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ORIGINAL RESEARCH

Characterization of Drug Resistance Patterns, Mutation Profiles and Prevalence of *Mycobacterium tuberculosis* in Shaoxing

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Objective: This study aimed to analyze drug resistance patterns, mutation profiles in *Mycobacterium tuberculosis* isolates and clinical characteristics of tuberculosis patients in Shaoxing, Zhejiang, China.

Methods: Clinical specimens and data from tuberculosis patients admitted in 2024 were collected. Cultures were established using the MGIT liquid culture system, and drug susceptibility to twelve anti-tuberculosis agents (four first-line and eight second-line) was assessed by the microbroth dilution method. Mutations in the *rpoB* gene, *katG* gene, and *inhA* promoter were identified using a DNA microarray chip assay.

Results: Among 268 *Mycobacterium tuberculosis* isolates, 62 (23.1%) exhibited resistance to at least one anti-tuberculosis drug. These comprised 21 (7.8%) mono-resistant, 25 (9.3%) poly-resistant, and 16 (6.0%) multidrug-resistant strains, including 3 (1.1%) classified as pre-extensively drug-resistant and 1 (0.4%) as extensively drug-resistant. Among rifampicin-resistant isolates, mutations at codons 531 (47.4%) and 526 (21.1%) of the *rpoB* gene were most frequent, while the *katG* Ser315Thr substitution was detected in 44.8% of isoniazid-resistant strains. Compared with primary cases, re-treated patients were more frequently over 50 years of age, exhibited a higher prevalence of pulmonary cavities, and showed significantly elevated rates of drug resistance ($P < 0.05$).

Conclusion: Our findings indicate that although the overall prevalence of drug-resistant tuberculosis in Shaoxing remains low, the resistance patterns are heterogeneous. These results underscore the need for comprehensive drug susceptibility and genetic testing to guide effective treatment strategies.

Keywords: *Mycobacterium tuberculosis*, multidrug resistance, drug sensitivity test, DNA microarray, clinical characteristics

Introduction

Tuberculosis (TB), caused by the *Mycobacterium tuberculosis* complex, remains a major global health challenge and is now the leading cause of mortality from infectious diseases worldwide.[1] According to the World Health Organization (WHO) Global TB Report 2024, an estimated 10.8 million new cases were reported in 2023, corresponding to an incidence of 134 per 100,000 population. In the same year, approximately 400,000 new cases of multidrug- or rifampicin-resistant tuberculosis (MDR/RR-TB) were recorded.[2] In 2023, China reported an estimated 741,000 new TB cases, corresponding to an incidence of 52 per 100,000 population, making it the third-largest contributor to the global TB burden. During the same year, an estimated 29,000 MDR/RR-TB cases were recorded, representing 7.3% of the global total and ranking China fourth worldwide for MDR/RR-TB.[2,3] Drug-resistant tuberculosis (DR-TB) is classified as either primary resistance, arising from direct infection with drug-resistant *Mycobacterium tuberculosis*, or acquired resistance, which emerges during treatment and is largely driven by poor therapeutic outcomes, non-adherence, substandard drug quality, and insufficient infection control.[4,5] The emergence of DR-TB, particularly MDR-TB, pre-extensively drug-resistant (pre-XDR), and extensively drug-resistant (XDR-TB) forms, has markedly undermined treatment success and poses substantial challenges to clinical management. Monitoring DR-TB and tailoring treatment regimens and preventive strategies accordingly are essential to reducing the global TB burden.[6,7] MDR-TB

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remains a critical public health challenge worldwide, threatening the effectiveness of TB control programmes. MDR-TB is defined by resistance to the two first-line drugs, rifampicin (RIF) and isoniazid (INH), and is primarily driven by genetic mutations. Mutations in the *rpoB* gene are detected in 95–99% of RIF-resistant strains, while *katG* mutations account for 60–95% of INH resistance, and *inhA* promoter mutations contribute to 8–43%.[8,9] Molecular diagnostics for *Mycobacterium tuberculosis* (MTB) drug resistance have been widely implemented over the past three decades. As tuberculosis management shifts from standardized regimens toward more personalized approaches, detailed knowledge of drug-resistance patterns in MTB and the clinical profiles of patients are essential to guide clinical decision-making and optimize treatment strategies. Compared to Ningbo and Hangzhou, the research on *Mycobacterium tuberculosis* in Shaoxing remains relatively limited.[10,11] However Shaoxing City Center for Disease Control and Prevention has only analyzed the spatiotemporal distribution of tuberculosis from a prevention and control perspective, lacking comprehensive data on *Mycobacterium tuberculosis* strains and clinical characteristics of affected patients.[12] DNA microarray assays, which integrate PCR and reverse hybridization, enable detection of RIF and INH resistance within six hours, while simultaneously identifying associated mutations in the *rpoB* and *katG* genes and the *inhA* promoter.[13] In many previous studies, many authors have described the detection efficiency of Xpert MTB/RIF, and whole-genome sequencing (WGS) for different samples,[14,15] but there were few comprehensive analysis about DNA microarray assays. Furthermore, DNA microarray assays provide earlier, clearer and more interpretable results for the identification of multidrug-resistant tuberculosis (MDR-TB). Therefore, in this study, we characterized the drug-resistance patterns and mutational profiles of MTB isolates from Shaoxing, Zhejiang, in 2024, and examined the clinical features of affected patients. These insights provide a foundation for optimizing anti-tuberculosis treatment strategies.

Materials and Methods

Study Population and Data Collection

This study was conducted at the Affiliated Hospital of Shaoxing University, the sole designated center for the treatment and research of TB and DR-TB in Shaoxing. The hospital delivers comprehensive care for tuberculosis patients, assesses treatment efficacy in both outpatient and inpatient settings, manages cases with comorbidities, and provides guidance to primary healthcare providers. The hospital also functions as the designated referral center for tuberculosis patients with complications from other institutions. From January to December 2024, samples from inpatients were collected, and demographic and clinical data were retrieved from medical records. Patients were stratified into two groups according to treatment history: new cases and retreatment cases. New cases were defined as individuals with no prior exposure to anti-tuberculosis therapy, those who had received an incomplete course of standardized treatment, or those who had undergone irregular therapy for less than one month. Retreatment cases were defined as patients who had received irregular or inappropriate anti-tuberculosis therapy for at least one month, as well as those with prior treatment failure or relapse.[16]

MTB Culture

All specimens were processed with N-acetyl-L-cysteine–sodium hydroxide (2% NaOH) for digestion and decontamination. Cultures were performed using the BACTEC MGIT 960 automated system (Becton Dickinson, MD, USA) according to the manufacturer's instructions. Positive cultures were confirmed by acid-fast staining with Auramine O and by the SD BIOLINE TB Ag MPT64 rapid test (Standard Diagnostics, Korea).

MTB Drug Susceptibility Testing

Drug susceptibility testing was conducted using the Sensititre™ MTB MYCOTB assay (Thermo Scientific™, TREK Diagnostic Systems, UK) in accordance with the manufacturer's protocol. The 96-well microtiter plates contained isoniazid (INH), rifampicin (RIF), streptomycin (SM), ethambutol (EMB), ofloxacin (OFX), moxifloxacin (MXF), amikacin (AM), kanamycin (KM), rifabutin (RFB), para-aminosalicylic acid (PAS), ethionamide (ETH), and cycloserine (CYC). Briefly, bacterial suspensions were adjusted to a 0.5 McFarland standard in deionized water using an ultrasonic disperser. A 100 µL aliquot was added to Middlebrook 7H9 broth, vortexed for 30s, and 100 µL of the mixture was inoculated into each well of the MIC plate. Plates were sealed and incubated at 35–37 °C for 7–10 days. The *Mycobacterium tuberculosis* reference strain H37Rv (ATCC 27294) was used as a control. Multidrug

resistance (MDR) was defined as resistance to both RIF and INH. Pre-extensively drug-resistant TB (pre-XDR-TB) was defined as MDR-TB with additional resistance to either fluoroquinolones (FQ) or a second-line injectable drug, but not both. Extensively XDR-TB was defined as MDR-TB with resistance to at least one FQ and one injectable agent.[17,18]

DNA Microarray Detection

DNA microarray kits were obtained from CapitalBio Corporation (Beijing, China). The assay employed oligonucleotide probes targeting mutations at codons 511, 513, 526, 531, and 533 of the *rpoB* gene within the RIF resistance-determining region (RRDR) to identify RIF resistance, and additionally screened for mutations at *katG*315 and *inhA*-15 to assess INH resistance.[19] A 10–20 μL bacterial suspension (≥1.0 McFarland) was mixed with 80 μL nucleic acid extraction buffer, vortexed for 10 min, incubated at 95 °C for 5 min, and centrifuged at 12,000 r.p.m. for 1 min. PCR amplification, chip washing, drying, and hybridization were performed according to the manufacturer's protocol, and results were scanned and interpreted using a LuxScan 10K-B microarray scanner. Each sample was analyzed in triplicate. PCR cycling conditions consisted of an initial denaturation at 94 °C for 4 min, followed by 30 cycles of 94 °C for 40s, 56 °C for 50s, and 72 °C for 60s, with a final extension at 72 °C for 10 min.

Statistical Analysis

Comparisons of proportions were assessed using Pearson's chi-square test or Fisher's exact test, with statistical significance defined as $P < 0.05$. All analyses were conducted using SPSS version 24.0 (IBM, Armonk, NY, USA).

Results

Types of Specimen

A total of 268 *Mycobacterium tuberculosis* isolates were recovered from patient specimens. Of these, 112 (41.8%) originated from sputum, 88 (32.8%) from bronchoalveolar lavage fluid, 35 (13.1%) from pleural effusion, 12 (4.5%) from lymph node biopsies, 9 (3.4%) from pus, 4 (1.5%) from urine, 1 (0.4%) each from pericardial and cerebrospinal fluid, and 6 (2.2%) from secretions collected at other anatomical sites.

Resistance Patterns

Of the 268 *Mycobacterium tuberculosis* isolates analyzed, 206 (76.9%) were susceptible to all tested first- and second-line anti-tuberculosis agents, whereas 62 (23.1%) exhibited resistance to at least one drug. Among the resistant isolates, 21 (7.8%) were classified as mono-resistant, 25 (9.3%) as poly-resistant, and 16 (6.0%) as MDR. Among the MDR-TB isolates, 3 (1.1%) were classified as pre-XDR and 1 (0.4%) as XDR (Table 1). The mono-resistant isolates comprised 6 (28.6%) resistant to streptomycin (SM), 4 (19.1%) to INH, 1 (4.8%) to RIF, 3 (14.3%) to EMB, 2 (9.5%) to ETH, and 5 (23.8%) to CYC. Among the poly-resistant isolates, 16 (64.0%) exhibited resistance to two anti-TB drugs, 6 (24.0%) to three drugs, and 3 (12.0%) to four drugs (Table 2). Within the MDR-TB group, 10 (62.5%) were resistant exclusively to first-line agents, 2 (12.5%) pre-XDR strains showed additional resistance to fluoroquinolones (FQs), and the single XDR strain was resistant to all tested drugs (Table 3). Overall, resistance to RIF and INH was observed in 19 (7.1%) and 29 (10.8%) isolates, respectively.

Detection of Mutated Codons in Resistance Genes Using DNA Microarray Chip

Mutational profiles of resistance-associated genes are summarized in Table 4. Among RIF-resistant isolates, 17 (89.5%) harbored mutations within the *rpoB* gene, most frequently at codon 531 (10 isolates, 52.6%) and codon 526 (5 isolates, 26.3%), with one strain exhibiting mutations at both sites. Additional mutations were identified at codons 516 (2 isolates, 10.5%) and 511 (1 isolate, 5.3%), whereas no alterations were detected at codons 513 or 533. Among INH -resistant isolates, 26 (89.7%) carried mutations in either *katG* or the *inhA* promoter. Specifically, 13 isolates (44.8%) exhibited the

Table 1 Distribution of Different Drug Resistance Types

Drug Resistance	Total (n=268)	
	n	%
Any resistance	62	23.13
Monoresistance	21	7.84
Polyresistance	25	9.33
MDR-TB	16	5.97
Pre-XDR–TB	3	1.12
XDR-TB	1	0.37
Unclassified MDR-TB	12	4.48

Table 2 Drug Resistance Profiles of Poly-Resistant Strains

Drug Resistance	Total (n=25)	
	n	%
Resistance to two drugs		
SM+INH	4	16.00
INH+EMB	2	8.00
EMB+CYC	9	36.00
RIF+ETH	1	4.00
Resistance to three drugs		
RIF+RFB+CYC	1	4.00
SM+EMB+ETH	4	16.00
INH+EMB+CYC	1	4.00
Resistance to four or more drugs		
SM+EMB+PAS+CYC	1	4.00
SM+INH+EMB+ETH+CYC	1	4.00
SM+INH+OFX+MXF+ETH	1	4.00

Table 3 Drug Resistance Profiles of MDR-TB

Drug Resistance	Total (n=16)	
	n	%
MDR-TB resistant to first-line or second-line anti-TB drugs		
INH+RIF	4	25.00
INH+RIF+SM	3	18.75
INH+RIF+SM+EMB	3	18.75
INH+RIF+ETH+CYC	1	6.25
INH+RIF+SM+EMB+ETH	1	6.25
Pre-XDR-TB		
INH+RIF+SM+OFX+MXF+PAS+ETH+CYC	1	6.25
INH+RIF+EMB+OFX+MXF+RFB+PAS+ETH+CYC	1	6.25
INH+RIF+SM+EMB+AM+KM+RFB+ETH+CYC	1	6.25
XDR-TB		
INH+RIF+SM+EMB+OFX+MXF+AM+KM+RFB+PAS+ETH+CYC	1	6.25

Table 4 Pattern of Gene Mutations Detected by DNA Microarray Chip Method

Drug Resistance Patterns	Resistance Gene	Mutation Type		No. (%) of Strains
RIF resistance pattern (n=19)	rpoB	511(CTG→CCG)	Leu511Pro	1 (5.26%)
		513(CAA→AAA)	Gln513Lys	–
		513(CAA→CCA)	Gln513Leu	–
		516(GAC→GTC)	Asp516Val	2 (10.53%)
		516(GAC→TAC)	Asp516Tyr	–
		516(GAC→GGC)	Asp516Gly	–
		526(CAC→TAC)	His526Tyr	3 (15.79%)
		526(CAC→GAC)	His526Asp	1 (5.26%)
		526(CAC→CTC)	His526Leu	–
		526(CAC→CGC)	His526Arg	–
		531(TCG→TTG)	Ser531Leu	7 (36.84%)
		531(TCG→TGG)	Ser531Trp	2 (10.53%)
		533(CTG→CCG)	Leu533Pro	–
		526(CAC→GAC), 531(TCG→TTG)	His526Asp, Ser531Leu	1 (5.26%)
INH resistance pattern (n=29)	katG	315(AGC→ACC)	Ser315Thr	13 (44.83%)
		315(AGC→AAC)	Ser315Asn	4 (13.79%)
	inhA	–15(C→T)		7 (24.14%)
	katG+inhA	315(AGC→ACC), –15(C→T)	Ser315Thr, −15 (C→T)	2 (6.90%)

Note: →, mutation direction and site.

Ser315Thr substitution in *katG*, 4 (13.8%) carried the Ser315Asn variant, 7 (24.1%) harbored the –15C→T mutation in the *inhA* promoter, and 2 (6.9%) contained mutations in both *katG* and *inhA*.

Characteristics of TB Patients

A total of 247 new cases and 21 relapse cases of TB were included in the analysis (Table 5). There were no significant differences between new and relapse cases in terms of gender (χ^2=0.143, P=0.705), residence (χ^2=0.104, P=0.747), infection type (χ^2=0.164, P=0.685), underlying disease including COPD (χ^2=0.466, P=0.495), hypertension (χ^2=0.614, P=0.433), diabetes (χ^2=0.446, P=0.504) and hepatitis B (χ^2=1.044, P=0.307), symptoms including cough (χ^2=0.432, P=0.511), low fever (χ^2=0.029, P=0.864), hemoptysis (χ^2=1.598, P=0.206) and night sweat (χ^2=0.053, P=0.819). Relapse cases were more likely than new cases to occur in individuals over 50 years of age (χ^2=7.582, P<0.01), to be associated with pulmonary cavities (χ^2=3.947, P<0.05), and to exhibit higher rates of drug resistance (χ^2=13.124, P<0.01), including MDR-TB (χ^2=27.778, P<0.01), these differences were statistically significant.

Discussion

Drug resistance represents a critical obstacle to TB control, heightening the risk of treatment failure and facilitating ongoing transmission within communities.[20] In newly diagnosed TB cases, drug resistance is most often attributable to direct transmission, whereas in relapse cases it is frequently acquired during treatment. Timely and accurate drug susceptibility testing (DST) is therefore essential to guide regimen optimization and to mitigate the risk of further resistance development.[21,22] In this study, we present, to our knowledge, the first investigation of drug resistance profiles and mutation patterns of MTB strains isolated from TB patients in Shaoxing. The majority of isolates were derived from pulmonary TB cases, whereas only a minority was associated with extrapulmonary disease. Approximately one-quarter of the isolates exhibited resistance to at least one anti-TB drug, with 7.1% resistant to RIF. As a cornerstone of TB therapy, RIF resistance is of particular concern, given that more than 90% of RIF-resistant strains are also resistant to INH.[23,24] In this study, most RIF-resistant isolates were classified as MDR-TB, including pre-XDR and XDR variants. These strains displayed variable resistance to fluoroquinolones (OFX, MXF) and second-line injectable agents (AM, KM), underscoring the challenges they pose to clinical management. Timely and accurate drug susceptibility testing remains essential to guide effective therapy.

Table 5 Demographic and Clinical Characteristics of New and Relapse TB Patients

Characteristics		New Case (n = 247) n (%)	Relapse Case (n=21) n (%)	χ^2	*P*
Demographic characteristics	Male	163 (65.99%)	13 (61.90%)	0.143	0.705
	Age (>50)	111 (44.94%)	16 (76.19%)	7.582	<0.01
	Low weight	140 (56.68%)	17 (80.95%)	4.699	0.030
Residence	Urban	74 (29.96%)	7 (33.33%)	0.104	0.747
	Rural	173 (70.04%)	14 (66.67%)		
Infection type	Pulmonary TB	216 (87.45%)	19 (90.48%)	0.164	0.685
	Extrapulmonary TB	31 (12.55%)	2 (9.52%)		
Underlying disease	COPD	44 (17.81%)	5 (23.81%)	0.466	0.495
	Hypertension	104 (42.11%)	7 (33.33%)	0.614	0.433
	Diabetes	24 (9.72%)	3 (14.29%)	0.446	0.504
	Hepatitis B	4 (1.62%)	1 (4.76%)	1.044	0.307
	Tumor	8 (3.24%)	0	—	—
	HIV	1 (0.40%)	0	—	—
Symptoms	Cough	136 (55.06%)	10 (47.62%)	0.432	0.511
	Low Fever	63 (25.51%)	5 (23.81%)	0.029	0.864
	Hemoptysis	25 (10.12%)	4 (19.05%)	1.598	0.206
	Night sweat	31 (12.55%)	3 (14.29%)	0.053	0.819
Laboratory parameters	Albumin reduction	83 (33.60%)	9 (42.86%)	0.735	0.391
	Leukocytosis	39 (15.79%)	5 (23.81%)	0.907	0.341
Pulmonary CT	Cavity	77 (31.17%)	11 (52.38%)	3.947	<0.05
	Cheese necrotic lesion	34 (13.77%)	6 (28.57%)	3.342	0.068
Resistant phenotype	MDR-TB	7 (2.83%)	6 (28.57%)	27.778	<0.01
	Other resistance types	39 (15.79%)	10 (47.62%)	13.124	<0.01

Conventional phenotypic assays for detecting drug-resistant MTB are limited by the slow growth rate of the organism, often leading to substantial delays. By contrast, DNA microarray–based methods, which target gene mutations underlying resistance, significantly reduced the turnaround time.[13,25] Compared with Xpert MTB/RIF-which detects resistance only to RIF-DNA microarray-based assays enable the simultaneous identification of resistance to both RIF and INH. Although Xpert MTB/RIF provides a short turnaround time for individual samples, its overall throughput is constrained by the instrument's module capacity. In contrast, DNA microarray-based methods offer high throughput and can generate results within six hours.[14] Regarding WGS, while it provides comprehensive genomic information, it requires cultured isolates, incurs high costs, and involves a longer workflow. These factors limit its suitability as a primary diagnostic method in routine clinical settings. By comparison, DNA microarray-based assays are more cost-effective, faster and importantly, can be applied directly to clinical specimens, making them well aligned with the needs of rapid clinical diagnostics.[15] In this study, the most frequent *rpoB* mutation associated with RIF resistance was Ser531Leu. Notably, one isolate carried concurrent mutations at codons 526 and 531. These findings are consistent with previously reported patterns of *rpoB*-mediated resistance.[19] The predominant mutation conferring INH resistance was the *katG* Ser315Thr substitution, a variant previously associated with high-level resistance. Defining the prevalence of *katG* and *inhA* mutations provides clinically relevant insights that can inform the selection of more effective therapeutic regimens. Ethionamide may serve as an effective substitute in cases where resistance is attributable solely to *katG* mutations, whereas high-dose INH may remain a viable therapeutic option for isolates harboring only *inhA* mutations.[26–28] In this study, all 16 MDR-TB strains harbored identifiable gene mutations; however, two RIF-resistant and three INH-resistant isolates exhibited phenotypic resistance in the absence of corresponding mutations at the targeted

loci. This discrepancy suggests the involvement of alternative genetic alterations or additional resistance mechanisms. Previous studies have shown that mutations in the *rpoA* and *rpoC* genes of *Mycobacterium tuberculosis*, which encode the α and β′ subunits of RNA polymerase, may also confer resistance to RIF. These compensatory mutations may play an important role in restoring bacterial fitness and facilitating the emergence and transmission of MDR strains in vivo. For INH resistance, in cases where mutations result in the loss of the *katG* gene encoding the *KatG* catalase–peroxidase, mutations in the promoter region of the *ahpC* gene—which encodes alkyl hydroperoxide reductase C (*AhpC*) with a function similar to *KatG*-can lead to ahpC overexpression, thereby compensating for the loss of *katG* activity.[29,30] In addition, nonspecific resistance may arise through the activity of efflux pumps (eg, Rv3065, Rv1410c). Overexpression of these efflux pumps can reduce the intracellular concentration of antibiotics, preventing the drug from reaching its target and enabling the development of subpopulations exhibiting high-level resistance.[31] Nevertheless, despite their advantages in delivering rapid results that support early initiation of appropriate therapy and help reduce the transmission of drug-resistant strains, DNA microarray–based assays have inherent limitations. Their mutation-detection scope is restricted, and they may fail to identify uncommon mutations or those located outside canonical resistance-associated loci. Moreover, current DNA microarray platforms cannot detect resistance-associated mutations for second-line drugs. These limitations reduce their utility for guiding the treatment of multidrug-resistant *Mycobacterium tuberculosis* and ultimately constrain their broader clinical applicability.[32] Thus, DNA microarray–based assays may serve as a valuable adjunct for the rapid identification of MDR-TB strains, but should be applied in conjunction with conventional drug susceptibility testing to ensure comprehensive resistance profiling.

Unlike most bacterial infections, TB treatment is lengthy and complex, and many patients require retreatment due to treatment failure or relapse. In this study, patients were stratified into two groups: new cases and relapse cases. Overall, no significant differences were observed between the two groups in terms of living environment, clinical symptoms, comorbidities, or diagnostic indicators. However, relapse cases were more frequently observed among individuals over 50 years of age, which may reflect challenges in treatment adherence due to limited supervision. By contrast, younger patients—particularly those under 18 years of age—demonstrated significantly better outcomes. Moreover, the higher prevalence of pulmonary cavities among relapse cases suggests more advanced disease, a finding consistent with previous reports from the region.[33] Importantly, the proportion of drug resistance—including MDR-TB—was significantly higher in relapse cases than in new cases. This may reflect shortcomings in initial treatment, where insufficient consideration of individualized regimens and underlying resistance-associated mutations contributed to the emergence of drug-resistant MTB. Therefore, systematic detection of resistance-associated mutations, coupled with individualized treatment strategies, is essential to curb the emergence and transmission of drug-resistant MTB.

However, some limitations of this study need to be considered. First, the sample size was relatively small, precluding assessment of temporal trends. Second, the genetic analysis was limited to INH- and RIF-resistant strains, without examining resistance determinants in isolates resistant to second-line drugs. Future work will expand the cohort and employ broader detection strategies to provide a more comprehensive understanding of resistance mechanisms.

Conclusion

To our knowledge, this is the first study to characterize drug resistance patterns, mutation profiles of *Mycobacterium tuberculosis*, and associated clinical features in Shaoxing. These findings provide baseline data that may inform regional TB control strategies and guide clinical management. Although the overall prevalence of drug-resistant TB in Shaoxing was relatively low, resistance patterns were heterogeneous. Standardized treatment regimens, under selective pressure, may inadvertently amplify and disseminate resistance, thereby increasing the risk of MDR-TB, pre-XDR-TB and XDR-TB. These findings underscore the need for individualized treatment strategies guided by both drug susceptibility testing and molecular profiling of resistance-associated mutations.

Ethics Approval and Informed Consent

This study complies with the Declaration of Helsinki and was reviewed and approved by the Medical Ethics Committee of the Affiliated Hospital of Shaoxing University (Approval No. 2025-002-01). The study was considered exempt from the requirement of informed consent as no identifiable patient information was collected and it exclusively focused on the

genomic characteristics of bacteria. The need for consent to participate was also waived by the ethics committee that approved our study.

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Author Contributions

All authors made a significant contribution to the work reported, whether that is in the conception, study design, execution, acquisition of data, analysis and interpretation, or in all these areas; took part in drafting, revising or critically reviewing the article; gave final approval of the version to be published; have agreed on the journal to which the article has been submitted; and agree to be accountable for all aspects of the work.

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Disclosure

The authors have no competing interests to declare.

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