

PERSPECTIVES

Bovine tuberculosis: a double-edged issue at the human/livestock/wildlife interface in Africa

Contributors: Alexandre Caron (CIRAD¹, RP-PCP²), Michel de Garine-Wichatitsky (CIRAD, RP-PCP) and François Roger (CIRAD)

BOVINE TUBERCULOSIS IN AFRICA

Bovine tuberculosis (bTB) caused by *Mycobacterium bovis* is a major neglected tropical disease and there are important gaps in understanding of the epidemiology of this animal disease and zoonosis (Hotez and Kamath, 2009; El Idrissi and Parker, 2012). Its impacts can be economic, as bTB decreases the level of livestock production for both local and export markets; sanitary, as bTB can be transmitted from animal to human populations, causing severe disease and mortality; social, when livestock ownership is a source of social status in rural communities; and detrimental to biodiversity conservation, when bTB threatens wildlife populations or when disease management options consider the possibility of wildlife control. In developed countries, although bTB was once thought to be under control, the disease is re-emerging

as a result of maintenance of the agent in new wild host species. In the developing world, bTB is widespread in animal populations, and the animal and human health surveillance systems are not adapted to detect the infection efficiently or to assess its real impact on both host populations (Thoen *et al.*, 2009).

In Africa, the epidemiological situation of bTB in livestock and human populations is highly variable. In many cattle populations, the disease is chronic and largely asymptomatic until latter stages of disease. There is little information about the disease in small ruminants; although recent studies have indicated that goats in Africa are more prone to *Mycobacterium tuberculosis* infection than to bTB (Deres, Conraths and Ameni, 2013), bTB is known to occur in goats in Europe (Napp *et al.*, 2013). Small ruminants could therefore be an important host for the spillover of *M. tuberculosis* to humans

and vice versa. The extent of this spillover is unknown because of the lack of local diagnostic capacity to detect extra-pulmonary tuberculosis (TB), the major form of bTB in humans (Durr *et al.*, 2013); the few studies providing information on this aspect indicate absence (Tschopp *et al.*, 2010) or low prevalence of bTB in humans (Thoen *et al.*, 2009). The implications of a high prevalence of human immunodeficiency virus (HIV) for bTB susceptibility and prevalence in African rural populations are also largely unexplored, and human behaviour such as raw milk consumption can be an important additional risk factor. The high mammal diversity that still occurs in some areas of Africa provides additional hosts for *M. bovis*. In the Great Limpopo Transfrontier Conservation Area (GLTFCA) of southern Africa, for example, bTB has been shown to occur in more than 16 wild species (A.L. Michel, pers. comm.), but the role of each species in maintaining the



Cattle owner and herd in the Zinder area of the Niger, 2006

¹ International Cooperation Centre of Agricultural Research for Development: www.cirad.fr

² Research Platform Production and Conservation in Partnership: www.rp-pcp.org

disease is unknown or still debated, as are the impacts of the disease on different species.

The spatial extent and intensity of wildlife/livestock/human interfaces in Africa are highly variable. Interface areas range from double fences separating conservation areas (e.g. national parks) from other land-use types (e.g. communal land), to integrated mixed systems where wildlife and livestock production coexist (e.g. tourism and meat production). Some interface areas are marked by porous physical barriers, which can take the form of buffer zones around wildlife conservation areas, where human activities are regulated (e.g. wildlife hunting concessions), or environmental land-use boundaries such as rivers, which can attract wild and domestic ungulates and facilitate interactions (Kock *et al.*, 2014). Many of these interface areas share important characteristics: they occur in semi-arid and arid areas where poor human communities with little access to human and animal health services struggle to make a livelihood from small-scale farming, environmentally constrained cultivation and the legal or illegal harvesting of natural resources (Giller *et al.*, 2013). Limited availability of resources such as water and grazing land, especially during the dry season, promotes interactions among wildlife, livestock and human populations, increasing the risk of pathogen transmission. There is potential for these interface areas to play an important role in the epidemiology of bTB in Africa.

Across Africa, these interfaces span large tracts of land, but regional differences can arise as a result of historical and political contingencies. In western Africa, wildlife has been largely extirpated and its role in the epidemiology of bTB is probably very limited because the interface with livestock is localized around a few remaining wildlife conservation areas. In this region, *M. bovis* is therefore maintained mostly in livestock populations.

In central Africa, forest environments do not provide opportunities for intense contacts between wildlife and livestock species because forage resources are widely distributed and freely available. Although few data are available, it seems likely that these limited interface areas do not play an important role in bTB epidemiology.

In eastern Africa, *M. bovis* is endemic in wild and domestic ungulate populations (Tschopp *et al.*, 2010), but its epidemiology in the region's ecosystems has not attracted much interest until recently (e.g. Tschopp *et al.*, 2010; Roug *et al.*, 2014) and many gaps in knowledge remain. Eastern Africa has conserved extensive wildlife populations and several countries rely heavily on the wildlife industry for tourism. Expanding pastoral and agropastoral human populations in dry

savannahs encroach increasingly on to natural areas, but overall densities of wildlife and livestock are relatively low, except in areas of Ethiopia, where there are large cattle and wild ungulate populations.

In southern Africa, bTB at wildlife/livestock interfaces has been the focus of several studies, probably because the pathogen was introduced and spread in the Kruger National Park ecosystem in South Africa, where the implications for the conservation of wildlife

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mobilized the scientific community. Interface areas in southern Africa include fenced areas (e.g. Kruger National Park or country-wide fenced systems in Namibia and Botswana) and unfenced boundaries on the periphery of conservation areas. Recent initiatives to create transfrontier conservation areas in this region have drawn attention to the human and animal health issues associated with these complex socio-ecosystems (Osofsky, Cumming and Kock, 2008). The disease is spreading in some regions of southern Africa, and is endemic in others, with livestock/wildlife interfaces playing an important role in the inter-species spillover and spread of the pathogen.

THE ECOLOGY OF bTB IN MULTI-HOST SYSTEMS IN AFRICA

At wildlife/livestock interfaces, bTB evolves in complex multi-host systems. Each wild or domestic host can play an epidemiological role in the maintenance and spread of the pathogen, and lack of understanding of these roles can compromise the success of control strategies. Implementing a test-and-slaughter strategy in livestock populations will fail if a wild maintenance host repeatedly reintroduces the infection into the domestic animal population. Similarly, failure to understand the role of small ruminants in bTB or TB epidemiology can compromise control measures in cattle and human infection. Adopting a more functional approach to identify the key hosts in disease epidemiology has been proposed as a way of improving knowledge of – and therefore surveillance and

control strategies for – infectious diseases in Africa, including emerging diseases (Caron, Morand and Garine-Wichatitsky, 2012).

In South Africa, cattle imported from Europe have been retrospectively identified as the source of bTB. In the 1950s and 1960s, cattle from farms neighbouring the southern boundary of the Kruger National Park acted as a source of bTB for wildlife in the park when bTB spilled over to African buffalo (*Syncerus caffer*). Since then, *M. bovis* has spread in wildlife populations, reaching the northern tip of the park in 2005 and emerging in a buffalo population in the Gonarezhou National Park in Zimbabwe, despite the 40 km of communal land separating the two parks (de Garine-Wichatitsky *et al.*, 2010; Kock *et al.*, 2014). Molecular studies indicate that buffaloes, and probably greater kudu (*Tragelaphus strepsiceros*), have become maintenance hosts for bTB in this ecosystem (Michel *et al.*, 2009), although buffaloes do not seem to be clinically affected by *M. bovis* infection. It is suspected that most other wild species act as dead-end hosts, i.e. they can be infected by bTB but do not pass it on to other animals, although the effects at the species level can be severe. For example, bTB seems to be relatively aggressive in the lion population via consumption of infected buffaloes, with potential consequences on the tourism industry, for which the lion is a key species. Recent studies have collected more information on the presence of bTB at other cattle/buffalo interfaces in southern Africa (Jori *et al.*, 2013; Tanner *et al.*, 2014). In this region, the lechwe kob (*Kobus leche kafuensis*) has also been shown to maintain bTB close to wildlife/livestock interfaces in Zambia (Munyeme *et al.*, 2010).

As well as the biodiversity conservation issues related to the spread of bTB in wildlife populations, another important issue is the risk of spillback of bTB from a wildlife reservoir to naive cattle populations. The emergence of bTB in the buffalo population of the Gonarezhou National Park in Zimbabwe underlines the threat of such spillback, and also of spillover to human populations, directly through bushmeat consumption or indirectly through cattle or goats (de Garine-Wichatitsky *et al.*, 2010; Caron *et al.*, 2013). The buffalo population in GLTFCA could become a spatial vector, acting as a host population bridging cattle populations in South Africa and Zimbabwe. While spillback of bTB from a wildlife maintenance host to a domestic host seems to be rare in Africa (de Garine-Wichatitsky *et al.*, 2013a), recent studies suggest that it is possible (Munyeme and Munang'andu, 2011; Musoke *et al.*, 2013).

These studies underline the complex epidemiology of bTB at the wildlife/livestock interface and the need to disentangle the role of each host to understand the



Cattle herds drinking at a Mwenezi River pool during the dry season. On one side of the river is Gonarezhou National Park, on the other, Malipati communal land, 2008



Buffaloes on the run in Gonarezhou National Park, Zimbabwe. The species has the capacity to move undetected into anthropogenized land, triggering potential for bTB spillover from wildlife to cattle, 2008

pathogen dynamics in socio-ecosystems. The risk of bTB transmission between wild and domestic species, and ultimately to humans, is documented, but questions remain regarding the sanitary, economic and social consequences of the disease.

BOVINE TUBERCULOSIS – A NEGLECTED TROPICAL DISEASE OR NOT A PROBLEM?

Estimating the impacts of bTB on human, livestock and wildlife populations is difficult because of the chronic form of the disease. In western and eastern Africa, although bTB is endemic in cattle populations, animal and public health authorities do not consider it a priority disease. The lack of diagnostic capacities to differentiate *M. bovis* in humans from the human pathogen *M. tuberculosis* blurs the impact of bTB on human populations. A more relevant question concerns the *relative* impact of bTB in its hosts, as most hosts harbour communities of pathogens that can have impacts on their health and production (Caron *et al.*, 2013). Small-scale farming communities would probably rank bTB below tick-borne diseases and other more deadly diseases of their livestock (de Garine-Wichatitsky *et al.*, 2013b), while veterinary services generally prioritize diseases with high economic impacts, such as foot-and-mouth disease, and largely ignore bTB. In addition to descriptive epidemiology of bTB in African contexts, three areas of research could help decision-makers to assign appropriate priority to bTB surveillance or control:

- *Impact of bTB on human and animal populations:* What are the health and production consequences of having endemic bTB in host populations?

While the impact of bTB in cattle populations in the northern hemisphere has been documented, little information is available on African contexts (Mwacalimba, Mumba and Munyeme, 2012). Notably, the interplay among bTB, the immune system and other diseases (e.g. brucellosis, Rift Valley fever, tick-borne diseases) could increase the overall disease burden in host populations (e.g. Ezenwa *et al.*, 2010).

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- *Understanding bTB at human/livestock/wildlife interfaces:* Studying the relationship between the type of host contact and pathogen transmission could help identify the types of interface, seasons and drivers of host contact leading to bTB spillover/spillback, which will be specific to local contexts (e.g. Miguel *et al.*, 2013). Detailed ecological and social studies would be required to identify the relevant risk factors.
- *Diagnostic tools:* The development of bTB diagnostic tools adapted to wildlife,

livestock and human hosts could help improve field detection and discrimination between bTB infection and the presence of other mycobacteria (Chambers, 2013). A recent study investigating the relationship between the presence of *Fasciola hepatica* and bTB diagnosis in cattle in the United Kingdom of Great Britain and Northern Ireland highlights the need to investigate the effect of multi-pathogen conditions on bTB diagnostic sensitivity (Claridge *et al.*, 2012).

TRANSLATING RESEARCH INTO MANAGEMENT AND CONTROL OPTIONS

For countries prioritizing bTB, research on bTB epidemiology at wildlife/livestock/human interfaces can have a positive influence on surveillance and control, as surveillance systems need to be adapted to the specific situations of these interfaces. In multi-host systems, research can identify which host(s) should be sampled to detect the pathogen or to estimate its prevalence cost-effectively. Optimizing surveillance systems at these interfaces – including by taking advantage of local opportunities such as surveillance on bush meat and hunted wildlife – and adapting them to the multi-pathogen context will increase the efficiency of veterinary services in resource-limited environments. The integration of heterogeneous data from surveillance into risk analysis tools can facilitate estimation of the risk of spillover and/or spread between susceptible host populations (Etter *et al.*, 2006). Research can also help prevent disease spillover/spillback into new host populations by offering management options for human/livestock/wildlife interfaces.

Decreasing contacts between infected and naive hosts will limit the local spread of bTB, so adapted farming practices such as reducing the shared use of pasture and water by wild and domestic ungulates can be explored when the risk of contact is understood in the local spatio-temporal context (e.g. whether it is based on hotspots of transmission or seasonal risk of contacts). When bTB is endemic in host populations, its control or eradication is difficult, and it may be necessary to learn to live with the infection. In an endemic situation, management options will need to be identified for reducing the impact of bTB on livestock and wildlife host populations in a multi-pathogen context, and for minimizing human exposure to the pathogen. Collaboration with farmers, local veterinary services, wildlife managers and the public health sector should result in the design of socio-economically acceptable sanitary management plans to promote sustainable livestock production in African contexts. For example, the zoonotic transmission can be greatly reduced by implementing basic hygiene measures if acceptable for local traditions (e.g. boiling milk). The impact of bTB in production animals needs to be assessed: does bTB really have an impact on local production (i.e. is bTB a priority disease for local farmers?). There is room for participatory approaches that merge distinct spheres of knowledge, bringing scientific information to local communities and translating communities' knowledge into information for the scientific community to come up with appropriate and locally acceptable control or management measures.

The situation of bTB at human/livestock/wildlife interfaces is complex and can only be tackled through interdisciplinary approaches that bridge epidemiology, ecology, economics and social sciences, as recommended by the One Health and EcoHealth approaches (Pfeiffer, 2013). These approaches should aim at reducing the risk of bTB spillover to important populations, and reducing the impact of the disease on animal and humans. ³⁶⁰

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