The prevalence of bovine tuberculosis in cattle at the wildlife/livestock interface in the Mnisi community, South Africa

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Introduction

Bovine tuberculosis (BTB) is caused by *Mycobacterium bovis* (*M. bovis*), of the *Mycobacterium tuberculosis* complex. The pathogen has a wide host range including humans, wildlife, livestock as well as domestic animals. The disease has great implications in livestock productivity, conservation of endangered wildlife and public health due to its zoonotic potential (Firdessa *et al*., 2012). Reports have mentioned the endemic levels and potential spread of BTB in South African game reserves, particularly the Kruger National Park (Michel *et al*., 2006). However, limited to no research has been conducted to investigate the potential spill-back of BTB into livestock, especially in communities' bordering the game reserves at the wildlife/livestock/human interface.

Objective

To investigate the prevalence and epidemiology of bovine tuberculosis in livestock in the Mnisi community.

Materials and Methods

Intradermal tuberculin test and Interferon gamma assay

At 15 dip-tanks located in Mnisi, 1167 cattle were tested for bovine tuberculosis using the comparative intradermal tuberculin skin test (CIDT) (Figure 1). The IFNɣ assay was used as an ancillary test to the CIDT in this study. Whole blood of animals (n = 4) with a CIDT bovine bias > 4 mm and selected animals (n = 7) with bovine bias between 2 – 4 mm were collected and stimulated with four purified protein derivatives (PPD) (bovine PPD, avian PPD, fortuitum PPD, pokeweed PPD) for the interferon gamma (IFNɣ) assay.

Isolating and identifying Mycobacterium tuberculosis complex organisms

Animals that tested positive based on the CIDT and/or interferon gamma were purchased from the owner and slaughtered for a detailed meat inspection. Lymph nodes and organ samples with typical BTB lesions were collected and cultured for mycobacteria. Isolates identified as acid-fast bacilli using Ziehl-Neelsen staining were speciated by PCR and genetically characterized using VNTR typing (Hlokwe *et al*., 2013). Phylogenetic analyses of the obtained genotypes in comparison with other isolates from domestic and wild animals in South Africa was carried out using UPGMA (Unweighted Pair Group Mean Average) as well as the maximum parsimony tree (Bionumerics software package version 6.6; Applied Maths, St-Martin-Latem, Belgium).

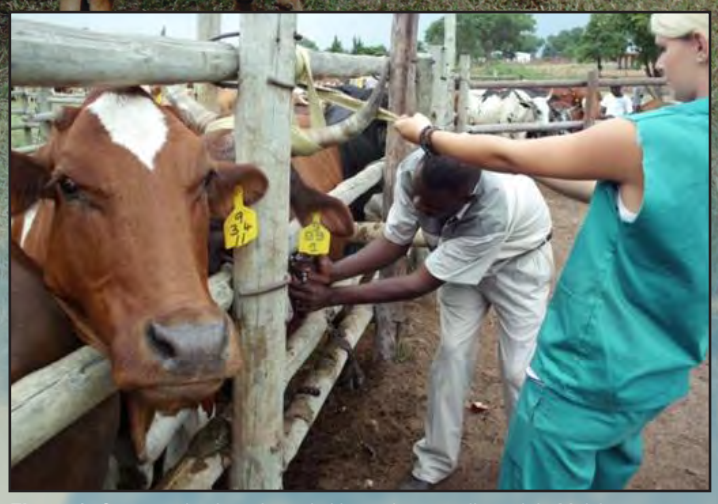

Figure 1: Comparative intradermal skin testing at a dip tank in Mnisi

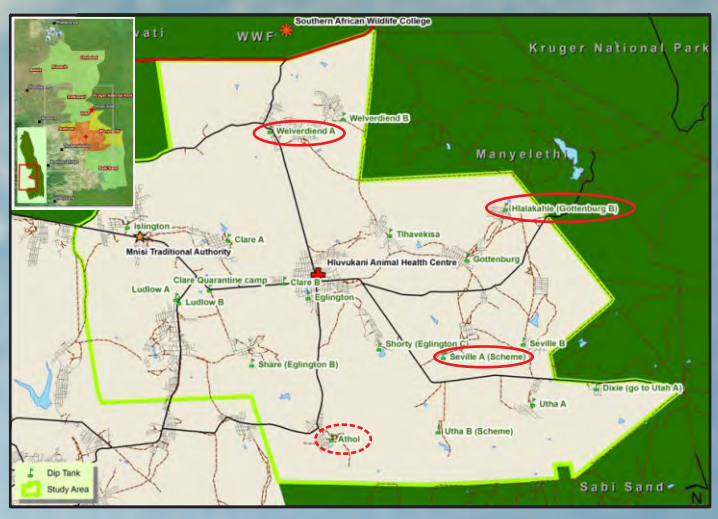

Figure 2: Map of Mnisi community area showing the dip tanks of study. Red circles indicate the dip tanks at which BTB positive cattle were detected.

Results

Bovine tuberculosis was detected at a low prevalence of 0.34 % at individual animal level and 26.7 % at dip-tank level. Dip-tanks identified as BTB infected were mainly located in close proximity with game reserves (Figure 2). Meat inspection showed that animals with lesions typical for BTB (Figure 3) were mainly localised and affected predominantly the thoracic lymph nodes; only one of the animals slaughtered had a lesion in the lung lobe. All *Mycobacterium* isolates were identified as *Mycobacterium bovis* and characterised genetically as VNTR 1, designated the original Kruger *M. bovis* strain (Figure 4).

Discussion

Great efforts have been implemented by governments and private game reserve owners to minimize the interaction between wildlife and livestock in neighbouring communities, in an attempt to control disease outbreaks at the wildlife/livestock interface. However, this study provides the first evidence of BTB spill-back from wildlife in the Kruger National Park into cattle in a neighbouring community.

Conclusion

BTB spill-back from the endemically infected Kruger National Park is an imminent risk to the livestock in neighbouring communities and mandates increased control efforts.

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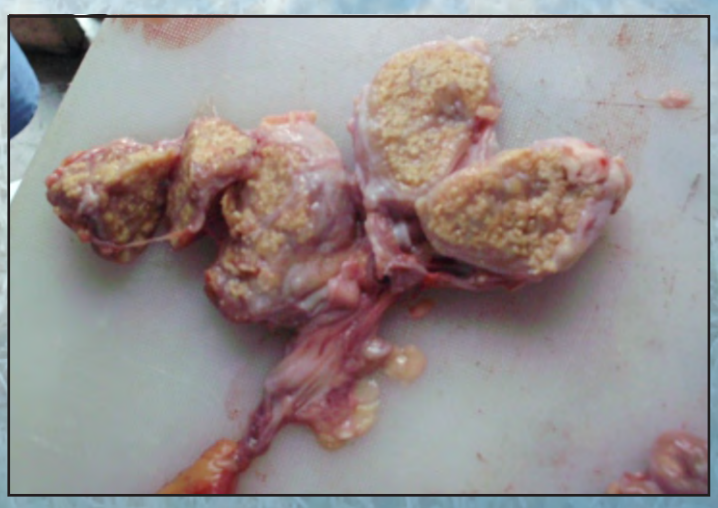

Figure 3: Typical calcified TB lesions in the lung lymph node of a skin test positive animal identified at Welverdiend A dip tank.

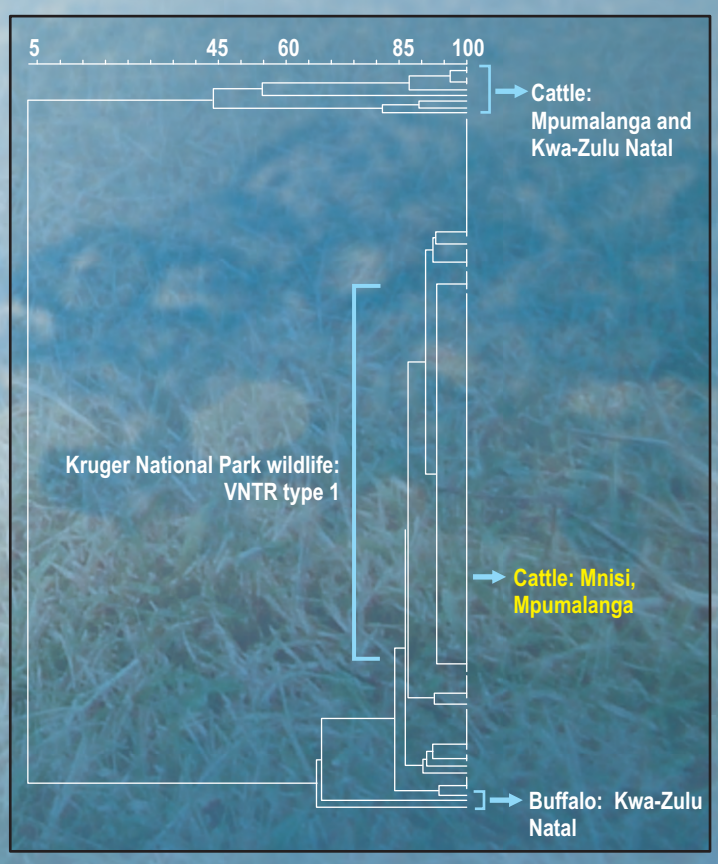

Figure 4: Dendrogram depicting the genetic homology between isolates obtained in this study with isolates from the Kruger National and other outbreaks in SA.

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