

Prevalence of bovine tuberculosis in cattle slaughtered in abattoirs in Taraba State, Nigeria

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ABSTRACT: Bovine tuberculosis is a serious zoonotic disease caused by *Mycobacterium bovis* and other members of the *Mycobacterium tuberculosis complex* (MTBC). The disease affects mainly cattle but can also affect humans and other domestic and wild mammals. The disease poses serious health risks to humans and livestock. The study investigated the prevalence of bovine tuberculosis in cattle slaughtered in abattoirs in Taraba State, Nigeria. The study was conducted between February and May 2023. The study adopted a cross-sectional design. The study was conducted in the Jalingo, Bali and Wukari abattoirs, representing Taraba North, Taraba Central, and Taraba South senatorial zones, respectively, selected based on the number of cattle slaughtered daily. A systematic random sampling technique was used for cattle selection, and the lungs of 400 slaughtered cattle were sampled. A proportionate distribution based on the abattoir's slaughter capacity was used, 80% (320) of the samples from Jalingo abattoir and 10% (40) each to Bali and Wukari slaughter slabs. Acid-fast bacilli detection and polymerase chain reaction techniques were the laboratory techniques that were utilised in this study. Bovine tuberculosis was found to have a prevalence of 1.5% (6/400) in cattle slaughtered in Taraba State through acid-fast bacilli detection. Out of the six tissue samples that tested positive for acid-fast bacilli, 2(33.3%) samples were identified as *Mycobacterium tuberculosis complex* (MTBC), and 1(16.7%) sample was identified as *Mycobacterium bovis* through Polymerase Chain Reaction (PCR) analysis. These findings highlighted the presence of bovine tuberculosis in slaughtered cattle in Taraba State, with a considerable proportion of positive cases detected. These findings pose a risk to food safety in Taraba State, with potential for zoonotic transmission.

Keywords: Abattoirs, Bovine, *Mycobacterium bovis*, Prevalence, Taraba State.

INTRODUCTION

Bovine tuberculosis (BTB) is a long-lasting disease that is spread from animals to humans. It is mostly caused by the rod-shaped bacteria *Mycobacterium bovis* (Smith *et al.*, 2006), along with other bacteria in the *Mycobacterium tuberculosis complex* (MTBC) (Brosch *et al.*, 2002). *Mycobacterium bovis* is a type of acid-fast bacillus that is classified within the *Mycobacteriaceae* family and the *Mycobacterium* genus (Smith *et al.*, 2006). *Mycobacterium bovis* primarily affects cattle, but it can also infect humans and induce a disease with comparable pathological

characteristics to *Mycobacterium tuberculosis*, which is highly harmful to humans (Biet *et al.*, 2005). Several studies have documented the presence of *Mycobacterium tuberculosis*, which is responsible for tuberculosis in humans and *Mycobacterium bovis* which causes bovine tuberculosis in cattle (Cadmus *et al.*, 2010; Krajewska *et al.*, 2015; Gelalcha *et al.*, 2019). Bovine TB can infect cattle, humans, non-human primates, goats, cats, dogs, pigs, buffalo, badgers, possums, deer, and bison (Grange, 2001). Bovine TB can be spread by breathing in infected

aerosol droplets, coming into direct contact with an infected animal, being in a contaminated environment, or eating milk and meat that are contaminated with *Mycobacteria* (Yahyaoui-Azmi *et al.*, 2017). Bovine TB causes mycobacterial mastitis, which releases germs into milk. Unpasteurized milk can spread the bacterium to humans (Garnier *et al.*, 2003). The Northern Nigerian "fura da nono," made with unpasteurized milk, may also cause TB. Nomadic herders who live near their animals also drink unpasteurized milk, increasing infection risk (Jenkins *et al.*, 2011). Multiple investigations have shown bovine TB in Nigerian abattoirs. Labourers who do not use protective gear are at risk for bovine TB (Cadmus *et al.*, 1999).

Bovine TB has symptoms similar to those of human tuberculosis. It causes prolonged coughing, weakness, and thoracic granulomas (Taylor *et al.*, 2007). Granulomas may spread to the genitalia (Shitaye *et al.*, 2006). However, clinical signs may include muscle weakness, trouble breathing, a lack of appetite, poor physical condition, and a persistent cough. Lymphadenopathy may clog airways, digestive tracts, and blood vessels, especially in the head and neck, worsening the animal's disease (Ramos *et al.*, 2015). Extra-pulmonary lesions, such as pin-point tubercles on gastrointestinal organs, describe generalised bovine TB (Cantres-Fonseca *et al.*, 2018). The lesions' symptoms resemble *Mycobacterium tuberculosis* (Grange, 2001; Adane *et al.*, 2020). Caseous necrosis lesions are seen in the tuberculous lung (Ramos *et al.*, 2015) and tuberculous granulomas are a pathognomonic sign of the condition (Wangoo *et al.*, 2005).

The prevalence of bovine tuberculosis in Nigeria varies from 0.5% in Oyo, a state in the southwest with a small livestock population, to 12.27% in Gombe, a state in the northeast with a high concentration of animals (Aliyu *et al.*, 2009). Incidents of bovine tuberculosis infections have been reported in the Eastern region of the country (Itah and Udofia, 2005). A study conducted in Jos, North-central Nigeria, revealed a prevalence of 15.4% of *Mycobacterium bovis* in human pulmonary infections (Oragwa *et al.*, 2017).

Nigeria is positioned as the sixth country with the highest burden of tuberculosis among the 30 nations classified as having a high tuberculosis burden worldwide. Furthermore, Nigeria bears the greatest burden of tuberculosis in Africa (WHO, 2022). Therefore, the objective of this study is to determine the current prevalence of tuberculosis in cattle that are often slaughtered in Taraba State, Nigeria.

METHODOLOGY

Study location

The study was conducted in abattoirs of three out of the sixteen Local Government Areas (LGA), the 3 LGAs were Jalingo metropolis, Bali and Wukari in Taraba State, Nigeria; each representing a senatorial zone, Taraba

North, Taraba Central and Taraba South, respectively. The State is situated within the geographical coordinates of latitude 6°25'N to 9°30'N and longitude 9°30'E to 11°45'E (Figure 1). It experiences a tropical continental climate. Taraba State, the second-largest state in Nigeria with a land area of around 60,291 km², has a population of over 2.3 million people, as recorded in the 2006 population census (National Population Commission, 2006). The state experiences an annual growth rate of 3.1%. Cattle slaughtered at the abattoirs are sourced from the cattle markets in Taraba State (Tella cattle market, Iware cattle market, Bantaji cattle market, Garba-Chede cattle market, Mararraba-Donga cattle market); these are the primary livestock markets in the State that accept cattle from the northern region of Nigeria and bordering African nations such as Cameroon, Mali, Chad, and Niger. The slaughter capacity of 45-55, 5-10 and 7-15 cattle per day was registered from Jalingo abattoir, Bali slaughter slab and Wukari Slaughter slab, respectively (Taraba State Government, 2022).

Study design and data collection

Sample size determination

The formula described by Thrusfield (2007) was used to determine the sample size for the study.

$$N = Z^2 P (1-P)/d^2$$

Where: n = Sample size, Z = Appropriate value for the standard normal deviation for desired confidence level = (1.96), P = Anticipated prevalence rate, Q = 1-P, D = Desired absolute precision (2%), P = Prevalence of (4.10%) Bikom *et al.*, 2021).

$$N = \frac{1.96^2 \times 0.041(1-0.041)}{0.02 \times 0.02} = 378 \text{ (minimum sample)}$$

A minimum sample size of 378 samples is required. However, 400 samples were collected from slaughtered cattle to test for bovine tuberculosis from the selected zonal abattoirs of Taraba State for proportionate sampling. Accordingly, out of the 400 cattle, a proportionate distribution was used to allocate the sample size for the three Local Government Areas in the State, giving a share of 80% (320) to Jalingo abattoir and 10% (40) each to Bali and Wukari slaughter slabs. This was based on their slaughter capacity of 45-55, 5-10 and 7-15 cattle per day for Jalingo abattoir, Bali slaughter slab and Wukari Slaughter slab, respectively (Obialigwe *et al.*, 2024).

Sampling technique

The study was carried out from February to May 2023 in the abattoirs in Taraba State. A systematic random sampling technique was used for cattle selection. On

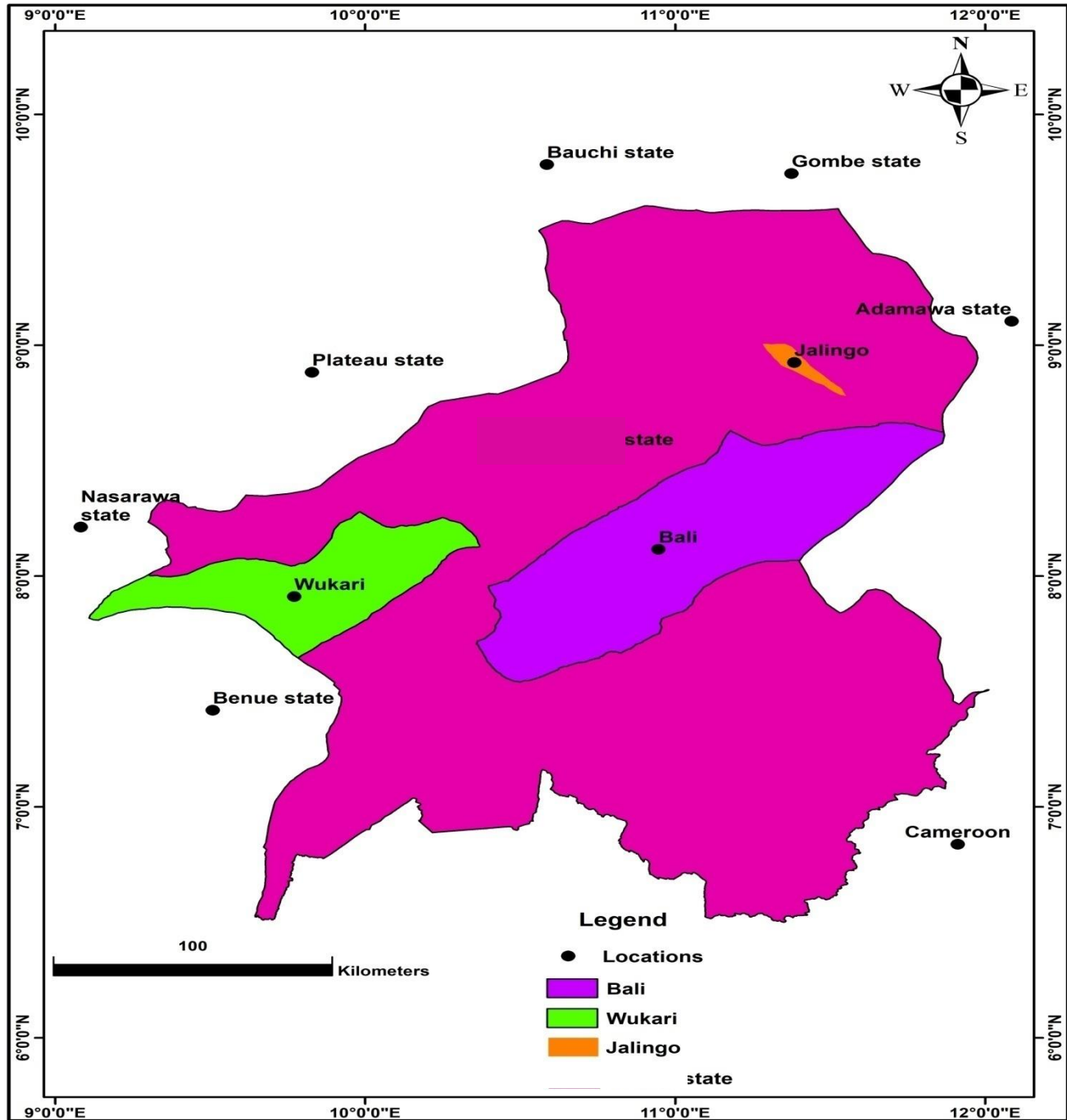


Figure 1. Map of Taraba State and the Study Areas in Taraba State, Nigeria. The map was created in ArcMap version 10.7 (ESRI Co., Redlands, California, USA)® with data from the Nigerian Geological Survey Agency (NGSA).

average, 45-55, 5-10 and 7-15 cattle from Jalingo abattoir, Bali slaughter house and Wukari Slaughter house, respectively, were slaughtered daily. Jalingo LGA was selected to represent Taraba North, Bali, Taraba Central and Wukari LGA to represent Taraba South. The n^{th} term (sampling interval) for the systematic random sampling method was calculated by dividing the total population size by the desired sample size (n). Based on the calculated

sampling interval of four for Jalingo abattoir, and three for Wukari and Bali slaughter houses, respectively. Hence, every fourth slaughtered cattle was sampled in Jalingo abattoir, and every third cattle was sampled in both Wukari and Bali Slaughter houses. Daily, the first cattle was selected by balloting between 1 to 4 in Jalingo abattoir and between 1 to 3 in both Wukari and Bali Slaughter house. Thereafter, every fourth cattle (by adding 4 to the initial

number picked) was selected till the sample size of 320 in Jalingo abattoir was achieved. Also, at both Wukari and Bali slaughter house, every third cattle (by adding 3 to the initial number picked) was selected till the sample size of 40 each in Wukari and Bali slaughter house was achieved.

Sample collection

Cattle were selected by systematic random sampling in Jalingo, Wukari and Bali abattoirs. During the postmortem inspection of the carcasses in the abattoir under a bright-light source, the lung tissues of the selected cattle were sampled for subsequent examination for bovine tuberculosis. Data of the sampled cattle, such as sex and breed, were determined and documented as described by Nwankwo *et al.* (2019). The slaughtered cattle were classified as either young or adult, which was carried out at the abattoir after slaughter using the time of appearance and the degree of wear of the temporary and permanent teeth as described by Torell *et al.* (2003). The body condition of the cattle was assessed using the modified body score condition method developed by Moran (2005). The cattle in the study were classified into four groups based on their body condition scores. i) Good: cattle exhibiting no visible bones and displaying clear signs of fat accumulation; ii) Moderate: cattle without visible bones and displaying minimal or no evidence of fat accumulation; iii) Emaciated: thin cattle with prominent ribs and hip bones; iv) Highly emaciated: cattle with extremely thin flesh covering, prominently protruding ribs and hip bones, and significant depression of the lumbar fossa (Moran, 2005). Samples were collected and labeled into a sterile screw-capped, leak-proof specimen containers (with 0.9% normal saline solution to keep them moist and to maintain cell viability) and were stored at 4°C and were later transported in a sealable pack and were put inside a cooler containing ice pack to National Veterinary Research Institute (NVRI) Vom, where analysis were carried out at the Central Diagnostic Laboratory and Biotechnology Laboratory.

Laboratory test procedure

Ziehl-Neelsen staining technique

After thawing at room temperature, 5 g of each lung tissue was pulverised using a sterile mortar and pestle and homogenised in 10 mL of sterile normal saline solution for 10 minutes. The homogenates were sterilised for 15 minutes in 2 ml of 4% NaOH. Using phenol red as an indicator, the sterilised solution was neutralised with 1% (0.1N) HCl. Finally, 15 minutes of 3000 rpm centrifugation concentrated the solution. The liquid component was discarded. A small amount of each completely processed sample's solid portion was used to generate a thin Ziehl-

Neelsen staining layer. The pellet loops were delicately spread over a pristine, oil-free microscopic slide, left to dry in the air, and then fastened by applying heat, following the method outlined by Ahmad *et al.* (2017). The stained slide was then drenched with concentrated carbol fuchsin on an iron rack. It was then gently cooked for 5 minutes to avoid boiling. After rinsing, the slide dried naturally. After drying, the slide was covered with 3% v/v acid alcohol for 2–5 minutes until the smear was light pink. Then, it was cleaned with clean water and dried naturally. The smear was then dyed with methylene blue for 1–2 minutes. The stain was removed using purified water and left to dry naturally. The dyed slides were examined using a light microscope with an x100 objective lens and oil immersion to identify acid-fast bacilli. The presence of pinkish-red rod-shaped bacteria on a blue-black background indicates acid-fast positivity, which strongly confirms TB (Ahmad *et al.*, 2017).

Polymerase Chain Reaction (PCR) Technique

Acid fast positive samples to Ziehl-Neelsen staining were further subjected to Polymerase Chain Reaction (PCR) analysis.

DNA Extraction & Purification: Approximately 25mg of the lung tissue sample was homogenised with a pestle and mortar, and then 200µl of the homogenised lung tissue was added to a 1.5 ml microcentrifuge tube containing 80 µl PBS, and 100 µl Buffer ATL was added. The DNA extraction and purification were performed as described by the manufacturer QIAGEN (2016).

PCR Reaction Mix (Master Mix): The PCR reaction mix was prepared for each primer, which typically includes the following components: DNA template, primer, PCR buffer, dNTPs (dATP, dGTP, dCTP, dTTP), Taq DNA polymerase, MgCl₂, and Nuclease-free water. Two separate PCR reaction mixes were prepared for each primer (Table 1). PCR for each primer set was done with the following reaction mixture: 10µl of DNA Template, 1x TE reaction buffer [containing 10mM Tris-HCl (pH 8.3), 50mM of KCl, 1.3mM of MgCl₂, and 0.001% of gelatin], 2.5U Taq polymerase, 0.2 mM of each deoxynucleosidetriphosphate (dNTPs), and 75 pmol/µl of each primer (Table 1) and 6.5µL of Nuclease-free water was prepared.

DNA Amplification Protocols: The PCR amplification was performed using GeneAmp PCR System 9700(Applied Biosystem®) thermal cycler with the following conditions as described by Sposito *et al.* (2014) with slight modification:

Initial denaturation – the reaction mixture was heated at 95°C for 5 minutes to denature the DNA template. After an

Table 1. List of primers used in this study.

Primer	Primer sequence	Expected band size (bp)	Reference
TB1	5'-CCTGCGAGCGTAGGCGTCGG-3'	123 base pairs (bp) <i>MTBC</i> fragment	Eisenach <i>et al.</i> (1990)
TB2	5'-CTCGTCCAGCGCCGCTTCGG-3'		
<i>PncAMB-1.2</i>	5'-ATGCGGGCGTTGATCATCGTC-3'	186 base pairs (bp) <i>M.bovis</i> fragment	DeLosMonteros <i>et al.</i> (1998)
<i>PncAMB-2</i>	5'-CGGTGTGCCGGAGAAGCCG-3'		

MTBC Fragment: The MTBC (*Mycobacterium tuberculosis complex*) fragment are specific DNA sequence targeted by the TB1 primer. This sequence is characteristics of bacteria within the *Mycobacterium tuberculosis complex*, which includes *Mycobacterium tuberculosis*, *M. bovis*, *M. africanum*, *M. orygis*, *M. microti*, *M. canettii*, *M. caprae*, *M. pinnipedii*, and *M. suricattae*. *PncAMB-1.2* and *PncAMB-2* Primers: are specific for *Mycobacterium bovis*. These primers target a unique DNA sequence resulting in an expected band size of 186 base pairs, which is used to distinguish *M. bovis* from other members of the *Mycobacterium tuberculosis complex*.

initial denaturation step (at 95°C for 5 minutes), 40 amplification cycles (to amplify the target DNA exponentially) was performed as follows: Denaturation at 94°C for 1minute (to separate the DNA strands into two single strands, in order to expose the target region for subsequent amplification), annealing at 68°C for 1 minute (to allow the primers to bind to their complementary sequences on the single-stranded DNA template) and primer extension at 72°C for 1 minute (to allow the DNA polymerase to extend the primers along the DNA template, resulting in the synthesis of new DNA strands). After the last cycle, a final extension step was performed at 72°C for 10 minutes to ensure that all the remaining single-stranded DNA templates are fully extended (Sposito *et al.*, 2014).

Gel Electrophoresis: After amplification, the PCR products were resolved and analysed by using 1.5% agarose gel electrophoresis. The 1.5% agarose gel was created by measuring 1.5g of agarose powder and dissolving it in a conical flask with 100 ml of TBE buffer. The mixture was then heated in a microwave oven for 1-3 minutes until it completely liquefied. After that, it was cooled by gently swirling at room temperature. A volume of five microliters (μ l) of ethidium bromide was introduced into the molten gel, which was subsequently poured into a gel caster equipped with a comb. The gel was then allowed to solidify, after which the combs were removed. The gel caster tray was carefully placed in the electrophoresis tank, and the gel was totally submerged in the buffer solution (TBE).

The first lane (well) of the gel was loaded with the 100 base pair (bp) DNA molecular weight marker (2 μ l). Purified DNA from the reference strains *M. tuberculosis* (H₃₇R_v) (1 μ l) and *M. bovis* (1 μ l) (AF2122/97 reference genome) were used as the positive controls to validate the tested samples, and nuclease-free water was used as a negative control to rule out the possibility of PCR contamination (Chitale *et al.*, 2022; Farrel *et al.*, 2019). The samples were carefully loaded into the additional wells of the gel. Gel electrophoresis was done at 100v for 1 hour, and the gel was carefully removed from the tank. Finally, the gel was immediately visualised using BioRadGelDoc[®] imager (Musawa *et al.*, 2021).

Statistical analysis

Statistical Package for the Social Sciences (SPSS) Version 25 (IBM[®] Statistics) was used to perform descriptive and inferential statistics. The data obtained were presented using frequency and percentage. Prevalence of bovine tuberculosis was calculated by dividing the number of positive samples by the total number of slaughtered cattle inspected over a period of time and presented as percentage. The Pearson Chi-square test was used to determine a possible association between bovine tuberculosis infection and the age, breed, body condition score, and sex of the sampled cattle processed for Ziehl-Neelsen microscopy. Descriptive and inferential statistics were used to summarise the data that were obtained (percentages, 95% confidence interval and values of $p < 0.05$ were considered significant throughout the study).

RESULTS

Ziehl-Neelsen microscopy

Out of the 400 slaughtered cattle sampled, 90 were male and 310 were female, having 2 (2.22%) and 4 (1.29%) frequencies for acid-fast bacilli (Table 2) (Figure 2). The mean age of the slaughtered cattle is 1.18 ± 0.387 SD years. The young cattle (73) and adult cattle (327) were 1 (1.37%) and 5 (1.53%) acid-fast bacilli positive, respectively. The association between bovine tuberculosis and the age of cattle was not statistically significant ($p > 0.05$) (Table 2).

In this survey, the slaughtered cattle breeds revealed that Wadara had the highest acid-fast bacilli percentage, 4 (1.38%), while Sokoto Gudali 1 (1.61%), Red Bororo 0 (0%) and White Fulani had 1 (5.88%), respectively. The association between bovine tuberculosis and breeds of slaughtered cattle was not statistically significant ($p > 0.05$) (Table 2).

Furthermore, out of the slaughtered cattle sampled, the distribution of acid-fast bacilli positive samples among the slaughtered cattle body condition score surveyed revealed

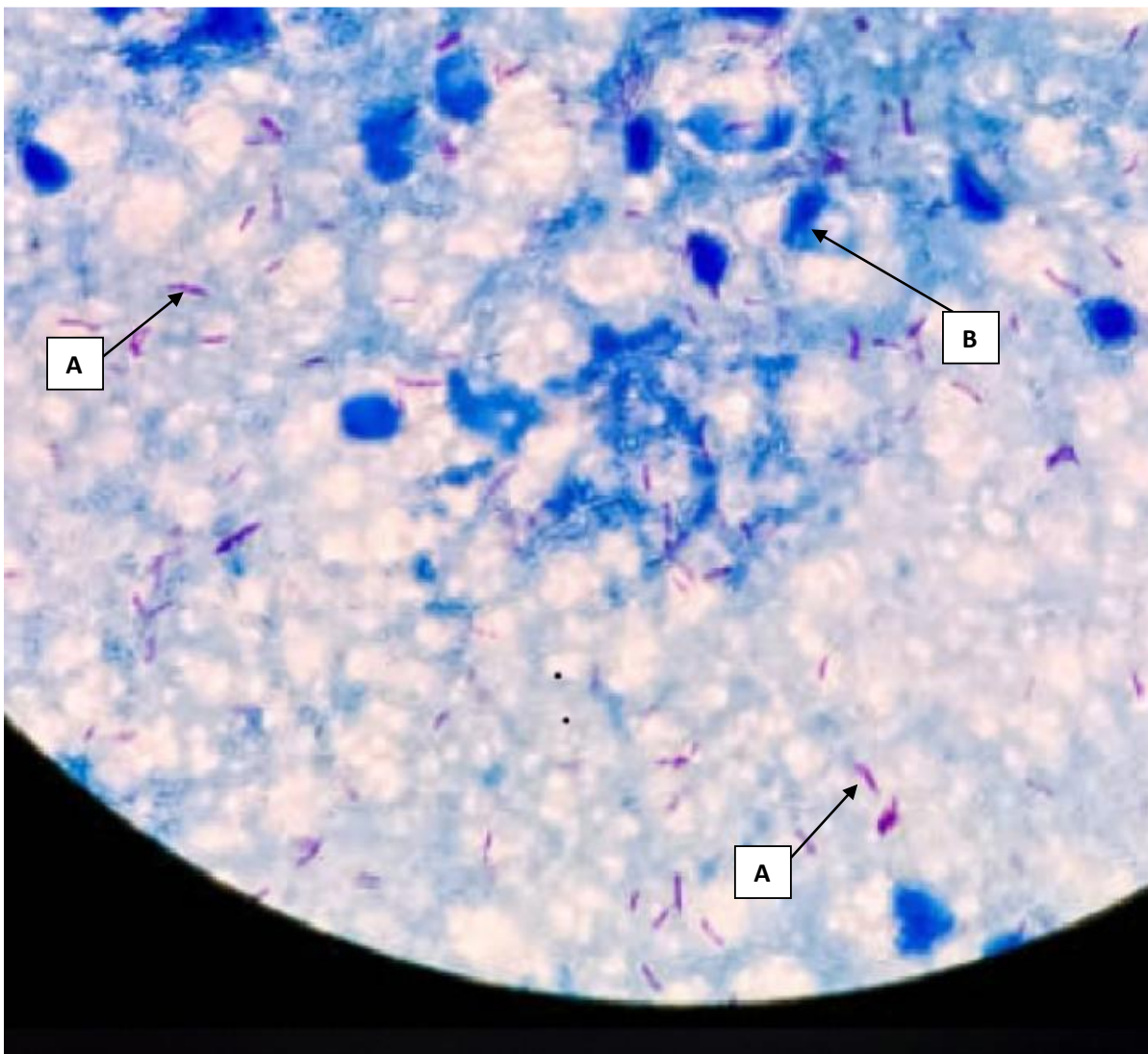


Figure 2. Acid-fast bacilli appeared pinkish (A) in a bluish background (B), detected in lung tissue from slaughtered cattle (x100).

that highly emaciated cattle had the highest percentage of acid-fast bacilli 2 (10.53%), followed by emaciated cattle 3 (4.41%). Slaughtered cattle with the body condition score, moderate and good had a prevalence of 1 (0.47%) and 0%, respectively. The association between bovine tuberculosis and body condition score of slaughtered cattle was statistically significant ($p = 0.001$) (Table 2).

An overall prevalence of 1.5% (6/400) bovine tuberculosis in the slaughtered cattle's lungs sampled at abattoirs across the three geopolitical zones (Northern, Central and Southern) of Taraba State was obtained. Out of these, 1.9% (6/320) were found in the Northern Taraba (Jalingo), 0 (0%) each found in the Central Taraba (Bali) and Southern Taraba (Wukari), respectively (Table 2). There was no statistically significant association between bovine tuberculosis in different parts of the State ($p > 0.05$) (Table 2).

Polymerase Chain Reaction (PCR)

Out of the 6 tissue samples from the slaughtered cattle that tested positive to acid-fast bacilli, two samples (2/6) were positive for *M. tuberculosis complex (MTBC)* by PCR, amplifying the 123bp fragments, while one tissue sample (1/6) was positive for *M. bovis* amplifying the 186bp fragment (Figure 3).

DISCUSSION

The study has revealed a 1.5% prevalence of bovine tuberculosis among slaughtered cattle by identification of acid-fast bacilli using Ziehl-Neelsen microscopy. The slightly low prevalence in this study may be due to the sampling technique utilised for the study and the disease

Table 2. Acid-fast bacilli in cattle slaughtered at the abattoirs in Taraba State, base on Ziehl-Neelsen Microscopy.

Variables	Number of cattle sampled	Mean±Standard Deviation	Ziehl-Neelsen Staining (Positive %)	Ziehl-Neelsen Staining (Negative)	Chi-Square (χ^2)	p-value
Location of abattoir						
Jalingo	320		6 (1.88)	314		
Wukari	40	1.3±0.641	0 (0)	40	1.523	0.467
Bali	40		0 (0)	40		
Age						
Young	73		1 (1.37)	73		
Adult	327	1.18±0.387	5 (1.53)	321	0.014	0.907
Sex						
Male	90		2 (2.22)	88		
Female	310	1.78±0.418	4 (1.29)	306	0.410	0.522
Breed						
White Fulani	290		4 (1.38)	286		
Sokoto Gudali	62		1 (1.61)	60		
Red Bororo	31	1.44±0.811	0 (0)	31	2.512	0.473
Wadara	17		1 (5.88)	17		
Body condition score						
Good	101		0 (0)	101		
Moderate	212		1 (0.47)	211		
Emaciated	68	2.01±0.784	3 (4.41)	64	16.856	0.001*
Highly emaciated	19		2 (10.53)	18		

*The statistical test used is Chi-Square (χ^2) and $p < 0.05$ is considered significant.

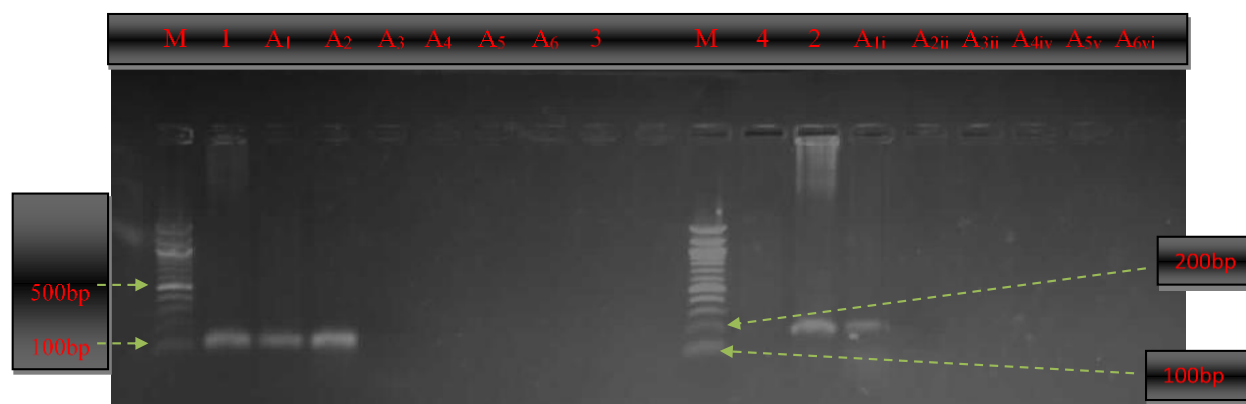


Figure 3. Agarose gel image showing amplified 123bp (*MTBC*) and 186bp (*M. bovis* species-specific fragment). Electrophoresis on 1.5% agarose gel. Lane M: DNA molecular weight marker (100bp DNA ladder); Lanes 1 & 2 are positive controls (*M. tuberculosis* H₃₇R_v and *M. bovis* respectively); Lanes 3 & 4 are negative controls (nuclease-free water); Lane A₁ & A₂ are positive samples to *MTBC* showing 123bp bands; Lane A_{1i}: showing positive sample diagnostic for *M. bovis* at 186bp band. Lane A₃, A₄, A₅, A₆, A_{2ii}, A_{3iii}, A_{4iv}, A_{5v}, & A_{6vi} are all negative samples.

condition of the slaughtered cattle. The low prevalence in this study could also be a result of the low sensitivity of Ziehl-Neelsen staining for detecting *Mycobacterium bovis*, especially in tissues with a low bacterial load.

The prevalence of bovine tuberculosis (1.5%) in this study is lesser than the prevalence of 3.56% reported by

Bikom *et al.* (2021) through acid-fast bacilli detection in Cross River State. Ahmad *et al.* (2017) reported a prevalence of 16% acid-fast bacilli-positive tissue through purposive sampling of carcasses with nodular lesions in Zamfara State, Nigeria. Other reports with higher prevalence of bovine tuberculosis include the prevalence

of 6.5% by Ejeh *et al.* (2014) in Otukpo, Benue State, using Ziehl-Neelsen microscopy, using purposive sampling.

Conversely, this present study prevalence is comparable to 1.4% reported by Nwanta *et al.* (2011) in Enugu State, Nigeria, but higher than the prevalence of 0.056% by Ziehl-Neelsen staining that was reported by Musawa *et al.* (2021) in Sokoto State. Variations in prevalence have been linked to confounding factors such as slaughtered cattle disease status, environmental factors, and sampling technique (Awah-ndukum *et al.*, 2012). The above prevalence reports reaffirm the endemicity of bovine tuberculosis in Nigeria.

This study reveals that adult cattle had a higher prevalence of tuberculosis than the younger ones. The research revealed that the risk of having bovine tuberculosis is significantly associated with the age of the slaughtered cattle. Furthermore, the high number of adult cattle with bovine tuberculosis in this study reaffirms that tuberculosis is a chronic disease. The finding was similar to previous reports that tuberculosis was more common among adult cattle (Bikom *et al.*, 2021; Lawan *et al.*, 2020).

The prevalence of tuberculosis in this study was higher among male slaughtered cattle than cows. The high number of bovine tuberculosis in male cattle might be due to the fact that few bulls are kept longer on the farm to mount the cows. Although, the number of female slaughtered cattle sampled was more than the bulls. The finding was similar to the previous report that tuberculosis was more common among male cattle (Kapalamula *et al.*, 2023).

This study revealed that Wadara breeds had the highest percentage of acid-fast bacilli. Although, high number of White Fulani breed was sampled in this study than other cattle breeds. The breed of cattle has been considered, among other factors, to be associated with the persistence of bovine tuberculosis infection (Alvarez *et al.*, 2014).

The results of this study indicate that tuberculosis was more common in cattle with severely malnourished body condition scores compared to those with fair or moderate body condition scores. Moreover, this study also noted a substantial correlation between body condition scores and bovine tuberculosis infection. This work provides additional evidence that tuberculosis is a chronic and debilitating disease that causes gradual weight loss in infected cattle. Furthermore, this outcome aligns with the discoveries of Lawan *et al.* (2020), who observed a greater prevalence of bovine tuberculosis in cattle with a thin body condition score compared to those with optimal and overweight body condition scores. The present study corroborates the findings of Ejeh *et al.* (2014), which indicated a higher prevalence of bovine tuberculosis in cattle with a lean body condition score compared to those with medium and fat body condition scores.

The results of this study showed that PCR is a highly sensitive test that can be used as a confirmatory test alone or in combination with other traditional methods, such as postmortem examination, the Tuberculin Skin Test, and

Ziehl-Neelsen staining, to eliminate the chance of a false-positive result. The current study suggests that *Mycobacterium bovis* may not be the only reason for the significant number of acid-fast bacilli detected in the sampled slaughtered cattle at post-mortem. *Mycobacterium tuberculosis* complex and other acid-fast bacilli organisms, like *Nocardia* and *Rhodococcus equi* may also be involved. The present study detected the presence of *Mycobacterium tuberculosis* complex that was not *M. bovis*, although the study did not precisely detect *M. tuberculosis* from any of the Slaughtered cattle sampled, but previous research report by Cadmus *et al.* (2010) and Jenkins *et al.* (2011) have shown that the presence of this species (*M. tuberculosis*) can be detected in slaughtered cattle in Nigeria. However, it is also reasonable to hypothesise that human-to-animal transmission of *M. tuberculosis* may exist in the research area due to the high prevalence of HIV/AIDS and coexisting human tuberculosis illnesses (Taraba AIDS Control Agency, 2018).

Limitations

The study focused on the three Taraba State abattoirs in three of the state's sixteen LGAs. This may not reflect state-wide bovine TB prevalence. Ziehl-Neelsen staining and PCR may not identify all bovine TB cases, especially those with low bacterial loads or atypical presentations. Ziehl-Neelsen staining may not reveal bTB in samples with low bacterial burdens due to its limited sensitivity. PCR cannot identify an active infection from immunisation or exposure, and more so, dead or non-viable bacteria might cause false-positive findings.

Conclusion

The study revealed a 1.5% prevalence of bovine tuberculosis among slaughtered cattle in Taraba State, Nigeria, with cases detected primarily in the Jalingo abattoir. Laboratory analysis identified *Mycobacterium tuberculosis* complex (MTBC) and *Mycobacterium bovis* in the positive samples, confirming the zoonotic risk posed by these pathogens. Bovine tuberculosis was more prevalent in adult cattle, males, and those with poor body condition scores, particularly emaciated and highly emaciated animals.

This research lays the groundwork for future policy decisions that will enhance human health by reducing the risks associated with bovine tuberculosis. The study has established the existing prevalence of bovine tuberculosis in cattle that have been slaughtered for human consumption in Taraba State. This study reaffirms the prevalence of bovine tuberculosis in Nigeria and exposes the human population to a zoonotic risk.

Based on the findings, the study recommended that

stricter and more comprehensive meat inspection protocols should be implemented in abattoirs across Taraba State. Targeted education programs for farmers, butchers, and consumers on the risks of zoonotic transmission should be conducted, emphasising the dangers of consuming unpasteurized milk and undercooked meat.

The future studies could adopt a "One Health" approach by examining the interaction between bovine tuberculosis in cattle and potential human health implications, promoting a holistic understanding of the issue.

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ETHICAL DECLARATION

Ethical approval was sought from the University of Ilorin Research Ethics Review Committee before commencement of the study, with the ethical approval number UREC/FVM/PG20/68VA002.

CONFLICTS OF INTEREST

The authors have stated that there are no competing interests.

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