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Sero-prevalence of Bovine Brucellosis and associated risk factors in mbeya region, Southern highlands of Tanzania

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ABSTRACT

A cross-sectional study was conducted to establish the seroprevalence of brucellosis and associated risk factors in indigenous and exotic breeds of cattle from 178 farms in Mbeya region. A total of 1211 cattle (929exotic cattle from 108 commercial farms and 282 indigenous cattle from 70 traditional farms) were tested for *Brucella* antibodies using the Rose Bengal Plate Test (RBPT) and competitive Enzyme Linked Immunosorbent Assay (c-ELISA) as screening and confirmatory tests, respectively. The overall animal-level seroprevalence was 9.3%; 11.3% (95% CI: 9.4–13.5) in indigenous cattle and 2.8% (95% CI:1.4–5.6) in exotic cattle. Further, the overall herd level seroprevalence was 32.0%; 50.5% (95% CI: 40.9–59.9) in indigenous cattle and 4.2% (95% CI: 1.3–12.4) in exotic cattle. Infections were higher in cattle aged 6–10 years old, (39.8%; 95% CI: 31.2–49.1) followed by those aged 1–5 years (5.8%; 95% CI: 4.8–6.6) and 11–15years old (2.7%; 95% CI: 0.8–8). When compared to cattle sampled from herds size of 1–50, those sampled from the herd sizes of 51–100 and 101–150 had higher odds of brucellosis seropositivity [(OR = 3.6, CI: 1.76–7.16, $p < 0.001$) and (OR = 3.0, CI: 1.09–8.04, $p = 0.033$). The odds of seropositivity in animals which calved on pasture was 3.0 (CI: 1.1–7.8, $p = 0.028$) compared to those that calved at home. Brucella seroprevalence was also observed to vary according to districts, with Mbarari district recording the highest (45.4%). It is evident from the study that Brucellosis is present in Mbarari, Mbeya and Momba districts of Mbeya Region. The findings of this study provide some baseline data that could contribute to the design and implementation of brucellosis control measures in the study areas.

1. Introduction

Brucellosis is an infectious bacterial zoonotic disease commonly caused by members of genus *Brucella* (World Health Organisation (WHO), 2006). To date, the genus *Brucella* consists of eleven species (Smirnova et al., 2013). It is usually caused by *Brucella abortus* in cattle, *B. melitensis* in goats and sheep, *B. ovis* in sheep, *B. suis* in pigs and *B. canis* in dogs. The disease is also caused by *Brucella neonate* in desert wood rat, *B. ceti* in cetaceans, *B. pinnipedialis* in pinnipeds, *B. microti* in common vole (*Microtus arvalis*) and *B. inopinata* isolated in human but not in animal. *Brucella papionis*, isolated from baboons (*Papio* species) (Whatmore et al., 2014). However, *B. abortus*, *B. mellitensis* and *B. suis* remains the important causes of *Brucella* associated morbidity and mortality worldwide (Ciocchinia et al., 2014). Some *Brucella* species are also maintained in wildlife populations such as zebra (*Equus burchelli*), buffalo (*Syncerus caffer*), wildebeest (*Connchaetes vardonii*) and eland antelope (*Taurotragus oryx*) (Godfroid, 2002) and pose a risk of transmission between domestic and wild animals, especially when they share grazing grounds and watering points (Pandey et al., 1999).

In many developed countries, the disease has been brought under control with assciated decrease in economic losses attributable to it (Muma et al., 2006). The disease in animals causes abortions, infertility, reduced milk production, neonatal mortality, hygroma, epididymitis and orchitis. The disease may hinder international trade due to restrictions impossed by international veterinary regulations on animal movement. *B. abortus, B. mellitensis, B. suis and B. canis* are usually transmitted between animals by contact with the placenta, foetus, fetal fluids and vaginal discharges from an infected animal (Maurin, 2005). Although ruminants are usually asymptomatic after their first abortion, they can become chronic carriers, and continue to shed *Brucellae* in milk and uterine discharges during subsequent pregnancies (The Center for Food Security and Public Health (CFSPH), 2009).

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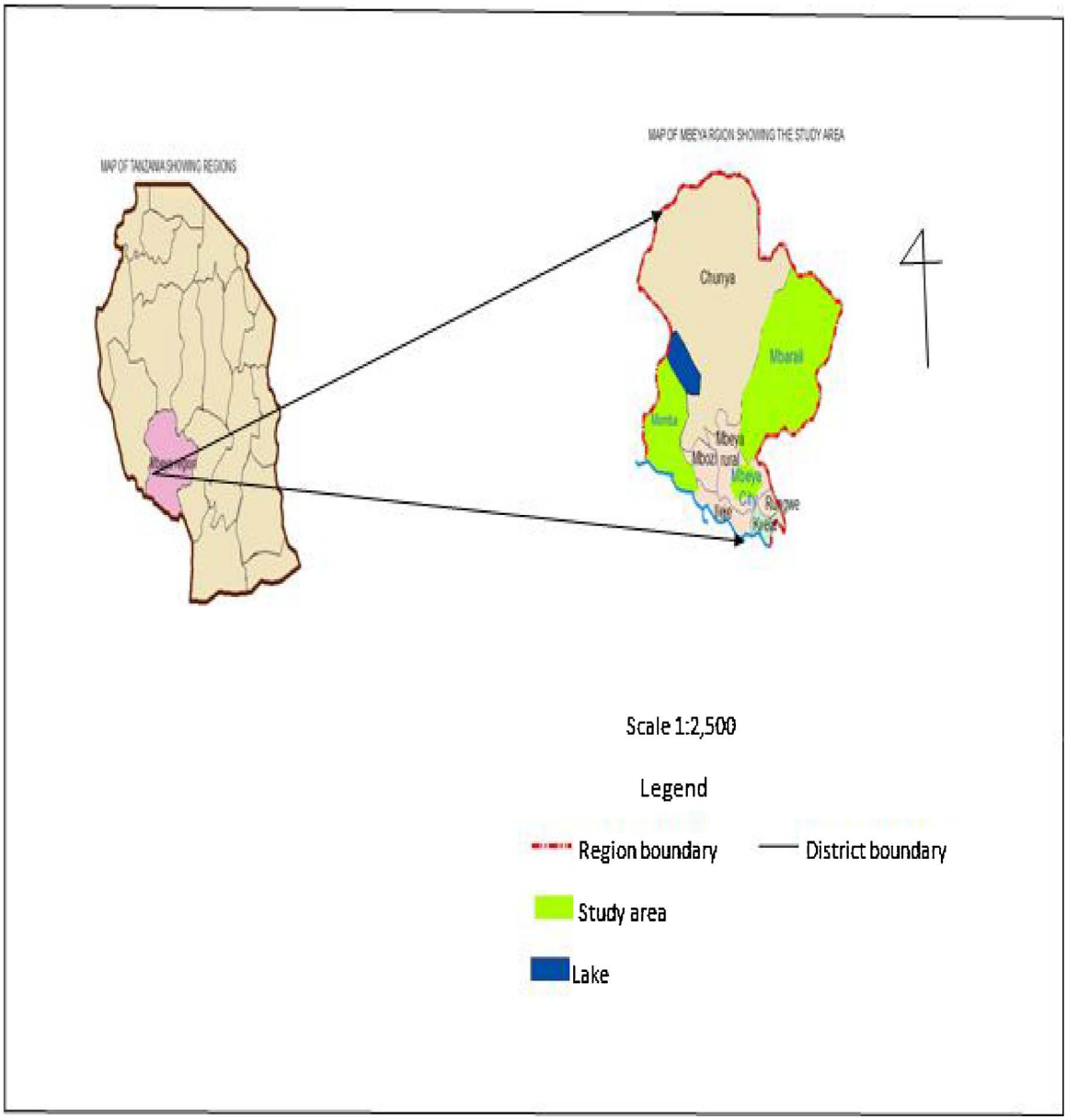

Fig. 1. The insert is the Map of Tanzania showing study districts.

In Tanzania, the extent and factors associated with brucellosis are not well understood although some studies have been done in some parts of the country (Shirima, 2005; Swai et al., 2005; Weinhäupl et al., 2000). It has been reported to occur in livestock at the prevalence of 6.2% in Arusha and Manyara regions (Shirima, 2005), 12.2% in Kilimanjaro (Swai et al., 2005) and 12–14% in Eastern zone (Weinhäupl et al., 2000). The aim of this study was to determine the individual and herd level seroprevalence of Brucella infections in cattle reared under traditional (indigenous cattle) and commercial farming (exotic cattle) systems in Mbeya and identify risk factors associated with Brucella infections in cattle.

2. Materials and methods

2.1. Study area

A cross-sectional study was carried out in Mbarari, Mbeya and Momba districts in Mbeya Region of Southern highlands of Tanzania (Fig. 1) from August 2015 to January 2016 with the purpose of determining seroprevalence and risk factors associated with occurrence of brucellosis in cattle. Currently, Momba district is located in the new administrative region of Songwe. The three districts can further be categorized into two settings, namely, rural communities which include Mbarari and Momba districts and urban communities which comprise Mbeya City Council. The former comprises the majority of agropastoralists whereas the later comprise commercial farmers who are mostly dairy cattle keepers.

The region lies about 5500 feet above sea level and experiences subtropical highland climate with humid summers and dry winters. The temperature ranges between −6 °C in the highlands and 29 °C on the lowlands. The average rainfall per year is 900 mm. According to the 2012 national census, the region had a human population of about 2,707,410. The main economic activity in the region is crop production followed by livestock keeping. The dominant animal species are cattle (911,889) followed by goats (275,659) (Mbeya regional Commissioner office, 2012). Others include sheep, pigs, guinea fowls, ducks, geese and rabbits. In Mbeya region, cattle rearing is a mainstay of the household economy as they provide draught power for tillage in crop production,

main sources of protein (milk and meat) and provide income through the live animal sales.

2.2. Study animals

Blood for serum was collected from 1211 cattle owned by individual farmers comprised of Short horn Zebu and Ankole (hereafter referred to as indigenous cattle) in Mbarari and Momba and Friesian dairy cattle (herein after referred to as exotic breed) in Mbeya district and part of Mbarari district. Herd selection was done randomly and based on farmers consent. Only animals with no history of brucellosis vaccination, both male and female, were enrolled in the study.

2.3. Study design and sample size calculation

A cross-sectional sero-epidemiological study with a two-stage design was carried out between July and December 2015. To calculate the required number of farms/households to be sampled in order to estimate the seroprevalence of brucellosis infected herds, an expected herd prevalence (P_{ex}) of 40.6% (Chimana, 2012), desired absolute precision (d) of 10% and confidence level of 95% was applied as described by Chulaluk (Chulaluk, 2009), where $n = 1.96^2 P_{exp} (1\text{-}P_{exp})/d^2$ resulting into a required sample size of 93 farms/households.

The resulting sample size was multiplied by the design effect (D) of 1.4 calculated using the formula D = 1 + (b-1) roh (Otte and Gumm, 1997). The average number of samples per cluster (b) was 10 and intra cluster correlation coefficient or rate of homogeneity (roh) was 0. 1 (Zolzaya et al., 2014). The final sample size included 186 farms/households. In order to determine the number of households to be sampled in each district, proportionate sampling was employed whereby 70, 68 and 48 herds were sampled in Mbarari, Momba and Mbeya districts, respectively. Sampling was planned to at least select 10 animals from each herd, bringing the total number to be sampled to 1860. A total of 1211 blood samples from 178 herds were randomly collected from three districts; 550 samples were collected from Mbarari district; 425 blood samples from agro-pastoral were collected from Momba districts as well as 236 blood sample from exotic dairy cattle were collected from Mbeya district (Table 1). Selection of study villages and households/farms was done using a random sampling approach. The list of all villages keeping cattle and eligible herds for each district was generated with the help of local veterinarian, farmers and village leaders. It should be noted that few herds were sampled in both Mbarari and Momba districts due to resource constraint and poor accessibility; whereas more herds were sampled than estimated in Mbeya district due to small herd sizes and easy accessibility of the herds.

2.4. Sampling and collection of epidemiological data

Approximately 5 ml of blood was obtained by a veterinarian via a jugular vein puncture of apparently health cattle using a well labelled plain vacutainer tube with 21G blood collection needle (BD vacutainer® Eclipse™ Blood collection needle). The samples were left to clot at room temperature overnight and subsequently centrifuged at 3000 rpm for 10 min to obtain clear serum. Pipette was used to transfer serum into 2 ml labelled sterile Eppendorf's and stored between 4 and 8 °C in mobile refrigerator. Serum samples were then transferred to the University of Zambia, School of Veterinary laboratory and stored at −20 °C until examined. Sample transfer was done after obtaining the export permit No 0000001545 from Tanzania Ministry of Livestock and Fisheries Development and an Import permit No 16/2015/(VTHQ/8/3/20) from the Zambian Department of Veterinary Services.

Table 1
Cattle sample distribution by study area, including planned and obtained number of samples.

Study area	Target herds	Herd sampled	Target number of animals	Animal sampled
Mbarari district	70	55	700	550
Momba district	68	54	680	425
Mbeya city council	48	69	480	236
Total	186	178	1860	1211

After blood collection, heads of the households were interviewed using a pre-tested structured questionnaire on the issues concerned with cattle management including husbandly practices, breeding methods, animal replacement and interaction with wildlife with the aim of obtaining the epidemiological data.

2.5. Serological sample testing

2.5.1. Rose Bengal plate test

All collected sera samples were screened using Rose Bengal Plate Test (RBPT) manufactured by Ubio Biotechnology Systems Pvt Ltd for *Brucella* antibodies according to the test procedure recommended by OIE (OIE: Terrestrial manual, 2009). Briefly, 20 µl of RBPT antigen and 20 µl of the test serum were placed alongside on one well of the glass plate and mixed quickly and thoroughly. The slide was rocked gently from side to side for 4 min. After 4 min of rocking, any visible agglutination was considered positive result.

2.5.2. Competitive Enzyme Linked Immunosorbent Assay (C-ELISA)

RBPT positive sera were then subjected to competitive Enzyme Linked Immunosorbent Assay (c-ELISA) as confirmatory test, adopting a test procedure and interpretation of results as recommended by the manufacturer (Svanova Biotech AB SE-751 Uppsala, Sweden). The assay was conducted according to the manufacturer's instructions. Briefly, 45 µl of sample dilution buffer was placed in each well that was used for serum and control sample, respectively. A total of 5 µl of controls samples were added in duplicate in appropriate wells, followed by addition of 5 µl of dilution buffer into appropriate wells. Thereafter, 5 µl of test samples were added into each appropriate well. In addition, 50 µl of mAb-solution were added into all wells, followed by sealing the plate. Mixing of the reagents was done by placing the plate on the plate shaker. After incubation and rinsing four times with PBS-tween buffer, 100 µl conjugate solution were added to each well. After rinsing it again, 100 µl of substrate solution were added followed by incubation at room temperature for 10 min with subsequence addition of 50 µl of stop solution to each well. The optical densities (OD) of the controls and samples were measured at 450 nm in a microplate photometer (Huma reader, EPSON LQ-1170, MODULE: P641A) within 15 min after the addition of the stop solution to prevent fluctuation in OD values. The percentage inhibition values (PI) for controls and samples were calculated using the formula defined by the ELISA kit manufacturer as here under:

$$PI = 100\text{-}(\text{Mean OD}_{samples/Ctrl} \times 100)$$

$$\text{Mean OD }_{conjugatecontrolCc}$$

According to the ELISA kit manufacturer, serum was regarded as positive when the PI value was ≥ 30%. Only animals positive to both RBPT and c-ELISA were regarded as *Brucella* seropositive.

2.6. Data management and analysis

Collected epidemiological data and laboratory results on Brucellosis seropositivity outcome was entered and cleaned in the Microsoft Excel before being imported into STATA 13® statistical software (Statacorp, College Station, TX, USA) for analysis. Categorical variables were summarized as frequency and percentages; continuous variables were summarized as proportions. An animal was considered to be seropositive when it tested positive on both RBPT and c-ELISA methods. A

herd was defined as the total number of cattle belonging to the same household and it was considered seropositive if at least one cattle become positive to both RBPT and c-ELISA.

Using STATA 13® as a tool for data analysis, two steps were involved to investigate the association between the individual and herd level factors with brucellosis seroprevalence outcome. First, all potential risk factors were screened for statistical association with the outcome variable in univariable logistic regression analysis. Only variables with p-values < 0.20 in univariate analysis were included in the second step (Multivariate logistic regression analysis). Variables not statistically significant in the univariable analysis, but with a known association with brucellosis or suspected to be a potential confounder were also included in the multivariable analysis. The variables which resulted in a change of ≥ 25% in the coefficient estimates of other predictors compared to its absence in the model were considered to have potential confounding effect. The model was constructed by a forward stepwise selection of variables utilizing likelihood ratio test and a p-value ≤ 0.05. The degree of association between or among each risk factor was assessed using the chi-square test. The discriminatory ability of the model was then assessed using the receiver operating characteristics (ROC) and goodness of fit was assessed using the Hosmer-Lemeshow goodness-of-fit check.

3. Results

A total of 1211 serum samples out of the planned 1860 were collected from 178 out of 186 expected cattle herds (Table 1). The overall brucellosis seroprevalence at individual and herd level was 9.3% (95%CI: 0.08–0.11) and 32.0% (95%CI: 0.6–0.7), respectively. Individual *Brucella* seroprevalence was significantly higher in indigenous cattle breed (11.3%) compared to exotic breed of cattle recorded at 2.8% (Table 2). The results of univariable analysis showed that history of abortion, sharing grazing land, geographical area, herd size, retained placenta and calving area increased the risk of cattle acquiring *Brucella* infection at individual animal level (Table 3). There was strong association between antibodies against *Brucella* species and retained placenta (OR = 4.32; 95% CI: 1.46–12.83–) (Table 3).

At herd level, bovine brucellosis was reported to be higher in indigenous breed (50.5%) than exotic breed (4.2%) (Table 4). History of abortion, geographical area and herd size were positively associated with increased herd level *Brucella* seropositivity (Table 5). With respect to herd size, there was a strong association between herds with 51–100 cattle (Table 5) with *Brucella* seropositivity.(OR = 2.0).

3.1. Multivariable logistic regression analysis

Results of multivariable analysis are summarized in Table 3. Compared with animals sampled from herds size of 1–50 cattle, those sampled from the herd sizes of 51–100 and 101–150 had higher odds of brucellosis seropositivity [(OR = 3.6, CI: 1.76–7.16, p < 0.001) and (OR = 3.0, CI: 1.09–8.04, p = 0.033). The odds of seropositivity in animals which calved in the pasture was 3.0 (CI: 1.1–7.8, p = 0.028) compared to the odds of those which calved at home. The odds of seropositivity in animals sampled from Momba and Mbeya districts was 4.4 (CI: 1.0–19.6, p = 0.05) and 12.0 (CI: 2.7–54.7, p = 0.001) compared to the odds of animal sampled from Mbarari district. The assessment of the predictive accuracy of the multivariable model based on the area under the curve (AUC) derived from the receiver operating characteristic curve analysis (AUC = 0.76), suggesting that the final model provided good discrimination.

The Hosmer-Lemeshow goodness-of-fit check showed that the model fitted the data (x2 = 10, d.f. 7, p = 0.16) (Table 5) and the area under the Roc Curve analysis gave the area of 0.90, indicating the model had good predictability.

4. Discussion

The aim of this study was to determine the seroprevalence of *Brucella* infections in cattle in selected districts of Mbeya region and identify associated risk factors. From our study, there was evidence of previous cattle exposure to brucellosis in the study area. The present study has revealed higher seroprevalence of bovine brucellosis in indigenous cattle rearing areas (Mbarari and Momba districts) than those rearing exotic dairy cattle (Mbeya district) both at individual animal and herd levels. The potential risk factors included large herd size, animals calving on the pasture, and production areas; whereby cattle reared in Momba and Mbeya districts had a higher prevalence.

The overall animal level seroprevalence in our study was higher than that reported earlier in Tanzania (Chitupila et al., 2015; Karimuribo et al., 2007; Swai and Schoonman, 2010). In Sub-Saharan Africa, the reported herd level seroprevalence in our study was higher when compared to the 25.0% in Zimbabwe (Matope et al., 2011a) but lower when compared to the 40.10% in Angola (Mufinda et al., 2014); 45.9% in Ethiopia (Yohannes et al., 2013) and 35.3% in Ghana (Folitse et al., 2014). Comparing the grazing system, the results in traditional setting obtained from our study was higher than that obtained in Niger (Boukary et al., 2013), Uganda (Nizenyimana and Mwiine Comparative, 2013) and in Zimbabwe (Gomo et al., 2017) but lower when compared to Nigeria (Mai et al., 2012) and Angola (Mufinda et al., 2014). In commercial grazing system, the individual animal prevalence obtained in our study was lower compared to that obtained in Nigeria (Mai et al., 2012) and Zimbabwe (Matope et al., 2011a) but was found to be similar with that from Uganda (Nizenyimana and Mwiine Comparative, 2013) and relatively high to that found in Niger (Boukary et al., 2013). The low level of *Brucella* seroprevalence in our study can be explained by the fact that pastoral system are undergoing major social transformations suggesting that pastoralism is shrinking due to increased human population density, increased exotic crop farming, urbanization, climate change and increased demand for game ranching. The shrinking of pastoral system results into the rise of intensive and semi-intensive grazing systems which calls for better animal management and reduction of contact with other herds resulting into a breakdown of *Brucella* transmission chain. The seroprevalence results observed in our study was found to be slightly similar with those reported by Dean et al. (2013) in Togo and by Chatikobo et al. (2008) in Rwanda.

4.1. Risk factors influencing Brucella seropositivity

The prevalence of bovine brucellosis in Mbeya region of Tanzania has been noted to vary with geographical variables and husbandry practices. This is similar in most part of Sub-Saharan Africa (Mc Dermott and Arimi, 2002), where cattle management practices (Mc Dermott and Arimi, 2002; Mekonnen et al., 2010; Chimana et al., 2010; Maurice et al., 2013; Kaltungo et al., 2015) intermingling of different livestock species (Godfroid et al., 2011; Muma et al., 2006) are reported to influence brucellosis prevalence. The prevalence was observed to be higher in pastoral herds (11.3%) and lower in exotic herds (2.8%) that mostly practiced zero grazing. This corroborates with the findings earlier reported (Kadohira et al., 1997; Mc Dermott and Arimi, 2002). High prevalence in pastoral system was associated with breakdown in disease control measures including poor or absence of surveillance infrastructure, the difficulties of collecting information and transporting samples to the laboratories from highly mobile herds and limited resources devoted to animal disease control. However, low prevalence of brucellosis in exotic cattle can be explained by application of good husbandry and veterinary practices, good veterinary practices as well as other preventive measures.

High prevalence of brucellosis was recorded in cows with a history of abortion (14.2%) compared to 6.4% in non-abortive cows. This findings was statistically significance (P = 0.045) and it can be explained by the fact that infection due to *Brucella* species accounts for

Table 2
Results from univariable logistic regression analysis of potential risk factors for bovine brucellosis at animal level by demographic variables and husbandry practices.

Variable	Level	No.	Distribution%	Proportion positive%	95%CI	P-value
Sex	Male	94	7.8	12.8	7.4–21.2	0.24
	Female	1117	92.2	9.0	7.5–10.9	
Area	Mbarari	550	45.4	16.5	13.7–19.9	0.00
	Momba	425	35.1	4.7	3.1–7.2	
	Mbeya	236	19.5	0.8	0.2–3.3	
Management	Traditional	928	76.6	11.3	9.4–13.5	0.00
	Exotic	283	23.4	2.8	1.4–5.6	
Herd composition	Cattle only	971	80.2	6.9	5.5–8.7	0.00
	Cattle and goat	240	19.8	19.1	14.7–24.7	
Abortion	Yes	86	7.1	14.2	8.8–21.9	0.00
	No	1125	92.9	6.4	5.1–8.0	
Retained placenta	Yes	33	2.7	5.3	2.4–11.4	0.08
	No	1178	97.3	2.5	1.7 − 3.6	
Animal source	Home breeding	1098	90.7	9.4	7.9–11.4	0.39
	Brought In	112	9.3	7.1	3.6–13.6	
Grazing land	Communal	929	76.7	92.9	86.3–96.4	0.00
	Individual	282	23.3	75.0	72.4–77.5	
Calving area	Home	1155	95.4	4.6	3.5–6.1	0.92
	Pasture	66	4.6	4.4	1.8–10.2	
Disposal of aborted foetus	Thrown	1165	96.2	3.6	2.7–5.0	0.38
	Buried	46	3.8	5.3	2.4–11.4	
Contact with other herds	Yes	929	76.7	75.0	72.4–77.5	0.00
	No	282	23.3	93.0	86.4–96.4	
Herd size	1–50	614	50.7	17.7	11.7–25.9	0.00
	51–100	324	26.8	35.4	27.1–44.7	
	101–150	167	12.9	31.0	23.1–40.1	
	151–200	40	3.3	7.0	3.6–13.6	
	201–250	4	2.5	3.5	1.3–9.1	
	251–300	0	0	0	0	
	301–350	0	0	0	0	
	351–400	46	3.8	5.3	2.4–11.4	
Age	1–5(years)	696	57.5	5.8	4.8 − 6.6	0.74
	6–10(years)	502	41.5	39.8	31.2–49.1	
	11–15(years)	13	1.0	2.7	0.8–8	
Disposal of retained placenta	Thrown	1165	96.2	3.6	2.7–4.9	0.38
	Buried	46	3.8	5.3	2.4–11.4	

Table 3
Final multivariable logistic regression model for Brucellosis in cattle sampled from Mbarari, Momba and Mbeya districts.

Variable	Odds ratio	P-value	95% CI
Herd size (number of cattle)			
≤50	Ref.		
51–100	1.8	0.071	0.95–3.42
101–150	3.57	< 0.001	1.78–7.16
151–200	3.00	0.031	1.11–8.13
201–250	1.91	0.301	0.56–6.54
> 250	1.46	0.477	0.51–4.18
Calving area			
Home	Ref.		
Pasture	2.96	0.028	1.12–7.84
District			
Mbarari	Ref.		
Momba	4.43	0.050	1.00–19.62
Mbeya	11.99	0.001	2.63–54.68

significant proportion of abortion in indigenous cattle (Muma et al., 2012; Matope et al., 2011b). The finding is in agreement with that reported by Muma et al. (2006) and could be explained by the fact that communal grazing system allows intermingling of animals of different herds and species having different disease status.

The variation in bovine seroprevalence in the different geographical region was associated with the cattle grazing system where it was reported higher in those districts that kept cattle under the traditional management system (Mbarari and Momba) and less in the commercial setting (Mbeya district). These findings agreed with those reported by Muma et al. (2006). However, the findings from our study were found to be statistically insignificant ($P \leq 0.05$) and this can be explained by the fact of seroprevalence was highly dependent on the type of grazing system.

In those herds where both cattle and small ruminants were kept, there was a higher individual level *Brucella* seroprevalence than in herds that raised only cattle. The explanation for this could only be clear if isolation and genotyping of Brucella species could be done to see whether there is existence of *Brucella mellitensis* in the study area which can account for increased Brucella seroprevalence in mixed herds.

5. Conclusion and recommendations

The sero-surveillance studies of brucellosis in cattle suggest that brucellosis is endemic in Mbarari, Mbeya and Momba districts in Mbeya region. However, the information on the economic impact and diversity of *Brucella* species prevailing in the study area is still lacking and is an area of further research. Therefore, identification of Brucella species from livestock and humans in Mbeya Region before engaging on eradication programs is recommended. Further, research on the status of brucellosis in all potential livestock species and human as well as

Table 4
Seroprevalence of bovine brucellosis at herd level in different variables.

Variable	Level	No	Distribution	Prop. positive	95%CI	P-value
Management	Traditional	107	60.11	50.50	40.9–59.9	0.00
	Exotic	71	39.99	4.2	1.3–12.4	
Area	Mbarari	55	30.90	76.4	63.2–89.9	0.00
	Momba	54	30.34	24.1	14.4–37.4	
	Mbeya	69	38.76	2.9	0.7–11.1	
Abortion history	Yes	36	20.22	6.7	3.9–70.9	0.33
	No	142	79.78	2.6	19.4–33.9	
Retained placenta	Yes	29	16.29	37.9	22.1–56.8	0.18
	No	149	83.71	30.9	23.9–38.8	
Animal source	Home breeding	133	74.72	36.3	27.6–43.9	0.02
	Brought Inn	45	25.28	22.2	12.3–36.9	
Grazing land	Communal	108	60.67	50.0	40.6–59.4	0.01
	Individual	70	39.33	4.2	1.3–12.6	
Calving area	Home	172	96.63	30.2	23.8–37.6	0.03
	Pasture	6	3.37	83.3	31.8–98.1	
Disposal of foetus	Thrown	177	99.44	31.6	25.2–38.9	–
	Buried	1	0.56	1	–	
Disposal of retained placenta	Thrown	177	99.44	31.6	25.1–38.9	–
	Buried	1	0.56	1.0	–	
Contact with other herds	Yes	108	69.67	43	1.4–12.6	0.00
	No	70	39.33	50.0	40.6–59.4	

Table 5
Summary results of multivariable logistic regression analysis of risk factors with depended Brucella seropositivity in cattle at herd level.

Variable		Odds Ratio	P-value	95%CI
Area	Mbarari district	1.0	0.01	0.09–0.73
	Momba district	2.0	0.00	0.00–0.15
	Mbeya district	–	–	
Herd size	1–50	1.00	0.05	1.01–8.80
	51–100	2.0	0.02	1.39–30.06
	> 100	–	–	
History of abortion			0.09	0.85–10.18

correlation of brucellosis in human and animals should be done in the study area. The findings of this study could contribute to the design and effective implementation of brucellosis control measures in the study areas and areas with similar epidemiological patterns.

Author contributions

Sagamiko, F.D and Muma, J.B conceived and designed the study; Sagamiko,F.D, Hang'ombe, B and Muma, J.B performed the laboratory work; Sagamiko,F.D, Muma J.B, Hang'ombe, B, Karimuribo, E, Mwanza, A.M and Sindato, C analysed the data and wrote the paper.

Conflict of interest

The authors declare no conflict of interest on the study.

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