INVESTIGATING THE SPATIAL DISTRIBUTION OF BOVINE TUBERCULOSIS (BTB) HERDS OF CATTLE IN NAMWALA DISTRICT OF ZAMBIA

By

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DECLARATION

I, Novan Tembo, do hereby declare to the Senate of The University of Zambia that this dissertation is my own original work and that it has neither been nor concurrently being submitted for a higher degree award in any other university.

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ABSTRACT

The overlap in grazing pastures and water points at the wildlife-livestock interface area among different wildlife species and livestock have been recognised as "hot" spots for disease transmission. It is a major driver for bovine tuberculosis (bTB) occurrence in the Kafue flats. To investigate this phenomenon, Geographical Positioning System (GPS) coordinates representing 96 herds across 20 villages were captured alongside biological and risk factor data. The GPS coordinates were transferred into Arc-View 3.2 and laid onto the map of Namwala district. To understand relationships with the environment, map overlays were done to incorporate physical features including National Parks, Game Management Areas (GMA) and flood plains. In addition, Questionnaires were administered across 96 independent households to assess risk factors of bTB transmission to livestock.

The results revealed a spatial distribution of the disease in cattle in Namwala district of Zambia, with an ecological interplay in the high bTB prevelance areas which were a function of existing resreviour hosts. That was particularly significant in the eastern interface areas of the District where autocorrelation between high prevalence in cattle and the environment was found to be significant using Moran's I statistic (p-value=0.006). This indicated the marked tendency for aggregation of the positive bTB cases which may be due to the overlapping effect of cattle and wildlife in grazing areas. Further, on epidemiological studies, a total of 35 herds were found positive representing a prevalence of 36.4% (95% CI=26.7-46.3%). Individual herd prevalence across the study area ranged from 0% to 14% (95%=2.4-26.2%). The possible risk factors contributing to the spread of the disease to livestock were contact with wildlife during grazing and at water points. We also looked at the potential for bTB to be transmitted to humans. Risk factors underlying such possible transmission included low BCG vaccination at only 30%, only 40% having knowledge of bTB and only 26% reporting boiling of milk while frequency of drinking milk at least three times a week was as high as 82%. On logistic regression, cattle sharing watering points with wild animals were 5.5 more likely to belong to bTB positive herds.

The use of GIS in this epidemiological study has shown that bTB is skewed to the Eastern side of Namwala in distribution. Mitigation measures against this disease should therefore prioritise this region of the district.

DEDICATION

To whoever gives their best in the pursuit and unreserved sharing of scientific knowledge for believing in the power of science to make this world a better place!

To the Fully Proud Tembo, Magiya Manda and Paul Manda families, for preparing me to play my role in that endeavour.

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AIDS   Acquired Immuno Deficeincy Syndrome

BCG   Bacillus Calmette-Gurin; A tuberculosis vaccine

bTB   bovine Tuberculosis

CDC   Centre for Disease Control

CI   Confidence Interval

CPR   Common Pool Resource

GIS   Geographical Information Systems

GMA   Game Management Area

GPS   Geographic Positioning System

HIV   Human Immunodeficiency virus

M. bovis   Mycobacterium bovis

MTC   Mycobacterium Tuberculosis Complex

O.R   Odds Ratio

TB   Tuberculosis

WHO   World Health Organisation

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CHAPTER ONE

1.0 INTRODUCTION

Bovine tuberculosis (bTB) caused by *Mycobacterium bovis* is a major zoonotic disease of worldwide economic and public health importance, especially in developing countries where control measures are neither formulated nor enforced (Sudre *et al.,* 1992). Bovine tuberculosis belongs to closely related bacteria classified under members of the *Mycobacterium tuberculosis* complex (MTC). Bovine tuberculosis (bTB) has been shown to exhibit a wide host range and preference than most pathogens within the MTC, making it a very important emerging zoonotic pathogen (Filliol *et al.,* 2006). Among the MTC, *Mycobacterium tuberculosis* (*M. tb*) is the most common cause of human tuberculosis, but an unknown proportion of cases are due to *Mycobacterium bovis (M. bovis)* (Cosivi *et al., 1998).* The relatively low incidence of development of open (infectious) pulmonary tuberculosis due to bTB in humans is almost certainly due to immunological factors that could be abrogated in concurrent HIV infections (Cosivi *et al.,* 1998). Thus there is every reason to be seriously concerned that the HIV pandemic might fuel an increase in human tuberculosis cases due to bTB (Humblet *et al., 2009).*

The World Health Organisation (WHO) has declared the new resurgence of TB a global emergency. Globally, approximately 1.86 billion people are infected with TB, implicating TB as the greatest cause of death due to a single pathogen, second only to the human immunodeficiency virus (HIV) (Ashford *et al.,* 2001). The burden is made worse by the contribution of bTB. In some developed countries, bTB has been brought under control, with subsequent decrease in economic losses attributable to it

(Humblet *et al.,* 2009). A consequence of the reduced burden of infections in animals in these countries is a reduction in human tuberculosis cases resulting from *M. bovis* (Muma *et al.,* 2013). The situation is different in most developing countries such as Zambia where bovine tuberculosis (bTB) is still endemic. Currently the global incidence rate is growing at approximately 0.4% per year, with a much higher rate observed in sub-Saharan countries, Zambia included (WHO factsheet 10/4/2012). Sustained infection of bTB in animals implies that millions of people in rural African communities are daily at risk because of life style, eating habits, and poor hygienic conditions which favour infections. Under the World Health Organization (WHO), Zambia is ranked in Group three on the Global TB rankings based on the prevalence and incidence of all forms of human tuberculosis (WHO, 2012). Unlike Group one which implies that a country has no Tuberculosis problem and Group two where it is a minor problem, Group three implies that TB is a major problem (Sitima *et al.,* 1997).

In Zambia, the incidence of tuberculosis has been on the increase (WHO, 2011). At the same time, Elliot *et al.,* (1990) reported that by 1989, of the total number of patients who were receiving anti-tuberculosis therapy in Zambia, 73% of them were sero-positive for HIV. Although statistical figures show significant levels of tuberculosis infection among human populations in Zambia, very little information is available to ascertain how many of the observed human tuberculosis cases can be attributed to infections due to bTB (Cook *et al.,* 1996). Further, Cook and co-workers reported that there is a positive correlation relationship between rearing animals and acquiring bTB in Zambia. These researchers found a high prevalence of tuberculosis in humans, especially those with concurrent HIV infection in the Monze district of Zambia (Cook *et al.,* 1996). It is well known, that *M. tuberculosis* will be

largely responsible for the new TB cases and deaths, but an unknown and potentially important proportion will be caused by bTB. The direct correlation between bTB infection in cattle and the disease in the human population has been well documented in industrialized countries, whereas little information is available from developing countries where risk factors for bTB infection in both animals and humans exist in high proportions (Ashford *et al.,* 2001).

Understanding the distribution of a disease is important in the formulation of control strategies. Moreover, the distribution is also important in the appreciation of the extent of disease prevalence. Although there are a number of reports on bTB infections in cattle, only a few of them are on distribution of the disease. (Oloya *et al.,* 2007; Kazwala *et al.,* 2001). Up-to-date information on the risk factors is required in the light of high HIV/AIDS prevalence in sub-Saharan Africa (Anon. 2000; Berkley *et al.,* 1990), moreover, animal protein (meat and milk) is highly required to mitigate the impact of the HIV/AIDS pandemic, but bTB infections threaten this resource (Bandara and Mahipata, 2002). The World Bank estimates that the disease accounts for 26% of all avoidable adult deaths in less developed countries. So serious is the threat of tuberculosis that in 1993 the World Health Organization took the unprecedented step of declaring this disease a global emergency (WHO 2002). HIV infections render a person infected by MTC agents much more likely to develop overt tuberculosis and the evolution of the disease is considerably accelerated. About 20% of all forms of TB cases in Africa are believed to be related to HIV (Tanser and Suer, 2002).

Sustained infection requires not only better study techniques but ones which present results in ways that are easier to appreciate and thus easier to use in formulating control measures. One such way of better understanding and presenting results is the capture of exact geographical points of disease occurrence to determine where to direct resources (Dirk *et al.,* 2009). According to WHO, in order to properly plan, manage and monitor any public health program it is vital that up-to-date relevant information is available to decision makers at all levels of the public health system. This must be done with available data taking into consideration disease transmission dynamics, demographics, availability of and accessibility to existing health and social services as well as other geographic and environmental features. Geographical Information Systems (GIS) provide ideal platforms for the convergence of disease specific information and their analyses in relation to population settlements surrounding social and health services and natural environment. GIS allows policy makers to easily visualize problems in relation to existing health and social services and the natural environments and so more effectively target resources (WHO, 2012).

Mapping has been used historically in public health context. An example is the well-known maps of cholera cases around Broad Street Pump in London in the mid-1800s (Matthews 1998). Maps help in identifying populations at risk and thus help to direct intervention. The identified groups can also help in control since they have to be involved but should be identified first. Geovisualisation or GIS mapping is the use of computer aided graphical methods to visualize geospatial information and is a technique which is being used to help guide health service planning, public health interventions and inform the public about disease hot-spots (Douglas *et al.,* 2010). The aim in health mapping is not to identify statistically significant relationships but

to first gain insight in understanding the ways in which health status varies over space and to reveal the potential drivers behind this variation. GIS helps to counter the problem of non-user-friendly presentation of results encountered in disease control (Ellen and Cromley, 2003).

Multi-faceted and interdisciplinary approach to disease control demands more complicated responsibility sharing across physicians, Veterinarians, social scientists and politicians by virtue of formulating policies, under the banner of "One Health." The use of geospatial mapping makes it easy to visualize data leading to easier analysis. Graphical presentation has a way of appealing more to human perception. With such heightened appreciation of data important control strategies such as disease modelling and policy on diseases can be formulated. GIS has been used to describe sources and distributions of disease agents and identified regions in time and space where people may be exposed to environmental and biological agents and to finally map and analyse spatial and temporal patterns in health outcomes (Ellen and Cromley, 2003). Such information is critical in effective implementation of disease control strategies.

The modelling capacity offered by GIS is directly applicable to understating the spatial variation of disease and its relationship to the distribution of risk factors and health care systems (Tanser and Suer, 2002). Public health practice needs timely information on the course of disease and other health events to implement appropriate actions and GIS is an innovative technology for generating this type of information. Due to infrastructural and cost constraints, there is a lack of reliable statistics and disease reporting in Africa. Additional study techniques are therefore

needed to address that problem. GIS can help significantly in this area by filling the gaps through empirical disease modelling techniques (Tanser and Suer, 2002). GIS can therefore be used to model tuberculosis in Zambia which is one of the leading causes of death worldwide killing more people aged over 5 years of age along with AIDS, malaria and diarrhoea (theglobalfund.org, 2013). Before modelling however, it is important to get the pattern of disease using mapping (Ellen and Cromley, 2003). That is because disease transmission is linked to spatial and spatiotemporal proximity and transmission is more likely to occur if at risk individual are close to each other in space and time (Bell *et al.,* 2006).

In order to control Bovine Tuberculosis (bTB) in livestock it is important to begin by finding out where the disease is prevalent, what risk factors are favouring the prevalence and how much the livestock owners know about it and then allow them to become an integral part of control strategy (Munyeme *et al.,* 2012)

1.1 JUSTIFICATION OF THE STUDY

The impact of TB in terms of morbidity, mortality and spread varies substantially with demographic profile so that identifying the most exposed or affected populations becomes a key aspect of planning and targeting interventions (Tatem *et al.,* 2012). One challenge of public health is to improve the public's perception of the extent of the TB pandemic and application of science in finding solutions thereby facilitating the more widespread use of up to date scientific evidence (Bell *et al.,* 2006). The production of attractive and informative maps complements the formal analysis of spatial epidemiological data and as a result of visual impact they have, it is likely that maps will influence the recipient much more than accompanying

statistics (Rezaeian *et al.,* 2004). There has been no work conducted in Zambia using GIS to study the pattern of bTB spatial distribution

Previous investigations on zoonotic tuberculosis had focused on reporting the presence of the disease in animals and humans without application of geospatial tools to get information on the exact extent of the problem. This study was therefore designed to investigate the spatial distribution of bTB in cattle in Namwala District of Zambia and provide more information on tuberculosis and the association that exists in this previously identified high prevalence setting in livestock.

1.2 SIGNIFICANCE OF THE STUDY

The impact of TB on human health has been devastating worldwide with more than 3.5 million dying annually from TB, with bTB being responsible for 3% of these cases (Cosivi *et al.,* 1998). In Zambia, the high HIV prevalence of 14.3% countrywide continues to fuel all forms of TB with WHO estimating that 70% of Zambian TB patients are infected with HIV. TB is the leading cause of death among HIV infected persons (CDC, 2012).

The results of the study will be important in helping decision makers make informed choices on how much resources to allocate to bTB control based on the location and extent of the problem. The maps highlighted where the vulnerable populations are. The affected population will benefit by virtue of having been identified and hopefully will be placed on the agenda of tuberculosis control. Having been identified, the populations will also be made to actively participate in implementation of control strategies.

1.2.1 Research questions

1. What is the spatial distribution of bTB in cattle in the known high prevalence areas of Namwala District?

2. What factors influence the spatial and temporal distribution of bTB in animals and zoonotic transmission to humans in Namwala District?

3. Would GIS results be complementary with earlier findings from traditional descriptive epidemiological techniques?

1.3. Objectives

1.3.1 Principal objective/ General Objective

The principal objective of this study was to investigate the spatial distribution of bTB in cattle in Namwala district of Zambia and its associated public health implications.

1.3.2 Specific objectives

1. To determine the spatial distribution of bTB in Namwala District of Zambia

2. To determine possible factors influencing the spatial distribution of bTB in cattle and zoonotic transmission to people in Namwala District

3. To assess the complementarities of GIS results with earlier traditional descriptive epidemiological study results.

CHAPTER TWO

Literature Review

2.1 Background

2.1.1 Namwala

Namwala is a district in Southern province of Zambia (Figure 3.1) and lies in the Kafue basin (Figure 3.1). It is bound by Kafue National Park on the West and Lochinvar National park on the East. It also has Kafue flats Game Management Area (GMA) on the East, Namwala GMA on the North and Billi GMA on the South. Southern province has the highest cattle density in Zambia and it (Namwala) has the highest density of all the districts. It is highly dependent on cattle rearing. Cattle owners practice transhumance type of grazing where they take their animals to the plains for more pastures. The local tribe is the Ila who drink a lot of unpasteurised milk (Sitima *et al.,* 1997).

The HIV rate is at 2/1000 and all forms of TB at 5/1000 (Namwala District Development Plan 2006-2010). The district has the highest condemnation rates of bTB in the province. Higher cattle density account for bTB in connection with the practice of transhumance grazing which exposes livestock to reservoir hosts including Lechwe because of being in Kafue basin a haven for the Lechwe (Munyeme *et al.,* 2012). People have been known to contract the disease thorough consumption of unpasteurised milk such that *M. bovis* has been isolated from the animals and the people themselves (Malama *et al.,* 2013). HIV influences pathogenesis of the disease in people (Hunagy *et al.,* 2013; Malama *et al.,* 2013). Prevalence of bTB is as high as 30% in the cattle of the district (Sitima *et al.,* 1997). In a study by Muma *et al.,* (2013), they found that Monze had the highest prevalence

of bTB and there was no difference with Namwala. They found that the highest spoligotype indicative of bTB were in samples from Namwala district.

2.1.2 Kafue Lechwe

BTB in wildlife forms a stable reservoir such that *M. bovis* has been characterised from Kafue Lechwe (*Kobus Lechwe Kafuensis*) (Malama *et al.,* 2013). The Kafue Lechwe are an effective disseminator of bTB more so with the habit of overcrowding which promotes the sharing of the pathogen (Munyeme and Munang'andu 2011). Where animals mix with Lechwe disease transmission has been observed to occur with a case of a Kafue Lechwe found dead with tubercles on a ranch where bTB was diagnosed in Central province as one example. Kafue Lechwe has a role as a maintenance host and *M. bovis* is known to circulate in them. Prevalence is high in the interface area in Lochinvar National Park (Munyeme *et al.,* 2013). In fact, positive bTB was found in 14-35% of post-mortems in Kafue Lechwe confirming it as an important reservoir (Zieger *et al.,* 1998). Moreover, Fiztgerald *et al.,* (2012) found that 24% of the sampled Kafue Lechwe had gross lesions indicative of bTB from 2004 to 2008. The disease is also found in Wild Boars and African Buffaloes in South Africa but in Zambia the Lechwe remains the important reservoir. Kafue Lechwe prefer swamps and live in groups which promotes disease propagation (Fiztgerald *et al.,* 2012). Flooding in the swampy areas also disseminates the infectious agent.

A lot of research has previously been done implicating the Kafue Lechwe in the sustenance and spread of bTB. With regards to spread to livestock, mixing in the plains is the contributing factor (Munyeme *et al.,* 2012). Moreover, older animals are more affected as well as those with poor body condition. The large herds in Namwala

usually contain the two susceptible animal groups. Taken orally the infectious agent can be emitted as aerosols during rumination (Fiztgerald *et al.,* 2012). Aerosol transmission is more effective while large doses are needed for oral transmission. Once in the livestock the disease is spread from cattle to cattle. Animal movement on foot also sheds the disease in the routes of movement (Humblet *et al.,* 2009).

2.1.3 Tuberculosis in Humans

Tuberculosis is an infectious chronic respiratory disease which usually attacks the lungs but can also damage other parts of the body. It is usually spread through aerosols from an infected individual to a susceptible individual. There are mainly two types including the human and animal types. It has been controlled in many parts of Europe and North America but remains a huge problem in Asia and Sub-Saharan Africa. In people, diagnosis is done by culturing of sputum. It can be treated using antibiotics including Isoniazid, Rifampicin, Pyrazinamide and Ethambutal (WHO, 2014; CDC, 2014). The control of the disease is mainly through vaccination and public health measures such as avoiding overcrowding and boiling of milk. While most cases are from person to person, people can also get the disease from cattle through drinking of contaminated milk. The disease also affects cattle where it is a major problem in sub-Saharan cattle populations. Diagnosis in cattle is through the tuberculin skin test. To control the disease in animals test and slaughter is used to cull off the positive animals. Moreover, avoidance of contact with wildlife which tend to harbour the disease also helps in prevention (OIE, 2013).

Tuberculosis results from infection with members of the *Mycobacterium tuberculosis* complex (MTC). The constituent agents including *Mycobacterium tuberculosis* and

mycobacterium bovis affect wildlife, domestic animals and humans (Biet *et al.,* 2005). With the increasing overlapping of habitants of the three host categories, tuberculosis has been compounded by cross-infection resulting in wildlife acting as reservoir of the agents not only from domestic animals but humans as well. Humans have also come to be hosts of bTB (Biet *et al.,* 2005). Zoonotic tuberculosis (bTB) now accounts for an appreciable amount of cases of tuberculosis in humans (Munyeme *et al.,* 2010).

Tuberculosis has been a scourge of mankind since antiquity (Hall, 1985) and according to Mostowy *et al.* (2002), the causative agent of tuberculosis, *Mycobacterium tuberculosis,* has been known for some 120 years and the disease continues to plague humanity. He further observed that tuberculosis is a disease which few countries are free of. It is very ancient where lesions have been found in Egyptian mummies (Hall, 1985). It is an infectious disease, characterised by slow progressive development of tubercles in almost any organ of the body except the skeletal muscles.

According to the WHO report of 2006, Tuberculosis is ranked 7th most morbidity causing disease in the world and is the leading cause of death from a curable infectious disease. TB incidence is highest in Africa (290/100000 persons per year) as is the annual rate of increase in number of cases (6%). It further states that world-wide 7-12% of all new TB cases in adults aged 15 to 49 are attributable to HIV infection with proportions at 31% in Africa. Jamshid and co-workers (2010) reported that TB was responsible for 25% of preventable deaths worldwide. They reported that the infectious dose is very low and inhaling less than ten bacteria may cause an

infection. A third of the world's populations are thought to be infected with *Mycobacterium tuberculosis* which is about 2 billion people (WHO, 2012). About 5 to 10% of latent infections develop to active tuberculosis from immunosuppression among which the causes include HIV. An untreated patient can affect 10 to 15 people annually. It is a major cause morbidity and mortality in countries especially in Africa. WHO declared TB a 'global emergency' in 1994 (WHO 2002). Moreover, the devastation of tuberculosis is borne out by figures from the *globalfund.org* indicating that 14 million people worldwide are infected with active tuberculosis. The number of deaths was 1.4 million in 2011 which is high (O'Grady *et al.,* 2012). The majority of deaths were reported in the developing world. Over 95% of deaths occurred in low and middle income countries (WHO, 2012) where Zambia lies. More concern was highlighted by the rising number of children co-infected with HIV and TB (Chintu *et al.,* 2007). In Zambia the proportion of TB patients testing positive for HIV increased from 22% in 2006 to 84% in 2010 and 70% were HIV positive (Kapata *et al.,* 2012). The influence of HIV is so high such that someone who is living with HIV is 20 times more likely to develop active tuberculosis than someone who is HIV negative (WHO, 2012). TB is now the leading cause of death among people living with HIV (*The Fund Information note*, 2011).There is also the emerging problem of drug resistance (Raviglione *et al.,* 1995). In fact the multi-drug resistance has already become established worldwide (Farmer *et al.,* 1998). According to the WHO TB fact sheet of 2012, multi drug resistance is present in virtually all countries it has surveyed which include Zambia. Sub-Saharan Africa has the highest burden of new cases. Further the report stated that someone in the world is newly infected with TB bacilli every second and 5% to 10% who are infected with TB become actively sick. Tuberculosis remains the leading infectious disease cause

of death worldwide killing more people aged over 5 years of age than AIDS, Malaria, diarrhoea and all other tropical diseases combined (WHO, 2012).

2.1.4 Bovine Tuberculosis

Mycobacterium bovis is a major cause of animal tuberculosis and human extra-pulmonary tuberculosis (bTB) especially in developing countries such as Zambia (Cosivi *et al.,* 1998). All forms of tuberculosis including bTB are the major and potentially lethal opportunistic infection in patients with HIV/AIDS infections. A study conducted in Zambia on bTB found an association between tuberculin positive cattle and tuberculosis in humans (Cook *et al.,* 1996 in Munyeme *et al.,* 2008). Herd size has been found to have an influence on prevalence of bTB (Kazwal *et al.,* 2001 in Munyeme *et al.,* 2008). Southern province has one of the highest cattle populations in Zambia (Aregheore, 1994). Large herd sizes makes farmers take their animals into the plains for more pastures where their animals mix with wildlife. In fact, in a study by Cook *et al.,* (1996) cattle in lager herds were more likely to give a positive bTB reaction. They also found that ten households reported a human case of tuberculosis (TB) during preceding 12 months. The herds or these households were six times more likely to have tuberculin positive animals than herds in households without a reported TB case.

The problem of bTB is summed up by Cosivi *et al.,* (1998) who stated that while tuberculosis is one of the most widely spread infectious diseases and a leading cause of death due to a single infectious agent among adults in the world with *M. tuberculosis* being the most common cause, there are unknown proportions caused by *M .bovis*. In developing countries non pasteurisation of milk and low government

control measures on bTB contribute. They reiterated that TB is the major opportunistic infection in HIV infected person such that dual HIV and *M. bovis* has been reported even in industrialised countries. HIV pandemic in countries with *M. bovis* in animals' favours zoonotic transmission (leads to bTB). Close contact between animals and people and poor hygiene also contribute. Cosivi *et al.,* (1998) reported that the danger of transmission of bTB between diseased cattle and farm workers is high. While the disease is widely distributed it is often neglected in most developing countries. In Africa only seven countries apply test and slaughter policy and consider bTB a notifiable disease. Zambia is one of them. That however, hasn't helped to curb the disease.

The impact of TB is considerable, with more than 3.5 million people dying annually with bTB being responsible for 3% of these cases (Cosivi *et al.,* 1998 in Munyeme *et al.,* 2010). The importance of bTB is further enhanced by the fact that *M. bovis,* the cause of bTB is resistant to pyrazamide, an important drug in tuberculosis treatment. The resistance necessitates a nine month instead of the short course of TB treatment which is possible with pyrazamide. Higher mortality rates during treatment of tuberculosis generally may be associated with *M. bovis*, multi drug resistance and HIV co-infection (Timothy *et al.,* 2008). Melinda *et al.,* (2008) reported a case of a hunter acquiring cutaneous *M. bovis* from infected deer supporting the need for public health precautions with regard to wildlife acting as a reservoir of *M. bovis*.

According to Cosivi *et al.,* (1998) in Munyeme *et al.,* (2009), bTB is an important disease of both economic and public health importance. In low income countries bTB is still prevalent and is responsible for significant economic loss in animal

production. Cosivi *et al.,* (1998) stated that global prevalence of human tuberculosis due to *M. bovis* has been estimated at 3.1% of all human cases. In countries where a majority of poor rural pastoral communities depend on cattle for livelihood bTB is reported to be a constant threat (Munyeme *et al.,* 2009). Lack of information on bTB in many African countries, Zambia inclusive, has reduced the attention given to this infectious agent in terms of prioritising resources devoted to control of animal disease. According to Nawal *et al., (*2009), HIV makes bTB a serious public health threat to persons at risk. In their study they established that 30.5 to 40% of examined cattle and farm workers were infected with bTB. Timothy *et al.,* (2008) also reported that *M. bovis* appears to be contributing to sustaining the TB incidence in some bi-national communities in the USA where *M. bovis* the causative agent of bTB accounted for 45% of all culture positive cases in children.

The highest rate of increase in HIV is in sub-Saharan Africa where 20-40% of young adults are infected. Life expectancy is low between 30 to 40 years instead of approaching 70 years which may be possible without the pandemic (Pearson *et al.,* 2006). The prevention of HIV and all forms of TB (bTB or Human tuberculosis) requires focused effort to control. The focussed control is required more especially in areas of high HIV prevalence such as Zambia as a matter of great urgency (Corbett *et al.,* 2003). Many infected persons frequently receive the diagnosis of HIV infection or AIDS after having TB diagnosed at a health facility. The proportion of HIV infected TB patients who die during TB treatment is high with an estimate of 6% to 39% dying during TB treatment in sub-Saharan Africa (Sousak *et al.,* 2007). Deaths occurring in first few months after TB diagnosis are more likely TB related whereas deaths occurring later are more likely to be attributable to other HIV related illness

(Sousak *et al.,* 2007). Likelihood that an infected HIV positive person will develop active TB of any kind is significantly higher; 5-10% per year. Thus HIV positive people who suffer from latent tuberculosis have 80% chance of developing TB at some point in their life time in contrast to 10% chance of HIV negative people (Kathryn 2011).

2.2 Tuberculosis in Zambia

Worldwide Tuberculosis remains a major problem especially in Asia and Africa where in the latter, Sub-Saharan region where Zambia lies, is the hardest hit by the pandemic (WHO, 2012). Tuberculosis prevalence in Zambia is high. The prevalence has been compounded by HIV leading to the situation where Zambia has the 10th highest co-infection rate of tuberculosis and HIV in the world (USAID, 2012). TB is the leading cause of death among HIV infected persons (Centre for Infectious Disease Research in Zambia, 2007). That has impacted on agriculture which is a major sector in Zambia. About 97% of the rural population is engaged in agriculture which is about 45% of the total population. Agriculture is the main source of income such that Agriculture contributes about 18% to real GDP taking up 39% of the economy from non-traditional exports (Frimmo, 2012).

The period of increasing TB between 1990 and 2000 coincided with an increase in HIV/AIDS while the decrease can be attributed to improved TB care (Kapata *et al.,* 2011). While the existence of a vaccine against the disease helps, it is widely recognised that BCG provided inconsistent and often inadequate protection against tuberculosis with the decline in protection increasing with increasing age at

vaccination (Fine *et al.,* 2001). The Tuberculosis refers to both the *M. tuberculosis* and *M. bovis* types.

"Baseline epidemiological data have persistently reported findings of bovine tuberculosis in both wild and domestic animals in Kafue (Munyeme *et al.,* 2012). In Zambia reported cases of bTB go as far back as 1947 and were reported in Kabwe and Mazabuka districts by the Veterinary Department. Abattoir compilation studies on epidemiology have indicated that the disease is not homogeneously distributed. Lack of pasteurisation of milk and association of animal and human population increase the risk of transmission of bTB (Munyeme *et al.,* 2011). Moreover the lack of regular tests has led to increased incidence. Other factors include high bTB prevalence in Kafue lechwe in Zambia and resistance to first line antibacterial drug (pyrazamide) as well as general lack of knowledge contributing to the need for more concerted efforts" (Munyeme *et al.,* 2012). Marcotty *et al.,* (2009) stated that test and slaughter and pasteurisation may have worked in industrialised countries but may not be optimal control tools in Africa. He suggested that control strategies should first fit the needs and perceptions of local communities.

Yieshm *et al.,* (2008) stated that potential interventions in TB control are complex and require innovative study techniques to provide rigorous evidence needed to inform health policy makers to ensure resources are used optimally. According to Olalekan *et al.,* (2009), evidence shows that there is no decline in number of deaths from all forms of TB among HIV positive people in Africa. There also exist the differences in different sub regions. Notably, Africa has the highest rates of both HIV and all forms of TB in the world. They propose that using existing health data, GIS based techniques can provide opportunity to clarify and quantify the health burden

from TB-HIV deaths in highly endemic areas which in their study was found to be southern Africa. BTB is a neglected zoonosis. Main risk is poorly documented and there are uncoordinated efforts and failure in control strategies. Notably, there is no doubt that environmental factors are of major importance in the perpetuation of bTB in livestock (Hall, 1985). Environmental factors also happen to be the basis of geographically based information systems (GIS) (Burrough and Mcdonnell, 1998).

2.3 Use of Geographical Information Systems in Disease Mapping

Among the uses of epidemiology is the acquisition of information on the ecology and natural history of a disease. Natural history of infectious agents is only identifiable when it studied in the context of their ecosystems. Ecosystems are related to communities and their environments (Thrashfield, 1986). Ecosystems make up important geographical features which are amenable to the use of GIS and Tuberculosis, especially the animal type, is a geographically dependent disease (Tanser and Suer 2003).

Geovisualisation or GIS mapping is the use of computer aided graphical methods to visualise geospatial information. It is a technique which has begun to be used to help guide health service planning, public health interventions and inform the public about disease hot-spots (Douglas *et al.,* 2010). Geographic information systems facilitate analysis of associations between location, environment and disease to document the non-random distribution of diseases. Geospatial analysis using GIS was actually developed for problems in environmental and life sciences in particular ecology and epidemiology. Spatial statistics typically result from the observation rather than experimentation. The data can be represented using coloured spots on the

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map to convey information of location and intensity of information of concern (Dirk *et al.,* 2009). GIS involves observations where absolute location and relative positioning are taken into account. A linkage between GIS and spatial analysis is considered to be an important aspect in development of GIS into a research tool (Luc *et al.,* 2011). According to Openshaw *et al.,* (2012), a common starting point in the analysis sequence is the map generated by GIS. GIS is an effective tool to monitor and control various infectious diseases. It helps to solve the problem of visualisation and provides spatial data attributable to disease. Visualisation is probably the most commonly used spatial analysis method which results in maps that describe patterns and which are useful for both simulating more complex analysis patterns and for communicating the results. Exploration of spatial data involves the use of statistical methods to determine whether observed patterns are random in space. Modelling introduces the concepts of cause effect relationships using both spatial and non-spatial data sources to explain or predict spatial patterns. Tools for mapping include Google-Earth and Microsoft Virtual-Earth for descriptive statistics (Dirk *et al.,* 2009). Mapping only produces maps but analysis requires other tools such as Microsoft MapPoint, Arc Explorer, Epi-Map and Arc-GIS which is probably the most commonly used commercial packages.

GIS is not a new field as evidenced by field epidemiology and geographical analysis by John Snow on local water pumps in London in 1850's (Matthew, 1998; Bell *et al.,* 2006). GIS works in conjunction with Geography which is an important factor that leads to non-uniformity in disease distribution. One tool that enables researchers to easily investigate trends and question the nature of disease distributions in advance is GIS as patterns can reveal trends in disease dynamics. GIS according to Matthew,

(1998) helps in location of disease occurrence, distribution, changes that may have occurred, assessment of impact of intervention or relationships and systematic patterns of regions. GIS also offers flexibility in utilising different techniques for mapping data through the use of area based counts and point based data types. Until recently the use of GIS in the study of infectious disease has been low. Matthew (1998) concluded by saying GIS allows researchers to display data at different resolution and aggregation in order to convey information. All this feeds into the ultimate goal of improving surveillance of high risk populations upon identification.

Burrough and McDonnell, (1998) also stated that disease risk is known to be associated with environmental variables and factors such as presence of local wildlife reservoir species and cattle movement (which are important features in Zambia). They further stated that data for epidemiology focus on attributes of the data but if coordinates are also collected spatial patterns of epidemiological problems can also be investigated. Investigation aimed at describing and understanding the processes that influence the occurrence of disease can benefit greatly from access to digital information systems that represent the environment within which these processes operate. The information helps to highlight high risk areas and divide areas based on prevalence (Wen Y.K. and Ming W, 2011). According to Nunes (2007); Onozaka and Hagihara (2007) in Rindra *et al.,* (2009), several epidemiological processes may result in strong spatial patterns relating to risk or incidence. They observed that, for example, pathogen dispersal may be highly localised, susceptible hosts may be clumped together or control strategies may be spatially restricted. They also note that probability of transmission declines dramatically with distance from infected host. Factors affecting spatial positions of pathogens and hosts and probability of

encounters are thus important in disease dynamics. They further noted that TB is known as a disease prone to spatial aggregation or clustering. Understanding heterogeneity provides useful insight into local epidemic control. That makes a case for the importance of understanding spatial distribution using mapping which picks up geographical points. Liu *et al.,* (2012) attested that several studies have shown that spatial distribution of TB is non-random and clustered. He stated that spatial analysis conducted to explore spatial epidemiology can provide guidance for formulating regional prevention strategies and increase the public health intervention's effectiveness. Meanwhile Silva *et al.,* (2003) argue for the possibility of using results of their study of spatial distribution of tuberculosis for implementation of equitable local health policies and health surveillance measures since their study identified households with the highest risk and most heavily affected age groups using GIS techniques. The study also identified at risk groups to help in health surveillance and implementation of control policies. Adrain *et al.,* (2012), observed that at present geographic information systems (GIS) are among the most useful tools in epidemiology as they can be used to identify geographical areas and population groups with higher risk of sickness or premature mortality and which thus need higher care or health information and monitoring of disease in time and space. They reported that GIS was used to identify locations of TB transmission and incidence in USA from 1993 to 2000. Still in the USA, according to Ellen and Cromley, (2003) GIS applications have described sources and geographical distribution of disease agents, identified regions in time and space where people may be exposed to environmental and biological agents and mapped and analysed spatial and temporal patterns in health outcomes. According to Dirk *et al.,* (2009) the sequence followed in Geovisualisation may involve firstly visualising spatial patterns

in data then describing these spatial pattern and finally attempting to explain the observed patterns. This helps to predict changes in patterns and to use the explanations derived to inform decision making and guide policy formulation. Identifying areas of highest prevalence is important so that public health specialists and planners can be aware of increased risk and possible causes in their locality, so as to target individual and population interventions (Dirk *et al.,* 2009).

After maps have been created, the significance of observed patterns have to be explored. Spatial autocorrelation analysis is a method that has been widely used to explore the spatial pattern of variables in many fields. Moran's I is one of the statistics used to estimate the strength of the spatial auto-correlation, and the significance of the spatial auto-correlation can be tested. Spatial autocorrelation analysis can identify spatial clusters (positive autocorrelation) and spatial outliers (negative autocorrelation). Spatial autocorrelation is an assessment of the correlation of a variable in reference to spatial location of the variable. According to Waldhor *et al.,* (1996) spatial distribution of rates used in epidemiology actually raise the need for the use of autocorrelation. He reported that in order to provide the first answer to the question of autocorrelation the well-known spatial autocorrelation coefficient frequently used is Moran's I. Jackson *et al.,* (2010) also states that Moran's I is a widely used spatial statistic for detecting global spatial patterns. He stated that investigation of global clustering patterns across regions is very important in spatial data analysis. Moran's I is the more popular test statistic for spatial autocorrelation and can be calculated using readily available statistical packages including STATA. (Xiao *et al.,* 2012).

According to WHO (2012), in order to properly plan and manage and monitor any public health programme it is vital that up-to-date information is available to decision makers at all levels of public health system. The production of attractive and informative maps complements the formal analysis of spatial epidemiological data and as a result of visual impact that they have, it is likely that maps will influence the recipient much more than accompanying statistics. (Rezaian *et al.,* 2004).

Douglas *et al.,* (2009) argued that the majority of the world's disease burden is in Africa. They therefore suggested that geographical information systems, GIS, technology can be an important tool of great potential for health research and management in Africa. They said spatial modelling capacity offered by GIS is directly applicable to understanding the spatial variation of disease and its relationship to environmental and health care system. WHO on the other hand states that GIS allows policy makers to easily visualise problems in relation to existing health and social services and the natural environments and so more effectively target resources. WHO also states that public health practices need timely information on the course of disease and other health events to implement appropriate actions and GIS are an innovative technology for generating this type of information.

Risk communication is an essential element in this process with the objective being to present scientific outputs in ways that are understandable to non-scientists. One of the mechanisms for improving the transparency and widespread understanding of scientific evidence is to use visual methods of presentation in order to make fairly quantitative results easier to comprehend which is where maps can be particularly

useful (Bell *et al.,* 2006). Such maps can be created by collection of GIS coordinates and transferring onto maps using ArcGIS. GIS is capable of presenting maps that allow visualisation of spatial pattern of phenomena. After visualisation, the question of pattern and association to environment, time variation and spatial concentration are asked (Bell *et al.,* 2006). Exploratory analysis leads to modelling relationships between events and characteristics of an individual using pattern analysis. None the less, maps can be enough to make decisions of resource allocation based on patterns observed (Gilbert *et al.,* 2012).

Ability to map environmental factors associated with disease is important in infectious disease control. Ease of use with proper training allows for surveillance data to be within reach of even the smallest health departments. Detailed maps can be revised infinite number of times enabling creation of a variety of new types of maps that could be useful in public health management and practice (Matthew, 1998). Ideally communities would with the help of GIS have ability to have health information from various data sources for efficiency and centralisation in order to recognise spatial patterns that may suggest where cost-effective public health interventions can be applied.

2.3.1 Challenges to GIS in Spatial prediction of Disease occurrence

According to Thomas *et al.,* (2003) considerable scepticism exists in many quarters about the role of mapping and spatial analysis in the study of disease patterns and resource allocation as maps may misidentify clusters and causes. There are also pitfalls inherent in analytical systems that depend upon approximations and potentially inappropriate boundary sets. Moreover, some problems may arise when

interpreting the maps where problems may either be exaggerated or underappreciated due to reliance on legends and the contrast used such as in the case of choropleth maps (Thomas *et al.,* 2003). Further challenges include paucity of qualified staff who can effectively utilise GIS tools. While Africa can indeed greatly benefit from the enhanced understanding of diseases, results may only be as good as assumptions employed in analysis (Tanser and Suer 2002). Moreover, the mapping needs to be followed by statistical assessment and experimental challenge of the hypothesis before inferences in relation to cause and effect can be drawn. When testing hypothesis the most basic approach is to examine maps of disease occurrence visually together with data from other map layers for the purpose of formulating theoretical hypothesis (Tanser and Suer 2002).

2.3.2 Why Geographical Information Systems

The use of Global positioning systems and geographical information systems in disease surveys and reporting is becoming increasingly routine enabling a better understanding of spatial epidemiology and the improvements of surveillance and control strategies. GIS has been widely applied to understanding the management of malaria in Africa (Tanser and Suer, 2002). It has been used to map malaria vectors, their habitants and infection. It has also been used in management and control of malaria to measure the effects of access to malaria treatment to evaluate the effects of intervention strategies (Tanser and Suer, 2002). GIS is not the complete solution to understanding distribution of disease and the problems of public health but it is an important way in which to better illuminate how humans interact with their environment to create or deter health. The objectives of spatial epidemiology analysis are the description of patterns, identification of disease clusters and

explanation or prediction of disease risk. Maps are useful for identification of areas with suspected elevation in risk and formulation of hypothesis about disease aetiology and assessing needs for health resource allocation (Dirk *et al.,* 2009). The disease impact in terms of morbidity, mortality and spread varies substantially with demographic profile so that identifying the most exposed or affected populations becomes a key aspect of planning and targeting interventions (Tatem *et al.,* 2012)

According to Goswamin *et al.,* (2012) Epidemiology stresses the importance of understanding three components of the disease including people involved, the time of disease outbreak or transmission and location of transmission. However, he says many epidemiological studies in the past have failed to examine the role that spatial patterns play in the development of trends in disease in ways that go beyond descriptive methods. Geography helps to understand factors that lead to non-uniformity of disease distribution such as physical and environmental factors. GIS screening can effectively penetrate populations with high disease burden and poor healthcare access since linkage of vulnerable populations to care remains challenging and will require creative interventions to impact morbidity (Goswamin *et al.,* 2012).

The use of GIS is low in Africa such that whilst there have been numerous critiques of the application of GIS technology to health problems in the developed world, it has been less clear whether the technology is both applicable and sustainable in an African setting (Frank *et al.,* 2002). Muray *et al.,* (2009) demonstrated that combining qualitative techniques with GIS mapping may improve the understanding of potential TB transmission within a community and guide public health interventions to enhance control efforts. Matthew *et al.,* (1998) observed that global

control of tuberculosis remains poor. In their study, the results yielded were useful for a Houston based TB surveillance in tracking the spatial trends in TB cases over the year.

It remains to be seen if GIS can be used with the level of success recorded in the developed world. Due to the potential it has in helping with the control of health problems, it was chosen as a tool for our study. Namwala was used due to easier access to act as the study area but the results may be used in other areas. It has large cattle herds and lies in the Kafue basin where bTB has been demonstrated to occur in previous studies (Munyeme *et al.,* 2012). GIS was to be used to map the pattern of bTB as understanding of distribution helps in disease control. Maps generated by GIS help to highlight problems. One of the mechanisms for improving the transparency and widespread understanding of scientific evidence is to use visual methods of presentation in order to make fairly abstract quantitative results easier to comprehend and that is where maps are particularly useful (Bell *et al.,* 2006).

CHAPTER THREE

Materials and Methods

3.1   Study areas

The study was conducted from October, 2012 to March, 2013. It was conducted in Namwala district of Zambia located at 15°45'S and 26 °27'E. Namwala district is located in Southern province of Zambia (Figure 3.1) and has the highest cattle density in the country (Sitima *et al.,* 1997). It is home to the Ila people who keep large herds of cattle (Sitima *et al.,* 1997). They practice transhumance grazing which involves taking their animals to the plains.

The district lies in the Kafue basin (Figure 3.2) bordered by Kafue National park on the west, Namwala GMA in the North, Billi GMA in the South and on the East is the Lochinvar national park a haven for Kafue Lechwe. Kafue Lechwe are known to harbour bTB as a maintenance reservoir host (Munyeme *et al.,* 2012). In the grazing fields livestock inadvertently mix with wildlife including Kafue Lechwe running the risk of contracting bTB.
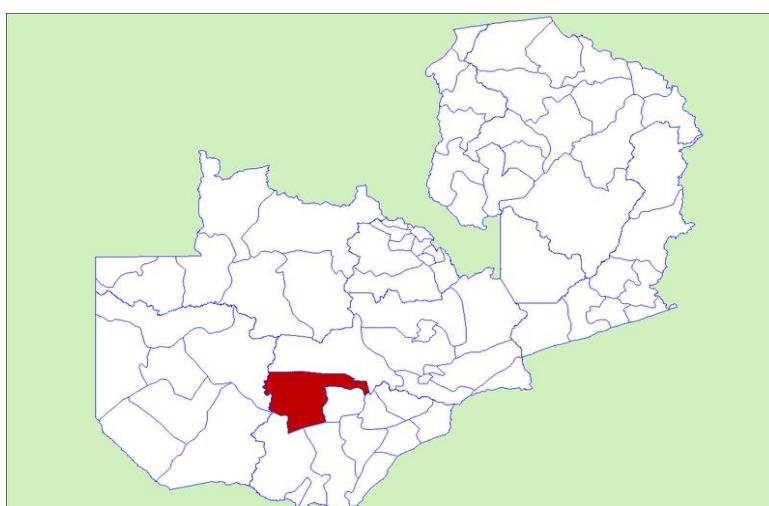
Figure 3.1: Map of Zambia, showing the geographical location of Namwala District (*Shaded part*) in Southern Province in relation to other Districts in Zambia.

Besides being a main cattle producing area in Zambia, the study area was chosen because previous reports had intimated the existence of high bTB prevalence than the surrounding areas (Munyeme *et al.,* 2011). Further the people in this area have a tradition of drinking raw milk which has been considered a risk factor for exposure to *M. bovis* (Sitima *et al.,* 1997).

Figure 3.2 Detailed Map of Namwala District, showing the names of some of the villages and areas under study, insert shows the Map of Zambia.

3.2.0   Study design

The study was conducted as a cross-sectional study. The two major slaughterhouses in Namwala were included to obtain daily bTB condemnation rates collected over a six-month period. Data was collected to follow up on the origin of the bTB infected

cattle to collect GIS coordinates and to administer questionnaires (Appendix 1). Autocorrelations was also tested using Moran's I (Appendix 2)

3.2.1 Abattoir

The study commenced with collection of daily condemnation data from the two abattoirs in Namwala (Figure 3.3). From abattoir condemnations, trace back was done to go out to the areas of origin of the bTB positive cattle to obtain GIS information (Appendix 3) and administer questionnaires. At the abattoir, the animals were checked for clinical signs indicative of bTB, including emaciation and coughing which are the most important clinical signs (Figure 3.4). The positive cases were those with lungs that had tubercles and caseous material as shown in Figure 3.5.

Figure 3.3 ZAMBEEF abattoir Namwala District (2012). (One of the abattoirs visited where data on condemnations was collected to effect trace-backs).

A positive herd was one from which an animal was condemned at the abattoir and there was still at least one animal showing clinical signs of bovine tuberculosis upon

trace-back and interviews. For confirmation, records from Animal Health inspectors were referenced. The information from Animal Health inspectors was used as secondary data in our study. Animal Health inspectors had visited the farms to certify tuberculosis status.

Figure 3.4. Animals before slaughter at abattoir. Animals are checked for bTB before slaughter by inspection to check for coughing and emaciation.

The post-mortem results were coupled with ante mortem findings including emaciation and coughing. For identification of positive herds we relied on data from Animal Health inspectors who had records of farms which still had the disease and we also examined the herds.

Figure 3.5 Condemned lungs due to infection with suspected bovine Tuberculosis. The picture shows lungs with tubercles as can be seen from raised points on lung tissue.

3.2.2 Questionnaire Survey

The survey was done using purposive sampling. The questionnaire survey was conducted among the households whose herds had a positive animal condemned as being bTB positive on post-mortem at the abattoirs. The survey was in order to find practices that may be possible risk factors contributing to the disease contraction by livestock and possible transmission to people and to locate positive herds based on positive cases. That was done by referring to data gathered by Animal Health inspectors on herd positivity to identify herds that still had at least one positive animal. The Animal Health inspectors screened the herds using a tuberculin skin test but herd owners were also interviewed on relevant clinical signs of bovine tuberculosis. A closed ended pre-tested structured questionnaire was used to collect data on age, sex, grazing behaviour, drinking water sources and other production factors of cattle reared (Appendix 1).

3.2.3 Inclusion Criteria

The carcases selected for trace back to points of origin were those condemned as having pathological lesions indicative of bovine tuberculosis based on caseous material in the lungs or tubercles at post-mortem. The people interviewed were therefore those who had taken at least an animal to the abattoir and had at least one carcass condemned within the previous twelve months. A positive herd was one from which a condemned carcass originated and at least one animal was positive for tuberculosis as diagnosed by Animal Health Inspectors using a tuberculin skin test.

3.2.4 Spatial Data

The study aimed to map the spatial distribution of the bovine tuberculosis positive herds based on positive cases as determined at the two abattoirs. The points of origin of the positive individual animals were geo-referenced. Interviews were also conducted in the households owning the respective herds from which the positive cases originated. The follow-up was made possible by the records of the owners as compiled by the abattoirs. The follow-up therefore helped to link the positive cases to the herds in order to map the spatial distribution of the positive bTB herds.

3.2.4.1 Collection of GIS data

A trace back system was employed where geographical points were collected from points of origin of the carcasses deemed positive for bTB on post-mortem examination. The geographical points were captured using a hand held GPS device and recorded.

3.3 Sample Size Determination

$$n = \frac{Z^2 * p * (1 - p)}{d^2}$$

$$n = \frac{(1.96)^2 * (0.80) * (0.20)}{(0.05)^2}$$

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Where;

n=   is the required sample size

z=   Confidence level: conventional = 95% = 1 - a; therefore, a = 0.05 and $z_{(1-a/2)}$ = 1.96 = value of the standard normal distribution corresponding to a significance level (1.96 for a 2-sided test at the 0.05 level). [The critical value for the 95% confidence level]

p=   Previous studies estimated the prevalence to be around 80%

d=   Precision (absolute): we'd like the result to be within 5% of the true value

The sample size of 246 was the number of bTB positive animals to be traced back based on condemnations after slaughter at the abattoirs that were to be used in the study. Therefore, a total of 246 herds were supposed to be visited and interviews conducted in 246 households from where the positive animals originated. Only 96 herds could be visited due to resource constraints.

3.4 Data analysis

Descriptive Statistics: The database establishment was in Microsoft Excel® before transferring to Stata SE12 for Windows (Stata Corp. College Station, TX) for analysis. The database included bio-data and bTB test results. The proportion of bTB infected cattle in the animals slaughtered at the two slaughterhouses was

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estimated. Individual prevalence was calculated using STATA by expressing the number of bTB positive heads of cattle as a proportion of the respective herd size. The overall prevalence was also calculated using STATA as the total number of positive animals in the study area, as recorded by Animal Health inspectors, as a proportion of the total heads from the 96 herds (Table 4.1). The geographical positions of the herds were collected as coordinates (Table 4.2).

Geospatial Data: The collected coordinates were processed and transferred onto maps of Namwala to show bTB occurrence. The general pattern helped to determine how bTB distribution relates to the interface area. The processing and creation of maps was done in Arc-GIS 3.2. The points were firstly transferred onto an Excel spreadsheet for cleaning and conversion to GIS amenable data. The cleaned data was stored as a text file which was transferred into ArcGIS 3.2 to lay on the processed maps of Namwala district. The map layering included combination of shape files to show important features of the district including most importantly, the flood plains, the rivers, Game Management Areas and National Parks. The captured coordinates were laid on the created maps to gain an understanding of how they relate to those important geographical features such as the flood plains, the Game Management Areas and National Parks. The Game Management Areas and National Parks have been known to play a role in being the basis for the interface of wildlife and domestic animals where transmission of bTB has been known to occur (Munyeme *et al.,* 2012; Malama *et al.,* 2013). The analysis attempted to show how the location of animals found positive for bTB related to the interface which was a risk factor for the disease. Since animals don't necessarily wander into national parks while wild animals don't restrict themselves to the parks, a buffer zone where mingling may occur was

postulated. Based on findings from a study in brazil using GIS indicating that buffer zones range from 0.45 to 27.95 kilometres (Brenda *et al.,* 2010) we created a buffer zone of 30 kilometres from the parks which was the area within which most points of origin of the bTB positive animals lay. To gain more insight into the relationship of bTB and the interface, shape files of the Game Management Areas were also added to the maps which completely captured the collected coordinates indicating the relationship between the two. To further understand how significant the coordinates were in terms of following geographical location, we employed Moran's I (Appendix 2) to test significance played by location. Moran's I measures whether a correlation observed is statistically significant or occurs by chance (Moran, 1950). For the test Stata 12 was used. While other statistical tests including Geary's C may be used, only the code for Moran's I was available to run the test in Stata.

CHAPTER FOUR

Results

4.1 Descriptive results

Using trace back system based on abattoir survey reports, a total of 96 herds of cattle from 20 different geo-captured villages in Namwala district were sampled for bTB positivity. The herd positivity was based on condemnation at the abattoirs and further information on relevant clinical signs gathered during interviews after tracing back to villages of origin of the individual animals condemned and reference to information recorded by Animal Health inspectors. The grazing systems or cattle keeping enterprises ranged from farmers practicing plain grazing (grazing in the flood plains) in the lacustrine flood plains of the Game Management Areas (GMAs), those that practised transhumance and farmers who had sedentary herds which were always in the Villages. Out of the 96 herds of cattle, 7 (7.3%, 95% CI; 2.0-12.6%) practiced sedentary/village grazing, (the practice of not taking cattle to the plains), whilst 87 (90.6%, 95% CI; 84-96.5%) practiced transhumance (seasonal movement of animals to the plains based on availability of pastures) cattle grazing system. Only 2 herds (2.1%, 95% CI; 0-4.9%) of the 96 sampled herds were kept in the plains almost permanently. From these, a total of 35 herds were found positive representing a herd level prevalence of 36.4% (95% CI=26.7-46.3%). Individual animal prevalence ranged from 0% to 14% (95%=2.4-26.2%) across the 96 herds (Table 4.1).

There were more positive herds in the eastern part of Namwala District towards Lochinvar National Park and this area formed the biggest interface area between cattle and the Kafue Lechwe antelopes.

4.2 Prevalence by strata

There was an overall significant difference in bTB prevalence across the 20 villages studied based on individual animal data ($p=0.001$). Based on results for condemnation of carcasses the individual herd prevalence of TB ranged from 0 to 14% (95%=2.4-26.2%) while the overall prevalence was 36.4% (95% CI=26.7-46.3%). In most areas the prevalence was around 3% (Table 4.1)

Table 4.1 The individual prevalence of bTB from the 20 Villages geo-captured.

Location	Area prevalence %	95% C I
Namwala central	14	2.4-26.2
Chinyemu	0	n/a
Baambwe	8.6	0-18
Kawalizhi	11.4	0.5-22.3
Musongwa	2.8	0-8.5
Mbeza	5.7	0-13.6
Mbeza	5.7	0-13.6
Kwa Nico	8.6	0-18.1
Chitongo	2.9	0-8.5
Maala	2.9	0-8.5
Maala	5.7	0-13.6
Nakwanza	8.6	0-18.1
Kantengwa	2.9	0-8.5
Mahungu	2.9	0-8.5
Butele	5.7	0-13.6
Kabulamwanda	2.9	0-8.5
Kasaka	0	n/a
Kasenga	0	n/a
Shikolopa	0	n/a
Shimbizi	8.5	0-18.1

4.3 Spatial distribution of villages within Namwala District

All these studied areas had their GPS locations collected as coordinates (Table 4.2).

Distribution of study villages that were traced back using abattoir data is presented in

Figure 4.1 below as solid dots. All the 20 villages fell within the catchment areas of

the 3 main health centres; Namwala District Hospital, Maala Rural Health Centre and

Chitongo Rural Health centre. These were the only health centres that were offering

TB screening in human patients, with Namwala District hospital acting as a referral

hospital for the other health centres. Figure 4.1 indicates the overlap of bTB positive

herds within a 30km buffer of Lochinvar National park (shown by a large black

circle within Figure 4.1), which had more positive cattle herds than those in the

30km buffer of Kafue National park.

4.4 Geospatial results

Table 4.2 The coordinates of the 20 villages geo-captured in the study and the average herd size per location.

Area of origin	South	East	Average Herd Size
Namwala central	-15.75	26.43	21
Chineyu	-15.8	26.43	18
Baambwe	-15.77	26.5	25
Kawalizhi	-15.77	26.57	22
Musongwa	-15.9	26.1	19
Mbeza	-16.07	27	90
Mbeza	-16.05	27.03	89
Kwa Nico	-16.08	26.92	71
Chitongo	-16.03	26.93	95
Maala	-15.72	26.72	12
Maala	-15.73	26.73	29
Nakwanza	-15.68	26.75	13
Kantengwa	-15.77	26.87	14
Mahungu	-15.8	26.33	19
Butele	-16	26.93	175
Kabulamwanda	-15.87	26.87	205
Kasaka	-15.95	26.97	130
Kasenga	-15.87	26.77	106
Shikolopa	-15.92	26.95	100
Shimbizi	-15.7	26.37	177

The captured locations lay between 26.1°E and 27.03°E and -15.68°E and -16.08°E. The herd had to be considered for the auto-correlation analysis using Moran's I**. (**Table 4.3.)
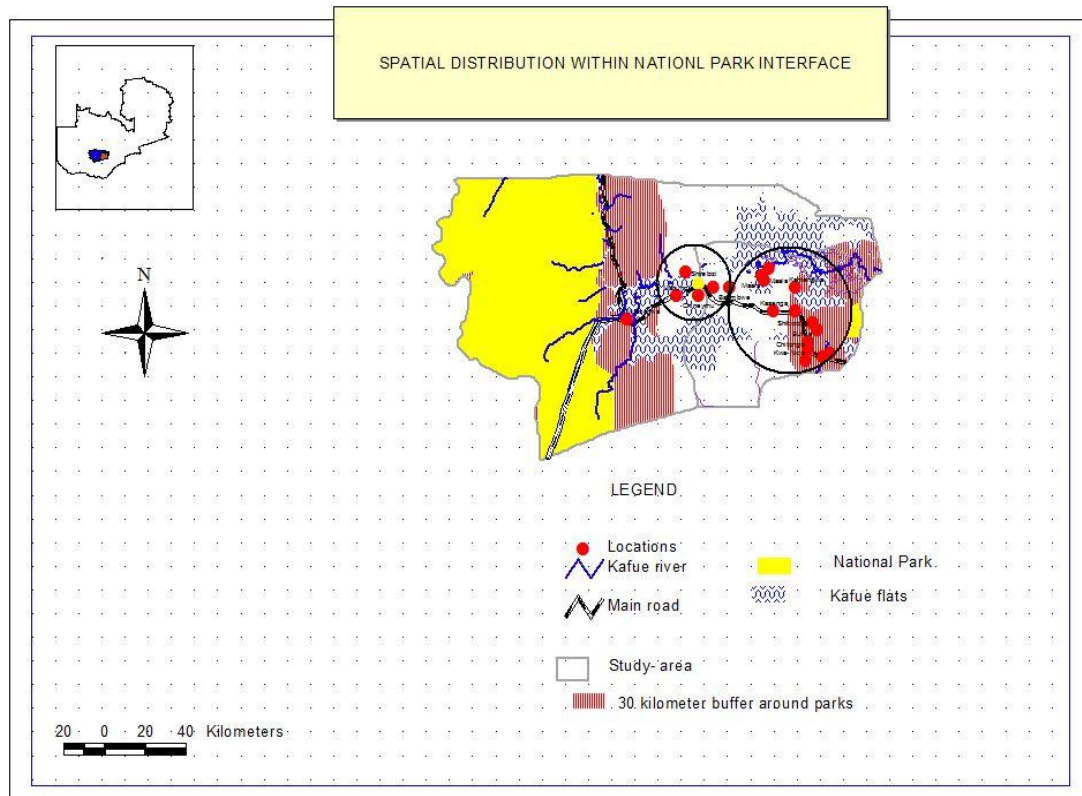
Figure 4.1 Spatial distribution of villages (dots) which had positive cattle herds in proximity to interface areas and National Parks, black circles within the figure indicate the approximate geographical distribution in relation to size of cattle herds being positive.

The smaller black circle within Figure 4.1 indicates mainly cattle herds around Namwala Central, Baambwe areas and those near or in proximity to Maala region. Majority of cattle herds that were found to be positive belonged to the villages in the eastern part of Namwala District 70% (*n*=14 villages), with 50% (*n*= 10 villages) being located deep inside the buffer zone (the GMA) between the open areas and the National Park.

When Game Management areas were considered, the bTB positive herds still tended to fall within the areas where mixing with wildlife occurs. The positive herds were

within a ten kilometre buffer of the Game management areas. Refer to Figure 4.2 below,
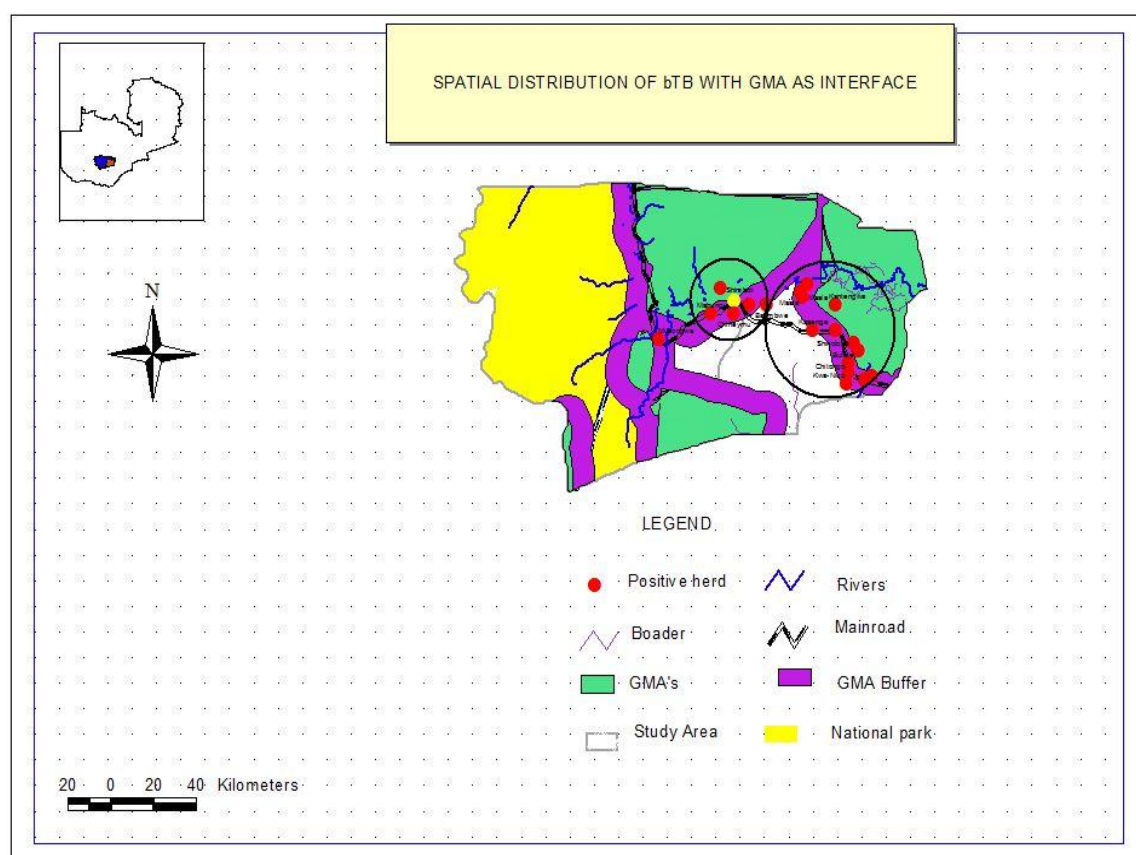
Figure 4.2 Showing the bTB cases within a 10 kilometre buffer of the Game Management Areas.

4.5 Test for Auto-Correlation

To test for correlation of positive bTB herds in the observed geographical areas, Moran's I was used which indicated a considerable correlation with a *p*-value of 0.006. The test was done in Stata with herd size used as a proxy. The formula for the test is given in Appendix 2. The correlation was meant to test whether the tendency to occur in a given geographical area was statistically significant based on the influence of either GMA's or National parks leading to aggregation or whether the pattern occurred by chance.

Table 4.3 The test for autocorrelation was done using Moran's I.

	Moran's I				
					p-value
Variables	I	E(I)	Sd (I)	Z	*
Herd Size	0.18	-0.053	0.093	2.519	0.006
* 1-tail test					

Note; the variables are explained in **Appendix 2**. Sd is the standard deviation of I.

4.6 Demographic characteristics of study populations

Demographic characteristics of the respondents were as follows: gender, female headed households represented 1% of the respondents, (95% CI; 0-3.1%), whilst male headed households represented 99%. (95% CI; 96.9-100%) of the respondents. Similarly, 70% of the respondents were living within the buffer zones of the National Parks, with close to 60% coming from the eastern GMAs close to Lochinvar National park. The minimum number of people living in a household was 2, whilst the maximum number was 39.

A total of 20 village clusters were studied and these formed 96 respondents who correspondingly had 96 cattle herds. A range of biologically plausible risk and deterministic factors for possible zoonotic transmission of bTB were studied and carefully examined on their effect within the study populations and are initially expressed as proportions The possible factors included high frequency of drinking unpasteurized milk at 81%, (95% CI, 78.0-97.8) with the frequency of drinking at least three times a week, being a maintenance factor. Other plausible factors for zoonotic transmission included low number of those boiling their milk at only 26%

(95% CI; 17.1-35.0) low BCG vaccination at 29%, (95% CI; 19.9-38.4). Other

factors are as outlined in the table below (Table 4.4).

Table 4.4 Summary of biologically plausible deterministic and risk factors that were considered across all the study villages and their proportional representation.

Risk Factor	Proportion %	Confidence Interval
Positive Herd	36.46	26.7-46.30
BCG Vaccination	29.17	19.9-38.4
Treated for TB	65.63	56.0-75.3
TB Knowledge	40.63	30.6-50.6
Sour Milk Drinking	79.2	70.9-87.4
Boiling Milk	26.04	17.1-35.0
Freq. of drinking Milk more than three times a week	81.25	78.0-97.8
Keeping Cattle	97.95	93.3-99.7
Condemnation	66.67	57.1-76.3
Drinking Water Sharing	91.67	86.0-97.3
Contact with Wildlife	52.08	41.9-62.3

4.7 Univariate analysis

When considered independently, some of the significant factors that showed high

proportional representativeness as contributing to disease transmission to livestock

and maintenance therein, included high contact between domestic animals and wild

animals at 92% (95% CI; 86.0-97.3) and the low level of knowledge on bTB at only

41%, (95% CI; 30.6-50.6). On univariate analysis of independent variables at herd

level, four main factors were observed to have had independent effect on TB herd status (Table 4.5 below).

Table 4.5 Some risk factors which were considered significant at univariate analysis.

Risk Factor	$\chi 2$	P. value
contact with wildlife	9.42	0.002
movement to the plains	10.12	0.001
sharing drinking water with wildlife	5.62	0.017
condemnation at abattoir due to bTB	5.76	0.016

Note: Variables with Fisher's exact $p \leq 0.25$ were identified as risk factors for inclusion in the multivariable model (and all the above variables thus transferred for analysis in the multivariate analysis logistic regression model)

Some variables had marginal effect whilst others had no effect. Of these variables, the most significant were contact with wildlife, being transhumant, moving cattle herds to the plains (thus moving of cattle to the plains for grazing for certain parts of the year), and cattle sharing grazing ground and drinking water as well as having animals being condemned at the abattoir, these came out very prominent.

Contact with wildlife when assessed independently showed a significant effect in TB prevalence (Fisher's exact $\chi^2 = 9.42$, $p = 0.002$). Moving animals to the plains was noted to be significantly associated with TB positivity ($\chi^2 = 10.12$; $p = 0.001$). Similarly, cattle herds that were seen to share drinking water and share grazing grounds had a significant effect on finding a herd positive within it ($\chi^2 = 5.62$; $p = 0$. 017). Cattle herds from which when taken to the abattoir for slaughter, had at least one animal condemned within the preceding twelve months before the study period, showed a significant effect on TB positivity ($\chi^2 = 5.76$; p = 0.016).

TABLE 4.6 Herd-level risk factors for bovine tuberculosis (bTB) positivity in cattle herds of Namwala District (*n*=96) in Zambia. Results from the final multivariable logistic regression model

Variable	Level	*b*	SE(*b*)	P value	OR	95% Conf. Interval (OR)
Constant		1.3	1.1	0.19	-	-
Contact with Wildlife	Yes	0.94	0.2	0.0.48	0.24	0.15-3.86
	No	-	-		1	-
Movement of cattle to the plains	Yes	1.2	1.1	0.09	0.28	0.32-2.40
	No	-	-	-	1	-
Sharing grazing & drinking water with wildlife	Yes	1.5	1.3	0.01	5.51	4.1-73.4
	No	-	-	-	1	-
Organs Condemned at abattoir due to TB	Yes	0.5	0.4	0.04	1.1	0.29-1.3
	No	-	-	-	1	-

Results from the final multivariate logistic regression model.

Where;

b   is a constant

SE (b) is the standard error of the constant

OR   Odds Ratio

4.8 Multivariate analysis of factors associated with bTB positivity in cattle

The multiple logistic regression model identified contact with wildlife, being transhumant (thus moving of cattle to the plains for grazing for certain parts of the year), cattle sharing grazing ground and drinking water as well as having animals being condemned at the abattoir due to suspected tuberculosis in the herd as factors having significant effect on herd bTB status (Table 4.6). The Hosmer-Lemeshow goodness-of- fit check showed that the model fitted the data well with n=96, $\chi^2 = 5.2$ and P= 0.52. Cattle herds that were reported to be sharing grazing grounds and drinking water with wild animals concurrently had a significantly higher chances of having bTB (OR=5.5, 95% CI; 4.1-73.4) when contact with wildlife and having animals being condemned at the abattoir due to suspected tuberculosis are controlled.

Similarly the experience of having cattle condemned at the abattoir due to suspected tuberculosis, or exhibiting tuberculosis lesions had significant protective effect on bTB status as such owners took some precautionary measures including test and slaughter (OR=1.1, 95% CI; 0.32-2.40) when contact with wildlife, being transhumant and cattle sharing grazing ground and drinking water were constant. Contact with wildlife as well as movement of cattle to the plains without actual sharing of drinking water and grazing pastures were found to have a protective effect on bTB herd status (OR=0.24, 95% CI; 0.15-3.86) and (OR=0.28, 95% CI; 0.32-2.40) given that the other two variables in the model are held constant.

4.9 Effect of herd size on tuberculosis positivity in cattle in Namwala District

There was a positive association between herd size and herd level bTB status (Figure 4.3, below). The positive association that exists between herd size and bTB prevalence is statistically confirmed using a Lowess smoother scatter plot incorporating a trend line (Figure 4.3). The figure clearly shows that increase in herd

bTB positivity is correspondingly associated with an increase in the herd size. The effect of herd size on bTB prevalence is markedly noted in smaller herds as well as in larger herds, with average herd sizes having somewhat a subtle effect (Figure 4.3), where the likelihood of getting at least one positive animal correspondingly increased with the increase in the size of the herd. Marked effect of herd size was seen in herds between 2 to 9 animals which were observed, then subtle changes between herds with 50 to 250 animals and those above 250 animals showed a marked increase in herd positivity (Figure 4.3).
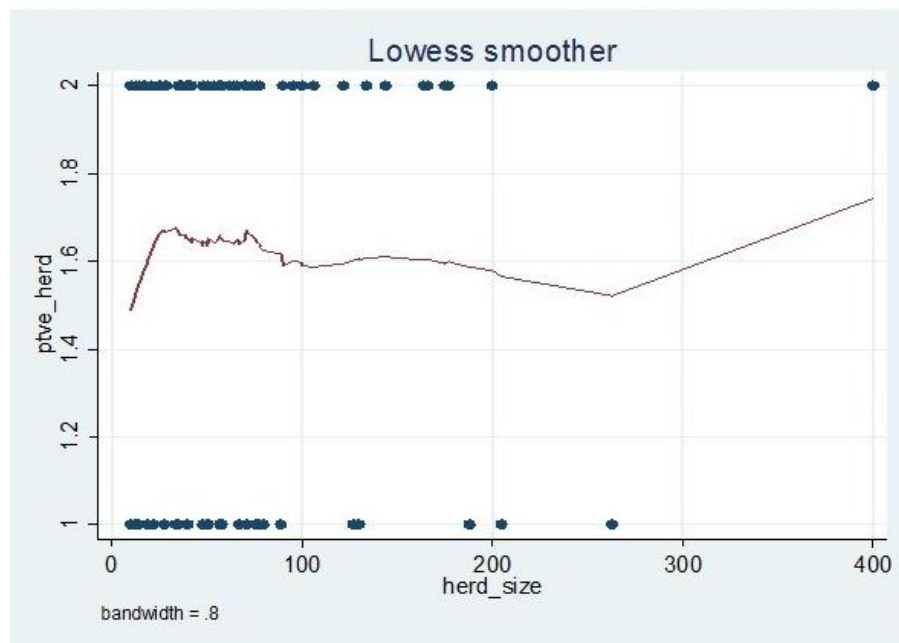
Figure 4.3 The effect of herd size on bTB positivity in Namwala District according to Lowess smoother (*n*=96). Herd sizes as large as 250 tend to increase the chances of bTB positivity markedly.

4.10 Complementarities between generated GIS data and Traditional Epidemiological Data

The results obtained under this study have highlighted complementarities between traditional epidemiological techniques and GIS technology. In the study done, there

was aggregation observed where more bTB cases tended to occur towards the eastern region of Namwala which is congruent with earlier findings from traditional techniques (Munyeme *et al.,* 2011). Our results have highlighted further the complementarities in the evidence generated by the positive bTB herd patterns in the buffer zones being influenced by Lechwe antelope population (eastern GMA) compared to the western GMAs of Namwala District where there are no Lechwe antelopes. Traditional epidemiological studies have indicated that the Lechwes are the reservoirs of bTB and are found in the eastern GMA's (Hang'ombe et al, 2012).

From our generated maps, large herds were mostly the ones in the interface areas and those practicing transhumance systems of grazing patterns. Herd size was seen to have an influence on bTB prevalence as identified using traditional epidemiological analysis and this was clear on generated maps too.

CHAPTER FIVE

Discussion

BTB has a complex epidemiology with both cattle-to-cattle and wildlife-to-cattle transmissions. Transmission to humans can also occur. The number of animals shedding the infectious agent such as the many Kafue Lechwe in Kafue basin and large number of susceptible hosts such as the large herd sizes in Namwala promote disease transmission from wildlife to livestock. Larger herds are usually driven into the plains as they look for more pastures. Larger herds also tend to have older animals and those in poor body condition and thus more susceptible hosts. The contact in grazing areas and water points promotes transmission to livestock and in turn people get the disease from consumption of untreated milk. (Robin *et al.,* 2012). Factors underlying risk of transmission to humans includes non-testing of the disease, low BCG vaccination and lack of pasteurisation of milk. (Robin *et al.,* 2012). Moreover, there is an association between all types of tuberculosis including bTB and poverty as well as malnutrition (Moda *et al.,* 1996). Namwala is one of the districts with high levels of poverty in the country (Namwala Development Plan 2010). Matthew (1998) said geographical information science is a very important tool for use in disease mapping as well as public health surveillance to assist in identifying high risk groups such as the farmers who consume untreated milk in the district. Linkage of affected populations to care remains challenging and will require creative interventions to impact morbidity (Goswamin *et al.,* 2012). Such creative tools include GIS which was the tool used in this study.

The results obtained from this study starting from trace-back system of suspected abattoir bTB positive cattle, and their geo-spatial referencing have revealed the spatial distribution of the disease in cattle in Namwala district of Zambia. The results

have particularly highlighted that there is an ecological interplay in the spatial distribution of bTB in the high bTB prevelance area of Namwala District which is itself a function of the existence of the resreviour hosts particularly in the eastern interface areas of the District. These results are further congruent with earlier traditional epidemiological results of bTB being more or less proportionately high in areas with Kafue lechwe antelope populations (Munyeme *et al.,* 2010).

Despite these findings and earlier studies, bTB remains a huge problem in Namwala district of Zambia as was indicated from abattoir results. Across the study District, the disease burden at herd level was found to be as high as 36.4% (95% CI 26.7-46.3%). That confirms earlier findings of high prevalence of bTB in Namwala district (Fitzgerald *et al.,* 2012; Zieger *et al.*, 1998). The individual prevalence based on animals condemned at the abattoirs and those testing positive in the respective herds in relation to total animals in the respective herds was similarly as high as 14% (95% CI=2.4-26.4%). While the disease has been persistently reported for some time now (Munyeme *et al.,* 2011), it seems to have either remained stable or actually spreading which may be explained by risk factors contributing to its sustenance coupled with the lack of preventive and control measures in place. Due to the above observations, this study investigated factors related to either spread, sustenance as well as other risk factors associated with bTB positivity among cattle herds being high in Namwala District of Zambia. The univariate analysis incriminatingly pointed at a broad range of factors as being possibly explanatory to bTB transmission in the district. One of the major factors observed for the high bTB prevalence in the District was related to the old system of traditional livestock keeping, especially the transhumance system. The transhumance system exposed cattle to the Lechwe

antelopes, which have been identified as untreatable reservoir hosts of bTB occurrence in the Kafue flood plains. Other herd level factors were the large herd sizes. It is having large herds that forces farmers to look for more pastures and end up in the plains inhabited by wild animals. In Namwala District, some cattle owners owned several thousand heads of cattle (Muma *et al.,* 2009, Munyeme *et al.,* 2010). While animals are also driven to the west of the district, the maps revealed a spatial distribution skewed towards the Eastern region. That may be indicative of the role played by Lochinvar national park and Namwala GMA which are habitants of Lechwe (reservoirs of bTB). Maps were therefore able to bring out the role played by geographical factors, in this cases National parks and GMA's in bTB sustenance in the environment. This was further complicated by the sharing of common pool resources (CPRs), such as grazing grounds and drinking water through large assemblages of different cattle herds. Such factors have contributed to the continuum of the bTB transmission intra and between herds. When considered independently, some of the significant factors that showed high proportional representativeness as contributing to disease transmission and maintenance in humans besides low level of knowledge on bTB at only 41%, (95% CI; 30.6-50.6) was the correspondingly high contact between domestic animals and wild animals at 92% (95% CI; 86.0-97.3). The most important factor that may be sustaining the disease in the domestic animals, could be the level of knowledge of bTB among farmers being as low 41%, (95% CI; 30.6-50.6) and thus 60% of the people may not be employing precautionary measures against the disease. Maybe with more information farmers may be testing and culling positive animals. Moreover, with more knowledge farmers may lessen the contact of their livestock with wild animals where reservoirs are. The three main risk factors as determined on univariate analysis were contact with wildlife being

highly significant (*p*-value=0.002), movement to the plains which was also highly significant (*p*-value=0.001) and sharing of drinking water (*p*-value=0.017) all of which can be attributed to a strong effect of mixing between wildlife and domestic animals (Table 4.5).

Multiple logistic regression model identified contact with wildlife, being transhumant (thus moving of cattle to the plains for grazing for certain parts of the year), and cattle sharing grazing ground and drinking water as well as having animals being condemned at the abattoir due to suspected tuberculosis in the herd as factors having significant effect on herd bTB status. Cattle herds that were reported to be sharing grazing grounds and drinking water with wild animals concurrently had significantly higher odds of a positive bTB status (OR=5.5, 95% CI; 4.1-73.4) given that contact with wildlife and having animals being condemned at the abattoir due to suspected tuberculosis are controlled.

While there were no tests done to ascertain the occurrence of bTB in humans during the study, it can be assumed that some human cases were related to the disease originating in animals. The assumption is borne out by the fact that at least 65% of those interviewed had reported being treated for tuberculosis and had bTB positive herds. Other studies have investigated such animal to human transmission (Malama *et al*., 2013). BTB has been known to be transmissible through drinking water to animals (Philips *et al.,* 2003), and in turn can be transmitted to humans if unpasteurised milk or contaminated carcasses are consumed. Moreover Malama *et al.,* (2013) confirmed cases of tuberculosis in humans of Namwala resulting from *M.bovis* which was isolated and identified using molecular diagnostics. Therefore, while the problem of bTB is bad enough in livestock, it's made worse by the fact that

it also affects human beings. The possibility of some cases of tuberculosis in the people of Namwala known to be from *M. bovis* (bTB) is well documented (Malama *et al.,* 2012). Risk factors related to the possible occurrence of the disease in human populations were also investigated. Most importantly, results showed high frequency of respondents consuming non-pasteurised milk at 81%. Consumption of raw milk has a huge role in zoonotic transmission (Munyeme *et al.,* 2011). Only 26% of those interviewed indicated boiling their milk before consumption. Further, drinking of sour milk was as high as 79% when considered as the main ration consumed at least once per week. Further plausible factors for possible transmission to humans as a zoonotic risk included low number of those boiling their milk at only 26% (95% CI; 17.1-35.0) coupled with low level of BCG vaccination among children at 29% (95% CI 19.9-38.4%).

The contact with wildlife which also leads to disease transmission to domestic animals (Biet *et al.,* 2005) was as high as 52% and the sharing of drinking water at 91.67% in those interviewed. Contact with wildlife seems to be the primary factor since wildlife have been known to harbour bTB (Hang'ombe *et al.,* 2012). Moreover, Lechwe antelopes found in Lochinvar National Park are important reservoirs of the disease (Munyeme *et al.,* 2011). The influence of contact is highlighted by the maps generated in the study which indicate the geographical areas where the majority of bTB cases were originating from. From these maps, it was evident that the relative space covered by positive herds occurred along the GMAs of the Lochinvar National Park, the sanctuary of the Lechwe antelopes (Figure 4.1 and 4.2). The occurrence of bTB was more in the herds closer to Lochinvar national park in the eastern region than in the western part of Namwala. Further data indicates that 70% of the

respondents living within the buffer zones of the national parks reported having lost an animal at the abattoir due to suspected tuberculous lesions.

To test for association with the geographical area Moran's I was used and yielded a p-value of 0.006 indicating a strong correlation or clustering of bTB positive herds being more likely to occur in the GMA of the Lochinvar National Park (eastern interface of Namwala District), than on the western interface area, where there were no Lechwe antelopes. Most bTB positive herds were within buffer zones of national parks within a 30 kilometre radius and the buffer of Game management zones within a 10 kilometre buffer (Figures 4.1 and 4.2).

The results therefore indicate a spatial distribution of bTB as being clustered and closer to Lochinvar National Park game management areas, as obtained through the application of GIS tool in public health as has been done many times in other areas (Adrian *et al.,* 2012; Wen and Ming 2011). The study identified the at risk populations as those in the interface of national parks and game management areas. Moreover populations closer to Lochinvar national park appear to be the more vulnerable to contracting bTB. In coming up with strategies to control the disease, those in the eastern part should receive more resources commensurate with higher burden of the disease they bear in Namwala.

Traditional epidemiology has reported bTB in Namwala for a long time but GIS was not used to associate epidemiological observations and spatial distribution of the disease. The tools of traditional epidemiological study such as questionnaires and reference to past data helped show risk factors of bTB while GIS identified at risk groups in relation to geographical location. GIS has been used to identify at risk

populations (Adrian *et al.,* 2012) and to track disease progression (Goswamin *et al.,* 2012). Both animal and people at-risk populations were equally identified in the study conducted. It is also hoped that results of the study can be applied to track changes and effectiveness of control against bTB strategies once formulated and applied in Zambia. Matthew *et al.,* (1998) observed that global control of tuberculosis remains poor and this is particularly true in countries such as Zambia.

According to Goswamin *et al.,* (2012) epidemiology stresses the importance of understanding three components of the disease including people involved, the time of disease outbreak or transmission and location of transmission. However, the paper notes that many epidemiological studies in the past have failed to examine the role that spatial patterns play in the development of trends in disease in ways that go beyond descriptive methods. Geography helps to understand factors that lead to non-uniformity of disease distribution such as physical and environmental factors. The environmental factors observed in the study included national parks and GMA's with bTB reservoir animals.

GIS is an important tool in understanding nature of distribution of diseases. In this particular study, GIS was used to display the distribution of bTB in Namwala. The transmission of bTB was found to involve large cattle herd sizes which have to go into the plains (interface area) for more pastures and end up mixing with wild animals (bTB reservoirs). To be contracted by the people risk factors as outlined in Tables 4.4 and 4.5 should be optimally at play.

The use of GIS is low in Africa. Despite numerous critiques of the application of GIS technology to developed world health problems, it has been less clear whether the technology is both applicable and sustainable in an African setting (Frank *et al.,*

2002). With more of such results as obtained in the study and availing such to policy makers more time is needed to see if that will be the case in Zambia. Muray *et al.,* (2009) demonstrated that combining qualitative techniques with GIS mapping may improve the understanding of potential TB transmission within a community and guide public health interventions to enhance control efforts. Similarly, in this particular study, we have combined quantitative data mining techniques with GIS mapping to come up with the better understanding of the extent of the bTB problem in Namwala District of Zambia.

GIS as demonstrated was able to show complementarities between traditional epidemiological techniques and GIS. While traditional epidemiology captured risk factors by understanding demographical, biological, as well as social factors that lead to disease such as risk behaviours, the mapping captured those groups or helped to show where they are found in space in relation to these other factors. Looking at the generated maps it is easy to see that there is an extensive region where bTB occurs in Namwala and more importantly to see that even then it is more towards some parts such as the eastern part.

Namwala has always been known to have bTB and that it is concentrated more in the interface. The study reveals that the eastern part has even more cases and maps make it easier to appreciate those earlier findings (Munyeme *et al.,* 2010, Munyeme *et al.,* 2011). By capturing the prevalence and using ArcView3.2 to relate the prevalence to environmental factors such as national parks and game management areas and flood plains the study demonstrated the applicability of the map overlays in understanding disease distribution and how that relates to environmental factors as shown in

Figures 4.1 and 4.2 showing bTB prevalence within the buffers of national parks and game management areas.

According to Bascore *et al.,* (2004) in Sara *et al.,* (2005), GIS has emerged as an important component of many projects in public health and epidemiology. Looking at the conducted study, this assertion has been qualified by the findings that confirmed the interface area in the eastern part of Namwala as a priority area. In that regard, while the district may need resources for control of tuberculosis, the eastern interface area would take precedence. Maps can also be used to monitor progress following control and advocacy (Bell *et al.,* 2006). The created maps can therefore act as a reference point to help gain insight into how the disease occurrence changes by looking at the changes in the maps which can be created later. Finally, maps can be used to identify areas where further data are needed. For example, while there was prior knowledge of the prevalence of bTB in Namwala, the actual areas were not precisely identified. The research highlighted the areas of highest prevalence as captured by the maps.

Upon creation of the maps and laying of GPS points we assumed the possibility of a buffer zone playing a role as an area of mixing in the interface. In a study by Brenda *et al., (*2010) in Brazil on how far wild animals can wonder from their inhabitants, they proposed buffer zones ranging from 0.45km to 27.95km. We therefore postulated a buffer zone of 30km from the national park boundaries in our analysis. Figure 4.1 shows the map based on the buffer zone of such perimeter. GPS coordinates lay within GMA areas themselves without applying buffers. The map based on the Game Management areas is shown in figure 4.2. Animals tend to wander from the parks while domestic animals graze near to the parks thus the

possibility of the buffer zone where mixing can occur and ultimately disease transmission.

The possibility of wildlife transmitting tuberculosis to domestic animals has been reported before (Hang'ombe *et al.,* 2012). According to Hang'ombe *et al., (*2012), Kafue Lechwe found in Kafue basin has been described as feral reservoir of bTB in Zambia. It was observed that bTB is not homogeneously distributed with high prevalence rates recorded within and around Kafue basin. There is an interface of grazing land for both wild and domestic animals. Moreover, according to Munyeme *et al.,* (2008), in their study on bovine tuberculosis, true prevalence at herd level was estimated at 49.8% (95% CI 37.9-61.7%). Bovine tuberculosis status was highly associated with area and husbandry practices. The disease prevalence was seen to vary according to area of study with cattle herds reared in the interface areas showing high prevalence. Our study confirmed those findings. Mary and Eric (2004) stated that epidemiology generally centres on understanding how the occurrence of a disease relates to potential explanatory factors. Furthermore, it is not uncommon to include for consideration when available the spatial locations at which cases of the disease occur. They posit that arguably one of the most fundamental tasks in spatial epidemiology is the characterisation of the spatial distribution of disease through the creation of maps. That is what the research project achieved by coming up with the maps in Figure 4.1 and Figure 4.2.

Model building follows mapping. Modelling aims to identify relevant individual factors that play a role in producing an observed pattern of spatial distribution. In our project, we turned to descriptive statistics to understand the risk factors at play to produce the maps created. Disease modelling aims to simulate events in nature to find out how processes play out to produce disease with the aim of predicting future

events or gaining purchase on disease control. Traditional epidemiology says the danger of transmission between diseased cattle and farm workers is well established (Cosivi *et al.,* 1998). GIS application has already been used to describe sources and geographical distributions of disease agents, identified regions in time and space where people may be exposed to environmental and biological agents and mapped and analyzed spatial and temporal patterns in health outcomes. (Ellen and Cromley 2003). All those factors were identified by the study including eastern populations and practices including transhumance grazing and other CPR's such as water points. According to Thrushfield (1985) control of disease involves use of natural history of disease which involves understanding of ecology. Ecology is part of geographical data which is a major component of GIS technology. Tanser and Suer (2003) described TB as an environmentally dependent disease. Even in our study bTB seems to depend on GMA's and National parks which are environmental features.

GIS involves observations where absolute location and relative positioning are taken into account (Luc *et al.,* 2012). It is well established that an untreated patient of tuberculosis can infect 10 to 15 people annually thus the importance of identifying those at risk populations (Jamshid *et al.,* 2010). Marcotty *et al.,* (2009) observed that main risk of TB is poorly documented and there are uncoordinated efforts and failure in control strategies which may be helped by creation of maps as was done in the study to guide control strategies. Matthew *et al.,* (1998) also stated that GIS uses already available data and maps generated help in having health information for efficiency and centralization. The fact that according to Rezaian *et al.,* (2004), maps tend to influence the recipient much more than accompanying statistics highlights the added benefit of GIS as it ensures that traditional epidemiological results become more useful. That is because the high appeal leads to more efforts towards control

more so with areas of high prevalence clearly highlighted by generated maps. Traditional epidemiological results including prevalence can now be used in conjunction with maps generated. The production of attractive and informative maps complements the formal analysis of spatial and epidemiological data (Rezaian *et al.,* 2004).

Overall, the findings of tuberculosis in and around the Kafue Basin have earlier been demonstrated by researchers who diagnosed the disease in cattle and the Lechwe (wildlife) populations (Gallagher *et al.,* 1972, Dillmann 1976, Stafford 1991 and Pandey *et al.,* 1998). All these researchers recognized the likelihood of the pivotal role the Lechwe was to serve as a source of a non-treatable reservoir host of the disease to cattle due to the interaction which was observed between these two species of animals, and the exiting high prevalence of the disease in Lechwe antelopes. Of particular interest was Namwala District which had the highest prevalence even by early studies by Munyeme and co-workers (Munyeme *et al.,* 2009, Munyeme *et al.,* 2010). The District is centrally located right inside the Kafue plains with almost all its entire cattle population being found in the Kafue flats. It is no wonder then that the generated maps showed bTB prevalence skewed towards the eastern region of Namwala where the Lechwe are found. This scenario added to the suspicion of Lechwe proximity and having TB positive reactor cattle in the herds. In a similar study conducted in interface areas of the Kafue Basin GMAs it was observed that TB positivity was influenced by the proximity to the Lechwe antelopes (Cook *et al.,* 1996), although this potential association merited further investigation due to the non-availability of more detailed information especially in relation to the risks posed by infected Lechwe. The results of this study add in a little way to that missing information. Results obtained have revealed the spatial distribution of the disease in

cattle with areas having kafue lechwe antelopes, indicating larger areas of overlapping high prevalence of bTB in both cattle.

BTB remains a huge problem that has to be given a lot of attention. In fact, even to this day in spite of pasteurisation and test and slaughter having been used successfully to bring down the incidence in the West (Marcotty *et al.,* 2009), still there are cases of bTB in countries such as USA especially in the bi-national communities (Timothy *et al.,* 2008). It follows that a country like Zambia with low levels of pasteurisation has a bigger problem. Hopefully the results obtained will help in addressing the problem.

CHAPTER SIX
Conclusion

Based on the results obtained we conclude that the spatial distribution of bTB in Namwala follows the interface area where the Lechwe antelopes overlap with cattle in terms of grazing ground and watering points. More importantly, the results showed that the prevalence is much higher in the eastern region of the district. The eastern region also happens to be closer to Lochinvar National Park an important habitat of Lechwe antelopes which are known to harbour bTB (Hang'ombe *et al*., 2012). The association between tuberculosis occurrence and the interface was demonstrated by the Moran's I obtained in the spatial analysis giving the *p*-value of 0.006 when herd size was taken into account as a risk factor for the disease.

The fact that the occurrence of tuberculosis was captured using GIS to create the maps showing prevalence also indicates the complementarity of GIS with traditional epidemiological investigations. The complementarity can also be demonstrated by the fact that the maps captured the prevalence towards the eastern region which agrees with earlier studies indicating that Lechwe harbour the disease (Munyeme *et al.,* 2012; Muma *et al.,* 2013). Meanwhile, the underlying cause of bTB appears to be mixing with wildlife with as many as 52% of the herds sharing grazing pastures with wildlife and as many as 92% sharing drinking water points. Herd size has a huge role as a risk factor in the contraction of bTB by livestock from wildlife. That is because it is huge herds that have the need to look for more pastures and thus end up in the plains where wild animals harbouring bTB also graze from. Finally, besides herd size other important risk factors contributing to occurrence of bTB can be concluded to include lack of knowledge of disease transmission at 60% thus farmers do not take precautionary measures to protect their animals.

BTB is also a problem in people. Important risk factors that may account for occurrence of the disease in humans include the use of raw milk at 79% while only 26% boil their milk even when the frequency of drinking milk at least three times a week was as high as 81%. The results highlight the importance of GIS in that the created maps can direct where resources are expended in Namwala which is by far the cardinal and fundamental importance of GIS in health sciences.

GIS a mathematical tool was used to identify animal and human populations at risk of the disease. A corroboration of human health personnel, veterinarians and GIS specialists among others would help to tackle the disease. One health approach in the control of the disease would thus be the best approach (Malama *et al.,* 2013). The spatial distribution and important factors driving transmission of bTB in Namwala were empirically demonstrated and it is hoped that allocation of control measures will be guided by the maps generated.

This study revealed the pattern of distribution of positive bTB herds in the high prevalence area of Namwala district and also attempted to answer the question of what might be causing the pattern which we came up with upon creation of maps using collected coordinates. The use of GIS in this epidemiological study has shown that bTB is skewed to the Eastern side of Namwala in distribution. Mitigation measures against this disease should therefore prioritise this region of the district.

CHAPTER SEVEN

Recommendations

The results obtained in the project have underscored the areas needing urgent attention in terms of control of bTB. It's clear from the results that being in the interface area and more specifically the eastern GMAs of Namwala District raises the likelihood of herds being bTB positive. The interface area would require more resources and sensitisation for the control of bTB. The obtained GPS coordinates are actually very useful in directing the interventionists to the actual area precisely to within meter radius of affected parts. The coordinates can also be useful in case of further research to precisely target the area of study. The people in the region need sensitisation on the need to use precautionary measures including most importantly, the boiling of milk. The people also have to be sensitised on the need to avoid mixing wildlife with their domestic animals. Water points can be cordoned off to avoid mixing with wildlife and taking in the infective organism during the drinking of water. Other measures may include strengthening the testing of animals for the disease to slaughter those that may potentially be a source of infection to the rest of the herd. The farmers need to understand that tuberculosis can be insidious and chronic thus their herd can harbour carriers. Since contact was the most important factor, some measures meant to restrict contact between wildlife and livestock can help in disease control. Electrified fences have helped but that has not been instituted for Kafue Lechwe in Zambia. Other methods that can be employed include wild life vaccines as baits (Fitzgerald *et al.,* 2012). Such control measures would be easy to employ since the animal populations which are vulnerable and implicated in bTB transmission have been identified.

Having used GIS to detect areas of bTB occurrence where with good resource allocation, the disease can be controlled; we recommend the adoption of GIS in studying other diseases.

There is need to commit resources towards training in the use of the technology so that even more robust analyses can be used in studying the disease. The creation of maps used in the project and the spatial analysis used were basic. More training would enable the production of even more informative maps and the use of more robust statistical tests. More resources can also help in the production of such detailed maps and more complete and better results generally. There is need to train people in use of more software in the use of this technology to study diseases. That would include involving personnel with more know-how on the use of the different software and spatial analytic skills.

We recommend the use of the technology to the study of diseases including cholera where outbreaks are experienced every year to show using visual maps of Lusaka and therefore enable detection of the actual areas where resources can be directed to manage the outbreaks. Other diseases include Rift Valley fever and African swine fever among others whose maps may help to understand areas of occurrence and from there gain insight into the problem and formulate mitigation measures.

REFERENCES

1.   Adrian Z.B, Marvel H.T, and Lilia P.B.M., 2012. Spatial and Temporal Distribution of Tuberculosis in the state of Mexico. The Scientific World Journal, 12, p 7

2.   Anon., 2000. Annual report of the department of research and specialist services. Lusaka: Government printers

3.   Anoshivan K, and Jamshid Y.C 2010. Spatial distribution of tuberculosis in Mazandaran province-Iran: Spatial-Temporal modelling. Tanaffos journal 9(3): 15-21

4.   Anseli, Luc. Unknown year. Spatial data analysis with GIS; An introduction to application in the social sciences. Santa Barbara, CA 93106: National centre for geographic information and analysis univerisity of California.

5.   AREGHEORE. Country profiles/zambia [Online].

6.   Armbruster C.1994. 'Infections with Mycobacterium tuberculosis and MOTT (Mycobacteria other than tuberculosis) in HIV infected and AIDS patients'. Wien Med Wochenschr;144(8-9):182-6

7.   Armin G, Nafomon S, and Etienne F. 2006. Mapping Malaria transmission in west and central Africa. Tropical Medicine and International Health. 2(7), pp.1032-1046.

8.   Ashford D.A, Whitney E, Raghunathan P. and Cosivi O. 2001. Epidemiology of selected Mycobacteria that infect humans and other animals. Rev Sci Tech; 20:325-37.

9.   Bandara A.B and Mahipala MB. 2002. Incidence of brucellosis in Sri Lanka: an overview. Vet Microbiol; 90:197-207.

10.   Berkley S. 1990. AIDS in Sub-Saharan Africa: an overview. Prog Rep Health Dev South Afr:5-9.

11.   Biet F., Boschiroli M.L., Thorel M.F and Guilloteau L.A 2005 Zoonotic aspects of Mycobacterium bovis and *Mycobacterium avium* -intracellular complex (MAC) Vet Res May-June; 36 (3) : 411-36

12.   Brenda A, Renato C.and Carlos E.V., 2010. How can we estimate buffer zones of protected areas? A proposal using biological data, Brazilian journal of nature conservation, December 165-17 8(20)

13. Bruin, J. 2006. Newtest: command to compute new test. UCLA: Statistical Consulting Group. http://www.ats.ucla.edu/stat/stata/ado/analysis/.

14. Burna M., Salome D., Silvia A., Jan H., Claudio J.M.L., Sven D.C.P., Paul D.V.H and Jakob Z. 2013. Zoonotic *Mycobacterium bovis* induced tuberculosis in Humans. Emerging infectious diseases volume 19 number 6-June 2013.

15. Chintu C. 2007. Tuberculosis and Human Immunodeficiency virus co-infection in children; management challenges. Paediatric Respr. Rev.8(2), pp.142-7.

16. Cook AJ, Tuchili LM, Buve A, Foster SD, Godfrey-Fausett P, Pandey GS, and McAdam KP. 1996. Human and bovine tuberculosis in the Monze District of Zambia-a cross-sectional study. Br Vet J; 152:37-46.

17. Corbett E.L, Watt CJ, and Walker N. 2003. The growing burden of tuberculosis: global trends and interactions with the HIV epidemic. Arch Intern Med.163(9), pp.1009-21.

18. Cosivi O., Grange J.M., Darbon C.J., Raviglione M.C., Fujikura T., Cousins D., Robinson R.A., Huchzermeyer H.F., de Kantor and Meslin F.X 1998. Zoonotic tuberculosis due to *Mycobacterium bovis* in developing countries Emerg. Infect Dis 1998 Jan-Mar; 4(1) 59-70 PMCID:PMC 2627667

19. Dirk P, Tim R, Mark S, Kim S, David R and Archie C, 2009. Spatial Analysis in Epidemiology, Oxford University Press, Great Clarendon Street, Oxford OX2 6DP, Oxford New York. Pp1-6, 9-14, 23, 26 and 31.

20. Douglas, Nobel D, Smith D, and Mathar R. 2012. Feasibility study of Geo-spatial Mapping of Chronic disease risk ti inform public health commissioning. BMJ. 2(711).

21. Ellen and Cromley E. 2003.GIS and Disease. Annual Review of Public Health. Vol. 24, pp.724.

23. Elliott AM, Luo N, Tembo G, Halwiindi B, Steenbergen G, Machiels L, Pobee J, Nunn P, Hayes RJ, and McAdam KP. 1990. Impact of HIV on tuberculosis in Zambia: a cross sectional study. BMJ 1990; 301:412-5.

24. Ernest Jawetz, Joseph L M and Edward A. A 1984. A Review of Medical Microbiology, Lange medical publications, California. Pp228-233

25. Farmer P. and Kim JY. 1998. Community based approaches to the control of multi-drug resistant tuberculosis: introducing "DOT-plus". BMJ. 317(7159), pp.671-4.

26. Fightingtuberculosis.org 2012. [online]. [Accessed November 2012].

27. Fine E.P. 2001. BCG: the challenge continues. Scand J Infect Dis. 33(4), pp.243-5.

28. Fitzgeral S.D and Kaneene J.B 2012. wildlife reservoirs of bovine tuberculosis worldwide hosts, pathology surveillance and control, diagnostic centre for population and animal health 4125 Bedmat Road, Lansing MI 489110(2012)

29. Frank C. T. and David K. S. 2002. The application of Geographical Information Systems to Public Health Problems in Africa, a review in International Journal of Health Geographica. 2002 1:4

30. Frimno G.M Unknown Year True contribution of Agriculture to Economic Growth and Poverty reduction, Malawi, Mozambique and Zambia, Synthesis pp 13 to 14.

31. Gilberto G, Antonio M.M and Suzana D.F, and Mariha S.C. Unknown year. Spatial analysis and GIS; A primer. [online].

32. Goswamin N.D., Hecker E,J., Vickey C., Ahean M.A., Ox G.M *et al.,* 2012. Geographic information system-based screening for TB, HIV and Syphilis (GIS-THIS): A cross sectional study Plos One 7(10); e46029 doi 10.1371/journal. Pone.0046029

33. Hall H.T.B. 1985. Diseases of Livestock in the Tropics. United Kingdom: Longman.

34. Han'gombe M.B, Munyeme M., Nakajima C., Fukushima Y., Suzuki H, Matandiko, Ishii A, Mween A.S and Susuki Y. 2012. *Mycobacterium bovis* Infection at the Interface Between Domestic and Wild Animals in Zambia BMC Veterinary Research 2012 8:221

35. HealthMapping.com 2007. [online].

36. Humblet M.F, Boscholi M.L and Saegeman C, 2009. Classification of worldwide bovine tuberculosis risk factors in cattle; a stratified approach. Veterinary Research 2009 Sep-Oct 40(5): 56 DOI 10.1051/vetrer/2009032

37. Hunagy Z.Y, Boer W.F, Largeveld F., Xu C., Tebaru B.K., Berlingieri F and Princh h.H 2013 Dilution effect in bovine tuberculosis: risk factors for

regional disease occurrence in Africa Proc Biol Sci 2013 June 26;280(1765) 20130624vDOI 10.1098/rspb.2013.0624

38. Jackson MC, Huang L, Xie Q, and Tiwari RC. A modified version of Moran's I. Int J Health Geogr. 2010 Jun 29;9:33. doi: 10.1186/1476-072X-9-33.

39. Kapata N, Chanda K.P, O'Grady J. 2011. Trends of Zambia's tuberculosis burden over the last two decades. Tropical Med. Inter health. 16(11), pp.1404-9.

40. Kapata N., Chanda K.P, Grobasch M.P. 2012. Scale up of TB and HIV program collaborative activities in Zambia- a 10 year review. Tropical Medicine Inter. Health. 17(6), p.76.

41. Kathryn D. 2011. Molecular Epidemiology in Tuberculosis. Davis, USA.

42. Kazwala RR, Daborn CJ, Sharp JM, Kambarage DM, Jiwa SF, Mbembati NA. 2001. Isolation of Mycobacterium bovis from human cases of cervical adenitis in Tanzania: a cause for concern? Int J Tuberc Lung Dis 2001; 5:87-91.

43. Malama S, Tohansen J.B, Muma J.B Mwanza S, Berit D and Godfroid J 2013. Isolation and molecular characterisation of *Mycobacteria bovis* from Kafue Lechwe (*Kobus lechwe Kafuensis*) from Zambia, tropical animal Health prod(2014) 46:153-157 DOI 10.1007/511250-013-04-66-4

44. Malama S. 2013. Norwegian school of Veterinary Science (2013, December 10) Tuberculsois in Zambia, spread, control of infection, Science daily.

45. Malama S., Bwalya J.B., and Godfroid J 2013. A review of Tuberculosis at the wildlife-livestock-human interface in Zambia Infect Dis Poverty 2013 2;13

46. Marcotty, Matthys F, Godfroid J. 2009. Zoonotic tuberculosis and brucellosis in africa; neglected zoonoses or minor public health issues? Annals of tropical medicine and parasitology. 103(5401-411), p.411.

47. Mary M.L and Eric D.K, 2004. A multi-scale method for disease mapping in spatial epidemiology, Statistics in medicine, statistics med.2004;00;1-1

48. Matthew L.S. 1998. The utility of geographical information systems (GIS) and spatial analysis in tuberculosis surveillance in Harris county, Texas 1995-1998. Texas.

49. Melinda J, Joshua M, Paul B 2008. Human mycobacterium bovis infection and bovine tuberculous outbreak In Michigan, 1994-2007. Emerging Infectious Diseases., p.657.

50. Moda G, Daban C.J, Grange J.M and Cosivi O 1996. The Zoonotic Importance of Mycobacteria bovis, Veterinary Public Health Service, Tubercle and Lung Disease 05/1996: 17(2) 103-8 DOI: 10.1016/50972-847996 90022-2

51. Mostowy S. and Behr MA. 2002. Comparative genomics in the fight against tuberculosis: diagnostics, epidemiology, and BCG vaccination. AM J Pharmacogenomics. 2(3), pp.189-96.

52. Mota E.F, Silva V.L, and Palm J.S and Costa M.C. 2003. Spatial distribution of tuberculosis mortality in Salavador, Bahia, Brazil. Cad Saudepublica. 19(4), pp.915-22.

53. Muma J.B, Syakalima M., Munyeme M., Zulu V.C and Kuruta 2013. "Bovine Tuberculosis and Brucellosis in traditionally managed Livestock in Selected Districts of Southern province of Zambia" Vet Med Int 2013; June.

54. Munyeme M, John B. M, Munang'andu H .M, Clovice Ka, Eystein and Martin T. 2010. Cattle Owners awareness of Bovine Tuberculosis in high and low prevalence settings of the Wildlife-Livestock Interface areas in Zambia. BMC Veterinary Research 2010 6:21

55. Munyeme M, Muma J.B, Rigouts L.S, Nambota A.M, Phiri I.G.K Samui K.L, Ding P and Tryland M 2008. Effects of livestock/wildlife interface on the epidemiology of bovine tuberculosis in the Kafue basin of Zambia, preventive vet med 2008(85) 317-328

56. Munyeme M, Rigouts L, Shaputa I.C, Muma J.B, Tryland M, Skjerve E and Bent D 2009. Isolation and Characterisation of Mycobacterium bovis strains from Indigenous Zambian cattle using Spacer oligonucleotide typing technique BMC Microbiology 2009, 9:144 DOI:101186 1471-2180-9-144

57. Munyeme M. and Munang'andu H. 2011. A review of bovine tuberculosis in the kafue basin ecosystem. Veterinary Medicine International. 211.

58. Munyeme M, Muma J.B, Skjerve E. 2008. Risk factors associated with bovine tuberculosis in traditional cattle of the livestock/wildlife interface area in Kafue basin of Zambia. Elsevier Preventive Veterinary Medicine. 85, pp.317-328.

59. Munyeme M, Muma J.M, Samui K.L. 2009. Prevalence of Bovine tuberculosis and animal level risk factors for indigenous cattle under different grazing strategies in the Livestock/Wildlife interface areas of Zambia. Tropical Animal Health. 41, pp.345-352.

60. Munyeme M. 2011. Epidemiological investigations of zoonotic tuberculosis in Livestock/wildlife interface areas of the Kafue basin Zambia. Norway.

61. Muray E.J., Maraig B.J., Mans G., BeyersN., Ayles H., Godfrey-faussett P., Wallman S., Bond V. 2009. A Multidisciplinary method to map potential tuberculosis transmission hot spots in high burden communities. Int J Tuberc Lung dis 2009 June; 13(6) 767-74

62. Nawal, Moley A.H, Soliman Y.A . 2009. Bovine tuberculosis in dairy cattle farm as a threat to public health. African Journal of Microbiology Research. 3(8), pp.446-450.

63. Nester, Anderson, Roberts, and Pearson and Nester. 2004. Microbiology; A human perspective. New York: Mcgraw Hill.

64. Nigel U., Philip S., Seif R., Ferdinand M., Mbanya., Kitange H., Louise H., Richards E., Terry A., Albert 2001. Non-communicable diseases in sub-Saharan Africa: where do they feature in the health research agenda? Bull World health organ vol 79 n.10 genebra Jan.2001.

65. Nsubuga P., Mark E.W., Stephen B.T., Mark A.A., Stephen B.B., Clair V.B., Tom M.C., Victoria E., Rubina I., Dan S., Donna F.S., Robert V.T., Maya V and Muray T 2006. Disease Control priorities in developing Countries, 2nd edition, Chapeter 53.

66. O'Grady J, Bates M, and Chilukutu L. 2012. Evaluation of Xpert MTB/RIF. Clinical Infectious Diseases. 55(9), pp.1171-8.

67. OIE/terrestrialmanual(online 01/04/2014)

68. Olalekan A.U, Ismael Y, and Khalide A and Mubashir B.U. 2009. A trend analysis and sub-regional distribution in number of people living with HIV and dying with TB in Africa,1991 to 2006. International Journal of Health geographics.

69. Oloya J, Kazwala R, Lund A, Opuda-Asibo J, Demelash B, Skjerve E, Johansen TB, Djonne B. 2007. Characterisation of mycobacteria isolated from slaughter cattle in pastoral regions of Uganda. BMC Microbiol 2007; 7:95.

70. Openshaw P. Unknown year. Developing appropriate spatial analysis methods for GIS.

71. Patrick K.M., Manuel B., Teresa N.Q., Joseph O., Denise D., Kenneth C.J., Gerry B., Karan P.S and Stephen E.W, 2004. Using GIS technology to identify areas of tuberculosis transmission and incidence, International Journal of health geographic 2004 3;23 doi10. 1186/1476-07 2X-3-23

72. Philips C.J., Foster G.R., Morris P.A., and Teverson R., 2003. The transmission of Mycobacterium bovis Infection to cattle, Res Vet Sci 2003 Feb; 74(1):1-15

73. Praveen K.T, Nathawat M.S and Ablishekm, 2011. Role of GIS and GPS in vector borne disease mapping; a case study, Department of geography, Banaras Hindu university, Varanasi (2011)

74. Raviglione M.G , Snider DE JR, and Kochi A. 1995. Global Epidemiology of tuberculosis. Morbidity and Mortality of a Worldwide epidemic. JAMA. 273(3), pp.220-6.

75. Rindra V.R, Philipe S, Fanjasoa R, and Arthur R. and Vincent R. 2009. Spatial clustering of pulmonary tuberculosis and impact of the care factors in Antananarivo city. Tropical medicine and international Health. 14(4), pp.429-437.

76. Robin A.S, Adrian R.A and Stanley W.J.M 2012. Herd Level Risk Factors for Bovine Tuberculosis, A literature review, Veterinary Medicine International Volume 2012(2012), Article ID 621210

77. Sara P, Simon B, Hannah K, Silvio M, David M, and Allen, 2005. Mapping the global distribution of trachoma. Bulletin of the world health organisation, December 2005, 83(12)

78. Simon I.H., Graham A., and David J.R 2007. "Global Mapping of Infectious diseases: methods, Examples and Emerging applications; Emerging infectious Diseases 2007 April; 13(4):674

79. Sitima A.M.C, Pandey G.S 1997. Viability of *M. bovis* in traditionally sour milk and prevalence of bovine tuberculosis in Namwala district of Zambia, International science symposium 9-11h April, Lusaka Zambia.

80. Sousak Aksup 2007. Antiretroviral Therapy during Tuberculosis Treatment and Marked Reduction in Death rate of HIV infected patients, Thailand Emerging Infectious Diseases July 2007 pp1001.

81. Stone J., Brown F., and Drbniewsk 2011. Human *Mycobacterium bovis* infections in London and South East England. Clinical microbiology 2011.

82. Tanser F.C, and Le Sueur D. 2002. The Application of geographical information systems to important public health problems in Africa. Int J Health Geogar. 2002; 1:4. doi:10.3201/eid0202.960202 [PMC free article] [PubMed] [Cross Ref]

83. Tatem A.J, Adamo S, Bharti N, Castro M, Dorelien A, Fink C, Mendelsohn J, Montana L, Montegomery M.R, Nelson A, Noor A.M, Pindolia D and Yetman G and Balk D. 2012. Mapping Populations at Risk: Improving Spatial Demographic Data for Infectious Disease Modelling and Metric Derivation, Popul Health Metr. 2012 May;10(1):8.

84. The application of geographic information systems (GIS) to illustrate geographical distribution of notifiable diseases in KSA during the 1990's. Saudi Arabia Ministry of Health.

85. The application of geographical information systems to public health problems in Africa 2002. A review, International journal of health geographica. 1(4).

86. The global fund information note: HIV collaborative activities. July, 2011.

87. Thomas C. R and Cecil G. 2003. Geographic Information Systems and Public Health. Annu. rev. public health 2003.24:1-6

88. Thrashfield, M. 1986. Veterinary Epidemiology. London: Butterworth & Co. Ltd.

89. Timoty C.R, Maria M, Kathleen S, Moser SK, Bridine and Steffenie A.S. 2008. Tuberculosis from Mycobacterium bovis in Bi-national communities United States. Pp 909-912 Emerging Infectious Diseases June 2008.

90. Training Manual for the Second Third Country Training Program Course, Zoonosis Module by University of Zambia School of Veterinary Medicine in conjunction with JICA. 6th November to 20th December,2000. Pp19-27

91. USAID. 2011. Tuberculosis profile for Zambia USAID. [online]. [Accessed June 2011].

92. Using GIS to Map Diseases In Developing Countries/Leannevalleys.webs.Com(Accessed 06/06/2012)

93. Waldhör T. The spatial autocorrelation coefficient Moran's I under heteroscedasticity Stat Med. 1996 Apr 15-May 15;15(7-9):887-92.

94. Wang T, Xue F, Chen Y. 2012. The spatial Epidemiology of tuberculosis in Linyi city, China, 200-2010. BMC public health. 12(885).

95. WHO factsheet no.104. 2012. [online].

96 WHO/tuberculosis [online] 01/03/2011/12/13

97. WOOD, Peter. 2006. Understanding Immunology. Pearson Prentice Hall.

98. World Assembly of delegates of the OIE in May 2009 on Bovine Tuberculosis

99. www.who.com/gis(Accessed August 2012)

100. www.ats.ucla.edu/stat/stata/faq/morans_i.htm (accessed 06/12/13)

101. Xiao-Ni Huo, Hong Li,Dan-Feng Sun,Lian-Di Zhou, and Bao-Guo 2012. Li Combining Geostatistics with Moran's I Analysis for Mapping Soil Heavy Metals in Beijing, China Int J Environ Res Public Health. 2012 March; 9(3): 995-1017.

102. Yieshm A, Sismanidis C, Beyer S.N . 2008. ZAMSTAR the zambia South Africa TB and HIV reduction study; design of a 2x2 factorial community randomised trial. 79(63).

103. Zieger U., Pandey G.S, Kriek N.P.J and Caudwel A.E 1998. tuberculosis in kafue Lechwe (*Kobus lechwe kafuensis*) and in bush buck (*Tragelaphus scriptus*) on a game ranch in central province Zambia; case report, Journal of the south African veterinary association issue 3 vol 69 p.98-101 1998 September.

ANNEX

Appendix 1 Questionnaire

ANIMQ

A SURVEY TO DETERMINE DISTRIBUTION OF BTB IN CATTLE OF

NAMWLA DISTRICT

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SECTION ONE: IDENTIFICATION

Day of visit:…………………………......................................……......

Farm Sampling No:……………………………....................................……....

Farm location:………………………………………………………….

Zone	Herd/Village	GPS Coordinates

Owner's   name   and   Address   (Area):………………….................

....

Name of person interviewed:…………………...

Relation of the person interviewed:

1. Owner ☐   2. Family member ☐   3. Care taker ☐

Number of members in the household

☐

Name of interviewer:…………………...

Q1. Do you own animals?

Yes ☐

No ☐

Q2. Do you come in contact with animals

Yes ☐

No ☐

Q3. What kind of contact

Herding of animals ☐

Milking of animals ☐

Q4. What type of animals do you have on this farm/village and what is the herd size

of your cattle?

Cattle	Sheep	Goats	Pigs	Others (Specify)

Q5. Do you enclose your animals at night

Yes ☐

No ☐

Q6. If YES in (2) above, how close are the animals

1 very close ☐   2 spread out ☐

Q7. What is the size of the enclosure in relation to number of animals?

1 small ☐   2 right size ☐   3 big ☐

Q8.   Do you receive any veterinary supportive services?

0. Yes…….….………...☐

1. No…….….………...….☐

If   yes

specify……………………………………………………………………..

SECTION TWO: FEEDING AND ANIMAL MOVEMENT PATTERNS

Q9.   If you practice grazing what type of grazing is it?

0. Own pastures…………….………...

☐

1. Only communal pastures…….………………...

☐

2. Own and communal pastures…….….……………...

☐

Q10. Do your animals come into contact with wild animals?

Yes   ☐

No   ☐

If yes specify the type of wild animals…...

Q11. For how long do your animals come into contact with wild animals?

Less than a month …………..☐

3-6 months …………….. ....☐

All year round….…………….. ...☐

Q 12. Do you move your animals to the plains on certain times of the year for search of grazing land?

Yes ☐

No ☐

Q 13. Where do your animals drink water?

Own watering points…………………………………………………………. ☐

Shared / Communal watering points……………………………………………. ☐

Own and communal watering points…………………………………………… ☐

Q 14. Do your animals share drinking water with wild animals simultaneously?

Yes ☐

No ☐

DISEASE AND DISEASE CONTROL

Q15. Have you taken some animals to the abattoir in the past 24 months?

Yes ☐

No ☐

Q16. Have you ever thrown away lungs or part of lungs due to nodular (hard growths) on them or at an Abattoir?

Yes ☐

No ☐

Q17. If Yes in question above, has there been an animal from your herd which had lungs/other organs condemned?

Yes ☐

No ☐

Q18. If yes in question above, were you told what condition it was?

Yes ☐

No ☐

Q19. If yes in question above, what was the condition?

    Specify………………

Q 20. Did any animal die in your herd in the last 12 months?

Yes ☐

No ☐

Q21. Has any animal shown weight loss and coughing?

Yes ☐

No ☐

If   yes,   give   the   identity   of   the

animals…………………………….........................

Q22. If any animal has shown the signs what was done about the problem?

0. Treated ……………………...…..☐

1. Culled …………………….......................................…..........☐

2. other……...…………..

Q23.   Do you have animals that show signs of weakness and lethargy on this farm?

0. Yes ☐

No ☐

If yes, give the identity of the animals…………………………….......................

Q 24. Do you have very thin and emaciated (wasted away) animals in your herd?

Yes ☐

No ☐

Q 25. Did any animal showing the signs in Q20 & 21 above die?

Yes ☐

No ☐

Q26. What measures would you take if you observed some of these signs?

Isolate the animal immediately ☐

Call a veterinarian ☐

Attempt to treat it ☐

If you would treat it how would you treat the animal?

Specify…………………………………………………………………………

Q 27. Have you ever heard about bovine tuberculosis (bTB)?

Yes ☐

No ☐

Q 28. If YES, do you know how its spread?

Yes ☐

No ☐

Q 29. Are you aware of bTB in wildlife?

Yes ☐

No ☐

Q30. Have you heard of a disease called tuberculosis?

Yes ☐

No ☐

Q31. Has any of your animals ever been condemned due to tuberculosis?

Yes ☐

No ☐

Q32. How do you think animals get Tb?

From other animals ☐

From people ☐

From wildlife ☐

Other…………………………………………………………

Q33. Do you think you it is possible to prevent tuberculosis in cattle?

Yes ☐

No ☐

Q34. If (Yes) how would you prevent tuberculosis transmission to your herd?

Avoiding mixing animals from other herds ☐

Avoiding mixed grazing ☐

Reducing contact with wild animals ☐

Other (specify).,……………..

Q35.   How often do you conduct disease preventive measures against Tuberculosis and how?

0. None……………………….…………………………………...............☐

1. Regular (at least once per year)…………......................................☐

2. Irregular (once after many years)...☐

4. Specify……………………….

Q36.   Are your family members vaccinated against Tuberculosis?

Yes ☐

No ☐

Q37.   Has any member of your family been treated for Tuberculosis?

Yes ☐

No ☐

Q38.   Do you drink milk?

Yes ☐

No ☐

Q39.   Do you boil your milk?

Yes ☐

No ☐

Q40   Do you sell your milk to the people around you?

Yes ☐

No ☐

Appendix 2. Moran's I

The Moran's I statistic for spatial autocorrelation is given as:

$$I = \frac{n}{S_0} \frac{\sum_{i=1}^{n} \sum_{j=1}^{n} w_{i,j} z_i z_j}{\sum_{i=1}^{n} z_i^2} \tag{1}$$

where z_i is the deviation of an attribute for feature i from its mean $(x_i - X)$, $w_{i,j}$ is the spatial weight between feature i and j, n is equal to the total number of features, and S_0 is the aggregate of all the spatial weights:

$$S_0 = \sum_{i=1}^{n} \sum_{j=1}^{n} w_{i,j} \tag{2}$$

The z_I-score for the statistic is computed as:

$$z_I = \frac{I - \mathrm{E}[I]}{\sqrt{\mathrm{V}[I]}} \tag{3}$$

where:

$$\mathrm{E}[I] = -1/(n-1) \tag{4}$$
$$\mathrm{V}[I] = \mathrm{E}[I^2] - \mathrm{E}[I]^2 \tag{5}$$

Appendix 3 GEOGRAPHICAL POSITIONING SYSTEM (GPS) READINGS OF ALL THE STUDY VILLAGES

	Area of Origin	South	East	Elevation	TIME	WAY POINT	Ecology	Cattle	Questionnaires	Cattle Tested
		Namwala GPS points: Human TB Patients with Sputum positives								
1	Namwala Central	?	?	?	No. Data	?	?	?	yes	-
2	Chineymu	15°48' 11.81"	026°26' 16.01"	1023m	7:26 AM	97	Forest	Yes	yes	-
3	Baambwe	15°46' 15.81"	026°30' 28.74"	998m	8:13 AM	98	grassland/plains	Yes	yes	-
4	Kawalizhi	15°46' 59.63"	026°34' 01.96"	1005m	11:01 AM	99	Mixed	Yes	yes	-
5	Musongwa	15°54' 33.96"	026°06'	1001m	11:44	100	Mixed	Yes	yes	-

			01.57"		AM					
6	Mbeza	16°04' 01.30"	027°00' 57.05"	1001m	16: 17 PM	101	Mixed	Yes	yes	-
7	Mbeza	16°03' 32.21"	027°02' 01.21"	997m	16:48 PM	102	Mixed	Yes	yes	-
8	Kwa-Nico	16°05' 31.74"	026°55' 17.60"	1001m	18:08 PM	103	Forest	Yes	yes	-
9	Chitongo	16°02' 16.75"	026°56' 43.30"	1012m	9:49 AM	104	Forest	Yes	yes	-
10	Maala	15°43' 32.45"	026°43' 45.27"	995m	10:57 AM	105	open grassland	Yes	yes	-
11	Maala	15°44' 04.18"	026°44' 20.67"	997m	11:45 AM	106	plains	Yes	yes	-
12	Nakwanza	15°41' 00.14"	026°45'	991m	14:59	107	Mixed	Yes	yes	-

				59.98"		PM				
13	Kantengwa	15°46' 50.98"	026°52' 18.15"	997m	12:40 AM	108	Plains	Yes	yes	-
14	Mahungu	15°48' 40.96"	026°20' 58.17"	1013m	16:19 PM	109	Mixed	Yes	yes	-
15	Butele	16°00' 05.69"	026°56' 05.30"	1032m	8:53 AM	110	Mixed	Yes	yes	-
16	Kabulamwanda	15°52' 15.76"	026°52' 29.80"	1010m	11:40 AM	111	Forest	Yes	yes	-
17	Kasaka	15°57' 47.41"	026°58' 57.83"	999m	13:48 PM	112	Mixed	Yes	yes	-
18	Kasenga	15°52' 18.46"	026°46' 25.42"	1023m	15:00 PM	113	Forest	Yes	yes	-
19	Shikolopa	15°55' 03.65"	026°57'	992m	15:34	114	Mixed	Yes	yes	-

				52.02"		PM						
20	Shimbizi	15˚42' 00.65"	026°22' 07.04"	995m		16: 58 PM	115	Mixed	Yes	yes	-

The coding was done over three days