



## Update on the Situation of Tuberculosis in Africa's Wild Life

KOUENGOUA KOUENGOUA ARMELLE PRUDENCE<sup>1\*</sup>, YESSINOU ROLAND<sup>2</sup>, NANKAM CHIMI ROLAND<sup>1</sup>, FOTSAC DZOUSSE MULLER<sup>1</sup>, KOUAM ALAIN<sup>1</sup>, DJUIKWO FELICITE<sup>1</sup>, FACHO BALAAM<sup>1</sup>, AWAH NDUKUM JULIUS<sup>3</sup>, FAROUGOU SOUAIBOU<sup>2</sup>

<sup>1</sup>Université des Montagnes Bangangte Cameroon; <sup>2</sup>University of Abomey Calavi, Benin; <sup>3</sup>University of Bamenda Cameroon.

**Abstract** | Bovine tuberculosis eradication is an actively ongoing research subject, mostly in developed countries due to its impact on economy, public health and conservation. Researches on bovine tuberculosis (bTB) in under developed countries still remain stagnant or not really progressing even though it is an endemic disease in cattle. Cattle are considered as the main host of this disease but other studies have shown that several wildlife species are involved in the maintenance and transmission of bTB. Recent studies on the status of bTB at the wildlife-cattle interface have gained relevance in recent years. Awareness on the status of bTB in the African wildlife is a paramount step for ensuring control, surveillance in cattle. This review systematically addresses data available on bovine tuberculosis in Africa's wildlife. This article has given an overview of the factors related to prevalence, host, causal agents, methods of diagnostics, risk factors. After several screenings, six articles were considered for this systematic review. East and Southern Africa countries carry on most researches on bovine tuberculosis in wildlife. Available studies assessed the status of wild mammal, carnivore. Further researches to improve the knowledge on the status of bovine tuberculosis in wildlife in Africa are still needed in order to allow proper disease monitoring in wildlife-cattle and human.

**Keywords** | Bovine Tuberculosis, Wildlife, Africa

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\***Correspondence** | Kouengoua Kouengoua Armelle Prudence, Université des Montagnes Bangangte Cameroon; **Email:** kouenpru@yahoo.com

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## INTRODUCTION

Tuberculosis is a chronic infectious disease caused by members of the *Mycobacterium tuberculosis* complex (MTBC). It affects livestock, wildlife, and humans (Poirier et al., 2019). The members of this complex have shown the ability to infect a large diversity of natural populations of non-domesticated, and domesticated species worldwide (Caminiti, et al., 2020). Proven to be zoonotic pathogens in public health, it has also been identified in several wild animals including cervids in North America, badgers in Great Britain, feral pigs in Europe, brush-tailed possums in New Zealand, and buffaloes in South Africa (Fitzgerald and Kaneene, 2012).

Bovine tuberculosis becomes detrimental to biodiversity conservation, where it threatens wildlife populations or when disease management options consider the possibility of wildlife control (Alexandre Caron et al., 2014). In Africa, where it is a regional threat, the epidemiological situation of bovine tuberculosis (bTB) in livestock and human populations is highly variable (Hutcheon, 1880), reasons being there are very few countries with a structured surveillance system to know its distribution and information about its occurrence. The first recorded case of bTB in Africa's cattle was diagnosed in South Africa in 1880. Although bTB in cattle occurs widely in Africa, the diagnosis is mainly dependent on the detection of macroscopic lesions during meat inspection of carcasses in abattoirs (Awah-Ndukum

In Africa's wildlife the first detection of *M. bovis*, was during a destructive outbreak of the disease in South Africa (Paine and Martinaglia, 1929) in greater kudu (*Tragelaphus strepsiceros*) and a few other wildlife species. Several studies in Sub-Saharan Africa have shown the existence of tuberculosis in cattle and wildlife. Though knowledge gaps remains, the spill over of bTB from cattle to wildlife has already been described on several occasions; affecting a diversity of wildlife species in a wide range of protected areas of Sub-Saharan Africa (Jori et al., 2013).

This study aims to review the present state of bovine tuberculosis in Africa's wildlife, in other to see how far the gaps on the awareness have been filled.

## METHOD

A systematic bibliographic review was conducted on the situation of bovine tuberculosis in Africa's wildlife by searching PubMed, Google Scholar and Agora. No time limitation was imposed. The search criteria were specified in advance and the search was executed on 31/03/2022 and last updated on 26/03/2023. The search strings used were the following: "endemics" OR "epidemiology" OR "risk factors" OR "population at risk" OR "health correlates" AND "bovine tuberculosis" OR "mycobacterium bovis infection" AND "cattle" AND "wildlife" AND "Africa". Abstracts selection was according to their relevancy and excluded if dealing exclusively with cattle, human or other geographical regions out of Africa. Articles were reviewed in full text. For each article, the extracted data included country of the study, authors, year of publication, wildlife host, method of study (Test), samples, number of animal samples, number of positive sample (%), and risk factors. Information were summarized and presented in Table (1).

## RESULTS

The bibliographic search yielded 171 articles. These searches were combined and duplicates were removed. Fig. (1) depicts the flow of the selection process. One hundred and fifty eight (158) articles were excluded after screening. One hundred and thirty one (131) articles were assessed for eligibility, fourteen (14) were excluded with reasons that didn't meet all inclusion criteria. Six (6) articles were selected as of interest to the present review.

### CHARACTERIZATION OF PUBLISHED ARTICLES

The studies were published through the period 2002-2023. The regional distribution of studies was East Africa (4), Southern Africa (2). The studies enrolled six authors from

five countries. The regional distribution of studies was Mozambique (2), Zambia (2), Tanzania (2), South Africa (1), and Zimbabwe (1). The follow up duration of the study ranged from three to seven years. The studies were of high quality. Types of studies were cross sectional and retrospective studies. Most of the studies were conducted on the field. Approximately all the included studies were published during the last decade of our review as from 2010 to 2023 as shown in Table (1).

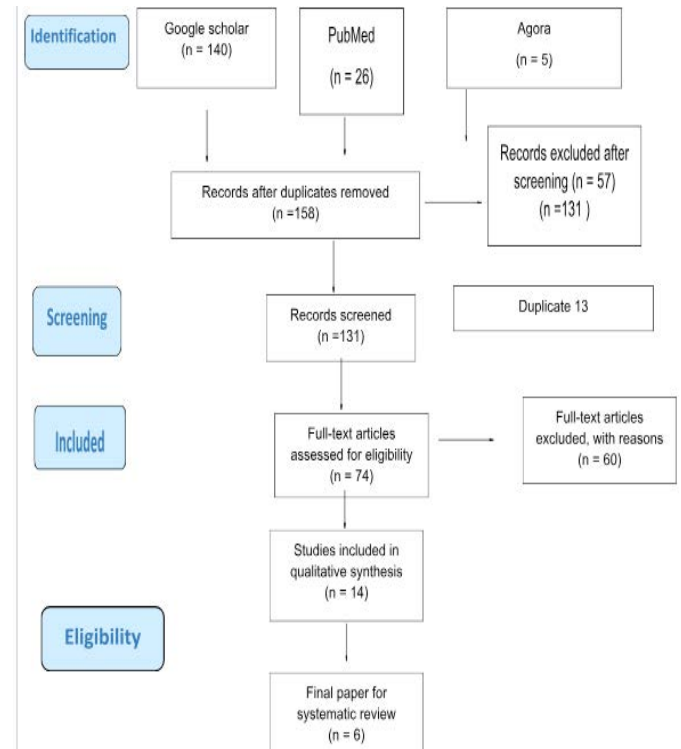


Figure 1: Diagram of included and excluded records of systematic review

### PREVALENCE RATES

Different species of wild animals are diagnosed for bovine tuberculosis mostly the African buffalo (*Syncerus caffer*) and the percentage of positive bTB reactors in buffalo was 8.06 % using Bovid TB Stat-Pak® at the Limpopo National Park Mozambique. In South Africa, forty one (41) isolates from buffalo, four (4) isolates from lion, two (2) isolates from baboons and one (1) from a warthog were confirmed as *M. bovis*. In Uganda the prevalence of the disease may vary from 5 to 30% in warthogs (*Phacocoercus africanus*) at the Queen Elizabeth National Park. *M. bovis* was isolated from 11.1% (2/18) migratory wildebeest (*Connochaetes taurinus*) and 11.1% (1/9) topi (*Damaliscus lunatus*) sampled systematically in 2000. Spoligotyping results revealed that one *M. bovis* isolate from one African civet (*Civettictis civetta*) is belonged to SB0133 spoligotype. Thirty-five working African elephants (*Loxodonta africana*) were screened for *Mycobacterium tuberculosis*

**Table 1:** Characteristics of included studies in the review

Country	Authors	Year of Publication	Hosts	Tests	Sample (tissue/ lait ou autre)	Size of host sample examined	Prevalence of Mycobacterium bovis in animals (%)
Mozambique	Tanner et al. 2015	not mentioned	African buffalo ( <i>Syncerus caffer</i> )	ELISA	Serum	62	5/62 (8.06%)
Mozambique	Tanner et al. 2015	Not mentioned	Cattle ( <i>Bos indicus</i> )	ELISA	Serum	2445	24/2445 (0.98%)
Zambia	Hang'ombe et al 2012	2006-2010	Cattle ( <i>Bos indicus</i> )	Culture, PCR	Tissue	315	37/315 (11.75%)
Zambia	Hang'ombe et al 2012	2006-2010	Antelope ( <i>Kobus lechwe Kafuensis</i> )	Culture, PCR	Tissue	75	15/75 (20 %)
South Africa	Sichewo et. al 2019	2012-2017	Cattle ( <i>Bos indicus</i> )	Culture	Nasal swab	99	9/99 (9.09%)
Tanzania	Katale et al. 2014	2010-2013	Cattle ( <i>Bos indicus</i> African buffalo ( <i>Syncerus caffer</i> ), African civet ( <i>Civettictis civetta</i> )	Culture, PCR multiplex	Tissue	606	6/606 (0.99 %)
Zimbabwe	Rosen et al. 2017	2014-2016	African elephant ( <i>Loxodonta africana</i> )	MTB Complex antibodies using the Elephant TB Stat-Pak and the DPP Vet TB Assay for elephants	Whole blood	35	6/35 (17.14 %)
Tanzania	Katale et al. 2017	Not mentioned	African buffalo ( <i>Syncerus caffer</i> )	Gamma interferon	Whole blood	102	2/102 (1.96 %)

complex antibodies using the Elephant TB Stat-Pak and the DPP Vet TB Assay for elephants. Six of thirty five elephants (17.14%) were seropositive.

**HOST EPIDEMIOLOGICAL STATUS, IDENTIFICATION OF MEMBERS OF THE MYCOBACTERIUM TUBERCULOSIS COMPLEX AND METHODS OF DIAGNOSIS OF M. BOVIS**

African buffaloes (*Syncerus caffer*) are regarded as the likely maintenance hosts of bTB usually in Africa; and epidemiological evidence has been gathered to support this view based on the characterization of populations maintaining high bTB prevalence rates despite long-term lack of contacts with cattle. Other reported hosts are considered spill over, such as lions, African civet, and elephant. Bovine tuberculosis has been confirmed by culture in 29 free-ranging African wildlife species. Only African buffaloes (*Syncerus caffer*), greater kudu (*Tragelaphus strepsiceros*), and Kafue lechwe (*Kobus lechwe kafuensis*) are established maintenance hosts (Renwick et al., 2007; Michel et al., 2009, 2015; Munyeme et al., 2010; Clifford et al., 2013), but there are strong indications that warthogs (*Phacochoerus africanus*) and lions (*Panthera leo*) also have the potential to become maintenance hosts

(Michel et al., 2015).

The methods of diagnosis of *M. bovis* from the wildlife species are not different from those used on cattle; such as culture - the gold standard method - followed by PCR, are same for human, cattle and wildlife, followed by interferon gamma assay, rapid lateral flow assay, intradermal tuberculin test, serological assay, inspection and gpc. Certain diagnostics are coupled for more precision such as culture and PCR; interferon gamma assay, couple to spoligotyping; lateral flow assay, couple to culture, lateral flow assay, couple to interferon gamma assay. GeneXpert, spoligotyping permits to show that there are similarities between *M. bovis*, from wildlife (African buffalo, antelope) and *M. bovis* from cattle or humans. Some are more specific to the species.

**RISK FACTORS**

Most studies conducted in wildlife in Africa, are in Mozambique, Ethiopia, Zambia, Tanzania, Botswana, South Africa, Zimbabwe. Mammals are the wildlife species mostly diagnosed for tuberculosis, such as African buffalo, kafue antelope, whom are considered as maintenance hosts, potentially responsible for the transmission of *M. bovis* to cattle. Other species are also diagnosed such as elephant,

warthog, and lion. Information concerning age and sex of animals are not reported. Most of the wild tested animals are adults. One of the factors mentioned concerning the possible transmission of bTB between wildlife and cattle is the sharing of same grazing lands and concerning cattle and human is the consumption of un-pasteurised milk.

## DISCUSSION

There are few studies done in other parts of Africa as far as wildlife is concerned. It might be because of the non accessibility to wild, specific lack of required equipment, lack of policies on wildlife conservation or expensive requirements of wildlife animals. The regional distribution of tuberculosis in Africa's wildlife is mostly in East Africa and Southern Africa. Meanwhile researches on *M. bovis* in cattle and human are much more available, because bTB is endemic in cattle. Moreover, the disease is of economic, sanitary, and public health importance. Most epidemiological studies done in the wildlife are cross sectional studies, mostly conducted on the field, requiring at some point specific methods of diagnosis, if not for the molecular and gross lesions detection which are main diagnosis done. Approximately all the included studies were published during the last decade of our review as from 2010 to 2020. A comparatively large number of studies address molecular epidemiology. Overall prevalence rates reported for bovine tuberculosis in *Syncerus caffer* (buffalo) is among the highest record for these species worldwide (Katale et al., 2014; Tanner et al., 2015; Katale et al., 2017; Sichewo et al., 2020). Prevalence rates have also been noted in lion, baboon, warthog (Sichewo et al., 2020), Kafue lechwe antelope (*Kobus leche Kafuensis*) (Bengis et al., 2004; Munyeme et al., 2010), migratory wildebeest (*Connochaetes taurinus*) and 11.1% (1/9) topi (*Damaliscus lunatus*) (Cleveland S. et al., 2007). Among the wildlife species mostly studied we also have the kafue lechwe antelope (Bengis et al., 2004; Munyeme et al., 2010; Hang'Ombre et al., 2012). Most studies did not report about age and sex differences. African buffaloes (*Syncerus caffer*) are regarded as true highly likely maintenance hosts of bTB usually in Africa. Other studies present greater kudu (*Tragelaphus strepsiceros*) as possible likely maintenance host too. The same kafue lechwe antelope is considered as high maintenance host posing a potentially high risk of transmission of *M. bovis* to livestock, other wildlife, and to members of the local communities (Munyeme et al., 2010; Malama et al., 2013). Other studies describe the kafue lechwe antelope (*Kobus leche Kafuensis*) as feral reservoirs of bTB in Zambia (Bengis et al., 2004; Munyeme et al., 2010). All other reported hosts are considered as dead end spill over hosts. *M. bovis* were found along other pathogens such as *Mycobacterium intracellulare* who was the most frequently isolated species (20 isolates, 36.4%) from human, cattle and wildlife

followed by *M. lentiflavum* (11 isolates, 20%), *M. fortuitum* (4 isolates, 7.3%) and *M. chelonae-abscessus* group (3 isolates, 5.5%) (Katale et al., 2014) in Tanzania. In South Africa, due to sudden death in meerkats (*M. suricattae Suricata suricatta*), inspection was carried out after euthanasia, to discover the cause of death which was *Mycobacterium Suricattae*, (Patterson et al., 2017). The methods used to diagnose mycobacteria in cattle, and human, are the same ones used for wildlife. Nevertheless at some point of time specific diagnosis like the Elephant TB Stat-Pak and the DPP VetTB Assay for elephants (Rosen et al., 2017), are adopted. Risk factors that govern bTB epidemiology and transmission in wildlife and wildlife-livestock remain largely unknown in sub-Saharan Africa.

## CONCLUSION

The present study updated information on bovine tuberculosis in Africa's wildlife. This improved the knowledge on tuberculosis. Even though most studies in wildlife are recent, it is noted that, studies are mostly carried out in the east and southern part of Africa. Tuberculosis is present in African wildlife, through non-tuberculous mycobacterial, and zoonotic mycobacteria. These causative agents have already been diagnosed through culture, serological assay, and molecular characterisation. The study reported tangible information on the status of African wildlife as regard tuberculosis. In Cameroon, studies on bovine tuberculosis in wildlife remain unknown. This review is intended to update awareness, and to foster more research on risks transmission of tuberculosis from wildlife to domestic animals, and human.

## DATA AVAILABILITY STATEMENT

The documents we consulted for this systematic review were selected through search engines PubMed, Google Scholar, and Agora. The search criteria were specified in advance and the search strings used were the following: "endemics" OR "epidemiology" OR "risk factors" OR "population at risk" OR "health correlates" AND "bovine tuberculosis" OR "mycobacterium bovis infection" AND "cattle" AND "wildlife" AND "Africa".

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## CONFLICT OF INTEREST

The authors declare that they have no conflict of interests.

This review will highlight the situation of wildlife in Africa, and emphasise on what is done, and what has to be done.

## AUTHORS CONTRIBUTION

Prudence KKA and Roland Y: Sample and data collection. Roland C and Muller F: Data analysis and drafted the manuscript. Alain K, Felicite D, and Balaam F: Drafted the manuscript. Ndikum A and Souaibou F: Designed the study and drafted the manuscript. All authors have read, reviewed, and approved the final manuscript.

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