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MAPPING EXPOSURE OF CATTLE TO RIFT VALLEY FEVER VIRUS ALONG THEIR MIGRATORY ROUTES

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DECLARATION

This thesis is my original work and has not been presented for a degree in any other university.

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This thesis has been submitted for examination with our approval as the university supervisors.

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DEDICATION

This work is dedicated to my grandparents Mr. and Mrs. Kipkwe Binott for embracing the importance of education and becoming champions in their generation by taking their children to school including my aunts in an era when girl child education was overlooked. In so doing, my parents, Mr. and Mrs. Reuben Binott Mosomtai were able to pass on the mantle of education to me and my siblings.

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LIST OF ACRONYMS

AUC	Area Under Curve
BBMM	Brownian Bridge Motion Model
CDC	Centre for Disease Control
CO_2	Carbon dioxide
ECOWAS	Economic Community of West African States
ET	Evapotranspiration
FMD	Foot and Mouth Disease
GLM	Generalized Linear Model
GPS	Global Positioning System
ID	Identification
IgM	Immunoglobulin M
IPCC	Intergovernmental Panel on Climate Change
KMOH	Kenya Ministry of Health
MAXENT	Maximum Entropy
MCP	Minimum Convex Polygon
MODIS	Moderate Resolution Imaging Spectroradiometer
NDVI	Normalized Differentiated Vegetation Index
NEP	North Eastern Province
NIR	Near Infrared
NSD	Net Squared Distance
RNA	Ribonucleic Acid
RVF	Rift Valley Fever
RVFV	Rift Valley Fever Virus
ROC	Receiver Operating Curve
SDM	Species Distribution Modeling
SRTM	Shuttle Radar Topographic Mission
TBE	Tick Borne Encephalitis
TWI	Topographic Wetness Index

ABSTRACT

Aedes mosquito is the primary vector for Rift Valley fever virus which affects humans and animals. Virus transmission pathways in animals occurs when bitten by infected mosquito or when viremic animals relocate to new regions with competent mosquitoes. Though Rift Valley fever is a transboundary disease with serious economic consequences, movement of viremic animals in search of pasture or trade in spreading the diseases is not fully understood. This research was undertaken in order to better understand the cattle spatial ecology, especially for pastrolist and their interaction with vectors habitat.

Using 11 collared herds between 2012 to 2015, kernel density estimator was used to established their utilization distribution while species distribution modeling was used to map vector distribution. The environmental layers used to map environmental space of the sample vectors included topographic wetness index, soil type, phenological variables from satelitte derived normalized difference vegetatoon index (NDVI) and Africlim bioclimatic envelopes. The animal movement patterns were further used to characterize the herd's core grazing areas using generalized linear modeling.

The animal tracking results showed that all herds had limited movement during rainy seasons while during dry seasons they covered an average of 120km in 10 days in search of pastures. Climatic conditions, vegetation seasonality, evapotranspiration and soil types were key determinants of space use within home ranges (p value < 0.05). Similar environmental layers contributed most in defining suitable vector habitats for mosquito species. A vector distribution map generated with an accuracy of Area Under Curve of 0.76 showed suitable habitat coinciding with core grazing areas.

Results indicated that movement patterns of pastarolist and vectors habitats are majorly influenced by climatic conditions and vegetation seasonality. Distance covered in search of pasture has the potential of introducing the disease in new regions. Vector control and vaccination of animals, therefore, require to be focused in core grazing areas to reduce disease spread.

Key words: Species distribution modelling, Livestock movement, Rift Valley fever, Generalized linear model

CHAPTER ONE: INTRODUCTION

1.1 Background

Rift Valley Fever (RVF) is a zoonotic disease that affects human and animals. In animals, it causes necrotic hepatitis, haemorrhages, and abortion with high mortality in domesticated animals especially the ewes (Chamchod et al., 2016). In human, RVF infection presents with; fever, myalgia, headache and in severe cases, it causes encephalitis, renal failure, fatal hepatitis and haemorrhagic fever. In addition, recent findings on RVF virus (RVFV) indicate its association with miscarriages in women (Baudin et al., 2016). The World Organization for Animal Health (OIE) classifies RVFV as high impact transboundary pathogen which has been endemic to Africa until recently when an outbreak was recorded in Arabian Peninsula and Yemen in 2000 (Nanyingi et al. 2015; Shawky 2000; Murithi et al. 2011). The disease was first confirmed in 1930 in a farm in Kenya after a successful virus isolation that established that the found virus strain belong to the genus *Phlebovirus* of the family *Bunyaviridae* viruses (Ogara et al. 2014; Sindato et al. 2014; Britch et al. 2013;). The virus is transmitted through bites by infected mosquitoes or by coming in contact with body fluids of infected animals (Balenghien et al. 2013; Klous et al. 2016). *Aedes* species are the primary vectors that maintain the virus through transovarial transmission during interepizootic periods while secondary vectors of *Culex*, *Anopheles* and *Mansonia* species amplify RVF spread resulting in outbreaks (Arum et al., 2015).

The disease is endemic to Africa, however, in recent years it has spread to Madagascar, Saudi Arabia and Yemen, and it is increasingly recognized as a major transboundary disease threat (Murithi et al. 2011; Shawky, 2000). According to a review by Shawky (2000) the first suspected cases of RVF in Saudi Arabia (Jizan province) and the borders in Northern Yemen (Wadi Mawr, El-Zuhrah district in Al-Hodeidah Governorate) were reported on the 10th of September 2000. During the outbreak, he noted that 3,289 suspected cases were reported and over 638 human deaths were confirmed. Other outbreaks have also been reported in Sudan, Egypt, Cameroon, Central African Republic, Mali, Mauritania, Madagascar, Nigeria, Senegal, Somalia, South Africa, Zambia and Zimbabwe (Munyua et al. 2010; Murithi et al. 2011; Shawky 2000; Soti et al. 2013). During the 1977/1979 outbreak, for instance, over 200,000 people in Egypt were

affected, and this resulted in over 600 deaths. In the 1997/1998 outbreak over 100,000 people were affected in East Africa, and 450 people died in Kenya alone (Munyua et al., 2010a).
Changes in climate has been associated with the occurrence of RVF specifically during the El Nino phenomenon (Anyamba et al., 2001). Flooding that results from excessive rainfall provides breeding grounds for mosquito vectors increasing their population. Especially in East Africa, climate change has caused insurgence of vectors into new ecological zones (FAO, 2009). During the 2006/2007 outbreak in Kenya, for instance, 15 new counties reported outbreaks for the first time (Mosomtai et al., 2016; Murithi et al., 2011; Nanyingi et al., 2015). Anyamba et al. (2011), Britch et al. (2013) and Gachohi et al. (2012), suggest that variation in climate lead to extreme temperatures, storm surges, flooding or droughts which in turn affects the population of arthropod vectors that transmit diseases.

Rainfall also increases vegetation growth which provide hibanation possibilities for the vectors, food and host availability while drought periods forces the vectors to accumulate around household increasing contact with humans (Anyamba et al. 2011). Anyamba et al., (2009) alluded that in most semiarid areas, precipitation and green vegetation abundance are major determinants of arthropod and other animal population dynamics. He noted that there is a close relationship between ‘green vegetation’ development and breeding and upsurge patterns of some insect pests and vectors of disease such as mosquitoes and locusts. His findings was also confirmed by Hightower et al. (2012) where he used geocoded location of confirmed cases of RVF in human to identify the relationship between the surrounding environment and RVF outbreaks. He found out that the lower NDVI in the first 10 days of November of 2006 describes an area that is more arid than the rest of the country. The increased rainfall preceeding the outbreak period provides water to rehydrate desiccated mosquito eggs in soil. A dense bush vegetation cover therefore provides landing zones and resting areas that would be desirable to vectors.

Movement of viremic animals to new regions propagates the spread of RVF by being bitten by competent vectors within these regions, consequently, infecting other animals thus, enabling animal to animal transmission (Arum et al., 2015). This movement is as a result of two major factors; trade and nomadism. The disease burden associated with legal and illegal trade, especially at international level, has been recorgnize globally (Fèvre et al., 2006; Shawky, 2000), however, the same case is not true to nomadic pastoralism (FAO 2004). Nomadic pastoralism is a main source of livelihood for over 200 million households globally practiced in arid and semi arid regions and it is a core aspect in the culture of the people who practice it (Schrepfer & Caterina, 2014). Pastoralist mobility is dependent on climatic factors that are important for livestock production. Their grazing strategies are influnced by availability of water and pastures therefore, usage of an area is dependent on meeting this conditions and avoiding it when the conditions deteroriates and this inturn determine their migratory routes (Young et al., 2016). These regions where water and pastures are available are also suitable RVF vectors habitats. In Kenya, pastoralist who largely occupy northern and north eastern part of the country share similar migratory pattern as East Darfur and this regions have been hard hit by several RVF outbreaks over the years (Murithi et al., 2011).

1.2 Statement of the problem

RVF is a disease with high socio-economic impact. During the 2006/2007 outbreak, Kenya lost ~Ksh. 40 billion across all market chains. The vector ecology continually expands in that with every new outbreak there is an increase in vector species that are competent to host the virus (Murithi et al., 2011). There is also policy biasness that restricts only movement of viremic animals in international trade overlooking localized movements such as pastoralism and localized trade especially during interepizootic periods. Knowledge on the role played by nomadic pastoralism in maintaining and spreading RVF has not been fully exploited. Most research so far has been focusing on entomological (Britch et al., 2013; Glancey et al., 2015; LaBeaud et al., 2008; Linthicum et al., 1985; Sutherland et al., 2011) and environmental characteristics (Anyamba et al., 2010; Kiplimo et al., 2014; Sindato et al., 2014; Soti et al., 2013b) that proliferates RVF outbreaks. Movement ecology provides immense opportunity to understand movement behaviour of livestock and this will deepen insights on potential contribution of livestock movement in spreading diseases (Bourouiba et al. 2010; Caron et al. 2016). Furthermore, understanding the vector ecology and their interaction with livestock while grazing will improve accuracy of any possible early warning systems. Quantifying the impact of livestock movement in spreading RVF virus will not only help in improving prediction models but will also help the government in making informed policies.

1.3 Objectives

This research analyses the exposure of cattle to Rift Valley fever virus along their migratory. The specific objectives include;

1. To determine vector habitats and cattle home range
2. To identify environmental characteristics within cattle home ranges
3. To establish the relationship of vector habitats and cattle home ranges

1.4 Research Questions

1. Where are the suitable vector habitats and core home ranges?
2. What are the environmental characteristic of the home ranges?
3. What are the relationship between suitable vector habitat and cattle home ranges?

We hypothesize that cattle grazing areas lie within suitable habitat zones for vectors thus increasing their exposure to the virus.

1.5 Justification

Like most arboviruses, RVF is driven by a complex interaction of mosquito vector populations and vertebrate hosts in different habitat types under varying environmental conditions (Arum et al., 2015; Linthicum et al., 1985; Sang et al., 2010; Shawky, 2000). During previous outbreaks, key primary vectors of RVF virus were identified (Sang et al., 2010) but the limited understanding of their ecology in diverse ecological zones and the interplay with the nomadic pastoral systems along the major livestock movement routes are largely unknown. For these reasons, this study seeks to analyze cattle movement routes in order to understand resource utilization i.e. where they spend a lot of time grazing and how do they often utilize that area, water points, distance moved between forage sites etc., and this will provide the new insights on the exposure of cattle to mosquito biting. Analyses of cattle movement pathways (trajectories) also integrate each cattle location into the larger context of the spatial distribution of the population and changing environmental conditions through time, as well as individuals' constraints, behavior, and survival (Neumann et al., 2015). Movement dynamics of livestock and its role in spreading RVF has not yet been used in understanding RVF outbreaks, therefore, the information obtained from this research will be very valuable to the science community and in filling in a research gap on the role of cattle movement in spread and maintenance of RVFV. It is also envisaged that tracking of animal movement will permit identification of areas where introduction or amplification of the disease could potentially occur from wild disease reservoirs or hosts due to a high density of RVF vector populations. This could contribute to the enhanced understanding of RVF epidemiology and present opportunities for strategic disease prevention.

1.6 Scope and limitations

The study is limited to counties where GPS collars have been deployed and the surrounding counties due to cross boundary movements of cattle/livestock. The information obtained will only be inferred to the time the GPS were operational. Similarly, remote sensing data covering the collared periods will be used to understand the environmental characteristics. A major challenge faced was low signal areas where the collared animals grazed and hence a gap in data captured occurred in some time periods. Due to high cost of high resolution satellite imagery with high temporal resolution, which would be ideal in analyzing cattle movement at the landscape level, Moderate Resolution Imaging Spectroradiometer (MODIS) satellite data was used with other ecological covariates. Vector sampling was conducted only during the beginning of the rainy season, however, understanding viral activity in both seasons is vital, therefore, future research should incorporate doing vector sampling during the dry season also.

CHAPTER TWO: LITERATURE REVIEW

2.1 Introduction

Rift Valley Fever (RVF) is an acute mosquito borne viral disease affecting livestock, such as cattle, sheep, goats, camels, buffalo as well as humans ((CDC), 2007; Anyamba et al., 2010; Breiman et al., 2008; Linthicum et al., 1987; Munyua et al., 2010; Murithi et al., 2011; Shawky, 2000). The Rift Valley fever virus (RVFV) is an arbovirus of the genus *Phlebovirus* of the family Bunyaviridae, and replicates in mosquitos and in vertebrates (Britch et al., 2013; Lutomiah et al., 2014; Ogara et al., 2014; Sang et al., 2010). The prefix *bunya* refers to a place in Uganda (Bunyamwera) were the family prototype (Bunyamwera virus) was first isolated (Shawky, 2000).

The name of the RVF is derived from the Rift Valley in Kenya, where the disease was first reported among livestock in the early 1900s, whereas the virus was first isolated in 1931 (Anyamba et al., 2010; Arum et al., 2015; Murithi et al., 2011; Shawky, 2000). The virus can be transmitted to vertebrates both by bites of the mosquito vector and through contact with body fluids of infested animals. The mosquito transmission occurs mainly through *Aedes* and *Culex* species but also by *Mansonia*, *Anopheles* etc (Nguku et al., 2010; Owange et al., 2014; Sindato et al., 2014; Tchouassi et al., 2014; Tigoi et al., 2015). In different regions, different species of mosquitoes may prove to be the predominant vector (Shawky, 2000). Moreover, *Aedes* mosquitoes are capable of transovarial transmission to offspring via eggs which lead to new generations of infected mosquitoes hatching from their eggs. In this way the virus is able to stay within the ecosystem, as the eggs of these mosquitoes may survive for periods of up to several years in dry conditions until periods of rainfall or inundation occur and the infected mosquitoes hatch from the eggs and transmit the virus to the host (Hightower et al., 2012; Munyua et al., 2010; Shawky, 2000). As it was already mentioned above, the virus can also be transmitted through direct handling of infected animals or meat and contact with blood and other body fluids of infected animals. It is expected to be a result of the slaughtering or handling of infected animals or touching contaminated meat during the preparation of food. It is also mentioned, that the consumption of raw milk of infected animals could be a possible transmission process. Even airborne transmission was reported among laboratory workers dealing with virus cultures (Ogara et al., 2014; Shawky, 2000).

In domestic ruminants the disease causes high mortality in young animals and sudden onset of abortions in pregnant animals (Britch et al., 2013; Gachohi et al., 2012; Munyua et al., 2010a; Murithi et al., 2011). Adult cattle and sheep may suffer mortality rates of 10-30% or higher; that depends mostly on the nutritional state of the animal. For animals that are younger than seven days, fatality rates may approach 100%. Of the mentioned potential animals to get infected, sheep appear to be more susceptible than cattle; goats and camels are less susceptible (Britch et al., 2013; Gachohi et al., 2012; Nguku et al., 2010; Ogara et al., 2014). The incubation rates for animals are characterized to be rather short. Widespread abortion, infertility, and rapidly fatal neonatal disease are typical of outbreaks among cattle and sheep (Shawky, 2000).

In humans diagnosed with RVF, the disease often proceeds uncomplicated with symptoms such as an acute febrile illness (Munyua et al., 2010b). The incubation period varies from two to six days and even during this time people may show no symptoms. Febrile illness symptoms often come with sudden onset of fever of more than 38°C for more than 48 hours. Accompanying symptoms can be headache, general weakness, nausea, backache, diarrhea, or abdominal pain. The symptoms last between two and seven days. After that time the immune system response to infection becomes detectable with the appearance of immunoglobulin M (IgM) antibodies (Shawky, 2000). But in some cases more serious complications occur, ranging from fatal hemorrhagic disease, meningoencephalitis, renal failure, blindness, and in very few cases even death. The human case-fatality rate is approximately 0.2 to 5 % (Britch et al., 2013; Sindato et al., 2014). Patients with hemorrhagic fever (less than 1 % of cases) may remain viremic for up to 10 days and show the highest case-fatality rate, which can be as high as 50 % (Shawky, 2000).

2.2 Historic development of RVF outbreaks

After the disease was confirmed in 1930 (Anyamba et al., 2009; Breiman et al., 2008; Britch et al., 2013; Gachohi et al., 2012; Linthicum et al., 1985; Munyua et al., 2010; Murithi et al., 2011; Sindato et al., 2014; Soti et al., 2013), one of the earliest reported outbreaks occurred in 1950-1951 in Kenya. Murithi et al. (2011) reviewed annual records of reported livestock diseases in

Kenya from 1910 to 2007 from the Department of Veterinary Services at Kabete. Before the major outbreak, he noted that the disease was only confined in Nakuru County from 1912 - 1936 specifically in Naivasha, Marura, Ndabibi, Ol Magogo, and Njoro (Figure 1a). No RVF cases were reported between 1936 and 1950 in the country.

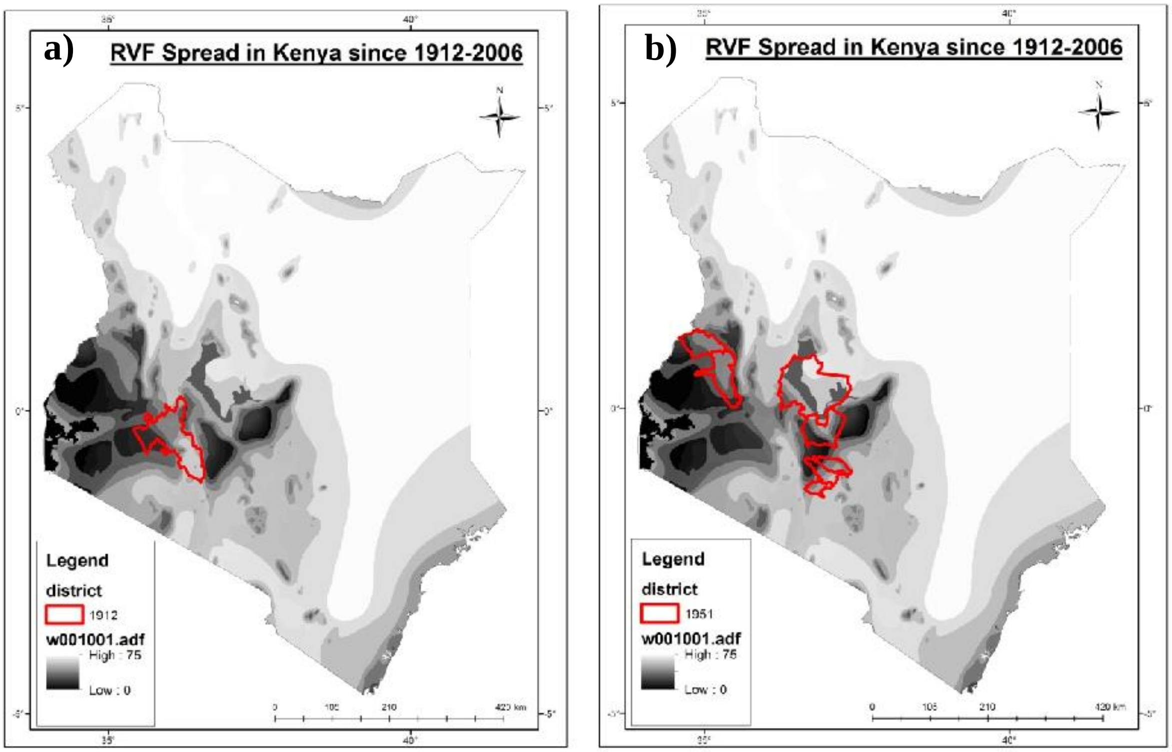


Figure 1:New districts affected by a) 1912 to 1936 outbreak b) 1950 to 1951 outbreak (source: Murithi et al., 2011)

During the 1950 -1951 outbreak, 8/69 (12%) administrative districts (now Counties) were involved. This were; Nakuru where the disease was first reported, Trans Nzoia, Uasin Gishu, Laikipia, Thika, Nyeri and Maragwa, and Nairobi (Figure 1b) (Murithi et al., 2011). Only one of these newly reporting districts, Laikipia district, borders the Nakuru district. Another national epizootic affecting the same eight districts was re- ported in 1955.

Another major outbreak occurred in between 1960 to 1964 where more districts reported the disease for the first time. 22/69 districts (32%) were involved including all of the districts involved during the 1951 and 1955 epizootics. These districts (now counties) were; Narok, Kajiado, West Pokot, Garissa, Wajir, Mandera, Isiolo, Marsabit, Machakos, Makueni, Kwale, Kilifi, Tana River and Kiambu (Figure 2a) (Murithi et al., 2011). From 1965 to 1996, national epizootics were reported in 1967–1968 (12 districts) ; 1970–1971 (three districts), 1977–1978 (11 districts); 1981 (eight districts); 1983 (nine districts); and 1989–1991 (nine districts) (Murithi et al., 2011). Isolated localized outbreaks were reported in 1965 (two districts), 1969 (two districts), 1985–1986 (one district) and in 1987–1988 (one district). A large epizootic in 1997–1998 involving the 22 districts also occurred. All of the affected districts had previously reported RVF outbreaks and this supports majorly accepted hypothesis that RVF virus becomes enzootic in certain ecologies (Murithi et al., 2011).

In 2006–2007, the most extensive RVF epizootic involving 33/69 districts was reported (Murithi et al., 2011; Munyua et al., 2010b). This epizootic represented the first reported RVF disease activity in 15 districts (now counties), including Baringo, Samburu, Kirinyaga Murang'a, Taita-Taveta, Lamu, Malindi, Kitui, Meru, Mwingi, Moyale, Embu, and Mbeere (Figure 2b) (Murithi et al., 2011). He also noted that nine districts that had previously reported RVF outbreaks did not report cases in the 2006–2007 epizootic and that surveillance was more comprehensive during this epizootic than at any previous time; therefore, some of the newly reporting districts may have had scattered low number of RVF cases in livestock that went unrecognized during previous epizootics.

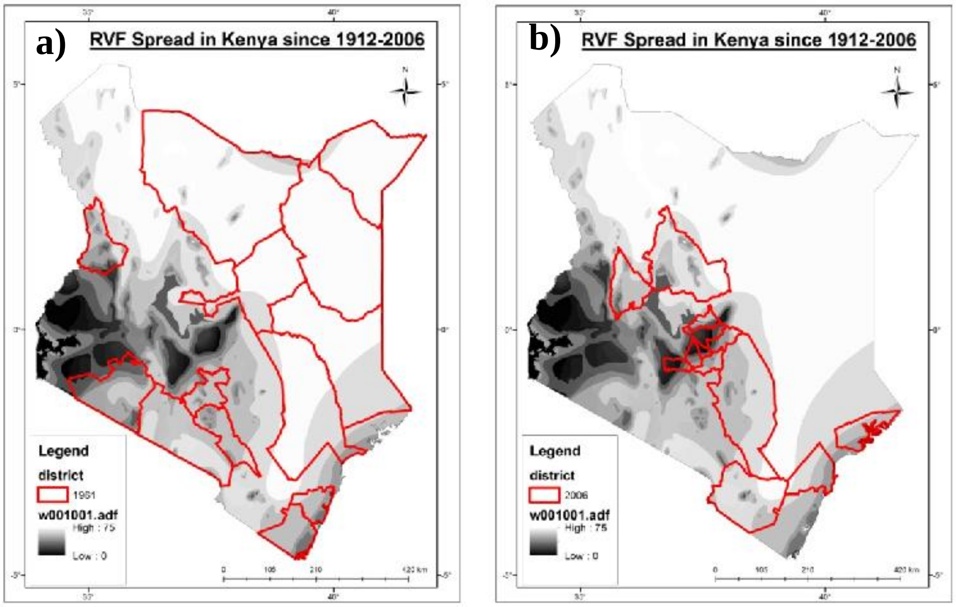
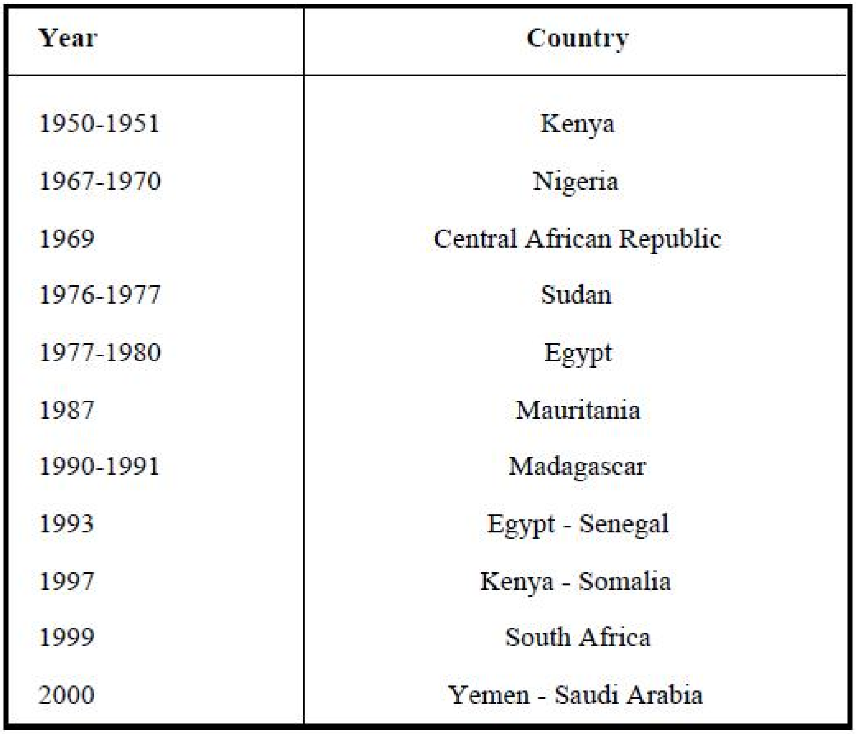


Figure 2:New districts affected by a) 1960 to 1964 outbreak b) 2006 to 2007 outbreak (Murithi et al., 2011)

So far only the Western and Nyanza provinces, located on the southwestern region of the country, has never reported human or livestock RVF outbreaks by 2007 even though flooding from the Yala and Nzoia rivers are common with high mosquito vectors in these regions during seasons of heavy rainfall (Murithi et al., 2011).

Outside Kenya, outbreaks have been reported in Sudan, Egypt, Cameroon, Central African Republic, Mali, Mauritania, Madagascar, Nigeria, Senegal, Somalia, South Africa, Tanzania, Zambia and Zimbabwe (Anyamba et al., 2010; Munyua et al., 2010a; Murithi et al., 2011; Nguku et al., 2010; Ogara et al., 2014; Shawky, 2000). Now the disease is endemic to Africa (Anyamba et al., 2010; Munyua et al., 2010a; Murithi et al., 2011; Nguku et al., 2010; Ogara et al., 2014; Shawky, 2000) however, in recent years it has spread to Madagascar, Saudi Arabia and Yemen, and it is increasingly recognized as a major transboundary disease threat (Murithi et al. 2011; Shawky, 2000). According to a review by Shawky (2000) first suspected cases of RVF in Saudi Arabia (Jizan province) and the near borders in Northern Yemen (Wadi Mawr, El-Zuhrah district in Al-Hodeidah Governorate) were reported on the 10th of September 2000. The table below shows major oubreaks that have occure in the half of the centuary.

Table 1: Major outbreaks in the world (source: Shawky, 2000**)**



Year	Country
1950-1951	Kenya
1967-1970	Nigeria
1969	Central African Republic
1976-1977	Sudan
1977-1980	Egypt
1987	Mauritania
1990-1991	Madagascar
1993	Egypt - Senegal
1997	Kenya - Somalia
1999	South Africa
2000	Yemen - Saudi Arabia

2.3 Environmental characteristics of RVF outbreaks

RVF outbreaks typically occur in 5-15 year intervals and in interepidemic/epizootic periods occurrence is sporadic (Lichoti et al., 2014). Breiman et al. (2008), Britch et al. (2013), Gachohi et al. (2012), Linthicum et al. (1985, 1987), McMahon et al. (2014), Ogara et al. (2014) and Sindato et al. (2014) associates these outbreaks to periods of above normal rainfall events and/or higher temperatures associated with the warm phase of El Niño. During those events mosquitos have enlarged potential breeding sites which allow hatching of multiple species of *Aedes*, the primary vectors, which eventually feed on nearby vertebrate animals and thereby transmitting the virus (Britch et al., 2013; Linthicum et al., 1987; Muturi et al., 2013; Ochieng et al., 2013; Soti et al., 2013b). Although outbreaks are often associated with heavy rainfall and flooding and also have reoccurred in the same locations, it is important not to consider these factors as the only environmental criteria for RVF outbreaks. Besides the climatological impacts, the geological and geographical factors should be characterized and considered as well (Hightower et al., 2012)

Beside rainfall, factors that could be considered may be predominant soil types, specific landforms, the role of ecological zones, land use, elevation, vegetation (e.g. NDVI), etc. In a case study by Hightower et al. (2012) these parameters were examined. For example, they concluded that soil types which were associated with increased RVF incidence were solonetz, calcisols, solonchalks, and planosols. They were present in 72 % of areas with grid cells where cases occurred. Furthermore, RVF incidence was higher in areas with clay or very clayey soils. For landforms, plains were categorized as prominent before any other, because this landform allows flood waters to pool more easily and provide larval habitat. His finding were in agreement with (CDC) (2007); Anyamba, Linthicum, & Tucker (2001); Anyamba, Linthicum, Mahoney, Tucker, & Kelley (2002); Arum et al. (2015); Davies, Linthicum, & James, (1985); Gachohi et al., (2012); Glancey, Anyamba, & Linthicum, (2015); Hassan, Ahlm, Sang, & Evander, (2011); Kiplimo Jusper, Waithaka, H.E., Notenbaert, (2014); Linthicum et al., (1987); Martin et al., (2008); Ochieng et al., (2013); Soti et al., (2013) and Shawky, 2000). An example of specifically Kenyan geologic features in the Rift Valley, which plays also an important role in RVF risk assessment/mapping, is the so called *dambo*. Dambos are shallow depressions located often near rivers filled with water during the rainy season. They can be up to a kilometer in length and several hundreds of meters in width. Often they are encompassed by a large vegetation cover due to a constant presence of water and act as potential breeding sites for mosquitoes. Even during the dry seasons they remain greener than other areas (Shawky, 2000).

Also RVF incidence were reported in the Somali acacia ecological zone located in North Eastern Part (NEP); characterized as semiarid areas where shrubbery grasses and occasionally trees are growing (Anyamba et al., 2002, 2012; Nguku et al., 2010; Ochieng et al., 2013; Ogara et al., 2014). Even the elevation played an important role. They found out that the majority of RVF cases occurred at elevations below 500 m; no case occurred above 1.100 m, whereas 30 % of Kenya is at an elevation of 1.000 m or higher. For the NDVI variable it was noticeable that case locations had significantly higher NDVIs than non-case locations. The vegetation normally increases after long lasting rainfall. The rainfall then provides water to rehydrate desiccated mosquito eggs in soil and the vegetation (for example a dense bush vegetation cover) could provide landing zones and resting areas. A combination of these factors while providing optimal vector habitat at each life stage, can be considered as an optimal vector environment (Hightower et al., 2012). Another important circumstance for RVF distribution is an adequate number of hosts available. Therefore, census data and the distribution of animals is a helpful means to predict the risk (Balenghien, 2013).

2.4 Climate change and RVF occurrence

Climate changes may affect the three fundamental components of the epidemiological cycle of RVF, namely: vectors, hosts and virus. The consequences of global warming on vectors, in particular, may be many. The hatching dynamic of *Aedes* mosquitoes, the main reservoir of RVF in Africa, strongly depends on the rainfall pattern (Anyamba et al., 2001). *Aedes* females lay eggs in pond mud. Although these eggs become desiccated when ponds dry up, they remain viable for several years or even decades in the dry mud. The ovaries and ovarian ducts in a mosquito infected with RVF can transmit the virus to the nascent eggs (Hassan et al., 2011; Hightower et al., 2012). When infected via transovarial transmission, eggs allow the virus to persist in the field during dry and/or inter-epizootic periods. Eggs need to be flooded to hatch. Heavy rainfall results in a massive hatching episode and, consequently, the development of a large vector population (Sang et al., 2010). Then, once infection has been amplified in livestock, secondary vectors such as *Culex* and *Anopheles* species, which breed in semi-permanent pools of water, become involved in the transmission of the virus (Swanepoel & Paweska, 2011).

In East Africa, outbreaks were clearly correlated with the unusual heavy rainfall associated with El Niño (Anyamba et al., 2001, 2002, 2009, 2010, 2012), which consequently flooded many Aedes breeding habitats. El Niño-Southern Oscillation events are a combined ocean atmosphere phenomenon, involving changes in the temperatures of surface waters in the tropical Pacific and in its closely linked atmospheric counterpart, the Southern Oscillation (Martin et al., 2008). El Niño-Southern Oscillation events involve a large exchange of heat between the ocean and the atmosphere, and affect: global mean temperature, trade winds, tropical circulation and precipitation (Martin et al., 2008; McMahon et al., 2014). As mentioned in the IPCC report, heavy rainfall events are likely to become much more frequent in years to come and: 'extremes of the hydrological cycle, such as floods and droughts are apt to be enhanced with global warming (Toure, 2010). In fact, the increase in rainfall in East Africa, extending into the Horn of Africa, is robust across the entirety of the models surveyed in the IPCC report (Drake et al., 2013). Thus, it may be assumed that the frequency and severity of RVF outbreaks on this part of the continent will increase. This could also affect other countries that import animals from Africa, such as some islands in the Indian Ocean. One example is Comoros, which is dependent on the importation of livestock from Kenya and Tanzania – countries where RVF is endemic (Martin et al., 2008).

The correlation between outbreaks of RVF and periods of heavy rainfall observed in East Africa does not apply to West Africa (Kiplimo et al., 2014). However, RVF is also endemic in some sub-Saharan countries. Recent studies conducted in the Ferlo region of Senegal, which included daily mosquito catches and rainfall records (Soti et al., 2013), demonstrated that several generations of *Aedes* can emerge during the same rainy season, depending on: the succession of rains and dry periods, consecutive changes in the water levels of temporary ponds and the flooding of quiescent eggs laid on the shores areas. This mechanism could be the way the disease persists at low incidence levels (Ochieng et al., 2013). This situation would worsen with longer durations of dry days between periods of more intense precipitation during the rainy season (allowing the draining of the ponds and the embryogenesis of eggs), a scenario clearly predicted for some regions of Africa (Martin et al., 2008)

2.5 Management of RVF outbreaks

To prevent the transmission and infection of the disease, it is important to consider several measures that need to be taken which target animals, mosquitoes, as well as humans. To protect healthy animals, it is possible to apply a sustained program of animal vaccination. Depending on the situation, both killed and live attenuated vaccine, can be used. For example, live attenuated vaccine may cause abortion or birth defects in pregnant animals and gives a following three-year immunity, whereas killed vaccines do not cause these effects but two inoculations and annual revaccination is required. Furthermore, it is recommended not to use common needles for vaccination, to disallow the movement of non-vaccinated animals from affected areas, to spray animals by using safe insecticides and to regularly perform a surveillance of susceptible animals. In case of already infected animals, notification and rapid burial of dead animals is important. For combatting against the mosquitoes and their distribution, it is relevant to remove any stagnant water body or water collection to prevent mosquitoes from laying their eggs, for example discarded tires, barrels and old buckets. Weekly treatment of water bodies that cannot be removed should be treated with insecticides in appropriate concentration (Shawky 2000).

Human protection of RVF is divided in several categories, such as individual measures, community measures, and prevention of occupational hazards which are important to follow because no vaccine for humans is yet available. Individual measures include sleeping indoors, using bed nets during sleep, putting screens on windows, wearing clothes that protect the whole body, to use a mosquito repellent for exposed areas of the body, to avoid sitting near vegetation during evening hours where the mosquito activity is rather high, to avoid contact with animals, and if that’s not possible, to wear gloves, masks, and gowns for protection, and to always wash hands well after contact with animals. Community measures include active health education so the public awareness of the disease and their prevention increases. Furthermore, it is necessary to implement regular disease surveillance. For the prevention of occupational hazards, it is significantly relevant to wear gloves, masks and other protective clothes if exposed to infected animals or humans and their tissue, blood or other fluids (Shawky 2000).

2.6 RVF outbreak 2006-2007 in Kenya

In Garissa District in North Eastern Province (NEP), several cases of unexplained fatalities associated with fever and generalized bleeding were reported to the Kenya Ministry of Health (KMOH) in mid-December 2006. Immediately it was initiated to take serum samples from the patients to test on any link to RVF or other diseases. In 10 of the first 19 examined patients RVFV RNA or immunoglobulin M (IgM) antibodies against RVFV were found in the serum samples. Evidence for other diseases was not found, all serum specimens were negative for yellow fever, Ebola, Crimean-Congo hemorrhagic fever, and dengue viruses (CDC 2007). By December 20, a total of 20 deaths had been reported. The official outbreak was confirmed due to the isolation of RVFV from the specimens and was further underpinned by reports of livestock deaths and unexplained animal abortions in NEP. Eventually the outbreak spread to nearby provinces and districts and resulted in 404 human cases with 118 deaths as of January 25, 2007 (CDC 2007).

Three different cases were identified. A suspected case was defined as acute onset of fever (>37,5°C) with headache or muscle and joint pain in a person with no other known cause of acute febrile illness. A probable case was defined as acute onset of fever in a person with unexplained bleeding, vision deterioration, or altered consciousness. A confirmed case was defined as a suspected or probable case with laboratory confirmation of RVFV. A gender or age specific characteristic could not be identified. Figure 2 shows the distribution of reported RVF cases and the corresponding percentage. It is prominent that mainly the east and south were affected. This is probably due to the unusually heavy rainfall in eastern Kenya during October until December 2006. They were three times the average for that period during the preceding eight years and 12 times the rainfall in 2005. Massive flooding in great parts of Kenya, particularly NEP occurred (CDC 2007). Figure 3 gives an overview of the rainfall in 10-day periods in Kenya during the 2006-2007 outbreak, whereas the yellow dots show actual RVF case locations. The first epidemic period occurred from mid-December of 2006 to mid-January of 2007 in NEP, which can be derivated by the first heavy rainfalls during November 11-20 in that region. Another epidemic period occurred between mid-January and peaked in early February of

2007 in Baringo County (in the western part of Kenya) initiated by heavy rain falls between December 21-30.

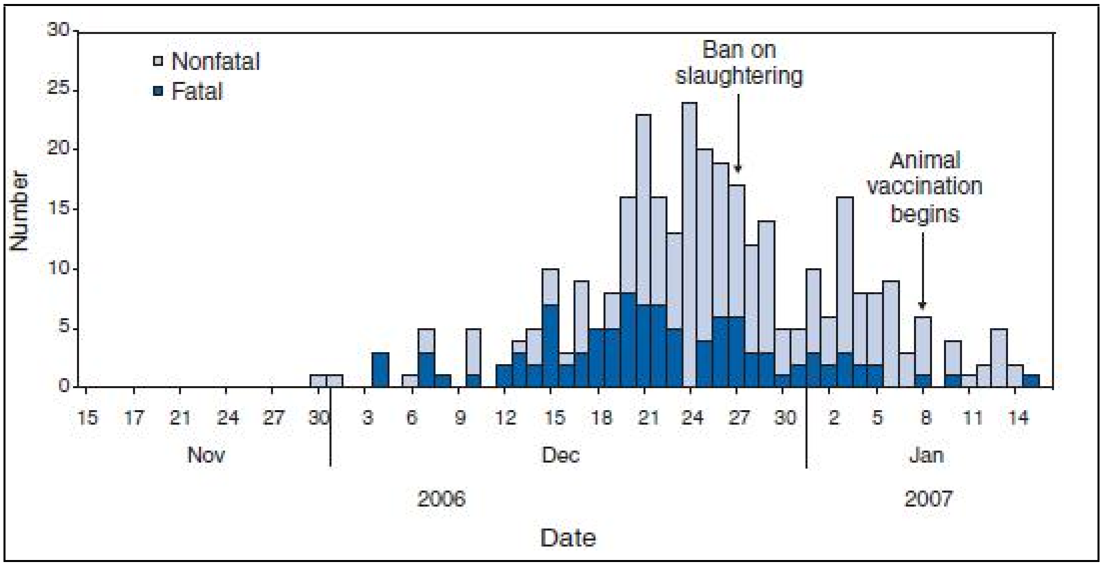


Figure 3:Number of reported RVF cases (n=330), by date of illness onset in Kenya for November 2006-January 2007 (CDC 2007: 75)

Figure 3 shows a diagram with the number of reported RVF cases by date of illness onset, divided in fatal and nonfatal outcomes. First RVF cases occurred already by the end of November, but the actual outbreak started in mid-December. After a ban on slaughtering was state-imposed, it is noticeable that the severity of the outbreak started to decrease. This happened again after animal vaccination started in early January of 2007 (CDC 2007).

2.7 Role of Remote Sensing in the analysis of RVF epidemics

Earlier predictive studies by Linthicum et al., (1987) used satellite derived NDVI and rainfall to assess the potential for RVFV activity in two ecologically distinct RVF enzootic areas in Kenya which indicated a positive correlation between NDVI and high mosquito population, hence the high likelihood of RVF occurrence. Using a 19-year-old NDVI data, a mask was created to identify areas where RVF was more likely to occur in the savannah ecosystems of Africa. In East Africa, there was a strong correlation between predicted risk areas and observed outbreaks of RVF from 1981 to 2000; these outbreaks were more likely to occur during warm ENSO events in East Africa while cold ENSO events in Southern Africa triggered RVF outbreaks (Anyamba et al., 2009).

A climatic RVF risk-monitoring model was proposed in predicting the potential spatial and temporal distribution by using NDVI anomaly and elevated sea surface temperature (SST). The model retrospectively detected previous three outbreaks (1982 - 83, 89 and 1997 - 98) which correlated with positive SST and NDVI anomalies and also predicted, almost accurately, the areas for 2006 - 2007 outbreak areas in East Africa (Anyamba et al., 2010). Despite high success in predicting outbreak areas times and areas, the coarse resolution of 8 km may overgeneralize the risk and it was, therefore, useful for small-scale areas as countries and not continental scales.

Spatiotemporal analysis employing climatic and environmental variables was used in combination with vector surveillance data to predict potential outbreaks in Horn of Africa, Sudan, and Southern Africa with suitable areas of eminent epidemics identified with a lead time of 2 - 4 months. Accurate prediction timelines by optimal model performance were enhanced with precise animal and human disease data (Anyamba et al., 2010). Using time series analysis of NDVI from September 1997 to April 1998, RVF suitable areas were identified in Kenya with a lead time of 5 months, these received anomalous rainfall which led to favorable conditions for emergence of RVFV vectors. This has been supported by recent studies by Anyamba et al. whose improved methods led to first the prospective prediction of RVFV circulation enabling accurate prediction with lead times of 2-4 months before outbreaks (Anyamba et al., 2001, 2002, 2010).

2.8 Animal movement and disease transmission

Domestic and wild animal population movements are important in the spread of disease. There are many recent examples of disease spread that have occurred as a result of intentional movements of livestock or wildlife. A review done by Fèvre et al., (2006) examined several issues that relate to movement of domestic and wild animals and discusses the risks that these movements entail at local, regional and global scales with regard to the spread of disease. The authors highlighted some of the infectious diseases that resulted in outbreaks. For instance, In late January or early February 2001, Foot and Mouth Disease (FMD) was introduced to a pig farm in the north of England. The disease spread through the pig herd probably occurring with three waves of infection and amplification, however, FMD was not notified to the authorities until it was identified during a routine meat inspection at a slaughterhouse. Another example was given of *Trypanosoma evansi*, a pathogen responsible for surra in livestock that spread in south east Asia, particularly in the Philippines where there was high mortality in those areas in which the parasite had been detected. The spread was blamed on the movements of livestock as part of herd improvement program.

In Africa, livestock are one of the few tradable commodities available to millions of poor households, particularly those living in the more arid regions of sub- Saharan Africa. There are well-established trade routes across the continent that supply the large coastal populations of west and central Africa and the Arabian peninsula (Fèvre et al., 2006). According to Nanyingi et al., (2015) and Shawky, (2000), RVF outbreak in Arabian Penisula in 2000 was associated with livestock trade with horn of africa. In Madagascar, Mayotte and Comoros Islands, introduction of RVF is suspected to be caused by movements of viremic animals along trade routes.(Balenghien et al., 2013). Gachohi et al. (2012) and Ogara et al. (2014) noted that during RFV outbreaks, cattle movement amplify the spread of the disease, and this forces the government to stop all livestock movement, slaughtering and selling animal products during the outbreak period (Gachohi et al. 2012, Ogara et al. 2014). This was supported by Ogara et al. (2014) when they did risk pathway analysis to investigate the possibility of entry, release, exposure and eventual consequences of the RVF in Ijara, Kenya. He found out that the virus spread through mosquito bites, environmental contamination by infected carcasses or aborted foetuses and movement of infected animals and humans, leading to massive losses of lives, livelihoods and trade.

Movement of an organism is also influenced by its biological and external factors driving its movement (Dodge et al., 2013). Environmental conditions may trigger certain movement patterns or invoke a particular behavioral response, and thus determine local movements or long-distance migrations (Dodge et al., 2013). Livestock migration pattern in semi arid regions is influenced by the need to look for water and pasture. Young et al., (2016) monitored pastoralist in Darfur and noted that pastoralist move north-south migration because the southern parts of East Darfur are too wet for livestock in the rains, exactly when northern pastures are wet enough, while conversely, northern areas are lacking in forage and water in the dry season, when these resources are available further south. A research done by Caron et al. (2016) on African buffalo movement across the Great Limpompo Transfrontier Conservation Areas which cuts across

Limpopo (Mozambique), Kruger (South Africa), and Gonarezhou (Zimbabwe) national parks found out that subadult female out of the 68 collared buffalo had extra ordinary long distance movement. Young buffalo dispersed further than the adults to reduce the chances of inbreeding. They said female also tested positive for RVF among other zoonotic disease that were tested and therefore concluding that animal movement played a major role in the spread of diseases among distant populations, across protected areas and international borders.

2.9 Research gap

Even though high economic burden is involved in managing zoonotic diseases, the impact it has on developed and developing countries differ (FAO, 2009). Most zoonotic diseases in developed countries are under control majorly because of functional institutional infrastructure in place. Europe for instance has established a digital system where animal registration is made and therefore it is possible to trace the movement of an individual cattle among premises and this data is available at a national level (Barjardi et al., 2011). Framework such as the bovine tuberculosis (bTB) risk-based trading (RBT) schemes have been adopted in England and Wales to reduce the spread of bTB during trade (Adkin et al., 2016). Adkin et al., (2016) noted that there was reduction in sale of infected cattle when provision of bTB risk score of the farm was compulsory to the potential purchasers alluding to the potential the scheme had in preventing farmers from buying infected animals.

Dispite overwhelming evidence on the importance of animal movement in spreading RVF, major research especially in developing countries are focused on environmental (Flick & Bouloy, 2005; Glancey, Anyamba, & Linthicum, 2015; LaBeaud et al., 2008; Linthicum, Bailey, Davies, & Tucker, 1987; Linthicum, Davies, Kairo, & Bailey, 1985; Lutomiah et al., 2014; Munyua et al., 2010; Murithi et al., 2011; Muturi et al., 2013; Nguku et al., 2010; Ochieng et al., 2013; Ogara, Kasiiti, Gathura, & Landmann, 2014; Owange et al., 2014; Sang et al., 2010; Shawky, 2000; Sissoko et al., 2009; Swanepoel & Paweska, 2011; Tchouassi et al., 2013, 2014; Tigoi et al., 2015; Woods et al., 2002), entomological (CDC, 2007; Anyamba et al., 2009, 2010; Anyamba, Linthicum, Small, Britch, & Tucker, 2012; Anyamba, Linthicum, & Tucker, 2001; Anyamba, Linthicum, Mahoney, Tucker, & Kelley, 2002; Breiman et al., 2008; Kiplimo Jusper, Waithaka, H.E., Notenbaert, 2014; Linthicum et al., 1987; Martin et al., 2008; McMahon, Manore, Hyman, LaBute, & Fair, 2014; Muga, Onyango-Ouma, Sang, & Affognon, 2015; Ng'ang'a, Bukachi, &

Bett, 2015; Ogara et al., 2014; Sindato et al., 2014; Soti et al., 2013) and molecular (Freire et al., 2012; Grobbelaar et al., 2011; Lutomiah et al., 2014; Tchouassi et al., 2013) aspects of the disease.

Several research studies have identified that movement of viremic animal amplify the disease, however, exactly how is yet to be determined. Movement ecology provides immense opportunity to understand movement behaviour in animals and this will deepen insights on its potential contribution in spreading of infection diseases (Bourouiba et al., 2010; Caron et al., 2016). With the advancement in tracking technology using GPS, movement of organism can be obtained at high spatial and temporal resolution which was not possible before. Computational technology and statistical advancement has also provided more opportunity of extracting relevant information from this huge telemetry data. In managing zoonotic disease, this localized movement and its potential in spreading diseases can be exploited especially in developing countries where they don't have infrastructure put in place of monitoring movement of individual livestock.

This research brings in a holistic understanding of RVF occurrence by combining entomological, environmental and animal movement patterns, an approach that has not been explored before. Central to this work is the insights gained on pastoralist migratory patterns and the role it plays in maintaining the virus during inter-epizootic periods.

CHAPTER THREE: METHODOLOGY

3.1 Study area

The study area stretches from Isiolo County E36.724, N2.282 to Lamu county E41.6921, S3.2230 traversing Meru, Tana River and Garissa Counties respectively (Figure 1) spanning over an area of 121,357.44km2. The study area borders Somalia from the eastern side of Garissa county, Wajir, Marsabit and Samburu counties borders from the eastern, northern and western part of Isiolo county respectively while Tana River and Meru counties are bordered by Kitui to the West and Tharaka Nithi to the south respectively. The elevation of the study area ranges from 5, 199M at Mt. Kenya in Meru county which is the highest mountain in Kenya to the shores of Indian Ocean in Lamu and Tana River counties.

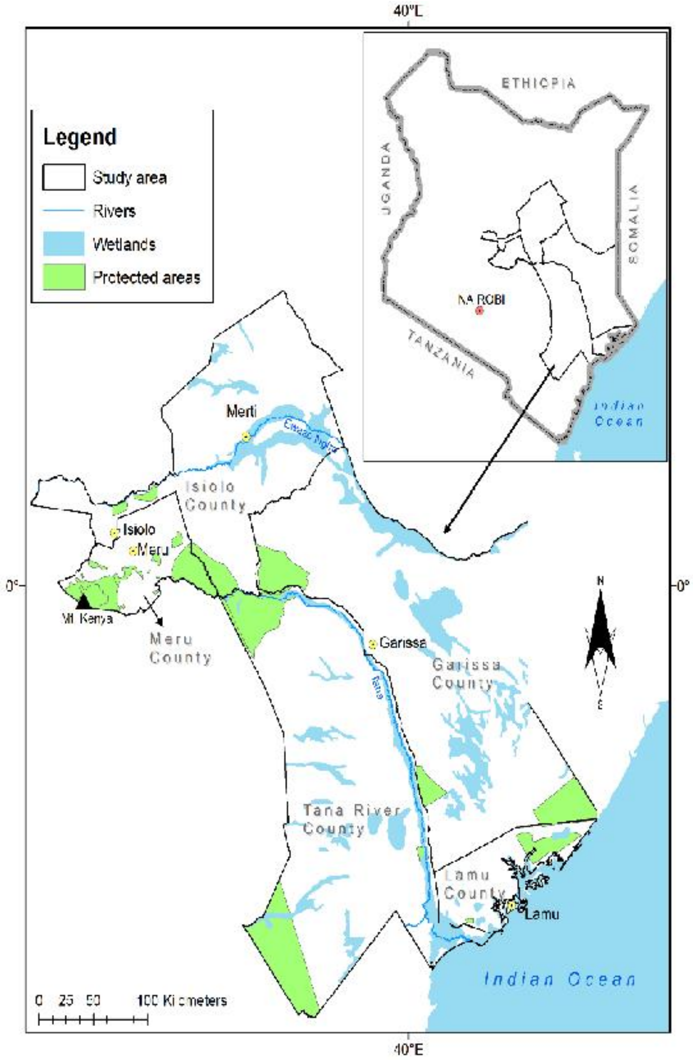


Figure 4:Location map of the study area

Two permanent rivers traverse the study area sourcing from Mt. Kenya; Tana River with a delta characterized by large irrigation schemes which have been associated with providing ideal breeding spaces for RVF vector (Arum et al., 2015), and Ewaso Nyiro River which traverses through Isiolo with a large wetland at Merti that provides pasture for pastoralist during the dry season (Figure 1). The soil types are largely clayey (Kiplimo et al., 2014) coupled with seasonal flooding which provides a suitable habitat for mosquito vectors (Mosomtai et al., 2016). Lamu, Isiolo, Garissa and Tana River counties are covered by savannah type vegetation (Arum et al., 2015) with several national parks and game reserves located within the study area (Figure 1). Wildlife like buffalos, waterbuck, gazelles etc. have shown to be reservoirs of RVF virus (Britch et al., 2013). The community are mainly pastoralist who mainly settle around water points and dambos and live closely with their animals increasing the chances for zoonotic disease contraction (Ogara et al., 2014).

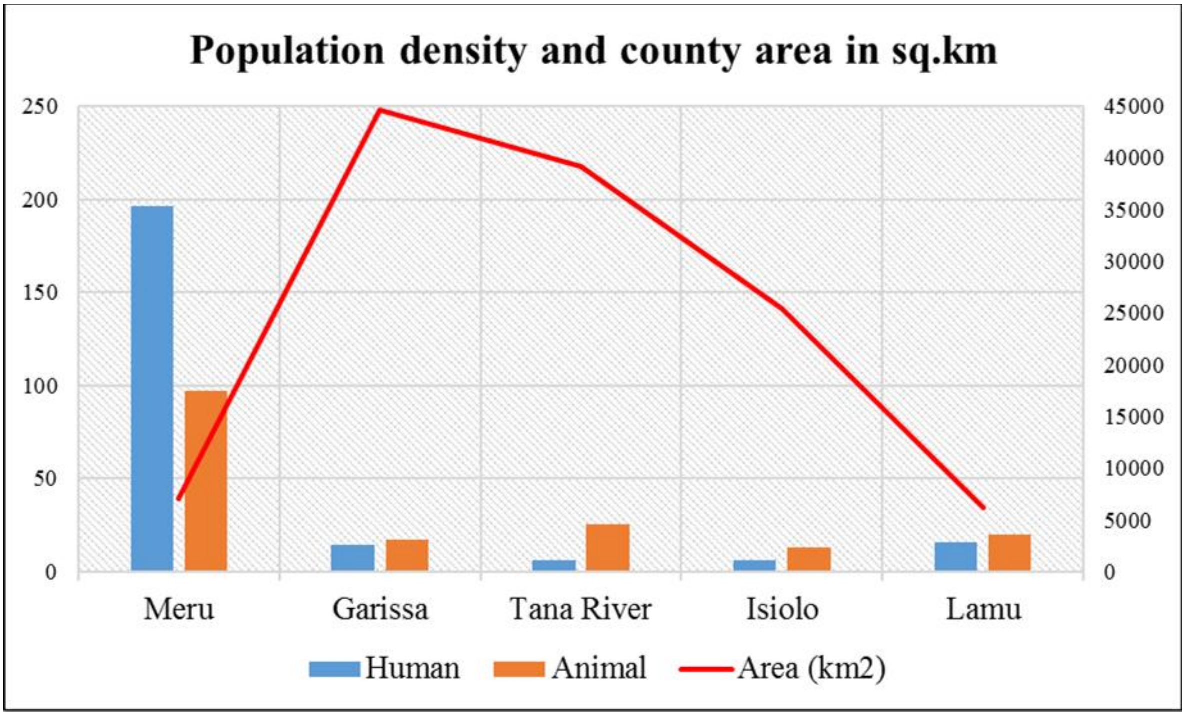


Figure 5: Size of county area (sq. km) and population density for both human and animal

In the study area Garissa county has the largest landmass with highest population of livestock compared to all the counties in the study area. However, Meru county has the highest population for both human and animal even though it has the least number of livestock and landmass. The big county sizes in the arid areas allow for nomadic pastoralism which is the main source of livelihood for the communities residing there. Garissa County has a population of 623,060 according to the 2009 census and is traditionally occupied by the Somali ethnic group and over 80% of the land is used for livestock production. The sparse population of approximately 14 persons/km2 of the district is found concentrated around the water sources and also around small market centers (Arum et al., 2015). Tana River county has a population of 240,075 according to the 2009 census distributed in 47,414 households. It is inhabited by a mixture of Orma and Somali communities who are pastoralist, with large herds of livestock, consisting mainly of cattle, sheep and goats. Isiolo county is largely occupied by the following Cushitic communities Oromo-speaking Boran and Sakuye, the following communities are found Turkana, Samburu, Meru, Somali and other immigrant communities from other parts of the country.

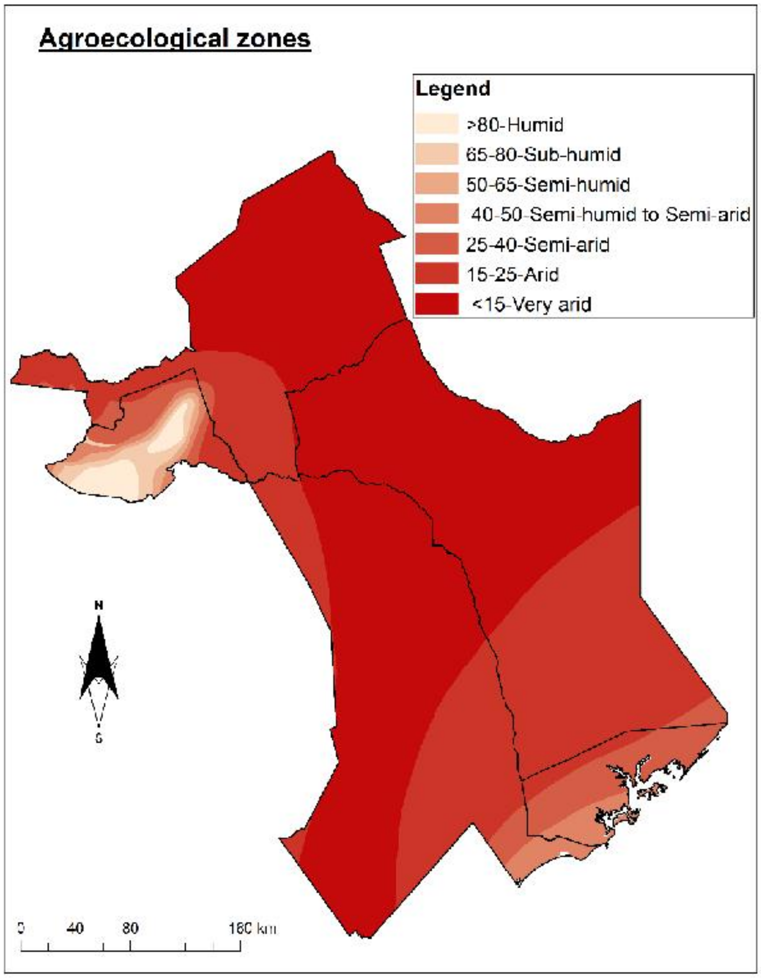


Figure 6: Map for the agro-ecological zones of the study area

Isiolo, Garissa, Tana River and Lamu counties are arid regions characterized by averaged daily temperatures ranging from 20 – 35^{0}C while Meru county is very humid with temperature ranging from <10^{0}C in Mt Kenya to 20^{0}C at the slopes of the mountain (Figure 3). Rainfall is bimodal; the long rains occurring from March to May and the short rains in October to December with occasional variation. In the arid region rainfall amount ranges from 300 – 800mm annually with extreme cases occurring rarely during El Nino resulting to excessive flooding. The vegetation is majorly open shrubland with woody acacias in the arid

3.2 Data and materials

a) Cattle movement data

Trajectory data from pastoralist was obtained from 2012 – 2016 from 11 collared herds from Garissa, Tana River and Isiolo counties herein referred to as Garissa, Tana River and Isiolo herds respectively (Table 2). Garissa herds were collared between September 2012 to June 2014 while Tana River and Isiolo herds were collared from August 2013 to 2016. The herds were identified with the following Collar IDs; 1172, 1175, 1178, 1179, 1174, 1177 for Garissa herds, 4168, 4169 for Tana river herds and 4006, 4167, 4170 for Isiolo herds. The herds comprised of 700 – 1000 cattle and were identified via focused group discussion with acceptance by owners who were familiar with different movement corridors used by the community (Owange et al., 2014). The temporal resolution for transmitting the location of the herds was after every one hour during the day only, however, there were several times when the collars failed to transmit because the animals were either out of range of the satellites or when the battery life ended. Garissa herds had two months of missing data due to out of coverage while Isiolo and Tana River herds had six months of missing data due to end of battery life before being replaced.

Table 2: Summary of vector layer datasets

Description	**Data**	**Source**	**Period**	**Resolution**
Cattle movement	GPS collars	11 Herds	Sep 2012 - Jul 2016	1 hour fixes
Mosquito sampling	Lat, long	GPS	Apr/Dec 2012 - 2015	long and short rains
	County boundaries	Open data portal	N/A	1:50,000
	Protected areas	ILRI portal	N/A	1:50,000
	wetlands	ILRI portal	N/A	30M
	Rivers	ILRI portal	N/A	N/A

b) Mosquito sampling

Mosquito occurrence data was obtained from published work. Arum et al., (2015) and Sang et al. (in press) articulate the procedure in which mosquito sampling was done. While trapping mosquitoes, GPS location were taken which are used as occurrence data for species distribution modelling for mosquito distribution (Table 2).

c) Other GIS layers

County boundaries wetlands, rivers and protected areas layers that were used to generate location map were obtained from Open data portal (http://www.opendata.go.ke/) and International Livestock Research Institute GIS website (http://192.156.137.110/gis/search.asp).

d) Environmental layers

16-day composite images of NDVI from the 250-m MODIS MOD13Q1 product (collection 5) for the years 2001-2015 were processed. The MOD13Q1 time-series image data was atmospherically corrected (Vermote et al., 2002). The images were smoothed utilizing a Whittaker smoother algorithm (Atzberger & Eilers, 2011) to reduce residual noise such as clouds and cloud shadow. The MOD13 product includes the 250-m near-infrared (NIR), the red reflectance (RED) and the NDVI data layer. Monthly images of Evapotranspiration from 1 km MOD16 were also obtained and used as a proxy for rainfall for the same period of time as NDVI and since it is a calculated index no pre-processing required (Mu et al., 2005). These data were downloaded from the Earth Explorer data portal. Digital soil type data was obtained from the Kenya Soil Survey data set (Sombroek et al., 1982). Soils that exhibit a high degree of water retention potential, as determined by their physical and chemical properties, are known to provide suitable RVF vector breeding conditions. 30m digital elevation model (DEM) data from the Shuttle Radar Topographic Mission (SRTM) was processed to compute areas where water can potentially collect in the landscape. Firstly, the DEM was corrected for artifacts within low lying areas and water bodies using selective filtering (Grohman, Kroenung, & Strebeck, 2006).

Table 3: Summary of environmental data

Data	Source	Period	Resolution
Evapotranspiration	MOD 16	2012 - 2015	1km
soil type	Soil Survey of Kenya	Revised 1997	1:50, 000
Elevation	USGS	N/A	30m

animal density	FAO	N/A	5km
NDVI	MOD 13Q	2012 - 2015	250m

For simulation of the mosquito species distribution in the study area, current climatic conditions at one kilometer grid resolution from the AfriClim data set were used (Platts et al., 2015). These variables were preferred because they provide high resolution projections for the African continent (Lovett, 2015; Mwalusepo et al., 2015). This data set contains grids of temperature, rainfall and derived bioclimatic summary variables (Table 5).

Table 4: Bioclimatic variables obtained from AfriClim

Data	Description	units	Period
bio1	Mean annual temperature	^{0}C	1961-1990
bio2	Mean diurnal range in temperature	^{0}C	1961-1990
bio3	Isothermality	^{0}C	1961-1990
bio4	Temperature seasonality	^{0}C	1961-1990
bio5	Max temp warmest month	^{0}C	1961-1990
bio6	Min temp coolest month	^{0}C	1961-1990
bio7	Annual temp range	^{0}C	1961-1990
bio10	Mean temp warmest quarter	^{0}C	1961-1990
bio11	Mean temp coolest quarter	^{0}C	1961-1990
bio12	Mean annual rainfall	mm	1961-1990
bio13	Rainfall wettest month	mm	1961-1990
bio14	Rainfall driest month	mm	1961-1990
bio15	Rainfall seasonality	mm	1961-1990
bio16	Rainfall wettest quarter	mm	1961-1990
bio17	Rainfall driest quarter	mm	1961-1990
mi	Annual moisture index		1961-1990
mimq	Moisture index moist quarter		1961-1990
miaq	Moisture index arid quarter		1961-1990
dm	Number of dry months	month	1961-1990
llds	Length of longest dry season	month	1961-1990
pet	Potential evapotranspiration	mm	1961-1990

3.3 Methods

The methodology adopted for this study is summarized in Figure 7 and involved vector habitat analyses, characterizing the home range environment through generalised linear modelling and species distribution modelling

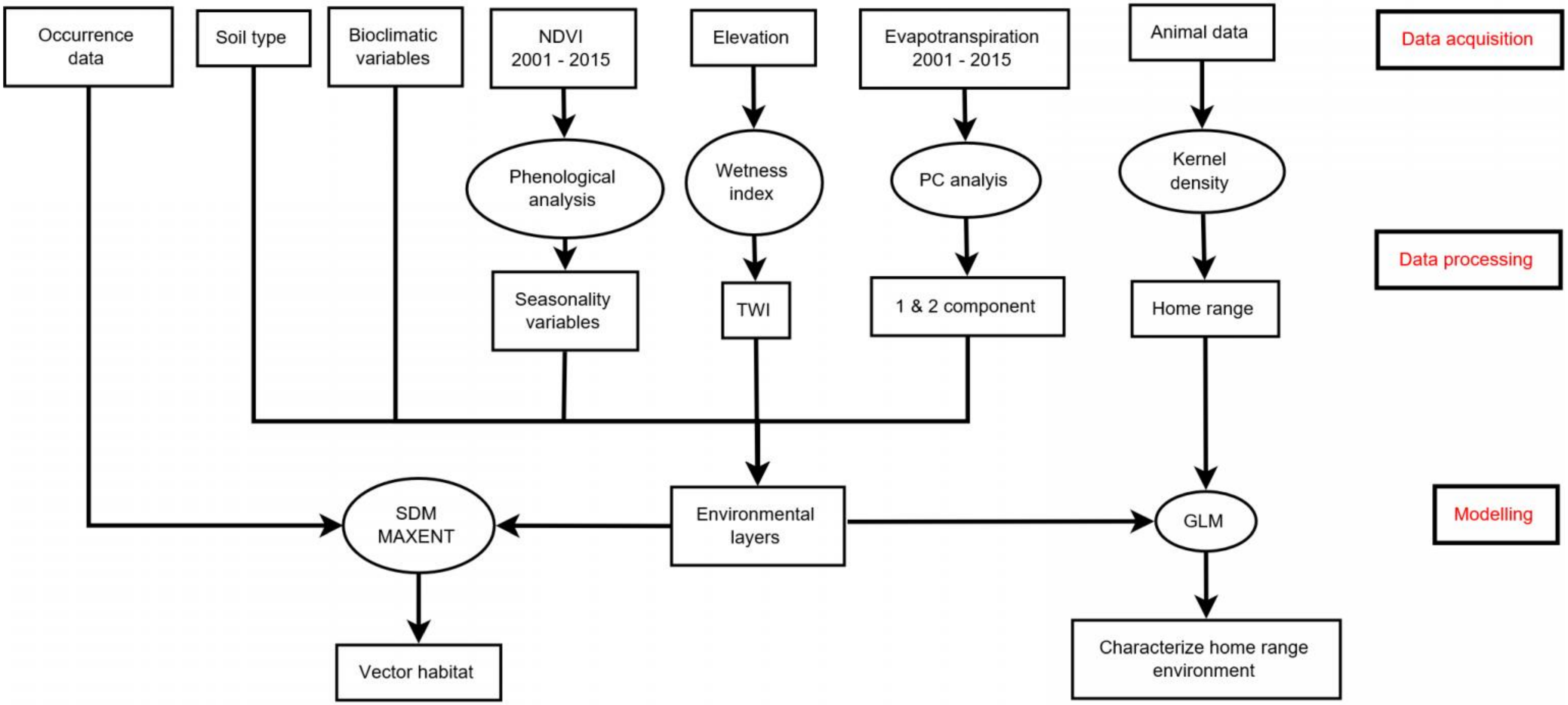


Figure 7: Methodology flowchart diagram

3.3.1 Research approach

This research made use of data driven approach. Data driven approach make use of computational intelligence, machine learning technique, artificial intelligence etc to establish pattern within the data (Solomatine et al., 2008). Computational intelligence was used to establish cattle grazing areas, topographic wetness and vegetation seasonality. Machine learning technique, specifically, Maximum Entropy was used to establish vector distribution which used sample training data to model the rest of the data sets. Finally, linear regression was used to establish relationships between cattle grazing areas with the climatic conditions that were suitable.

3.3.2 Seasonality analysis

Remotely sensed variables on vegetation productivity dynamics from Moderate Resolution Imaging Spectroradiometer (MODIS) time series data were analyzed using TIMESAT. TIMESAT analyses phenology signals found in time series satellite data by fitting local functions to the time series data points, then combines them into a global model (Clark et al., 2010; Jamali et al., 2015). Thereafter a smooth model function is used to extract phenology variables for each growing season, which in turn reduces the influence of residual signal noise in the NDVI time series data (Foi et al., 2008; Shen et al., 2013) and data dimensionality (Fu & Wang, 2003; Hinton & Salakhutdinov, 2006). Function-fitting parameters used in TIMESAT for this study were: Savitzky-Golay filter procedure, 3- and 4-point window over 2 fitting steps, adaptation strength of 3.0, no spike or amplitude cutoffs, season cutoff of 0.0, and begin and end of season threshold of 20%.

3.3.3 Evapotranspiration analysis

Principle component analysis was performed on the ET time-series data spanning from 2001 - 2015 in order to reduce data dimensionality and maximize data variability over the observation period (Mosomtai et al., 2016). This is achieved by extracting the underlying structure i.e. the principal components in the data. These underlying structures are achieved by establishing the directions (eigenvector) in which the most variance (eigenvalue) in the data exists. The eigenvector with the highest eigenvalue in the data makes up the first principal component and depending on the number of dimensions of the data, the maximum number of principal components generated is equal to the number of the dimensions. However, the first eigenvector is orthogonal to the second therefore, the variance that was not explained in the first component is explained in the second until all the information in the data is captured. Mostly very few components contains most of the information, therefore only the significant component with 99% of the variance were selected for analysis (Gulrez & Al-Odienat, 2015)

3.3.4 Topographic wetness index analysis

TWI was calculated to extract topographic features based on steadiness of wetness (Landmann et al., 2010). Steadiness of wetness is defined as the contribution the slope and the upstream contributing area would make to a specific unit area in terms of water retention capacity (Beven & Kirkby, 1979). SAGA GIS was used to extract TWI from the 30m elevation data from SRTM (Boehner & Selige, 2006).

3.3.5 Home range estimation

According to Horne et al. (2007), home range is defined as that area criss-crossed by an animal in its normal activities of food gathering, mating, and caring for young. Within home range, we have core areas that are frequently used by the animal than other places probably because it has enough food sources or home sites (Walter et al., 2011). Utilization distribution map describes this intensity of use within the home ranges with contour boundaries defining the space use percentage where 50% describes the core areas while 99% describes the entire home range (Worton, 1987). A review done by Walter et al (2011) identified several advances in methods used to map home ranges. In this study we used Kernel Density Estimator (KDE) to identify cattle utilization distribution using the cattle telemetry data (figure 2) (Hengl, 2008). Even though KDE erroneousness in estimating home ranges has been identified (Skarin et al., 2015) and improvements such as Brownian Bridge Movement Models (BBMM) suggested (Horne et al., 2007), data gaps within our data posed a challenge in using advance methods. For instance, while trying to use BBMM it was difficult to predetermine GPS error (Laver & Kelly, 2008). KDE was implement in ArcGIS 10.2.2 using the movement ecology extension (ArcMET) by (Wall, 2014)

3.3.6 Species distribution modelling (SDM)

MAXENT default settings with a few alterations was used aimed at attaining precise and accurate predictions (Merow et al., 2013; Phillips & Dudík, 2008). Twenty percent (20%) of occurrence records were withheld from each model to be used as independent test data. A regularization multiplier of three was used to spread out the predictions and reduce overfitting and ten replicate runs was set to obtain a robust model. Due to increased replication, random seed was used to select different random test/run partition for each run. A 10 percentile training presence threshold' was used which predicts the 10% most extreme presence observation as absent (Cord et al., 2014) to eliminate outliers from the model. Modelling was performed under current bioclimatic, vegetation and topographical conditions.

Threshold independent area under curve (AUC) of receiver operating characteristic (ROC) analysis model (Phillips & Dudík, 2008) was used to asses model performance. The area under a ROC curve indicates the probability that presence (sensitivity) versus absence (specificity) or background points (Yackulic et al., 2013) were ordered correctly by a classifier. AUC values of zero indicate impossible occurrence area while one indicate optimal occurrence area or perfect ordering (Du et al., 2014). Swets (1988) discriminatory power with slight modification was used to rank the models as; i) excellent = 0.90-1.00, ii) good = 0.80-0.89, iii) fair = 0.70-0.79, iv) poor = 0.60-0.69, and v) fail = 0.50-0.59. T-test was used to test the susceptibility of cattle to mosquito bites within their home range. Points were selected randomly over the study area and pixel values for each random points were extracted for both home range and vector habitat map to test the hypothesis. Figure 7 summarizes the methodological flowchart.

3.3.7 Generalized linear modelling

Generalized Linear Model (GLM) was used to characterized the cattle home ranges using the same environmental layers used to model vector distribution. GLM constitutes a family of models with flexibility when modelling the response variable (Guisan & Zimmermann, 2000). 1000 random GPS points from the trajectory were selected and their pixel values extracted for environmental layers and home range raster. Gaussian family of GLM with logit link function was used to model the response variable. Furthermore, two sample T-test was used to prove the exposure of cattle to mosquito habitat by selecting 100 random points within their home ranges.

Pixel values were extracted for both home range map and vector habitat map to test the hypothesis (Skarin et al., 2015)

CHAPTER FOUR: RESULTS AND ANALYSIS

4.1 Seasonality analysis

Seasonality parameters extracted from TIMESAT are shown in figure 12 whereby; (a) beginning of season, (b) end of season, (c) length of season, (d) base value, (e) time of middle of season, (f) maximum value, (g) amplitude, (h) small integrated value, (h+i) large integrated value.

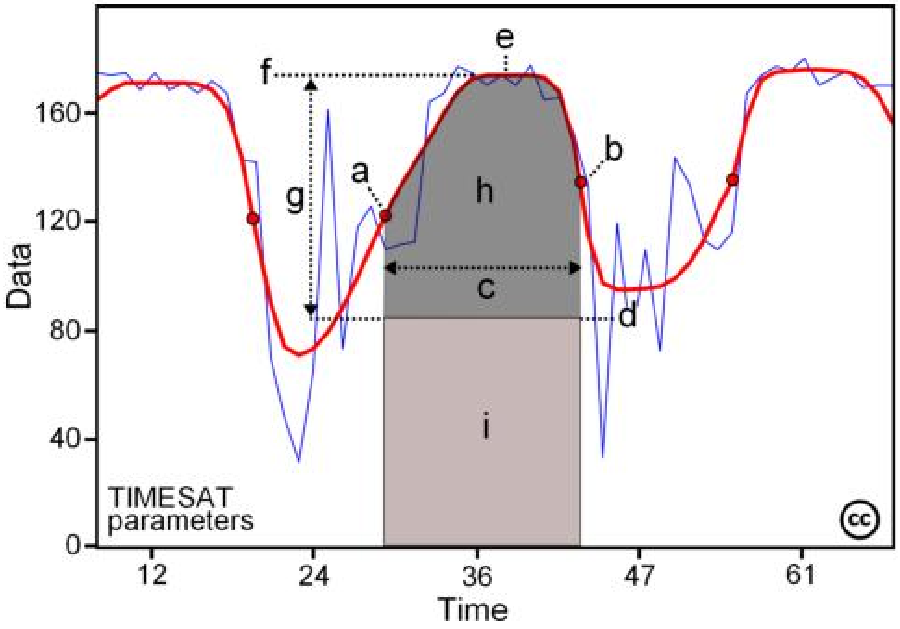


Figure 8: Seasonality parameters extracted in TIMESAT

Amplitude measures the total increase of greenness of vegetation when it rains. High increase is noted in Meru County with the least change occurring at the border of Garissa and Isiolo county and in Mt. Kenya. Since Meru county is an agricultural area the high increase in greenness is as a result of crop grown during the rainy season. In Garissa and Isiolo where least change is observed, it is as a result of bareland with little vegetation that characterizes the area. High maximum NDVI during the season is noted in Lamu county where we have Mangroove forest as well as the Mboni forest that is characterized by savannah vegetation. Beginning, end and middle of the season have the same pattern in all the counties. Largely Isiolo county is covered by vegetation that hardly responds to increase in greenness describing an area covered by shrublands that are ever green through all the season or bareland area. Meru and Tana River County largely record increase and decline of greenness within the same period describing similar vegetation type. Even though Tana River depend mainly on pastoralism, they also practice agricultural farming during wet seasons as indicated by beginning and end of season. Apart from Meru county and the coastal region in Lamu county, the region has short length of seasons which is a characteristic of arid regions. The rains do not last longer periods.

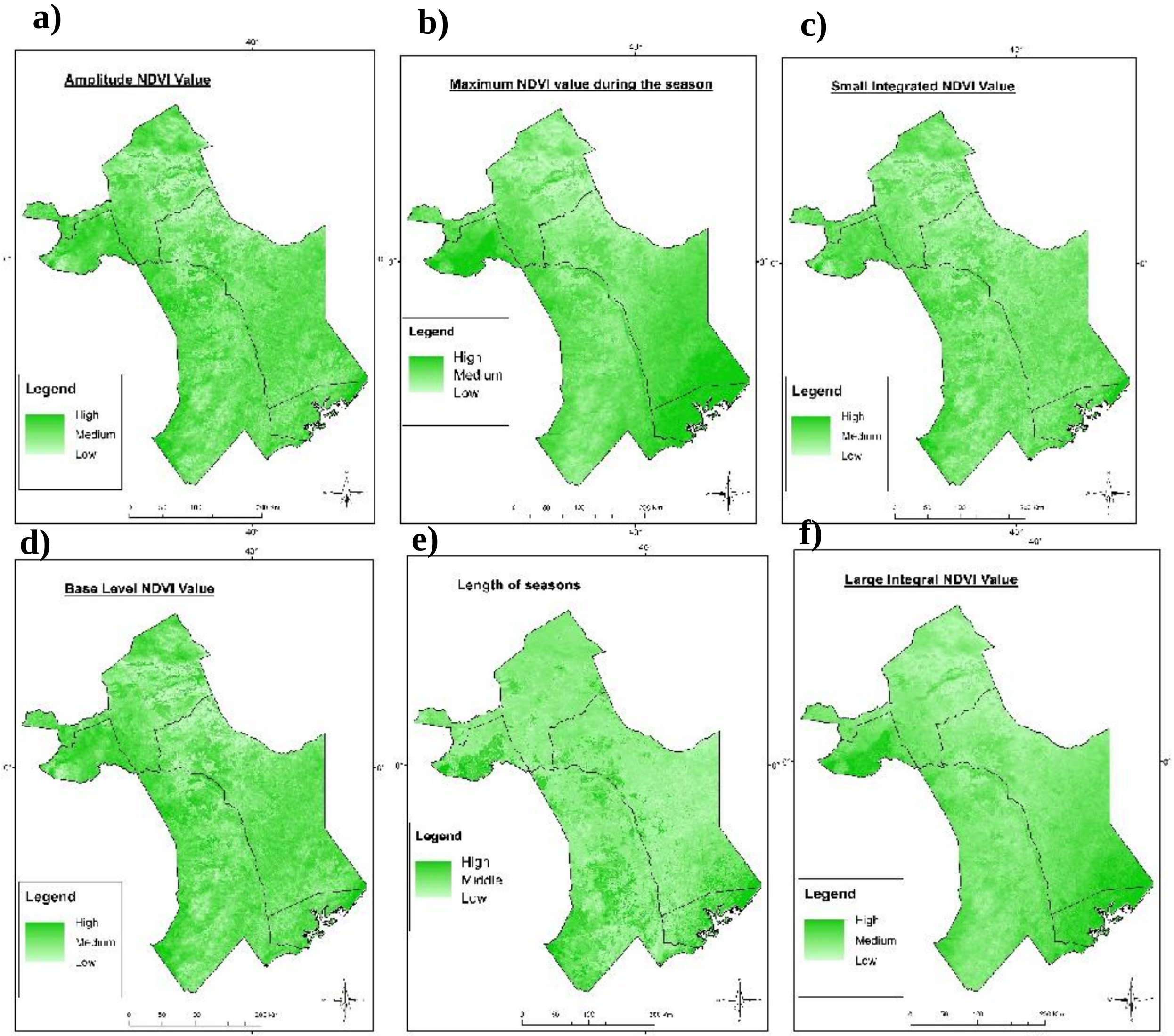


Figure 9:Maps of seasonality parameters from NDVI spanning from 2001-2015 extracted from TIMESAT represented by a) Amplitude, b) Maximum NDVI value in the season, c) Small integral value, d) Base NDVI value, e) Length of season and f) Large integral value

4.2 Evapotranspiration characteristics

To reduce data dimensionality and multi-collinearity but at the same time maximizing on the variance in the data (Mosomtai et al. 2016; Mu, Zhao, and Running 2005), first and second component for evapotranspiration (ET) were obtained from principal component analysis. The two component describe 99% of the variance in the data. ET represents the sum of water lost via transpiration and evaporation from surface water bodies and soils. It is highest in summer and regions closer to the equator because of high levels of solar radiation (Mu, Zhao, and Running 2005). Figure 11 represent the two component whereby the first component (PC1) is orthogonal to the second one (PC2). This means that the variance that were not captured in the first component is captured in the second. High variability in ET is represented by the red color while the green represent no change. There were no clear patterns in PC1as compared to PC2.

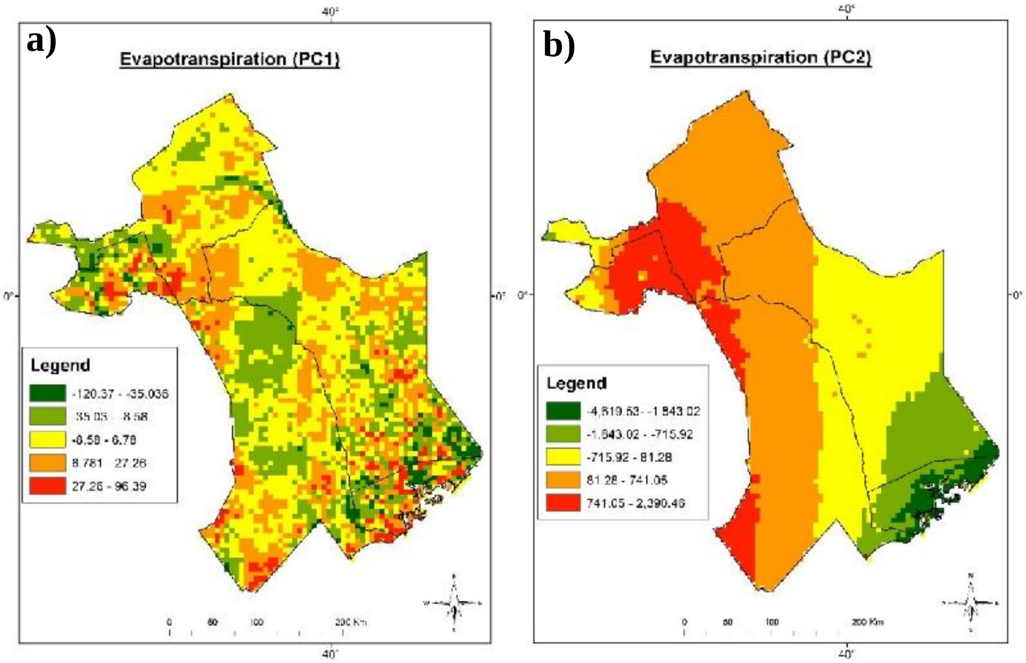
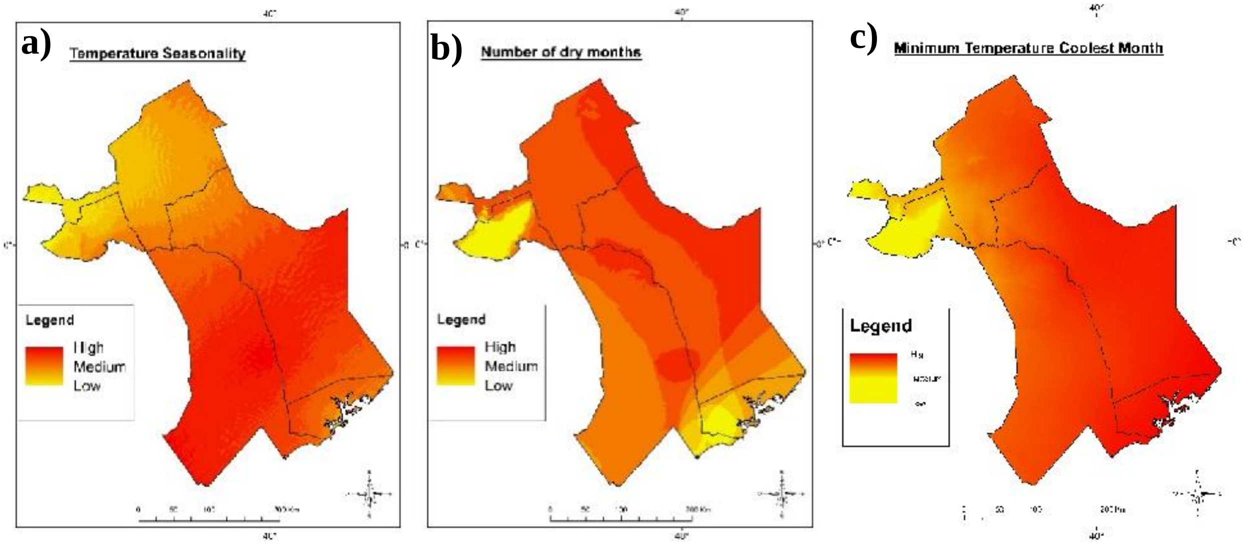


Figure 10: Map of the first a) and second b) principal components of evapotranspiration

Pockets of high ET variability is noted across the study area in PC1 with medium variability represented in Yellow to Orange color largely covering the area. In PC2, highest variability occurs at the slopes of Mt. Kenya at Meru and Isiolo County with least variability occurring at Lamu county.

4.3 Climatic characteristics

Temperature variability in wet and dry season are lowest in Meru and Isiolo county but highest in Tana river and Garissa county. The minimum temperature during the coolest month which is July, is lowest in Mt. Kenya and Meru county while highest in Garissa, Tana River and Isiolo counties. Due to aridity of Garissa, Tana River, Lamu and Isiolo counties, the temperatures there are still higher compared to Meru county. The high temperature influences the vegetation type and the amount of evapotranspiration especially during excessive rainfall. Garissa and Isiolo county have the longest number of dry months in a year compared to Meru and the border of Lamu and Tana River county county at Tana River delta (figure 14). Like the temperature characteristics, the highest rainfall during the wettest and driest month is in Meru County while the rest of the study area receive low rainfall. Isiolo receives the least amount of rainfall during the driest quarter while Meru receives the highest.



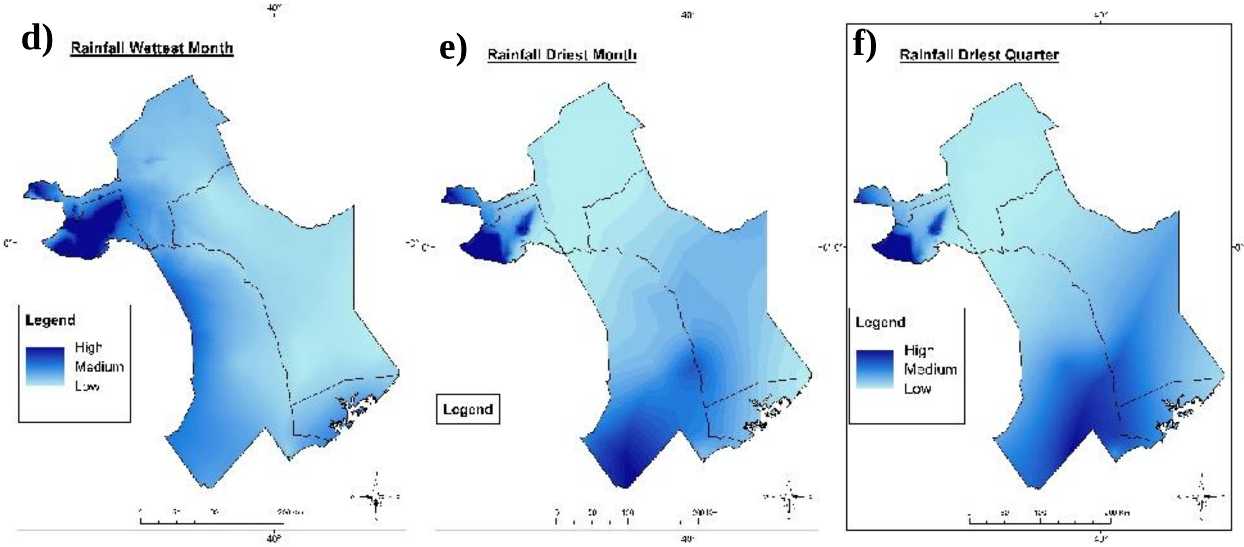


Figure 11: Maps showing climatic characteristics of the study area whereby a) Temperature seasonality, b) Number of dry months c) Minimum temperature coolest month, d) Rainfall wettest month, e) Rainfall driest month and f) Rainfall driest quarter

4.4 Topographic characteristics

Topographic wetness index (TWI) estimates predicted water accumulation in a region from an uphill area. TWI has been used to estimate malaria risk caused by mosquitoes (Cohen et al., 2010). Garissa, Lamu and part of Isiolo and Tana River counties have the highest level of water accumulation.

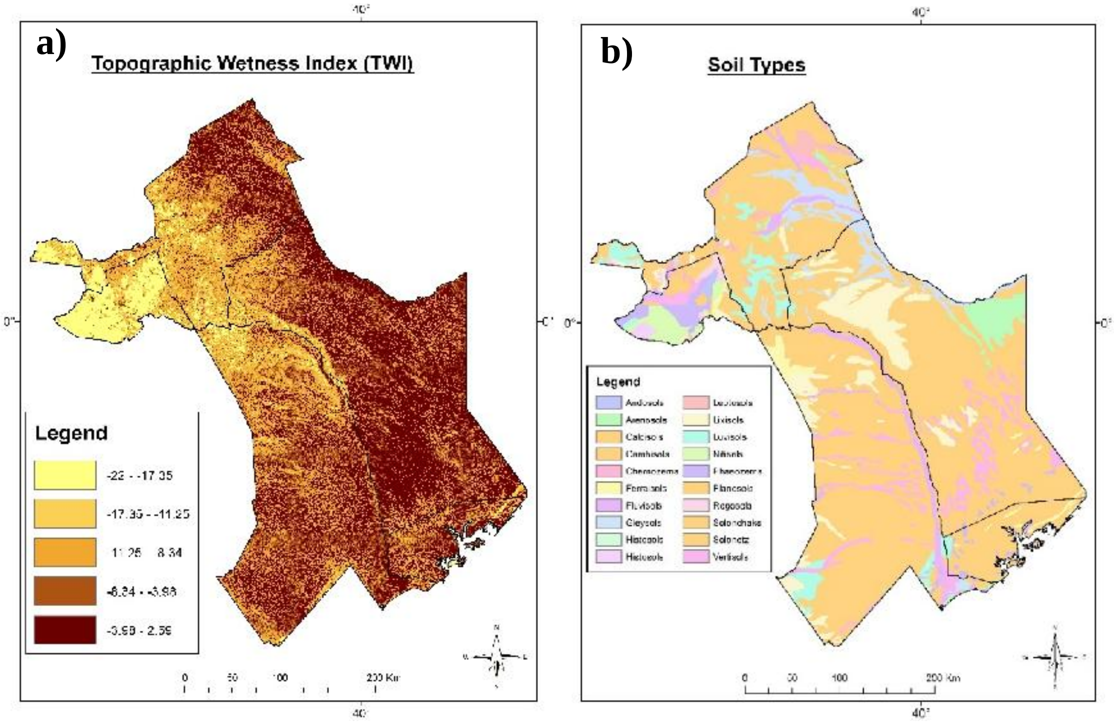


Figure 12: Maps showing TWI (a) and soil types (b) of the study area

The low lying topography allows for flooding and accumulation of water in dambos which are suitable habitats for mosquitoes. Meru county and specifically Mt. Kenya has unsuitable area for water accumulations which is indicated by the low index. Soil types are also key determinant for mosquito habitats. Hydric soils which have high water rentention abilities elongates flooding periods. Tana River, Lamu, Garissa and Isiolo are largely covered by these type of soil types. Solonchanks, solonetz, calcisols, cambisols and planosols represented in brown colour in Figure 15 are dominant in these counties except in Meru county.

4.5 Home range estimation

Movement trajectory data of the collared herds were classified into three major groups namely; Garissa, Tana River and Isiolo herds represented in red, green and blue colour respectively as shown in figure 6. A total of 42,156 points were obtained during the monitoring period. Isiolo herds were spatial apart from each other while Garissa and Tana River herds were grazing together with similar movement patterns. Even though Garissa and Tana River herds were in different counties, some of the herds interacted together due to the shared Tana River which is a major source of water for the herds.

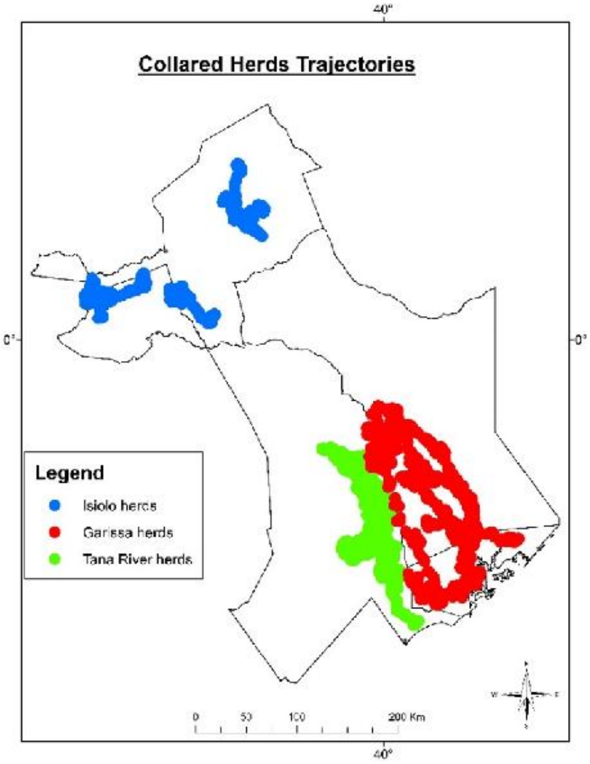


Figure 13: Trajectory map of the collared herds

Garissa herds had eight core areas which was defined by 50% space use; Bura, Hindi, Degurdei, Dondori, Masalani, Witu, Gedilun and Boni which was 18.4% of the total home range (figure 9). Herd 1172, 1175 and 1174 never interacted throughout the monitoring period. Their home ranges were confined around Hindi and witu for herd 1172 and Bura and Degurdei for herd 1175 and 1174. The rest of the herds moved freely from Bura and Degurdei to Witu, Hindi and Dondori having stop Overs at Masalani, Boni and Gedilun interacting with the herds that never moved. Herd 1179, 1177 and 1178 were in Hindi, Witu and Dondori respectively when collared in September 2012 until beginning of November 2012 before moving up North. Herd 1178 spent a year grazing in Gedilun which is part of Boni forest from April 2013 to March 2014, herd 1179 grazed in Boni between December 2012 to March 2013, June 2013 to August 2013 and November 2013 to January 2014. All these period were during the dry seasons. The same was true to herd 1177 which was in Masalani from June 2012 to August 2013 and December 2013 to January 2014. Notably, during the wet season throughout the monitoring period, the three herds were in Bura and Degurdei until the end of the season.

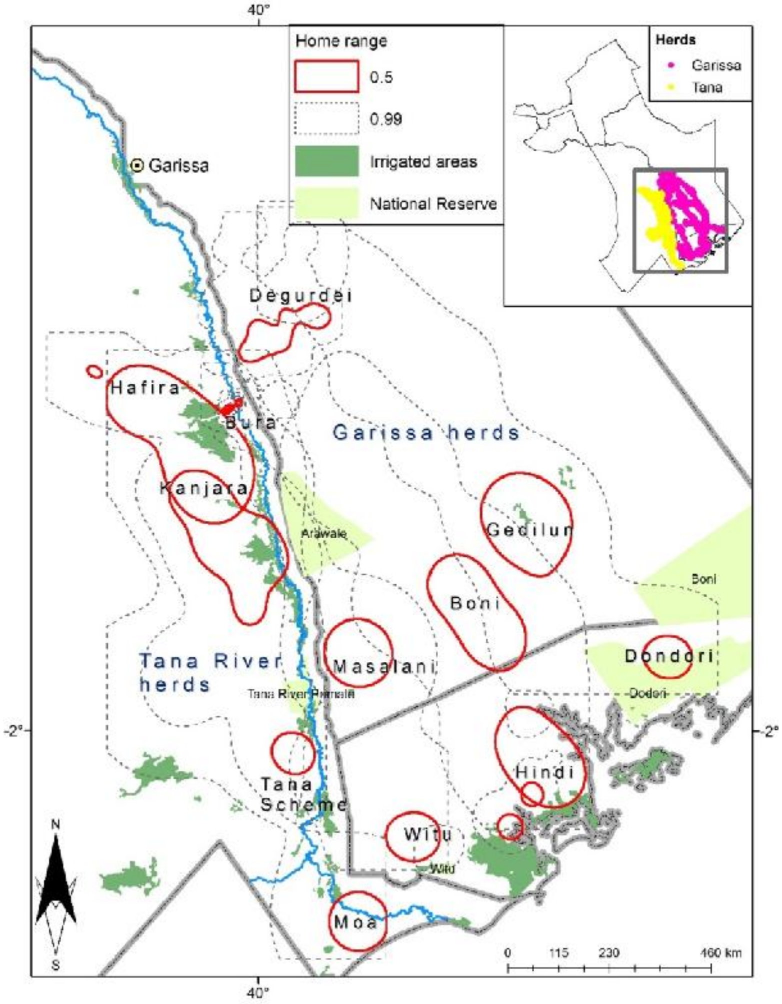


Figure 14: Home range map for Tana River and Garissa herds

Tana River herds also had similar pattern of movement even though in different county. When collared herd 4168 and 4169 were in Hafira, they moved to Kanjara during the short rainy period between November and December 2013. In January 2014, which is the beginning of dry season that last upto march, they moved south before going back to Kanjara at the beginning of wet season in April to June. From August they moved south again and herd 4169 spent three months grazing at Tana scheme while herd 4168 proceeded to Tana delta at Moa and graze there until end of the dry season. When the short rains began they went back to Kanjara again. The herds cover approximately 120km in search of pastures during the dry season. Herd 4168 for instance covered about 150km in 10days to get to Tana delta and when the short rains began they went back to Kanjara in less than 10days covering the same distance.

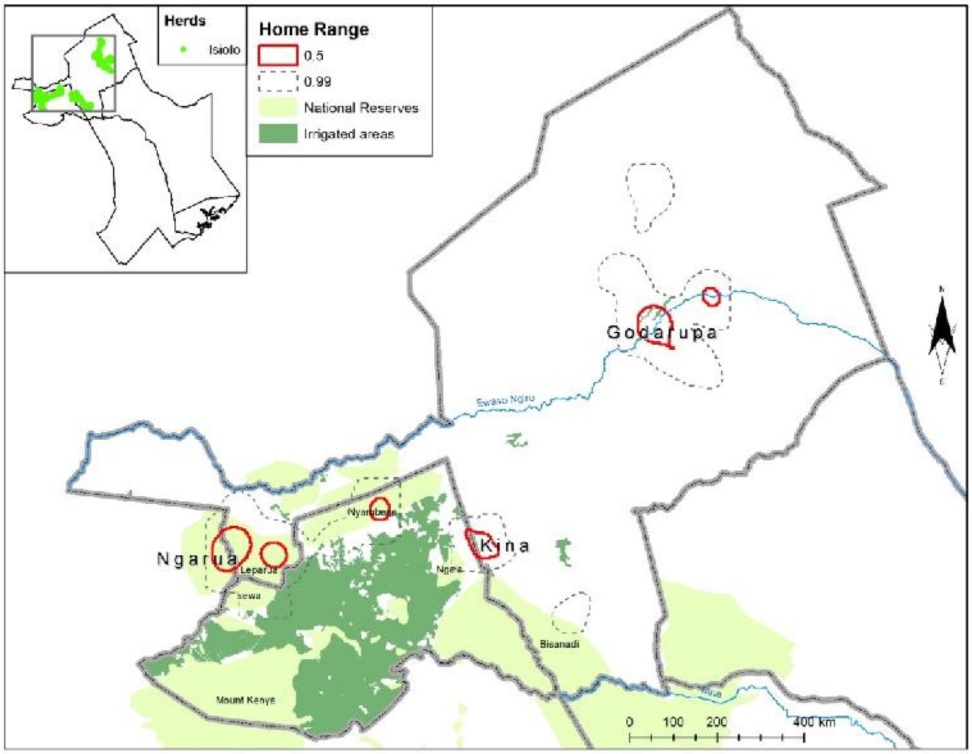


Figure 15: Home range map for Isiolo herds

Isiolo herds did not have a large home range as Garissa and Tana River herds. Herd 4006 grazed in Ngarua from the time it was collared until the end of June 2014, then it moved to Nyembene national reserve until the end of the dry season. The home range for the herd was within Leparua community conservancy, Lewa conservancy and part of Mt. Kenya national park traversing part of the irrigated areas. Herd 4167 home range was confined within Kina from September 2013 until December 2014 then it moved south when the dry season began and grazed around Bisandi national reserve. Herd 4170 grazed almost entirely at Godarupa in both seasons and moving either North, South or East during wet seasons and spending less than two months. The core grazing areas is within a large wetland in Merti with small pocket of irrigated land.

Movement of viremic animals has been known to be an amplifying factor during RVF outbreaks however quantifying its impact or understanding the dynamics of how it contributes in amplifying the disease is unclear especially in developing countries (Balenghien et al., 2013). Role of livestock movement especially as a result of trade in spreading diseases has been exemplified by a review done by Fèvre et al. (2006) and its effect quantified by Adkin et al.

(2016). Developed countries are in a better position in quantifying these dynamics due to established infrastructure which is not available in developing countries (Bajardi et al., 2011). Core grazing areas are the hotspot for virus infection and reinfection. These areas are distinctively used according to seasons, for instance Bura, Kanjara and Degurdei are core grazing areas for wet season while Gedilun, Boni and Dodori are used during dry season. This grazing strategy is similar to the one observed by pastoralist in East Darfur in Sudan where they move south on dry season and north on wet season. This is because the southern area gets too wet on rainy season while the northern part is wet enough to sustain their livestock. On dry season, the forage is available in the south when the north is too dry for their livestock (Young et al., 2016). Furthermore, infection rate within these core grazing areas varies depending on the season with high infection rate happening during the wet season. This reiterates several research that have demonstrated the importance of rainfall for transmission and maintainannce of RVF virus (ref). Interviews conducted by Ogara et al. (2014) showed that rainfall was a high risk factor identified by informants for RVF occurrence.

4.6 vector distribution

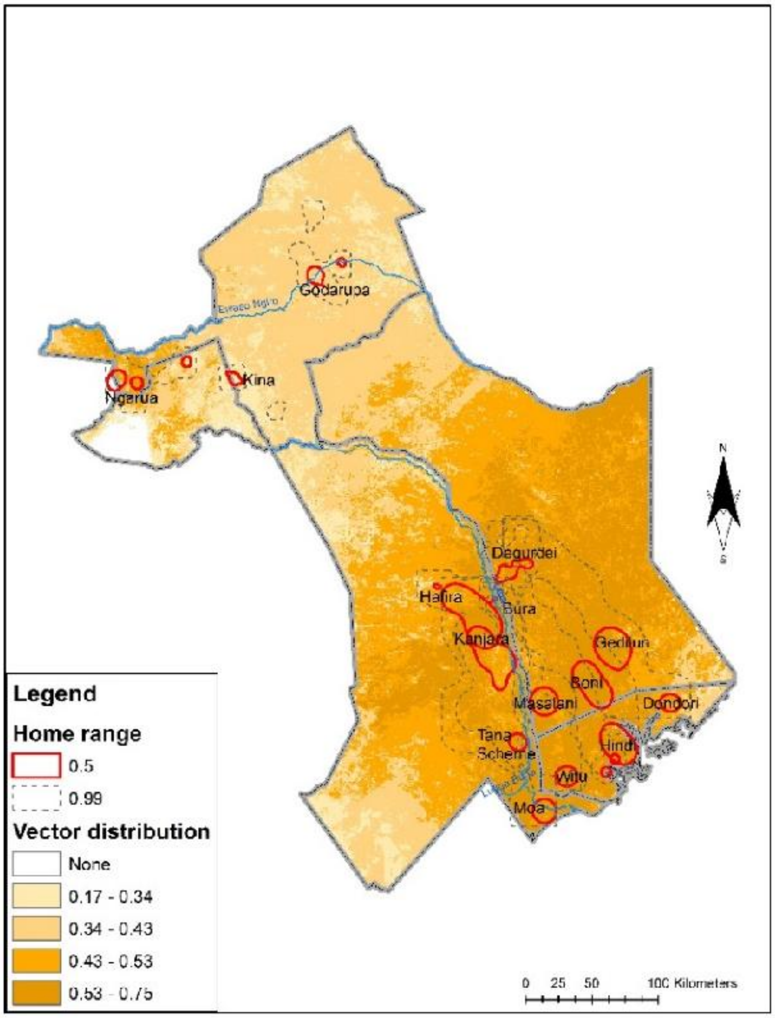


Figure 16: vector distribution map overlaid with cattle home range

A probability map of vector distribution was generated with and accuracy of AUC 0.76 (figure 16). The deep colour represents areas highly suitable for mosquito habitats while the light colour represents the least suitable habitats. Garissa, Lamu and Tana River counties are largely covered by suitable habitats for RVF vectors compared to Isiolo and Meru county while Mt. Kenya was mapped unsuitable vector habitat. All the core grazing areas are within highly suitable vector habitats except for Kina and Godarupa which had a lower suitability. Key environmental variables that contributed in defining the vector habitat in the model were; rainfall driest month (53.5%), evapotranspiration (23.7%), amplitude (13.7%) and maximum NDVI value in the season (7.5%) (table 5).

Table 5: variable contribution in mapping vector habitat

Variable	*Percent contribution*
Rainfall driest month	53.5
Evapotranspiration (PC2)	23.7
Amplitude	13.7
Max. NDVI value in the season	7.5
End of season	0.9
Mean temp. coolest quarter	0.6
Temperature seasonality	0.1
Middle of the season	0
Rainfall seasonality	0
Soil	0
Large integral	0
Small integral	0
Length of season	0

Suitability for mosquito habitat within the study area is high especially in Tana River, Garissa and Lamu counties. Diversity and abundance of mosquito vectors sampled at some of the occurrence points used in generating the vector distribution map are identified by Arum et. al (2015). He noted that more vectors were trapped during the rainy season especially the long rains compared to the dry season and this explains the high seroprevalence observed in the herds during the wet season. This is in line with key determinant of vector distribution identified by the model. Rainfall driest month contributed the most in defining the vector habitat which describes a semi-arid climatic conditions. The horn of Africa which is endemic to RVF is characterized by this type of climatic condition with mean NDVI ranging between 0.15 – 0.4 and mean annual rainfall of 100 and 800mm (Anyamba et al., 2009). All RVF outbreaks in Kenya since 1950 has been associated with abnormally high rainfall greater than 600mm in the semi-arid regions mostly occurring during El Nino rains (Anyamba et al. 2009; Murithi et al. 2011). *Aedes* eggs already infected through transoviral transmission can withstand harsh climatic conditions such that when it floods their population increases. During the interepizootic periods, water collecting in dambos maintains the *Aedes* population couple with human modification of landscape such as creation of irrigation schemes which mimics flooding events that occurs during El Nino (Mosomtai et al., 2016). The study area has several national irrigation schemes which is part of home range of the herds collared with Bura irrigation scheme being within one of the core grazing areas (Figure 4). Outbreaks in Egypt and Senegal for instant were related to human modification of landscape through creation of Aswan dam and irrigation schemes in the Nile river (Drake et al., 2013).

Evapotranspiration and vegetation seasonality variables (amplitude and maximum NDVI value of the month) were also key parameters in defining vector habitat. The rate of ET depends on solar radiation which is highest in semi-arid regions, soil moisture, vegetation type and stage development of the plant (Mu et al., 2005). The ET rate (flux) in the study area is maximum during El Nino periods due to water lost through surface water due to flooding and 'greening' of the vegetation. The savannah type vegetation in the study area experiences greener-than-normal vegetation conditions described by Hightower et al. (2012) and Anyamba et al. (2009) which is described in the model by the amplitude while the maximum development stage of the plant is described by the maximum NDVI value of the month. High humidity as a result of high ET rate provide suitable habitat for the vectors to thrive with the green vegetation creating resting grounds (Hightower et al., 2012).

4.7 Home range characteristics

Climatic conditions, vegetation seasonality, evapotranspiration and soil types were key spatial determinants within home ranges (p value < 0.05) (Table 7). Minimum temperature coolest month, length of the longest driest season, rainfall wettest month and rainfall driest quarter were significant climatic determinant while, maximum NDVI value, length of the season and large integral were significant phenological determinant of space by the herds. Notably, there were variabilities within home ranges between the herds from the same county and between counties. For instance, home ranges for Garissa herds were significantly influenced by rainfall driest month while it was not for all Isiolo herds especially herd 4170. Herds which were confined in one place throughout the monitoring period in Garissa (herd 1172, 1174, 1175) and herd 4170 in

Isiolo were similarly influence by vegetation seasonality, specifically amplitude and maximum NDVI value of the season. Space use for both Tana River and Isiolo herds were influence by evapotranspiration while it varied among herds in Garissa. Topographic Wetness Index only contributed to space use for herd 4169 and 4170 in Isiolo and herd 1178 and 1179 which moved north-south depending on the season in Garissa. 14 soil types were significant within the study area with Solonetz and Vertisols being the common soil type within all the home ranges. Isiolo herds grazed in diverse soil types (12) compared to Garissa (8) and Tana River (6) herds. Herd 1177 traverse within significant soil types when migrating north-south while confined herds grazed within significant soil types as well. From the results, determinants factors for favourable vector habitat are similar to the ones that determine core grazing areas for herds. This was further affirmed by the hypothesis results in Table 6 that indicate cattle core grazing areas were within suitable vector habitats

Table 6: Hypothesis results

County	*Herds*	*P values*
Isiolo	h4006	6.52E-14
	h4170	0.00949
	h4167	5.77E-07
Garissa	h1172	0.001437
	h1174	< 2.2e-16
	h1175	< 2.2e-16
	h1177	< 2.2e-16
	h1178	< 2.2e-16
	h1179	0.08451
Tana River	h4168	0.000796
	h4169	< 2.2e-16

Table 7: *P* values for explanatory variables in determining home ranges

	Isiolo				*Tana river*			*Garissa*			
Variables	***h4006***	***h4167***	***h4170***	***h4168***	***h4169***	***h1172***	***h1174***	***h1175***	***h1177***	***h1178***	***h1179***
(Intercept)	0.00	0.00	0.92	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00
Rainfall driest month	**0.01**	0.78	**1.00**	0.07	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**
Min. temperature coolest month	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	**0.01**	**0.00**	**0.00**	0.07
Temperature seasonality	**0.00**	0.07	**0.00**	**0.00**	-	**0.00**	0.22	0.30	0.80	0.59	0.23
Rainfall wettest month	**0.00**	**0.01**	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	0.61	**0.00**	**0.00**
Rainfall driest quarter	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	**0.04**	**0.00**	**0.00**	**0.00**	**0.04**
Base value	0.58	0.56	0.70	**0.01**	0.29	0.43	**0.03**	**0.00**	**0.00**	0.85	**0.00**
Number of dry months	0.08	**0.01**	**1.00**	**0.01**	**0.00**	**0.00**	NA	NA	0.05	**0.00**	**0.00**
Length of longest dry season	**0.00**	**0.00**	0.96	0.16	**0.00**	**0.00**	NA	NA	0.11	**0.00**	**0.00**
Amplitude	0.33	0.23	**0.00**	0.24	**0.01**	**0.00**	**0.00**	**0.00**	0.19	0.07	0.42
Max. NDVI value in the season	0.59	**0.02**	**0.00**	0.73	0.05	**0.00**	**0.00**	**0.00**	0.06	0.07	**0.00**
Middle of the season	0.11	**0.01**	0.27	**0.00**	0.29	**0.00**	0.23	**0.00**	0.42	0.54	**0.00**
Length of the season	**0.00**	**0.01**	**0.00**	**0.00**	0.16	**0.00**	0.08	**0.00**	0.69	0.46	0.46
End of season	0.85	0.33	0.39	**0.00**	0.57	0.15	0.48	0.25	0.03	0.33	**0.00**
Large integral	**0.00**	**0.02**	**0.00**	0.16	**0.00**	**0.00**	**0.03**	**0.01**	0.58	**0.02**	**0.00**

Evapotranspiration	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	0.69	0.37	**0.01**	**0.00**	**0.00**	0.07
Topographic Wetness Index	0.05	**0.00**	**0.00**	0.10	0.64	0.36	0.01	0.44	0.47	**0.00**	**0.00**
Gleysols	-	**0.00**	0.10	**0.01**	-	-	-	-	-	-	-
Luvisols	-	-	-	0.74	-	-	-	-	**0.00**	-	-
Phaeozems	**0.00**	-	-	**0.00**	-	-	-	-	**0.00**	0.91	0.59
Planosols	-	-	0.28	**0.00**	-	**0.00**	0.61	-	**0.00**	0.45	0.87
Solonetz	-	**0.00**	**0.00**	0.23	0.15	-	**0.02**	**0.00**	**0.00**	**0.00**	**0.00**
Vertisols	**0.00**	-	-	0.47	**0.00**	-	0.12	**0.00**	**0.00**	**0.00**	**0.01**
Ferralsols	-	**0.00**	-	-	-	-	-	-	-	-	-
Nitisols	-	**0.00**	-	-	-	-	-	-	-	-	-
Regosols	**0.00**	0.15	-	-	-	-	-	-	-	-	-
Cambisols	**0.00**	-	-	-	-	-	-	-	-	-	-
Chernozems	0.89	-	-	-	-	-	-	-	-	-	-
Fluvisols	0.37	-	-	-	-	-	-	-	-	-	-
Lixisols	**0.00**	-	-	-	-	-	0.07	-	-	-	-
Lleptosols	-	-	-	-	-	-	-	-	**0.03**	-	-
Solonchanks	-	-	-	-	-	-	-	**0.00**	-	-	-

Pastoralist migration and space use for cattle grazing were determined by similar factors as the vector habitats. Their movement are driven by availability of water and pasture which is clearly demonstrated in the model by the significant variables (table 3) (FAO, 2009). Rainfall wettest month and rainfall driest quarter influences space use differently; during wet season green vegetation is available within the study area and this is described by the large integral and maximum NDVI value of the season while the water is accessible due to flooding and dambos hence the limited cattle movement, however, during the dry season the herds move to location where the vegetation is greener than the surrounding area and the accessible water are mostly the dambos and according to Arum et al., (2015) most of them settle around this dambos. From the collared herds during wet season they were at ‘home’ (Bura, Kanjara, Degurdei, Ngarua) while during dry season they migrate further to Dodori, Boni, Witu and Gedilun. Pastoralism is the main source of livelihood to many people living in the semiarid region in the horn of Africa.

Their grazing strategies which is passed on from generation to generation is no longer sustainable due to adverse effects of climate change. The collard herds had a clear pattern of defined core grazing areas during wet and dry season which is similar to the one identified by Young et. al (2016) in Darfur, Sudan. Length of the longest dry season which mostly occurs during the drought periods results to over use of core grazing areas and longer distance covered in search of pastures. Suitable vector habitats even during dry season coincide with core grazing areas, this makes herds susceptible to mosquito bites which enable the vectors to lay eggs and transmit the virus (Owange et al., 2014). 14 suitable soil types were identified that defined space use with Solonetz and vertisols being the common soil type in all the home ranges. The hydric nature of these soil provide suitable habitat for *Aedes* to lay the eggs (Kiplimo et al., 2014; Sindato et al., 2014). Interaction of the herds with wildlife also increases their susceptibility to RVF, for instance, Dodori which was one of the core grazing areas during dry season, is a national reserve while the herds in Isiolo grazed in several national reserves. Wildlife such as buffalo has been tested positive with RVF antibodies (Britch et al., 2013).

CHAPTER FIVE: CONCLUSION AND RECCOMENDATION

5.1 Conclusion

In developing countries, unregulated cattle movement is the biggest threat to spread of infectious disease especially from countries where political instability exist (Fèvre et al. 2006). The 2000 RVF outbreak in the Saudi Arabia and Yemen is reported to have been introduced by smuggled livestock from Somalia according to Shawky (2000). It is estimated that ~75,000 cattle move from Somalia to Kenya annualy and due to collapse government infrastructures, there no export controls measure hence diseases known to have been circulating in Somalia are introduced to Kenya (Fèvre et al. 2006, FAO 2004). FAO (2009) noted that there is also biasness in policy development regarding managing zoonotic diseases whereby emphasis are placed on movement of viremic animal at international level and continue to receive attention from policy makers and researchers leaving out local movement.

Furthermore, only commercial livestock are able to live up according to international regulation requirements which is not the case for pastoralist community in developing countries (FAO 2004). Most of them cannot afford vaccines coupled with their cultural practices that constantly keep them in close contact with animals making them the most vulnerable communities to zoonotic diseases (Abdi et al. 2015). In most developing countries, the cost of preventing diseases like vaccination has proven to be high which has forced many national institutions to respond to crises instead of focusing on prevention (FAO, 2009). In Kenya for instance, during RVF outbreaks livestock movement is banned however there is no restriction during enzootic periods which could potentially be the vital time when the virus is encroaching new ecologies (Mosomtai et al., 2016)

This research aimed at understanding the role of cattle movement and their interaction with vectors in maintaining and transmitting RVF virus along their migratory routes. We hypothesized that cattle core grazing areas are within suitable vector habitats therefore they are continually bitten while grazing allowing the vector to lay fertilized eggs that will hatched in flooded environment. This was achieved by mapping suitable vector habitats and cattle home ranges. Furthermore, home range characteristics were determined using the following environmental variable, seasonality parameters from NDVI, bioclimatic variables and topographic parameters that involved topographic wetness index and soil types. In defining cattle home ranges telemetry data from collared herds in Garissa, Tana River and Isiolo counties were used. Kernel density estimator was used to estimate home range while generalized linear model was used to identify space use determinants. Vector habitat was mapped by using sample occurrence data in the study area. Using Maxent which is a machine learning technique, the sample occurrence data was used to identify similar environmental characteristics within the study area and their probability of suitability.

Core grazing areas were defined by 50% space used. Garissa herds had eight core areas which was only 18.4% of the total home range. Some of the herds never interacted throughout the monitoring period. Their home ranges were confined in Lamu and Garissa county however the rest of the herds moved freely from Garissa to Lamu county having stop Overs at Masalani, Boni forest and Gedilun and coming in contact with the herds that never moved. The Tana River herds also had similar movement pattern as Garissa herds even though they were in different county. During the dry season the animal migrated south to Lamu county and during wet seasons they moved up north in Garissa county. Notebly, some of the core grazing areas during dry season included Dondori game reserve, Tana River delta and Boni forest. In Isiolo, core garzing areas in dry season were in Lewa conservancy, Nyambene national reserve and Leparua community conservancy. Garissa, Lamu and Tana river counties are largely covered by suitable vector habitats therefore most of the core grazing areas identified were within highly suitable vector habitats. Climatic, phenology and topographic characteristics were important variables in defining vector habitats, similarly, these variables were also determinant factors for core grazing areas for cattle.

Animal movement is a risk path way for animal-animal transmission along their migratory routes. This is evidently shown by interaction of migrating herds with both herds that were confined in Lamu and Garissa county. Migrating viremic herds can introduce RVFV in new regions with suitable vector habitats when they come in contact with other herds. Wildlife are known reservoirs for RVFV. Some of the core grazing areas identified are within national reserves therefore, livestock are susceptible to infections in search areas. Also, large irrigation schemes in Tana Delta mimics similar conditions as flooding which maintains vector population throughout the seasons.

Pastoralist migration pattern and space use for cattle grazing are determined by similar factors as the vector habitats. Their movement are driven by availability of water and pasture. Climate change continues to be an important factor that determines pastoralist behaviour and occurrence of RVF. Long dry seasons will increase distance moved by pastoralist in search of pastures and perhaps forcing them to stay longer in national reserves hence increasing the exposure of livestock to RVFV. Also, the vector ecology is expanding especially when the humid regions become warmer due to climate change.

5.2 Recommendation

There is need to give equal attention to movement of livestock as a result of pastoralism apart from trade. The is a high potential of spread of the virus undetected far and wide if no policies are put in place and regular vaccination of animals especially in cross border migration. For pastoralist, vaccination should always be administered in core grazing areas just before the rainy season starts. This will reduce chances for animal spreading the virus along it's migratory route. Vector control such as spraying should be administered in this core grazing areas since they are equally suitable habitat for mosquitoes. Government veterinary services should be funded more and the legislation governing the livestock sector should be updated for regular inspection of animals to reduce movement of viremic animals especially during inter-epizootic periods. Pastoralist should also call a veterinarian even in remote rural areas when they see symptoms of RVF.

To improving RVF early warning systems and disease surveillance in developing countries, models should incorporate movement of animal. Even though most developing countries do not have infrastructure in place to monitor movement of individual cattle, earth observation technology, specifically GPS tracking provide a potential that can be explored further. Recent models have also failed to accurately pinpoint the location and timing of the next epidemic. This calls for collaborative research efforts that attempt to combine serological, climatic, and ecological data for greater area prediction models that will bridge the uncertainty in RVF spatial and temporal patterns. If a warning is issued, countries have the power to prioritize and prepare, enabling proactive prevention like vaccination versus a reaction to fight an epidemic.

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