



Prevalence of Bovine Tuberculosis in Cattle and Cattle-Derived Products in Indonesia: A Systematic Review and Meta-Analysis

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Abstract | Bovine tuberculosis (bTB), primarily caused by *Mycobacterium bovis* (*M. bovis*), is an important zoonotic disease in developing countries, including Indonesia. This study aimed to estimate the pooled prevalence of bovine tuberculosis in cattle and cattle-derived products in Indonesia and to evaluate its implications within a One Health framework. A systematic literature search was conducted in PubMed, ScienceDirect, Google Scholar, and Portal Garuda following PRISMA 2020 guidelines. Studies published between 2000 and 2025 reporting the prevalence of *M. bovis* or members of the *Mycobacterium tuberculosis complex* (MTBC) in cattle or cattle-derived products in Indonesia were included. Data were extracted on study characteristics, sample types, diagnostic methods, and prevalence estimates. Meta-analysis was performed using MetaXL 5.3 software with a random-effects model and Freeman–Tukey double arcsine transformation. A total of 9 studies met the inclusion criteria and were included in the meta-analysis. The pooled prevalence of bTB was 8.0% (95% CI: 0.0–23.0), with substantial heterogeneity ($I^2 = 98\%$). Subgroup analysis showed higher prevalence in milk samples 17.0% (95% CI: 0.0–56.0) compared with non-milk samples 2.0% (95% CI: 0.0–6.0), in dairy cattle prevalence 13.0% (95% CI: 0.0–38.0) compared with beef cattle 0.2% (95% CI: 0.0–1.0) and in PCR-based methods 10.0% (95% CI: 0.0–29.0) compared with non-PCR based methods 5.0% (95% CI: 0.0–17.0). However, these findings should be interpreted cautiously due to wide confidence intervals and considerable variability across studies. In conclusion, bovine tuberculosis has been reported in cattle and cattle-derived products in Indonesia, although the overall estimate remains uncertain. Strengthening surveillance and implementing integrated One Health approaches are important to improve disease control.

Keywords | Bovine tuberculosis, *Mycobacterium bovis*, *Mycobacterium tuberculosis complex*, Indonesia, Prevalence, Meta-analysis

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INTRODUCTION

Tuberculosis (TB) is a major infectious disease affecting both humans and animals worldwide. The disease is caused by members of the *Mycobacterium tuberculosis complex* (MTBC), with *Mycobacterium tuberculosis* being

the primary cause of TB in humans (Kurniati *et al.*, 2019). However, another important species within this complex, *Mycobacterium bovis*, is responsible for bovine tuberculosis (bTB), a chronic infectious disease primarily affecting cattle and other mammals. The disease has significant zoonotic potential and remains a public health concern in

many developing countries (Kemal *et al.*, 2019).

Although the global burden of TB is largely driven by *M. tuberculosis*, zoonotic tuberculosis caused by *M. bovis* remains a concern, particularly in low and middle income countries where close contact between humans and livestock is common and food safety practices may be inconsistent (Borham *et al.*, 2022). In Indonesia, which is among the countries with a high burden of human tuberculosis, the specific contribution of zoonotic transmission remains unclear due to limited routine differentiation between *M. bovis* and *M. tuberculosis* in diagnostic systems.

Bovine tuberculosis is primarily transmitted among cattle through inhalation of aerosols, direct contact, or contaminated feed and water (Dejene *et al.*, 2016). Humans may acquire infection through inhalation of aerosols from infected animals or through the consumption of raw or unpasteurized milk and improperly cooked meat products (Borham *et al.*, 2022). However, evidence on the extent of zoonotic transmission in Indonesia is still limited, and most available information is derived from localized studies with varying methodologies

In Indonesia, available studies on bovine tuberculosis are fragmented across regions and differ substantially in terms of diagnostic approaches, sample types, and study designs. Some studies have reported the detection of *Mycobacterium bovis* or MTBC in cattle or cattle-derived products, while others have reported no positive findings. This variability makes it difficult to draw general conclusions about the epidemiological situation of *bovine tuberculosis* at the national level.

Systematic reviews and meta-analyses can be used to synthesize available evidence and provide an overall estimate of disease occurrence. However, when substantial heterogeneity is present, the pooled estimates should be interpreted with caution and considered as indicative rather than definitive measures of prevalence. In this context, a meta-analysis can still be useful to identify patterns, highlight data gaps, and explore sources of variability across studies. Therefore, this study aimed to systematically review and synthesize available evidence on *bovine tuberculosis* in cattle and cattle-derived products in Indonesia. In addition, this study sought to estimate pooled prevalence and explore variations across studies based on sample type, cattle type, and diagnostic methods, while acknowledging the limitations associated with heterogeneous data.

MATERIALS AND METHODS

STUDY DESIGN

This study was conducted as a systematic review and meta-analysis to synthesize available evidence on the

prevalence of *bovine tuberculosis* (bTB) in cattle and cattle-derived products in Indonesia. The review was carried out in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 guidelines to ensure transparency and consistency throughout the study selection process (Haddaway *et al.*, 2022).

The review process followed four main stages: identification, screening, eligibility assessment, and inclusion. In the identification stage, relevant studies were retrieved from selected electronic databases using predefined search strategies. During the screening stage, titles and abstracts were examined to remove clearly irrelevant studies. Full-text articles of potentially eligible studies were then assessed based on predefined inclusion and exclusion criteria. Studies that met *all* criteria were ultimately included in the meta-analysis.

LITERATURE SEARCH STRATEGY

A comprehensive literature search was conducted to identify studies reporting the prevalence or detection of *Mycobacterium bovis* or members of the *Mycobacterium tuberculosis* complex (MTBC) in cattle and cattle-derived products in Indonesia. The search was performed across several electronic databases, including PubMed, ScienceDirect, Google Scholar, and Portal Garuda, to ensure broad coverage of both international and Indonesian publications. The search strategy combined relevant keywords related to the disease, host, and geographical context. The main search terms included “*bovine tuberculosis*”, “*Mycobacterium bovis*”, “*Mycobacterium tuberculosis complex*”, “cattle”, “milk”, and “Indonesia”. These terms were combined using Boolean operators such as “AND” and “OR” to refine the search. Where applicable, variations of keywords and synonyms were also considered to maximize the identification of relevant studies. The search was limited to articles published between 2000 and 2025 and written in English or Indonesian. This time frame was selected to capture both earlier and more recent evidence relevant to the epidemiology of *Bovine tuberculosis* in Indonesia. All retrieved records were compiled and organized prior to the screening process.

ELIGIBILITY CRITERIA

Studies were selected based on predefined inclusion and exclusion criteria to ensure the relevance and consistency of the data included in this review. Studies were eligible for inclusion if they met the following criteria: (1) conducted in Indonesia, (2) reported the detection or prevalence of *Mycobacterium bovis* or members of the *Mycobacterium tuberculosis complex* (MTBC) in cattle or cattle-derived products, (3) provided sufficient numerical data, including the total number of samples examined and the number of positive cases, and (4) were published

between 2000 and 2025 in either English or Indonesian. No restrictions were applied based on diagnostic methods, as variations in diagnostic approaches were expected and considered relevant for exploring heterogeneity across studies. Studies reporting zero positive results were also included, as they provide important information for prevalence estimation and help reduce potential publication bias. Studies were excluded if they were review articles, editorials, commentaries, or other publications without primary data. Experimental studies conducted under controlled laboratory conditions that did not reflect field or surveillance data were also excluded. In addition, studies with insufficient methodological information or incomplete data for calculating prevalence were excluded. When multiple publications reported the same dataset, only one study was included to avoid duplication. Grey literature, including non-indexed journal articles and institutional publications, was considered eligible provided that the studies met the inclusion criteria and reported sufficient primary data.

STUDY SELECTION PROCESS

The study selection process was carried out in several stages following the PRISMA framework. After all records were identified and compiled, duplicate articles were removed. The remaining studies were then screened based on their titles and abstracts to identify those that were potentially relevant to the objectives of this review. Full-text articles of the selected studies were subsequently retrieved and assessed against the predefined inclusion and exclusion criteria. This step ensured that only studies meeting all criteria were included in the final analysis. The screening and eligibility assessment were conducted independently by two reviewers. Any discrepancies between reviewers were discussed and resolved through consensus to ensure consistency in the selection process. The overall selection process was documented using a PRISMA flow diagram, which presents the number of records identified, screened, excluded, and included at each stage of the review.

DATA EXTRACTION

Data extraction was conducted using a standardized data extraction form to ensure consistency across studies. Information extracted from each eligible study included the name of the first author, year of publication, geographical location of the study, type of cattle (dairy or beef), type of sample examined, diagnostic methods used, species of *Mycobacterium* detected, total number of samples tested, and number of positive samples. To improve accuracy, data extraction was performed independently by two reviewers. The extracted data were then compared, and any discrepancies were discussed and resolved through consensus. This process was applied to minimize potential errors and ensure the reliability of the extracted dataset. The

collected data were used to calculate prevalence estimates for each study and to support subgroup analyses based on study characteristics such as sample type, cattle type, and diagnostic methods. These variables were also considered important for exploring potential sources of heterogeneity among the included studies.

QUALITY ASSESSMENT

The methodological quality of the included studies was assessed using the Joanna Briggs Institute (JBI) Critical Appraisal Checklist for Studies Reporting Prevalence Data (Munn *et al.*, 2020). This tool consists of nine domains evaluating key aspects of study quality, including the appropriateness of the sampling frame, sampling method, adequacy of sample size, clarity of study description, validity and reliability of the diagnostic methods, consistency of measurement, and appropriateness of statistical analysis. Each study was assessed independently by two reviewers. For each domain, responses were categorized as “yes,” “no,” or “unclear.” Discrepancies between reviewers were discussed and resolved through consensus to ensure consistency in the assessment process. The overall quality of each study was determined based on the number of criteria fulfilled. Studies meeting 7–9 criteria were classified as high quality, those meeting 4–6 criteria as moderate quality, and those meeting three or fewer criteria as low quality. The results of the quality assessment are presented in a dedicated table. The quality assessment was used to provide an overview of the methodological rigor of the included studies and to support the interpretation of the findings, particularly in the context of heterogeneity across studies.

STATISTICAL ANALYSIS

The meta-analysis was performed using MetaXL5.3 software to estimate the pooled prevalence of *bovine tuberculosis* (bTB) across the included studies. Given the expected variability in study design, sample types, and diagnostic methods, a random-effects model was applied to account for both within-study and between-study variation. To address the presence of studies with very low or zero prevalence, the Freeman–Tukey double arcsine transformation was used prior to pooling the data. This approach helps stabilize variance and allows the inclusion of studies reporting zero events without introducing computational issues. The pooled prevalence was presented along with 95% confidence intervals (CI). Heterogeneity among studies was assessed using Cochran's Q test and the I^2 statistic. The I^2 value was interpreted as an indicator of the proportion of total variation attributable to between-study heterogeneity. Given the high level of heterogeneity observed, the pooled estimates were interpreted with caution and were considered as indicative of general patterns rather than precise measures of national prevalence. Subgroup analyses were conducted to explore

potential sources of variability based on sample type, cattle type, and diagnostic methods. All results were reported descriptively, and emphasis was placed on identifying patterns and differences across studies rather than drawing definitive conclusions from the pooled estimates.

RESULTS

STUDY SELECTION

The literature search identified a total of 4,111 records from electronic databases. After removing 753 records that were identified as ineligible through automated tools, 3,358 records remained for title and abstract screening. Of these, 3,265 records were excluded as they were not relevant to the study objectives. A total of 93 articles were then assessed for full-text eligibility. Among these, 6 articles could not be retrieved. The remaining 87 full-text articles were evaluated in detail, resulting in the exclusion of 78 studies for several reasons, including studies not conducted in Indonesia (n = 54), lack of prevalence data (n = 23), and duplicate data (n = 1). Finally, 9 studies met all inclusion criteria and were included in the meta-analysis. The detailed study selection process is presented in the PRISMA flow diagram (Figure 1).

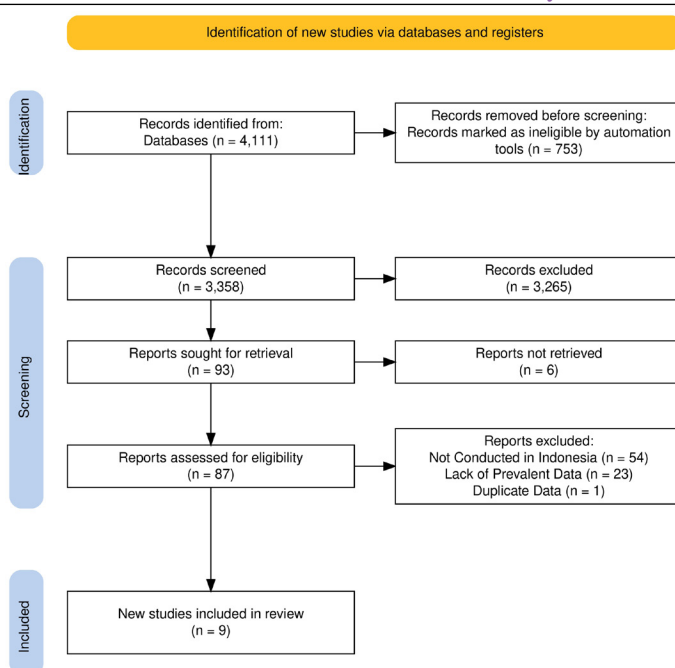


Figure 1: PRISMA flowchart of studies selection of meta-analysis of bovine tuberculosis in Indonesia.

Table 1: Studies Included in the meta-analysis.

No	Author and year	Province	Cattle type	Sample type	Diagnostic method	Sample size	Cases
1	Purwanta <i>et al.</i> (2014)	South Sulawesi	Dairy	Milk	PCR	60	6
2	Agung <i>et al.</i> (2015)	South Sulawesi	Dairy	Milk	PCR	60	28
3	Juwianto <i>et al.</i> (2018)	West Java	Dairy	Tissue	Histopathology + PCR	10	1
4	Darsana <i>et al.</i> (2015)	Bali	Beef	Tissue	PCR	4513	0
5	Putra <i>et al.</i> (2013)	Bali	Beef	Blood	ELISA	180	1
6	Daulay <i>et al.</i> (2017)	West Java	Dairy	Feces	TST + PCR	202	8
7	Putra <i>et al.</i> (2023)	Central Java, Yogyakarta, East Java	Dairy	Milk	PCR	163	0
8	Desire <i>et al.</i> (2024)	East Java	Dairy	Milk	PCR + Ziehl-Neelsen	94	66
9	Sari <i>et al.</i> (2025)	West Java	Dairy	Milk	PCR + Ziehl-Neelsen	60	0

Table 2: JBI critical appraisal checklist for included studies.

No	Studi	1	2	3	4	5	6	7	8	9	Skor	Category
1	Purwanta <i>et al.</i> , 2014	Y	N	Y	Y	Y	Y	Y	Y	U	7	High
2	Agung <i>et al.</i> , 2025	Y	N	Y	Y	Y	Y	Y	N	Y	7	High
3	Juwianto, 2018	N	N	N	Y	N	Y	Y	N	N	3	Low
4	Darsana <i>et al.</i> , 2015	Y	Y	Y	Y	Y	Y	Y	Y	Y	9	High
5	Putra <i>et al.</i> , 2013	Y	N	U	Y	Y	Y	Y	N	U	5	Moderate
6	Daulay <i>et al.</i> , 2017	Y	Y	Y	Y	Y	Y	Y	Y	Y	9	High
7	Putra <i>et al.</i> , 2023	Y	Y	Y	Y	Y	Y	Y	Y	Y	9	High
8	Desire <i>et al.</i> , 2024	Y	N	Y	Y	Y	Y	Y	Y	Y	8	High
9	Sari <i>et al.</i> , 2025	Y	N	U	Y	Y	Y	Y	N	U	5	Moderate

Q1: Sample frame appropriate? 2: Sampling method appropriate? Q3: Sample size adequate? Q4: Subjects and setting described? Q5: Data analysis coverage sufficient? Q6: Valid diagnostic method? Q7: Measurement reliable? Q8: Statistical analysis appropriate? Q9: Response rate adequate? Y= Yes; N= No; U= Unclear; Score Interpretation: 7-9 = High; 4-6 = Moderate ≤3 = Low

Table 3: Pooled prevalence of bovine tuberculosis in Indonesia and subgroup meta-analysis.

Categories	No. of studies	Prevalence		Heterogeneity			p-value for subgroup difference
		Pooled (%)	95% CI	Q	p-value	I ²	
Overall	9	8.0	0.0-23.0	531.65	<0.01	98%	
Subgroup analysis							
Sample Type							<0.01
Milk samples	5	17.0	0.0-56.0	275.43	<0.01	99%	
Non-milk samples (tissue, blood, feces)	4	2.0	0.0-6.0	39.63	<0.01	92%	
Cattle type							<0.01
Dairy	7	13.0	0.0-38.0	293.44	<0.01	98%	
Beef	2	0.2	0.0-1.0	4.72	0.03	79%	
Diagnostic method							<0.01
PCR	8	10.0	0.0-29.0	530.44	<0.01	99%	
Non-PCR	5	5.0	0.0-17.0	72.37	<0.01	94%	

STUDY CHARACTERISTICS

A total of 9 studies published between 2013 and 2025 were included in the meta-analysis. These studies were conducted in several regions of Indonesia, including West Java, Central Java, Yogyakarta, East Java, Bali, and South Sulawesi. However, it is important to note that the included studies were geographically concentrated in a limited number of provinces, and several major regions in Indonesia were not represented. Most of the included studies focused on dairy cattle, while only a small number of studies investigated beef cattle populations. This imbalance reflects the greater availability of data from dairy production systems but may also influence the overall findings of the meta-analysis. The characteristics of the included studies are summarized in Table 1. The types of samples analyzed varied across studies, including milk, tissue, blood, and fecal samples. Among these, milk samples were the most frequently examined. Differences in sample types may influence the detection of *Mycobacterium bovis*, as each sample type reflects different biological processes and diagnostic contexts. A range of diagnostic methods was used across the included studies. Polymerase chain reaction (PCR) was the most commonly applied method, either as a standalone test or in combination with other techniques such as tuberculin skin testing (TST), histopathology, enzyme-linked immunosorbent assay (ELISA), and Ziehl–Neelsen staining. Variations in diagnostic methods may contribute to differences in reported prevalence across studies.

The total sample size varied substantially across studies, ranging from small-scale investigations with as few as 10 samples to larger studies involving several hundred samples, and one study including more than 4,500 samples. In addition, the number of positive cases varied considerably, with some studies reporting no positive findings and others reporting relatively high detection rates. Overall, the variation in study locations, sample types, cattle populations, diagnostic methods, and sample sizes

indicates substantial heterogeneity among the included studies, which should be considered when interpreting the pooled results.

QUALITY ASSESSMENT

The methodological quality of the included studies was assessed using the Joanna Briggs Institute (JBI) critical appraisal checklist for prevalence studies. Overall, most studies were categorized as having moderate to high methodological quality, indicating that the majority of the included studies provided adequate methodological information and appropriate approaches for prevalence estimation. However, some studies showed limitations related to sample representativeness, small sample size, and insufficient reporting of sampling procedures, which may have influenced the reliability of the reported prevalence estimates. The quality assessment results of the included studies are summarized in Table 2.

ANALYSIS FOR OVERALL POOLED PREVALENCE AND SUBGROUP ANALYSIS OF BOVINE TUBERCULOSIS

The pooled prevalence of bovine tuberculosis (bTB) in cattle and cattle-derived samples in Indonesia was estimated using a random-effects model, resulting in an overall prevalence of 8.0% (95% CI: 0.0–23.0). The analysis revealed substantial heterogeneity among the included studies, as indicated by a high Cochran's Q statistic ($Q = 531.65$, $p < 0.001$) and I^2 value of 98%, suggesting considerable variability across studies as can be seen in Figure 2. The pooled prevalence estimates and subgroup analysis results are summarized in Table 3. Subgroup analysis based on sample type showed that studies using milk samples tended to report higher prevalence estimates (17% [95% CI: 0.0–56.0]) compared with studies using non-milk samples, including tissue, blood, and fecal samples (2% [95% CI: 0.0–6.0]) as shown in Figure 5. However, the confidence intervals were wide and included zero, indicating substantial uncertainty in the estimates.

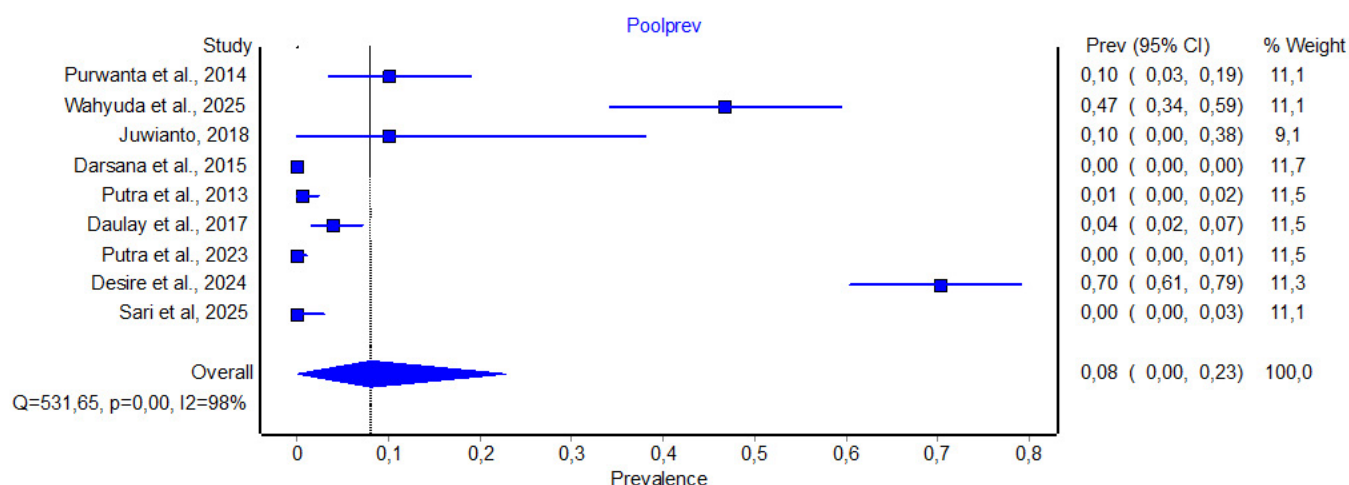


Figure 2: The forest plot of meta-analysis pooled prevalence of bovine tuberculosis in Indonesia.

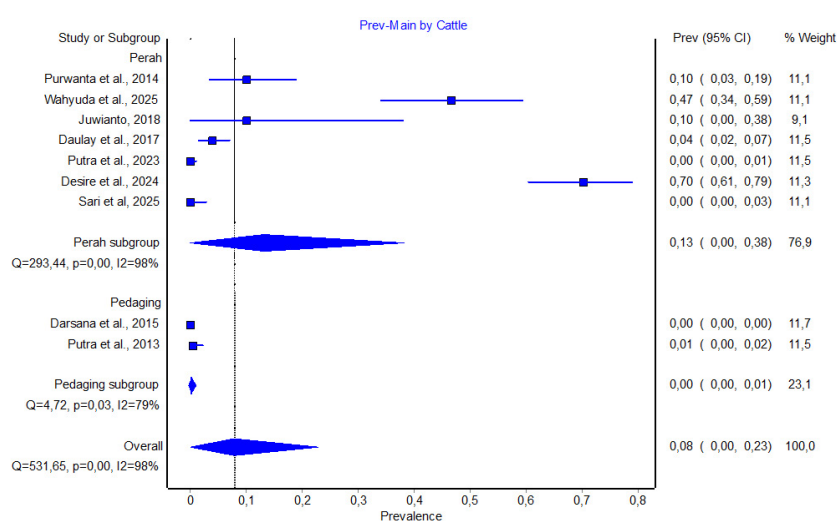


Figure 3: The forest plot of Subgroup analysis based on cattle type of bovine tuberculosis in Indonesia.

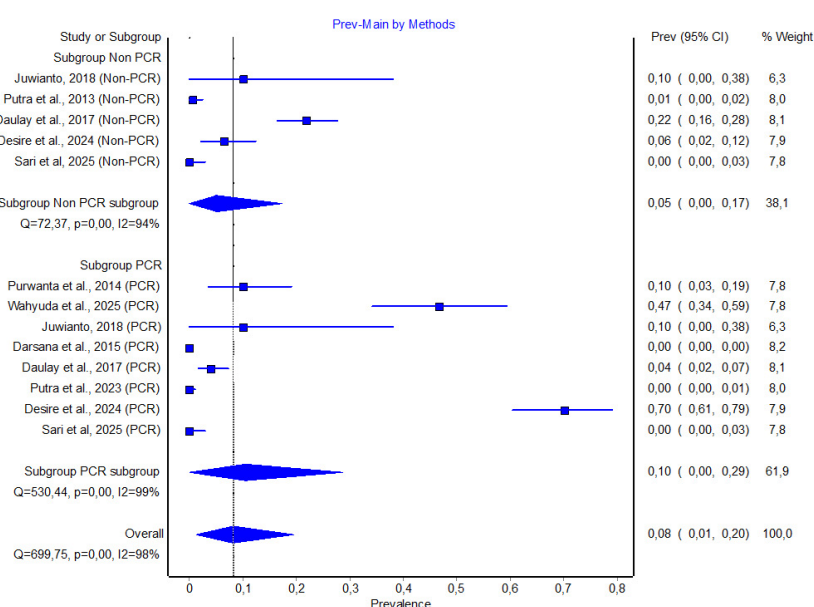


Figure 4: The forest plot of Subgroup analysis based on Diagnostic Methods of bovine tuberculosis in Indonesia.

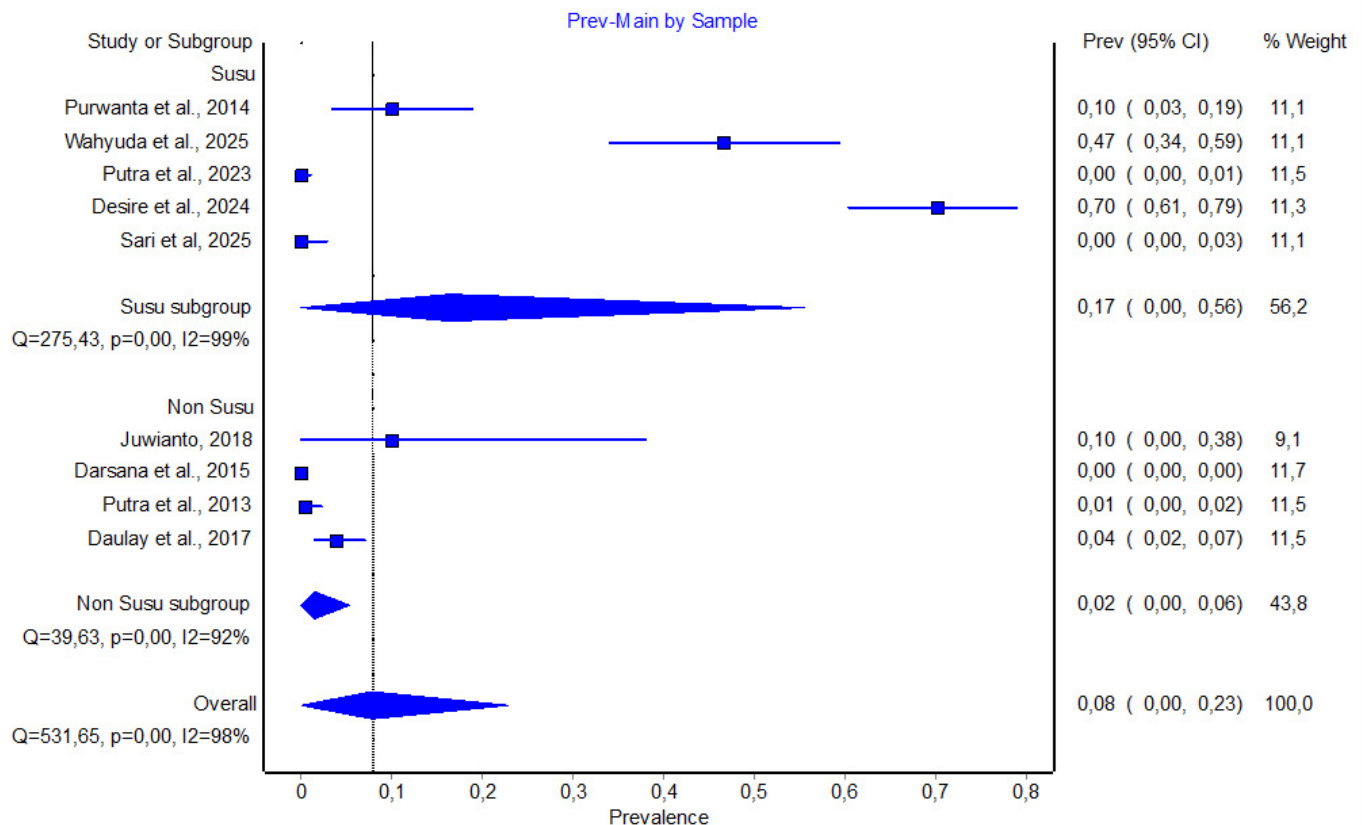


Figure 5: The forest plot of Subgroup analysis based on sample type of bovine tuberculosis in Indonesia.

Similarly, subgroup analysis based on cattle type indicated that studies involving dairy cattle reported higher prevalence (13%; 95% CI: 0.0–38.0) compared with those involving beef cattle (0.2%; 95% CI: 0.0–1.0), as shown in Figure 3. Despite these differences, heterogeneity remained high within subgroups, suggesting that these factors alone do not fully explain the observed variability. Subgroup analysis based on diagnostic methods showed that studies using PCR-based methods reported slightly higher prevalence (10%; 95% CI: 0.0–29.0) compared with non-PCR methods (5%; 95% CI: 0.0–17.0) as presented in Figure 4. Nevertheless, these differences should be interpreted cautiously due to variations in study design, sample types, and diagnostic approaches across studies. Overall, the high level of heterogeneity and wide confidence intervals indicate that the pooled estimates should be interpreted as indicative patterns rather than precise measures of prevalence.

DISCUSSION

This systematic review and meta-analysis suggests that bovine tuberculosis has been reported in cattle and cattle-derived products in Indonesia; however, the pooled estimate should be interpreted as an approximate summary rather than a precise measure of national prevalence. The overall pooled prevalence was 8.0% (95% CI: 0.0–23.0),

but the extremely high heterogeneity ($I^2 = 98\%$) indicates substantial variability across studies. Therefore, the pooled result is better understood as a general indication of available evidence rather than a definitive estimate of disease burden.

When compared with findings from other countries, the estimated prevalence in this study appears broadly similar. A meta-analysis conducted in Pakistan reported a pooled prevalence of approximately 6.06% (Schrish *et al.*, 2025), while studies in Bangladesh reported around 7% (Islam *et al.*, 2024) in India approximately 7.3% (Srinivasan *et al.*, 2018), and in Ethiopia about 5.8% (Sibhat *et al.*, 2017). However, these comparisons should be interpreted cautiously, as they are also based on heterogeneous datasets with different study designs and diagnostic approaches.

Subgroup analysis based on sample type indicated that studies using milk samples tended to report higher prevalence compared with non-milk samples. This finding is biologically plausible, as *Mycobacterium bovis* can be excreted in milk, particularly in animals with systemic infection or mammary involvement (Collins *et al.*, 2022; Kemal *et al.*, 2019). At the same time, this difference may also reflect variation in diagnostic context, since milk, tissue, blood, and fecal samples represent different biological pathways and are not directly comparable. Previous studies

have also highlighted that raw milk consumption may contribute to zoonotic tuberculosis transmission (Borham *et al.*, 2022; Desta *et al.*, 2022).

A similar pattern was observed in the comparison between dairy and beef cattle, where dairy cattle tended to show higher prevalence. This may be associated with differences in management systems, as dairy cattle are typically kept for longer production periods and may experience more prolonged exposure to infectious agents (Clasen *et al.*, 2024; Vries and Marcondes, 2020). In addition, closer contact between animals and farm workers in dairy production systems may facilitate transmission within herds (Dejene *et al.*, 2016). However, it should be noted that the included studies were geographically concentrated, and differences observed between cattle types may also reflect regional variation rather than purely biological differences.

The subgroup analysis based on diagnostic methods showed slightly higher prevalence in PCR-based studies (8%) compared with non-PCR methods (5%). This pattern is consistent with previous findings indicating that molecular techniques such as PCR have higher sensitivity and specificity compared with conventional diagnostic methods (Ferrari *et al.*, 2024; Siala *et al.*, 2017). PCR is capable of detecting MTBC DNA even at low bacterial loads or when organisms are not viable (Hida *et al.*, 2012). Nevertheless, this comparison should be interpreted with caution because the included studies differed in sample types, study designs, and combinations of diagnostic methods.

It is also important to consider that the methodological quality of the included studies varied. While most studies were classified as moderate to high quality, one study was categorized as low quality based on the JBI critical appraisal (Munn *et al.*, 2020). This study had limitations in terms of sampling approach and representativeness, which may have contributed to variability across studies and influenced the overall heterogeneity. Therefore, its findings should be interpreted with caution in the context of the pooled analysis.

From a public health perspective, the findings of this study highlight the potential relevance of bovine tuberculosis within a One Health context. Transmission of *Mycobacterium bovis* involves interactions between animal health, human health, and environmental factors (Borham *et al.*, 2022). Individuals who are in close contact with cattle, such as farmers, veterinarians, and slaughterhouse workers, may be at increased risk of exposure (Palmer *et al.*, 2012). However, it is important to note that this study did not include human data, and therefore the extent of zoonotic transmission in Indonesia cannot be directly determined.

Overall, this study indicates that bovine tuberculosis has been detected in cattle and cattle-derived products in Indonesia, but the available evidence remains limited and heterogeneous. Future research with more representative sampling, standardized diagnostic approaches, and broader geographic coverage is needed to improve the understanding of bovine tuberculosis epidemiology in Indonesia.

STUDY LIMITATIONS

This study has several limitations that should be considered when interpreting the findings. First, the number of available studies was relatively limited, with only nine studies meeting the inclusion criteria. In addition, these studies were conducted in a limited number of provinces, meaning that several regions of Indonesia were not represented. As a result, the findings may not fully reflect the national situation.

Second, there was substantial heterogeneity among the included studies ($I^2 = 98\%$), indicating considerable differences in study design, sampling approaches, diagnostic methods, and sample types. This high variability makes it difficult to interpret the pooled estimate as a single, precise measure of prevalence. Third, the use of different diagnostic methods across studies may have influenced the reported results. Variations in sensitivity and specificity between molecular and conventional methods could lead to differences in detection rates, which may contribute to the observed variability.

In addition, the included studies differed in terms of sample types and study settings, including variations between dairy and beef production systems. These differences may have introduced additional variability that was not fully accounted for in the analysis. Furthermore, variation in study quality, including the presence of one study categorized as low quality, may have contributed to the observed heterogeneity and should be taken into account when interpreting the results.

Finally, although studies reporting zero prevalence were included, the possibility of publication bias cannot be entirely ruled out. Due to the limited number of studies, a formal assessment of publication bias was not performed. Despite these limitations, this study provides a useful overview of the available evidence and highlights important gaps that should be addressed in future research.

CONCLUSION

This systematic review and meta-analysis provides a synthesis of available evidence on bovine tuberculosis (bTB) in cattle and cattle-derived products in Indonesia. The findings suggest that bovine tuberculosis has been

reported in several regions and sample types; however, the pooled prevalence estimate should be interpreted with caution due to substantial heterogeneity among studies. Subgroup analyses indicated that higher prevalence estimates were observed in milk samples and dairy cattle, as well as in studies using PCR-based diagnostic methods. Nevertheless, these patterns should be understood as indicative trends rather than definitive differences, given the variability in study design, sample types, and diagnostic approaches.

Overall, the results highlight the need for strengthened surveillance and more standardized research approaches to better understand the epidemiology of bovine tuberculosis in Indonesia. From a public health perspective, the findings support the importance of a One Health approach that integrates animal health, human health, and food safety sectors, particularly in settings where close contact with livestock and consumption of animal products may increase exposure risks. Future studies with more representative sampling, consistent diagnostic methods, and broader geographic coverage are needed to provide more reliable estimates and to support evidence-based control strategies.

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NOVELTY STATEMENT

This study provides an updated systematic review and meta-analysis of bovine tuberculosis in Indonesia by incorporating more recent studies and broader subgroup analyses, including cattle type, sample type, and diagnostic methods. In addition, this study highlights the potential role of cattle-derived products and emphasizes the importance of a One Health approach for bovine tuberculosis surveillance and control in Indonesia.

AUTHOR'S CONTRIBUTION

Andi Muh Zulkifli contributed to literature searching, study selection, data extraction, statistical analysis, interpretation of results, and manuscript drafting.

Wahiduddin contributed as a research supervisor, study design and methodology, provided scientific guidance throughout the research process, and critically revised the manuscript.

Andi Zulkifli contributed as a research supervisor and

contributed to methodological guidance and manuscript revision.

Masni contributed through academic input, constructive feedback, and improvement of the manuscript

Stang contributed through academic evaluation, scientific suggestions, and manuscript review.

GENERATIVE AI AND AI ASSISTED TECHNOLOGY STATEMENT

The authors declare that no generative AI and AI assisted technology was used in the creation of this manuscript.

CONFLICT OF INTEREST

The authors have declared no conflict of interest.

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