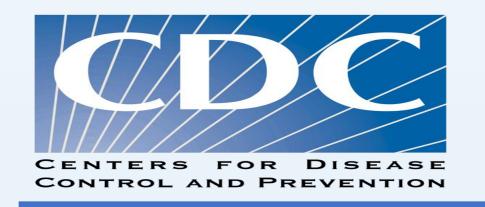
# Mycobacterium bovis infection in cattle at the wildlife/livestock interface in northern KwaZulu-Natal province, South Africa

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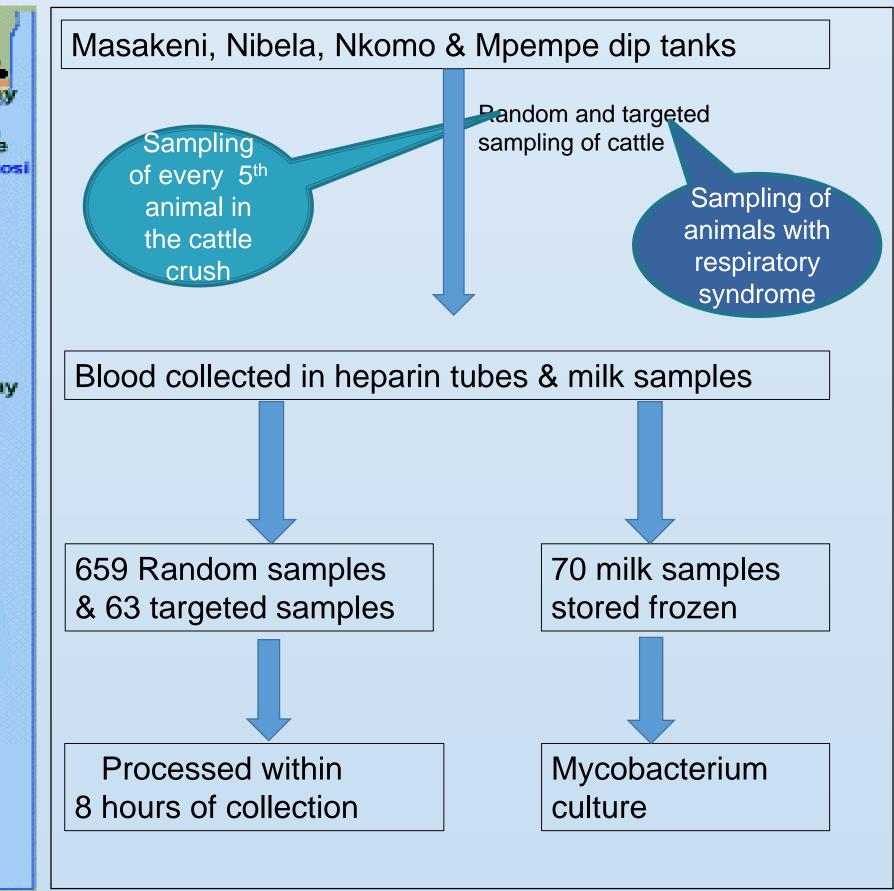


#### Introduction

Bovine tuberculosis (bTB) is a chronic respiratory disease of cattle caused by Mycobacterium bovis (M. bovis). The disease is characterised by progressive formation of tuberculous lesions in lung tissue, lymph nodes and other organs and results in production losses and trade restrictions. Although cattle and the African buffalo are known as maintenance hosts for M. bovis, it has a wide range of warm blooded hosts that include other wild and domestic animals and humans (Ayele et. al, 2004). Bovine tuberculosis is classified as a significant zoonotic disease (OIE,2006). M. bovis transmission to humans occurs primarily through consumption of contaminated milk or through direct contact with infected animals (Michel et al. 2010). The role of zoonotic TB in human TB in South African populations is unknown. The aim of this study was to determine the prevalence of *M. bovis* infection in communal cattle in Big 5 False Bay Municipality, uMkhanyakude district, Kwa-Zulu Natal and formed the first phase in a One Health investigation into the epidemiology of M. bovis infection at the wildlife/livestock/human interface.

### Materials & methods





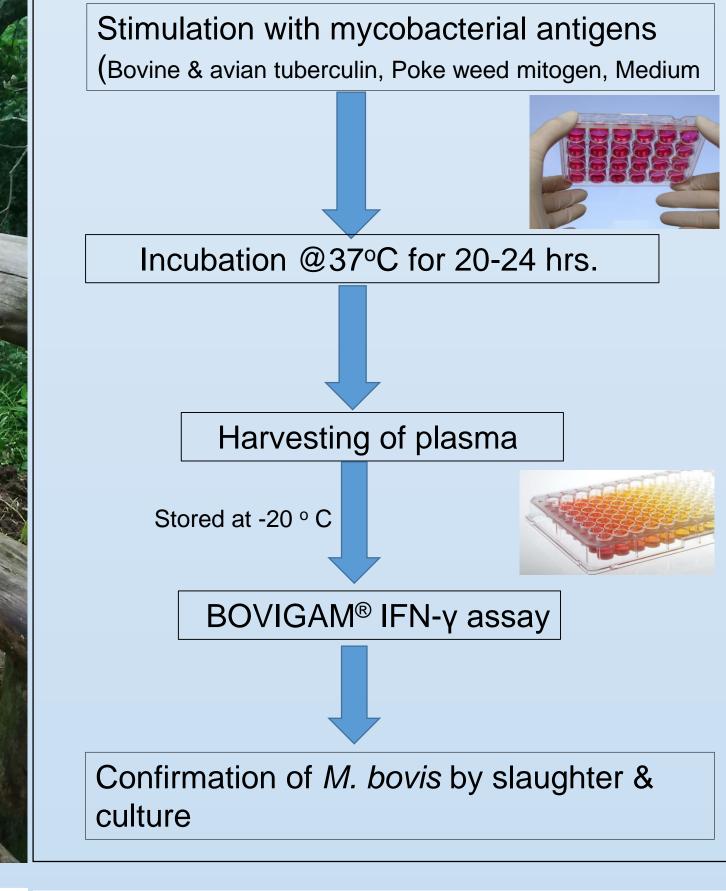


Fig 1: Study area: Northern KZN, uMkhanyakude district, Big 5 False Bay

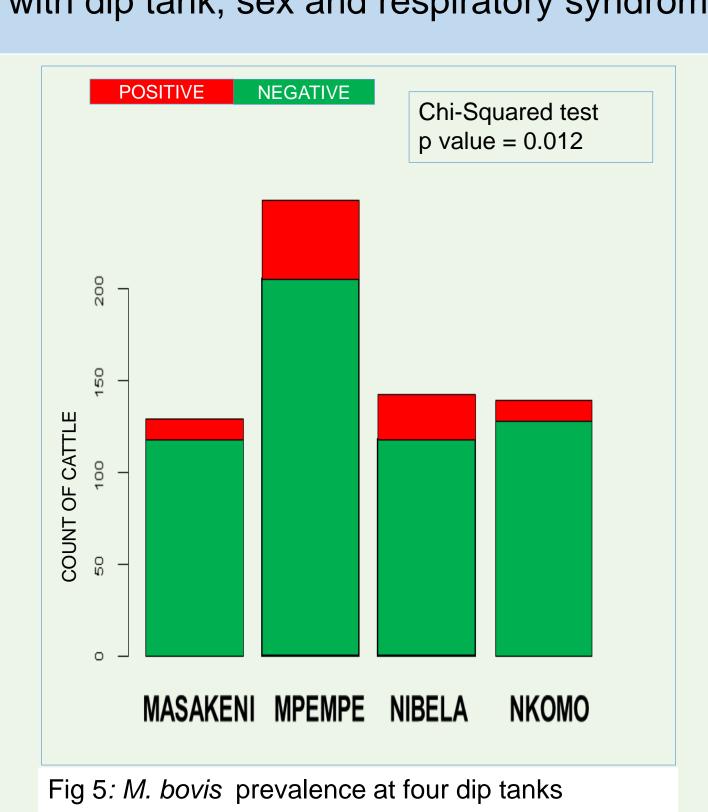
Fig 2 Flow diagram for sample collection at the four dip tanks

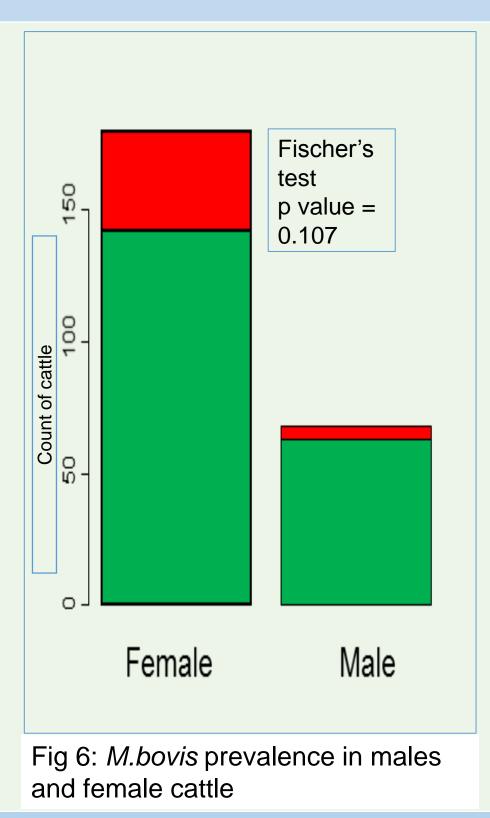
Fig. 3:Cattle in the cattle crush during blood collection

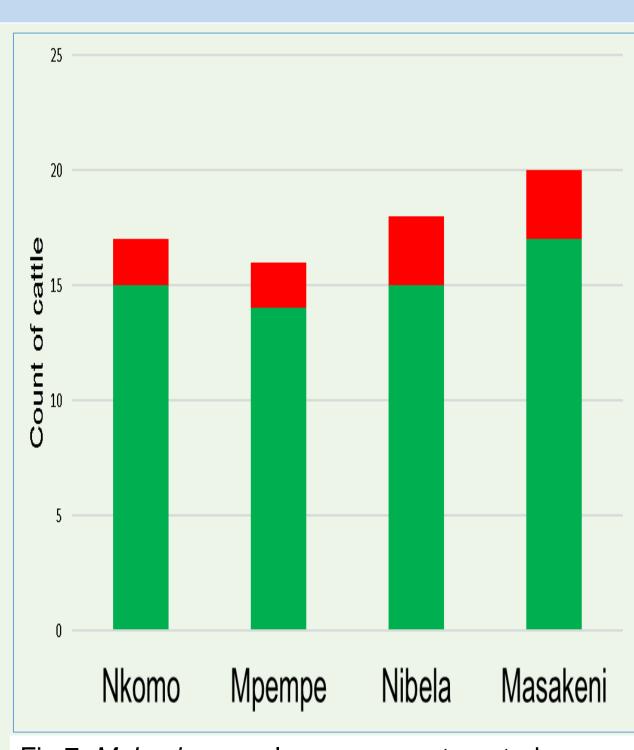
Fig 4: Flow diagram for the processing of the blood samples in the laboratory

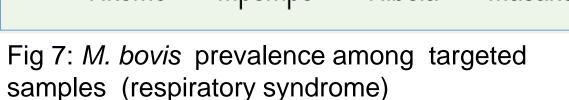
#### Results

A total of 722 cattle were tested at four dip tanks using the Bovigam assay of which 99(13.7 %) were classified as bovine reactors (Musoke et. al. 2015). The prevalence in association with dip tank, sex and respiratory syndromic sampling are shown in figures 5 – 7. Slaughter of three bovine reactors confirmed the presence of granulomatous lesions (figure 8 A and B).









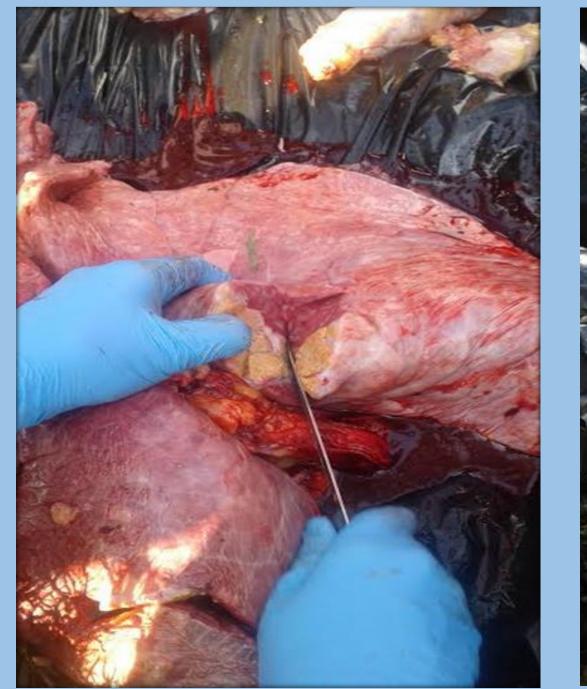




Fig 8: Post mortem findings in bovine reactor cattle. Multiple confluent caseous necrotic lesions in the lungs (A) and the enlarged pre-scapular lymph node (B)

## Discussion



Significantly different prevalences were detected at the four dip tanks, implying different levels of *M. bovis* exposure. There was no significant association between sex and *M. bovis* infection confirming that male and female cattle were equally susceptible to bTB. The prevalence in targeted samples (respiratory syndrome) was slightly higher than in randomly sampled animals (20% versus 17%), meaning that the majority of bTB infected cattle did not show clinical (respiratory) signs, hence respiratory signs are an unreliable indicator of bTB.

#### References

1.Ayele, W. Y., Neill, S. D., Zinsstag, J., Weiss, M. G., & Pavlik, I. (2004). Bovine tuberculosis: an old disease but a new threat to Africa. The International Journal of Tuberculosis and Lung Disease: The Official Journal of the International Union against Tuberculosis and Lung Disease, 8(8), 924–937. 2.Michel, A.L., Muller, B., van Helden, P.D. 2010. Mycobacterium bovis at the animal-human interface: A problem, or not? Veterinary Microbiology, 140, 371–381.

3.Musoke, J., Hlokwe, T., Marcotty, T., Du Plessis, B. J. A., & Michel, A. L. (2015). Spillover of mycobacterium bovis from wildlife to livestock, South Africa. Emerging Infectious Diseases, 21(3), 448–451. 4. OIE (2006) Office International des Epizooties Terrestrial manual: World Health Organization for Animal Health, Paris: Office International des Epizooties