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Understanding the epidemiology of TB-HIV co-infection in Indonesia: evidence from the 2023 national TB registry

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ABSTRACT

Introduction Tuberculosis (TB) and HIV co-infection remain a significant public health challenge in Indonesia. Therefore, this study aims to identify the determinants and epidemiological characteristics of TB-HIV co-infection using data from the 2023 national TB registry.

Methods The study procedures were carried out using a cross-sectional design, analysing univariate, bivariate and multivariate associations between TB-HIV coinfection status and demographic, clinical and health service factors among patients with TB.

Results Among 22 698 patients with TB, 94.8% were HIV negative, with a predominance of males (58.8%) and adults aged 30–59 years (49.8%). The majority of the patients were treated in healthcare facilities located in Western Indonesia, had pulmonary TB (93.8%), bacteriological diagnosis (55.5%) and achieved a cure (85.9%), while the remaining 14.1% included patients who died, were lost to follow-up, or had incomplete treatment outcomes. The most common nutritional status among patients was normal nutritional status (44.4%). In the multivariate analysis, clinical diagnosis remained the strongest predictor of TB-HIV co-infection (OR 2.446; 95% CI 2.154 to 2.778; p<0.001). Other significant predictors included male sex (OR 2.096; 95% CI 1.835 to 2.395), extrapulmonary TB (OR 1.337; 95% CI 1.075 to 1.662) and undernourished status, which showed lower odds of TB-HIV co-infection compared with overweight or obese patients (OR 0.809; 95% CI 0.676 to 0.967).

Conclusions This study highlights TB-HIV co-infection as the primary outcome, emphasising the role of demographic, clinical, nutritional and regional disparities in influencing co-infection risks. The findings underscore the need for integrated TB-HIV diagnostic and management strategies, including nutritional support and targeted interventions focusing on high-risk populations and health service accessibility to strengthen early detection and treatment outcomes.

WHAT IS ALREADY KNOWN ON THIS TOPIC

⇒ Co-infection of tuberculosis (TB) and HIV remains a major public health challenge in high-burden countries, including Indonesia. Previous studies have suggested that demographic and clinical factors such as sex, age and diagnostic method may influence HIV positivity among patients with TB, but national-level evidence has been limited.

WHAT THIS STUDY ADDS

⇒ This study, using data from the 2023 national TB registry (SITB), found that 5.2% of patients with TB were HIV positive. Male sex, older age, clinical diagnosis (vs bacteriological) and treatment outcome were significantly associated with HIV positivity. Among these, clinical diagnosis was the strongest predictor, with clinically diagnosed patients with TB being approximately 2.4 times more likely to be HIV positive.

HOW THIS STUDY MIGHT AFFECT RESEARCH, PRACTICE OR POLICY

⇒ The findings underscore the importance of strengthening integrated TB-HIV diagnostic and treatment services across Indonesia, particularly in regions with limited laboratory capacity. Policies should prioritise universal HIV screening among all patients with TB—especially those diagnosed clinically—and enhance diagnostic infrastructure to improve early detection and outcomes for co-infected individuals.

INTRODUCTION

Tuberculosis (TB) and HIV remain two of the most significant overlapping epidemics in developing countries, including Indonesia. The dual burden of TB-HIV co-infection poses a major public health challenge because each disease accelerates the progression and worsens the prognosis of the other. In 2024, Indonesia reported 17136 cases of TB–HIV co-infection, reflecting the increasing convergence of these two epidemics and the persistent gaps in prevention, diagnosis and treatment.[1] Countries with a high TB burden, including Indonesia, continue to be the focus of global strategies addressing TB/HIV co-infection and multidrug-resistant or rifampicin-resistant TB under the WHO 2021–2025

strategic framework. TB is ranked as the second highest contributor to global disease burden, accounting for approximately 10% of cases worldwide and remains a leading cause of morbidity and mortality in Indonesia.[1 2] In 2023, Southeast Asia accounted for 45% of the global 10.8 million reported TB cases,[1] underscoring the regional importance of TB control.[1 3] Globally, TB remains the leading cause of death among individuals living with HIV due to the profound immunosuppression associated with HIV infection.

Case notifications play a central role in evaluating TB programme performance. The 2022 national TB report indicated that approximately 75% of estimated TB cases were detected, leaving 25% undiagnosed or unreported. Among reported cases, adults accounted for 84.7% and children under 15 years for 15.3%.[3] Under-reporting is frequently driven by diagnostic and reporting challenges,[4] particularly among children, where TB is clinically difficult to detect and often under-prioritised.[5 6] TB-HIV co-infection further complicates diagnosis and treatment, often requiring coordinated service delivery and integrated care pathways.[7]

Addressing TB-HIV co-infection in Indonesia is increasingly urgent due to rising HIV incidence and the complex clinical management required for co-infected individuals. Co-infected patients face a higher risk of extrapulmonary and drug-resistant TB forms.[1] Therefore, identifying factors associated with HIV status among affected patients is crucial for developing targeted interventions, improving health outcomes and progressing towards elimination goals,[8] making early identification of associated determinants essential for targeted interventions and improved health outcomes.[8] All patients with TB accessing directly observed treatment short-course (DOTS) services are required to undergo HIV testing unless previously documented. HIV-positive patients must initiate antiretroviral therapy (ART) within 2–8 weeks after starting TB treatment, and all testing outcomes must be recorded within the National Tuberculosis Information System (SITB).[3 9]

TB-HIV surveillance in Indonesia is currently conducted using routine data collected from healthcare facilities implementing collaborative activities. Data were obtained from both TB and HIV services, using the Tuberculosis Information System (SITB) and the HIV/AIDS Information System (SIHA). Integrated surveillance relies on two systems: SITB for TB and SIHA for HIV/AIDS. Differences in data completeness, system fragmentation and limited interoperability often lead to discrepancies in reported outcomes.[10] Technical barriers, internet instability and limited digital literacy among health workers continue to hinder optimal data reporting at the primary care level.[11] Strengthening data integration and improving SITB–SIHA interoperability remain essential priorities for accurate monitoring and surveillance.[12] This study aims to describe the demographic, clinical and healthcare characteristics of patients with TB stratified by HIV status and identify factors independently associated with HIV co-infection using national TB registry data from 2023, supporting Indonesia's goal of ending the TB and HIV epidemics by 2030.

METHODS

Study design and participants

The current study used a cross-sectional design using secondary data extracted from the 2023 Tuberculosis Information System (SITB), a national surveillance database managed by the Indonesian Ministry of Health. The SITB dataset included routinely collected and standardised patient level data from public and private healthcare facilities across all provinces in Indonesia. The study population comprised all registered patients with TB in the 2023 SITB dataset. The inclusion criteria were individuals with a confirmed TB diagnosis and available data on HIV status. The primary outcome variable was defined as HIV status among patients with TB, dichotomously categorised as HIV-positive or HIV-negative, representing TB-HIV coinfection. Records with incomplete or missing values for the primary outcome variable or essential independent variables were excluded from the analysis. A total of 22 698 patients with TB who met the eligibility criteria were included in this study, and this design enabled the identification of socio-demographic and clinical characteristics associated with HIV status among patients with TB within a defined time frame, without follow-up.

Patient and criteria

The study population comprised all patients with TB recorded in the 2023 Tuberculosis Information System (SITB), a national surveillance database managed by the Indonesian Ministry of Health. The inclusion criteria encompassed individuals of all age groups who had been diagnosed with either pulmonary or extrapulmonary TB and had documented HIV status data. Only patient records with complete information on key socio-demographic and clinical variables including sex, age, geographical location of the healthcare facility (based on time zone), diagnostic method, treatment outcome and nutritional status were included in the analysis. Records with missing, incomplete or inconsistent data on HIV status or other critical demographic and clinical variables were excluded from the final dataset. A complete case analysis approach was applied to handle missing data.

Study variables

This study used secondary data from the 2023 Tuberculosis Information System (SITB), by Indonesia's Ministry of Health. The primary objective of this study was to identify factors associated with HIV status among patients diagnosed with TB across Indonesia. The dependent variable was HIV status, dichotomously categorised as either HIV positive or HIV negative. Independent variables included a range of socio-demographic and clinical characteristics, selected based on their epidemiological relevance to TB-HIV coinfection.

Socio-demographic variables comprised sex and age group. Sex was recorded as a binary variable (male or female). Age was classified according to the WHO guidelines into seven categories: infants (0–1 year), toddlers (1–5 years), children (6–12 years), adolescents (13–19 years), young adults (20–29 years), adults (30–59 years) and older adults (≥60 years). This stratification facilitated a nuanced analysis of age-related susceptibility and exposure to TB-HIV coinfection.

Geographical location of healthcare facilities was categorised based on Indonesia's official time zones Western Indonesia Time (WIB), Central Indonesia Time (WITA) and Eastern Indonesia Time (WIT) to reflect regional diversity and potential disparities in healthcare access and service distribution, particularly regarding HIV testing and treatment availability.[13]

Clinical variables included the anatomical site of TB infection, diagnostic method, treatment outcomes and nutritional status. The anatomical location of TB was categorised as either pulmonary or extrapulmonary. Type of diagnostic confirmation was classified into two categories: (1) clinical diagnosis, based on signs, symptoms and radiological findings without laboratory confirmation; and (2) bacteriological diagnosis, confirmed through acid-fast bacilli smear microscopy, interferon gamma release assay, tuberculin skin test or rapid molecular testing such as GeneXpert MTB/RIF.[14]

Treatment outcomes were classified based on SITB records into three primary categories: cured, treatment failure and deceased. Nutritional status among patients with TB was assessed using age-appropriate methods. For children aged 0–60 months, nutritional status was evaluated using weight-for-length/height Z-scores. For individuals older than 60 months, nutritional status was determined based on body mass index. Classification of nutritional status followed the 2020 Nutritional Guidelines issued by the Indonesian Ministry of Health and was grouped into three categories: undernourished, normal and overweight/obese.[15]

Data analysis

Data from the 2023 SITB database were cleaned, processed and analysed using IBM SPSS Statistics software. Descriptive statistics were used to summarise the characteristics of the study population (univariate analysis). Bivariate logistic regression was conducted to examine the association between each independent variable and HIV status among patients with TB. Variables with a p value<0.25 in the bivariate analysis were included in the multivariate logistic regression model to identify factors independently associated with HIV status. Multivariate logistic regression was performed in two stages. Model I served as the initial full model, including all selected independent variables. Variables with a p value>0.05 were assessed for potential confounding effects. Non-significant variables that were not identified as confounders were excluded from the model. Model II represented the final model, retaining only variables that were statistically significant or identified as confounders. Adjusted ORs and 95% CIs were reported. Statistical significance was set at a p value<0.05.

Potential sources of bias inherent in the use of secondary data from a national registry, such as selection bias, information bias and reporting bias, were carefully considered. To reduce selection bias, the analysis included only cases with complete and verified data on HIV status and key variables. Misclassification of variables such as HIV status, TB type and diagnostic method was minimised by excluding implausible or inconsistent entries and cross-validating relevant fields. Additionally, regional variation in reporting completeness was addressed by including geographical location in the model. Although the cross-sectional design limits causal inference, multivariate modelling was used to control for potential confounders and strengthen the internal validity of the associations observed.

RESULTS

Patient characteristics

Based on secondary data from the Tuberculosis Information System (SITB) in 2023, 5.2% of patients with TB were HIV positive, underscoring the need for integrated TB-HIV management. An overview of the demographic and clinical characteristics of the study population revealed that most participants were male (58.8%), with the adult age group (30–59 years) comprising 49.8% of the total sample. The majority of patients received care from healthcare facilities located in the WIB, with most TB cases being pulmonary (93.8%) and diagnosed bacteriologically (55.5%). The predominant treatment outcome was 'cured' (85.9%), and the most common nutritional status among participants was 'normal' (44.4%) (table 1).

Based on table 2, it was found that the difference in the proportion of HIV-positive cases between males and females was 3.3%. The association between sex and HIV status yielded a p value<0.001, indicating a statistically significant relationship between sex and HIV status. The OR was (OR 2.096; 95% CI 1.835 to 2.395), meaning that males had a 2.096 times higher risk of being HIV positive compared with females.

The difference in the proportion of HIV positivity between young adults and the elderly was 7.4%. The association between age group and HIV status resulted in a p value<0.001 for the categories of children, young adults and adults compared with the elderly, indicating a significant relationship between age and HIV status. For the young adult group, the OR was (OR 0.116; 95% CI 0.083 to 0.162), meaning young adults had a 0.116 times lower risk of being HIV positive compared with the elderly.

The difference in the proportion of HIV positivity between healthcare facilities located in WIT and WIB was 7.4%. The association between healthcare facility location and HIV status showed a p value<0.001 for WIT and WITA categories compared with WIB, indicating a

Table 1 Socio-demographic and clinical characteristics of patients with TB in Indonesia, 2023 (n=22 698)

Characteristic	Frequency	Percentage
HIV status		
HIV positive	1183	5.2
HIV negative	21 515	94.8
Sex		
Male	13 352	58.8
Female	9346	41.2
Age (year)		
Infant (0–1)	158	0.7
Toddler (1–5)	1075	4.7
Child (6–12)	679	3.0
Adolescent (13–19)	1562	6.9
Young adult (20–29)	4162	18.3
Adult (30–59)	11 294	49.8
Elderly (60+)	3768	16.6
Healthcare facility location		
WIT (Central Indonesia Time)	976	4.3
WITA (Eastern Indonesia Time)	2958	13.0
WIB (Western Indonesia Time)	18 764	82.7
Anatomical location		
Extrapulmonary TB	1399	6.2
Pulmonary TB	21 299	93.8
Type of diagnosis confirmation		
Clinical	10 102	44.5
Bacteriological	12 596	55.5
Treatment outcome		
Deceased	1411	6.2
Failed	1779	7.8
Cured	19 508	85.9
Nutritional status		
Underweight	9113	40.1
normal	10 081	44.4
Overweight	3504	15.4

Data derived from the 2023 Tuberculosis Information System (SITB), Ministry of Health, Republic of Indonesia.
TB, tuberculosis.

significant relationship. For the WIT group, the OR was (OR 0.228; 95% CI 0.190 to 0.273), meaning that patients in healthcare facilities in EIT had a 0.228 times lower risk of being HIV positive compared with those in WIB.

The difference in the proportion of HIV positivity between patients with extrapulmonary TB and pulmonary TB was 1.6%. The association between disease site and HIV status had a p value of 0.011, indicating a significant relationship. The OR was (OR 1.337; 95% CI 1.075 to 1.662), meaning that patients with extrapulmonary TB had a 1.337 times higher risk of being HIV positive compared with those with pulmonary TB.

The difference in the proportion of HIV positivity between clinical and bacteriological diagnosis was 3.2%. The association between diagnosis type and HIV status resulted in a p value of 0.011, indicating a significant relationship. The OR was (OR 1.930; 95% CI 1.713 to 2.175), meaning that patients diagnosed clinically had a 1.930 times higher risk of being HIV positive compared with those diagnosed bacteriologically.

The difference in the proportion of HIV positivity between undernourished/malnourished patients and overweight/obese patients was 1.1%. The association between nutritional status and HIV status yielded a p value of 0.020, indicating a significant relationship. For the undernourished/malnourished group, the OR was (OR 0.809; 95% CI 0.676 to 0.967), meaning they had a 0.809 times lower risk of being HIV positive compared with overweight/obese patients.

Based on the information presented in table 3, Model I serves as the initial multivariate logistic regression model, incorporating all variables under consideration in the analysis. This comprehensive approach allowed for the simultaneous evaluation of each variable's independent association with HIV positive status. The results obtained from this initial model indicated that nearly all included variables demonstrated statistically significant associations with HIV positivity, as evidenced by p values <0.05. This level of significance suggests a reliable and non-random relationship between these variables and the outcome of interest. However, one notable exception to this pattern was the variable labelled 'anatomical location', which yielded a p value exceeding the threshold for statistical significance (p>0.05). This finding implied that, within the context of the full model, anatomical location did not exhibit a meaningful association with HIV positive status.

Following these initial findings, the next analytical step was to assess the potential for confounding effects that might influence the relationship between the variables and HIV status. To this end, the 'anatomical location' variable was removed from the model due to its non-significant p value. The rationale for this exclusion was to refine the model by eliminating variables that do not contribute significantly to explaining variation in the outcome, thus enhancing the interpretability and parsimony of the final model. After removing this variable, the researchers calculated the percentage change in the ORs for the remaining variables to determine whether 'anatomical location' acted as a confounding factor. This calculation involved comparing the ORs of the reduced model (Model II) to those of the initial full model (Model I). The change in OR was expressed as a percentage, representing the extent to which the ORs of the other variables shifted when 'anatomical location' was excluded. The results showed that for all remaining variables, the percentage change in ORs was less than 10%. This finding is generally interpreted as an indication that

Table 2 Factors associated with TB-HIV patients in Indonesia, 2023 (n=22 698)

Variable	HIV status				P value	OR (95% CI)
	HIV positive		HIV negative			
	n	%	n	%		
Sex						
Male	879	6.6	12 473	93.4	<0001	2.906 (1.835 to 2.395)
Female	304	3.3	9042	96.7		
Age (year)						
Infant (0–1)	2	1.3	156	98.7	0.807	0.837 (0.200 to 3.494)
Toddler (1–5)	15	1.4	1060	98.6	0.364	0.758 (0.417 to 1.378)
Child (6–12)	24	3.5	655	96.5	<0.0010	0.293 (0.175 to 0.489)
Adolescent (13–19)	32	2.0	1530	98.0	0.005	0.513 (0.321 to 0.820)
Young adult (20–29)	352	8.5	3810	91.5	<0.001	0.116 (0.083 to 0.162)
Adult (30–59)	718	6.4	105 763	93.6	<0.001	0.158 (0.115 to 0.218)
Elderly (60+)	40	1.1	728	98.9	ref	ref
Healthcare facility location						
WIT (Central Indonesia Time)	164	16.8	812	83.2	<0.001	0.228 (0.190 to 0.273)
WITA (Eastern Indonesia Time)	194	6.6	2764	93.4	<0.001	0.655 (0.558 to 0.770)
WIB (Western Indonesia Time)	825	4.4	17 939	95.6	ref	ref
Anatomical location						
Extrapulmonary TB	94	6.7	1305	93.3	0.011	1.337 (1.075 to 1.662)
Pulmonary TB	1089	5.1	20 210	94.9		
Type of diagnosis Confirmation						
Clinical	709	7.0	9393	93.0	<0.001	1.930 (1.713 to 2.175)
Bacteriological	474	3.8	12 122	96.2		
Treatment outcome						
Deceased	277	19.6	1134	80.4	<0.001	0.169 (0.145 to 0.196)
Failed	133	7.5	1646	92.5	<0.001	0.511 (0.422 to 0.618)
Cured	773	4.0	18 735	96.0	ref	ref
Nutritional status						
Underweight	528	5.8	8585	94.2	0.020	0.809 (0.676 to 0.967)
Normal	489	4.9	9592	95.1	0.787	0.975 (0.814 to 1.168)
Overweight	166	4.7	3338	95.3	ref	ref

Analysis based on the 2023 SITB dataset; outcome variable: HIV status among patients with TB.
TB, tuberculosis.

'anatomical location' did not have a confounding effect on the associations between the other variables and HIV status. Consequently, based on these statistical considerations, 'anatomical location' was excluded from the final model.

Model II therefore represents the final and more refined multivariate logistic regression model. This model retained only those variables that exhibited statistically significant associations with HIV positive status, excluding the 'anatomical location' variable. The results of Model II further confirmed that several key variables remained significantly associated with HIV positivity, with p values all below 0.05. These variables included sex, age, healthcare facility location, type of diagnosis confirmation, treatment outcome and nutritional status. Their retention in the final model underscores their independent and meaningful contributions to explaining the likelihood of an individual being HIV positive.

Among these variables, the type of diagnosis confirmation emerged as the most strongly associated factor with HIV status, indicated by an exceptionally significant p value of <0.001. This strong association suggests that the method by which a diagnosis was confirmed plays a critical role in predicting HIV positivity. More specifically, the OR for individuals diagnosed clinically was estimated at 2.446. This means that, after adjusting for sex, age, healthcare facility location, treatment outcome and nutritional status, individuals with a clinical diagnosis

Table 3 Multivariable logistic regression of factors associated with HIV status among patients with tuberculosis, Indonesia, 2023

	Model I		Model II	
Variable	**P value**	**OR (95% CI)**	**P value**	**OR (95% CI)**
Sex				
Male	<0.001	2.227 (1.937 to 2.561)	<0.001	2.238 (1.947 to 2.572)
Female (ref)	–	–	–	–
Age				
Infant	0.997	0.997 (0.231 to 4.301)	0.998	1.002 (0.232 to 4.329)
Toddler	0.127	0.623 (0.339 to 1.145)	0.124	0.620 (0.337 to 1.140)
Child	<0.001	0.241 (0.142 to 0.408)	<0.001	0.242 (0.143 to 0.411)
Adolescent	<0.001	0.338 (0.209 to 0.546)	<0.001	0.341 (0.211 to 0.551)
Young adult	<0.001	0.077 (0.055 to 0.108)	<0.001	0.077 (0.055 to 0.108)
Adult	<0.001	0.108 (0.078 to 0.150)	<0.001	0.109 (0.078 to 0.151)
Elderly (ref)	–	–	–	–
Healthcare facility location				
WIT	<0.001	0.246 (0.202 to 0.299)	<0.001	0.246 (0.202 to 0.299)
WITA	<0.001	0.678 (0.572 to 0.805)	<0.001	0.678 (0.572 to 0.804)
WIB (ref)	–	–	–	–
Anatomical location				
Extrapulmonary TB	0.428	0.908 (0.715 to 1.153)		
Pulmonary TB (ref)	–	–	–	–
Type of diagnosis confirmation				
Clinical	<0.001	2.477 (2.173 to 2.822)	<0.001*	2.446 (2.154 to 2.778)*
Bacteriological (ref)	–	–	–	–
Treatment outcome				
Deceased	<0.001	0.162 (0.137 to 0.190)	<0.001	0.162 (0.137 to 0.191)
Failed	<0.001	0.579 (0.475 to 0.706)	<0.001	0.579 (0.475 to 0.706)
Cured (ref)	–	–	–	–
Nutritional status				
Underweight	0.019	0.797 (0.660 to 0.963)	0.016	0.793 (0.656 to 0.957)
Normal	0.360	0.915 (0.758 to 1.106)	0.342	0.912 (0.755 to 1.102)
Overweight (ref)	–	–	–	–

*Statistically significant at p < 0.001
TB, tuberculosis; WIB, Western Indonesia Time; WIT, Eastern Indonesia Time; WITA, Central Indonesia Time.

were approximately 2.4 times more likely to be HIV positive compared with those who received a bacteriological diagnosis. Furthermore, the 95% CI for this OR ranged from 2.154 to 2.778, which reflects a precise and statistically robust estimate of the association. Taken together, these findings highlight the importance of diagnostic methods and related clinical factors in understanding and predicting HIV infection within the studied population.

DISCUSSIONS

This study analysed 22 698 patients with TB recorded in Indonesia's 2023 SITB (National Tuberculosis Information System). The dataset provided demographic and clinical variables essential for understanding the epidemiology of TB-HIV co-infection. Of all recorded TB cases, 1183 (5.2%) were HIV-positive, while 21 515 (94.8%) were HIV-negative. As indicated in the results, the majority of patients were HIV-negative (94.8%), male (58.8%) and most belonged to the adult age group of 30–59 years (49.8%). Multivariate analysis showed that Model II, representing the final logistic regression model, demonstrated significant associations (p<0.05) between HIV status and several key variables including gender, age, healthcare facility zone, diagnostic type, treatment outcomes and nutritional status.[16–18] This co-infection rate aligns with global patterns in high-burden settings and underscores the continuing convergence of TB and HIV epidemics in Indonesia.

Most patients presented with pulmonary TB (93.8%), the predominant form due to its transmissibility and diagnostic accessibility through sputum-based tests. Extrapulmonary TB, though less common (6.2%), is more frequently associated with HIV and may be underdiagnosed due to limited access to specialised diagnostic tools.[19] More than half of patients (55.5%) were bacteriologically confirmed through diagnostic methods such as smear microscopy or culture, which remain the diagnostic gold standard for TB because of their reliability in confirming active disease.[20 21] Treatment outcomes showed that 85.9% of patients were recorded as cured, reflecting effective implementation of DOTS strategies and adherence to standardised protocols.[22 23] This high cure rate also suggests functional collaboration between TB and HIV treatment programmes, which typically integrate ART for co-infected patients.[24 25]

Gender distribution showed that 58.8% of patients with TB were male, consistent with global epidemiological patterns. The proportion of HIV-positive cases differed by 3.3% between males and females, and gender was significantly associated with HIV status. Males were 2096 times more likely to be HIV-positive than females, potentially reflecting higher exposure to behavioural risks such as unprotected sex, substance use and lower rates of timely healthcare-seeking.[26 27] Men often present later for diagnosis, which may lead to co-infection being detected at the time of TB diagnosis.[28–30] However, other studies found no gender-related differences in TB-HIV co-infection prevalence. For instance, Alemu *et al* reported that gender was not associated with TB-HIV coinfection among newly diagnosed patients who are HIV positive in Ethiopia.[16] Such inconsistencies may arise from regional differences, sample characteristics or the progression of localised HIV epidemics.

Regarding age, adults aged 30–59 accounted for the largest group of TB cases (49.8%), followed by young adults aged 20–29 (18.3%) and the elderly aged 60+years (16.6%). These findings highlight that productive age groups carry the highest burden of TB, which has implications for national productivity and household stability. Although TB cases among children and adolescents are much lower, they still indicate ongoing transmission. Elderly individuals are at increased risk of TB-HIV co-infection due to immunosenescence, comorbidities and cumulative exposure.[31] Their higher interaction with healthcare services may also increase detection rates of HIV.[32] Late-life HIV diagnoses in elderly individuals are often discovered during TB evaluations.[33 34] Conversely, studies from other regions have identified higher HIV prevalence among younger adults, driven by behavioural risk exposure and lower HIV testing rates among youth.[31]

Healthcare facility location was also a significant determinant. Most patients (82.7%) received care in WIB, followed by WITA at 13.0% and WIT at 4.3%. This distribution mirrors population density and reflects the concentration of healthcare infrastructure in the western region. Urban areas in WIB provide greater access to diagnostic services, explaining the higher number of bacteriologically confirmed cases and TB diagnoses.[35] The difference in HIV-positive proportions between WIB and WIT was 7.4%, and facility location was significantly associated with HIV status. Facilities in WIT were 0.228 times less likely to report HIV-positive patients with TB than those in WIB, reflecting disparities in access, testing capacity and potential under-reporting.[35] This was also likely that these diagnostic methods were more widely available and accessible at the healthcare facilities, specifically those in the WIB region, contributing to the higher number of bacteriologically confirmed cases.[3] Geographical differences may indicate systemic inequalities in service availability and HIV programme implementation.[36]

Pulmonary TB accounted for 93.8% of cases, while extrapulmonary TB represented 6.2%. This is expected, as pulmonary TB is more infectious and easier to detect via sputum-based diagnostic tools.[37] Extrapulmonary TB is more common among immunocompromised patients, particularly those with HIV, which aligns with the elevated HIV rates found in this subgroup in further analyses. The difference in the proportion of HIV-positive cases between patients with extrapulmonary TB and pulmonary TB was 1.6%. The relationship between disease location and HIV status resulted in a p value of 0.011, showing a significant association between the two. Studies have shown that HIV alters immune responses, increasing susceptibility to TB dissemination beyond the lungs.[38]

The OR was 1.337, meaning that patients with extrapulmonary TB were 1.337 times more likely to be HIV-positive compared with patients with pulmonary TB, with a 95% CI of 1.075 to 1.662. The difference in the proportion of HIV-positive cases between clinical and bacteriological diagnoses was 3.2%. The relationship between diagnostic type and HIV status produced a p value of 0.011, showing a significant association between these two. The OR was 1.930, meaning that clinical diagnoses were 1.930 times more likely to result in an HIV-positive status compared with bacteriological diagnosis, with a 95% CI of 1.713 to 2.175. The higher odds (OR: 1.930) of HIV-positive status in clinically diagnosed TB cases could reflect the difficulty of bacteriological confirmation in immunocompromised patients.[21 24]

The majority of TB cases were diagnosed bacteriologically (55.5%), while 44.5% were clinically diagnosed. Bacteriological confirmation is considered the gold standard for TB diagnosis. However, clinically diagnosed cases still represent a significant proportion, possibly due to challenges in sputum collection or smear-negative TB, which are more common among HIV-positive patients. These findings stress the importance of strengthening diagnostic capabilities, particularly for populations with a higher likelihood of clinical TB presentation. However, the substantial proportion of clinically diagnosed cases highlights persistent diagnostic challenges, especially in populations with HIV, who often present with

smear-negative or extrapulmonary TB, making sputum-based detection more difficult.

In Model II, it could be concluded that the factor strongly associated with HIV status was the diagnostic type. The p value for this association was <0.001, suggesting a significant relationship between diagnostic type and HIV status, even after controlling for gender, age, healthcare facility location, treatment outcome and nutritional status. Reinforcing existing evidence that HIV-positive patients are more likely to receive clinical rather than bacteriological diagnoses

In the final Model II, diagnostic type maintained the strongest association, with an OR of 2.446 (95% CI 2.154 to 2.778; p<0.001). HIV-positive individuals frequently present with extrapulmonary involvement or low bacillary load, making bacteriological confirmation difficult.[39] The importance of considering HIV screening and linkage to care, specifically among clinically diagnosed patients with TB, as this subgroup appeared to carry a disproportionately higher HIV burden. The data showed that 85.9% of patients were recorded as cured, with 7.8% experiencing treatment failure and 6.2% recorded as deceased. The high cure rate reflects effective implementation of DOTS (directly observed treatment, short-course) and suggests generally good programme performance. Research in Nepal also reported a comparable success rate, showing that consistent drug supply and patient supervision improve outcomes from DOTS twelfth class.[40] The studies in Brazil reported even with DOTS in place still having main challenges such as the commitment from the patients to do the treatment.[41] However, the non-negligible rates of death and treatment failure indicate a need to investigate comorbidities, particularly HIV and barriers to treatment adherence.

Among patients in this research, 40.1% were underweight, 44.4% had normal nutritional status and 15.4% were overweight. Malnutrition is a well-established risk factor for TB, weakening host immunity and increasing susceptibility. In HIV-positive individuals, specifically those with low CD4 counts, sputum production was often inadequate and smear-negative TB was more common. The difference in the proportion of HIV-positive cases between poor/nutritionally inadequate status and overweight/obesity status was 1.1%. The relationship between nutritional status and HIV status resulted in a p value of 0.020, showing a significant association between nutritional status and HIV status.[42 43]

The high proportion of undernourished patients underscores the directional relationship between TB and malnutrition. Interestingly, HIV-positive status was slightly more associated with overweight/obesity, a finding that may reflect medical-associated weight gain or improved nutritional support in managed programmes. Based on nutritional status assessments, most respondents were classified as having normal nutritional status (44.4%). This could show relatively stable health conditions among the patients, which could contribute to better treatment responses.[44] Adequate nutrition was essential for maintaining immune function, and those with normal nutritional status could have a higher likelihood of responding well to TB and HIV treatment.[42 43] This data did not show the socioeconomic conditions of the patients in the study, or how the patients had access to adequate food and healthcare services.

While SITB provides comprehensive national data, several limitations must be acknowledged. As a secondary dataset, SITB is limited to variables collected for national reporting and excludes key factors such as socioeconomic status, comorbidities beyond HIV, ART adherence, behavioural risks and underlying conditions. Data completeness may vary by region due to inconsistent reporting, resource limitations or geographical barriers, especially in remote settings. Being cross-sectional, the dataset cannot infer causality. Diagnostic bias may occur because HIV testing availability and bacteriological diagnostic capacity differ across regions. These limitations highlight the need for enhanced data quality assurance, improved diagnostic standardisation and complementary research approaches.

Future studies should integrate SITB with other health information systems to obtain more comprehensive risk factor data. Longitudinal designs are needed to assess treatment outcomes over time, understand the impact of co-infections and capture dynamic interactions between TB and HIV. Additionally, regional comparative analyses can help identify disparities in TB-HIV services and guide targeted intervention strategies.

CONCLUSIONS

Using national surveillance data from 2023, this study provides updated insights into TB-HIV co-infection in Indonesia. HIV prevalence among patients with TB highlights the continuing burden of dual infections. Gender, age, facility type, anatomical TB site, diagnostic method, treatment outcome and nutritional status were significantly associated with HIV status. Clinical diagnosis—defined as TB identified without bacteriological confirmation through imaging, symptom assessment or clinician judgement—emerged as the strongest predictor of HIV positivity. This reflects diagnostic challenges among extrapulmonary TB cases, children and immunocompromised individuals with limited access to definitive testing. Because TB and HIV diagnoses are interlinked, strengthening integrated diagnostic pathways, expanding imaging and laboratory capacity and ensuring universal HIV testing for all patients with TB are essential to reduce disparities and improve TB-HIV care.

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