EISSN: 2707-0425

East African Journal of Science, Technology and Innovation, Vol. 5 (3): June 2024

Seroprevalence and Potential Risk Factors for Lumpy Skin Disease Seropositivity in Tanga and Pwani Regions in Tanzania

[1]MAKOGA F T., [1]NASSORO Y R., [1]KAFYULILO N Z., [1]MAYENGA C., [1]CHANG'A J S., [1]BITANYI S., [2]NJAU E P., [2]CHENGULA A*

[1]Tanzania Vaccine Institute (TVI), Tanzania Veterinary Laboratory Agency (TVLA), Dar es Salaam, Tanzania.
[2]Department of Microbiology, Parasitology and Biotechnology, Sokoine University of Agriculture, Morogoro, Tanzania

***Corresponding Author**: fredymakoga212@gmail.com

Abstract

Lumpy skin disease (LSD) is an important viral disease of cattle and water buffalo affecting all breeds and all ages. Presently, the disease is among the global threats to the cattle industry due to its rapid spread and high morbidity. A cross-sectional study was conducted in Tanga and Pwani region in Tanzania from December 2022 to February 2023 to determine seroprevalence and potential risk factors associated with LSD serostatus. Sera from 200 unvaccinated cattle from 88 herds were tested for the presence of Lumpy skin disease virus (LSDV) antibodies using capripox double antigen multispecies commercial ELISA kit (ID. vet Innovative Diagnostics-France). Assessment of potential risk factors for LSD serostatus was achieved using a pretested standard questionnaire administered to the herd owner or designated representative. Descriptive statistics and chi-square, were used to analyse data. Anti- LSD antibodies were detected with an overall seroprevalence of 13.5% (CI 9.06-19.03) and 22.73% (CI =14.47- 32.89) at animal and herd levels, respectively. Seropositivity varied significantly between age categories of cattle ($\chi2$=4, p =0.0444), size of the herds ($\chi2$ = 12.65, p =0.0004), grazing system ($\chi2$ =7.3, p= 0.0069), location ($\chi2$= 6.54, p=0.0152), introduction of new animals in the herd ($\chi2$ =9.4, p=0.0021) and breeds of cattle ($\chi2$ =9.4, p=0.0021). Serostatus also varied significantly between herds where breeding bulls are shared and herds where breeding bulls are not shared. This is the first study of its kind in Tanzania to detect LSDV antibodies in unvaccinated cattle using serological technique in Tanzania. This study provides baseline information on LSD for planning further studies that can help in implementation of effective control measures.

Keywords: *Lumpy skin disease; seroprevalence; cattle, risk factors; Tanzania*

Received: 24/01/24
Accepted: 20/06/24
Published: 28/06/24

Cite as, *Makoga et al., (2024)*. Seroprevalence and Potential Risk Factors for Lumpy Skin Disease Seropositivity in Tanga and Pwani Regions in Tanzania. *East African Journal of Science, Technology and Innovation 5(3).*

Introduction

Lumpy skin disease (LSD) is an important viral disease of all breeds and ages of cattle and water buffalo. The causative agent of LSD is Lumpy Skin Disease Virus (LSDV) which belongs to the family poxviridae a member of the genus Capripoxvirus (Diallo and Viljoen, 2007). Lumpy skin Disease Virus (LSDV) is a large brick-shaped enveloped double-stranded DNA virus with about 150kbp genome size (Diallo and Viljoen, 2007). Lumpy skin disease is endemic in many sub-Saharan countries and is responsible for the poor performance of the livestock industry and

threatens country, regional, and global food security (Kiplagat *et al*., 2020). Lumpy skin disease was first reported in Zambia in 1929 and the first report of LSD outbreak in Tanzania was recorded in 1981 (Baldacchino *et al.,* 2013). The disease causes high morbidity and leads to devastating economic losses from drop in milk production, loss of draught power, loss from permanent damage to hide, mortalities, increased veterinary costs, and reduced market price (Gambo *et al.*, 2018, Kiplagat *et al*., 2020, Ratyotha *et al*., 2022). Due to its high economic impact and rapid spread across borders, LSD is among World Organisation for Animal Health listed notifiable transboundary diseases (Clemmons and Alfson, 2021, WOAH, 2021).

Lumpy skin disease transmission is mainly mechanically by blood feeding vectors including biting flies (*Stomoxys calcitrans)*, tick and mosquitoes (Chihota *et al*, 2001, Issimov *et al*., 2020, Calistri *et al*., 2020). Therefore, controlling vectors especially during outbreaks is crucial for limiting the transmission of LSDV by vectors. There is paucity of data on the role of vectors and their variation between regions on the epidemiology of LSD impacting its control (Makoga *et al*., 2023) . In endemic areas, vaccination is regarded as the most cost-effective means of controlling LSD, however, lack of reliable, effective and affordable vaccine is a worldwide challenge (Bead, 2016), which when coupled with low vaccine coverage as reported in Tanzania, augurs poorly for its control. Currently LSD is understood to be endemic in all African countries except in Morocco, Algeria, Tunisia and Libya (Tuppurainen *et al*., 2017). The prevalence of LSD ranging from 6.4% to 19.5% at animal level has been reported in Ethiopia, Uganda and Egypt (Gari *et al*., 2010, Abera *et al*., 2015, Ochwo *et al*, 2019, Hasib *et al*., 2021 and Selim *et al*, 2021). Reports of LSD occurrence outside Africa are available and linked to international trade in animals and animal products, and weak regulatory frameworks governing animal movement between different countries (Tuppurainen *et al*., 2017). Lumpy skin disease outbreaks outside Africa have been reported in Middle East, Asia and Europe (Wilhelm and Ward, 2023). Outbreaks in Middle East have been reported since 1990 in Kuwait, Lebanon, Yemen, United Arab Emirates, Bahirain, Israel and Oman (Tuppurainen and Oura, 2012). In Asia and Pacific region, the disease was first reported in north China and Baghladesh in 2019 (WOAH, 2021). The disease spread further to Chinese Tapei, Nepal, Bhutan, Vietnam, Myanmar and Hong Kong where it was confirmed in 2020 (WOAH, 2021).

Several epidemiological factors are associated with LSD occurrence such as age, sex, mean annual rainfall, communal grazing and water sources, introduction of new animals, herd size, animal breed, and sources of replacement stock (Gari *et al*., 2012; Ochwo *et al*., 2019; Selim *et al*., 2021). Introduction of new animals, sharing of grazing areas and water sources for cattle is a common practice in Tanzania (Makoga *et al*., 2023), which increases the risk of LSD transmission.

Early detection is a pre-requisite towards successful disease control, however, this requires well estalished and equiped laboratory in terms of infrastures and personnel (Kayesh *et al.,* 2020). Various techniques are available for detection of LSDV and dignosis of LSD. Some of the diagnostic method include clinical signs, serological method, viral isolation in embryonated chicken eggs or cells/tissue, and molecular detection by Polymerase Chain Reaction (PCR) and sequencing (Milena *et al*., 2019, Krešic *et al*., 2020, Amin *et al*., 2021, Saltykov *et al*., 2021). Presently there is no test for differention between natural infection and vaccinated animals (DIVA). Virus Neutralization test (VNT) is widely used as gold standard for LSDV serological diagnosis (WOAH), 2021), however, Milena *et al.,* (2019) showed high degree of agreement between Enzyme-Linked Immunosorbent Assay (ELISA) and VNT that justifies the suitability of both tests in detecting anti- LSDV (Krešic *et al.,* 2020). ELISA is a method with the ability to detect LSDV antibodies produced following vaccination or natural infection from 20 days to 7 months after exposure (Sprygin *et al*., 2018, Calistri *et al*., 2020, Krešic *et al.,* 2020). ELISA is relatively cheap hence can be used especially when large number of samples are to be screened (Milena *et al*., 2019). Nevertheless, molecular techniques remain superior over serological technique with later being time consuming and failing to distinguish

LSDV from other Capripox members (Soliman and Abdelrahman, 2008).

Tanzania is among the countries with largest cattle population in Africa while diseases are one of the many reasons for poor performance of the livestock subsector (URT, 2010). To improve the performance of livestock subsector in Tanzania, disease control is one of the government priorities through the Ministry of Livestock and Fisheries (URT, 2017). However, the success of disease control program depends on the knowledge on the epidemiology of diseases, and the associated risk factors, a missing link in Tanzania. This study therefore sought to provide epidemiological information on LSD in Tanzania by estimating the seroprevalence and potential risk factors for LSDV serostatus in Tanga and Pwani regions. This will help in adding to the scarce epidemiological knowledge on LSD in Tanzania and potentially contributes to better understanding of the diseases as a primer for its control.

Material and Methods

Study area

This study was conducted in Tanga and Pwani regions which are among the 26 administrative regions in Tanzania mainland. Tanga is located on northeast of Tanzania bordering Kenya and Kilimanjaro in the north, Manyara region to the west, Morogoro and Pwani region to the south and Indian ocean to the east. Tanga has a total area of 26,667 km^2 divided into 11 administrative districts. The average temperature and annual precipitation in Tanga are 26^{o}C and 982 mm, respectively. Pwani region is located on eastern part of Tanzania with 26.2^{o}C average temperature and average annual precipitation of 995 mm. Pwani has a total area of 32547 km^2 divided into eight (8) administrative districts and borders Tanga region to the north, Morogoro to the west and Lindi region to south and surrounds Dar es Salaam to east. According to the national Agricultural census 2019/2020, Tanga and Pwani region has a total of 1.5milion and 739,101 cattle respectively (URT, 2021). Livestock diseases is one of the major challenges in cattle production in Tanga and Pwani region with diseases such as East coast fever, trypanosomiasis, anaplasmosis, Lumpy skin disease, food and mouth disease and black quarter disease and brucellosis have been reported to occur in the area (URT, 2021). Figure 1 is a sketch of the study area.

Study design

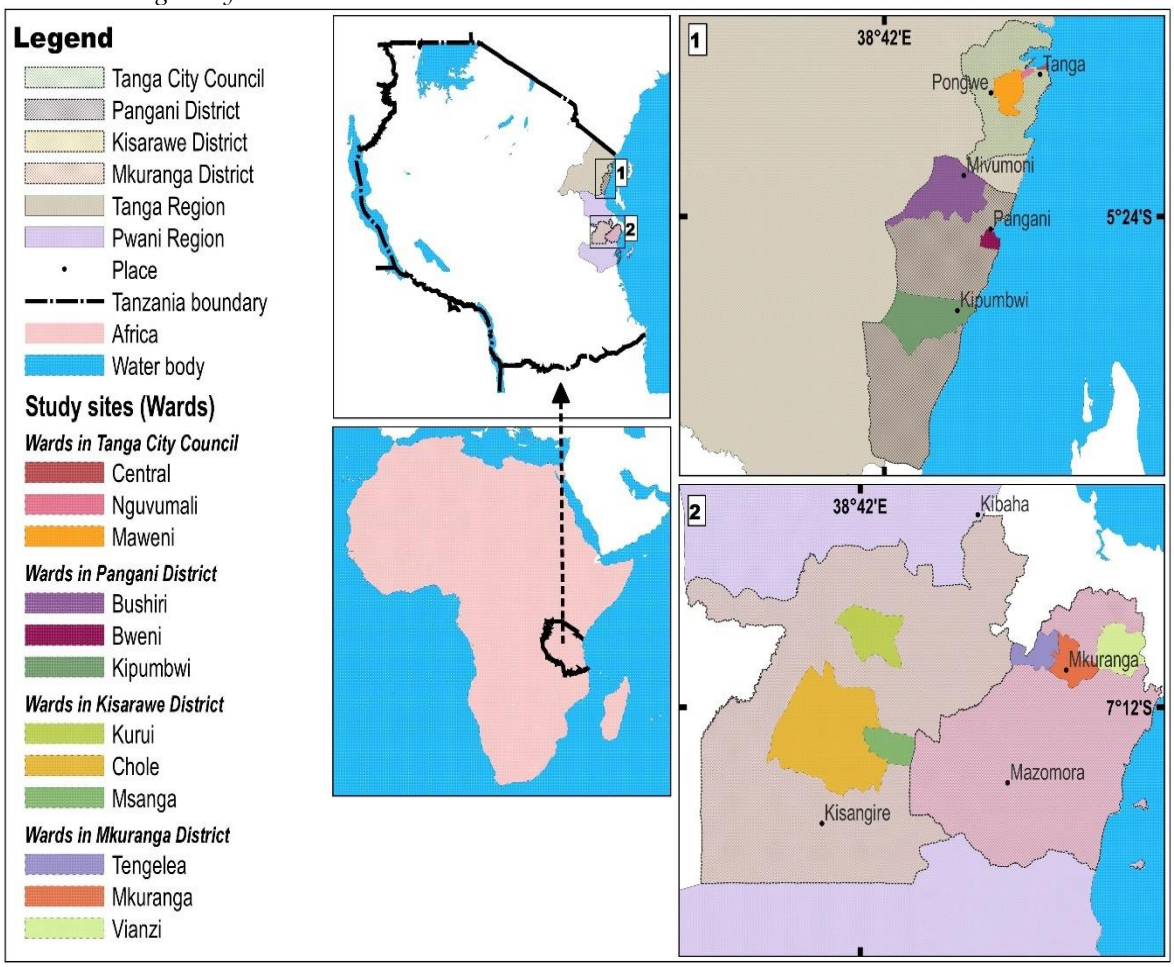
This was a cross-sectional study conducted in Tanga and Pwani regions from December 2022 to February 2023. A multistage sampling method was employed where districts and wards were selected purposively based on accessibility, presence of different farming system, geographical representativeness and farmers willingness to participate in the study following consultations with District Veterinary Officers. Districts which were included in the study are Pangani and Tanga city district from Tanga region and Mkuranga and Kisarawe districts from Pwani. Three wards were included from each district namely Kipumbwi, Bweni and Bushiri from Pangani district, Maweni, Central and Nguvumali from Tanga city council. In Pwani region, Vianzi, Mkuranga and Tengelea participated from Mkuranga district while Kurui, Chole and Msanga from Kisarawe district participated in the study. On the day of field visit, the ward Extension Officers prepared list of households from which systematic random sampling employed to select households/herds for sample collection. The first household in the list were selected and then one household after every three-household in the list was selected. The list had a total of 352 household in the two regions. Only herds with at least three animals were included and a range of 1-5 unvaccinated animals aged 6 months and above were selected. Based on age, animals were categorized into 6 -11 months, 12-48 months and above 48months as calves, young and adults, respectively. Herds were also categorized according to their size into small (1-5), medium (6-20) and large (above 20 animals).

Sample size estimation

Sample size was estimated according to Thrusfield (2007) at 95% confidence level and 5% absolute precision. 10% expected prevalence rate was considered for sample size estimation based on the reported prevalence by Ochwo *et al.,* (2019) in Uganda. From the formula the estimated sample size was 139 cattle, to increase precision a total of 200 cattle from 88 herds were sampled.

Figure 1

Sketch showing study area



Sample collection

Whole blood was collected by venipuncture from the jugular vein into plain vacutainer tube and maintained in upright position at room temperature to allow clotting and separation of sera. Sera were extracted within 12 hours of collection using pipette and transferred into 1.8ml sterile cryovials. Sera were packed in cool box with icepacks before transporting to Center for Infectious Disease and Biotechnology (CIDB) Laboratory for processing and stored at -20^{o}C until analysis.

Determination of seroprevalence

Detection of LSDV antibodies was achieved using Capripox Double Antigen Multi-species commercial ELISA kit ((ID.vet Innovative Diagnostics-France) (Milena *et al.*, 2019, Ochwo *et al.*,2019), following the manufacturer's protocol. Briefly, optical density was measured at 450nm using ELISA microplate and sample percentage was estimated as

$$SP=\frac{(ODsample-ODnc)}{ODpc-ODnc}\ X100.$$

All sample with SP value greater than 30% regarded positive.

Where, ODsample is optical density of the sample, ODnc is optical density of the negative control and OD pc is optical density for positive control.

Seroprevalence were determined using the following formula

Animal level seroprevalence

$$= \frac{Animal\ tested\ posive}{Total\ animals\ tested} \text{x}100$$

Herd Level seroprevalence

$$= \frac{Herd\ tested\ posive}{Total\ herds\ tested} x100$$

Assessment of potential risk factors

This was achieved using a pretested standard questionnaire administered to the herd owner or designated representative. Potential risk factors included are age of animals, sex, region, herd size, grazing system, breeding system, source of breeding bull, location and introduction of new animals into the herd**.**

Data analysis

Analyses were carried out using Epi Info Statistical Package Version 7.2.5 (Centers for Disease Control and Prevention, Georgia, USA). Descriptive statistics used to analyse seroprevalence data and results presented in tables while chi- square test was employed to compare the seroprevalence between categories of the selected potential risk factors.

Results

Characteristics of the study population

Table 1 summarizes characteristics of the study population. The study examined two hundred (200) cattle from the two regions where 114 (57%) were from Tanga region and 86 (43%) from Pwani region. The total number of animals examined per district were 72 (36%) in Pangani, 42 (21%) in Tanga city, 40 (20%) in Mkuranga and 46 (23%) in Kisarawe. Out of the examined cattle, (53.5%, n= 107) were indigenous (53.5%, n= 107). Over 70% of cattle examined in this study were grazed communally, and came from the herds where breeding is done naturally (85%, n =117).

Table 1

Characteristic of the study population

Parameter	Category	Total	Proportion %
Animal per region	Tanga	114	57
	Pwani	86	43
Animals per district	Pangani	72	36
	Tanga city	42	21
	Mkuranga	40	20
	Kisarawe	46	23
Number of herds per district	Pangani	29	33
	Tanga city	28	31.8
	Mkuranga	15	17.0
	Kisarawe	16	18.2
Sex	Female	166	83
	Male	34	17
Age	6-11 month	58	29
	>1-4years	62	31
	>4years	80	40
Herd size	Small	25	12.5
	Medium	74	37.5

	Large	101	50.5
Breed	Indigenous	107	53.5
	Cross-breed	93	46.5
Grazing system	Zero grazing	59	29.5
	Communal grazing	141	70.5
Breeding system	Natural	170	85
	Artificial	23	11.5
	Both	7	3.5
Location	Urban	42	21
	Peri-urban	57	28.5
	Rural	101	50.5

Prevalence

Animal level prevalence

A total of 200 cattle were tested for the presence of antibodies against LSDV of which 27 cattle were positive (seroprevalence 13.5% (CI= 9.06-19.03). The highest seroprevalence was recorded in Pangani district (18.06%, CI= 9.98-28.6) with Kisarawe and Mkuranga having a seroprevalence of 17.39% (CI= 7.82-42.42) and 15.8% (CI= 5.7%-29.84), respectively. All sera from Tanga city council were negative for anti-LSDV.

Herd level seroprevalence

Twenty (20) herds had at least one cattle tested positive for LSD antibodies leading to an overall apparent herd seroprevalence of 22.73% (CI =14.47- 32.89). Kisarawe had the highest apparent herd seroprevalence of 37.7% (CI =15.2-64.57), while Pangani had seroprevalence of 34.48% (CI= 17.94-54.33) and Mkurangahad seroprevalence of 26.67% (CI= 7.79- 55.1).

Table 2 summarizes result on statistical inference of variation in seroprevalence between categories of the selected potential risk factors where LSDV seroprevalence varied significantly with age of cattle (χ^2=4, p =0.0444) with the highest prevalence in cattle aged >4 years (18.75% CI=10.0-29.03). Seroprevalence also varied significantly with herd size (χ^2 = 12.65, p =0.0004). Between herd size categories, cattle from large herd size had the highest rate of seropositivity (22.7%, CI=15.02-32.18). Moreover, significant variation in seroprevalence was observed with grazing system (χ^2 =7.3, p =0.0069) where cattle from the communal grazing system had the highest prevalence (17.75%, CI=11.82-25.05) and lowest prevalence in cattle from zero grazing system (3.39% CI=0.41-11.71). In the present study, location was another potential risk factors observed to have a varying LSDV serostatus between rural, urban and peri-urban location (χ^2 6.54, p=0.0152) where higher rate of seropositivity was observed in animals from rural area location (22.77% CI=15.02-32.18) than in peri-urban (7.02%, CI=1.95-17.00) and urban (0%, CI=91.59-100). Furthermore, when LSDV seroprevalence between animals from herds with and without history of introducing new animals compared, the variation was statistically significant (χ^2 =9.4, p=0.0021). Prevalence in animals from the herds with and without history of introducing new animals was (26.53%, CI=14.95-41.07) and 9.27% (CI=5.16-15.07) respectively. In our study, comparison in seroprevalence was made between indigenous cattle (21.51%, CI= 13.66-31.24) and cross breed (6.54%, CI=2.67-13.02). This difference in seroprevalence between the two breeds was statistically significant (χ^2 =9.5, p=0.002). Furthermore, seroprevalence varied with source of breeding bull in which higher rates of seropositivity was observed animals from the

herds where breeding bulls are shared (19.57%, CI=12.34-27.93) than in animals from the herd with own breeding bull or use artificial insemination

Table 2

Statistical Inference of Variation in Prevalence between Categories of the Selected Potential Risk Factors

Factor	Category	Total	Prevalence (%)	CI	χ^2	P value
Age	6-11month	58	6.90	1.96-16.73		
	1-4 years	62	12.90	5.74-23.85	4.04	0.0444*
	>4 years	65	18.75	10.0-29.03		
Region	Tanga	114	11.40	6.21-18.71	0.999	0.320
	Pwani	86	16.28	9.20-25.80		
Herd	Small	25	8.00	0.98-26.03	12.65	0.00004*
	Medium	74	2.70	0.33-9.42		
	Large	101	22.7	15.02-32.18		
Sex	Female	166	15.06	9.99-21.45	2.02	0.154
	Male	34	5.88	0.72-19.68		
Grazing	Communal	116	17.75	11.82-25.05		
	Zero grazing	59	3.39	0.41-11.71	7.3	0.0069*
Breeding	Natural	170	14.12	9.26-20.27		
	Both	7	0	59.04-100	0.42	0.521
	Artificial	20	13.04	2.78-33.59		
Breeding bull source	Shared	109	19.27	12.34-27.93		0.001*
	Own	65	3.08	0.37-10.68		
Location	Peri-urban	57	7.02	1.95-17.00	6.54	0.0152*
	Rural	101	22.77	15.02-32.18		
	Urban	42	0	91.59-100		
Animal introduction	No	151	9.27	5.16-15.07	9.4	0.0021*
	Yes	49	26.53	14.95-41.07		
Breed	Cross	93	6.54	2.67-13.02	9.5	0.002*
	Indigenous	107	21.51	13.66-31.24		

Ref =Reference, *=significant at p≤0.05

Discussion

In the present study, cattle from all farming systems in the surveyed area were involved in the study. Our study observed communal grazing and natural breeding in majority of the herds in the surveyed area. This is in line with the report in the previous study by Makoga *et al*, (2023) were communal grazing and natural breeding appeared to dominate the cattle production system. This is presumably due to presence of large unoccupied land that allow communal grazing. However, this is a traditional farming which is linked to low productivity and poor performance of the livestock subsector. Domination of natural breeding could be a sequel of uncontrolled breeding in communal grazing. Therefore, there is a need for extension knowledge provision to farmers on the use of the available land resource to grow improved pasture and to promote improvement of cattle breed by adopting the use improved semen to improve productivity (Notenbaert *et al*., 2020, URT, 2010).

This study is the first in Tanzania to confirmed LSDV antibodies in cattle by serological technique. Detection of antibodies in unvaccinated cattle in Tanga and Pwani regions suggests presence of this economically important disease (LSD) and the possibility that cattle are being exposed to LSDV. The present study has established an apparent seroprevalence of 13.5% and 22.73% at herd and animal level,

respectively. Our study also assessed potential risk factors for LSDV serostatus where variation in seroprevalence was observed to be significant between different age categories of cattle, grazing system, herd size, location, breeds of cattle, introduction of new animals in the herd and source of breeding bulls which are therefore, potential risk factor.

The observed overall seroprevalence of 13.5% at animal level is lower than what early reports described in Egypt, where prevalence higher as 19.5% was reported (Selim *et al*., 2021). The prevalence of 8.1%, 6.4%, 8.7%, and 7.6% which is lower than the seroprevalence observed in the present study have been reported in Ethiopia and Uganda (Gari *et al*. 2010, Abera *et al*. 2015, Ochwo *et al*. 2019, Hasib *et al*. 2021)). Similarly, variation in seroprevalence observed at herd level where our study established seroprevalence of 22.73% which is lower than 72.3% reported in Uganda (Ochwo *et al*., 2019) and close to 20.8% reported in Ethiopia (Dubie *et al*., 2022). The effect of variability in management practices, geographical location, climatic conditions and season on different drivers of LSD including vector population, are the possible reasons for the observed variation in seroprevalence. Different study designs and testing methods have been used to establish seroprevalence which can also contribute to the observed variability.

Anti-LSDV were not detected in all cattle samples from Tanga city council. This gives the impression that in the city there is a limited exposure to LSDV, perhaps due to low population of biting vectors attributed to increased human activities in cities which is known to interfere with breeding and resting places for vectors (Malele *et al*., 2011). Additionally, management system such as indoor feeding of cattle due to scarcity of land resource in most cities and existence of by-laws that restrict animal movement in cities, could also contribute to low exposure to LSDV.

Moreover, our study observed variations in LSDV serostatus between districts in the surveyed area which agrees with previous studies in Ethiopia where LSDV seroprevalence varied significantly between administrative zones (Gari *et al*., 2012). This is a possible indication that the exposure rate to LSDV varies between districts which is likely attributed to variation in prevalence, and distribution of vectors between districts, which are the determinants of LSDV transmission as reported by Chihota *et al*, (2001) and Issimov *et al*., (2020).

LSD seroprevalence was higher in cattle aged >4 years than in young cattle group aged below 4 years. Similar finding have been reported by Ochwo *et al*., (2019) and Amin *et al*., (2021). The observed higher seroprevalence in older cattle is linked to increased exposure and production stress which increase the susceptibility of cattle to LSD and other diseases. Due to possible endemicity of LSD in the area as documented by Tuppurainen *et al*, (2017), natural passive immunity in calves can also explain the variability in prevalence between different age groups of cattle.

The seroprevalence in the present study was also higher in cattle from large herd sizes. This is consistent with previous report in Ethiopia by Dubie *et al*, (2022) and recent study in Tanzania by Makoga *et al*, (2023). Higher rate of seropositivity in cattle from large herd sizes can be associated with inadequate pasture to accommodate large number of animals leading to starvation and long-distance tracking of cattle to search for pasture and water especially during dry season where pasture resources are scarce. Long distance tracking and starvation increase the chance of exposure and susceptibility of cattle to vectors and diseases including LSD.

Moreover, the present study observed higher seroprevalence in communally grazed cattle than in zero-grazed cattle which is in line with findings documented early (Gari *et al*., 2010, Selim *et al*., 2021) . Close contact of cattle from different herds with unknown disease status increases the possibility of LSD transmission though contaminated pasture and water and possible increased efficiency of mechanical transmission by vectors and hence, higher seroprevalence in communal grazing compared to cattle in zero grazing system where interactions between herds is minimum

Furthermore, LSD seropositivity observed to be higher in animals in rural area location. This can be explained by environmental and demographic

factors which possibly determine the levels of animal exposure to vectors and LSDV. For instance, in rural areas the number of vectors which are important in facilitating LSDV mechanical transmission is likely higher due to presence of large an occupied land that favor vectors breeding unlike in urban areas where due to increased human activities, availability of unoccupied land is limited as explained by Malele *et al*., (2011)

Our study further reports variation in seroprevalence between animals from herds with and without history of introducing animals from other herds. Seroprevalence was specifically higher in herds where new animals were introduced through sharing of breeding bull and stock replacement. This findings mirrors early reports (Amenu, 2018, Issimov *et al*., 2020), who reported increase in risk to LSDV exposure with introduction of new animals in the herd. Lack of rapid and cost- effective diagnostic facilities and failure to quarantine new animals before introducing in the herd cold also contribute to the observed results

Unlike previous finding by Kiplagat *et al*. (2020) and Hasib *et al*. (2021) who found higher risk and prevalence of LSD in crossbred cattle, in the present study the scenario was different where seroprevalence was higher in indigenous cattle. The difference in seroprevalence between breeds of cattle in the surveyed area could be associated with variation in management practices. In most cases indigenous cattle are considered hard and resistance to most diseases as reported by Vordermeier *et al.* (2012), the level of management such as vaccination and vector control is possibly less stringent in indigineous breed than in cross-breed which are believed to be more delicate and susceptible to diseases (Hasib *et al*, 2021). This supports previous reports of LSD being a disease of all breeds of cattle (WOAH, 2021). Furthermore, due to their low productivity nature, in most cases indigenous breed cattle are found in the rural area where the possibility of beeing exposed to LSD increases due to presese of large unoccupied land which contribute to increase in abundunce and prevalence of vectors, the key player in LSD epidemiology.

This is the first study in Tanzania to report on LSD seroprevalence and potential risk factors for LSDV serostatus. Detection of LSDV antibodies in animals in Tanzania is an indication that LSDV, the causative agent of the economically important disease (LSD) is circulating in the cattle population in Tanzania and cattle are possibly frequently exposed. Due to high economic impact associated with LSD, this information justifies the need of planning and implementing effective control measures against this disease including provision of extension knowledge to livestock farmers on LSD. However, further studies to establish LSD prevalence and the associated risk factors countrywide is important. Molecular confirmation and characterization of the LSDV-circulating in Tanzania is important for generation of information which can contribute to better control of the disease and improve the performance of livestock sector and its contribution towards sustainable livelihood.

Acknowledgement

Authors are thankful to the Tanzania Veterinary Laboratory Agency for financial support to conduct this study. Thanks are extended specifically to Grace Gabriel Geda, Paulo Joseph, Bishop Magidanga, Katarina Anakleti, Mark Joseph Mark, Rosejane Moshy and Benson Lukas for their support during this study.

The study complied with the ethical standards; Ethical clearance granted by Research Ethics Committee at Sokoine University of Agriculture with approval number SUA/DPRTC/R/186/031. All participants freely consented to participate in this study.

Funding– This work was funded by the Tanzania Veterinary Laboratory Agency.

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