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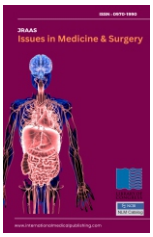

Research Article

Section: Pathology

Impact of Prior COVID-19 on the Demographics & Exposure Pattern of Tuberculosis Patients: A Cross-Sectional Study

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HIGHLIGHTS

- TB burden reversed during COVID
- COVID impact assessed in TB
- Young females predominated in TB
- TB contact predicts previous TB
- COVID factors not significantly associated

Key Words:
Tuberculosis
COVID-19
Mycobacterium Tuberculosis contact
Epidemiology
Cross-sectional study

ABSTRACT

Introduction: Tuberculosis (TB) remains a major global public health concern. Although TB mortality had been declining until 2019, it reversed during 2020–2021, as highlighted in the *Global Tuberculosis Report 2022*, largely due to disruptions caused by the COVID-19 pandemic. While COVID-19 has affected TB control programs worldwide, limited data exist on its impact on the demographic and exposure profiles of TB patients, especially in endemic regions. **Aim & Objective:** To assess the impact of prior COVID-19 infection on the demographics and exposure patterns of TB patients. **Materials & Methods:** This hospital-based cross-sectional study included 482 adult TB patients at a tertiary care center (January 2025-January 2026). Data on age, sex, previous TB history, TB contact, prior COVID-19 infection, vaccination status, steroid use, and hospitalization were collected. Statistical analysis included descriptive statistics, Chi-square/Fisher's exact test, and binary logistic regression to identify predictors of previous TB history and TB contact. **Results:** The mean age was 36.3 ± 15.98 years, with most patients aged 18–27 years (34.0%). Females constituted 63.3% of cases. Previous TB history was present in 54.4%, and 57.9% reported TB contact. Prior COVID-19 infection was documented in 57.3% of patients. A significant association was observed between TB contact and previous TB history ($p < 0.001$). Logistic regression showed that TB contact increased the odds of previous TB by approximately fourfold (OR = 4.04, 95% CI: 2.75–5.92). **Conclusion:** COVID-19 related factors showed no significant association with TB history or contact. Traditional risk factors, particularly TB contact and prior TB, remain key determinants, emphasizing the need to strengthen core TB control strategies.

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INTRODUCTION

Tuberculosis (TB), caused by *Mycobacterium tuberculosis*, is a chronic infectious disease that predominantly affects the lungs and remains a major public health concern worldwide [1]. *Mycobacterium tuberculosis* is a highly aerobic bacillus that primarily colonizes pulmonary tissue, although extrapulmonary involvement may occur. It is estimated that approximately one-quarter of the global population is latently infected with tuberculosis, constituting a vast reservoir for potential future disease [2]. Despite decades of global TB control efforts, tuberculosis continues to be among the top ten causes of death worldwide and remains the leading cause of mortality from a single infectious agent [3]. The global epidemiology of tuberculosis is shaped by a complex interplay of biological, social, and healthcare-related factors. Well-established risk factors for active TB disease include close contact with infectious TB cases, previous history of tuberculosis, socio-economic deprivation, and compromised host immunity [4]. In high-burden countries, household exposure and prior TB disease continue to play a central role in ongoing transmission and disease recurrence [5]. Understanding these exposure-related determinants remains fundamental to effective TB control strategies. In recent years, the coronavirus disease 2019 (COVID -19) pandemic has emerged as a major disruptor of global health-care systems, with significant implications for tuberculosis control [6]. The pandemic, caused by Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), rapidly evolved into a global health emergency following its emergence in late 2019 [7]. The unprecedented scale of the pandemic led to widespread lockdowns, reallocation of healthcare resources, and disruption of routine health services, including TB diagnostic and treatment programs [8]. A marked decline in TB case notifications was observed globally during the COVID-19 pandemic. In 2020, documented TB diagnoses decreased substantially compared to previous years [9]. However, this decline is widely believed to reflect underdiagnosis rather than a true reduction in TB incidence [10]. Reduced access to healthcare facilities, diagnostic delays, interruptions in TB prevention services, and misdiagnosis due to overlapping respiratory symptoms with COVID-19 have all been proposed as contributing factors [11]. The World Health Organization has warned that the COVID-19 pandemic may have reversed years of progress made toward global TB elimination [12]. Beyond healthcare system disruptions, concerns have been raised regarding the potential interaction between COVID-19 and tuberculosis at the individual patient level. Both TB and COVID-19 primarily affect the respiratory system and may present with similar clinical manifestations, including cough, fever, and breathlessness [13].

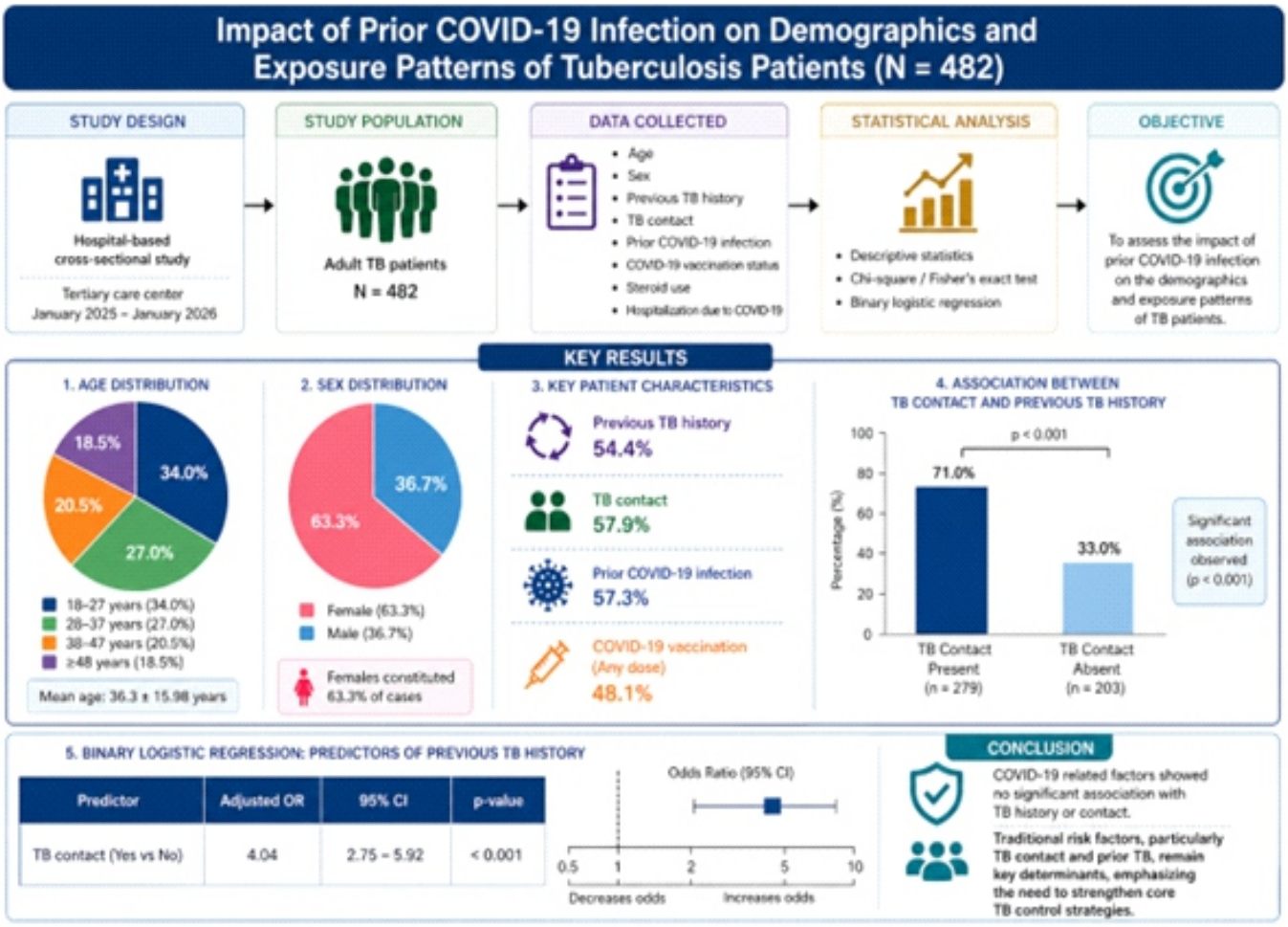

Figure 1: Study design and key findings showing TB contact as a significant predictor of previous TB with no association of COVID-19-related factors. ***Adopted from Biorender.com***

In TB-endemic settings, such overlap in clinical presentation may result in delayed recognition of tuberculosis, particularly in patients with persistent respiratory symptoms following COVID-19 infection [14]. Delayed diagnosis can lead to continued transmission, disease progression, and poorer outcomes. Several observational studies and case series have suggested that COVID-19 may unmask previously undiagnosed tuberculosis or accelerate the progression from latent infection to active disease, especially in individuals with pre-existing risk factors such as prior TB exposure or history of tuberculosis [15]. While the precise biological mechanisms underlying this association remain incompletely understood, the coexistence of immune perturbations, prolonged respiratory inflammation, and healthcare access barriers in the post-COVID period has raised important epidemiological concerns [16]. Previous history of tuberculosis is a recognized risk factor for recurrent or reactivated disease, particularly in settings with high back-ground transmission [17]. Similarly, close contact with infectious TB patients remains one of the strongest predictors of active TB development [18]. These exposure-related variables may assume heightened importance in the context of the COVID-19 pandemic, where routine contact tracing and preventive services have been disrupted [19]. Evaluating established TB risk factors alongside prior COVID-19 infection is therefore critical to understanding evolving patterns of TB presentation. Drug-resistant tuberculosis continues to pose a major challenge to global TB control efforts. Although not the primary focus of descriptive epidemiological studies, the burden of multidrug-resistant and rifampicin-resistant TB underscores the importance of early detection and uninterrupted treatment [20]. Pandemic-related disruptions have raised concerns about delayed diagnosis and treatment initiation, which may further contribute to adverse TB outcomes [21]. Despite growing interest in the interaction between tuberculosis and COVID-19, available data remain limited, particularly from single-center, real-world observational studies in TB-endemic regions [22]. Much of the existing literature has focused on TB-COVID co-infection or on healthcare system disruptions at the population level, with fewer studies examining the demographic and exposure profiles of TB patients in the post-COVID era [23]. Such descriptive analyses are essential to determine whether traditional exposure-related risk factors continue to predominate or whether COVID-19 related variables have independently altered TB epidemiological patterns. Characterizing demographic variables such as age and sex, along with key exposure-related factors including previous TB history, contact with TB patients, documented COVID-19 infection, and COVID-related clinical interventions, can provide valuable insights into contemporary TB epidemiology. These routinely collected clinical variables can inform targeted screening strategies, contact tracing policies, and posttreatment surveillance in high burden settings [24]. Evaluating whether COVID-19 infection or its related clinical management independently influences established TB exposure patterns is important for guiding public health prioritization in the post-pandemic era **Figure 1** shows overview of study design, methodology, and key findings assessing the impact of prior COVID-19 infection on demographics and exposure patterns among tuberculosis (TB) patients.

The present study was undertaken to describe the demographic and exposure profile of patients diagnosed with tuberculosis, with specific emphasis on prior COVID-19 infection, previous TB history, and contact with TB patients. Using a cross-sectional design, this study aims to determine whether traditional exposure-related risk factors remain predominant and to assess whether COVID-19 related variables independently influence TB history or contact patterns. The findings are expected to inform clinicians and public health practitioners regarding key exposure determinants and to support the continued prioritization of established TB control strategies in TB-endemic settings.

MATERIALS & METHODS

This hospital-based cross-sectional observational study included newly diagnosed tuberculosis confirmed by Gene Xpert, CBNAAT, AFB or culture. These patients diagnosed with tuberculosis during the study period of 1 year from JAN 2025 TO JAN 2026 at a tertiary care centre. Patients aged ≥18 years with complete demographic and exposure-related data were included, while those with incomplete records were excluded. Data were collected using a structured proforma and included age, sex, history of tuberculosis, history of contact with a tuberculosis patient, and history of prior COVID-19 infection. COVID-related clinical variables like covid vaccination status and steroid therapy along with hospitalization status were collected. Age was recorded in completed years, and all exposure variables were recorded as binary outcomes (Yes/No) based on patient history and medical records. Data were analyzed using descriptive statistics, with continuous variables expressed as mean ± standard deviation or median with interquartile range, and categorical variables as frequency and percentage. Associations between categorical variables were assessed using the Chi-square or Fisher's exact test, as appropriate, with $p < 0.05$ considered statistically significant. Ethical approval was obtained from the institutional ethics committee, and patient confidentiality was maintained.

RESULT

Demographic characteristics of the study population

A total of 482 patients diagnosed with tuberculosis were included in the study. The mean age of the study population was 36.3 ± 15.98 years, with an age range of 18–97 years. Female patients constituted 305 (63.3%) of the cohort, while 177 (36.7%) were male. The mean age among female patients was 35.88 ± 16.45 years, compared to 37.03 ± 15.14 years among male patients. No statistically significant difference in mean age

was observed between sexes (p = 0.443) (**Table 1**). breast carcinoma. When categorized into 10-year intervals, the highest proportion of patients was observed in the 18–27year age group (34.0%), followed by 28–37 years (19.7%). A progressive decline in frequency was noted with increasing age, demonstrating a clear predominance of young adults in the study population (**Table 2**). **Figure 2** (A & B) demonstrated that granulomas seen in a necrotic background.

Clinical Profile of the Study Population

A previous history of tuberculosis was reported by 262 (54.4%) patients, and 279 (57.9%) had a history of contact with a TB patient. Prior COVID-19 infection was reported by 276 (57.3%) individuals, while 277 (57.5%) had documented laboratory-confirmed COVID-19 positivity. COVID-19 vaccination was reported by 351 (72.8%) patients. A large proportion of patients received steroid therapy (84.6%) and required hospitalization (76.8%) during COVID-19 illness (**Table 3**).

Association Between TB Contact and Previous TB History

A Chi-square test was performed to examine the association between TB contact and previous tuberculosis (TB) history. All expected cell counts were greater than 5, satisfying the assumptions for the Chi-square test. A statistically significant association was observed between TB contact and prior TB history ($\chi^2(1) = 53.89$, $p < 0.001$). The effect size, measured using Cramér's V, was 0.33, indicating a moderate association. Fisher's exact test confirmed the statistical significance of this relationship ($p < 0.001$) (**Table 4**). Patients reporting TB contact were substantially more likely to have a history of previous TB compared to those without contact.

Logistic Regression Analysis

Binary logistic regression analysis was conducted to evaluate whether TB contact independently predicted previous TB history. The overall model was statistically significant (χ^2 (1) = 53.89, $p < 0.001$), indicating that TB contact significantly contributes to the prediction of prior TB. The regression coefficient for "TB Contact: No" was negative (B = -1.40, SE = 0.20, $p < 0.001$), indicating reduced odds of previous TB among individuals without TB contact. The corresponding odds ratio was 0.25 (95% CI: 0.17–0.36), meaning that individuals without TB contact had 75% lower odds of reporting previous TB compared to those with TB contact. Conversely, individuals with TB contact had approximately four times higher odds of previous TB (reciprocal OR ≈ 4.0). The model demonstrated an overall classification accuracy of 67.0%, with a sensitivity of 72.9% and specificity of 60.0%. Model fit indices were as follows: −2 Log Likelihood = 610.64, Cox & Snell $R^2 = 0.11$, Nagelkerke $R^2 = 0.14$, and McFadden's $R^2 = 0.08$, indicating modest but meaningful explanatory power (**Table 5**).

Multivariable Logistic Regression Analysis for TB Contact

Binary logistic regression analysis was performed to examine whether age, sex, prior COVID-19 history, and steroid therapy independently predicted TB contact (Yes vs No). The overall model was not statistically significant ($\chi^2(4) = 8.99$, $p = 0.061$; n = 482), indicating that these variables, taken together, did not significantly predict TB contact. Age showed a negative association with TB contact (B = -0.01, p = 0.076; OR = 0.99), suggesting that increasing age was associated with slightly lower odds of TB contact; however, this association did not reach statistical significance. Male sex was also not significantly associated with TB contact (B = -0.21, p = 0.277; OR = 0.81), indicating comparable odds of TB contact between males and females. Similarly, absence of prior COVID-19 infection was not significantly associated with TB contact (B = 0.14, p = 0.472; OR = 1.15). Steroid therapy status was likewise not a significant predictor of TB contact (B = -0.33, p = 0.225; OR = 0.72). Overall, none of the examined demographic or COVID-related variables independently predicted TB contact in this cohort.

Table 1. Demographic characteristics of patients diagnosed with tuberculosis

Variable	Value
Age (years), mean ± SD	36.3 ± 15.98
Age range (years)	18–97
Sex	
Female	305 (63.3%)
Male	177 (36.7%)
Age by sex (mean ± SD)	
Female	35.88 ± 16.45
Male	37.03 ± 15.14

Table 2: Age distribution of the study population (10-year intervals)

Age group (years)	n	%
18-27	164	34.0
28-37	95	19.7
38-47	49	10.2
48-57	22	4.6
58-67	18	3.7
68-77	8	1.7
78-87	2	0.4
88-97	3	0.6
Total	**482**	**100.0**

Table 3: Exposure and Clinical Profile of the Study Population (n = 482)

Variable	Yes n (%)	No n (%)
Previous TB history	262 (54.4%)	220 (45.6%)
TB contact history	279 (57.9%)	203 (42.1%)
Prior COVID-19 infection	276 (57.3%)	206 (42.7%)
Documented COVID-19 positive	277 (57.5%)	205 (42.5%)
COVID-19 vaccination	351 (72.8%)	131 (27.2%)
Steroid therapy during COVID -19	408 (84.6%)	74 (15.4%)
Hospitalization during COVID -19	370 (76.8%)	112 (23.2%)

Table 4: Association between TB Contact and Previous TB History (n = 482)

TB Contact	TB History: Yes	TB History: No	Total
Yes	191	88	279
No	71	132	203
Total	**262**	**220**	**482**

Table 5: Association of COVID-19–Related Variables with TB History and TB Contact (n = 482)

Exposure Variable	Outcome Variable	Yes / Yes	Yes / No	No / Yes	No / No	p-value
COVID History	TB History	140	136	122	84	0.064
COVID History	TB Contact	155	121	124	82	0.375
Documented COVID Positive	TB History	151	126	111	94	0.936
Steroid Therapy	TB History	222	186	40	34	0.955

No statistically significant associations were observed between COVID-19–related variables (COVID history, documented COVID positivity, or steroid therapy) and TB history or TB contact (all $p > 0.05$).

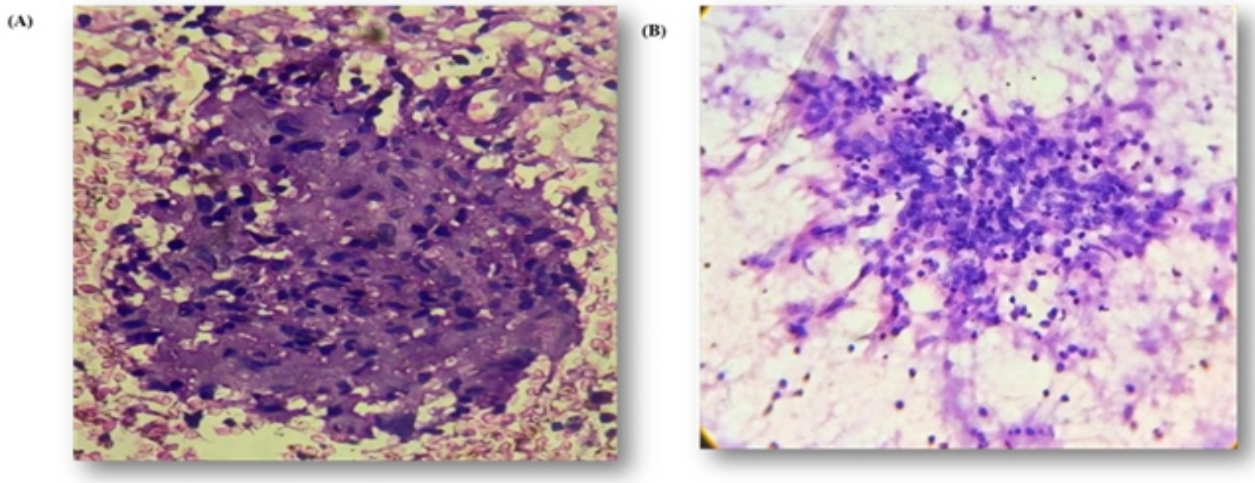

Figure 2: (A & B) Granuloma in the Background of Necrosis

DISCUSSION

The present cross-sectional study describes the demographic and exposure profile of patients diagnosed with tuberculosis in the context of prior COVID-19 infection and evaluates the association between key exposure variables [12]. The findings demonstrate a predominance of tuberculosis among young adults, a higher proportion of female patients, and a substantial burden of prior tuberculosis history and TB contact [25]. Importantly, while a strong association was observed between TB contact and previous TB history, prior COVID-19 infection was not independently associated with either TB history or TB contact [12]. The age distribution in this study demonstrated a clear predominance of younger individuals, particularly those aged 18-27 years, with a gradual decline in TB cases with increasing age [26]. This pattern is consistent with epidemiological observations from high TB-burden settings, where TB disproportionately affects young and economically productive age groups [27]. Increased social interaction, occupational exposure, and household crowding may contribute to higher transmission in this age group [30]. The right-skewed age distribution further supports this trend and underscores the need for targeted TB screening strategies among young adults [12]. Female patients constituted a higher proportion of the study population, contrasting with the traditionally reported male predominance in tuberculosis epidemiology [31]. However, several studies from resource-limited and TB-endemic regions have reported narrowing sex differences or context-specific variations in TB distribution [32]. Increased healthcare-seeking behaviour among women, improved access to diagnostic services, and enhanced case detection may partly explain this finding [26]. Social and cultural determinants influencing exposure patterns and healthcare utilization may also contribute (lonn). The absence of a statistically significant difference in mean age between male and female patients suggests comparable age related risk across sexes in the present cohort [33]. More than half of the patients in this study reported a previous history of tubrculosis [34]. This high proportion reflects the persistent challenge of recurrent or reactivated TB in endemic settings [35]. Previous TB is a well-recognized risk factor for subsequent disease due to residual lung damage, incomplete immune recovery, and continued exposure within high-risk environments. These findings emphasize the importance of long-term follow-up and preventive strategies among individuals with a prior history of tuberculosis. A similarly high proportion of patients reported a history of contact with a TB patient, underscoring the central role of exposure in TB transmission. The strong association observed between TB contact and previous TB history represents a key finding of this study. Patients reporting TB contact had approximately fourfold higher odds of previous TB, as demonstrated by both chi-square analysis and logistic regression. This association likely reflects clustering of TB within households or communities, where repeated exposure sustains transmission cycles [36]. The magnitude of the observed odds ratio indicates a clinically meaningful relationship [37], highlighting TB contact as a critical marker of ongoing transmission risk [38]. Logistic regression analysis further reinforced this observation by demonstrating that TB contact independently predicted previous TB history [39]. The consistency between bivariate and multivariable analyses strengthens the robustness of this finding and supports the hypothesis that exposure and disease recurrence remain closely linked in endemic settings [40]. These results reinforce the need for rigorous contact tracing, preventive therapy, and post-treatment surveillance among individuals with a history of TB [41,42]. In contrast, prior COVID-19 infection was not significantly associated with previous TB history [25]. Although a slightly lower proportion of prior TB was observed among patients with COVID-19 history compared to those without, this difference did not reach statistical significance [43]. Similarly, no significant association was observed between COVID-19 history and TB contact [50]. Documented laboratory-confirmed COVID -19 positivity and steroid therapy during COVID-19 illness were also not significantly associated with previous TB history. These findings suggest that COVID-19 infection and related clinical fa-

tors did not independently influence TB exposure patterns in this cohort [44]. The absence of statistically significant associations between COVID-related variables and TB history or contact is noteworthy [46]. While pandemic-related disruptions may have influenced healthcare access, diagnosis, and reporting, the underlying transmission dynamics in this population appear to remain driven primarily by traditional risk factors such as close contact and prior disease [45,47]. These findings caution against over-attribution of TB epidemiological patterns to COVID-19 exposure in the absence of clear supporting evidence [48,49]. From a public health perspective, the findings reinforce the continued importance of focusing TB control efforts on established exposure-related determinants. TB contact and previous TB history emerged as the most salient variables in this study, whereas COVID-19 history and related clinical factors did not demonstrate significant independent associations [50]. These results support sustained prioritization of contact tracing, active case finding, and post-treatment surveillance, even in the post-COVID era. The study has certain limitations that should be acknowledged. The cross-sectional design precludes causal inference, and temporal relationships between COVID-19 infection and tuberculosis diagnosis could not be established. Information on disease severity, timing between COVID-19 infection and TB diagnosis, and immunological parameters was not available. The reliance on self-reported history and medical records may introduce recall or documentation bias. Additionally, the single-center nature of the study may limit the generalizability of the findings. Despite these limitations, the study has several strengths [51]. The sample size was adequate, data completeness was high, and multiple analytical approaches were employed to examine key associations. The inclusion of logistic regression analysis allowed quantification of effect size and strengthened the interpretability of the findings. The study provides valuable real-world data from a TB-endemic setting and contributes to a nuanced understanding of tuberculosis epidemiology in the context of the COVID-19 pandemic. In conclusion, this study demonstrates that tuberculosis in the post-COVID period remains strongly associated with traditional exposure factors, particularly TB contact and previous TB history [51]. Prior COVID-19 infection was not independently associated with TB exposure or history in this cohort [49]. These findings underscore the continued importance of strengthening core TB control strategies and caution against attributing changes in TB epidemiology solely to COVID-19 without supporting evidence [33].

CONCLUSION

This cross-sectional study highlights that tuberculosis in the post-COVID period continues to be predominantly associated with established epidemiological risk factors. A high burden of disease was observed among young adults, with substantial proportions of patients reporting previous tuberculosis and history of TB contact. A strong and statistically significant association was demonstrated between TB contact and previous history of tuberculosis, reinforcing the role of close exposure in sustaining TB transmission in endemic settings. In contrast, prior COVID-19 infection was not independently associated with either previous TB history or TB contact. These findings underscore the continued importance of strengthening core tuberculosis control strategies particularly contact tracing, post-treatment surveillance, and targeted screening of high-risk groups-even in the post-pandemic era.

LIMITATIONS & FUTURE PERSPECTIVES

The present study has certain limitations that should be considered when interpreting the findings. The cross-sectional design precludes the establishment of causal relationships and limits the ability to determine temporal sequencing between COVID-19 infection and tuberculosis diagnosis. Information regarding the severity of COVID-19 illness, the interval between COVID-19 infection and TB detection, and relevant immunological parameters was not available, which may have restricted more detailed clinical interpretation. The study relied partly on patient-reported history and medical records, which may be subject to recall or documentation bias. Additionally, the single-center design may limit the generalizability of the findings to other populations or healthcare settings. Despite these limitations, the study provides valuable real-world evidence on tuberculosis epidemiology in a TB-endemic setting during the post-COVID period.

CLINICAL SIGNIFICANCE

The clinical significance of this study lies in its potential to bridge the gap between research findings and practical healthcare applications. It emphasizes the importance of trans-lating scientific observations into meaningful improve-ments in patient care, diagnosis, and treatment outcomes. By highlighting real-world relevance, the study contributes to evidence-based medical practice and supports informed clinical decision making. Ultimately, the findings aim to enhance patient quality of life, optimize therapeutic strategies, and promote better disease management in clinical settings.

ABBREVIATIONS

TB: Tuberculosis

COVID-19: Coronavirus Disease 2019

OR: Odds Ratio

CI: Confidence Interval

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AUTHOR CONTRIBUTIONS

All authors significantly contributed to the study conception and design, data acquisition, or data analysis and interpretation. They participated in drafting the manuscript or critically revising it for important intellectual content, consented to its submission to the current journal, provided final approval for the version to be published, and accepted responsibility for all aspects of the work. Additionally, all authors meet the authorship criteria outlined by the International Committee of Medical Journal Editors (ICMJE) guidelines.

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CONFLICT OF INTEREST

Authors declared that there is no conflict of interest.

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None

ETHICAL APPROVAL & CONSENT TO PARTICIPATE

All necessary consent & approval was obtained by authors.

CONSENT FOR PUBLICATION

All necessary consent for publication was obtained by authors.

DATA AVAILABILITY

All data generated and analyzed are included within this research article. The data sets utilized and/or analyzed in this study can be obtained from the corresponding author upon a reasonable request.

USE OF ARTIFICIAL INTELLIGENCE (AI) & LARGE LANGUAGE MODEL (LLM)

The authors confirm that no AI & LLM tools were used in the writing or editing of the manuscript, and no images were altered or manipulated using AI & LLM.

AUTHOR'S NOTE

This article serves as an important educational tool for the scientific community, offering insights that may inspire future research directions. However, they should not be relied upon independently when making treatment decisions or developing public health policies.

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