Quintessential One Health: A Bovine Tuberculosis Risk Analysis in South Africa

INTRODUCTION

Bovine tuberculosis (BTB), caused by pathogen Mycobacterium bovis, is an infectious disease of importance to domestic livestock, wildlife, and humans. Endemic to bovids, BTB is known to spill over into wildlife populations where they cohabitate. First identified in greater kudu and common duiker in 1928, BTB spilled over from infected cattle to African buffalo in South Africa's Kruger National Park in the 1990s. It has since been diagnosed in a multitude of species ranging from felids (lions, leopards, cheetahs) to canids (African wild dogs) to primates (baboons) to ungulates (eland, impala etc.); many of these species are already rare or in decline. The occurrence of BTB in wildlife constitutes an infectious feedback loop, potentiating re-exposure and infection for livestock, thus thwarting eradication efforts. The ability of M. bovis to cause spillover events and reside in various reservoir species makes it challenging to eradicate and presents a significant risk to wildlife health.



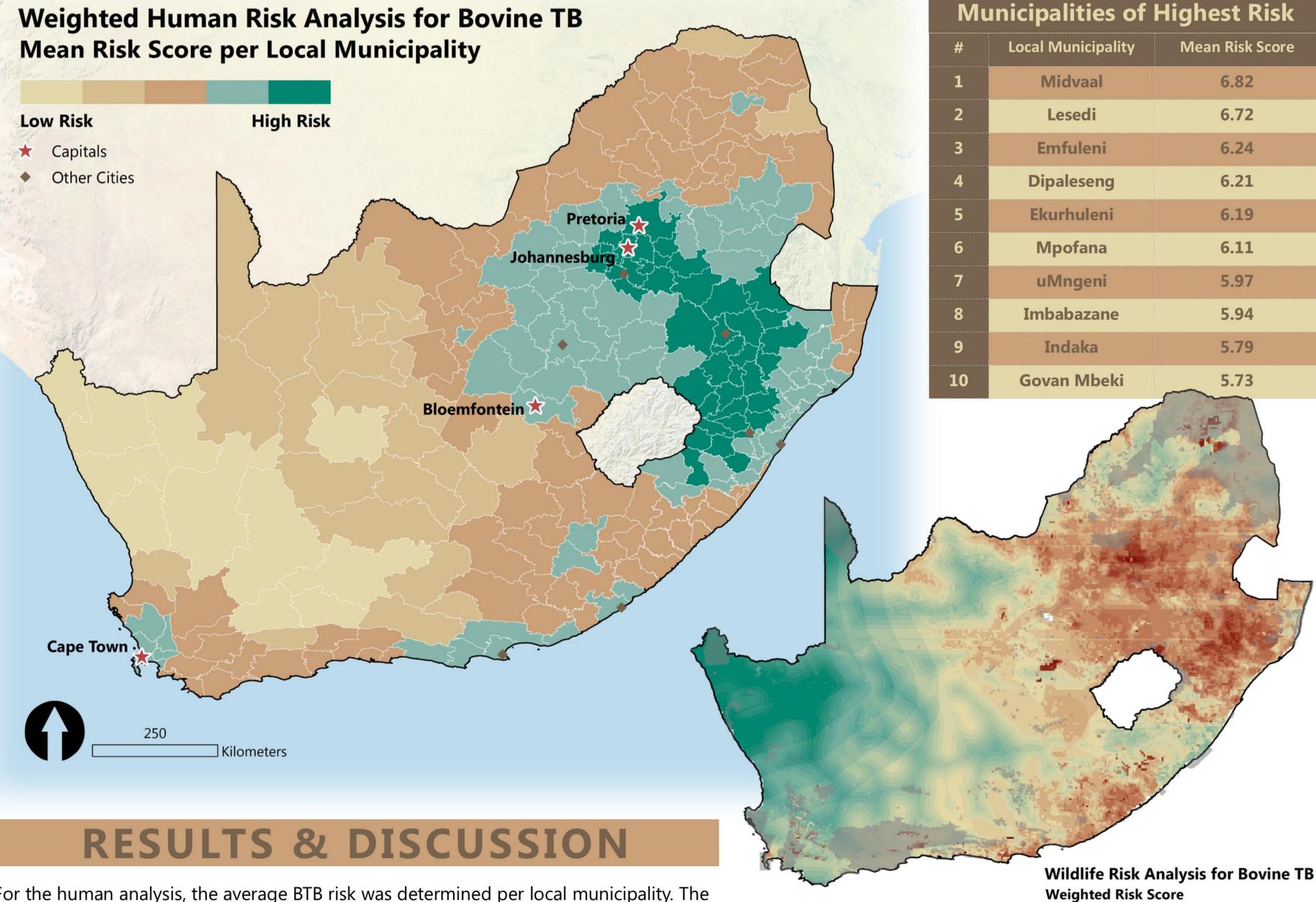
A noteworthy zoonosis for humans, BTB is closely related to M. tuberculosis, the causative agent of human tuberculosis (TB), and the leading infectious cause of death worldwide. Because developing nations often lack the resources for proper speciation, the exact proportion of BTB cases is unknown, and the true prevalence is suspected to be severely under-reported. However, due to reasons of increasing multi-drug resistance, it is of vital importance to make this distinc-

tion. On the South African landscape level, where wildlife is present to maintain the pathogen, where livestock range in close proximity to wildlife, and where livestock and people coexist, BTB remains a significant threat to public health, encapsulating how animal, human, and environmental factors collectively drive disease emergence and patterns.

Species of Conservation Interest Leopard **African Lion** Panthera pardus Panthera leo ULNERABLE **VULNERABLE African Wild Dog** Cheetah Lycaon pictus Acinonyx jubatus **ENDANGERED VULNERABLE**

METHODS

A weighted risk analysis was performed for both human and wildlife populations. A variety of tools was used for each analysis (ie. Euclidean Distance and Kernel Density), and each factor was converted to a raster and reclassified. Zonal Statistics was applied to the human analysis to determine average risk per local municipality. From the wildlife analysis, the hot zones of risk were manually compared to the ranges of vulnerable species to determine which species might be most susceptible based on geospatial factors. For humans, weight was assigned as follows: 30% HIV prevalence + 30% bovine density + 20% abattoir density + 20% dairy production. For wildlife, the weight was assigned as follows: 35% bovine density + 30% distance from African buffalo range + 20% distance from water + 10% distance from overlapping warthog and kudu range + 5% distance from independent kudu and warthog ranges.



For the human analysis, the average BTB risk was determined per local municipality. The absolute minimum and maximum scores possible were 0.5 and 8.9, respectively. Average scores per local municipality ranged from 0.63 to 6.82, with the minimum and maximum scores being 0.5 and 7.7, respectively. The highest average risk of BTB was 6.82, in the Midvaal Local Municipality, within the Sedibeng District Municipality, and the Gauteng Province. For the wildlife analysis, some high-risk areas overlapped with cheetah ranges, while African lions and African wild dogs seem to range in lower-risk areas. Leopard ranges expand across the extent of South Africa, so they may also be considered a potentially at-risk population.

The value of such a vulnerability project is multifold. Public health agencies can use this geospatial analysis to establish targeted surveillance and prevention programs, engage in public outreach, and disseminate food safety, hygiene, and biosecurity information in highly at-risk areas. This project can also inform conservation efforts, identifying key regions and populations at risk. BTB is also notably a *global* disease, with varying risk factors. This methodology can be repeated in other regions and modified for different factors. For example, BTB is also a problem in invasive brush-tailed possums in New Zealand, badgers in the UK, and white-tailed deer in Michigan.

There are some limitations to this geospatial analysis. Many livestock production risk factors are challenging to represent geographically, such as age, breed, and various management practices. Other excluded datasets include wildlife population density, other immunosuppressive diseases, food safety (ex. milk pasteurization vs. souring), and hygiene factors. In addition, wildlife migration routes and livestock movement across the landscape are critical factors influencing BTB ecology, and due to difficulty in presenting such information, were not considered in this analysis. Furthermore, higher spatial resolution may be more informative in the implementation of targeted surveillance programs. Finally, my chosen factors approximate human population density, but perhaps a more nuanced analysis incorporating environmental and human-independent factors may be more suitable.

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Protected Areas

High Risk

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Projection: Africa Albers Equal Area Conic

Data Sources: Global Administrative Areas (GADM), IUCN Red List of Threatened Species, South Africa Protected Areas Database (SAPAD), Statistics South Africa, FAO Global Network, Milk Producers Organization, South African National HIV Prevalence, Incidence, and Behaviour Survey, 2012, ESRI Datamaps 10

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SPATIAL ANALYSIS FACTORS

HIV Prevalence

Immunosuppression can leave patients susceptible to opportunistic pathogens like M. bovis. HIV is one of the most common coinfections with TB globally, and increases likelihood of developing overt clinical signs and severe disease. For this analysis, the average prevalence of HIV by district municipality was reclassified.

Dairy Production

The highest prevalence of BTB arises where intensive dairy production occurs. The consumption of raw, unpasteurized milk is considered the most important route of transmission from livestock to humans. The average milk production per local municipality was converted to a raster and reclassified before analysis.

Bovid Density

As bovids are the natural hosts of *M. bovis*, people who work closely with livestock and wildlife that range in the same territories are more at risk of pathogen transmission. This spatial factor was reclassified and incorporated into both analyses.

Abattoir Density

The impact of BTB is felt disproportionately by developing countries that lack preventative measures. Slaughterhouse employees are more likely to directly contact infected tissues. This problem is magnified when food safety testing is lacking. Kernel Density was run on data points denoting South African abattoirs.

Reservoir Ranges African buffalo are a confirmed maintenance host for M. bovis, capable of harboring infection and further dissemination. Greater for the bacterium. The spread of BTB is most likely to occur where

kudu and common warthog are also suspected to be reservoirs wildlife and domesticated animals intermingle. For this analysis, Euclidean Distance was run with species ranges, then reclassified. Ranges of BTB Reservoir Species

