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REGULAR ARTICLES

Prevalence and risk factors associated with *Theileria parva* infection in cattle in three regions of Tanzania

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Abstract Ticks and tickborne diseases (TBDs) are serious constraints to cattle production in Tanzania and other tropical and subtropical countries. Among the TBDs, East Coast fever (ECF) is the most important as it causes significant economic losses to the cattle industry in Tanzania. However, control of ECF in Tanzania has continued to be a challenge due to inadequate epidemiological information. The main objective of this study was to determine the epidemiological situation of *Theileria parva* infections in cattle kept under pastoral and agro-pastoral farming systems in Mara, Singida, and Mbeya regions of Tanzania. Blood samples were collected from 648 cattle in the three regions. Genomic DNA was extracted and amplified in a polymerase chain reaction (PCR) using *T. parva*-specific primers targeting the 104-kD antigen (P104) gene. In addition, information was collected on the possible risk factors of *T. parva* infection (animal age, region, animal sex, tick burden, tick control method, and frequency of acaricide application). The prevalence of *T. parva* across the three regions was 14.2%. There was variation in prevalence among the three regions with Mara (21.8%) having a significantly higher ($p = 0.001$) prevalence than the other regions. Moreover, Mbeya exhibited relatively lower prevalence (7.4%) compared to the other regions. Factors found to be significantly associated with an animal being PCR positive for *T. parva* were region ($p = 0.001$) and tick burden ($p = 0.003$). Other factors were not found to be significant predictors of being PCR positive for *T. parva*. The present study showed high variation in tick burden and *T. parva* prevalence across the regions. Therefore, different strategic planning and cost-effective control measures for ticks and *T. parva* infection should be implemented region by region in order to reduce losses caused by ticks and ECF in the study area.

Keywords East Coast fever · *Theileria parva* · Tickborne diseases · Risk factors · Cattle

Introduction

Ticks and tickborne diseases (TBDs) are important constraints to the improvement of livestock production in Tanzania and other sub-Saharan countries (Norval et al. 1992; de Castro 1997; Pegram et al. 2000; Swai et al. 2007). These diseases cause high morbidity and mortality and lead to reduced growth rate, milk production, and fertility. They also increase costs of livestock production due to ticks and TBDs control and/or treatment (Young et al. 1988; Minjauw and McLeod 2003; Jongejan and Uilenberg 2004). The costs associated with control and treatments of these diseases are high. For example in 1997, about US$54.7 million was used in Tanzania to control ticks and TBDs and the total loss

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associated with cattle mortality was estimated to be US$364 million (Kivaria 2006).

The important TBDs of cattle in Tanzania and other countries in sub-Saharan Africa include East Coast fever (ECF) (caused by *Theileria parva*), babesiosis (caused by *Babesia bigemina and Babesia bovis*), anaplasmosis (caused by *Anaplasma marginale*), and heartwater (caused by *Ehrlichia ruminantium*) (Norval et al. 1992; Kocan et al. 2003; Bock et al. 2004). Among the TBDs, ECF is one of the most important as it causes huge economic losses in cattle production in Eastern, Central, and Southern Africa (Giblin 1990; Norval et al. 1992; Minjauw and McLeod 2003). It has been reported in 12 countries in these regions, namely Tanzania, Kenya, Uganda, Burundi, Rwanda, Malawi, Mozambique, South Sudan, Democratic Republic of Congo (DRC), Zambia, Zimbabwe, and South Africa (Lawrence1991; Mukhebi et al. 1992; Mugisha et al. 2005). Economic losses caused by ECF can be categorized as direct, e.g., mortality and lowered milk production, and as indirect losses, e.g., cost of controlling the disease, cost of research, training, and extension services (Mukhebi et al. 1992; Jongejan and Uilenberg 2004). In Eastern African countries, including Tanzania, the cost of acaricide application, as a basic way of tick control, has been estimated to range between US$6 and US$36 per adult animal (Minjauw and McLeod 2003; Mugisha et al. 2005; Kivaria 2006). In addition, ECF is a main hindrance to the introduction of highly productive but ECF-susceptible taurine cattle, hence, hampering the development of the livestock sector significantly (Minjauw and McLeod 2003). In Tanzania, for example, the disease causes cattle deaths which accounts for 68% of the US$364 million annual total losses due to TBDs (Kivaria 2006). In unvaccinated zebu calves raised under pastoral conditions, ECF is responsible for annual mortality of 40–80% (Homewood et al. 1987, 2006; Kivaria 2006). In particular, the disease has been reported to kill about 920,000 cattle annually in Tanzania (Kivaria et al. 2007).

T. parva, the protozoan parasite that causes ECF, is transmitted cyclopropagatively and transtadially mainly by *Rhipicephalus appendiculatus*, a three-host tick, after being picked up from infected cattle (Giblin 1990; Norval et al. 1992). In cyclopropagative and transtadial transmission, the parasite undergoes cyclical changes while multiplying within two developmental stages (nymph and adult) of the vector (tick). Such kind of transmission has an implication in the sense that the vector is able to transmit the parasite to more than one host during the vectors life cycle. Existing methods for controlling ECF include vector (tick) control (Minjauwet al. 1997), use of tick resistant breeds (Willadsen 2004; Mwambene et al. 2012), immunization (vaccination) through infection and treatment method (ITM) (Radley et al. 1975; Uilenberg 1999; Di Giulio et al. 2009), and treating infected animals by chemotherapy (George et al. 2004; Ghosh et al. 2007). Acaricide application is the most common method used to control ticks in the tropics (Kagaruki and Loretu 1996). However, this method has major drawbacks, including development of resistance by ticks, food safety concerns (contamination of meat and milk wit toxic residues), environmental pollution, and high cost of production (George et al. 2004; Ghosh et al. 2007). Nonetheless, intensive application of acaricide by dipping or spraying at weekly intervals to control ticks is no longer advised, except for highly productive pure-bred *Bos taurus* dairy cattle (Pegram et al. 1993). Report by an FAO expert (Rome, 25–29 September 1989) suggests that the best way to control ticks and tickborne diseases is through establishment of enzootic stability (Jonsson et al. 2012), which seems to be practical in Tanzanian situation due to high prevalence levels of ticks and TBDs in some regions (Swai et al. 2005; Chenyambuga et al. 2010; Laisser et al. 2014).

The government of Tanzania used to subsidize acaricide to farmers in 1970s and 1980s, but later ended this program due to economic crises. As a result, most farmers stopped dipping their animals due to financial constraints and this led to increased level of tick challenge on animals, resulting in increased infection by TBDs and related losses (Norval et al. 1992; Swai et al. 2005; Chenyambuga et al. 2010; Laisser et al. 2014).Moreover, commonly implemented control strategies are not integrated in the traditional production systems; hence, the control efforts have not been matching with the enormity of the disease problem (Norval et al. 1992). Communal grazing is the main production system practiced by livestock keepers in Tanzania, whereby different herds from different households mingle during grazing and watering (Swai et al. 2005; Chenyambuga et al. 2010; Mwambene et al. 2012). This situation makes it difficult to control ticks and exposes cattle to high risk of tick infestation leading to increased *T. parva* infection if the animal is not tolerant/resistant.

Available methods for the diagnosis of *T. parva* infection include microscopic examination (Uilenberg 1981), xenodiagnosis (Mans et al. 2015), serological tests (Huang et al. 2004), and DNA-based assays (Odongo et al. 2010; Mans et al. 2015). Most of the existing information in Tanzania on the prevalence of *T. parva* infection is based on microscopic examination, serological test, and fewer reports based on DNA-based methods (Swai et al. 2005; Kivaria et al. 2007; Chenyambuga et al. 2010; Tarimo 2013; Laisser et al. 2014, 2016). DNA-based diagnostic techniques have been developed for a number of hemoparasites (Odongo et al. 2010; Mans et al. 2015). These techniques have proved to be sensitive, easy to use, can analyze a large number of samples, and can detect the parasites directly in clinical and environmental samples without culture (Salem et al. 1999; Criado-Fornelio 2007; Mans et al. 2015). The current study provides information on the prevalence of *T. parva* infection in cattle using a p104 based-polymerase chain reaction (PCR) method (Skilton et al. 2002). The p104-based PCR is able to identify current *T. parva* infection and has higher sensitivity and specificity than enzyme-linked immunosorbent assay (ELISA) (Skilton et al. 2002). This study aimed at establishing the prevalence and risk factors associated with *T. parva* infection in cattle kept under smallholder farming systems in Mara, Singida, and Mbeya regions of Tanzania. The results obtained from this study would help to enhance management decisions, including the design of effective control measures which can result into the improvement of the physical, economic, and social well-being of livestock and livestock keepers in rural areas.

Materials and methods

Study area

This study was conducted in Mara, Mbeya, and Singida regions of Tanzania representing three agro-ecological zones of the country, namely Lake zone, central zone, and Southern highlands, respectively. The Lake zone is within the main plateau, and its climate, vegetation, and rainfall are significantly influenced by the Lake Victoria. The zone comprises Mara, Mwanza, and Kagera regions. In this zone, *R. appendiculatus* is present in significant numbers throughout the zone, but the numbers decline further from the lake and its occurrence is not influenced by the season of the year. Most people in these areas practice mixed farming agriculture, with individuals owning large herds of cattle (up to 1000 herds) (Chiomba 1986). The central zone consists of five regions namely Shinyanga, Tabora, Kigoma, Singida, and Dodoma regions. In this zone, *R. appendiculatus* is present in the areas experiencing substantial amount of rainfall especially nearer to the lakes. Large number of people in this zone also own large herd sizes of cattle (Chiomba 1986). Southern highlands include Iringa, Mbeya, and Rukwa regions. High numbers of *R. appendiculatus* are found during the rainy season. Most farmers in these areas graze their cattle within the vicinity of the homesteads during the day and keep them in kraals during the night (Chiomba 1986).

Mara region has a total surface area of 30,150 km^2 located between latitudes 1° 0′ and 2° 31′ S and between longitudes 33° 10′ and 35° 15′ E (MRUF 2013). The region receives rainfall of between 900 and1500 mm with mean temperatures ranging from 18 to 35 °C (MRUF 2013). Singida region covers 49,341 km^{2}and is located in the central zone of Tanzania between longitudes 33° 27′ 5″ and 35° 20′ E and latitudes 3° 52′ and 7° 34′ S (SRSP 1997). Most parts of the region are arid with annual rainfall ranging between 500 and 800 mm. The region has mean annual temperatures ranging between 15 and 30 °C depending on season and altitude (SRSP 1997). Mbeya region is located in the western corner of the Southern highlands of Tanzania and lies between latitudes 7° and 9° S and between longitudes 32° and 35° east of Greenwich (MRSP 1997). Mean temperatures range between 16 °C in the highlands and 25 °C in the lowlands. Annual rainfall varies from 650 to 2600 mm and usually starts in October and goes through to May yearly (MRSP 1997).

Study design and sampling

A cross-sectional study was performed with the purpose of determining the prevalence and risk factors associated with *T. parva* infection in cattle. The study was conducted during the dry season between June and September 2015. A multistage sampling technique was used to obtain the appropriate sample size. Sampling frame were region, district, village, and household. Purposive sampling was employed to select regions and districts whereas villages, households, and animals were randomly selected. The choice of Mara, Mbeya, and Singida regions was based on the fact that in these three regions, there are three different breeds of cattle as well as different climatic conditions which may favor tick multiplication and distribution or presence of cattle populations with differing degrees of innate resistance to the *T. parva* infection. For example, Mara region is dominated with Tarime zebu cattle, while Singida region is dominated with Singida White (Mkalama white) zebu cattle. In Mbeya, there are mixtures of different zebu strains (Laisser et al. 2014, 2016, 2017). A simple random technique was employed to select herds and villages after developing a sampling frame of villages rearing indigenous breeds of cattle. However, only households who had at least ten cattle with all age groups (calves, weaners, and adults) were included in this study. In each herd, three cattle comprising calf, weaner, and adult were randomly selected. The sample size of (196) cattle in each region was obtained using the following formula described by Martin et al. (1987), with an expected prevalence of 15%, 95% confidence interval, and an absolute error of 5%. This gave a sample size of 196 cattle. The expected prevalence of 15% was used based on previous studies conducted in different parts of Tanzania (Tarimo 2013; Laisser et al. 2014; Kazungu et al. 2015). However, the sample size was increased from 196 to 216 in each region due to a positive response from livestock keepers. Therefore, a total sample of 648 cattle was included in the study.

Tick count and blood sample collection

Tick burden was assessed by collecting and counting the number of all visible ticks on cattle from one side of the body and the result multiplied by two. Tick burden (adult and nymph) on each animal were assessed as not seen (0 ticks), few (2 to

19 ticks), moderate (20–49 ticks), and abundant (≥ 50 ticks) as previously described by Simuunza et al. (2011) with few modifications. Blood samples were collected from jugular vein of each animal using 5-ml Vacutainer tubes containing ethylenediaminetetraacetic acid (EDTA). The tubes were labeled and kept in a cool box containing ice packs in the field and thereafter stored at − 20 °C at the Genome Sciences Centre, Faculty of Veterinary Medicine, Sokoine University of Agriculture pending further processing. In addition, during sampling, information on age of the animal, sex, frequency, and tick control method employed in each household was recorded. Age of each animal was determined as described by de Lahunta and Habel (1986).

DNA extraction

Genomic DNA from each blood sample was extracted using Quick-gDNA™ Blood MiniPrep Kit catalog nos. D3073 (Zymo Research Cooperation, USA), according to the manufacturer's instructions, and then eluted in 100 μl elution buffer. Afterwards, the concentration of purified genomic DNA was determined by spectrophotometer (NanoDrop™ One Spectrophotometer, Thermo Fisher Scientific).

Detection of *Theileria parva* infection

All cattle DNA samples were screened for the presence of *T. parva* infection using the nested polymerase chain reaction (nPCR) assay targeting the *T. parva*-specific 104-kD antigen(P104) gene (Skilton et al. 2002; Odongo et al. 2010).The outer and inner primers used were IL 3231 (5′-ATT TAA GGA ACC TGA CGT GAC TGC-3′), IL 755 (5′-TAA GAT GCC GAC TAT TAAT GACACC-3), and IL 4234 (5′-GGC CAA GGT CTC CTT CAG AAT ACG-3′) (IL 3232 5′ TGG GTG TGT TTC CTC GTC ATC TGC 3′), respectively. The outer and inner primers produced a 496- and a 277-bp fragment, respectively. Both polymerase chain reaction amplifications were done in a total volume of 10 μl comprising 1.0 μl 10× buffer, 6.35 μl nuclease-free water, 200 μM of dNTP,10 pmol of each of forward and reverse primers, 2.5 units of Ex Taq polymerase (Takara, Ostu, Japan), and 20 ng genomic DNA template, followed by vortexing and brief spin down to dissolve the pellet. For the second round, 1 μl of the primary PCR product was used as a template. Reaction conditions for both primary and secondary PCR involved initial denaturation at 95 °C for 5 min, followed by 30 cycles of denaturation at 94 °C for 30 s, annealing at 60 °C for 30 s, extension at 72 °C for 1 min, and a final extension at 72 °C for 5 min. The nPCR products were separated on 1.5% agarose gel and bands visualized in an ultraviolet (UV) transilluminator.

Data analysis

Initially, data were entered into a Microsoft Excel spreadsheet, before being transferred for analysis into the Statistical Analysis System (SAS) proprietary Software, Release 9.1 (SAS Institute Inc) for analysis. The chi-squared test was used to test for the association among categorical variables. The stepwise binary logistic regression model (Hosmer and Lemeshow 2000) was used to determine risk factors (predictors) associated with cattle being positive for *T. parva* on PCR. All variables with $p < 0.250$, in the univariate analysis, were included in the model. The variables included were region, age category, tick control method, frequency of tick control, sex of the animal, and tick burden. The binary logit link function produced the coefficient, p value, odds ratio (OR) together with the 95% lower and upper confidence intervals (CI). In order to determine whether each of the created models fitted the data, a non-significant Hosmer and Lemeshow goodness of fit test ($p > 0.05$) was used.

Results

A total of 648 cattle from the three regions (216 from each region) were sampled. Of these, 55.7% were females, while 44.3% were males. The prevalence of *T. parva* in each region is depicted in Table 1. The overall prevalence of *T. parva* across the three regions was 14.2%, with Mara having the highest prevalence (21.8%), followed by Singida (13.4%) and Mbeya (7.4%) (Table 1). The prevalence of *T. parva* was significantly higher ($p = 0.001$) in Mara than in the other two regions. Mbeya had the lowest prevalence in relation to the other regions. The influence of the risk factors such as age category, frequency of tick control, sex, tick burden, and tick control method on the prevalence of *T. parva* was also investigated. Tick-free cattle had significantly lower *T. parva* prevalence ($p = 0.002$) compared to other groups across the regions. Age of the animal and sex were not significantly associated with *T. parva* prevalence across the regions ($p > 0.05$) (Table 2).

In Singida region, cattle on which tick control was done every 2 weeks had significantly higher *T. parva* prevalence

Table 1 Prevalence of *T. parva* infection in the study area

Region	Cattle sampled	Positive (PCR)	Positive (%)
Mara	216	47	21.8
Singida	216	29	13.4
Mbeya	216	16	7.4
Overall	648	92	14.2

PCR polymerase chain reaction

than those on which ticks were controlled monthly or occasionally ($p = 0.04$). However, in Mara ($p = 0.751$) and Mbeya ($p = 0.653$) regions, there was no association between frequency of tick control and *T. parva* prevalence (Table 2). In Mara region, cattle that were dipped had significantly higher prevalence of *T. parva* than on those where other tick control methods were practiced ($p = 0.033$). In Mbeya, cattle that were dipped or hand sprayed had significantly lower *T. parva* prevalence than those where no tick control was practiced at all ($p = 0.001$). No significant differences were observed in *T. parva* prevalence among cattle subjected to different tick control methods in Singida region ($p = 0.987$). In Mbeya region, the prevalence of *T. parva* in cattle that had no ticks was significantly lower ($p = 0.015$) than those with few or moderate ticks. However, in Singida ($p = 0.626$) and Mara ($p = 0.257$) regions, no significant association was observed between the burden of ticks on cattle and the prevalence of *T. parva* (Table 2).

Table 3 Risk factors associated with the likelihood of being PCR positive for *T. parva* based on binary logistic regression model

Variable		Estimate	95% CI for estimate		*p* value
			Lower	Upper	
Age category	Young	2.00	1.04	3.46	0.057
	Weaner	1.34	0.75	2.41	0.925
	Adult[a]				
Region	Mara	3.23	1.67	6.18	0.001
	Singida	2.00	1.05	3.82	0.646
	Mbeya[a]				
Tick burden	Not seen	0.46	0.17	1.69	0.003
	Few	0.93	0.36	2.90	0.942
	Moderate	1.68	0.60	4.72	0.023
	Abundant[a]				

CI confidence interval

[a] Reference variable

The Hosmer and Lemeshow goodness of fit test was non-significant ($p = 0.617$), indicating that the model fitted the data. The maximum likelihood estimates for the final model for factors associated with cattle being positive on PRC to *T. parva* are presented in Table 3. The variables that were found to be significantly associated with cattle being PCR positive for *T. parva* were the region and tick burden. Cattle in Mara were three times (CI = 1.67–6.18, $p = 0.001$) more likely to be PCR positive for *T. parva* than those in Mbeya

Table 2 Factors associated with *T. parva* prevalence based on chi-squared test: *n* = number of animals

	Mara			Singida			Mbeya		
Risk factor	*n*	*T. parva* prevalence (%)	*p* value	*n*	*T. parva* prevalence (%)	*p* value	*n*	*T. parva* prevalence (%)	*p* value
Age category			0.243			0.291			0.277
Young	72	26.4		72	16.7		72	4.2	
Weaner	72	23.6		72	8.3		72	11.1	
Adult	72	15.3		72	15.3		72	6.9	
Frequency of tick control			0.751			0.04			0.653
Weekly	15	26.7		0	0		18	0	
Bi-weekly	15	20		30	26.7		90	1.1	
Monthly	30	16.7		51	17.7			0	
Occasionally	126	25.4		108	9.3			0	
Sex			0.782			0.06			0.418
Male	79	22.8		106	17.9		102	5.9	
Female	137	21.2		110	9.1		114	8.8	
Tick control method			0.033			0.987			0.001
Dipping	117	26.5		0	0		42	0	
Hand spraying	60	20		186	13.4		66	1.5	
Hand picking	9	11.1		0	0		0	0	
No tick control	30	10		30	13.3		108	13.9	
Tick burden			0.2573			0.626			0.015
None seen	67	14.9		102	12.8		87	1.1	
Few	79	22.8		100	13		122	11.5	
Moderate	38	31.6		12	25		7	14.3	
Abundant	32	21.9		2	0		0	0	

region. On the other hand, tick-free cattle were 0.46 (CI = 0.17–1.69, $p = 0.003$) times less likely to be PCR positive for *T. parva* than those which had abundant ticks. The other variables were not found to be significant predictors of cattle being PCR positive for *T. parva* ($p > 0.05$).

Discussion

East Coast fever caused by *T. parva* is an important disease that causes significant losses to the cattle industry in Tanzania and other sub-Saharan countries (Giblin 1990; Norval et al. 1992; Minjauw and McLeod 2003). The current study was carried out to determine the prevalence and risk factors of cattle being positive for *T. parva* in cattle kept under pastoral and agro-pastoral farming systems in Mara, Singida, and Mbeya regions of Tanzania. The results obtained showed that *T. parva* was prevalent across the three regions, indicating that cattle in the study areas were exposed to the infection. The overall prevalence (14.2%) for *T. parva* in the current study was relatively lower than that reported by Laisser et al. (2014) and Kazungu et al. (2015) in the Lake zone (27.7%) and in the northern part of Tanzania (19.7%), respectively, but higher than that reported by Tarimo (2013) in the eastern part of Tanzania (8.1%). These observed differences could have been influenced by factors such as inherent resistance of cattle to ticks and TBDs, virulence of the pathogens, and infection rate of ticks in the different regions (Moll et al. 1988; Laisser et al. 2016, 2017). In addition, this study was conducted during the dry season (June to September) when tick burden on cattle was significantly lower especially in Mbeya and Singida regions. Therefore, the prevalence of *T. parva* was expected to decrease due to lower tick burden during the dry season (Kerario et al. 2017), which in turn resulted in reduced intensity of transmission.

The difference observed in the magnitude of *T. parva* prevalence in the three regions could be attributed to the variation in tick abundance due to changes in climatic conditions, agro-ecological zones, host diversity (Lightfoot and Norval 1982; Laisser et al. 2017), level of host resistance, and different tick control practices among the regions (Punya and Hassan 1992). The observed higher prevalence in Mara region, relative to that of the other regions, could be attributed to poor tick control regime practiced in this region, especially in Tarime district (Laisser et al. 2014),where most farmers dip/spray their cattle occasionally because of lack of money to buy the acaricide. Moreover, most of the farmers in this region believed that their animals were tolerant to ticks. Because of these beliefs, most farmers were reluctant to dip/spray their animals. In addition, most of the dip tanks were not functioning at the time of conducting this study and the cost of acaricide was reported to be high such that a common farmer could not afford to dip his/her cattle (Peter Nyanja personal communication). Similar findings were reported by Laisser et al. (2014) in the same region but in different villages. Also, Swaiet al. (2007) obtained similar results in the Tanga region. Another reason as to why Mara exhibited higher prevalence of *T. parva* than the other regions could be that Serengeti and Tarime districts where the samples were collected are boarded by the Serengeti National Park, where there are large numbers of buffalos which are considered to be natural carriers of the *T. parva* parasite (Marcellino et al. 2012). Cattle and buffalo populations graze together in areas close to the national park during the dry seasons due to shortage of pastures and water in the communal grazing land. Since there is a presence of large number of *R. appendiculatus* in most of the national parks (Marcellino et al. 2012), especially at the end of the wet season, cattle grazing in areas close to the national parks was at high risk of being infected with *T. parva* parasite. The findings in this study are not different from those reported by Laisser et al. (2014) who reported a prevalence of 27.7% in Mara region.

The observed lower prevalence of *T. parva* parasite in Mbeya region could be attributed to the compulsory community managed dipping regime implemented in this region, which required each livestock farmer to dip his/her animals at a nominated frequency and the fact that the burden of the tick vector (*R. appendiculatus*) was relatively low in this region (Kerario et al. 2017). Compulsory community managed dipping system implemented and relatively lower tick vector in Mbeya might have contributed to the significant reduction of the level of *T. parva* infection in this region compared to Mara region. The higher prevalence of *T. parva* observed in Mara and Singida regions may be an indication that the current tick control methods practiced were not effective enough in protecting cattle from being infested with infective ticks. On the other hand, lower *T. parva* prevalence observed in cattle managed under dipping and hand spraying together with regular frequency of acaricide application in Mbeya region suggests that the control methods used in this region were quite effective in preventing cattle from being exposed to infective vectors and the fact that the burden of the vector tick of *T. parva* (*R. appendiculatus*) was low (Lynen et al. 2007; Kerario et al. 2017). In Uganda, the spatial distribution of *T. parva* parasite has been reported to imitate that of the tick challenge (Magona et al. 2011), where lower *T. parva* prevalence (4–5%) was reported in villages with low tick challenge and high prevalence (4–12%) was reported in villages with higher tick challenge.

In the current study, cattle from Mara were more at risk of being PCR positive for *T. parva* than those from Singida and Mbeya regions. This could perhaps be due to high population and wide spread of *R. appendiculatus* in relation to other tick species found in many parts of this region (Kerario et al. 2017). This study found that the large number of ticks in Mara was associated with poor tick control strategies undertaken in this region. Most of the farmers in this region dip/spray their cattle occasionally, especially when they observe large number of ticks on their animals (Kerario et al. 2017). Cattle with larger number of ticks were more likely to be PCR positive for *T. parva* than tick-free cattle. This observation is in agreement with the study by Magona et al.(2011) in Uganda who observed higher *T. parva* prevalence in villages with higher tick burden compared to the villages with lower tick challenge. The present study found no association between *T. parva* prevalence and sex of the animals in all the three regions, implying equal vulnerability of male and female cattle. Our findings concur with what was reported by Swai et al. (2007) in Iringa and Tanga regions of Tanzania and Marcellino et al. (2012) in the Central Equatorial State of South Sudan. However, the finding of this study is contrary to the results obtained by Muhanguzi et al. (2014) in Uganda, who reported that entire male cattle were associated with higher probability of *T. parva* infection than females and castrates.

In the present study, the results show that there was no variation in *T. parva* prevalence among different cattle age groups across the regions. This suggests that cattle with different age were equally susceptible to *T. parva* infection. This finding is in agreement with the results obtained by Laisser et al. (2014) who reported no variation among cattle age groups. However, our observation is different from other studies who reported higher prevalence in adult cattle in South Sudan (Marcellino et al. 2012), Uganda (Muhanguzi et al. 2010, 2014), and Iringa and Tanga regions of Tanzania (Swai et al. 2007). Furthermore, the study shows that there was no association between frequency of tick control and *T. parva* prevalence in Mara and Mbeya regions. Unexpectedly, cattle on which tick control regime was done every 2 weeks had significantly higher *T. parva* prevalence as compared to those on which ticks were controlled monthly or occasionally in Singida region. Improper and indiscriminate use of acaricides together with incorrect dilution, which all may result into development of resistant ticks (Kagaruki 1991; George et al. 2004), might have to a certain extent contributed to this situation in this region.

Conclusion

The current study indicates that *T. parva* prevalence was lower in Mbeya region where dipping system was regularly practiced, but higher in Mara region where dipping was occasionally practiced. The results show that the prevalence of *T. parva* was lower in tick-free cattle than in those with abundant ticks. Therefore, different strategic planning and cost-effective control measures should be implemented based on the magnitude of ticks and *T. parva* challenge in the study areas in order to reduce losses caused by ticks and ECF in the study area. Based on this study, two further studies can be recommended. The first study addressing the cost/benefit calculations of each control method for various tick burdens and tick control methods, and also for cattle populations with different degrees of innate resistance to ECF and the local ticks, and the second study characterizing *T. parva* isolates in Mara, Singida, and Mbeya regions of Tanzania in comparison to the Muguga cocktail vaccine (a registered vaccine for ECF in the country).

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Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

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