



DISEASE IN WILDLIFE OR EXOTIC SPECIES

Tuberculosis Caused by *Mycobacterium bovis* in a Capybara (*Hydrochoerus hydrochaeris*)

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Summary

Tuberculosis, associated with *Mycobacterium bovis*, was diagnosed *post mortem* in an adult female capybara (*Hydrochoerus hydrochaeris*), kept at the Pampulha Ecological Park, Belo Horizonte, Brazil, in a large metropolitan area. On post-mortem examination, there were numerous firm white nodules scattered throughout all lobes of both lungs. Tissue samples were collected for histological and microbiological examination. Microscopically, the pulmonary nodules were multifocal to coalescing granulomas and intralesional acid-fast bacilli were evident in Ziehl–Neelsen-stained sections of the lung and spleen. Colonies with morphological features of *Mycobacterium* spp. were isolated from lung samples and conventional polymerase chain reaction (PCR) with genomic DNA from the isolates was positive for *M. bovis*; sequencing indicated 100% identity with the region of difference 4 (RD4) of *M. bovis*. In addition, *M. bovis* DNA was detected in the lung by quantitative PCR. The finding of *M. bovis* in a capybara indicates a potential public health risk in a zoological collection.

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Keywords: capybara; *Mycobacterium bovis*; tuberculosis

Tuberculosis (TB) is a chronic and debilitating infectious disease, which may be caused by bacteria of the *Mycobacterium tuberculosis* complex (MTC), including *M. tuberculosis*, *Mycobacterium bovis*, *Mycobacterium africanum*, *Mycobacterium microti*, *Mycobacterium origi*, *Mycobacterium mungi*, *Mycobacterium caprae* and *Mycobacterium pinnipedii* (Huard *et al.*, 2006; Smith *et al.*, 2006). TB is considered an important emerging disease and one of the most important causes of death for adult people worldwide (WHO, 2015). Although human tuberculosis is most commonly caused by *M. tuberculosis*, *M. bovis* is responsible for an increasing number of cases (El-Sayed *et al.*, 2016).

Most MTC species have the ability to infect wild animals; however, the susceptibility, pathogenesis and immune response to infection vary according to the strain of *Mycobacterium* and host species (Lécu and Ball, 2011). Usually, infection of wild animals with *M. bovis* occurs when there is close proximity to infected cattle (Fitzgerald and Kaneene, 2013). Moreover, several wild animal species are naturally infected by *M. bovis*, and are therefore sources of infection for cattle (Alexander *et al.*, 2002; Fitzgerald and Kaneene, 2013).

In addition to cattle, which are the preferential host for *M. bovis*, several wildlife species have been recognized as reservoirs. Different host species have variable susceptibility to *M. bovis* infection and may be

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0021-9975/\$ - see front matter
<http://dx.doi.org/10.1016/j.jcpa.2016.05.014>

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considered as spillover hosts, which must be re-infected from other sources to maintain the infection, or maintenance hosts, which can maintain the infection (Ayele *et al.*, 2004). The brushtail possum (*Trichosurus vulpecula*), the African buffalo (*Synceurus caffer*), the Eurasian badger (*Meles meles*), the white-tailed deer (*Odocoileus virginianus*) and the European wild boar (*Sus scrofa*) are all considered maintenance hosts of *M. bovis* in their respective environments (Renwick *et al.*, 2007; Fitzgerald and Kaneene, 2013). The list of spillover hosts is extensive and includes wildebeest (*Connochaetes taurinus*), bush pig (*Potamochoerus porcus*), chacma baboon (*Papio cynocephalus*), cheetah (*Acinonyx jubatus*), common duiker (*Sylvicapra grimmia*), eland (*Taurotragus oryx*), honey badger (*Mellivora capensis*), impala (*Aepyceros melampus*), large spotted genet (*Genettati grina*), leopard (*Panthera pardus*), lion (*Panthera leo*), spotted hyena (*Crocuta crocuta*), warthog (*Phacochoerus aethiopicus*), elk (*Cervus canadensis*), sika deer (*Cervus nippon*), reindeer (*Rangifer tarandus*), mule deer (*Odocoileus hemionus*), fallow deer (*Dama dama*), Eurasian elk (*Alces alces*), goats (*Capra hircus*), Iberian lynx (*Lynx pardinus*), dogs (*Canis familiaris*), cats (*Felis catus*), sheep (*Ovis aries*), mink (*Lutreola vison*) and several other species (Ayele *et al.*, 2004; Gortazar *et al.*, 2012; Maas *et al.*, 2013; Viljoen *et al.*, 2015).

The capybara (*Hydrochoerus hydrochaeris*), the largest rodent, is widely distributed in South America (Alho and Rondon, 1987). These animals have high reproductive capacity and marked environmental adaptation. In addition, they have few natural predators, a factor that contributes to overpopulation, including in urban areas (Pereira and Eston, 2007). Monitoring these animals in urban areas is important since they can transmit several zoonoses. Their role in transmission of *Rickettsia rickettsii* is well established, but capybaras can also play a role in the transmission of *Leishmania* spp., *Leptospira* spp., *Trypanosoma* spp., *Enterobacteriaceae* (including *Salmonella enterica*), *Toxoplasma gondii* and ectoparasites (Chiacchio *et al.*, 2014).

A previous study that compared isolates of *M. bovis* included one isolate from a capybara that had been imported from Germany to the Czech Republic (Pavlik *et al.*, 2002). The only other documented case of mycobacterial infection in a capybara was a case of *Mycobacterium intracellulare* infection in Argentina (Pezzone *et al.*, 2013). The purpose of this report is to describe a case of *M. bovis* infection in a capybara in an ecological park in Brazil.

This was a free-ranging capybara that lived in an ecological park within the urban area of Belo Horizonte, Brazil. The animal had been captured as part

of a neutering programme and was found dead in captivity. Except for marked signs of emaciation, detailed clinical information was not available, and the animal had not been subjected to any treatment.

At necropsy examination, there were numerous firm white nodules, 1–2 cm in diameter, scattered throughout all lobes of both lungs (Fig. 1). An abscess was found in the mediastinum.

Samples of lung, liver, spleen, kidney, heart, pancreas, bronchial lymph node, tongue, stomach, large and small intestines, ovary and adrenal gland were fixed in 10% neutral buffered formalin, processed routinely and embedded in paraffin wax. Sections (5 µm) were stained with haematoxylin and eosin (HE) and sections of the lung and spleen were subjected to Ziehl–Neelsen (ZN) staining.

Microscopically, the pulmonary nodules were multifocal to coalescing granulomas, characterized by a core of necrosis, with occasional foci of mineralization, and surrounded by numerous epithelioid macrophages and multinucleated giant cells and some heterophils, lymphocytes, fibroplasia and fibrosis (Fig. 2). Similar smaller granulomas were observed in the spleen, liver (Fig. 3) and bronchial lymph nodes. Intralesional acid-fast bacilli were evident in ZN-stained sections of the lung and spleen (Fig. 4). In addition, there was diffuse thickening of the glomerular basal membrane and glomerulosclerosis, associated with moderate periglomerular and interstitial lymphocytic infiltration, which was interpreted as a membranous glomerulonephritis. There was a mild, multifocal lymphocytic infiltration in the heart and pancreas, with moderate interstitial fibrosis in the pancreas. No histological changes were observed in the tongue, stomach, small and large intestines, genital tract and adrenal gland.



Fig. 1. Gross appearance of the lungs showing multiple white nodules (0.1–1.0 cm diameter) scattered throughout all lobes. Bar, 3 cm.

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