

**RISK ASSESSMENT OF Q FEVER IN CATTLE KEEPING PASTORALIST
HOUSEHOLDS IN KAJIADO COUNTY, KENYA**

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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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DEDICATION

This work is dedicated “unto Him that is able.....” to my Parents Peter Marogo and Rhoda Kwamboka and to my siblings Janet, Amos, Dinah and Deborah. Thank you and May God bless you

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LIST OF ABBREVIATIONS

CAC	Codex Alimentarius Commission
CFSPH	Center for Food Security and Public Health
CFT	Complement Fixation Test
EFSA	European Food Security Authority
ELISA	Enzyme-Linked Immunosorbent Assay
FAO	Food and Agriculture Organization
IFA	Indirect Fluorescent Antibody test
KNBS	Kenya National Bureau of Statistics
LCV	Large Cell Variant
LPS	lipopolysaccharide
OIE	World Organization for Animal Health
PCR	Polymerase Chain Reaction
Ph	Potential of Hydrogen
SCV	Small Cell Variant
SDC	Small Dense Cells
UV	Ultra Violet
WHO	World Health Organization

ABSTRACT

Q fever (*Coxiella burnetii*) is an old zoonotic disease, believed to be widely present in ruminant populations worldwide. It is an occupational disease and like many animal diseases, it is likely that farm management practices have a direct impact on the presence and spread of Q fever within and between herds and to humans.

The current study was conducted to assess the health risk associated with Q fever infection in pastoralist households in Kajiado County, Kenya. The study carried out was specifically: 1) to identify potential exposure pathways for Q fever infection to pastoralist household members and; 2) to assess risk associated with Q fever infection in pastoralist households through the identified pathways in households with infected cattle. Data for the risk assessment were obtained from literature and a field survey conducted in three sub-counties in Kajiado County, namely, Namanga, Mashuru, and Ngong'. These study sites were purposively selected for the study based on the availability of livestock at the time the study was conducted in the month of November to December 2013. Selection of cattle in the selected sub-counties depended on availability of pasture and water and information provided by the local veterinarian personnel. A two-stage sampling method was used to select the villages with cattle herds in the selected sub-counties. Eighty-four cattle herds were randomly selected in the three sub-counties. A structured questionnaire was administered to household heads via personal interviews to collect data on their livestock management practices. Data collected on livestock management practices were used to identify the transmission pathways for Q fever infection to pastoralist household members.

A qualitative risk assessment was carried out to assess the health risk associated with Q fever using the Codex Alimentarius Commission framework, which comprises of hazard identification, hazard characterization, exposure assessment and risk characterization.

Two major transmission pathways, inhalation and ingestion, were identified. An event tree was constructed to show steps in the potential pathways that lead to human exposure to the pathogen, *Coxiella burnetii*, which causes Q fever. A risk assessment was then performed using data from the household questionnaire and secondary data from literature and other sources. The potential exposure pathways were identified including: Inhalation pathway through assisting during a reproduction event and without protection; Inhalation pathway through not cleaning/disinfecting boma/site after a reproduction event; Inhalation pathway through accumulation of animal waste/using it in the farm; and Ingestion pathway through consumption of contaminated raw milk. Risk associated with Q fever infection by pastoralist household through the identified pathways in households with infected cattle was estimated as: high in inhalation pathway through assisting during a reproduction event and without protection, and through not cleaning/disinfecting bomas/calving sites after a reproduction event; medium in inhalation pathway through accumulation of animal waste; and high, medium and low for Namanga, Mashuru, and Ngong, respectively, in ingestion of contaminated raw milk. Poor hygiene (self and that of the environment), ingestion of unpasteurized milk and its products and handling/assisting in any reproduction event without protection were among the identified steps through which the household members were exposed to the pathogen.

It is recommended that awareness of the disease Q fever among pastoralists should be enhanced. This will promote reduction of environmental contamination, pathogens spread and limit the risk to the public. The community should be educated on the various symptoms of the disease and the control measures that they can practice to reduce exposure to *Coxiella burnetii*.

CHAPTER ONE

1.0 INTRODUCTION

1.1 BACKGROUND INFORMATION

Q fever is an occupational zoonosis (Maurin and Raoult, 1999), caused by a gram negative obligate intracellular bacterium called *Coxiella burnetii* (Tissot-Dupont and Raoult, 2008). The bacterium is classified in the *Coxiellaceae* family in the order *Legionellales* of the *gamma* subdivision of *Proteobacteria* (Wilson *et al.*, 1989). In 1935, Q fever was first described by Derrick in Queensland Australia after an outbreak of a febrile illness among abattoir workers. It was named as “query fever” because the disease was of unknown origin and in 1937 Burnet and Freeman isolated the etiological agent and identified the organism as a *Rickettsia* species (Derrick, 1983). The disease can affect the general population living near infected herds or environment (van der Hoek *et al.*, 2010). The organism is highly resistant to environmental conditions (can persist up to 4 months in the environment) including drying, many common disinfectants and heat (Van Woerden *et al.*, 2004; Maurin *et al.*, 2007). The bacterium can be spread by wind and it is highly infectious by the aerosol route (Maurin and Raoult, 1999; EFSA, 2010). The ability of the organism to remain infectious in the environment for months increases the risk of spread to humans as its transmission is airborne.

The host range for *Coxiella burnetii* includes wild mammals, birds, arthropods (ticks), domestic mammals and reptiles (Arricau-Bouvery and Rodolakis, 2005). Sheep, goats, and cattle have been known to be sources of human infection as they are reservoirs of *Coxiella burnetii* (Rodolakis, 2006; Rodolakis *et al.*, 2007).

Q fever infection is transmitted from animal hosts to human hosts through inhalation of infected aerosols, ingestion of contaminated raw milk and dairy products (Arricau-Bouvery *et al.*, 2006) and contact with body fluids from an infected reservoir host (Rahimi *et al.*, 2011).

The disease in humans varies from asymptomatic seroconversion (60%), self-limiting febrile episodes to hepatitis or pneumonia (Maurin and Raoult, 1999; EFSA, 2010). The illness is generally characterized by endocarditis in chronic form, and sometimes can have a lethal outcome. Q fever also decreases the quality of life of the patients and causes severe levels of fatigue (Limonard *et al.*, 2010; Morroy *et al.*, 2011). In contrast, in ruminants *C. burnetii* infection is usually asymptomatic and diseased animals can shed intermittently the pathogen in faeces, urine, and milk and birth products. In ruminant herds clinical symptoms are largely represented by reproductive disorders, such as abortion, premature birth, dead or weak offspring, and infertility (Angelakis and Raoult, 2010; EFSA, 2010)

To date, Q fever occurrence studies in Kenya are limited especially in pastoralists' communities. The pastoralists' livelihood is in livestock and hence they have a very close association with their livestock. The current study aimed to fill the knowledge gap on the associated health risk of Q fever in both livestock and humans.

1.2 OBJECTIVES

1.2.1 General objective

The overall objective of this study was to assess the risks associated with Q fever infection in members of pastoralist households in Kajiado County.

1.2.2 Research questions

1. What are the potential pathways of exposure to Q fever infection to pastoralist household members?
2. What is the risk associated with Q fever infection in pastoralists household members through the identified pathways?

1.2.3 Specific objectives of the study were to

1. Identify potential exposure pathways for Q fever infection to pastoralist household members in Kajiado County.
2. Assess risk associated with Q fever infection by pastoralist households through the identified pathways.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Epidemiology of *Coxiella burnetii*

2.1.1 Etiology

Q fever is caused by *Coxiella burnetii*, a small, gram negative pleomorphic coccobacillus, obligate intracellular bacteria. The organism lives and replicates in monocytes and macrophages (Angelakis and Raoult, 2010).

2.1.2 Lifecycle of *Coxiella burnetii*

Coxiella burnetii enters the animal host and it is phagocytosed by macrophages. The ability to invade and grow within macrophages and monocytes is critical for its spread in different niches of the host. The organism can survive and divide in an acidified environment, the phagolysosome (Figure 2.1). Different genes are expressed by the large and small forms of the bacteria that enables it to survive in an environment that is acidified (Arricau-Bouvery and Rodolakis, 2005).

The cycle begins with entry of the spore in the eukaryotic cell causing acidification of the endosome of the phagosome. The small-cell variant (SCV) multiplies by transverse binary fission and differentiates to large-cell variants (LCV). Then the endosome fuses with the lysosome resulting in acidified phagolysosome. Multiplication of LCV occurs by transverse binary fission, then the LCV differentiates to SCV and polar endospore develops in LCV. Subsequently the SCV and spore are released out of the cell (Arricau-Bouvery and Rodolakis, 2005).

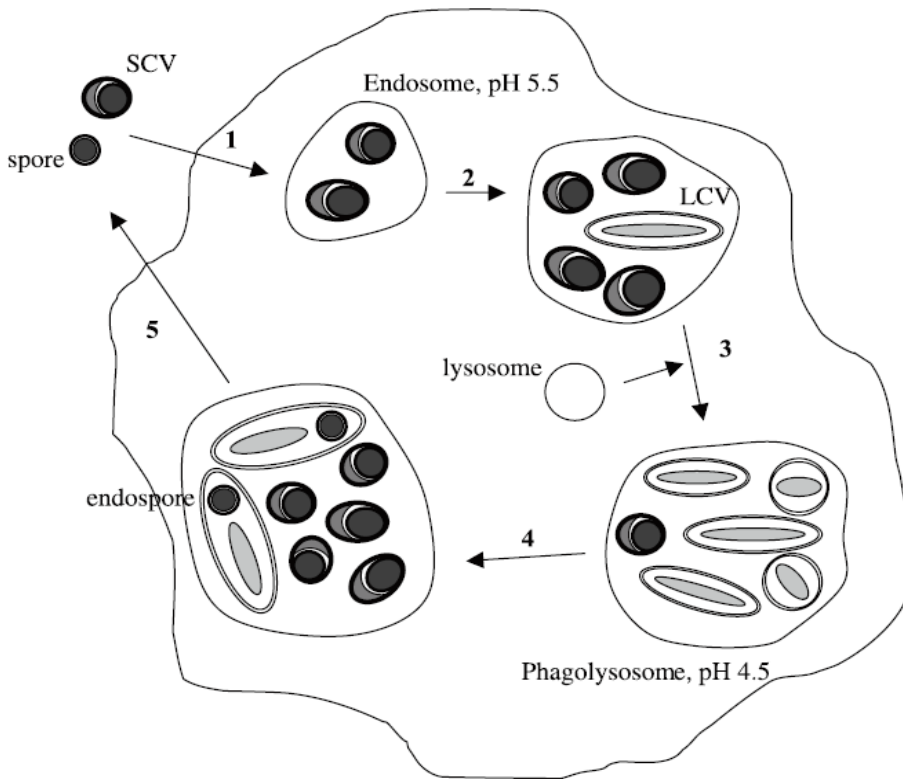


Figure 2.1: Lifecycle of *Coxiella burnetii*, causative agent of Q fever in macrophage/monocyte host cell (Arricau-Bouvery and Rodolakis, 2005)

Legend:

SCV- Small Cell Variant

LCV- Large Cell Variant

2.1.3 Developmental cycle and antigenic forms of *Coxiella burnetii*

The existence of *Coxiella burnetii* developmental cycle variants include the large cell variant (LCV), small cell variant (SCV) and small dense cells (SDC). They attribute to its ability to produce a small, dense, highly resistant spore-like form that is highly stable in the environment (McCaul and Williams, 1981; Coleman *et al.*, 2004). Small cell variant and SDC represent the metabolically inactive, extracellular and infectious forms of bacteria that can survive relatively extreme environmental conditions. The SCV is resistant to low or high Ph, heat, desiccation, (McCaul and Williams, 1981), pressure of up to 20,000ib/in², osmotic shock, UV light, chemical products such as ammonium chloride and disinfectants such as 0.5% sodium hypochloride (Heinzen *et al.*, 1999; Van Woerden *et al.*, 2004). The LCV undergoes sporogenic differentiation as it is the metabolically active form of the bacteria to produce spore-like forms that are highly resistant (Maurin and Raoult,1999) . The small-cell variants are highly stable in the environment (Angelakis and Raoult, 2010).

Coxiella burnetii exists in two antigenic forms, namely, phase I and phase II. They are morphologically identical, but differ in some biochemical characteristics including their lipopolysaccharide (LPS) composition. Phase I bacteria have a complete lipopolysaccharide (LPS) structure; it induces production of inflammatory cytokines in murine and human macrophages because it has an endotoxic activity. Phase II bacteria are produced by spontaneous mutations or large genetic rearrangements that result in the synthesis of truncated forms of LPS, which lack branched-chain sugars virenose and dihydrohydroxystreptose present in phase I LPS (Dellacasagrande *et al.*, 2000; Hoover *et al.*, 2002).

Phase I is highly infectious, whereas phase II is spore like and less infectious. *Coxiella burnetii* organisms isolated from infected animals or humans express phase I antigens and are highly infectious. Organisms expressing phase II antigens are less infectious and are recovered after the bacteria are passaged repeatedly in cell cultures or eggs. Experimentally, infected animals first produce antibodies to phase II antigens and later produce antibodies to phase I antigens (Maurin and Raoult, 1999).

2.1.4 Occurrence and modes of transmission

Q fever is an occupational zoonosis, though it can also affect the general population living near infected herds or environments (van der Hoek *et al.*, 2010). It has a worldwide distribution except in New Zealand where it has not been reported (Maurin and Raoult, 1999). A high level of exposure to *C. burnetii* has been indicated in Sub-Saharan Africa. This is in accordance to studies conducted that have reported a prevalence of *Coxiella burnetii* antibodies to range between 17- 37% (Kelly *et al.*, 1993; Mediannikov *et al.*, 2010) Several studies conducted in Africa i.e. Togo, Mali, Tanzania among others have indicated seropositivity in individuals tested (Steinmann *et al.*, 2005; Dean *et al.*, 2013; Prabhu *et al.*, 2011).

An investigation carried out in 50 travelers in Kenya who visited Maasai Mara showed that 8% (four) of the travelers contracted Q fever (Potasman *et al.*, 2000). Two of these cases further developed symptomatic infection and the remaining two had asymptomatic illnesses. This study also reported that the prevalence of antibodies to *C. burnetii* among Kenyan populations ranged from 10% to 20%. Moreover, various studies conducted in both pastoral and small holder farmers' regions in Kenya indicate occurrence of Q fever

among human and livestock populations (Knobel *et al.*, 2013; DePuy *et al.*, 2014; Muema *et al.*, 2017).

The host range of *Coxiella burnetii* includes many domestic, wild mammals and non-mammals, e.g. birds, reptiles and fish (Maurin and Raoult, 1999; Cutler *et al.*, 2007). The primary reservoirs of infections for man are domestic ruminants, mainly cattle, sheep and goats (Maurin *et al.*, 2007). Although rabbits, dogs and cats are not the major hosts of the pathogen, they can be infected and also transmit the infection to humans (Buhariwalla *et al.*, 1996).

An outbreak occurred in Switzerland where children over 15 years of age were found to be five times more likely to experience symptomatic infection relative to the younger ones less than 15 years of age (Raoult *et al.*, 2005). The study by Dupuis *et al.*, (1985) showed that young age seemed to be protective against *C. burnetii*. The clinical cases in children were shown to be equal in both girls and boys but at puberty the ratio changes whereby boys were more susceptible. The protective role of 17β - Estradiol which controls host responses to *Coxiella burnetii* could explain this. This has been validated in mice (Leone *et al.*, 2004; Tissot-Dupont *et al.*, 2007). This further explains why men are more often symptomatic than women, though they have equal seroprevalence. Thus, this shows that in the pathogenesis of Q fever gender and age play a role (Angelakis and Raoult, 2010; Gikas *et al.*, 2010).

Transmission to humans occurs mainly through inhalation of aerosols or dust contaminated with faeces of the infected animals, birth products, urine and through ingestion of raw milk and its products. Therefore, Q fever is mostly reported among people working with livestock.

Q fever is an occupational disease associated with the exposed person's occupation. Veterinarians, slaughterhouse workers, other livestock handlers, laboratory workers, rangers, and workers in animal-related industries being at a higher risk (Rauch *et al.*, 1987; EFSA, 2010; Angelakis and Raoult, 2011). In addition, individuals in contact with pets, e.g., cats and dogs are at an elevated risk (Maurin and Raoult, 1999). The bacterium is shed in milk, urine, faeces and is also shed in large numbers through placental and birth fluids of infected cattle, sheep and goats (Parisi *et al.*, 2006; Guatteo *et al.*, 2006; Guatteo *et al.*, 2007). Animals get infected through inhalation of aerosols from contaminated environment or ingestion of contaminated pastures, hay and straws (Maurin and Raoult, 1999). Ticks are considered as the natural primary reservoirs of *Coxiella burnetii* and are responsible for the spread of the infection in wild animals and for transmission of the pathogen to domestic animal (Norlander, 2000). Transmission of the pathogen to humans by ticks is unlikely (Beaman and Hung, 1989). Thus, ticks are considered to play a crucial role in maintenance of the organism in the environment (EFSA, 2010).

The organism is very stable in the environment and thus can survive for a long time and remain infective for a long period. It can remain stable in contaminated soil for up to 5 months and up to 2 weeks in aerosols (Tissot-Dupont and Raoult, 2008). Inanimate objects, e.g., wool, shoes, clothing, manure, straw and other materials contaminated with animal excreta can also serve as a source of infection to humans. Furthermore, spread of

the disease to humans can happen through indirect means (Tissot-Dupont and Raoult, 2008), e.g., handling of inanimate objects and inhalation of contaminated dust from farm vehicles (Arricau-Bouvery *et al.*, 2006). The organism can be shed in birth secretions and milk for several years by chronically ill animals thus making it an important source of human infection (EFSA, 2010).

2.1.5 Clinical manifestations of the disease in humans

Q fever has an incubation period of about 1-3 weeks in humans (Maurin and Raoult, 1999). Human clinical disease ranges from asymptomatic to severe. About 60% of humans infected with *Coxiella burnetii* present an asymptomatic form of the disease. Out of 40% that present with symptomatic form of the disease 38% have a mild disease that do not need hospitalization, 2% need hospitalization and of the hospitalized patients, 0.2% develop chronic infection (Maurin and Raoult, 1999). The symptomatic infection typically results in a mild, self-limiting, febrile-like disease (acute form). This acute form of the disease presents as a non-specific febrile illness that may occur together with hepatitis or pneumonia. It is characterized by sudden onset of fever (40.5° - 41.5° C), nausea, non-productive cough, diarrhea, weakness, profuse sweating, severe headache with retro-orbital pain, vomiting, chills, and chest or abdominal pain (Maurin and Raoult, 1999). Some patients develop chronic disease, that include endocarditis and other complications like vascular or osteoarticular infection (Parker *et al.*, 2006), chronic granulomatous hepatitis and infections of the reproductive organs (Maurin and Raoult, 1999; Angelakis and Raoult, 2010).

Children are less likely to develop the clinical form of the disease compared to adults (Maltezou and Raoult, 2002). Risk factors associated with greater likelihood to developing the disease include immunosuppression, age above 60 years, renal insufficiency, and pregnancy (Maurin *et al.*, 1999; Angelakis and Raoult, 2010). The clinical forms of the disease cause a great impact on patients, as it decreases the quality of life of the patients and causes severe fatigue (Limonard *et al.*, 2010). This has been reported in studies done a year after a Q fever outbreak in the Netherlands (Morroy *et al.*, 2011).

2.1.6 Clinical manifestations of the disease in animals

Coxiella burnetii infection in animals is generally asymptomatic but can induce pneumonia as well as delivery of weak offsprings, abortion and stillbirth- these being the most frequent clinical signs of the disease (Arricau-Bouvery and Rodolakis, 2005; Georgiev *et al.*, 2013). During the chronic phases of Q fever infection, the pathogen is persistently shed in urine and faeces, while during the acute phase of infection *C. burnetii* can be found in lungs, liver, spleen and blood (Arricau-Bouvery and Rodolakis, 2005). In carrier herds, i.e., the asymptomatic herds, they have the pathogen and can shed it but do not manifest the clinical signs of the infection. *Coxiella burnetii* is associated with chronic subclinical mastitis (Rodolakis *et al.*, 2007).

Infected bovine herds primarily shed *Coxiella* through birth products, milk, urine and faeces (Bouvery *et al.*, 2003; Courcoul *et al.*, 2011). The infection does not cause pathological changes in the lungs, heart, or liver unlike in humans. The site most often affected is the female reproductive system, mainly the placenta (Rodolakis, 2006).

The infection results in the shedding of large quantities of organisms into the environment as which forms a basis of infection for other animals and humans (Arricau-Bouvery and Rodolakis, 2005). Sheep primarily shed *C. burnetii* through faeces or vaginal mucus (Astobiza *et al.*, 2011) and goats mostly through milk (Berri *et al.*, 2002; Rodolakis *et al.*, 2007).

2.2 Diagnosis of Q fever in animals and humans

In both humans and animals Q fever is generally under- diagnosed and underreported probably due the non-specific nature of its clinical signs, the need for laboratory confirmation and lack of awareness of the disease in the medical and veterinary communities (Drancourt and Raoult, 2005). The World Organization for Animal Health (OIE, 2010) classified *Coxiella burnetii* as a Group 3 pathogen; therefore management of viable *C. burnetii* must be done in biosafety level 3 facilities and should be handled by experienced laboratory personnel only (Sidi-Boumedine *et al.*, 2010).

Q fever in humans is usually diagnosed by serology or Polymerase chain reaction (PCR). Indirect fluorescent antibody test (IFA) is usually used for diagnosing acute and chronic Q fever and patients at risk for chronic fever that are being followed up (Wegdam-Blans *et al.*, 2012). Serology can detect phases I and II of *C. burnetii* infection. In chronic form of Q fever Phase I IgG antibody titer is elevated and is higher than Phase II IgG antibody titer whereas in the acute form Phase II IgG antibody titer is elevated and is higher than the Phase I IgG antibody titer (Anderson *et al.*, 2009). In the first week of acute illness preceding antibiotic administration, serum or whole blood can be tested for *C. burnetii*

using PCR (Fournier and Raoult, 2003; Klee *et al.*, 2006). Treatment for Q fever should be administered as a negative PCR result does not rule out the disease.

C. burnetii can be detected in animals with serological or PCR tests. The serological testing methods available includes complement fixation test (CFT), enzyme-linked immunosorbent assay (ELISA) and indirect IFA tests. The antigen used in CFT regularly fails to detect antibodies particularly in sheep and goats as it is weakly sensitive though it is the OIE prescribed serological test (Field *et al.*, 2000; Porter *et al.*, 2011).

The ELISA and IFA tests efficiently bind IgM antibody which predominate during the acute phase relative to CFT (Sidi-Boumedine *et al.*, 2010). A rapid tool for the diagnosis of *Coxiella burnetii* which is sensitive and more specific is a PCR test used for identification of shedding animals (Hatchette *et al.*, 2001).

Coxiella burnetii, when considered as the etiological agent of abortion can be detected by histology and immunohistochemistry of placental cotyledons where available. Isolation of *C. burnetii* through culture is usually avoided because it is time-consuming, difficult, hazardous, and requires a biosafety Level 3 laboratory (Field *et al.*, 2000; McQuiston and Childs, 2002).

2.3 Treatment of Q fever in animals and humans

Doxycycline is the antibiotic of choice against *Coxiella burnetii* in man. It is the most effective treatment for preventing severe complications if it is started early in the course of the disease (Anderson *et al.*, 2013). Trimethoprim/sulfamethoxazole, fluoroquinolones or macrolides antibiotics can also be used (Maurin and Raoult, 1999; Anderson *et al.*, 2013).

In animals, the effectiveness of antibiotic treatments is not sufficiently documented and it is often used to decrease the number of abortions and the level of contamination of *Coxiella burnetii* during parturition (Arricau-Bouvery and Rodolakis, 2005). The prophylaxis based on antibiotic treatment reduces the risk of abortion, but it doesn't guarantee the eradication of the disease in the farm (Ruiz-Fons *et al.*, 2010).

2.4 Control and prevention of Q fever in animals and humans

Prevention measures are focused on avoiding exposure to humans mostly individuals at risk, to animals and environmental contamination. To reduce and prevent animal and environmental contamination, an antibody test should be done when introducing new animals to a Q fever free herd (Arricau-Bouvery and Rodolakis, 2005).

Parturition is important for the transmission of the disease in diseased animals and thus, equipment used to assist in parturition must be disinfected as well as the location. Aborted fetuses and placentas must be picked and destroyed so as to prevent ingestion by domestic and wild carnivores (Arricau-Bouvery and Rodolakis, 2005). People assisting in parturition should wear protective gear, i.e., gloves, boots, masks and must observe rigorous personal hygiene (Berri *et al.*, 2002; Rodolakis, 2006).

Manure should be treated with lime or calcium cyanamide (0.4%) before being spread on the field. Spreading of manure must never be performed when the wind blows as this could lead to spread of the disease far away (Maurin and Raoult, 1999; Arricau-Bouvery and Rodolakis, 2005). Antibiotic treatment with tetracycline can be used to reduce the number of abortions and quantities of *Coxiella burnetii* shed at parturition (Arricau-Bouvery and Rodolakis, 2005; Ruiz-Fons *et al.*, 2010). Transmission of the disease from

ticks to animals can be controlled through rigorous treatment of animals with acaricides. Pasteurization of milk from diseased animals is highly recommended. Individuals at risk, the public and health care professionals should be educated on sources of infection and various symptoms of the disease.

2.5 Risk assessment framework

This study followed a framework developed by Codex Alimentarius Commission (CAC, 1963) which is commonly used for food safety risk assessment. Risk assessment is the characterization of the potential adverse effects to life and health resulting from exposure to hazards (EFSA, 2008). Risk assessment consists of four steps including hazard identification, hazard characterization, exposure assessment, and risk characterization.

The outcome in each step is combined to represent a cause-and-effect chain from the prevalence and concentration of the pathogen to the likelihood and extent of health effects. Risk consists of both the likelihood and impact of disease (EFSA, 2008). According to steps in FAO, 2003:

Hazard identification

A hazard is something that is potentially harmful to humans, other animals, plants or the environment. Hazard identification is a process of identifying all the potential hazards in a given situation. Once a hazard has been identified, the risk associated with it can be estimated but a situation where there is no hazard the risk is unknown (EFSA, 2008) .

Hazard characterization

The characterization of the hazard identified involves describing and understanding the conditions under which the pathogen survives, grows, causes infection, transmits and dies, as well as the outcomes and impact of infection (EFSA, 2008) i.e. natural history.

Exposure assessment

Exposure assessment describes the pathways through which a pathogen is introduced to the environment or to a population of interest and consumed or comes into contact with humans. It describes the pathogen at subsequent steps from the point it is shed by the animal to consumption or coming into contact with humans or other animals. The pathogen is tracked and the likelihood of it being ingested or coming into contact with humans is estimated. It takes into account the frequency of contamination by the pathogen, the extent of contact with the pathogen, consumption patterns of contaminated food, and the role of the animal handler as a source of contamination (EFSA, 2008).

Risk characterization

Risk characterization involves integrating the information gathered in the previous steps to estimate the risk in a specified population. A risk estimate is a measure of the likelihood of exposure and severity of the adverse effects derived from a specific hazard, which could occur in a given population, including a description of the uncertainties associated with these estimates.

Risk question

This is a question asked to answer the risk associated with a hazard. In order to answer the risk question, assessment of the risk is necessary. This involves a process of identification of a hazard, analysis and evaluation of the risk associated with the hazard and determining the appropriate ways to eliminate or control the hazard.

2.6 Qualitative risk assessment framework

Qualitative risk assessment is an assessment that is generally descriptive or categorical in nature and permits ranking of risks (EFSA, 2008). It involves assessment where outputs of the likelihood of the outcome or the magnitude of the consequence are expressed in qualitative terms such as high, medium, low or negligible (FAO, 2003). In addition, it involves a comprehensive process to retrieve data and obtain a description of all the available information about a risk issue to arrive at a conclusion about the probability and magnitude of outcomes.

Being less dependent on quantitative data, it is commonly used for screening risks to determine whether they need further investigation and can be useful in the preliminary risk management activities (FAO/WHO, 2014).

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Study sites

This study targeted pastoralist cattle farmers in Ngong', Mashuru and Namanga sub-counties of Kajiado County, Kenya. Kajiado County is located to the Southern section of the Eastern Rift Valley in Kenya (Figure 3.1). The geographical coordinates of Kajiado County are $36.5^{\circ} 5' E$, $10^{\circ} 10' S$, $-30^{\circ} 10' S$. The county has a human population of 637,312 with 345,146 males and 342,166 females (KNBS, 2010) and covers an area of 21,292.7 km^2 and a density of 31.4 inhabitants/ km^2

The climate of the region is arid to semi-arid and falling between agro-ecological zones IV and V with very little potential for rain-fed cropping. The mean annual rainfall ranges from 500-1250mm with two wet seasons - the long rains occur during the month of March to May and the short rains from October to December. The vegetation varies from open grasslands, bushland to wooden grasslands (FAO, 2007).

The predominant land use and livestock management system in the region is free grazing with the main livestock species kept being cattle and small stock. The total number of cattle, sheep and goats population in Kajiado County was estimated at 411,840, 718,950 and 699,658, respectively (KNBS, 2010). Community land is communally held and used while livestock are managed by individual families (FAO, 2007).

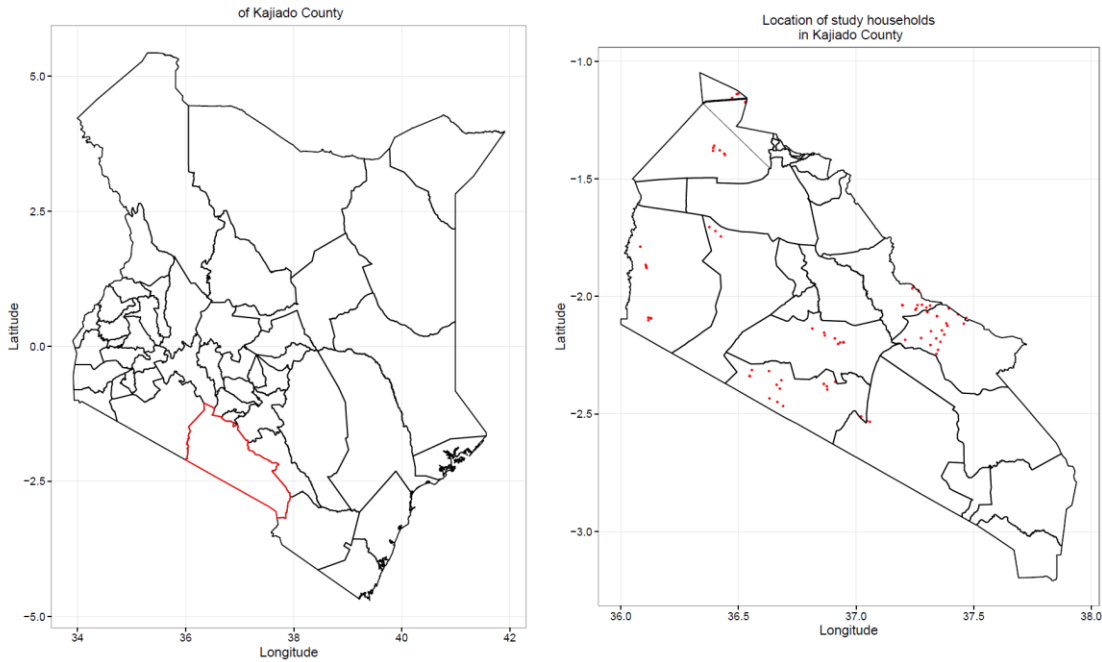


Figure 3.1: Map of Kajiado County showing the sites of study sub-counties

3.2 Selection of study sub-counties

The three study sites, namely, Mashuru, Namanga and Ngong' were purposively selected for the study. This study was nested within another study: a prevalence survey of Q fever in the target areas that generated part of the field activities and data presented in this thesis (Wakhungu, 2016). The selection was based on the availability of livestock at the time of the study which was conducted in the months of November to December 2013. Selection of cattle in the selected sub-counties depended on availability of pasture and water (which determines where the herds were located), and information provided by the local veterinary personnel.

3.3 Selection of households with cattle herds

A two-stage sampling method was used whereby villages with cattle herds in the selected sub-counties were listed in consultation with the local veterinary officer. Ten villages from each location were randomly selected from the provided list using computer-generated random numbers. A list of cattle herds from each of the selected villages was compiled with the help of the local extension officers and village elders. Approximately 8 herds in each village were randomly selected using computer generated random numbers.

3.4 Data collection

Data were collected through the administration of a structured questionnaire (Appendix 1). The questionnaire was administered to household heads via personal interviews.

Data collected through the questionnaires and used in this study included: Handling and disposal of aborted material and birth products; assisting in parturition; assisting during abortion; Milk consumption (raw, boiled, and fermented); Water sources; Animal waste management; and cattle husbandry practices.

3.5 Data handling and analysis

Data were entered into Microsoft excel 2010 and cleaned for analysis. This was then exported to Stata version 12 for statistical analysis. Proportions for each location were generated and 95% confidence intervals for each proportion was also generated using the same package. The fisher's test (some cells in 2 x 2 were <5) was used to test for statistical differences among the 3 study sub-counties for the different exposure methods.

The specific risk question addressed in this study was: What is the risk of Q fever infection through various transmission pathways to members of pastoralists' cattle farming households in Kajiado County? Hazard identification was conducted through consultation of scientific literature, databases such as those in the food industry, government agencies, and relevant international organizations, solicitation of expert opinions and personal communication. The data collected were also used in exposure assessment. The characterization of Q fever and *Coxiella burnetii* was based on the information and data retrieved through literature review. In this study, the exposure assessment was done by construction of a transmission pathway of the hazard from cattle to humans and estimation of the probabilities of occurrence of each step in the pathway. This was done based on information gathered from literature and questionnaires administered in the field. This incorporated extracting information from the published scientific articles, on the shedding patterns of *Coxiella burnetii* by cattle and the various ways in which it can be transmitted to humans. This involved literature search of the published scientific articles, reports from official organizations (EFSA, OIE), data from these and other relevant organizations and books as covered in (chapter 2). This information was used to decide on the most relevant transmission pathways for this pathogen which were then summarized in an event tree. An event tree describes graphically one or more chains of steps that lead to the event of interest. In this study, the event tree starts with cattle shedding *Coxiella burnetii* and working forwards through the potential transmission pathways, using binary logic (Figure 4.1). All steps individually must be necessary to cause the output event which is the exposure. The ultimate event was human ingesting or coming into contact with the bacterium, *Coxiella burnetii*.

The probability of exposure for each pathway was estimated by combining the likelihood of each step for each pathway as shown on the event tree (Figure 4.1). The likelihood of each step was based on information and data gathered during field work and/or from published literature. To estimate the overall likelihood of exposure for each pathway, likelihoods of each step were combined using the qualitative categories presented in tables 3.1 and 3.2. The qualitative measures were categorized as low, medium and high.

The quantitative probabilities generated from the data in the questionnaires and literature were transformed into qualitative measures according to the category they fall in (Tables 3.1 and 3.2). Specifically, the qualitative estimate for the probability of each step in the pathways was estimated separately using the scales defined in the respective tables. The qualitative estimates for the shedding step were obtained slightly different than those for the remaining steps in the pathway; this is because the estimates obtained through the literature for the shedding step are in very divergent scales as compared to the other steps in the pathway and therefore having the same qualitative categorization would have given biased estimates. Specifically, the scale used to categorize qualitatively estimates for the shedding step was adapted from Kasemsuwan *et al.*, (2009) (Table 3.1). For the remaining steps in the pathway, a different qualitative categorization was created in which the quantitative scale from 0 -100% was split in three equal categories corresponding to low (0-33%), medium (33.01-67%) and high (67.01 - 100%) (Table 3.2).

The overall probability estimate was calculated by combining qualitative probability estimates obtained from the various steps in the pathway using a matrix (Figure 3.2). In the combination matrix, the first step in a pathway corresponds to exposure 1 and the following step to exposure 2.

Depending on the length of the pathway, the combined steps become exposure 1 and then the following step is exposure 2 and the trend continues. The matrix was developed by (Kasemsuwan *et al.*, (2009) and it is based on the premise that since the resulting overall estimate is a conditional probability, the probability of an event is based on the occurrence of a previous event. Therefore, the overall probability cannot be higher than the lowest probability of the steps in the pathway (Kasemsuwan *et al.*, 2009).

In this study, the probability of a risk occurring through the identified potential pathways was calculated for each pathway separately. The final estimate of probability of exposure was based on the data collected and analyzed. These were expressed qualitatively as low, medium or high. The level of risk was determined; this was based on the likelihood of exposure and the impact of Q fever in humans and was then translated into one of the categories as shown in Figure 3.3 (EFSA, 2006).

Table 3.1: Quantitative interpretation of qualitative probability categories in the shedding assessment for facilitation of communication and interpretation

Probability categories	Prevalence %
Low	1
Medium	10
High	>10

Table 3.2: Quantitative interpretation of qualitative probability categories in the exposure assessment for facilitation of communication and interpretation

Probability categories	Likelihood of exposure to household members
Low	0 – 33%
Medium	33.01 - 67%
High	67.01 - 100%

Exposure 1	Exposure 2		
	Low	Medium	High
Low	Low	Low	Low
Medium	Low	Medium	Medium
High	Low	Medium	High

Figure 3.2: Matrix for combining probabilities (Kasemsuwan et al., 2009)

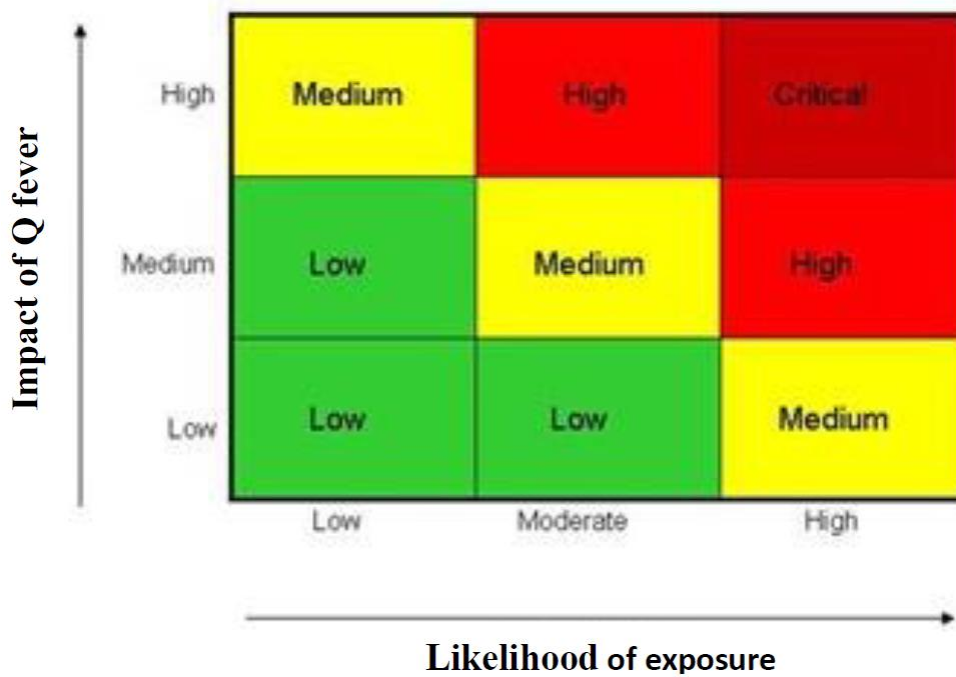


Figure 3.3: Matrix for risk characterization for likelihood of exposure to *Coxiella burnetii* an impact of Q fever (EFSA, 2006)

CHAPTER FOUR

4.0: RESULTS

4.1 Transmission pathways for Q fever in Kajiado County

4.1.1 Description of the transmission pathways

Two major transmission pathways of relevance to the target population in this study were identified (through information gathered from literature and questionnaire) through which *Coxiella burnetii* could move from cattle to humans including:

1. Inhalation- bacterium shed through urine and faeces contaminates the environment and clothes/hands and then inhaled through aerosols, dust or touching contaminated items; and
2. Ingestion- ingestion of raw milk and its products

These pathways were used to construct an event tree (Figure 4.1) which considered all ways through which the bacterium can be shed to the environment or through milk that can lead to farmers' exposure.

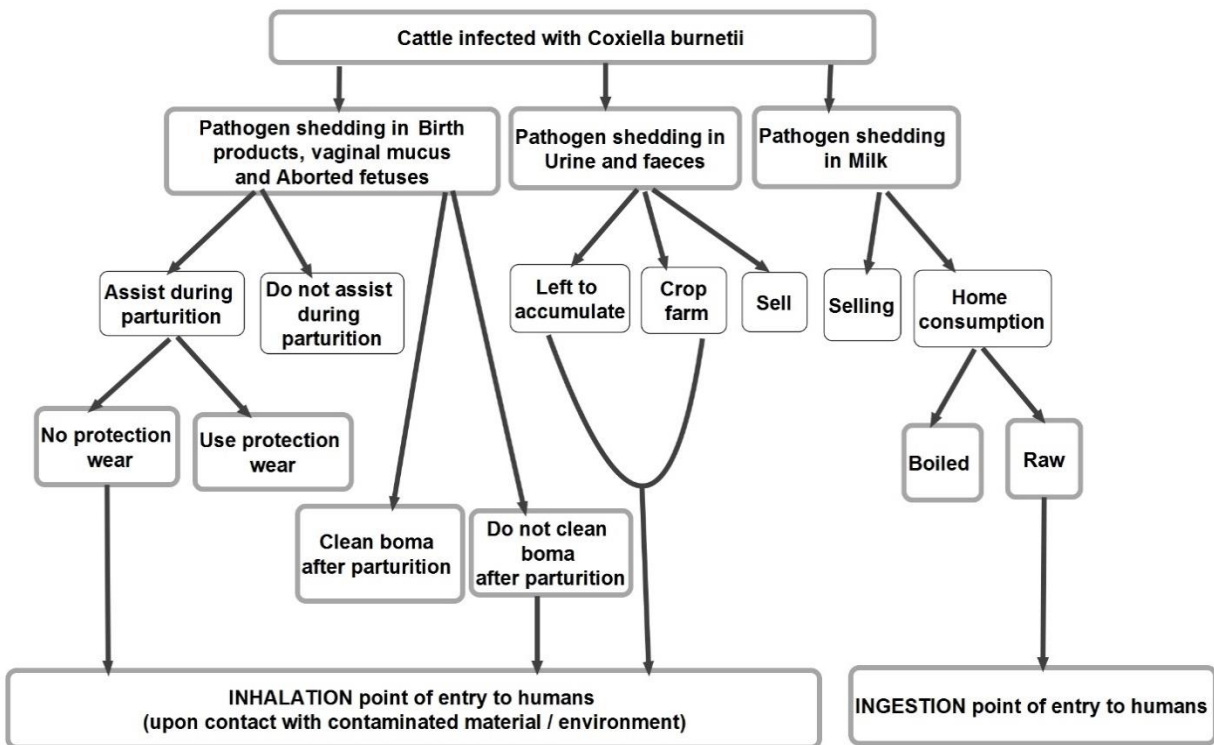


Figure 4.1: An event tree showing potential transmission pathways for *Coxiella burnetii* in Kajiado County

4.2 Qualitative risk assessment for the exposure of Q fever in Kajiado County

4.2.1 Hazard identification and hazard characterization

Coxiella burnetii was identified as the hazard of interest in this study. The literature review for this study formed the basis of the hazard identification. The outcomes are extensively described in Chapter 2. *Coxiella burnetii* has been reported in Kenya among the pastoralists: a study carried out in Kajiado County estimated the seroprevalence of Q fever (*Coxiella burnetii*) in cattle at 3.4% (Wakhungu, 2016). In another study conducted in Laikipia County, seroprevalence of 4%, 31%, 20%, and 46% were estimated in cattle, goats, sheep and camels, respectively (DePuy *et al.*, 2014). Higher rates were reported in a study conducted in Western Kenya among smallholder farmers which estimated a seroprevalence of 28.3% in cattle, 32.0% in goats and 18.2% in sheep (Knobel *et al.*, 2013). Seroprevalence of Q fever in humans was estimated in smallholder farmers in Western Kenya at 30.9% (Knobel *et al.*, 2013).

4.2.2 Exposure assessment

There are various ways identified in this study through which humans are exposed to the pathogen, *Coxiella burnetii*. A total of 84 households were surveyed in Kajiado County in this study, and estimates relevant for this risk assessment are presented in Table 4.1. Specifically, the proportion of farmers reporting either engaging or not engaging in exposure steps considered in this study was estimated from the field surveys. The estimates were broken down by sub-county, to see if there were major differences in farmers' practices in the different areas included in the study. In Ngong', consumption of raw milk at least sometimes was less practiced (30.4%) than in the other two sub-counties;

the difference was statistically significant ($P < 0.05$) (Table 4.1). All the other farmers' practices in the three sub-counties were similar as they were not statistically different as shown in Table 4.1.

Table 4.1: The proportion (%) of farmers potentially exposed to *Coxiella burnetii* through undertaking risk practices in relation to the steps along the pathways, by sub-county

Variable	Sub- county			p-value for χ^2 Fisher's exact test
	Namanga (95% CI)	Mashuru (95%CI)	Ngong (95%CI)	
Assisting cattle during a reproductive procedure	93.1% (83.6-102.6)	87.5 % (75.7-99.3)	91.3% (79.4-103.3)	0.895
Use protective gear during reproduction procedure	10.3% (-1.1-21.8)	9.4% (-1-19.8)	4.3% (-4.3-13)	0.786
Clean/disinfect boma after reproduction procedure	13.8% (0.8-26.8)	3.1% (-3.1-9.3)	0	0.095
Leaving cattle waste/manure to accumulate (not clean cattle waste)	82.8% (68.6-97)	75% (59.5-90.5)	65.2% (45-85.4)	0.390
Manure used in farms	17.2% (3-31.4)	15.6% (2.7-28.6)	17.4% (1.3-33.5)	1.000
Selling manure	0	9.4% (-1-19.8)	17.4% (1.3-33.5)	0.065
Consume milk with family	100%	96.9% (90.6-103.1)	100%	1.000
Consumption of raw milk (at least sometimes)	89.7% (78.2-101.1)	65.6% (48.7-82.6)	30.4% (10.9-49.9)	0.000

Legend:

CI - Confidence Interval

The probability of exposure in each step in the pathway was estimated qualitatively to the category they fall as shown in Table 4.2. In the identified pathways, the probability of exposure in the three sub-counties was found to be equal, and therefore the exposure estimation was conducted for all sub-counties combined except for consumption of raw milk at least sometimes which the probability was statistically different (Table 4.2).

Table 4.2: Probability estimates for the potential transmission pathways for *Coxiella burnetii*.

Pathway	Step in the pathway	Probability
Pathway 1: Inhalation pathway through assisting during a reproduction procedure and without protection.	Assisting cattle during any reproduction procedure	High
	Do not use protective wear during any reproduction procedure	High
Pathway 2: Inhalation pathway through not cleaning/disinfecting boma/ calving site after a reproduction procedure.	Do not clean/disinfect boma after any reproduction procedure	High
Pathway 3: Inhalation pathway through accumulation of animal waste/using it in the farm.	Cattle waste left to accumulate	High
	Cattle waste use in farm	Low
Pathway 4: Ingestion pathway through consumption of contaminated raw milk	Consume milk with family	High
	Consumes raw milk (at least sometimes): Namanga	High
	Mashuru	Medium
	Ngong'	Low

Pathway 1: Inhalation pathway through assisting during a reproduction procedure and without protection

Probability of an infected cattle shedding *Coxiella burnetii* in birth products and vaginal mucus has been estimated to be 19% (Guatteo *et al.*, 2006)- a high probability as shown previously in Table 3.1. The likelihood of exposure to farmers assisting during any reproduction procedure was high as well as that of assisting without using protection (Table 3.2, chapter 3) as interpreted from proportions of potential exposures generated in Table 4.1. The qualitatively interpreted estimated proportion of *Coxiella burnetii* shed in birth products and vaginal mucus was sought from literature review for this study. This interpreted probability was combined (using a matrix as shown in Figure 3.2, chapter 3) with the probability of exposure when assisting during any reproduction procedure and without protection gear collected during the survey and the overall probability of exposure was estimated as high.

Pathway 2: Inhalation pathway through not cleaning boma/site after a reproduction procedure

According to the data collected in the survey, 86.2%, 96.9% and 100% of Namanga, Mashuru and Ngong' households, respectively, did not clean the boma/ calving sites where a calving event had taken place. Infected animals shed high numbers of *Coxiella burnetii* during a reproduction procedure and highest numbers are shed when the procedure is abnormal (Rodolakis, 2006). In the environment *Coxiella burnetii* can survive for up to 4 months at a temperature range of 15-20⁰C (Van Woerden *et al.*, 2004).

The temperature range in Kajiado County is 14-34⁰C, therefore the pathogen can survive in the environment of Kajiado and thus the Likelihood of exposure in the three sub counties was high. The probability of shedding *Coxiella burnetii* to the environment was qualitatively estimated as high (19%) - from literature review. Data from the questionnaire estimated the probability of not cleaning the boma/ calving site where a reproduction procedure had taken place as high. The combined probability for each step in the pathway for not cleaning the boma/ calving site was high as demonstrated using the combination matrix in Figure 3.2.

Pathway 3: Inhalation pathway through accumulation of animal waste/using it in the farm.

Probability of cattle shedding *Coxiella burnetii* through faeces was estimated at 20.7% (Guatteo *et al.*, 2006). This probability of shedding through faeces was categorized as high as shown in Table 3.1. The likelihood of cattle waste to be left in the field was high. The proportion of household members using waste in own farm for crop farming was small as very few households practiced crop farming and thus the probability of this step was estimated as low. The households that used the manure for crop farming did not use the entire manure in the farm and therefore a lot was left to accumulate. Since the waste accumulates where livestock are kept at night, there was a high probability of exposure to the accumulated waste than the one used in the farm for crop farming. Overall, the probability of exposure through the accumulated cattle waste combined for each step in the pathway using the matrix in Figure 3.2 was medium.

Pathway 4: Ingestion pathway through consumption of contaminated raw milk

Probability of cattle shedding *Coxiella burnetii* through milk has previously been estimated at 24.4% (Guatteo *et al.*, 2006). This indicated a high probability of shedding the pathogen in milk as shown in Table 3.1.

Most respondents consumed milk with family members (probability of this step was high); 89.7%, 65.6% and 30.4% of Namanga, Mashuru and Ngong' households, respectively who consumed milk stated consuming raw milk at least sometimes.

The likelihood of exposure for Ngong' household members was low compared to Namanga and Mashuru which had a high and medium likelihood, respectively. Combining the probability of cattle shedding *C. burnetii* in milk (24.4% -as per literature review) and probabilities of exposure to *Coxiella burnetii* by household members in the three sub-counties as per the matrix in Figure 3.2, the overall probability of exposure through consumption of raw milk for Namanga and Mashuru and Ngong' was high, medium and low, respectively.

4.2.3 Risk characterization

The clinical symptoms of Q fever include non-specific febrile illness associated with pneumonia or hepatitis, sudden onset of fever, chills, profuse sweating, and severe headache, among others (Maurin and Raoult, 1999). A small proportion (2. 2%) of the patients may develop chronic infection including endocarditis and other complications (Angelakis and Raoult, 2010). Limonard *et al.* (2010) and Morroy *et al.* (2011) conducted studies that assessed the impact of Q fever one year onward since the infection, which showed that this disease causes a decrease in the quality of life of the patients and severe

fatigue. The clinical form of the disease was associated with inability to work and subsequent impact on livelihoods. Literature review identifies that the clinical form of the disease is not very common in infected people but the subclinical form is common. Even though the proportion of patients that manifest clinical form of the disease is low, the impact of the disease is substantial i.e. reduction of quality of life and severe fatigue. Thus, the impact of Q fever infection in the target population was given a qualitative value “medium”.

Risk characterization of Q fever infection to humans was done by combining the impact of Q fever and combined steps in each pathway to estimate the level of risk as follows:

Pathway 1: Inhalation pathway through assisting during a reproduction procedure and without protection

The likelihood of exposure to *Coxiella burnetii* through this pathway was high as described in the exposure assessment as per matrix in Figure 3.2. The impact of the resulting Q fever infection in humans was medium. Combining the exposure to *Coxiella burnetii* and the impact of Q fever infection in humans using the matrix in Figure 3.3, the level of risk was **high**.

Pathway 2: Inhalation pathway through not cleaning boma/ calving site after a reproduction procedure

The likelihood of exposure to *Coxiella burnetii* to humans through this pathway was high as described in the exposure assessment while the impact of the resulting infection in humans was medium. As per matrix in Figure 3.3, this combined exposure to *Coxiella burnetii* and subsequent impact of infection found that the level of risk was **high**.

Pathway 3: Inhalation pathway through accumulation of animal waste/using it in the farm

As per the exposure assessment the likelihood of exposure to *Coxiella burnetii* to humans through this pathway was medium and the impact of the resulting infection in humans was medium. Using the matrix in Figure 3.3 to combine the exposure to *Coxiella burnetii* and the ensuing impact of Q fever in humans, the level of risk was **medium**.

Pathway 4: Ingestion pathway through consumption of contaminated raw milk

The likelihood of exposure to *Coxiella burnetii* to humans through this pathway was medium for Namanga and Mashuru and low for Ngong' as per the exposure assessment. The matrix in Figure 3.3 combined the exposure to *C. burnetii* and the impact of the resulting infection in humans and the level of risk through this pathway for Namanga and Mashuru was **medium** and **low** for Ngong'.

CHAPTER FIVE

5.0 DISCUSSION

The current study found low to high risks associated with exposure of humans to *Coxiella burnetii* from infected cattle. While the estimates are high, it must be emphasized that these refer to human risk derived from exposure in cattle infected household. In other words, if a household has cattle infected with *Coxiella burnetii* and considering farming and milk consumption patterns among pastoralists in Kajiado, the likelihood of human exposure to this pathogen from cattle was substantial, and therefore the associated risk ranges from low to high.

A recent serological study of *Coxiella burnetii* on 300 samples from cattle in Kajiado County revealed a seroprevalence of 3.4% (Wakhungu, 2016): considering this estimate, the absolute risk of Q fever transmission from cattle to humans among pastoralists in Kajiado would be lower. Nevertheless, these results suggest that Q fever transmission from cattle to humans is possible and likely in pastoralist communities due to consumption of raw milk and not using protective clothing when calving and handling animals.

Infected animals shed high numbers of the pathogen, *Coxiella burnetii*, in the placenta and birth fluids at the time of an abortion or normal delivery and higher numbers are shed when the birth is abnormal (Rodolakis, 2006; Rousset *et al.*, 2009). A study by Van Woerden *et al.* (2004) found out that *Coxiella burnetii* can occur up to a concentration of 10^9 per placenta. As found in the current survey almost all respondents reportedly assisted in calving and while doing so, they did not have any protective gear.

The likelihood of exposure to the bacteria when this is happening is high for pastoralists in Kajiado because it is at this time that high numbers of the pathogen are shed. A study by (Madariaga *et al.*, 2003) showed that *Coxiella burnetii* is highly infectious with one organism proficient of causing a clinical infection in humans. An infected animal can have a full term pregnancy and have a normal delivery but will shed the pathogen in its birth products. The infected animals that experience abortion or any other reproduction complication attributed to *Coxiella burnetii* sheds the highest number of pathogens in its birth products (Rodolakis, 2006). In the current survey, almost all respondents assisted in any reproduction event (calving event, stillbirth, abortion). It was not possible to determine the causes of these reproduction events but it is likely some were due to *Coxiella burnetii* as can be depicted from the study carried out by Wakhungu (2016) in Kajiado County where a seropositivity to *Coxiella burnetii* of 3.4% was estimated. Consequently, if the reproduction event was attributed to *Coxiella burnetii*, then a high number of the pathogen was shed at that time thus increasing the risk of exposure to humans.

Humans most commonly contract Q fever through inhalation of air contaminated with *Coxiella burnetii* organism from animals aborting or birthing or contact with infected material, e.g. tissues, fluids, wool, straw (CFSPH,2006). Therefore, if the animals assisted at calving were infected, there was a likely direct contact of humans with the infected material and in the process inhalation of air that was already contaminated with the bacteria. This may therefore be a major transmission pathway giving a high level of risk to humans. These results are consistent with various epidemiological studies that demonstrate that inhalation of contaminated dust and aerosols are the primary mode of

transmission of *Coxiella burnetii* to humans (Johnson and Kadull, 1966; Maurin and Raoult, 1999).

Following calving or abortions, almost all the households surveyed did not clean or disinfect their bomas/ calving sites and did not dispose the cattle waste/manure. In a case where infected animal calves or abortions, the birth material and birth fluids containing *Coxiella burnetii* would be left at the site of parturition providing a source of infection to humans. A study conducted to investigate the quantity and spatial distribution of *C. burnetii* in the environment of goat farms found out that high quantities of *Coxiella burnetii* DNA were in goat housing/birthing areas (Kersh *et al.*, 2013). Also a study by (Sinclair *et al.*, 2008) indicated that the concentration of *Coxiella burnetii* in faeces lied in a range of 10^3 - 10^4 per gram faeces. Indeed, the pathogen in the birth products and faeces remains in the environment given the resistant nature of *Coxiella burnetii* (spore-like form) to environmental conditions including heat, pressure, many common disinfectants and drying (Heinzen *et al.*, 1999) increasing the risk of exposure to humans. In herds located in areas with high wind speed, open landscape, high animal densities and high temperatures, the risk of being infected reached very high values (Nusinovici *et al.*, 2015). Kajiado County is an arid to semi-arid region receiving a mean annual rainfall that ranges from 500-1250mm with a temperature range of 14-34⁰C (FAO, 2007). This makes the region favorable for the pathogen to thrive in, be spread and it is likely to persist for long in the environment providing a continuous source of infection to humans.

Infected animals shed *Coxiella burnetii* in milk. In cattle the pathogen can be shed persistently up to 13 months after calving (Arricau-Bouvery and Rodolakis, 2005). The bacteria can be destroyed in milk by high temperatures of pasteurization (CFSPH, 2007).

The infection by ingestion of raw milk is considered a minor factor in the transmission of *C. burnetii* to humans. It is a point of controversy and therefore the number of pathogens capable of causing Q fever has not been determined (Maurin and Raoult, 1999). Moreover, a study by Benson *et al.*, (1963) showed that drinking contaminated milk induced seroconversion in human volunteers but without clinical signs. This indicated that this is a possible route of transmission of the pathogen to humans. Of the surveyed households, 100% Namanga, 96.9% Mashuru, 100% Ngong' consumed milk from their livestock with family members and 89.7%, 65.6% and 30.4% of the households in Namanga, Mashuru and Ngong', respectively at least consumed raw milk. These results showed that residents from Namanga and Mashuru consumed raw milk more often as compared to Ngong' residents. Therefore, Namanga and Mashuru residents were at a higher risk of exposure to *Coxiella burnetii* as compared to Ngong' through this transmission pathway. Kajiado County is a pastoralist area predominantly inhabited by Maasai people whose customs allow various practices including consumption of raw milk. It is likely that Ngong residents, a peri-urban area of Nairobi, had embraced education on the importance of boiling milk before consumption relative to the other two sub-counties. Also, the fact that Ngong borders Nairobi County where there is modernization and education, the residents have learnt and embraced modern practices from their neighbors.

The surveyed households confirmed that they prepared fermented milk for consumption. The Ph. of fermented milk is 4.6 (Laligant *et al.*, 2003; Bouteille *et al.*, 2013). *Coxiella burnetii* can survive in an acidic environment as seen in its lifecycle whereby the Ph. in the endosome is 5.5 and that of the phagolysosome is 4.5 (Arricau-Bouvery and

Rodolakis, 2005). This showed that the pathogen can survive in fermented milk and humans are likely to be exposed to *Coxiella burnetii*.

In conclusion, inhalation is the main transmission pathway as the likelihood of exposure through this pathway is high. Namanga and Mashuru residents are more likely to get exposed to *Coxiella burnetii* through ingestion transmission pathway as compared to Ngong'. Controlling the steps in each pathway that lead to exposure to *Coxiella burnetii* is a potential measure that can be taken to reduce exposure to the pathogen.

CHAPTER SIX

6.0 CONCLUSIONS AND RECOMMENDATIONS

6.1 CONCLUSIONS

The following conclusions can be drawn from the study.

1. Four potential exposure pathways to *C. burnetii* were identified including:
 - a) Inhalation pathway through assisting during a reproduction event and without protection; the probability of exposure through this pathway was **high**;
 - b) Inhalation pathway through not cleaning/disinfecting boma/site after a reproduction procedure; this pathway had a **high** probability of exposure;
 - c) Inhalation pathway through accumulation of animal waste/using it in the farm; likelihood of exposure through this pathway was **medium**; and
 - d) Ingestion pathway through consumption of contaminated raw milk; probability of exposure was **high, medium** and **low** for Namanga, Mashuru and Ngong' respectively, through this pathway.
2. The level of risk ranged from low to high. The level of risk through:
 - a) Inhalation pathway through assisting during a reproduction procedure and without protection was **high**;
 - b) Inhalation pathway through not cleaning/disinfecting boma/site after a reproduction procedure was **high**;
 - c) Inhalation pathway through accumulation of animal waste was **medium**; and
 - d) Ingestion of contaminated raw milk for Namanga and Mashuru and Ngong was **high, medium** and **low**, respectively.

6.2 RECOMMENDATIONS

1. To reduce exposure to *Coxiella burnetii*, the use of protective gear, observing both environmental and personal hygiene, and consumption of boiled milk is highly recommended.
2. Awareness of the disease Q fever should be created through public education among pastoralists on the symptoms of the disease and its control and prevention measures.
3. Increased attention by the scientific community to this pathogen, *Coxiella burnetii*, in cattle raising communities is necessary as the health, economic and societal impacts of human infection are not negligible.
4. There is need to do further genomic characterization of *Coxiella burnetii* isolates from pastoral regions of Kenya to identify the strains found in these regions.

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APPENDICES

Appendix 1: Questionnaire for data collection on livestock keeping practices in Kajiado County.

Questionnaire Number:

Farm Code:

Farm Management practices (herd associated factors)

Reproductive disorders

1. Do you normally assist cattle during parturition?
 - a. Yes
 - b. No

2. And do you assist during any reproductive problem? (Mandatory)
 - a) Yes
 - b) No

3. Do you use any protective gear (gloves, masks, clothes) when assisting with the parturition or abortion of animals or whilst handling placentas and aborted fetuses?
 - a) Yes
 - b) No

4. If no, why not?

5. Do you separate cows during parturition from the rest of the herd? (Mandatory)
- a) Yes
 - b) No
6. Do you clean the site/boma after parturition? (Mandatory)
- a) Yes
 - b) No (go to question 77)
 - c) Don't know / not sure
7. If yes, how do you clean? (single choice)
- a) Cleaning with water
 - b) Cleaning with water and soap
 - c) Cleaning with water and disinfectant
 - d) Don't know
- Other (specify).....
8. Have you experienced any abortions and/or stillbirth in your cattle herd in the past year? (mandatory)
- a) Yes
 - b) No
9. If yes, how many cows were affected by any of these disorders in the last year? (it can't be more than the number of cows); if more than the number of cows – confirm.
-

10. Can you recall any other reproductive disorders in your herd in the last year?

(multiple choice)

- a. Dystocia (calf stuck at birth)
- b. Metritis (pus coming out from vulva)
- c. Weak calf
- d. Prolapsed (vagina/uterus coming out)
- e. Retained placenta (afterbirth membranes not coming out)
- f. None
- g. Other (specify) _____

11. How do you most frequently dispose of the aborted fetuses and placentas? (single choice) (Mandatory)

(**Tick one** mentioned as the most common)

- a) Burning
- b) Dumping
- c) Burying
- d) Feed to the cats/dogs
- e) Sell
- f) Eat
- g) Others (explain).....

GENERAL ZONOSSES EXPOSURE PRACTICES

12. What do you use the milk from YOUR cattle herd for? (multiple choice- mandatory)

- a) Consume within the family
- b) Sell to neighbors and members of the community
- c) Sell to local businesses (restaurants, hotels, schools, ...)
- d) Sell to milk vendors
- e) Sell to milk processing company
- f) Other (specify) _____

13. Do you consume raw milk? (Mandatory-single choice)

(Note: Raw being unprocessed milk, not boiled, not fermented, pasteurized or homogenized)

- a) Always
- b) Sometimes (primarily treated, but sometimes raw)
- c) No
- d) I don't know

14. Do you consume milk products made with raw milk? (Mandatory)

- a) Yes
- b) No (go to question 110)

15. If yes, which ones? (multiple choice)

- a) Yogurt
- b) Fermented milk (mala)
- c) Ghee
- d) Cheese
- e) Others (specify).....

16. How do you dispose the manure from the herd?

- a. Do not dispose
- b. Use in own crop farm
- c. Dispose by the road side
- d. Use it for biogas production
- e. Sell it
- f. Not sure / don't know
- g. Others (specify).....

