



SPECTRUM AND ANTIMICROBIAL SUSCEPTIBILITY PATTERN OF SECONDARY BACTERIAL INFECTIONS IN EXTRAPULMONARY TUBERCULOSIS: A CROSS-SECTIONAL OBSERVATIONAL STUDY

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ABSTRACT

Background: Extrapulmonary tuberculosis (EPTB) is a significant contributor to global morbidity. Secondary bacterial infections complicating EPTB lesions are understudied but can alter disease progression, delay clinical recovery, and accelerate antimicrobial resistance.

Aim & Objectives: To determine the burden, bacterial spectrum, and antimicrobial susceptibility patterns of secondary bacterial infections in patients with EPTB, and to identify associated host-related factors.

Methods: A hospital-based cross-sectional observational study was conducted at the Microbiology Laboratory of CRGH Hospital and Ruxmani Ben Deep Chand Gardi Medical College, Ujjain, India, from March 2023 to July 2025. Clinical samples (pus, pleural fluid, and tissue biopsies) from 67 EPTB patients were analyzed using standard phenotypic microbiological and antimicrobial susceptibility testing (AST) methods. Statistical associations were evaluated using Fisher's exact test.

Results: Secondary bacterial infections were confirmed in 7 of 67 patients (10.4%; 95% CI: 5.2–20.0%). The isolated pathogens were *Klebsiella pneumoniae* (n=3; 42.8%), *Pseudomonas aeruginosa* (n=2; 28.6%), and *Staphylococcus aureus* (n=2; 28.6%). Most isolates were recovered from pus samples (n=5; 8% of total pus specimens). All three *K. pneumoniae* isolates were multidrug-resistant (MDR, 100%), including one extensively drug-resistant (XDR, 33.3%) strain and two extended-spectrum β -lactamase (ESBL) producers (66.6%). Both *S. aureus* isolates were confirmed as methicillin-resistant *S. aureus* (MRSA) and were MDR (100%). Conversely, *P. aeruginosa* isolates remained fully susceptible to core anti-pseudomonal agents. No statistically significant associations were found between infection status and age, gender, behavioral habits, or comorbidities, though higher rates were observed in patients aged 45–60 years, diabetics, and chronic kidney disease (CKD) patients.

Conclusion: Secondary bacterial infections in EPTB are heavily dominated by highly resistant opportunistic pathogens like MRSA and ESBL/MDR *K. pneumoniae*. Routine microbiological surveillance and targeted antimicrobial stewardship are vital to optimizing therapeutic outcomes in EPTB co-infections.

Keywords: Extrapulmonary Tuberculosis, Secondary Bacterial Infection, Antimicrobial Resistance, Multidrug-Resistant Bacteria (MDR), Extensive Drug Resistant (XDR), Extended-Spectrum B-Lactamase (ESBL).

INTRODUCTION

Tuberculosis (TB) remains a dominant global public health threat. In 2024, an estimated 10.8 million individuals contracted TB globally, with India bearing the highest national burden⁽¹⁾.



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Extrapulmonary tuberculosis (EPTB) accounts for approximately 15% to 24% of all TB cases in India, with an elevated prevalence observed in immunocompromised individuals⁽²⁾. Managing EPTB poses distinct clinical dilemmas, including atypical clinical presentations, lower sensitivity of standard diagnostic tools, and delayed microbiological confirmation^(2, 3).

Secondary bacterial infections are an emerging, yet poorly characterized, complication in TB management. Co-pathogens can exacerbate tissue damage, mimic or mask progressive tubercular

lesions, prolong clinical recovery, and increase overall morbidity^(4, 5). While secondary respiratory bacterial co-infection rates in pulmonary TB are well-documented to hover between 10% and 15%—frequently involving *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Staphylococcus aureus*—corresponding data for EPTB remains remarkably scarce^(5, 6).

Host-related clinical and behavioral vulnerabilities heavily dictate susceptibility to both TB progression and secondary infections. Behavioral factors such as smoking and alcohol abuse compromise innate local tissue defenses and systemic immune responses^(7-9, 22). Metabolic and systemic disorders like Diabetes mellitus, HIV/AIDS, chronic liver disease, and chronic kidney disease (CKD) significantly impair cell-mediated immunity, increasing the risks of opportunistic bacterial invasion^(8-11, 16, 17).

Compounding this problem is the global surge in multidrug-resistant (MDR), extensively drug-resistant (XDR), and extended-spectrum β -lactamase (ESBL)-producing bacteria⁽¹²⁾. In resource-limited settings where empirical broad-spectrum antibiotic treatment is common, the absence of guided culture-based therapy drives poor clinical outcomes and accelerates resistance. Given the scarcity of data on secondary co-infections within EPTB lesions in India, this study investigated the demographic, behavioral, and clinical risk factors, alongside the phenotypic and antimicrobial susceptibility profiles of secondary bacterial isolates among EPTB patients^(4, 12).

MATERIALS AND METHODS

Study Design and Setting

This hospital-based cross-sectional observational study was conducted in the Department of Microbiology at R. D. Gardi Medical College and C.R.G. Hospital, Ujjain, Madhya Pradesh, India. The study duration spanned from March 2023 to July 2025. Institutional Ethical Committee approval was secured prior to initiation (IEC Ref. No: 02/2023).

Sample Size and Selection Criteria

Based on historical data by Shaddock et al., the assumed prevalence (P) of secondary bacterial infections among TB-positive cases was estimated at 36%⁽¹³⁾. Utilizing the standard sample size formula:

$$n = Z^2 \cdot P \cdot (100 - P) / e^2$$

Where (Z = 1.96) (under a 95% confidence interval) and an absolute error (e) of 5%, the ideal target sample size was calculated as (n = 369) patients. However, due to the specific focus on EPTB, strict adherence to inclusion timelines, logistical limits at a single center, and the need to maintain strict aseptic conditions when sampling deep extrapulmonary sites a highly defined cohort of 67 confirmed EPTB cases was enrolled and processed

during the study timeframe. To address this smaller realized cohort size and avoid statistical over-interpretation, strict non-parametric comparative tools - specifically Fisher's exact test-were utilized for all down-stream categorical cross-tabulations.

- **Inclusion Criteria:** All clinical samples (including lymph node aspirates, pus, pleural fluid, cerebrospinal fluid, and tissue biopsies etc.) obtained from verified EPTB-positive patients (both newly diagnosed and previously treated).
- **Exclusion Criteria:** Clinical specimens originating from non-extrapulmonary sites, patients negative for EPTB, and redundant duplicate samples from the same anatomical site of a single patient.

Data Collection

Clinical data were systematically gathered using a structured reporting tool. Recorded variables included age, sex, history of substance abuse (tobacco smoking and alcohol use), and pre-existing comorbidities (Type II Diabetes mellitus, HIV status, chronic liver disease, and CKD)^(7-9, 11, 14-17).

Laboratory Processing and Identification

All clinical specimens were collected in sterile containers under strict aseptic conditions. Initial screening involved direct light microscopy via Gram staining and acid-fast bacillus (AFB) staining. Mycobacterial tuberculosis presence was verified using Cartridge-Based Nucleic Acid Amplification Testing (CBNAAT).

To isolate aerobic secondary bacterial pathogens, specimens were inoculated onto 5% Blood Agar and MacConkey Agar plates and incubated aerobically at 37°C for 24 hours. Emerging bacterial growths were purified and identified to the species level utilizing standard Gram stain morphology and conventional biochemical profiling following established clinical guidelines^(18, 19).

Antimicrobial Susceptibility Testing (AST)

In vitro phenotypic susceptibility testing was executed via the modified Kirby-Bauer disk diffusion method on Mueller-Hinton agar, conforming strictly to the Clinical and Laboratory Standards Institute (CLSI, 2024) benchmarks⁽²⁰⁾. High-standard reference strains (*Staphylococcus aureus* ATCC 25923, *Escherichia coli* ATCC 25922, and *Pseudomonas aeruginosa* ATCC 27853) served as internal quality controls. Phenotypic definitions for MDR, XDR, and ESBL status were derived from international expert consensus guidelines⁽²¹⁾.

Statistical Analysis

Statistical calculations were performed using SPSS version 23.0 (SPSS Inc., Chicago, IL, USA). Quantitative values were described via frequencies and percentages. Due to the small sample size and sparse distribution of positive secondary infections, Fisher's exact test was applied to analyze categorical associations between clinical risk factors and

infection status. A two-tailed (p)-value (<0.05) denoted statistical significance, while values between (0.05) and (0.10) were interpreted as showing an analytical trend.

RESULTS

Prevalence and Patient Demographics

Out of 67 enrolled EPTB patients, secondary bacterial infections were detected in 7 individuals, yielding an overall prevalence of 10.4% (95% CI: 5.2%–20.0%). Stratified by gender, secondary infections occurred in 10.8% (5/46) of male patients and 9.5% (2/21) of female patients, displaying no significant difference (p=1.000).

Infection distribution across age cohorts demonstrated a concentration within mature adults. No infections were verified in patients aged (< 18) years (0/15) or (>60) years (0/12). Conversely,

infection rates were 15.3% (2/13) in the 18–30 age bracket, 10.0% (1/10) in the 30–45 bracket, and reached a peak of 23.5% (4/17) among individuals aged 45–60 years. This age-related cluster approached but did not achieve formal statistical significance (p=0.074).

Behavioral and Comorbidity Risk Profiles

Neither tobacco smoking (p=1.000) nor alcohol consumption (p=1.000) exhibited a statistically significant association with secondary infection rates. Among individuals managing comorbid Type II Diabetes mellitus, 33.3% (2/6) developed secondary infections compared to 8.1% (5/61) of non-diabetic patients (p=0.115). Notably, the sole patient presenting with pre-existing CKD in this cohort (100%) suffered from a secondary bacterial infection (p=0.104). Detailed risk factor profiles are summarized in Table 1.

Table 1: Association of Demographics, Behavioral Habits, and Comorbidities with Secondary Infections (n=67)

Riskfactor / Variable	Total (N)	Infection Present (N) (%)	Infection Absent (N) (%)	(P)-Value (Fisher's Exact)
Gender				1.000
Male	46	5 (10.8%)	41 (89.2%)	
Female	21	2 (9.5%)	19 (90.5%)	
Age Group (Years)				0.074
(≤18)	15	0 (0.0%)	15 (100.0%)	0.335
(>18) – 30	13	2 (15.3%)	11 (84.7%)	0.614
(>30) – 45	10	1 (10.0%)	9 (90.0%)	1.000
(>45) – 60	17	4 (23.5%)	13 (76.5%)	0.074
(>60)	12	0 (0.0%)	12 (100.0%)	0.336
Smoking				1.000
Yes	38	4 (10.5%)	34 (89.5%)	
No	29	3 (10.3%)	26 (89.7%)	
Alcohol Use				1.000
Yes	20	2 (10.0%)	18 (90.0%)	
No	47	5 (10.6%)	42 (89.4%)	
Diabetes Mellitus (Type II)				0.115
Yes	6	2 (33.3%)	4 (66.7%)	
No	61	5 (8.1%)	56 (91.9%)	
Chronic Kidney Disease (CKD)				0.104
Yes	1	1 (100.0%)	0 (0.0%)	
No	66	6 (9.1%)	60 (90.9%)	

Specimen Origin and Bacterial Spectrum

Pus aspirates (primarily from lymph nodes) comprised the vast majority of the clinical samples (62/67), 92.5%). The remaining samples consisted of 3 pleural fluids (4.4%) and 2 tissue biopsies (3.0%).

The 7 confirmed bacterial isolates were distributed across three species: *Klebsiella pneumoniae* (n=3),

42.8%), *Pseudomonas aeruginosa* (n=2), 28.6%), and *Staphylococcus aureus* (n=2), 28.6%). Pus specimens yielded 5 isolates (8.1% isolation rate within that category), comprising 2 *P. aeruginosa*, 2 *S. aureus*, and 1 *K. pneumoniae*. The single isolates recovered from pleural fluid ((1/3), 33.3%) and tissue biopsy ((1/2), 50.0%) were both identified as *K. pneumoniae*.

Table 2: Distribution of Secondary Bacterial Pathogens by EPTB Sample Type

Specimen Matrix	Samples Received N (%)	Total Isolates N (%)	Bacterial Identity Verified N
Pus/ Lymphnode Aspirate	62 (92.5%)	5 (8.1%)	Pseudomonas Aeruginosa (2) Staphylococcus Aureus (2) Klebsiella Pneumoniae (1)
Pleural Fluid	3 (4.4%)	1 (33.3%)	Klebsiella Pneumoniae (1)
Tissue Biopsy	2 (3.0%)	1 (50.0%)	Klebsiella Pneumoniae (1)
Total	67 (100%)	7 (10.4%)	K. Pneumoniae (3), P. Aeruginosa (2), S. Aureus (2)

Phenotypic Resistance Profiles and Susceptibility Patterns

The core epidemiological burden of drug resistance was concentrated within *K. pneumoniae* and *S. aureus*.

Klebsiella pneumoniae (n=3); All 3 isolates were confirmed as MDR (100%). Phenotypic tracking identified 2 isolates as ESBL producers (66.6%) and 1 isolate as XDR (33.3%). Susceptibility testing revealed that 2 out of 3 isolates (67%) were resistant to third-generation cephalosporins (Cefotaxime, Ceftriaxone, Ceftazidime) and Cefepime, with only 1 isolate (33%) remaining susceptible. Moderate susceptibility (67%) was maintained for β -lactam/ β -lactamase inhibitor combinations, aminoglycosides, fluoroquinolones, and carbapenems (Imipenem, Meropenem, Doripenem). Colistin retained absolute susceptibility (100%, 3/3). Described in details in Table 3 and 4.

Pseudomonas aeruginosa (n=2); Both strains demonstrated excellent susceptibility profiles.

Neither isolate exhibited MDR, XDR, or ESBL properties. They maintained 100% susceptibility to Piperacillin-Tazobactam, Ceftazidime, Cefepime, Tobramycin, Aztreonam, Colistin, and all tested carbapenems. Reduced susceptibility was restricted to fluoroquinolones, where 1 of the 2 isolates (50%) demonstrated resistance. Described in details in Table 3 and 4

Staphylococcus aureus (n=2); Both isolates were phenotypically categorized as MRSA (based on Cefoxitin resistance) and qualified as MDR (100%). They exhibited complete resistance (100%) to Penicillin, Erythromycin, Clindamycin, Ciprofloxacin, Levofloxacin, and Azithromycin. However, they remained fully susceptible (100%, 2/2) to Gentamicin, Vancomycin, Linezolid, Teicoplanin, Tetracycline, Cotrimoxazole, and Chloramphenicol. Described in details in Table 3 and 5

Table 3: Summary of Isolates Classified by Resistance Definitions (n=7)⁽²¹⁾

Microorganism	Total (N)	MDR N (%)	XDR N (%)	ESBL Producer N (%)	MRSA Status
Klebsiella Pneumoniae	3	3 (100.0%)	1 (33.3%)	2 (66.6%)	N/A
Pseudomonas Aeruginosa	2	0 (0.0%)	0 (0.0%)	0 (0.0%)	N/A
Staphylococcus Aureus	2	2 (100.0%)	0 (0.0%)	—	2 (100.0%)

Table 4: Antimicrobial Susceptibility Pattern of Gram Negative Bacteria N (%)

Antibiotic	Pseudomonas Aeruginosa (N=2) %	Klebsiella Pneumoniae (N=3) %
Amoxicillin-Clavulanic Acid	NT	2(67)
Piperacillin-Tazobactam	2 (100%)	2(67)
Ampicillin-Sulbactam	NT	2(67)
Cefotaxime	NT	1 (33)
Ceftriaxone	NT	1 (33)

Ceftazidime	2 (100%)	1(33)
Cefepime	2 (100%)	1(33)
Cefixime	NT	00
Cefoxitin	NT	1(33)
Amikacin	NT	2(67)
Gentamicin	NT	2(67)
Tobramycin	2 (100%)	2(67)
Ciprofloxacin	1 (50%)	1(33)
Levofloxacin	1 (50%)	1(33)
Imipenem	2 (100%)	2 (67)
Meropenem	2 (100%)	2 (67)
Ertapenem	NT	2(67)
Doripenem	2 (100%)	2(67)
Aztreonam	2(100%)	2(67)
Tigecycline	NT	2(67)
Colistin	2(100%)	3(100)
Minocycline	NT	2(67)
Tetracycline	NT	1(33)
Cotrimoxazole	NT	1(33)
Chloramphenicol	NT	1(33)
NT- Not Tested, As Per CLSI 2025, Recommended Antimicrobial Agents Were Tested		

Table 5: Antimicrobial susceptibility pattern of Staphylococcus aureus n(%)

Antimicrobial Agents	Susceptible 2 (%)
Penicillin	00
Cefoxitin	00
Erythromycin	00
Clindamycin	00
Gentamicin	2 (100)
Ciprofloxacin	00
Levofloxacin	00
Vancomycin	2 (100)
Linezolid	2 (100)
Teicoplanin	2 (100)
Tetracycline	2 (100)
Cotrimoxazole	2 (100)
Azithromycin	00
Chloramphenicol	2 (100)

DISCUSSION

Secondary bacterial co-infections within active extrapulmonary tubercular lesions represent an important clinical crossroad. In this study, the observed secondary bacterial infection rate of 10.4% aligns closely with the 10% to 15% co-infection range frequently recorded in pulmonary TB settings^(4, 5). This confirms that despite the distinct

anatomical environments of EPTB, structural tissue destruction and localized immune suppression create an identical niche for opportunistic bacterial pathogens.

Analyzing host demographic trends revealed a distinct, though statistically non-significant, cluster of secondary infections among patients aged 45–60 years (23.5%). This pattern matches earlier reports

by Mujahid et al. and Saini Manoj et al., who documented peak vulnerability to secondary bacterial complications within the third to sixth decades of life^(24, 25). Similarly, the higher infection rate among diabetic individuals (33.3%) and the absolute infection presence in the CKD patient, though limited by local statistical power, reflect well-established literature stating that metabolic and renal exhaustion compromise systemic immune surveillance and open windows for secondary bacterial migration^(8, 10, 16, 23).

The primary clinical specimens in this EPTB cohort were dominated by lymph node pus aspirates (92.5%). This mirrors classic epidemiological updates from India noting that peripheral lymphadenitis forms the single most common presentation of EPTB^(26, 27). The fact that multiple specimen types (pus, pleural fluid, and tissue biopsies) yielded active bacterial growths underscores that cold abscesses and necrotic tubercular tissue act as reservoirs for secondary pathogens.

The resistance profiles captured among the Gram-negative *K. pneumoniae* isolates present a serious therapeutic concern. The 100% MDR status, along with high ESBL rates and third-generation cephalosporin failure, highlights a regional expansion of critical-priority pathogens. This mirrors recent tracking across India where *K. pneumoniae* co-isolates in TB patients display extensive β -lactamase-mediated resistance, leaving colistin and select carbapenems as the only reliable therapeutic choices⁽²⁸⁻³⁰⁾.

In contrast, the preserved susceptibility of *Pseudomonas aeruginosa* to all primary anti-pseudomonal agents is highly encouraging. In intensive care units, *P. aeruginosa* develops broad-spectrum resistance due to heavy selection pressure from repeated antibiotic exposure. However, EPTB patients are typically managed in outpatient settings or general wards where anti-pseudomonal selection pressure is low, meaning these community-acquired or non-intensive strains often retain their baseline susceptibility⁽³¹⁻³³⁾. The moderate resistance seen against fluoroquinolones (50%) is a notable exception; this likely stems from the extensive use of fluoroquinolones (such as Levofloxacin or Ciprofloxacin) as second-line anti-tubercular agents or as empirical treatments for general infections⁽²³⁾. The 100% MRSA and MDR profile identified among *Staphylococcus aureus* isolates underscores a critical clinical reality. When empirical treatment is required for an EPTB patient suspected of harboring a secondary bacterial infection, traditional β -lactam antibiotics are highly likely to fail. While the absolute susceptibility of these MRSA strains to glycopeptides (Vancomycin, Teicoplanin) and Linezolid provides secure therapeutic backstops, it emphasizes that early bacterial culture and disk

diffusion testing are indispensable to avoid treating blindly and worsening regional resistomes^(35, 36).

Study Limitations

This study is primarily constrained by its single-center design and a small sample size (n=67), which reduced its statistical power and increased the likelihood of a Type II error. Consequently, compelling clinical trends (such as the associations with age, diabetes, and CKD) did not achieve formal statistical significance (p<0.05). Additionally, the lack of molecular assays prevented the genotypic confirmation of the phenotypic resistance mechanisms. Larger, multi-center trials are required to establish robust risk models and definitive empirical treatment algorithms.

CONCLUSION

Secondary bacterial infections complicate a subset of extrapulmonary tuberculosis cases and are predominantly caused by highly resistant opportunistic pathogens, such as methicillin-resistant *Staphylococcus aureus* (MRSA) and extended-spectrum β -lactamase/multidrug-resistant *Klebsiella pneumoniae*. These findings underscore the critical importance of performing routine microbiological cultures and antimicrobial susceptibility testing whenever a secondary infection is suspected in extrapulmonary lesions. Such practices are essential for implementing targeted, evidence-based antibiotic therapy.

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