Chapter 5
Tuberculosis in African Wildlife

Anita L. Michel and Paul D. van Helden

5.1 Introduction

Tuberculosis is an infectious, chronic, and usually fatal disease caused by members of the *Mycobacterium tuberculosis* complex (MTC) that are often able to cross species barriers between humans and domestic and wild animals. In wild animals, tuberculosis is primarily caused by spillover of *Mycobacterium bovis* infections from infected domestic cattle to free-ranging wildlife, while *M. tuberculosis* has long been known as, and still remains an important cause of death in captive wild animals in zoological collections worldwide, where close contact with humans facilitates its transmission to animals (Montali et al. 2001; de Lisle et al. 2001). *Mycobacterium tuberculosis* has been reported to cause generalized tuberculosis in a range of captive wildlife species. For more detailed information the reader is referred to recent literature focusing on tuberculosis in captive wildlife (Michel et al. 2013; Mikota et al. 2015; Miller and Lyashchenko 2015).

A growing number of MTC species, other than *M. bovis* and *M. tuberculosis*, able to cause lesions in infected animals has been identified in free-ranging wildlife in Southern and Western Africa (van Helden et al. 2009). The "Dassie bacillus" has been reported in rock hyraxes (*Procavia capensis*) as early as 1960, and appears to have established itself in this species (Parsons et al. 2008). A "member of the animal-adapted lineage of the MTC" was reported in free-ranging suricates (*Suricata*

A. L. Michel (✉)
Department Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, Onderstepoort, South Africa
e-mail: anita.michel@up.ac.za

P. D. van Helden
Division of Molecular Biology and Human Genetics, Faculty of Medicine and Health Sciences, South African MRC Centre for TB Research, DST NRF Centre of Excellence for Biomedical Tuberculosis Research, Stellenbosch University, Tygerberg, South Africa
e-mail: pvh@sun.ac.za

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suricatta) in the Kalahari Desert of the Northern Cape (South Africa), was later characterized as a new species, and was named *M. suricattae* (Parsons et al. 2013). A rare and slow-growing member of the antelope clade of the MTC, the "oryx bacillus," was recently isolated from a free-ranging adult African buffalo (*Syncerus caffer*) in KwaZulu-Natal, South Africa (Gey van Pittius et al. 2012). Infection with *M. mungi* is considered to be an emerging disease, and it is the cause of a high death rate in free-ranging banded mongooses (*Mungos mungo*) living in close proximity to humans in northern Botswana (Alexander et al. 2010). In 2013, an MTC strain closely related to the human-associated lineage 6 (also known as *M. africanum* West Africa type 2) was isolated from a chimpanzee in Côte d'Ivoire (Coscolla et al. 2013). The gregarious social behavior common to all these species is the most likely reason for their ability to sustain tuberculosis (TB). The impact of these newly identified organisms on their hosts and their zoonotic potential is currently unknown. (See Chap. 6 for more detailed information about these mycobacterial species.)

In this chapter, we collate the current knowledge about bovine tuberculosis (BTB) caused by *M. bovis* in free-ranging wildlife species in Africa.

5.2 Bovine Tuberculosis in African Wildlife Species

Although BTB in wildlife in Africa has been diagnosed in South Africa as long ago as the mid-1920s, the extent of the infection, and the ability of some of these infected species to act as maintenance hosts of the disease, only transpired recently. The full extent of the infection in wildlife in Africa and the role that these infected species play in the epidemiology of the disease in cattle are unknown, but it is assumed that it is an increasingly expanding infection as is seen in wildlife in South Africa, where buffaloes, at least, appear not to have been infected before the mid-1950s in the Kruger National Park (KNP) from where BTB spread to other species in the Park and in the surrounding areas.

The slow, progressive nature of tuberculosis is characteristic of the development of the disease in individual animals, and of its relentless and progressive spread in free-ranging wild animal populations. The disease becomes established in an ecosystem only once a wildlife species with the ability to maintain the infection independently, and to transmit the infection to other susceptible animals within the specific ecosystem becomes infected. Many of the species that become infected are incidental (dead-end or spillover) hosts, and they are likely to play a very limited role in the epidemiology of BTB in these infected ecosystems.

In Africa, BTB both in cattle and in wildlife is underdiagnosed and underresearched, and its prevalence is largely unknown (de Garine-Wichatitsky et al. 2013; Ayele et al. 2004; FAO 2012). There is a substantial body of evidence suggesting that free-ranging wildlife species contracted BTB from cattle in many

Table 5.1 Notification and control status of BTB in countries in Africa that reported *M. bovis* in wildlife (2014)

Country	BTB status cattle	BTB status wildlife	Notifiable cattle	Control cattle	Notifiable wildlife	Surveillance wildlife
Cameroon	+	+	Yes	Yes	No	No
Ghana	+	+	Yes	Yes	Yes	No
Mauritius	+	+	No	Yes	No	No
Mozambique	+	+	Yes	N/A	No	No
Nigeria	+	+	Yes	S	No	No
South Africa	+	+	Yes	Yes	Yes	No
Sudan	+	+	Yes	N/A	Yes	Yes
Tanzania	+	+	Yes	S	Yes	Yes
Togo	+	+	Yes	N/A	No	No
Uganda	+	+	Yes	N/A	No	No
Zambia	+	+	Yes	No	No	No
Zimbabwe	Last reported 1996	+	Yes	S	Yes	No

+, BTB infection or disease present; *N/A* no information available, *S* surveillance

different countries including in Africa, and that this spillover infection often remains undetected for decades (Palmer et al. 2012). It is therefore not surprising that all 12 countries in Africa that reported *M. bovis* infection in wild animals between 2000 and 2014, also reported BTB in cattle, although not always concurrently (Table 5.1). The actual number of African countries in which BTB occurs both in cattle and wildlife is likely to be higher as no information is available for many of these countries (OIE 2017a). In addition, widespread intermingling of livestock and wildlife at the wildlife/livestock interface is common in large parts of Africa, and this is known to enhance the transmission of *M. bovis* especially during times when there is competition for limited pastures and water (Caron et al. 2013). A lack of diagnostic facilities to confirm the infection in remote wildlife areas is a further impediment to accurate reporting and the inadequacy of the available information.

Of the 54 countries in Africa, BTB in cattle was reported in 89% (34/38) of those reporting disease information to the World Organization for Animal Health (OIE) between 2000 and 2014. No information was available for 13 countries, while one country reported absence and three countries had their last outbreak before 2000. Only those that reported the disease listed BTB as a notifiable disease in cattle and only nine of them require notification of BTB in wildlife (Table 5.2). Only 11 African countries have national BTB disease control policies and/or culling strategies (OIE 2017b) but prevention and control are often poorly implemented due to political, economical, and sociological constraints (Abdalla and Nganwa 2014; Awah-Ndukum et al. 2012).

In many countries, there are no regulations requiring the reporting of BTB outbreaks in wildlife. This is a hazardous practice since once the disease has established itself in a wildlife host, disease notification, surveillance, and monitoring to

Table 5.2 African wildlife species (excluding maintenance hosts) infected with *Mycobacterium bovis*

Common name	Scientific name	Location	References
Common duiker	*Sylvicapra grimmia*	Agricultural farmland	Paine and Martinaglia (1929)
Lion	*Panthera leo*	GKNPC and other game parks, South Africa	Keet et al. (1996), Michel et al. (2006) and Hlokwe et al. (2011)
Cheetah	*Acinonyx jubatus*	GKNPC, South Africa	Keet et al. (1996)
Leopard	*Panthera pardus*	GKNPC, South Africa	De Vos et al. (2001) and Michel et al. (2006)
Lesser kudu	*Tragelaphus imberbis*	Northern Tanzania	Cleaveland et al. (2005)
Topi	*Damaliscus lunatus*	Northern Tanzania	Cleaveland et al. (2005)
Chacma baboon	*Papio ursinus*	GKNPC and other parks	Keet et al. (1996, 2000a)
Yellow baboon	*Papio cynocephalus*	Ruaha ecosystem, south-central Tanzania	Clifford et al. (2013)
Olive baboon	*Papio cynocephalus anubis*	Kenya	Tarara et al. (1985)
Kirk's dik-dik	*Madoqua kirkii*	Ruaha ecosystem, south-central Tanzania	Clifford et al. (2013)
Vervet monkey	*Chlorocebus pygerythrus*	Ruaha ecosystem, south-central Tanzania	Clifford et al. (2013)
Honey badger	*Mellivora capensis*	GKNPC	Michel (2002) and Michel et al. (2006)
Large spotted genet	*Genetta tigrina*	GKNPC Ruaha ecosystem, south-central Tanzania	De Vos et al. (2001) and Clifford et al. (2013)
African civet	*Civettictis civetta*	Serengeti ecosystem, Tanzania	Katale et al. (2017)
Warthog	*Phacochoerus africanus*	Uganda South Africa (multiple locations)	Woodford (1982a, b), Kalema-Zikusoka et al. (2005) and Michel et al. (2009)
Bush pig	*Potamochoerus larvatus*	Hhluhluwe-iMfolozi Park, South Africa	Michel et al. (2009)
Impala	*Aepyceros melampus*	GKNPC South Africa Ruaha ecosystem, south-central Tanzania	Michel et al. (2006) and Clifford et al. (2013)
Bushbuck	*Tragelaphus scriptus*	GKNPC, South Africa	Hlokwe et al. (2014)

(continued)

Table 5.2 (continued)

Common name	Scientific name	Location	References
Eland	*Taurotragus oryx*	South Africa	Michel et al. (2006)
Blue wildebeest	*Connochaetes taurinus*	GKNPC, South Africa Northern Tanzania	Hlokwe et al. (2014) and Clifford et al. (2013)
Banded mongoose	*Mungos mungo*	GKNPC, South Africa	Brüns et al. (2017)
Giraffe	*Giraffa camelopardalis*	GKNPC, South Africa	TM Hlokwe, unpublished data (2013)
African wild dog	*Lycaon pictus*	GKNPC, South Africa	A Michel, unpublished data (2016)
Nyala	*Tragelaphus angasii*	South Africa	Hlokwe et al. (2014)
Black rhinoceros	*Diceros bicornis*	GKNPC, South Africa	Miller et al. (2017)
White rhinoceros	*Ceratotherium simum*	GKNPC, South Africa	P Buss, personal communication (2016)

GKNPC Greater Kruger National Park Complex

determine spread of the disease in wildlife are needed to effectively manage the epidemic, and to protect livestock populations from spillback from the wildlife hosts. No information about the nature of the infection is available in most of the countries that reported BTB in wildlife to the OIE, as very few of the data have been published in scientific journals.

To date, BTB has been confirmed by culture in 29 free-ranging African wildlife species. Of those only African buffaloes (*Syncerus caffer*), greater kudus (*Tragelaphus strepsiceros*), and Kafue lechwe (*Kobus leche kafuensis*) are established maintenance hosts (Michel et al. 2006, 2015; Renwick et al. 2007; 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 remainder of the species is considered to be spillover species (Table 5.2).

The characteristics of BTB in the maintenance hosts, and those that have the potential to become maintenance hosts are described in this chapter.

5.3 Maintenance Hosts of *Mycobacterium bovis*

*5.3.1 African Buffalo (*Syncerus caffer*)*

African buffaloes are probably the most important known wildlife maintenance host of BTB in Africa (Michel et al. 2006; Woodford 1982a, b). They are taxonomically closely related to domestic cattle, and exhibit the same gregarious social herd behavior (du Toit 2005). These characteristics are believed to create the ability for buffaloes to being infected with *M. bovis*, and to become a maintenance host.

Aerosol transmission of *M. bovis* because of the close contact between buffaloes within herds is the primary route of transmission of the infection in this species (Fitzgerald and Kaneene 2013). Herd sizes in the KNP vary substantially from as few as 50 to more than a 1000 buffaloes. These varying herd sizes are partly a function of seasonal fission and fusion events caused by environmental factors. These events ensure genetic exchange between herds, but they also facilitate the spread of BTB between herds (Cross et al. 2005). Normal dispersal behavior of single or small groups of buffalo heifers and bulls over considerable distances and fusion with new herds similarly cause gene flow and the spatial spread of BTB (de Vos et al. 2001; Michel et al. 2006; Caron 2014).

Once infected, the development of tubercles in buffaloes broadly follows the same stages of development and immunopathogenesis as has been described for domestic cattle. They appear to remain persistently infected, and are then, depending on the locality of the lesions, potential shedders of *M. bovis*.

In buffaloes, tuberculous lesions are more commonly found in the lymph nodes of the head and neck, tonsils, and in the lungs and associated lymph nodes. On many occasions, single, small lesions only are present in any one of the sites in which they usually occur. The appearance of the lesions in buffaloes varies substantially between animals, and when there is a florid reaction the lesions are poorly encapsulated and have a lardaceous appearance. Lesions often resemble abscesses caused by a number of pyogenic organisms, and these have often been dismissed as not tuberculous on the basis that the lesion is "merely an abscess." The lesions increase in size and number apparently as a function of the infectious dose and time. Generalization of infection following dissemination via the blood stream to multiple organ systems and serosal surfaces (miliary tuberculosis) is not uncommon and may occur in about 10% of diseased animals in a flock with a high BTB prevalence. The cumulative risk of exposure and infection over time results in a positively correlated association between age and the number of diseased animals (i.e., those with lesions; de Vos et al. 2001; Laisse et al. 2011). As the herd prevalence increases, the likelihood of recurrent exposure of individuals to invariably high doses of *M. bovis* increases, and more animals with advanced, generalized BTB can be expected to be present in the herd (de Vos et al. 2001). Additionally, with an increasing herd prevalence, BTB will be present more frequently in younger age groups, including calves. In very young calves with BTB, intrauterine transmission or transmission via milk is possible, but they appear to be rare events.

The long-term impact of BTB on the buffalo population is currently unknown as the disease is still spreading in a northerly direction following its entry in the south of the KNP. From the time of the estimated first infection of buffaloes in the south, it took about 50 years for the disease to reach the northern border of the Park, over a distance of about 500 km. Limited data about the effect of the disease on the buffalo population in the KNP reflect an increased vulnerability to drought and predation in herds with a high BTB prevalence (Jolles et al. 2005; Cross et al. 2009). These early indications could be a predictor of wider scale BTB-related ecological disruption that may be expected once the disease has developed to its full extent in that ecosystem (Caron et al. 2003). According to a recent mathematical model, it appears that BTB will have a more serious impact on cattle compared to buffaloes because of the difference in the transmission dynamics of the infection (Phepa et al. 2016).

*5.3.2 Greater Kudu (*Tragelaphus strepsiceros*)*

Greater kudus, one of the two subspecies of kudus, are large, gregarious antelopes that live in small groups in woodlands and bush lands where they browse on leaves of thorn trees of the genera *Acacia* and *Ziziphus*. Free-ranging greater kudus were among the first wild animals to be diagnosed with BTB in South Africa in the 1920s (Paine and Martinaglia 1929). Kudus are believed to contract the disease by different routes. One is the aerosol route in which case they develop multifocal tuberculous lesions in the lungs and associated lymph nodes with a distribution very similar to that seen in buffaloes and cattle. Generalization of the infection with hematogenous spread to organs, such as the spleen, liver, and kidneys, and to the serosal surfaces, has been observed. More frequently, and probably more importantly, *M. bovis* can be contracted percutaneously. In this instance, infection occurs at the site of lacerations in the oral and esophageal epithelium, and the thin skin of the inside of the ears by *M. bovis*-contaminated thorny twigs. Following infection of the parotid and retropharyngeal lymph nodes, typical pyogranulomas containing large numbers of mycobacteria develop. These lesions contain an abundant purulent exudate, and cause large irregular parotid and submandibular swellings. The pressure exerted by these lesions causes them often to rupture and to form draining sinuses from which bacilli-laden pus is shed into the environment including onto the browse.

The infection persists in localized kudu populations, at least for a considerable period of time (Michel et al. 2015), and for these reasons kudus are considered to be maintenance hosts, and they may become supershedders with the ability to effectively disseminate *M. bovis* within their home range and, perhaps more importantly, when they cross fences or are translocated to BTB-free ranches or conservation areas. Further support that they are maintenance hosts is provided by recent molecular epidemiological data that indicate that kudus maintain unique *M. bovis* strains in the absence of contact with buffaloes. In the KNP too, different populations of greater kudus are infected with either the common buffalo strain of *M. bovis* that occurs in the Park, or with a unique strain that only occurs in kudus in that region (Michel et al. 2009).

*5.3.3 Lion (***Panthera leo***)*

Bovine tuberculosis in free-ranging lions was first diagnosed in 1995 in the south of the KNP where, at that time, the prevalence of BTB in buffalo herds was the highest in the Park (Keet et al. 1996). Subsequent surveys showed that the prevalence of the disease in lions had the same south to north gradient as for the infection in buffalo herds, reflecting the spread of BTB in a northerly direction (Keet et al. 2000b; Rodwell et al. 2001). From 1993 to 2008, the prevalence of BTB in lions in the northern part of the KNP (low buffalo BTB prevalence zone) increased from 0 to 41% (Maas et al. 2012). In a study in 2017, the prevalence of BTB in the lion population was 33% in the central region, and 54% in the southern region where the infection appeared to have entered in the Park (Sylvester et al. 2017). *Mycobacterium bovis* infection in lions has also been reported in Tanzania where, compared to seronegative lions, serological data correlated with the presence of clinical signs and reduced survival times indicating the presence of the infection in lions, and its impact on *M. bovis*-infected prides (Cleaveland et al. 2005).

Lions are the only social felids, and they are the top predator in African ecosystems. Their status is listed as vulnerable by the International Union for Conservation of Nature (http://www.iucnredlist.org/apps/redlist/details/15951/0). Their sociality, communal cub rearing, communal hunting, their predilection to hunting buffaloes (a major prey species), and intraspecific aggression predispose them to becoming infected and to sustain the infection in prides once they become infected. Their preference for buffaloes as a prey species is greater during periods of drought when buffaloes are an easier prey due to their deteriorating body condition, weakness, and fission into smaller herds that make them more vulnerable to predation by lions (Mills 1995; Ferreira and Funston 2010; Tambling et al. 2013).

Tuberculosis is most frequently a subclinical but ultimately fatal disease in infected lions (Keet et al. 2000a), but there are currently insufficient data to calculate the mortality rate, the duration of the infection before death, or the average age at which they become infected, and how long after infection the onset of clinical signs is most likely to occur.

Lions may become infected by different routes, as reflected by the variable and inconsistent distribution of lesions in infected animals. During a kill and while feeding on infected buffalo carcasses, transmission of the infection may occur by the alimentary route, by aerogenous transmission of *M. bovis* while suffocating the prey, and during intraspecific aggressive behavior while feeding. Aggression while feeding also facilitates percutaneous transmission through bite wounds. The isolation of *M. bovis* from the mammary lymph nodes of some lionesses is not proof but an indication of a possible pseudo-vertical route of infection for suckling cubs. Similarly, the presence of a tuberculous endometritis in some females suggests that intrauterine transmission is also possible.

Dissemination of the infection followed by spread via the hematogenous and/or lymphatic route results in a generalized infection with the presence of miliary lesions mostly in the lungs but also in other organs (Keet et al. 2000a, b). Progression of an

M. bovis infection in lions, similar to other affected species, is generally slow, and body condition scoring during the early stages of the diseases is not useful to clinically detect lions with BTB (Maas et al. 2012). Exposure to consecutive high dose of *M. bovis* via different pathways may possibly contribute to a more rapid progression of the disease, with an earlier onset of the progressive emaciation and lethargy typically seen in advanced cases of the infection in lions. Bovine TB in lions is further characterized by the presence, in variable combinations in some animals, of swollen elbow joints caused by a tuberculous osteoarthritis, hygromas, lameness, corneal opacity, tuberculous panophthalmitis, a dull coat, and large, poorly healing skin lesions caused by the presence of subcutaneous tuberculous granulomas (Michel et al. 2015).

Visible lesions at necropsy in lions are limited to the lungs, skin, joints, and subcutaneous granulomas, and resemble those seen in domestic cats. The lesions are different from those seen in cattle and most other species. The lesions in the lungs are characterized by localized but poorly circumscribed areas of infection resembling an interstitial inflammatory reaction. Macroscopically the lesions in the lungs often contain cavities caused by bronchiectasis, and they contain a mucopurulent exudate containing large numbers of acid-fast bacilli. Histologically the lesions in the various tissues are characterized by a multifocal to confluent granulomatous inflammatory reaction seen as aggregates of predominantly macrophages lacking necrosis and the presence of Langhans giant cells typical of the tuberculous reaction in most other species (Keet et al. 1996). Tuberculous lesions in the lymph nodes of lions cannot be seen macroscopically, and the apparent absence of lesions there is thus not an indication of the absence of an *M. bovis* infection. When BTB is suspected in lions, it is mandatory to confirm the diagnosis by culture of a collection of specimens from the lungs, superficial and deep lymph nodes, the exudate from hygromas and affected joints, and from subcutaneous granulomatous lesions (Keet et al. 2000b).

The mounting evidence of the role of respiratory transmission of *M. bovis* infection in prides is currently the subject of an intense debate as to whether lions can be maintenance hosts under certain conditions. It is argued that once the infection has established itself in a critical mass of the population thus ensuring continuous pathogen circulation, that it could probably persist in lion prides in the absence of contact with buffaloes as the ongoing source of the infection. The likelihood that lions may become maintenance hosts is also dependent on their population size, and the long-term effects of BTB on the composition of the pride, and population dynamics.

Debilitating diseases, such as BTB, affect social species like lions in multiple ways. Apart from the direct effect on the health of individual animals, there is also an impact on the size of prides and their structure. Dominant male coalitions with BTB are probably evicted earlier because of the debilitating effects of the disease and the consequent increasing bouts of infanticide have an adverse effect on numbers and the composition of prides. The practice of communal hunting too provides support to lions with BTB allowing extended survival times and shedding of the pathogen over a longer period of time (Michel et al. 2006).

Lions are often translocated between conservation areas in Africa, and the risk of introducing lions subclinically infected with BTB into uninfected areas should always be considered.

*5.3.4 Warthog (*Phacochoerus africanus*)*

Bovine TB in warthogs was first diagnosed in the Queen Elizabeth National Park in Uganda by Woodford in 1982 who concluded that it was a spillover infection from African buffaloes (Woodford 1982a, b). It appears to have persisted both in buffaloes and warthogs in the Park since then, as BTB was still present in both populations when surveyed in 1997 (Kalema-Zikusoka et al. 2005). Warthogs with BTB were also found in several reserves and on private game farms in South Africa where they shared *M. bovis* strains carried by African buffaloes (Hlokwe et al. 2014). Lesions due to *M. bovis* are present both in the respiratory and gastrointestinal tracts. Warthogs are omnivores, and they opportunistically feed on carrion potentially containing *M. bovis* in addition to being exposed to environmental contamination with the pathogen. Once infected, close contact between members of family groups inside the confines of their burrows is thought to effectively facilitate aerosol transmission and the persistence of the infection within the family group. When warthog densities are low, BTB occurs as a sporadic spillover infection in them as their numbers are then too low to sustain the infection within the species. However, in the absence of predators, and when food is readily available and in abundance, the number of warthogs within an ecosystem can reach a threshold number at which they can sustain the infection within the population. Under these circumstances, the prevalence of the disease may vary from 5 to 30%, and they may then act as maintenance hosts (Michel et al. 2015).

*5.3.5 Kafue lechwe (*Kobus leche kafuensis*)*

Tuberculosis in Kafue lechwe was first diagnosed in 1946 (Munyeme et al. 2010). They are the dominant wildlife species in the Kafue Basin and live in very large herds. During the drier months of the year, cattle and lechwe intermingle on the dwindling pastures in the Basin, and congregate at watering points. The consistent high prevalence of BTB in lechwe (ranging from 20 to 36%) led to their classification as maintenance hosts of BTB (Gallagher et al. 1972; Clancey 1977). They have furthermore been identified as a risk factor for BTB in cattle (Munyeme et al. 2008), and they appear to be a source of spillback infection to cattle (Pandey 1998). The majority of tuberculous lesions is found in the lungs and associated lymph nodes, suggesting aerosol transmission. Generalization of the disease, following hematogenous spread, occurs in about 10% of diseased animals (Munyeme et al. 2010). The annual mortality rate ascribed to tuberculosis in a study conducted by Gallagher in

1972 was at least 20% (Gallagher et al. 1972), compared to the 10% in African buffaloes in the KNP (de Vos et al. 2001). (Refer to Chap. 23 for further information about tuberculosis in Kafue lechwe.)

5.4 Spillover Infection in African Wildlife Species

Transmission of BTB to spillover hosts is a "downstream" event in the epidemic curve of the disease in maintenance host(s), and its occurrence is dependent on a high prevalence of the disease in these hosts. In instances where an infected buffalo population has decreased markedly in size due to events such as drought or poaching, the prevalence of BTB in them, at best, was only slightly reduced or remained unchanged (de Vos et al. 2001; Kalema-Zikusoka et al. 2005), and they sustain the infection irrespective of the decrease in the number of animals.

Only a small number of the wildlife species diagnosed with BTB appears to play a role in the dissemination and maintenance of the disease. It is also difficult to predict whether infected spillover species may be responsible for transmission of the infection at the wildlife/livestock interface, but there is always a risk that they may transmit the disease to other species in one way or another.

To date, 26 spillover species have been reported (Table 5.1). It is likely that the disease may not have been reported in a number of species, while there may be those in which the disease has not been diagnosed. One can therefore expect that the number of African wildlife species infected with *M. bovis* will increase as time goes on.

Unless the conservation status of the infected spillover species is threatened or endangered, BTB is not likely to have a negative effect on their populations. Individual infected animals, however, will suffer the consequences of the infection.

5.5 Implications for Conservation and Trade

Infection of wildlife species with *M. bovis* has considerable implications for the national and international trade in livestock and wildlife because of the restrictions imposed by the international conventions governing trade with animals and their products from countries infected with *M. bovis*. These measures result in revenue losses for game farms and conservation areas particularly in Southern Africa where the different types of wildlife ranching are a profitable private enterprise. For the commercial wildlife industry that is rapidly evolving and expected to exceed the revenue generated from livestock farming in Southern Africa, quarantine regulations not only reduce the monetary value of breeding animals, but also prohibit the sale of live animals of the affected species (Munag'andu et al. 2006; de Garine-Wichatitsky et al. 2013; Michel et al. 2015; Hlokwe et al. 2016).

In some instances, BTB in ecosystems causes them to become conservation islands because of the limitations on the movement of BTB-infected wildlife from these areas, thus not only jeopardizing the conservation of endangered species but also preventing the free exchange of genetic resources between conservation areas.

5.6 Control of BTB in Free-Ranging Wildlife

While the long-term goal of eradicating BTB from domestic cattle has been achieved in many developed countries, it is unattainable in free-ranging wildlife populations, and very challenging in cattle, also in developed countries, in an environment where there is a coexistent wildlife maintenance host of the infection (Bengis et al. 2002; FAO 2012).

The choice of a suitable strategy for the control of BTB in wildlife depends on the primary conservation objectives for a particular ecosystem. African conservationists are faced with difficult choices and few options since they have an obligation to protect the species that host the pathogen, but they also have the responsibility of minimizing the risk of transmission of the disease to domestic cattle, other livestock, and humans at the interface. Additionally, they must also consider the potentially devastating impact on maintenance and spillover species, particularly when dealing with rare and endangered species.

Currently, *M. bovis* infection is not actively controlled in most affected African wildlife areas. In Southern Africa, fencing is used as a way of limiting the movement of BTB-infected animals (Jori et al. 2011), but flooding, elephant, and human activities disrupt them allowing BTB-infected animals to cross the interface at will. Game-deterrent fences are reasonably effective in restricting the movement of some animals, but a number of wildlife species including maintenance hosts of BTB, such as warthogs and kudus, cross intact fences at will either by jumping across them or by burrowing beneath them (Michel et al. 2006).

Control measures for BTB in free-ranging wildlife populations based on long-term interventions such as periodic mass capture followed by tuberculin testing and removal of positive animals can effectively reduce the prevalence of BTB and hence the infection pressure in the maintenance population in smaller conservation areas such as the Hluhluwe-iMfolozi Park (South Africa). Reduction in the prevalence rate reduces the risk of transmission to other wildlife species, and the possibility of spillback to cattle (Michel et al. 2015).

To effectively implement management strategies in wildlife populations, the BTB status of the infected population and neighboring domestic cattle should be monitored to gauge the impact of the control measures (Hlokwe et al. 2016).

5.7 Conclusion

In all likelihood vaccination remains the only control measure for BTB in wildlife populations. In the past decade, considerable progress has been made with the development of BTB infection models in various wild animal species including possums, badgers, African buffaloes, wild boars, and deer in which the efficacy of new vaccines can be tested. It remains to be seen whether a TB vaccine can be developed that will meet the requirements of efficacy, safety, affordability, and practicality to control BTB in African wildlife (Robinson et al. 2012; Buddle et al. 2013; Chambers et al. 2014; Gortazar et al. 2014; Palmer et al. 2014; Díez-Delgado et al. 2017).

Governments have an obligation to protect human and animal health at the interface of humans, domestic livestock, and wildlife. Given the significant economic impact of BTB on cattle farming and its zoonotic risk for human health, it is alarming that the situation in Africa over time has, at best, remained unchanged since the report by Cosivi et al. (1998) and despite experts calling for action to control the disease on the African continent (Olea-Popelka et al. 2017). This situation has now been exacerbated by the detection of BTB in a number of wildlife species, and their role as maintenance hosts of the disease.

African Governments must now take the expanding number of wildlife species infected with *M. bovis*, and the risk that they pose to the health and welfare of humans and livestock, into consideration if they want to act in the interest of their citizens and of conservation. Dealing with BTB, and attempting to control and eventually eradicate it, cannot be done without also taking the risks posed by the infection in wildlife, and the mostly unknown role that they play in the epidemiology of the disease in Africa, into consideration.

References

Abdalla E, Nganwa D (2014) Factors contributing to the transmission of bovine tuberculosis caused by *Mycobacterium bovis* and its control status in Sudan. In: Thoen CO, Steele JH, Kaneene JB (eds) Zoonotic tuberculosis: *Mycobacterium bovis* and other pathogenic mycobacteria, 3rd edn. Wiley, Hoboken, NJ, pp 159–174

Alexander KA, Laver PN, Michel AL et al (2010) Novel *Mycobacterium tuberculosis* complex pathogen, *M. mungi*. Emerg Infect Dis 16(8):1296–1299

Awah-Ndukum J, Kudi AC, Bah GS et al (2012) Bovine tuberculosis in cattle in the highlands of Cameroon: seroprevalence estimates and rates of tuberculin skin test reactors at modified cut-offs. Vet Med Int 2012:798502, p 13. https://doi.org/10.1155/2012/798502

Ayele WY, Neill SD, Zinsstag J et al (2004) Bovine tuberculosis: an old disease but a new threat to Africa. Int J Tuberc Lung Dis 8(8):924–937

Bengis RG, Kock RA, Fischer J (2002) Infectious animal diseases: the wildlife/livestock interface. Rev Sci Tech 21(1):53–65

Brüns AC, Tanner M, Williams MC et al (2017) Diagnosis and implications of *Mycobacterium bovis* infection in banded mongooses (*Mungos mungo*) in the Kruger National Park, South Africa. J Wildl Dis 53(1):19–29

Buddle BM, Parlane NA, Wedlock DN et al (2013) Overview of vaccination trials for control of tuberculosis in cattle, wildlife and humans. Transbound Emerg Dis 60(Suppl 1):136–146

Caron A (2014) Buffalo movements at the wildlife/livestock interface along the Limpopo River and consequences for pathogen transmission: preliminary results from the BUCATIN project 2010-2014, pp 12–15. RP-PCP and AHEAD GLTFCA Meeting, 12–15 May 2014, Dete, Hwange, Zimbabwe

Caron A, Cross PC, du Toit JT (2003) Ecological implications of bovine tuberculosis in African buffalo herds. Ecol Appl 13(5):1338–1345

Caron A, Miguel E, Gomo C et al (2013) Relationship between burden of infection in ungulate populations and wildlife/livestock interfaces. Epidemiol Infect 141(7):1522–1535

Chambers MA, Carter SP, Wilson GJ et al (2014) Vaccination against tuberculosis in badgers and cattle: an overview of the challenges, developments and current research priorities in Great Britain. Vet Rec 175(4):90–96

Clancey JK (1977) The incidence of tuberculosis in lechwe (marsh antelope). Tubercle 58 (3):151–156

Cleaveland S, Mlengeya R, Kazwala RR et al (2005) Tuberculosis in Tanzanian wildlife. J Wildl Dis 41:446–453

Clifford DL, Kazwala RR, Sadiki H et al (2013) Tuberculosis infection in wildlife from the Ruaha ecosystem Tanzania: implications for wildlife, domestic animals, and human health. Epidemiol Infect 141(7):1371–1381

Coscolla M, Lewin A, Metzger S et al (2013) Novel *Mycobacterium tuberculosis* complex isolated from a wild chimpanzee. Emerg Infect Dis 19(6):969–976

Cosivi O, Grange JM, Daborn CJ et al (1998) Zoonotic tuberculosis due to *Mycobacterium bo*vis in developing countries. Emerg Infect Dis 4(1):59–70

Cross PC, Lloyd-Smith JO, Getz WM (2005) Disentangling association patterns in fission-fusion societies using African buffalo as an example. Anim Behav 69:499–506

Cross PC, Heisey DM, Bowers JA et al (2009) Disease, predation and demography: assessing the impacts of bovine tuberculosis on African buffalo by monitoring at individual and population levels. J Appl Ecol 46(2):467–475

de Garine-Wichatitsky M, Caron A, Kock R et al (2013) A review of bovine tuberculosis at the wildlife-livestock-human interface in sub-Saharan Africa. Epidemiol Infect 141(7):1342–1356

de Lisle GW, Mackintosh CG, Bengis RG (2001) *Mycobacterium bovis* in free-living and captive wildlife, including farmed deer. Rev Sci Tech 20(1):86–111

de Vos V, Bengis RG, Kriek NP et al (2001) The epidemiology of tuberculosis in free-ranging African buffalo (*Syncerus caffer*) in the Kruger National Park, South Africa. Onderstepoort J Vet Res 68(2):119–130

Díez-Delgado I, Rodríguez O, Boadella M et al (2017) Parenteral vaccination with heat-inactivated *Mycobacterium bovis* reduces the prevalence of tuberculosis-compatible lesions in farmed wild boar. Transbound Emerg Dis 64(5):18–21

du Toit JG (2005) The African savanna buffalo, pp 78–105

FAO (2012) Tuberculosis. Animal Production and Health Division. http://www.fao.org/docrep/015/i2811e/i2811e.pdf

Ferreira SM, Funston PJ (2010) Estimating lion population variables: prey and disease effects in Kruger National Park, South Africa. Wildl Res 37(3):194–206

Fitzgerald SD, Kaneene JB (2013) Wildlife reservoirs of bovine tuberculosis worldwide: hosts, pathology, surveillance, and control. Vet Pathol 50(3):488–499

Gallagher J, Macadam I, Sayer J et al (1972) Pulmonary tuberculosis in free-living lechwe antelope in Zambia. Trop Anim Health Prod 4(4):204–213

Gey van Pittius NC, Perrett KD, Michel AL et al (2012) Infection of African buffalo (*Syncerus caffer*) by oryx bacillus, a rare member of the antelope clade of the *Mycobacterium tuberculosis* complex. J Wildl Dis 48(4):849–857

Gortazar C, Beltrán-Beck B, Garrido JM et al (2014) Oral re-vaccination of Eurasian wild boar with *Mycobacterium bovis* BCG yields a strong protective response against challenge with a field strain. BMC Vet Res 10(1):96

Hlokwe TM, Jenkins AO Streicher EM et al (2011) Molecular characterisation of *Mycobacterium bovis* isolated from African buffaloes (*Syncerus caffer*) in Hluhluwe-iMfolozi Park in KwaZulu-

Natal, South Africa. Onderstepoort J Vet Res 78(1):Art. #232, 6 pages. https://doi.org/10.4102/ojvr.v78i1.232

Hlokwe TM, van Helden P, Michel AL (2014) Evidence of increasing intra and inter-species transmission of *Mycobacterium bovis* in South Africa: are we losing the battle? Prev Vet Med 115(1–2):10–17

Hlokwe TM, de Klerk-Lorist LM, Michel AL (2016) Wildlife on the move: a hidden tuberculosis threat through introduction of untested species in an ecosystem. J Wildl Dis 52(4):837–843

Jolles AE, Cooper DV, Levin SA (2005) Hidden effects of chronic tuberculosis in African buffalo. Ecology 86(9):2358–2364

Jori F, Brahmbhatt D, Fosgate GT et al (2011) A questionnaire-based evaluation of the veterinary cordon fence separating wildlife and livestock along the boundary of the Kruger National Park, South Africa. Prev Vet Med 100(3–4):210–220

Kalema-Zikusoka G, Bengis RG, Michel AL et al (2005) A preliminary investigation of tuberculosis and other diseases in African buffalo (*Syncerus caffer*) in Queen Elizabeth National Park, Uganda. Onderstepoort J Vet Res 72(2):145–151

Katale BZ, Mbugi EV, Siame KK et al (2017) Isolation and potential for transmission of *Mycobacterium bovis* at human-livestock-wildlife interface of the Serengeti ecosystem, Northern Tanzania. Transbound Emerg Dis 64(3):815–825. https://doi.org/10.1111/tbed.12445

Keet DF, Kriek NPJ, Penrith ML et al (1996) Tuberculosis in buffaloes (*Syncerus caffer*) in the Kruger National Park: spread of the disease to other species. Onderstepoort J Vet Res 63 (3):239–244

Keet DF, Michel AL, Meltzer DGA (2000a) Tuberculosis in free-ranging lions (*Panthera leo*) in the Kruger National Park. In: Annual conference of the South African Veterinary Association, 26–28 September 2000, Pietermaritzburg, South Africa, pp 232

Keet DF, Kriek NPJ, Michel AL (2000b) Tuberculosis and its geographical distribution in free-ranging lions in the Kruger National Park. In: Third international conference on *Mycobacterium bovis*, 14–16 August 2000, Cambridge, UK

Laisse CJM, Gavier-Widén D, Ramis G et al (2011) Characterization of tuberculous lesions in naturally infected African buffalo (*Syncerus caffer*). J Vet Diag Invest 23(5):1022–1027

Maas M, Keet DF, Rutten VPMG et al (2012) Assessing the impact of feline immunodeficiency virus and bovine tuberculosis co-infection in African lions. Proc R Soc B Biol Sci 279 (1745):4206–4214

Michel AL (2002) Implications of tuberculosis in African wildlife and livestock. In: Gibbs EPJ, Bokma BH (eds) The domestic animal/wildlife interface. Issues for disease control, conservation, sustainable food production and emerging diseases, vol 969. Annals of the New York Academy of Sciences, New York, pp 251–255

Michel AL, Bengis RG, Keet DF et al (2006) Wildlife tuberculosis in South African conservation areas: implications and challenges. Vet Microbiol 112(2–4):91–100

Michel AL, Coetzee ML, Keet DF et al (2009) Molecular epidemiology of *Mycobacterium bovis* isolates from free-ranging wildlife in South African game reserves. Vet Microbiol 133 (4):335–343

Michel AL, Hlokwe TM, Espie IW et al (2013) *Mycobacterium tuberculosis* at the human/wildlife interface in a high TB burden country. Transbound Emerg Dis 60(s1):45–52. https://doi.org/10.1111/tbed.12099

Michel AL, de Klerk LM, Buss P et al (2015) Tuberculosis in South African wildlife: lions, African buffalo and other species. In: Mukundan H, Chambers M, Waters R et al (eds) Tuberculosis, leprosy and mycobacterial diseases of man and animals: the many hosts of mycobacteria. CABI, Oxfordshire, pp 365–385

Mikota SK, Lyashchenko KP, Lowenstine L et al (eds) (2015) Tuberculosis, leprosy and mycobacterial diseases of man and animals: the many hosts of mycobacteria. CABI, Wallingford, UK, pp 259–276

Miller MA, Lyashchenko KP (2015) Mycobacterial infections in other zoo animals. In: Mukundan H, Chambers M, Waters R et al (eds) Tuberculosis, leprosy and mycobacterial diseases of man and animals: the many hosts of mycobacteria. CABI, Wallingford, UK, pp 277–295

Miller MA, Buss PE, van Helden PD, Parsons SD (2017) Mycobacterium bovis in a free-ranging black rhinoceros, Kruger National Park, South Africa, 2016. Emerg Infect Dis 23(3):557–558. https://doi.org/10.3201/eid2303.161622

Mills MGL (1995) Notes on wild dog *Lycaon pictus* and lion *Panthera leo* population trends during a drought in the Kruger National Park. Koedoe 38(1):95–99

Montali RJ, Mikota SK, Cheng LI (2001) *Mycobacterium tuberculosis* in zoo and wildlife species. Rev Sci Tech Off Int Epiz 20(1):291–303

Munag'andu HM, Siamudaala VM, Nambota A et al (2006) Disease constraints for utilization of the African buffalo (*Syncerus caffer*) on game ranches in Zambia. Jpn J Vet Res 54(1):3–13

Munyeme M, Muma JB, Skjerve E et al (2008) Risk factors associated with bovine tuberculosis in traditional cattle of the livestock/wildlife interface areas in the Kafue basin of Zambia. Prev Vet Med 85(3–4):317–328

Munyeme M, Muma JB, Siamudaala VM et al (2010) Tuberculosis in Kafue lechwe antelopes (*Kobus leche kafuensis*) of the Kafue basin in Zambia. Prev Vet Med 95(3–4):305–308

OIE (2017a) http://www.oie.int/wahis_2/public/wahid.php/Diseaseinformation/statuslist

OIE (2017b) http://www.oie.int/wahis_2/public/wahid.php/Diseasecontrol/measures

Olea-Popelka F, Muwonge A, Perera A et al (2017) Zoonotic tuberculosis in human beings caused by *Mycobacterium bovis*—a call for action. Lancet Infect Dis 17(1):e21–e25

Paine R, Martinaglia G (1929) Tuberculosis in wild buck living under natural conditions. J Comp Pathol Ther 42:1–8

Palmer MV, Thacker TC, Waters WR (2012) *Mycobacterium bovis*: a model pathogen at the interface of livestock, wildlife, and humans. Vet Med Int 2012:236205

Palmer MV, Thacker TC, Waters WR et al (2014) Oral vaccination of white-tailed deer (*Odocoileus virginianus*) with *Mycobacterium bovis* Bacillus Calmette-Guerin (BCG). PLoS One 9(5): e97031

Pandey GS (1998) Studies of the infectious diseases of the Kafue lechwe (*Kobus leche kafuensis*) with particular reference to tuberculosis in Zambia, Dissertation, Azabu University, Tokyo

Parsons S, Smith SGD, Martins Q et al (2008) Pulmonary infection due to the dassie bacillus (*Mycobacterium tuberculosis* complex sp.) in a free-living dassie (rock hyrax—*Procavia capensis*) from South Africa. Tuberculosis 88(1):80–83

Parsons SD, Drewe JA, Gey van Pittius NC et al (2013) Novel cause of tuberculosis in meerkats, South Africa. Emerg Inf Dis 19(12):2004–2007

Phepa PB, Chirowe F, Govinder KS (2016) Modelling the role of multi-transmission routes in the epidemiology of bovine tuberculosis in cattle and buffalo populations. Math Biosci 277:47–58

Renwick AR, White PC, Bengis RG (2007) Bovine tuberculosis in southern African wildlife: a multi-species host-pathogen system. Epidemiol Infect 135(4):529–540

Robinson PA, Corner LAL, Courcier EA et al (2012) BCG vaccination against tuberculosis in European badgers (*Meles meles*): a review. Comp Immunol Microbiol Infect Dis 35(4):277–287

Rodwell TC, Kriek NP, Bengis RG et al (2001) Prevalence of bovine tuberculosis in African buffalo at Kruger National Park. J Wildl Dis 37(2):258–264

Sylvester TT, Martin LER, Buss P et al (2017) Prevalence and risk factors for *Mycobacterium bovis* infection in African lions (*Panthera leo*) in the Kruger National Park. J Wildl Dis 53 (2):372–376

Tambling CJ, Ferreira SM, Adendorff J et al (2013) Lessons from management interventions: consequences for lion-buffalo interactions. S Afr J Wildl Res 43(1):1–11

Tarara R, Suleman MA, Sapolsky R et al (1985) Tuberculosis in wild olive baboons, *Papio cynocephalus anubis* (Lesson), in Kenya. J Wildl Dis 21(2):137–140

Van Helden PD, Parsons SD, Gey van Pittius NC (2009) Emerging' mycobacteria in South Africa. J S Afr Vet Assoc 80(4):210–214

Woodford MH (1982a) Tuberculosis in wildlife in the Ruwenzori National Park Uganda (Part I). Trop Anim Health Prod 14(2):81–88

Woodford MH (1982b) Tuberculosis in wildlife in the Ruwenzori National Park, Uganda (Part II). Trop Anim Health Prod 14(3):155–160