314 (2025) 106443

Contents lists available at ScienceDirect

The Veterinary Journal

journal homepage: www.elsevier.com/locate/tvjl

Schmallenberg virus exposure in camels and donkeys: Potential reservoirs for trans-border spread in the Nigeria-Sahel region

Alex A. Adikwu [a,b,d,*], Theophilus I. Emeto [a,e,g], Paul F. Horwood [c,d,e], Olajide A. Owolodun [f], Andrew M. Adamu [c,d,e], Emmanuel O. Ngbede [j,k], Yiltawe S. Wungak [i], Hussaini G. Ularamu [i], Oyelola A. Adegboye [a,d,h]

[a] Public Health and Tropical Medicine, College of Medicine and Dentistry, James Cook University, Townsville, QLD, Australia
[b] Department of Public Health and Preventive Medicine, College of Veterinary Medicine, Joseph Sarwuan Tarka University, Makurdi, Nigeria
[c] Veterinary Science, College of Sciences and Engineering, James Cook University, Townsville and Cairns, Townsville, QLD, Australia
[d] Centre for Tropical Biosecurity, James Cook University, Townsville, QLD, Australia
[e] Australian Institute of Tropical Health and Medicine, James Cook University, Townsville, QLD, Australia
[f] Biotechnology Division, National Veterinary Research Institute, Vom, Nigeria
[g] World Health Organization Collaborating Centre for Vector-Borne and Neglected Tropical Diseases, College of Medicine and Dentistry, James Cook University, Townsville, QLD, Australia
[h] Menzies School of Health Research, Charles Darwin University, Darwin, NT, Australia
[i] Viral Research Division, National Veterinary Research Institute, Vom, Nigeria
[j] Institiute of Medical Microbiology and Hygiene, Saarland University, Homburg, Germany
[k] Department of Veterinary Microbiology, College of Veterinary Medicine, Joseph Sarwuan Tarka University, Makurdi, Nigeria

ARTICLE INFO

Keywords:
Schmallenberg
Transboundary
Seroprevalence
Camel
Donkey
Disease

ABSTRACT

Livestock trade and altered migration patterns have influenced the spread of transboundary animal diseases (TADs). Schmallenberg virus (SBV), an emerging arboviral pathogen transmitted by biting midges, causes severe birth defects and abortions, transient fever, diarrhea, and reduced milk production in ruminants, exemplifying a global threat to domestic livestock populations. This study investigated the exposure of camels and donkeys to SBV and identified potential risk factors that may influence introduction and spread. A total of 460 serum samples from camels (n = 230) and donkeys (n = 230) were screened for SBV antibodies using a commercial enzyme-linked immunosorbent assay (ELISA), and data on potential risk factors were collected. The observed seroprevalence of SBV was 56.5 % in camels and 11.3 % in donkeys. Univariate analysis demonstrated a significantly higher seroprevalence in older camels (P = 0.008; odds ratio (OR) = 2.3; 95 % confidence interval (CI): 1.25–4.27) and donkeys (P = 0.004; OR = 3.41; 95 % CI: 1.48–7.97). Seropositivity was not significantly influenced by sex, management system, or mixed species rearing. Multivariable analysis revealed geographic clustering of infection risk, with significantly higher odds of seropositivity in camels from Zangon Daura (OR = 4.73; 95 % CI: 1.33–20.4) and donkeys from Sule Tankarkar (OR = 4.46; 95 % CI: 1.20–17.9). Our findings suggest that camels and donkeys are exposed to SBV and might serve as reservoirs and potential sources for spread within the region. Further molecular studies are recommended for a deeper understanding of SBV transmission dynamics.

Introduction

Transboundary animal diseases (TADs) are infectious diseases with the potential to cause severe consequences when introduced into new territories through their impact on domestic animal populations, significant economic and food security implications, and capacity for international spread, requiring extensive control measures (Lubroth and Balogh, 2009; Clemmons et al., 2021). In West Africa, the border regions between Nigeria and the Sahel - encompassing Northern Nigeria, Southern Niger, and Chad - is a significant hub for agricultural trade (Pannhausen and Untied, 2010). Livestock migration patterns in this region have intensified, largely driven by urbanisation, demographic

* Corresponding author at: Public Health and Tropical Medicine, College of Medicine and Dentistry, James Cook University, Townsville, QLD, Australia.
E-mail address: alex.adikwu@my.jcu.edu.au (A.A. Adikwu).

https://doi.org/10.1016/j.tvjl.2025.106443
Received 8 August 2025; Received in revised form 16 September 2025; Accepted 16 September 2025
Available online 17 September 2025
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shifts, and rising incomes, creating conditions highly favorable for expanded intra-regional livestock trade (Hollinger and Staatz., 2015). It is estimated that over 60 % of the global dromedary camel and donkey populations are distributed across Africa, with these species playing crucial roles in import and export activities worldwide (Chu et al., 2015). The increasing cross-border movement of camels and donkeys in the Nigeria-Sahel region, influenced by expanding commercial activity, population growth, and desertification, combined with their vital contributions to agricultural services, transportation, and food systems, establishes these animals as potential sources for the introduction and spread of emerging TADs (Adamu et al., 2021; Salam et al., 2022).

The emergence of Schmallenberg virus (SBV) exemplifies the global vulnerability of domestic livestock to novel pathogens. SBV is an RNA orthobunyavirus, and causes disease in livestock, characterized by pyrexia, diarrhea, reduced milk yield, abortions, and congenital malformations. It has the potential to spread rapidly across herds when transmitting vectors, such as *Culicoides* spp., are present (Wernike et al., 2014). Although SBV was initially identified as a disease primarily of sheep, goats, and cattle (Reusken et al., 2012; Oluwayelu et al., 2018; Sibhat et al., 2018; Benfodil et al., 2025), subsequent epidemiological studies have detected SBV antibodies in horses (Rasekh et al., 2018), dogs (Wensman et al., 2013), pigs (Poskin et al., 2014) and various wildlife species, including red deer (Linden et al., 2012), mouflon, bison (Mullen and Murphree, 2019), llamas, and alpacas (Jack et al., 2012). SBV infection in camels has gained increasing attention in Europe and the Middle East. Wernery et al. (2013) reported an overall seroprevalence of 36.5 % among dromedaries from Pakistan, Sudan, and the United Arab Emirates. A subsequent study by Schulz et al. (2015) detected 62.4 % seropositivity in llamas and alpacas in Germany, while Pestil et al. (2021) reported 15.1 % seroprevalence among local dromedary camels in Turkey.

The expansion of camel trade in the Sahelian region, coupled with unregulated transboundary livestock movement routes utilised by pastoralists (Adamu et al., 2021), underscores the critical need for enhanced surveillance for transboundary, emerging and re-emerging pathogens. Robust surveillance systems function as an early warning system for pathogen introduction into the country, aiding in epidemic prevention and safeguarding both human and animal health. Epidemiological surveys provide policymakers with essential empirical evidence to assess disease outbreak probability and evaluate potential consequences, enabling the implementation of appropriate management measures for emerging and re-emerging diseases. This study evaluated the seroprevalence of SBV in camels and donkeys and investigated possible risk factors associated with SBV introduction and spread across the Nigeria-Sahel border region.

Material and methods

Study area

The research was conducted in the Sahelian region of Northern Nigeria, which shares borders with the Republic of Niger. The Sahel is a semi-arid region that serves as a transition zone between humid tropical Africa and the arid Sahara Desert, characterised by abundant sunshine and consistently high temperatures ranging from 36°C −42°C, alongside highly unpredictable low levels of rainfall, which often leads to prolonged droughts and intense floods in some instances (Eboreime et al., 2025). Nigeria houses approximately 296,100 camels (Camel Population by Country 2025) and around 1357,245 donkeys (Donkey Population by Country., 2025), which are predominantly located in the North-Western region (Ghude et al., 2020). Five local government areas (LGAs) were selected for this study: Maigatari, Babura and Suletankarkar from Jigawa State; along with Mai'adua, and Zangon Daura from Katsina State. These LGAs were chosen due to their significant camel and donkey populations, mainly driven by transhumance pastoralists activities. Additionally, Maigatari and Mai'adua host international livestock markets where animals, including camels and donkeys sourced from Niger Republic, Mali, Chad, and Cameroon, are traded (Adamu et al., 2022).

Study design and Sample collection

A convenience-based, cross-sectional study was conducted. The sample size was calculated using the formula for estimating proportions with specified precision (Thrushfield and Christley 2018), assuming an expected prevalence of 50 % (to maximise sample size for unknown true prevalence), a 95 % confidence level, and a desired precision of 5 %. This resulted in a minimum sample size of 225 animals per species, to which a 20 % contingency was added, leading to a target of 230 animals for both donkeys and camels. The animals were humanely restrained, and 5 mL of blood was drawn from each animal via venipuncture and transported to the laboratory. Subsequently, the samples were centrifuged at 4000 rpm for 15 min, after which the serum was aseptically extracted and transferred to labelled microtubes for storage at −20°C. Documented risk factors included the animal's sex, age, location, management systems employed by the owners, watering sources, and involvement in cross-border movements. Additional information collected included the purpose for rearing the animals and whether the camels and donkeys were kept alongside other animal species.

Serological detection of SBV antibodies

Serum samples from camels and donkeys were tested for antibodies against SBV using commercially available ID Screen® Schmallenberg virus indirect - multi-species enzyme-linked immunosorbent assay (ELISA) screening test kit (IDvet, Grabels, France), following the manufacturer's protocol. The manufacturers reported a sensitivity and specificity of 97.7 % and 99.7 % respectively, for the test. The plates were measured and recorded at an optical density (OD) of 450 nm using an ELISA reader spectrophotometer (Thermoscientific™ Multiskan™ MA, USA). The sample-to-positive ratio (S/P%) was calculated using the formula: S/P% = [(ODsample - ODnegative control)/(ODpositive control - ODnegative control)] × 100.Samples were classified as seropositive when S/P% exceeded 60 %, intermediate when S/P% values ranged from 50 % and 60 %, and seronegative when S/P% values were below 50 %.

Variables

Outcomes

The primary outcome is SBV serostatus (positive or negative) in camels and donkeys.

Predictors

The predictor variables documented included the animals' age, which was categorised into young (0–5 years) and adult (5 years and above) for camels. For donkeys, those 0–4 years old were classified as young, while those 4 years and above were considered adult. Sex was recorded as male and female, location was noted by local government areas (LGAs), and management systems were classified as semi-intensive or extensive. The purpose for rearing was designated as slaughter, milk, labour, or transportation. Water source was grouped as either a borehole, a well, or a stream. Mixed rearing was classified as "Yes" for camels and donkeys raised alongside other animal species, and "No" for animals not raised with other species. "Yes and "No" classifications were similarly used to indicate the history of cross-border movement for animals.

Data analysis

The apparent prevalence of SBV serostatus in camels and donkeys was calculated with Clopper–Pearson 95 % confidence intervals (CI),

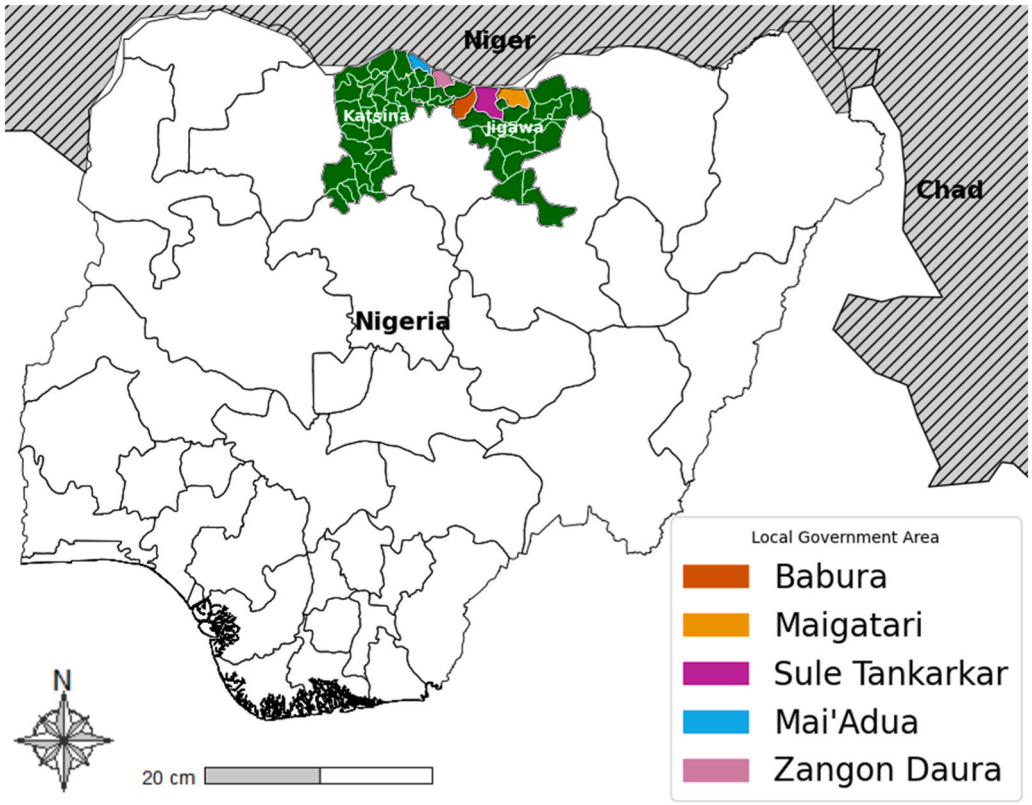

Fig. 1. Map of Nigeria showing LGAs bordering the Sahelian region.

while the true prevalence was estimated by adjusting the apparent prevalence for the reported specificity and sensitivity of the SBV ELISA screening test kit. Associations between animal seropositivity and predictor variables (such as species, age, sex, location, and management practices) were first assessed using univariate logistic regression. All variables were subsequently included in the multivariable logistic regression model. Results are presented as odds ratios (OR) and adjusted odds ratios (aOR) with their corresponding 95 % confidence intervals (CI) and associated p-values. All predictors were checked for multicollinearity using the generalized variance inflation factor (GVIF), adjusted for the degrees of freedom (McCullagh and Nelder, 2019). Only variables with low collinearity (GVIF values, 1–1.7) (Table 5) were considered in the multivariable logistic regression model. The final model was assessed using the Hosmer and Lemeshow method for goodness-of-fit and the receiver operating curve (ROC) for reliability (Hosmer and Lemeshow, 2000; Dohoo et al., 2009). All analyses were carried out in R version 4.3.3, and statistical significance was set at $p < 0.05$

Ethics

Ethical approval for the study was obtained from the Research and Ethics Committee of the National Veterinary Research Institute (Vom, Nigeria) with reference number AEC/02/115/22. This approval was acknowledged by James Cook University (JCU), acting as an external approval on the use of animal and human subjects for research board.

Results

Seroprevalence and risk factors of SBV in camels

The findings from 230 camels sampled across five LGAs revealed an overall apparent prevalence of 56.5 % (130/230). The true seroprevalence, adjusted for kit performance, was estimated to be 57.7 % (95 % CI: 50.9 – 64.4). Adult camels (over 5 years) showed a significantly higher rate of seropositivity, being 2.3 times more likely to be seropositive than younger camels (5 years or younger) (P = 0.008, OR=2.3, 95 % CI: 1.3–4.3). Although seroprevalence was higher in females (57.8 %, 95 % CI: 47.7–67.6) compared to males (55.5 %, 95 % CI: 46.4–64.3), this difference was not statistically significant (P = 0.69).

Seropositivity was identified in camels from all five LGAs. Univariate analysis indicated that Zangon Daura recorded the highest seroprevalence (73.3 %, 95 % CI: 54.1–87.7) and differed significantly when compared to Mai'Adua (P = 0.005, OR=4.1, 95 % CI: 1.6 – 11.6), which served as the reference LGA in the univariate model. The likelihood of seropositivity was significantly higher in camels utilised for farm labour than those raised for slaughter (P = 0.047, OR=2.3, 95 % CI: 1.0–5.4). The majority of camels were kept under extensive management systems (n = 173; 75.2 %), accessed drinking water from streams (n = 182; 79.1 %), and were reared alongside other animals (n = 207; 90 %). Nevertheless, there was no significant variation in seroprevalence based on management practices (P = 0.87), sources of water (P = 0.61), or interactions with other animals (P = 0.74). All sampled camels (100 %) participated in cross-border movement (Table 1), thus preventing its assessment as a variable risk factor within this study.

Table 1
Prevalence of SBV antibodies in camels and donkeys.

Species	No. sampled	No. positive	Apparent Prevalence (95 %CI)	True Prevalence (95 %CI)
Camel	230	130	56.52 % (49.85–63.02)	57.69 % (50.85 – 64.37),
Donkey	230	26	11.30 % (7.52–16.12)	11.27 % (7.38 – 16.22)

P < 0.0001, OR = 10.2, 95 % CI: 6.28–16.56

Table 2
Univariate logistic regression analysis of the presumed risk factors of SBV among camels.

Variable	Categories	n (%)	Positive (%, 95 %CI)	OR (95 %CI)	P-Value
Age	Young (0–5 yrs)	56 (24.3	23 (41.07, 28.10–55.02)	Ref	
	Adult (>5 yrs)	174 (75.7)	107 (61.49, 53.83–68.76)	2.29(1.25–4.27)	**0.008***
Sex	Male	128 (55.7)	71 (55.47, 46.43–64.25)	Ref	
	Female	102 (44.3)	59 (57.84, 47.66–67.56)	1.10 (0.65–1.87)	0.72
Location	Mai'Adua	50 (21.7)	20 (40.00, 26.41–54.82)	Ref	
	Sule Tankarkar	40 (17.4)	19 (47.50, 31.51–63.87)	1.36 (0.59–3.16)	0.48
	Babura	30 (13.0)	18 (60.00, 40.6–77.34)	2.25 (0.90–5.78)	0.09
	Maigatari	80 (34.8)	51 (63.75, 52.24–74.21)	2.64 (1.29–5.52)	**0.009***
	Zangon Daura	30 (13.0)	22 (73.33, 54.11–87.72)	4.12 (1.58–11.6)	**0.005***
Management systems	Semi-intensive	57 (24.8)	32 (56.14, 42.36–69.26)	Ref	
	Extensive/ Nomadic	173 (75.2)	98 (56.65, 48.91–64.15)	1.02 (0.56–1.86)	0.95
Rearing purpose	Slaughter/Meat	31 (13.5)	13 (41.94, 24.55–60.92)	Ref	
	Milk	100 (43.5)	57 (57.00, 46.71–66.86)	1.84 (0.82–4.22)	0.145
	Farm labour	96 (41.7)	60 (62.50, 52.03–72.18)	2.31 (1.02–5.36)	**0.047***
	Transportation	3 (1.30)	0 (0, 0–70.76)	0.91(0.08–10.43)	0.91
Watering source	Borehole	4 (1.7)	1 (25.00, 0.63–80.59)	Ref	
	Well	44(19.1)	25 (56.82, 41.03–71.65)	3.95 (0.46–83.3)	0.25
	Stream	182 (79.1)	104 (57.14, 49.61–64.44)	4.00 (0.50–81.7)	0.23
Mixed rearing	Yes	207 (90.0)	117 (56.52, 49.47–63.38)	Ref	
	No	23 (10.00	13 (56.52, 34.49–76.81)	1.00 (0.42–2.44)	1.00

Table 3
Univariate logistic regression analysis of the presumed risk factors of SBV among donkeys.

Variable	Categories	n (%)	Positive (%, 95 %CI)	OR (95 %CI)	P-Value
Age	Young 0–4 yrs	164 (71.3)	12 (7.32, 3.84–12.43)	Ref	
	Adult > 4 yrs	66 (28.7)	14 (21.21, 12.11–33.02)	3.41 (1.48–7.97)	**0.004***
Sex	Male	85 (37.0)	5 (5.88, 1.94–13.20)	Ref	
	Female	145 (63.0)	21 (14.48, 9.19–21.28)	2.71 (1.05–8.37)	0.05
Location	Maigatari	80 (34.8)	5 (6.25, 2.06–13.99)	Ref	
	Zangon Daura	30 (13.0)	2 (6.67, 0.82–22.07)	1.07 (0.15–5.29)	0.94
	Mai'Adua	50 (21.8)	4 (8.00, 2.22–19.23)	1.30 (0.31–5.17)	0.70
	Babura	30 (13.0)	5 (16.67, 5.64–34.72)	3.00 (0.78–11.60)	0.10
	Sule Tankarkar	40 (17.4)	10 (25.00, 12.69–41.20)	5.00 (1.64–17.20)	**0.006***
Management systems	Extensive/Nomadic	148 (64.3)	14 (9.46, 5.27–15.36)	Ref	
	Semi-intensive	82 (35.7)	12 (14.63, 7.80–24.17)	1.64 (0.72–3.74)	0.24
Watering source(s)	Stream	153 (66.5)	15 (9.80, 5.59–15.65)	Ref	
	Well	77 (33.5)	11 (14.29, 7.35–24.13)	1.53 (0.65–3.50)	0.31
Mixed rearing	Yes	179 (77.8)	19 (10.61, 6.51–16.08)	Ref	
	No	51 (22.2)	7 (13.73, 5.70–26.26)	1.3 (0.48–3.17)	0.58
Cross-border movement	Yes	126 (54.8)	10 (7.94, 3.87–14.11)	Ref	
	No	104 (45.2)	16 (15.38, 9.06–23.78)	2.11 (0.93–5.03)	0.08

Table 4
Multivariable logistic regression model for potential predictors of SBV seropositivity in camels.

Variable	Categories	Adjusted OR (95 %CI)	P-Value
Age	Young 0–5 yrs	Ref	
	Adult > 5 yrs	1.56 (0.75 – 3.26)	0.230
Location	Mai'Adua	Ref	
	Sule Tankarkar	1.10 (0.42 – 2.87)	0.844
	Babura	1.64 (0.57 – 4.83)	0.363
	Maigatari	1.97 (0.84 – 4.69)	0.120
	Zangon Daura	4.73 (1.33 – 20.4)	**0.023***
Management systems	Extensive/Nomadic	Ref	
	Semi-intensive	1.62 (0.57 – 4.94)	0.381
Watering source(s)	Borehole	Ref	
	Stream	6.88 (0.63 – 164.0)	0.139
	Well	4.58 (0.47 – 102.0)	0.223
Mixed rearing	Yes	Ref	
	No	0.45 (0.10 – 1.80)	0.278

Hosmer-Lemeshow goodness-of-fit test = 2.09, p-value = 0.955, ROC 0.643

Table 5
Multivariable logistic regression model for potential predictors of SBV seropositivity in donkeys.

Variable	Categories	Adjusted OR (95 %CI)	P-Value
Age	Young 0–4 yrs	Ref	
	Adult > 4 yrs	3.55 (1.41 – 9.22)	**0.0075***
Sex	Male	Ref	
	Female	2.54 (0.81 – 9.26)	0.129
Location	Maigatari	Ref	
	Zangon Daura	1.57 (0.17–11.0)	0.656
	Mai'Adua	2.96 (0.58–14.8)	0.180
	Babura	2.91 (0.66–13.3)	0.157
	Sule Tankarkar	4.46 (1.20–17.9)	**0.0279***
Management systems	Extensive/Nomadic	Ref	
	Semi-intensive	1.34 (0.483–3.71)	0.565
Watering source(s)	Stream	Ref	
	Well	1.49 (0.57 – 3.91)	0.416
Mixed rearing	Yes	Ref	
	No	0.73 (0.21 – 2.20)	0.587

Hosmer-Lemeshow goodness-of-fit test = 9.31, p-value = 0.316, ROC 0.531

Seroprevalence and risk factors of SBV in donkeys

Among the 230 donkeys evaluated, 26 (11.3 %) tested positive for SBV antibodies. The true seroprevalence was estimated to be 11.3 % (95 % CI: 7.38 – 16.22). Consistent with observations made in camels, adult donkeys exhibited a notably higher seroprevalence, with a likelihood of being positive 3.4 times greater than that of younger donkeys (P = 0.004, OR=3.4, 95 % CI: 1.5–7.9). Female donkeys showed higher levels of SBV antibodies (14.5 %, 95 % CI: 9.2–21.3) compared to male

donkeys (5.9 %, 95 % CI: 1.9–13.2), though this association was not statistically significant (P = 0.08).

The highest number of donkeys sampled was from Maigatari (n = 80, 34.8 %), yet this region displayed the lowest seroprevalence among all five LGAs. Moreover, donkeys sampled from Sule Tankarkar were five times more likely to be seropositive than those from Maigatari (P = 0.006, OR=5, 95 % CI: 1.6–17.2), with Maigatari serving as the reference LGA in the univariate model. A larger number of donkeys were raised under an extensive management system (n = 148; 64.3 %), but those under semi-intensive care revealed a higher seroprevalence (14.6 %, 95 % CI: 7.8–24.2), though this difference was not statistically significant (P = 0.34). Labour and transportation were the only purposes for keeping the donkeys that were screened (100 %). Although most donkeys were watered in the stream (n = 153; 66.5 %), donkeys that drank well water showed a higher seroprevalence (14.3 %, 95 % CI: 7.4–24.1), but this was not significant (P = 0.67). Donkeys that had no contact with other animals (13.7 %, 95 % CI: 5.7–26.3) exhibited more SBV antibodies compared to those raised in mixed settings (10.6 %, 95 % CI: 6.5–16.1), also not statistically significant (P = 0.51). Seropositivity was higher in donkeys that were locally domiciled (15.4 %, 95 % CI: 9.1–23.8) compared to donkeys involved in cross-border movement (7.9 %, 95 % CI: 3.9–14.1); however, this numerical difference was not statistically significant (P = 0.09). Univariate logistic regression revealed no significant correlation between SBV seropositivity in donkeys and factors such as management systems, water sources, mixed rearing, or cross-border movement.

Overall, the presence of SBV antibodies was considerably higher in camels compared to donkeys, with a 10-fold higher probability of being seropositive (P < 0.0001, OR = 10.2, 95 % CI: 6.3–16.6).

4. Discussion

The study revealed past exposure of SBV with a seroprevalence of 56.5 % in camels and 11.3 % in donkeys across five selected Sahelian LGAs in Nigeria. The observed high seroprevalence may be influenced by the ecological conditions of the Sahelian region, which are known to support significant vector populations (e.g., *Culicoides* spp.), and potentially by environmental factors like wind patterns that facilitate vector dispersal (Sedda and Rogers., 2013).

While camels demonstrated a significantly higher seroprevalence than donkeys, the hypothesis that this difference is solely attributed to higher cross-border movement in camels requires further investigation. In addition, Camel immunoglobulins, particularly their unique heavy-chain antibodies called nanobodies (VHHs), are significant for fighting diseases due to their small size, high stability, and ability to penetrate tissues and bind to unusual targets (Tillib, 2011). This may have also contributed to the high seropositivity observed. Our findings for donkeys indicated a numerically higher seroprevalence in locally domiciled animals (15.38 %) compared to those involved in cross-border movement (7.94 %), though this difference was not statistically significant. This suggests other factors, such as local environmental conditions or species-specific susceptibility, may play a substantial role. For camels, as all sampled individuals participated in cross-border movement, this factor could not be assessed as a differentiator for seroprevalence within the camel population, but it highlights the potential for widespread pathogen dissemination by this species.

Our results for camels are similar to the seroprevalence reported in New World Camelids (llamas and alpacas) by Schulz et al. (2015) in Germany. However, they differed from the findings of Wernery et al. (2013) and Pestil et al. (2021), who noted lower seroprevalence rates in dromedary camels in the UAE (36.5 %) and Turkey (15.1 %), respectively. These differences might be attributed to variations in vector density, local ecological conditions, husbandry practices, sampling strategies, or the timing of the study relative to local SBV transmission cycles. The high prevalence of SBV in camels also aligns with a study by Oluwayelu et al. (2018) on cattle and sheep, which also attributed their observed high prevalence to increased biting midges. The relatively low SBV seroprevalence in donkeys (11.3 %) is consistent with a study conducted on horses in Iran (Rasekh et al., 2018).

Univariate and multivariate analyses revealed significant differences among age groups, with older animals showing a higher likelihood of being exposed compared to younger ones in both camels and donkeys. This finding aligns with previous work on llamas and alpacas (Schulz et al., 2015) and other animal species; Wernike et al. 2014 in cattle, Veldhuis et al. 2014, and Sibhat et al. (2018), both from studies on dairy herds. However, Ferrara et al. (2023) reported a higher seroprevalence in younger animals from a study in cattle and water buffalo in Italy. The increased seropositivity in adult camels and donkeys might be attributed to cumulative exposure over multiple seasons. Studies investigating age-related risk factors in cattle have also indicated that adult animals' coat texture could potentially attract *Culicoides* spp. more than younger animals (Méroc et al., 2012; Benfodil et al., 2025). It is uncertain whether these characteristics contribute to the significant disparity observed between younger and older camels and donkeys, though considering similarities in skin texture and nutrition between camels and other ruminants, the possibility cannot be dismissed.

Evidence of viral exposure was detected at all sampling locations, with significant differences (P < 0.05) in the seroprevalence of SBV among camels and donkeys. The proportion of seropositive camels varied from 40 % at Mai'Adua to 73.33 % at Zangon Daura, while the seropositivity in donkeys ranged from 6.25 % at Maigatari to 25 % at Sule Tankarkar. The observed geographical variation in seroprevalence, particularly the elevated rates in camels at Zangon Daura and donkeys at Sule Tankarkar, aligns with expected patterns given the regional context. These higher seroprevalence levels are likely a reflection of the porous borders these areas share with the Republic of Niger, where established transhumance routes connect to grazing reserves frequented utilised by pastoralists and livestock traders. Livestock movements along these routes may increase exposure to disease vectors, while the proximity of an international livestock market in Maigatari could further increase transmission risk. This market serves as a convergence point for livestock from multiple states and countries, creating favorable conditions for contact between infected and susceptible animals. The role of such environments in facilitating disease transmission has been well-documented, with previous studies demonstrating that these settings are conducive for the circulation and dissemination of transboundary animal diseases (Martin et al., 2008; Di Nardo et al., 2014; Adamu et al., 2022). Camels primarily used for farming appeared to be at a significantly higher risk of SBV seropositivity compared to those kept for milk and meat (P < 0.05). This increased vulnerability could be attributed to their continual exposure to biting insects on farms, as they typically remain there for an average of 10.2 years, in contrast to those raised for meat and milk, which rarely exceed an average age of 7.8 years. Consistent with previous findings, the prevalence of SBV was unaffected by sex in both camels and donkeys, suggesting males and females face an equal risk of SBV infection in llamas and alpacas Schulz et al. 2015), horses (Rasekh et al., 2018), dairy cattle (Sibhat et al. 2018), and in cattle and sheep (Oluwayelu et al. 2018). Furthermore, factors such as management system, watering source, and mixed species rearing showed no significant correlation with SBV seroprevalence in camels and donkeys. This result implies that these factors may not notably affect the susceptibility or exposure of the screened camels and donkeys to the virus in this specific epidemiological context.

The study is not without limitations. First, convenience sampling was employed which may have introduced a certain level of bias. Additionally, the low ROC values (0.63 for camels and 0.53 for donkeys) suggest that while our models captured some significant associations and demonstrated acceptable goodness-of-fit (indicated by non-significant Hosmer-Lemeshow p-values) (Fagerland & Hosmer, 2012), they have limited discriminatory power in predicting individual animal serostatus. This suggests that important unmeasured covariates, such as specific vector abundance, microclimatic variations (temperature,

humidity, rainfall during peak vector seasons), and potentially host-specific immunological factors, were not included in our models. Moreover, the indirect multispecies ELISA kit used relies on a species conjugate that has been most often adopted for antibody detection in ruminants. Though the possibility of application for camels has been established (Schultz *et al.*, 2015), we are unsure about the effectiveness for donkeys. Furthermore, the ELISA kit (recommended by the manufacturer for SBV serology with high sensitivity and specificity in external validation studies - Bréard et al., 2013) is based on the viral N-protein, which may induce cross-reactivity with other members of the Simbu serogroup. While our study was able to detect antibodies in both camels and donkeys, the results should be cautiously interpreted. Future studies should strive to incorporate these environmental and epidemiological variables to develop more robust predictive models. Additionally, neutralization tests and molecular analyses should be employed to identify and confirm the circulating strains of SBV in camels and donkeys.

5. Conclusion

The widespread presence of anti-SBV antibodies was notably high in camels (56.52 %) and donkeys (11.3 %), with distribution across all the Nigerian LGAs included in the study bordering the Sahel region. The seropositivity rates for camels and donkeys were significantly associated with age and geographic location. Our findings suggest potential exchange and spread of the pathogen via transborder movement and further raises public health concerns regarding the role of these animals as reservoirs for the dissemination of this pathogen. Given the considerable cross-border movement of these animals, their role as potential contributors to the dissemination of SBV warrants further investigation, particularly concerning their capacity for disease transmission. Crucially, this study represents the first documented report of SBV seroprevalence in donkeys worldwide and camels within Africa, establishing a critical baseline for future research and surveillance efforts. Therefore, it is essential to conduct more thorough molecular studies, using RT-PCR to detect viral RNA to identify active infections and conduct sequence analysis to characterise circulating strains of SBV in these species. Such studies, combined with comprehensive investigations into vector dynamics, environmental factors, and the long-term outcomes of infection, will provide a more complete understanding of the epidemiological role of camels and donkeys in SBV transmission and inform targeted disease control strategies in the region.

Funding

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

CRediT authorship contribution statement

Olajide A. Owolodun: Validation, Supervision, Methodology, Investigation, Conceptualization. **Paul F. Horwood:** Writing – review & editing, Validation, Supervision, Conceptualization. **Theophilus I. Emeto:** Writing – review & editing, Validation, Supervision, Conceptualization. **Oyelola A. Adegboye:** Writing – review & editing, Validation, Supervision, Methodology, Formal analysis, Conceptualization. **Adikwu Alex A:** Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Software, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization. **Emmanuel O. Ngbede:** Writing – review & editing, Methodology. **Andrew M. Adamu:** Writing – review & editing, Methodology, Conceptualization. **Hussaini G. Ularamu:** Resources, Methodology, Investigation. **Yiltawe S. Wungak:** Resources, Methodology, Investigation.

Declaration of Competing Interest

The authors have nothing to declare.

Acknowledgment

The authors wish to thank the Directors of Veterinary Services in Jigawa and Katsina States for their support during the sampling process. We also thank the staff of the Viral Research Division, National Veterinary Research Institute, Vom for their assistance in the laboratory analysis.

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