



Spectrum of Additional Drug Resistance Among Patients with Rifampicin-Resistant Tuberculosis at a Tertiary Care Teaching Hospital in India: A Retrospective Cohort Study.

Dr. Shrinil V. Motka^{1*}, Dr. Dinesh C. Patel², Dr. Keyur M. Patel³, Dr. Krutesh S. Tripathi⁴, Dr. Amritlal T. Leuva⁵, Dr. Rajesh Makwana⁶, Dr. Meet Shah⁷, Dr. Miloni Trivedi⁸.

¹Senior Resident, Dr. M.K. Shah Medical College and Research Centre, Ahmedabad, Gujarat, India.

^{2,3}Associate Professor, Dr. M.K. Shah Medical College and Research Centre, Ahmedabad, Gujarat, India.

⁴Assistant Professor, Dr. M.K. Shah Medical College and Research Centre, Ahmedabad, Gujarat, India.

⁵Professor, Dr. M.K. Shah Medical College and Research Centre, Ahmedabad, Gujarat, India.

^{6,7,8}Third Year Resident, Dr. M.K. Shah Medical College and Research Centre, Ahmedabad, Gujarat, India.



Correspondence:

Dr. Shrinil V. Motka.

Senior Resident, Dr. M.K. Shah Medical College and Research Centre, Ahmedabad, Gujarat, India.

Email:

shrinilmotka232@gmail.com

Received: 15-03-2026

Revised: 25-04-2026

Accepted: 28-04-2026

Published: 02-05-2026

Abstract

Background: The emergence of multidrug-resistant tuberculosis (MDR-TB) is a threat to the accomplishments of the World Health Organization's (WHO) and India's End TB Strategy. The treatment of MDR-TB is less effective and more toxic when there is additional resistance to second-line drugs which makes the treatment more difficult.

Objective: To analyze the baseline susceptibility pattern and spectrum of additional drug resistance among patients with rifampicin-resistant tuberculosis (RR-TB) at a tertiary care center in Ahmedabad, Gujarat. **Materials and Methods:** A retrospective cohort study was conducted analyzing the records of 79 patients with RR-TB at Dr. M.K. Shah Medical College and Research Centre, Ahmedabad, between February 2022 and January 2026. Data encompassing patient age, gender, disease site categorized as pulmonary TB (PTB) or extrapulmonary TB (EPTB), HIV status and DRTB regimen given. **Results:** Out of 79 RR-TB patients, the majority were males (75.95%), with a mean age of 33 years. Pulmonary TB (PTB) was observed in 69 (87.3%) cases, while extrapulmonary TB (EPTB) accounted for 10 (12.7%) cases. Additional isoniazid resistance was identified in 15 (18.98%) cases. Fluoroquinolone resistance was noted in 23 (29.11%) cases. Within this category, Levofloxacin resistance is observed in 22 (27.84%), high-dose Moxifloxacin resistance is observed in 21 (26.58%) cases and low-dose Moxifloxacin resistance is observed relatively low in only 5 (6.32%) cases. Based on their resistance profiles, 56 (70.8%) of patients were initiated on a longer regimen, whereas 23 (29.1%) received a shorter regimen. **Conclusion:** Additional drug resistance, particularly to isoniazid and fluoroquinolone, remains a significant challenge in the management of RR-TB. Continuous surveillance and universal drug susceptibility testing (DST) are essential to formulate effective, individualized treatment regimens and prevent the amplification of resistance.

Keywords: multidrug-resistant tuberculosis (MDR-TB), rifampicin-resistant tuberculosis (RR-TB), Moxifloxacin, Levofloxacin, Isoniazid, Aminoglycoside.



This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC-BY) license (<http://creativecommons.org/licenses/by/4.0/>).

INTRODUCTION

Tuberculosis (TB) continues to represent a formidable public health challenge globally, and the relentless evolution of drug-resistant tuberculosis (DR-TB) threatens to derail the milestones outlined in the World Health Organization's (WHO) and India's "End TB Strategy". India bears the highest disproportionate burden of the disease, accounting for over a quarter of the global incident TB cases and a significant majority of the global multidrug-resistant TB (MDR-TB) and rifampicin-resistant TB (RR-TB) burden [1]. The transition from susceptible TB to RR-TB fundamentally alters the clinical approach, necessitating regimens that are historically more prolonged, inherently more toxic, and statistically less efficacious.

The programmatic management of RR-TB has evolved significantly, yet it is continuously challenged by the spectrum of additional drug resistance. While rifampicin resistance serves as a primary surrogate marker and operational entry point for MDR-TB treatment pathways, concurrent resistance to other critical first-line agents, such as isoniazid, and pivotal second-line core agents, particularly the fluoroquinolones (levofloxacin and moxifloxacin), drastically narrows therapeutic options [2,3]. Fluoroquinolones form the backbone of modern DR-TB treatment, and the amplification of resistance to these agents is directly correlated with delayed sputum culture conversion, increased relapse rates, and higher mortality. Consequently, the National Tuberculosis Elimination Programme (NTEP) in India has aggressively scaled up universal

Citation: Motka SV, Patel DC, Patel KM, Tripathi KS, Leuva AT, Makwana R, Shah M, Trivedi M. Spectrum of additional drug resistance among patients with rifampicin-resistant tuberculosis at a tertiary care teaching hospital in India: a retrospective cohort study. *Int. J. Med.*, 2026;**8**(5):1-6.

drug susceptibility testing (U-DST) using rapid molecular diagnostics to ensure early detection of these resistance profiles [4].

The current standard of care under the Programmatic Management of Drug-Resistant TB (PMDT) guidelines mandates tailoring treatment based on baseline resistance patterns. Patients are carefully triaged into either shorter, all-oral bedaquiline-containing regimens or longer, individualized regimens depending on their exposure history and the presence of additional fluoroquinolone or comprehensive baseline resistance [5]. However, the success of these standardized programmatic regimens relies heavily on accurate, localized epidemiological data. The resistance prevalence is not uniform across the Indian subcontinent; varying regional prescribing practices, patient compliance rates, and infection control measures create distinct geographical micro-epidemics of complex resistance patterns [6].

Despite national-level aggregate data, there is a critical need for granular, institution-level insights into the molecular epidemiology of DR-TB to guide empirical clinical decision-making. Tertiary care teaching hospitals serve as nodal referral centers for complex, treatment-experienced cases, providing a vital snapshot of the evolving resistance landscape. Therefore, this retrospective cohort study aims to systematically analyze the baseline susceptibility patterns and the specific spectrum of additional drug resistance primarily against isoniazid and fluoroquinolones among patients diagnosed with RR-TB at a tertiary care center in Ahmedabad, Gujarat. By mapping these resistance profiles to subsequent regimen allocation, this study seeks to underscore the critical necessity of comprehensive baseline DST in optimizing individualized therapy and mitigating the downstream amplification of extensively drug-resistant phenotypes.

MATERIALS AND METHODS

Study Design and Setting: -

A retrospective cohort study was conducted at Dr. M.K. Shah Medical College and Research Centre, Ahmedabad, Gujarat, India. The study evaluated patient data from February 2022 to January 2026. Data for this study was obtained from routinely maintained programmatic records under NTEP.

Participants and Case definition: -

All patients diagnosed with Rifampicin resistant tuberculosis (RR-TB) at Dr. M.K. Shah Medical College and Research Centre, Ahmedabad, Gujarat, India between February 2022 to January 2026.

- Rifampicin-Resistant Tuberculosis (RR-TB): A TB patient, whose biological specimen is resistant to R, detected using phenotypic or genotypic methods, with or without resistance to other anti-TB drugs. It includes any resistance to R, in the form of mono-resistance, poly-resistance, MDR or XDR.
- Multidrug-Resistant Tuberculosis (MDR-TB): A TB patient, whose biological specimen is resistant to both H and R with or without resistance to other first-line anti-TB drugs. MDR-TB patients may have additional resistance to any/all FQ or any other anti-TB drug.
- Pre-XDR Tuberculosis (Pre-XDR TB): TB caused by *Mycobacterium tuberculosis* strains that fulfil the definition of MDR/RR-TB and are also resistant to any fluoroquinolone.
- Extensively Drug-Resistant Tuberculosis (XDR-TB): RR/MDR-TB with additional resistance to at least one fluoroquinolone and at least one Group A drug (bedaquiline or linezolid), as per updated WHO definitions.

Variables: -

Data encompassing patient age, gender, disease site categorized as pulmonary TB (PTB) or extrapulmonary TB (EPTB), HIV status and DRTB regimen given.

Outcome: -

The primary outcome was the identification of additional drug resistance beyond rifampicin such as isoniazid (HR), levofloxacin (Lfx), moxifloxacin (Mfx), aminoglycoside (Am) was recorded. Based on the DST profiles and clinical assessment, patients were allocated to either a shorter regimen or a longer regimen as per NTEP guidelines. .

RESULTS

Demographic and characteristics

The study cohort comprised 79 RR-TB patients out of which 60 (75.95%) are male and 19 (24.05%) are female. The age ranging from 12 to 80 years with mean age is 33 years. For overall population most common age group is 16-20 years (n=13) for overall population, 26-30 years (n=10) for male group, 16-20 years and 20-15 years (n=4) for female group. Regarding the anatomical site of disease, pulmonary TB was the most prevalent manifestation, affecting 69 patients (87.3%), whereas 10 patients (12.7%) presented with extrapulmonary TB, including spinal and lymph node localizations. Only 1 (1.26%) patient having HIV positivity status.

Resistance pattern: -

Incidence of individual drug's resistance given below:

Table 1:- Shows incidence of individual drug's resistance.

Drug	Total (n=79)	Male (n=60)	Female(n=19)
Isoniazid (Total)	15 (18.98%)	10 (12.65%)	5 (6.32%)
High dose isoniazid (katG)	13 (16.45%)	9 (11.39%)	4 (5.06%)
Low dose isoniazid (inhA)	2 (2.53%)	1 (1.26%)	1 (1.26%)
Fluroquinolone (Total)	23 (29.11%)	18 (22.78%)	5 (6.32%)
Levofloxacin	22 (27.84%)	17 (21.51%)	5 (6.32%)
High dose moxifloxacin (Mfx _{high})	21 (26.58%)	17 (21.51%)	4 (5.06%)
Low dose moxifloxacin (Mfx _{low})	5 (6.32%)	3 (3.79%)	2 (2.53%)
Aminoglycoside	4 (5.06%)	2 (2.53%)	2 (2.53%)

- Isoniazid Resistance: Total Isoniazid resistance is observed in 15 (18.98%) of the cohort. The data indicates that high-dose isoniazid resistance associated with the katG mutation is the primary driver, accounting for 13 (16.45%) of cases, whereas low-dose isoniazid resistance from the inhA mutation is present in only 2 (2.53%) of cases. Males account for 10 (12.65%) of the total resistance, doubling the female rate of 5 (6.32%). None of the patient having both katG and inhA mutation simultaneously.
- Fluoroquinolone Resistance: This drug class demonstrates the highest overall incidence of resistance, affecting 23 (29.11%) cases of the total study population. It is predominantly seen in 18 (22.78%) males compared to 5 (6.32%) females. Within this category, levofloxacin resistance is observed in 22 (27.84%) cases and high-dose Moxifloxacin resistance is observed in 21 (26.58%) cases which are the most prevalent,
- while low-dose Moxifloxacin resistance is observed relatively low in only 5(6.32%) cases.
- Aminoglycoside Resistance: This represents the lowest incidence among the evaluated drugs, affecting only 4 (5.06%) patients of the total group. The resistance pattern for Aminoglycosides is distributed equally between males 2 (2.53%) and females 2 (2.53%).

Out of 79 patients, 23 (29.11%) patients having Pre-XDR-TB (R + FQ resistance) and 15 (18.98%) patients having MDR-TB (R + H ± FQ resistance). 21 patients having both Lfx and Mfx resistance. Out of which 20 patients having Lfx + Mfx_(low) resistance, 5 patients having Lfx + Mfx_(High) resistance, 4 patients having Lfx + Mfx_(low) + Mfx_(High) resistance.

Table 2:- Shows spectrum of multiple Drug resistance. R-Rifampicin, H-Isoniazide, Lfx-Levofloxacin, Mfx-Moxifloxacin, Am-Aminoglycoside. High- High dose, Low- Low dose.

Spectrum	Pattern	Total (n=79)	Male (n=60)	Female (n=19)
2 kinds of resistance drugs	R + H (KatG)	6 (7.59%)	4 (5.06%)	2 (2.53%)
	R + H (inhA)	2 (2.53%)	1 (1.26%)	1 (1.26%)
	R + Am	1 (1.26%)	0 (0%)	1 (1.26%)
	R + Lfx	1 (1.26%)	1 (1.26%)	0 (0%)
	R + Mfx (low)	1 (1.26%)	0 (0%)	1 (1.26%)
3 kinds of resistance drugs	R + Lfx + Mfx (low)	7 (8.86%)	6 (7.59%)	1 (1.26%)
	R + Lfx + Mfx (high)	1 (1.26%)	0 (0%)	1 (1.26%)
4 kinds of resistance drugs	R + H (KatG) + Lfx + Mfx (low)	5 (6.32%)	5 (6.32%)	2 (2.53%)
	R + Am + Lfx + Mfx (low)	2 (2.53%)	2 (2.53%)	0 (0%)
	R + Lfx + Mfx (low) + Mfx (high)	3 (3.79%)	3 (3.79%)	0 (0%)
5 kinds of resistance drugs	R + Am + Lfx + Mfx (low) + Mfx (high)	1 (1.26%)	0 (0%)	1 (1.26%)

DISCUSSION

Demographic Profile and Overall Cohort Characteristics

The present retrospective cohort study analyzed 79 laboratory-confirmed rifampicin-resistant tuberculosis (RR-TB) patients at a tertiary care teaching hospital in Ahmedabad, Gujarat, between February 2022 and January 2026. The cohort exhibited a distinct male predominance, with males constituting 75.95% of the study population. This finding is consistent

Citation: Motka SV, Patel DC, Patel KM, Tripathi KS, Leuva AT, Makwana R, Shah M, Trivedi M. Spectrum of additional drug resistance among patients with rifampicin-resistant tuberculosis at a tertiary care teaching hospital in India: a retrospective cohort study. *Int. J. Med.*, 2026;**8**(5):1-6.

with global and national epidemiological patterns of drug-resistant TB. Wang et al., in their three-year retrospective study from Fuyang City, China, similarly reported that 74.59% of their 181 drug-resistant TB (DR-TB) patients were male [7]. This may be attributed to greater occupational exposure, higher rates of tobacco and alcohol use, increased social mobility facilitating transmission, and a tendency toward delayed health-seeking behavior among male patients. The WHO Global Tuberculosis Report 2024 further corroborates that males bear a disproportionately higher TB burden across virtually all high-incidence nations [8]. The mean age of the present cohort was 33 years, with the highest case burden observed in the 16–20 years age group, indicating that the disease predominantly affects the economically productive younger population. Pulmonary TB (PTB) was the predominant disease manifestation, accounting for 87.3% of cases, while extrapulmonary TB (EPTB) constituted 12.7%. HIV co-infection was documented in only 1 patient (1.26). The relatively low HIV prevalence in our cohort is consistent with the national average, which is substantially lower than regions in Africa where HIV-TB co-infection dramatically amplifies drug-resistant TB transmission and worsens treatment outcomes [8].

Additional Isoniazid Resistance and Mutation Profile

Additional isoniazid (INH) resistance beyond rifampicin was identified in 15 patients (18.98%). The First National Anti-Tuberculosis Drug Resistance Survey (NDRS) of India reported that a high proportion of RR-TB patients were simultaneously resistant to isoniazid [9]. The comparatively modest H co-resistance rate of 18.98% observed in the present study may reflect earlier detection of RR-TB through implementation of universal drug susceptibility testing (U-DST) via GeneXpert MTB/RIF and line probe assays, potentially capturing patients at an earlier stage of resistance evolution before additional acquired mutations have accumulated.

Among the H-resistant cases, resistance mediated by the *katG* mutation (high-dose H resistance) was the predominant mechanism, accounting for 13 of 15 cases (86.67%), while *inhA* mutation-mediated low-dose INH resistance was identified in only 2 cases (13.33%). This distribution is clinically significant: *inhA* mutations retain a degree of susceptibility to high-dose isoniazid, potentially allowing its inclusion in optimized regimens, whereas *katG* mutations confer higher-level resistance that effectively precludes clinical utility of isoniazid at any dose. The preponderance of *katG* mutations in drug-resistant TB cohorts from India has been consistently documented in molecular epidemiological studies and aligns with global patterns where *katG* codon 315 substitutions are the dominant resistance determinants [10].

Fluoroquinolone Resistance: Prevalence and Comparison with Published Literature

Fluoroquinolone (FQ) resistance was the most prevalent form of additional resistance in this cohort, affecting 23 of 79 patients (29.11%). This is a critical finding, as fluoroquinolones specifically levofloxacin and moxifloxacin form the irreplaceable backbone of all contemporary DR-TB regimens, including the WHO-recommended shorter all-oral bedaquiline-containing regimen and the longer regimen [11]. Resistance to fluoroquinolones not only narrows therapeutic options but is also independently associated with significantly worsened treatment outcomes, including lower sputum culture conversion rates, higher relapse rates, and increased mortality in MDR-TB patients [12].

The FQ resistance rate of 29.11% in the present study is substantially higher than Suresh et al., in a large cross-sectional study of 833 MDR/RR-TB isolates from the IRL at Visakhapatnam, Andhra Pradesh, which reported additional FQ resistance in 14.2% of isolates [13]. In contrast, Sidiq et al., studying 374 MDR/RR-TB isolates at the New Delhi Tuberculosis Centre (NDTC), found levofloxacin resistance in 33.9% and moxifloxacin resistance (at 0.5 µg/mL) in 22.91% of isolates [14] figures more comparable to those observed in the present study. Studies from other Indian reference laboratories have reported FQ resistance among MDR-TB isolates ranging from 16.1% in Tamil Nadu and 17.1% in Kerala to 31% in Delhi and 33% in Karnataka [13], highlighting considerable inter-regional heterogeneity.

At the national level, the NDRS 2018 of India documented additional FQ resistance among MDR-TB patients at 21.82% [9]. The 29.11% rate in the present study exceeds both these benchmarks.

In the international context, Ahmad et al. reported ofloxacin resistance in 52.7% of 243 MDR-TB patients at a programmatic management unit in Peshawar, Pakistan substantially higher than the present cohort's FQ resistance rate [12]. A meta-analysis cited by both Ahmad et al. and Suresh et al. demonstrated a threefold greater risk of FQ resistance in TB patients exposed to FQ before TB diagnosis [12].

Levofloxacin versus Moxifloxacin Resistance: Differential Resistance Patterns

Within the FQ-resistant subgroup, levofloxacin resistance was documented in 22 patients (27.84%), while high-dose moxifloxacin resistance was noted in 21 patients (26.58%). Resistance at the low-dose moxifloxacin concentration was comparatively limited, affecting only 5 patients (6.32%). As Suresh et al. highlighted, moxifloxacin is active against strains with low-level resistance and can reduce mortality when administered at high doses, while retaining some bactericidal activity even with intermediate resistance (MIC 2.0 µg/mL) when combined with other second-line drugs [13]. The current WHO recommendation supports the use of moxifloxacin when there is resistance to earlier-generation fluoroquinolones such as ofloxacin, given its superior pharmacokinetic profile and enhanced antimycobacterial potency compared to first

Citation: Motka SV, Patel DC, Patel KM, Tripathi KS, Leuva AT, Makwana R, Shah M, Trivedi M. Spectrum of additional drug resistance among patients with rifampicin-resistant tuberculosis at a tertiary care teaching hospital in India: a retrospective cohort study. *Int. J. Med.*, 2026;**8**(5):1-6.

and second-generation FQs [11]. The present data shows that high-dose moxifloxacin resistance (26.58%) is only marginally lower than levofloxacin resistance (27.84%) while low-dose resistance (6.32%) is considerably less prevalent. This supports the rationale for routinely testing moxifloxacin at two concentrations in DST algorithms to preserve treatment options for a subset of patients who might otherwise be denied a potentially active drug.

Cross-Resistance Among Fluoroquinolones

A high degree of cross-resistance between levofloxacin and moxifloxacin was observed in this cohort. Of the 23 FQ-resistant patients, 21 demonstrated concurrent resistance to both levofloxacin and high-dose moxifloxacin, indicating that levofloxacin resistance reliably predicts high-dose moxifloxacin resistance in the majority of cases. This cross-resistance phenomenon is mechanistically well-established: FQ resistance in *M. tuberculosis* is predominantly mediated by mutations in the *gyrA* and *gyrB* genes encoding DNA gyrase subunits A and B, respectively. Specific *gyrA* mutations, particularly at codons 90 and 94, impair fluoroquinolone binding to the DNA gyrase complex, simultaneously reducing susceptibility across the entire fluoroquinolone class due to shared active site interactions [14]. This observation is consistent with findings by Sidiq et al., who reported that 85 of 127 (66.9%) levofloxacin-resistant strains were also resistant to moxifloxacin at 0.5 µg/mL, confirming the high frequency of cross-resistance between FQ class members [14]. Suresh et al. similarly observed that 89.8% of ofloxacin-resistant MDR-TB isolates were co-resistant to levofloxacin in their series [13]. Moxifloxacin monoresistance is not observed in the present study.

Pre-XDR-TB Burden and Implications for Regimen Allocation

Pre-XDR-TB, are identified in 23 patients (29.11%) in the present study. In the Sidiq et al. Delhi study, pre-XDR-TB of the FQ-type constituted 28.87% of MDR/RR-TB isolates [14], a proportion strikingly concordant with the 29.11% observed here. This convergence between a northern Indian reference laboratory cohort (Delhi) and the present western Indian tertiary center cohort (Ahmedabad) suggests that a comparable burden of pre-XDR-TB across geographically distinct Indian cohorts.

The direct consequence of the high FQ resistance prevalence was reflected in the treatment allocation pattern of this cohort: 56 patients (70.8%) required placement on the longer individualized regimen, while only 23 patients (29.1%) were eligible for the shorter all-oral regimen. Suresh et al. cited a study from Uttar Pradesh where FQ resistance was detected in 58.4% of MDR-TB patients by second-line LPA, rendering those patients ineligible for the shorter regimen [13].

Aminoglycoside Resistance

Aminoglycoside resistance was identified in 4 patients (5.06%), representing the lowest additional resistance rate. This is broadly consistent with patterns reported in comparable Indian studies. Sidiq et al. from New Delhi documented kanamycin resistance in 4.8% and capreomycin resistance in 6.4% of 374 MDR/RR-TB isolates [14]. Similarly, Suresh et al. from Andhra Pradesh found injectable second-line drug resistance to be substantially lower than FQ resistance in their series [13].

Drivers of Fluoroquinolone Resistance in Clinical Settings

Empirical prescription of fluoroquinolones for community-acquired pneumonia, acute exacerbations of chronic obstructive pulmonary disease, urinary tract infections, and undifferentiated febrile respiratory illnesses before TB diagnosis is confirmed represents a critical mechanism for the selective acquisition of FQ resistance in latent or undiagnosed TB patients. As cited by both Ahmad et al. and Suresh et al., a widely referenced meta-analysis demonstrated a threefold greater risk of FQ resistance in TB patients exposed to fluoroquinolones prior to TB diagnosis [12]. Ahmad et al., in their multivariate logistic regression analysis, identified previous TB treatment at private sector healthcare facilities (OR = 1.953, *p* = 0.034) as an independent predictor of ofloxacin resistance, attributing this association to frequent prescription of FQ for misdiagnosed respiratory infections and inadequate adherence to TB treatment protocols in non-programmatic settings [12].

In the present study, prior treatment history and FQ exposure data were not systematically available due to the retrospective design, representing a recognized limitation.

Importance of Universal Drug Susceptibility Testing

The findings of this study affirm the critical necessity of U-DST with mutation-level characterization for all RR-TB patients. The heterogeneity in resistance profiles documented in this cohort encompassing diverse patterns of RR-TB with various combinations of isoniazid, levofloxacin, moxifloxacin (at low and high concentrations), and aminoglycoside resistance demonstrates unequivocally that no single standardized empirical regimen can adequately address the treatment needs of all RR-TB patients. Suresh et al. similarly emphasized that knowledge of individual FQ drug resistance patterns prior to treatment initiation is essential to institute appropriate treatment regimens, avoid XDR-TB amplification through inadvertent FQ monotherapy, and prevent community transmission of extensively resistant strains [13]. Wang et al. in their

Citation: Motka SV, Patel DC, Patel KM, Tripathi KS, Leuva AT, Makwana R, Shah M, Trivedi M. Spectrum of additional drug resistance among patients with rifampicin-resistant tuberculosis at a tertiary care teaching hospital in India: a retrospective cohort study. *Int. J. Med.*, 2026;**8**(5):1-6.

Chinese cohort documented 33 distinct drug resistance profiles among 74 MDR-TB patients, with resistance to as many as 12 anti-TB drugs in individual cases, powerfully illustrating the complexity and heterogeneity of resistance profiles in tertiary referral centre cohorts [7]. The identification of 5 patients (6.32%) with low-dose moxifloxacin resistance but preserved high-dose susceptibility opens the possibility of high-dose moxifloxacin inclusion in otherwise limited regimens for these patients, a practice supported by pharmacokinetic modeling and clinical outcome data reviewed by Suresh et al. [13]. Similarly, the differentiation between katG and inhA mutations for isoniazid resistance provides actionable therapeutic information. Comprehensive baseline DST is thus not merely a diagnostic formality but a foundational determinant of individualized treatment quality and outcome.

Limitations

Several limitations of this study warrant acknowledgment. First, the retrospective design and single-centre setting limit the generalizability of findings to the broader RR-TB patient population in Gujarat or India. Second, complete treatment outcome data were not systematically captured, precluding analysis of the relationship between baseline resistance profiles and clinical treatment outcomes. Third, comprehensive prior treatment history and FQ exposure data were not routinely available in the medical records due to the retrospective nature of data collection, limiting the ability to characterize predictors of FQ resistance in this cohort. Notwithstanding these limitations, the study provides valuable institution-level epidemiological data that can directly inform local empirical treatment guidelines and reinforce the critical role of U-DST in optimizing individualized DR-TB management.

CONCLUSION

In conclusion, this study demonstrates that additional drug resistance particularly to fluoroquinolones constitutes a major and growing challenge in RR-TB management. The FQ resistance rate of 29.11%, with high cross-resistance concordance between levofloxacin and moxifloxacin, significantly constrains eligibility for the shorter all-oral regimen and necessitates individualized longer regimens for the majority of patients. The predominance of katG-mediated high-dose isoniazid resistance and the relatively low aminoglycoside resistance rate are also of clinical and programmatic relevance.

REFERENCES

1. World Health Organization. Global Tuberculosis Report 2024. Geneva: World Health Organization; 2024.
2. Udawadia ZF, Amale PT, Mullerpattan JB. The epidemiology of drug-resistant tuberculosis in India. *Infectious Disease Clinics of North America*. 2019;33(4):1063-1077.
3. Mase SR, Chorba T, Parks S, et al. Bedaquiline for the treatment of multidrug-resistant tuberculosis in the United States. *Clinical Infectious Diseases*. 2020;71(4):1010-1016.
4. Central TB Division, Ministry of Health and Family Welfare, Government of India. National Guidelines for Programmatic Management of Drug-Resistant Tuberculosis in India (PMDT Guidelines). New Delhi: Central TB Division; 2021.
5. Dholakia Y, Danawala Z, et al. Fluoroquinolone resistance in multidrug-resistant tuberculosis patients in Western India: Clinical implications and treatment outcomes. *Journal of Clinical Tuberculosis and Other Mycobacterial Diseases*. 2022;27:100310.
6. Sharma SK, Ryan H, Khaparde S, et al. Index-TB guidelines: Guidelines on extrapulmonary tuberculosis for India. *The Indian Journal of Medical Research*. 2017;145(4):448-463.
7. Wang W, Gao Y, Gao Y, Li T, Liu Y, Wang X, Fang X, Ding Y. Patterns of drug resistance and treatment outcomes in drug-resistant tuberculosis patients in Fuyang City: a three-year retrospective study. *Infect Drug Resist*. 2026;19:582909. doi:10.2147/IDR.S582909. (1)
8. World Health Organization. Global Tuberculosis Report 2024. Geneva: World Health Organization; 2024. (2)
9. Ministry of Health and Family Welfare, Government of India. Report of the First National Anti-Tuberculosis Drug Resistance Survey India 2014–16. New Delhi: Central TB Division; 2018. (3)
10. Zhao Y, Xu S, Wang L, Chin DP, Wang S, Jiang G, et al. National survey of drug-resistant tuberculosis in China. *N Engl J Med*. 2012;366(23):2161–2170. doi:10.1056/NEJMoa1108789. (4)
11. World Health Organization. WHO Consolidated Guidelines on Tuberculosis: Module 4: Treatment Drug-Resistant Tuberculosis Treatment. Geneva: World Health Organization; 2022. (5)
12. Ahmad N, Javadi A, Syed Sulaiman SA, Ming LC, Ahmad I, Khan AH. Resistance patterns, prevalence, and predictors of fluoroquinolones resistance in multidrug resistant tuberculosis patients. *Braz J Infect Dis*. 2016;20(1):41–47. doi:10.1016/j.bjid.2015.09.011. (6)
13. Suresh K, Vimala Y, Mohan N, Padmaja JJ. Additional resistance to any fluoroquinolones among multidrug-resistant Mycobacterium tuberculosis isolates from North Coastal Andhra Pradesh, India. *J Pure Appl Microbiol*. 2021;15(1):68–74. doi:10.22207/JPAM.15.1.01. (7)
14. Sidiq Z, Hanif M, Chopra KK, Khanna A, Jadhav I, Dwivedi KK. Second-line drug susceptibilities of multidrug- and rifampicin-resistant Mycobacterium tuberculosis isolates in Delhi. *Biomed Biotechnol Res J*. 2019;3:87–91. doi:10.4103/bbrj.bbrj_53_19. (8).