10.2147/IDR.S515231.**

**eCollection 2025.**

A Novel Nomogram to Differentiate Between Renal Tuberculosis and Nontuberculous

Renal Infection.

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**BACKGROUND:** To build a diagnostic nomogram for differentiating between renal

tuberculosis (RTB) and nontuberculous renal infection.

**METHODS:** Eligible patients were randomly categorized into derivation and

validation cohorts (7:3). Univariate and multivariate regression analyses were

conducted to filter variables and select predictors. Multivariate logistic

regression was employed for model construction and nomogram were used for

visualization. The nomogram was evaluated by Concordance index (C-index),

calibration curves and decision curve analysis (DCA).

**RESULTS:** Overall, 194 patients were included. The derivation and validation

cohorts included 75 and 61 patients and 32 and 26 patients with RTB and

nontuberculous renal infection, respectively. We included previous TB history,

CRP levels, fever, chronic infection and hydronephrosis in the construction of

the nomogram. A nomogram was developed and validated. This nomogram exhibited

good discrimination and calibration. The C-indices of this nomogram in the

derivation and validation cohorts was 0.99 and 0.98 (95% confidence intervals,

0.97-1.00 and 0.96-1.01), respectively. DCA revealed that the proposed nomogram

was useful for the differentiation.

**CONCLUSION:** The nomogram can differentiate between RTB and nontuberculous renal

infection.

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**17. Front Cell Infect Microbiol. 2025 Jun 30;15:1526740. doi:**

**10.3389/fcimb.2025.1526740. eCollection 2025.**

Metabolomics and lipidomics of plasma biomarkers for tuberculosis diagnostics

using UHPLC-HRMS.

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**INTRODUCTION:** Determining metabolic profiles during host-pathogen interactions

is crucial for developing novel diagnostic tests and exploring the mechanisms

underlying infectious diseases. However, the characteristics of the circulating

metabolites and their functions after Mycobacterium tuberculosis infection have

not been fully elucidated. Therefore, this study aimed to identify the

differential metabolites in tuberculosis (TB) patients and explore the

diagnostic value of these metabolites as potential biomarkers.

**METHODS:** Seventy-two TB patients and 78 healthy controls (HCs) were recruited as

the training set, while 30 TB patients and 30 HCs were enrolled as the

independent validation set. Metabolites in plasma samples were analyzed by

high-resolution mass spectrometry. Differential metabolites were screened using

principal component analysis and machine learning algorithms including LASSO,

Random Forest, and XGBoost. The diagnostic accuracy of the core differential

metabolites was evaluated. Pearson correlation analysis was performed.

**RESULT:** The metabolic profiling of TB patients showed significant separation

from that of the HCs. In the training set, 282 metabolites were identified as

differentially expressed in TB patients, with 214 metabolites validated in the

independent validation cohort. KEGG pathway enrichment analysis showed that the

differential metabolites were mainly enriched in lipid metabolism. Seven core

differential metabolites were identified by the three machine learning

algorithms. Receiver operating characteristic analysis revealed that Angiotensin

IV had high accuracy in diagnosing TB.

**CONCLUSION:** These newly identified plasma metabolites are expected to serve as

potentially valuable biomarkers for TB, potentially facilitating the diagnosis

of the disease and enhancing the understanding of its underlying mechanisms.

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**18. Front Cell Infect Microbiol. 2025 Jun 30;15:1600170. doi:**

**10.3389/fcimb.2025.1600170. eCollection 2025.**

Innovo GenMax MTB-RIF/INH: a moderate-complexity automated NAAT for rapid

simultaneous detection of Mycobacterium tuberculosis complex and

rifampin/isoniazid resistance.

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Y(1).

**Xichao Ou, Bing Zhao, Huiwen Zheng, Ruida Xing, Qian Sun, Zhonghua Qin, Lixia Zhang, Kai Cui, Yuanyuan Song, Yang Zheng, Yang Zhou, Shengfen Wang, Hui Xia\*, Yanlin Zhao\***

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**OBJECTIVE:** Given the increase of treatment failure, relapse and acquired

resistance observed in isoniazid (INH) resistance, there is an urgent to improve

rifampin (RIF) -priority based diagnostic strategies. Therefore, we evaluated

the performance of Innovo GenMax MTB-RIF/INH (GenMax), a moderate- complexity

automated nucleic acid amplification test (NAAT), for detecting Mycobacterium

tuberculosis complex (MTBC) and resistance to RIF and INH.

**METHODS:** Analytical sensitivity (limit of detection, LOD) was determined using

serial dilutions of Mycobacterium tuberculosis H37Rv (ATCC 27249) strains.

Diagnostic accuracy was assessed in clinical sputum specimens against

microbiological reference standards (MRS: positive by smear microscopy, culture

or Xpert MTB/RIF for diagnosis of TB) and phenotypic drug susceptibility testing

(DST). Discordant results were resolved by sequencing resistance genes (IS6110,

rpoB, katG, inhA, ahpC) and follow-up diagnosis results.

**RESULTS:** GenMax demonstrated a calculated LOD of 8.8 CFU/mL (95% CI: 7.4-11.4)

for MTBC, 674.1 CFU/mL (95% CI: 578.8-923.5) for RIF resistance, and 747.3

CFU/mL (95% CI: 613.7-1081.3) for INH resistance. In clinical evaluation, the

sensitivity and specificity for MTBC detection were 97.52% (95% CI: 92.38-99.36)

and 93.65% (95% CI: 88.91-96.53), respectively. For RIF and INH resistance,

sensitivities were 88.46% (95% CI: 68.72-96.97) and 85.19% (95% CI:

65.39-95.14), with specificity of 92.42% (95% CI: 82.50-97.18) and 94.12% (95%

CI: 84.86-98.10).

**CONCLUSION:** Innovo GenMax MTB-RIF/INH is a rapid and automated assay with high

sensitivity for MTBC detection, suitable for decentralized settings. While its

performance for RIF/INH resistance detection is competitive with existing

assays, its sensitivity remains gaps relative to WHO targets. Further

optimization, particularly through expanded probe coverage, is needed to bridge

this gap and ensure reliable detection in clinical settings.

Copyright © 2025 Ou, Zhao, Zheng, Xing, Sun, Qin, Zhang, Cui, Song, Zheng, Zhou,

Wang, Xia and Zhao.

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**19. Vaccine. 2025 Jul 12;62:127493. doi: 10.1016/j.vaccine.2025.127493. Online ahead of print.**

Mycobacterium tuberculosis Hsp70 as a cancer vaccine adjuvant: Immunomodulatory

mechanisms and tumor microenvironment remodeling.

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Heat shock proteins (HSPs), particularly the 70 kDa heat shock protein (Hsp70),

are crucial for cellular functions such as protein folding, refolding, and

regulation of protein activity. Mycobacterium tuberculosis Hsp70 (DnaK) has

attracted attention for its potential as a vaccine adjuvant due to its

immunostimulatory properties. This review covers the following topics: an

overview of cancer vaccines, introduction to Hsp70, research on DnaK in

dendritic cells (DCs), DnaK's role in the tumor immune microenvironment, its

safety profile, and insights for vaccine design. DnaK consists of an N-terminal

nucleotide-binding domain and a C-terminal peptide substrate-binding domain,

connected by a flexible linker. It has been shown to enhance DC maturation,

facilitate antigen presentation, and activate T cells. DnaK stimulates Toll-like

receptor 4 (TLR4) and CD40 on antigen-presenting cells, promoting both

maturation and the secretion of pro-inflammatory cytokines. Additionally, DnaK

can enhance antigen presentation through CD91 and DC-SIGN receptors on DCs.

However, the immunosuppressive environment within tumors poses challenges to DC

activation. DnaK may influence this tumor microenvironment by interacting with

macrophages, scavenger receptors, and natural killer (NK) cells, potentially

overcoming some of these barriers. Compared to traditional adjuvants like

lipopolysaccharide (LPS), DnaK has a favorable safety profile. Its conserved

structure and low toxicity make it a promising candidate for vaccine

development. Insights from studies on DnaK suggest strategies to improve vaccine

efficacy, such as combining it with TLR agonists and leveraging its interaction

with DC-SIGN to promote targeted activation of DCs. In conclusion, DnaK shows

significant potential as an adjuvant in vaccine design. Understanding its

structural and functional roles, as well as its effects on the immune

microenvironment, provides valuable insights for the development of more

effective and targeted vaccines against infectious diseases and cancer. Further

research is needed to elucidate its specific mechanisms of action and optimize

its use in vaccine formulations.

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Targeting alveolar macrophages in tuberculosis: Exploiting trained immunity for

novel therapeutic approaches.

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Tuberculosis (TB) is an airborne infectious disease caused by the Mycobacterium

tuberculosis (Mtb) complex organism. Alveolar macrophages (AMs) play key roles

in immune defense, antigen presentation, immune regulation, and immune secretion

during Mtb infection. Notably, AMs exhibit context-dependent dual functions:

protective and pathogenic. This duality is driven by the heterogeneous

composition of AM subsets and their distinct immune profiles. On one hand, they

fight against Mtb through a series of mechanisms to protect the host; on the

other hand, certain AM subsets may provide a permissive niche that facilitates

Mtb survival and persistence. Mtb possesses unique cell surface lipids and

secreted protein effectors that enable it to evade the killing effects of innate

immune cells and preferentially establish an ecological niche within AMs. AMs

not only strengthen their antibacterial capabilities through mechanisms such as

training immune memory, metabolic reprogramming, cytokine production, and

autophagy, but also collaborate with other immune cells to jointly maintain

immune balance within the body. Once this balance is disrupted, tuberculosis

infection may run rampant. Furthermore, this article summarizes the potential

role of different methods for inducing trained immune AMs in the treatment of

tuberculosis, including existing bacille Calmette-Guérin (BCG) vaccination and

emerging strategies such as lipopolysaccharide (LPS)-mediated Toll-like receptor

4 (TLR4) activation and Influenza A virus (IAV)-induced host trained immunity

activation, providing new ideas for the treatment of tuberculosis.

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**ahead of print.**

Integrative Metabolomics and Proteomics Analyses Reveal the Mechanism Underlying

Neurotoxicity of Rifampicin in HT22 Cells.

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Rifampicin is orally administered in the treatment of tuberculosis but is

sometimes accompanied with neurotoxicity. The mechanism behind

rifampicin-induced neurotoxicity remains unclear and need to be further

researched. To systematically explore this mechanism, integrative metabolomic

and proteomic analyses were performed to investigate rifampicin-induced injury

in HT22 cells. HT22 cells were treated with rifampicin at concentrations ranging

from 0-400 μg/mL, and cell viability and apoptosis were assessed. Subsequently,

cells treated with 0 μg/mL and 200 μg/mL rifampicin were collected for mass

spectrometry-based proteomic and metabolomic analyses, serving as the control

group and the rifampicin model group, respectively. Viability and apoptosis data

revealed dose-dependent injury after exposure to rifampicin, with 200 μg/mL

identified as a suitable dose for proteomic and metabolomic studies. In total,

253 proteins and 28 metabolites were shown to be dysregulated. In addition, our

integrated multi-omics analysis highlighted the glutathione metabolism pathway

as a central disrupted pathway in HT22 cells, leading to rifampicin-induced

neurotoxicity. Therefore, more efforts should be paid to explore the mechanism

of glutathione metabolism, and it may be a key therapeutic target for

alleviating rifampicin - induced neurotoxicity.

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Targeted next-generation sequencing for rapid tuberculosis detection: a

systematic review and meta-analysis.

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**BACKGROUND:** Targeted next-generation sequencing (tNGS) is an adjunct tool

endorsed by the World Health Organization (WHO) for tuberculosis diagnosis. The

study aimed to investigate the diagnostic performance of tNGS across different

clinical scenarios (populations, sample and tuberculosis types, and platforms),

which has not been comprehensively evaluated.

**METHODS:** A systematic literature search was conducted in PubMed, MEDLINE, Web of

Science, Wanfang Data, VIP, and CNKI to identify studies published in English

and Chinese from January 1, 2005, to October 14, 2024, that evaluated tNGS for

tuberculosis diagnosis using reference strains and original samples or isolates

from patients with presumptive or confirmed tuberculosis. Included studies were

assessed using the Quality Assessment of Diagnostic Accuracy Studies-2 tool

(QUADAS-2), and diagnostic accuracy was calculated against microbiological

reference standard and composite reference standard. The primary outcomes were

the pooled sensitivity and specificity. This study is registered with PROSPERO

(CRD42024560190).

**RESULTS:** Out of 3,383 records screened, 16 studies comprising 2,565 participants

were included in the meta-analysis. Overall, tNGS demonstrated a pooled

sensitivity of 0.86 (95 % CI, 0.77-0.91) and specificity of 0.95 (0.86-0.99).

The positive and negative likelihood ratios were 18.24 (5.61-59.26) and 0.15

(0.09-0.26). The diagnostic odds ratio and the area under the summary receiver

operating characteristic curve was 120.88 (26.93-542.57) and 0.95 (0.93-0.97),

respectively. The diagnostic performance of tNGS varied substantially depending

on sample type and sequencing platform, where the highest sensitivity was

observed with bronchoalveolar lavage fluid 0.91 (0.75-0.98) and the target

nanopore sequencing platform 0.85 (0.80-0.89). Furthermore, tNGS demonstrated a

significantly higher detection rate compared to GeneXpert MTB/RIF (odds ratio:

1.78 (1.39-2.29); p = 0.01).

**CONCLUSION:** tNGS demonstrates high diagnostic accuracy for tuberculosis, with

its performance influenced by sample type and sequencing platform. These

findings support the optimization of tNGS application in specific clinical

settings to enhance tuberculosis management.

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Clinical and Imaging Findings of Wrist Tuberculosis: A Study of 47 Patients.

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**PURPOSE:** This study aimed to describe the clinical and imaging features of

patients with wrist tuberculosis (TB) and to explore the importance of magnetic

resonance imaging (MRI) in the evaluation and treatment of wrist TB.

**METHODS:** The clinical and imaging data of 47 patients with wrist TB, diagnosed

through a combination of pathological (microbiological culture, polymerase chain

reaction, and histopathological examination) and clinical methods, were

retrospectively analyzed. The demographic characteristics, clinical symptoms,

laboratory tests, and imaging findings of these patients were recorded.

**RESULTS:** The mean age of the patients was 53.9 ± 15.3 years, and the time from

the onset of the patient's symptoms to the diagnosis of wrist TB was 16.2 ± 25.6

months. The main clinical manifestations included wrist pain (100%), wrist

swelling (97.9%), and limited wrist joint movement (89.4%). According to the

X-ray findings, wrist TB was classified into the synovitis stage (stage I, n =

22; 46.8%) and the bone erosion/destruction stage (stage II, n = 25; 53.2%). The

MRI manifestations included bone destruction (87.2%) and synovitis (100%), and

other manifestations included joint space narrowing (44.7%), tendon sheath

involvement (66.0%), abscess formation (42.6%), and rice body formation (12.8%).

Early bone destruction, not seen on plain radiographs (46.8%), was detected by

MRI examination. There was an increase in the proportions of dorsal soft tissue

abscesses and distal radioulnar joint abscesses detected by MRI examination in

stage II patients compared with stage I patients.

**CONCLUSIONS:** MRI can serve as an important adjunct in the diagnosis of wrist TB,

offering valuable insights into bone, joint, and soft tissue involvement that

may not be visible on plain radiographs.

TYPE OF STUDY/LEVEL OF EVIDENCE: Diagnostic IV.

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