

Seroepidemiology and Serotype Diversity of Foot-and-Mouth Disease Virus Among Domestic Ungulates Across Nigeria

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Abstract

Introduction: Foot-and-mouth disease (FMD) is a highly contagious viral infection of cloven-hoofed animals that causes substantial economic losses and severe disruptions to agricultural systems globally. It affects animal health and productivity in Nigeria but there is paucity of data across regions and among various animal species. This study determined the seroepidemiology and serotype diversity of the FMD virus (FMDV) among domestic ungulates including cattle, sheep, goats, and pigs, across all geopolitical zones in Nigeria.

Materials and methods: 1002 sera were collected from domestic ungulate animals (cattle n=511, sheep n=182, goat n=218 and pigs n=91) and were analyzed using commercial ELISA kits (ID Vet®, France and IZLER®, Italy) to antibody and serotype-specific antibodies to FMD. Metadata on individual species were collected through questionnaire uploaded on Kobocollect containing sociodemographic data, and distribution of FMD in Nigeria.

Results: The study revealed an overall rate of 45.7% for all the various species and regions in Nigeria with specific host prevalence of 69.7% for cattle, 26.9% for sheep, 20.6% for goats, and 8.8% for pigs. Serotype O was the most predominant (74.9%), followed by A (56.3%), SAT 2 (35.8%), Asia 1 (22.9%) and SAT 1 (16.8%). Kaduna had the highest prevalence (88.9%), while Cross River had the lowest (9.1%). Serotype co-infections were prevalent among cattle, with 32% exhibiting multi-serotype infections. Health status and body condition are major determinants of susceptibility, with unhealthy animals being five times more likely to test positive to FMD (OR = 5.479, $p < 0.001$).

Conclusion: We have systematically determined FMDV seroprevalence and serotype distribution in various domestic ungulate species across all the geopolitical zones in Nigeria. Our findings highlight the importance of improved surveillance networks to address regional patterns and prevalent serotype clusters. It reinforces the need for developing generic multivalent vaccination plans and provides essential data for national policy to improve livestock healthcare strategies and minimize the burden of FMD in Nigeria.

Introduction

Foot-and-mouth disease (FMD) is a highly contagious viral infection that affects cloven-hoofed livestock and wildlife, causing significant economic losses and severe socioeconomic problems. It is listed as a notifiable disease by the World Organization for Animal Health (WOAH) due to its wide distribution and potential to disrupt animal production systems. Globally, FMD circulate within 77% of the livestock population (OIE, 2021). FMD is caused by the Foot-and-Mouth Disease Virus (FMDV), a non-enveloped, single-stranded, positive-sense RNA virus of approximately 8.5kb in size. It belongs to the genus Aphthovirus in the family *Picornaviridae* and is surrounded by an icosahedral capsid composed of four structural proteins (Rueckert, 1990). There are seven immunologically distinct serotypes of FMDV (O, A, C, SAT 1, SAT 2, SAT 3, and Asia 1), with serotype O being the most prevalent globally (FAO, 2021). There is no cross-protection across these serotypes, and even among subtypes within a serotype, immune

protection is insufficient (Naveed, 2018). The disease is endemic and occurs year-round in Nigeria with seasonal outbreaks. Historical records trace the first reported outbreak to 1924 (Libeau, 1960), underscoring the long-standing presence and persistent challenge to livestock health and productivity in the country. In Nigeria, serotypes O, A, SAT 1, and SAT 2 have been documented historically, with a study stating the detection of antibodies against SAT3 across multiple states (Ehizibolo et al., 2013). The principal domestic hosts of FMDV are cattle, pigs, goats, and sheep (Ferris and Donaldson, 1992; Jamal et al., 2013). Among these, FMD manifests mildly in sheep and goats, sometimes resembling other vesicular disease like vesicular stomatitis (Blanco et al., 2002; FAO, 2024). Pigs, although susceptible, exhibit relatively lower risk for airborne transmission compared to cattle and sheep (Alexandersen and Donaldson, 2002). Transmission of the virus occurs by direct contact via respiratory droplets from infected animals, and indirectly through contaminated fomites such as vehicles, equipment, or personnel (Alexandersen et al., 2003). Though FMD typically causes low mortality (except in young calves), it has high morbidity and severely affects productivity. Infected animals show clinical signs including fever, lameness, and vesicle formation in the mouth, on the feet, and on the teats of lactating cows and the snouts of pigs (Grubman and Baxt, 2004). These vesicles eventually rupture, leading to painful erosions, excessive salivation, difficulty in eating, and reluctance to move, all of which impair the animal's performance. Economic losses are compounded by trade restrictions placed on meat and animal products originating from affected regions (FAO, 2025).

Routine prophylactic vaccination using inactivated FMD vaccines is recommended in endemic countries, but in Nigeria, it is largely restricted to a few dairy farms where trivalent vaccines targeting serotypes O, A, and SAT 2 are used (Lazarus et al., 2012). Despite being endemic, Nigeria has yet to implement a comprehensive FMD vaccination program. Control measures are typically cattle-focused, even though FMD affects all cloven-hoofed species (OIE, 2021). The situation is exacerbated by unrestricted transboundary animal movement, particularly at poorly regulated border posts in Africa including Nigeria (Bouslikhane, 2015; Woldemariyam et al., 2022) and limited access to vaccines by smallholder farmers in rural areas due to several factors like lack of awareness, lack of access, cost of the vaccine affecting sales by agro-veterinary infrastructures (Sopeju et al., 2025). Oyewusi and Talabi (2015) stressed the need for broader vaccination programs that include all susceptible species, improved disease surveillance, and the establishment of effective control posts along major livestock entry routes.

While numerous studies have been conducted on the epidemiology of FMD in Nigeria, Atuman et al. (2020) highlighted that seroepidemiological and serotyping investigations are inadequate despite the annual incidence. This gap in research underscores the need for updated and comprehensive surveillance activity. Therefore, we investigated the seroepidemiology FMD and determined the circulating serotypes of FMDV across various domestic ungulate species in all geopolitical zones in the country.

Methodology

Study Area

Border States of Niger Republic (Jigawa, Sokoto and Yobe State), Benin Republic (Niger, Ogun and Oyo States) and Cameroon (Adamawa and Taraba State). Other selected states (Plateau, Kaduna, Lagos, Ebonyi and Cross-River State). Ethical approval was obtained from Ethical Review Board of the National Veterinary Research Institute (NVRI), Vom with reference number AEC/02/148/24.

Study Population

Domestic ungulate animals (cattle, sheep, goat and pigs) from consenting farmers in our study areas were selected for the study. Samples were collected from 511 cattle, 182 sheep, 218 goats and 91 pigs located in our study areas. Blood samples were collected from individual animals using sterile needle and syringe, with the 5 ml of blood collected from jugular veins of cattle, sheep and goats and from the cranial vena cava in pigs.

Study design

This is a cross-sectional study, and we aseptically collected 5ml of blood from each of the jugular veins of cattle, sheep and goat and vena cava of pigs in our study.

Inclusion and Exclusion Criteria

Inclusion Criteria include weaned domestic ungulate animals from markets, farms or communities where there is an on-going or previous history of FMD outbreak. The exclusion Criteria include all domestic ungulate animals that are yet to be weaned and those found on farms or communities where there has not been history of FMD outbreaks were excluded. Border States are states that share boundary with neighbouring countries and with known international livestock trade. Non-border States are states without international cattle trade (with or without boundary with other countries). The sample size was calculated using the following formula with prevalence rate of 50% (Dohoo et al., 2003; Thrusfield, 2018). 1002 sera were obtained from cattle, sheep, goat and pigs in our study areas.

Serological Assay

Commercial ELISA kits (NSP and Serotype-specific for serotype A, O, SAT 1, SAT 2 and Asia 1) were used to detect the animals that were seropositive for FMD and the above-mentioned FMD serotypes. The kits were purchased from ID Vet (for NSP, Serotype O and A) and IZLER from Italy for Serotypes SAT 1, SAT 2 and Asia 1. Sera from the samples collected were first tested for positivity using NSP ELISA kits. The positive samples were then analyzed further for serotyping using serotype-specific ELISA kits for serotype O, A, SAT 1, SAT 2 and Asia 1. Each of the assays were carried out according to each of the manufacturers' instructions. The results of optical density (O.D.) values were validated, percentage

inhibition was calculated, and positivity was determined according to the standard provided by the manufacturer standard provided in the ELISA manuals.

Data Analysis

Questionnaires uploaded on Kobocollect were used to get information on the animal sampled and other information relevant to this study. Metadata generated from the sampled animals were transferred in an excel sheet with ascribed sample ID for each animal. Descriptive and inferential analysis of data was carried out using EXCEL and IBM SPSS to generate relevant figures.

Clinical Trial Number

Not applicable

Result

Seroprevalence of Foot and Mouth Disease (FMD) across Animal Species

The overall seroprevalence of Foot and Mouth Disease (FMD) is 45.7% (458/1002), with significant variation across species, Cattle had the highest seropositivity (69.7%), followed by sheep (26.9%), goats (20.6%), and pigs (8.8%) (Table 1). Logistic regression analysis further confirmed that cattle had the highest odds of seropositivity compared to pigs (reference category), (Table 2). Among cattle, females had a significantly higher seroprevalence (74%) than males (65.5%) ($\chi^2 = 4.35$, $p = 0.037$), but age was not a significant determinant. In sheep and goats, sex and age did not significantly influence seropositivity (Table 4). A similar trend was observed in pigs, where seropositivity did not differ significantly by gender or age (Table 2).

Geographical and Border Proximity Influence on Seroprevalence

Seroprevalence varied significantly across states, regions and geopolitical zones, with Kaduna states having the highest prevalence (88.9%), (Table 1). At the geopolitical zonal level, the North-Central (73.8%) and South-East (71.2%) had the highest seropositivity, as shown by the Logistic regression analysis. (Table 2). Among cattle, seropositivity was significantly higher in the South-East (95%) and North-Central (87.7%), with the lowest rates in the South-South (12.7%) ($\chi^2 = 121.63$, $p < 0.001$) (Table 1). For sheep, Ebonyi (100%) showed the highest rates, while Jigawa (9.1%) had the lowest seropositivity ($\chi^2 = 72.23$, $p < 0.001$). For goats, the highest prevalence was recorded in Plateau (60%) followed by Niger (50%), while Lagos (3.3%) had the lowest rates ($\chi^2 = 41.8$, $p < 0.001$). In pigs, Adamawa had the highest seroprevalence (100%) while Cross River (4.2%) had the lowest ($\chi^2 = 38.37$, $p < 0.001$) (Fig. 3). Proximity to international borders did not significantly influence seroprevalence, as border states (48.9% for Niger,

49.4% for Benin, and 45.7% for Cameroon) had similar rates to non-border states (43%) ($p = 0.403$) (Fig. 1).

Influence of Health Status and Body Condition on Seroprevalence

Health status and body condition significantly influenced FMD seroprevalence. Animals in poor body condition exhibited the highest seroprevalence (66.2%), while those in fair (49.2%) and good condition (39.5%) had lower infection rates ($p < 0.001$). Logistic regression analysis indicated that animals in poor condition were three times more likely to be seropositive than those in good condition ($OR = 3.008$, $p < 0.001$). Animals in fair condition had moderately increased odds of seropositivity ($OR = 1.484$, $p < 0.001$). Unhealthy animals demonstrated significantly higher seropositivity (66.9%) compared to apparently healthy ones (26.9%, $p < 0.001$), with unhealthy animals being over five times more likely to be seropositive ($OR = 5.479$, $p < 0.001$) (Table 2). Among cattle, animals in poor condition had the highest seroprevalence (80%) compared to those in fair (72.3%) and good condition (64.3%) ($p = 0.036$). Similarly, unhealthy cattle exhibited higher seroprevalence (76.7%) than apparently healthy cattle (52.1%, $p < 0.001$). Goats followed a similar pattern, with poor condition animals showing the highest seroprevalence (62.5%) ($p = 0.012$). Pigs and sheep did not exhibit statistically significant associations between health or body condition and FMD infection.

Serotype Distribution and Multi-Serotype Infections

The study identified five circulating FMD serotypes in Nigerian livestock, with serotype O being the most prevalent (74.9%), followed by serotype A (56.3%), serotype SAT2 (35.8%), serotype Asia1 (22.9%), and serotype SAT1 (16.8%). The prevalence of FMD serotypes also varied across Nigeria's six geopolitical zones and serotype O had the highest positivity rate in the North-West at 92.5%. A statistically significant association was found between geopolitical zone and serotype distribution ($p < 0.001$) (Fig. 3). Cattle exhibited the highest diversity serotype infection, while pigs had the least diversity. For cattle, 32% tested positive for two serotypes, 21.2% for three serotypes, 8% for four serotypes, and 8.7% for all five serotypes (Fig. 3). Goats and sheep had lower multi-serotype infection rates, while pigs were predominantly infected by single serotypes. Notably, 4.2% of cattle, 8.9% of goats, and 37.5% of pigs tested positive for FMD but not for any of the five major serotypes analyzed. Among multi-serotype combinations, O and A co-infections were most prevalent across all the four animal species, followed by O and SAT2. Chi-square values (p -values) suggested significant variation in serotype distributions across animal species, with p -values below 0.05 for most serotype combinations except specific cases such as SAT 2 and Asia 1 among goats and pigs (Fig. 2). Overall, serotype O and A emerged as the most prevalent combination across all animal types, with cattle showing the highest proportional distribution (Fig. 2). Lesser frequencies for combinations like SAT 2 and Asia 1, as well as SAT 1 and Asia 1, were consistently observed across species. The prevalence of specific serotype co-infections also differed based on health status. Unhealthy animals demonstrated higher prevalence across most serotype combinations, with significant associations observed for O and A ($p = 0.004$), O and Asia 1 ($p < 0.001$), and SAT 2 and Asia 1 ($p = 0.001$) (Fig. 3).

Table 1
Seroprevalence of Foot-and-Mouth Disease Across Animal Species and Demographics

Category	Subcategory	Seroprevalence	p-value
Animal Species	Cattle	69.7	< 0.001
	Sheep	26.9	
	Goat	20.6	
	Pigs	8.8	
Sex	Male	47.8	0.229
	Female	44.0	
Age Group	Adult	45.4	0.767
	Yearling	47.0	
	Young	38.9	
Body Condition	Poor	66.2	< 0.001
	Fair	49.2	
	Good	39.5	
Health Status	Apparently Healthy	26.9	< 0.001
	Unhealthy	66.9	
Geopolitical Zones	North-Central	73.8	< 0.001
	North-East	46.3	
	North-West	51.1	
	South-East	71.2	
	South-South	9.1	
	South-West	45.1	
Border Proximity	Border States	47.9	0.124
	Non-Border States	43.0	
Border Region	Northern Border States	47.6	0.295
	Southern Border States	49.4	
	Non-Border States	43.0	

Table 2
Logistic Regression Analysis of Factors Associated with FMD Seropositivity

Variable	Category	Odds Ratio (Exp(B))	95% CI (Confidence Interval)	p-value
Animal Species	Pig (Reference)	1.000 (Reference)	-	-
	Cattle	23.829	11.259–50.431	< 0.001
	Goat	2.699	1.217–5.984	0.015
	Sheep	3.822	1.724–8.474	0.001
Geopolitical Zone	South-South (Reference)	1.000 (Reference)	-	-
	North-Central	28.148	13.706–57.807	< 0.001
	North-East	8.616	4.662–15.925	< 0.001
	North-West	10.449	5.51–19.816	< 0.001
	South-East	24.667	10.781–56.434	< 0.001
	South-West	8.226	4.392–15.405	< 0.001
North/South	South (Reference)	1.000 (Reference)	-	-
	North	1.969	1.523–2.546	< 0.001
Body Condition	Good (Reference)	1.000 (Reference)	-	-
	Poor	3.008	1.814–4.987	< 0.001
	Fair	1.484	1.143–1.927	< 0.001
Health Status	Apparently Healthy (Reference)	1.000 (Reference)	-	-
	Unhealthy	5.479	4.177–7.186	< 0.001

Discussion

The findings of our study carry significant implications for understanding the epidemiology of Foot-and-Mouth Disease (FMD), offering critical insights into the dynamics of its spread across species, geographical locations, and health status of infected animals. Notable patterns in seroprevalence, serotype distribution, and co-infections reveal not only the nature of FMD transmission but also its complex impact.

One of the key findings was that the seroprevalence of FMD in Nigeria across various species is 45.7%, with variation in seroprevalence among animal species. Cattle exhibited the highest seropositivity (69.7%), followed by sheep, goats, and pigs, confirming species-specific susceptibility. This aligns with previous observations that cattle are more vulnerable to FMD even in shared ecosystems (Ehizibolo et al., 2019; Ploquin et al., 2025), highlighting the need to prioritise cattle in disease control programs. Differences between species at different locations point to the possible influence of environmental and management factors on infection dynamics, beyond intrinsic host characteristics.

Geographical disparities in seroprevalence were prominent in our study, with states in the North-Central and South-East zones recording the highest rates, while the South-South zone had significantly lower prevalence. Our findings mirror previous reports from Nigeria supporting disparities in the seroprevalence by region, with higher prevalence mostly recorded in the northern parts of the country (Begovoeva et al., 2023); Wungak et al., 2016; Fomenky et al., 2023). These patterns suggest that regional factors such as livestock movement, and ecological conditions play a crucial role in shaping FMD epidemiology. Interestingly, proximity to international borders did not significantly affect seroprevalence, challenging reports about cross-border transmission earlier reported by Babangida et al. (2017), and indicating that localized containment measures may be effective in limiting disease spread.

Health status and body condition emerged as strong determinants of seroprevalence. Animals in poor health or with low body condition scores were more likely to test positive for FMD, emphasizing the role of general well-being in disease susceptibility. In previous studies, health status and body condition scores have shown inconsistent associations with FMD seropositivity. While one study in Ethiopia found no significant link (Bahiru & Assefa, 2022), another in central Ethiopia established a clear correlation using multivariable logistic regression (Awel et al., 2021). However, our findings underline the role of the health status in animal susceptibility to FMD, which indicates the importance of improving livestock nutrition and overall care as part of broader disease prevention efforts, particularly in vulnerable animal populations.

Our study also identified distribution of the different serotypes with serotype O being most prevalent in all the species, then followed by serotype A, SAT 2, SAT 1 and Asia 1. Our study also identified some animals that did not test positive to any of the five serotypes analyzed in this study. While SAT 3 have been previously reported in Nigeria (Ehizibolo et al., 2013), there is a lack of evidence indicating the circulation of serotype C in Nigeria. Nonetheless, our finding of new serotype, Asia 1, suggests that both serotypes may be circulating within various animal populations in Nigeria and should therefore be considered in future research study. Another view to this finding may be that new topotypes are

emerging with similar antigenic variants with those serotypes that are not known to be circulating in this part of the world. Furthermore, serotype Asia 1 has been reported to be geographically restricted to Central Asia (Knowles & Samuel, 2003; Roeder & Knowles, 2008), however, this study provides evidence of its circulation in Nigeria which may, in the actual sense, be an evolutionary drift of one or more of the commonly circulating serotypes in Nigeria towards serotypes Asia 1. Furthermore, some of the animal species that tested positive for FMD but not for any of the five major serotypes analyzed indicate the potential circulation of overlooked strains such as serotype SAT 3, C or a new one that has not been reported.

There are also complex trends of FMD epidemiology, especially with regards to the patterns of multi-serotype co-infections; in which cattle recorded the highest prevalence of co-infections and multiple serotypes. A key finding of this study is the widespread dominance of the O and A serotype combination across all examined animal species. The same pattern is seen with O and SAT 2 in all animal species except sheep. This consistent pairing emerged as the most prevalent co-infection pattern, suggesting a strong epidemiological foothold and possible adaptation of these serotypes within the Nigerian livestock population. The recurring presence of O and A across species underscores their role as a primary driver of multi-serotype FMD infections in the country. These findings have important implications for FMD control strategies. The cross-species dominance of O and A highlights the critical need for vaccines that robustly target both serotypes, ideally through polyvalent formulations. However, cattle showed other serotype combinations with SAT 2 and Asia 1 (15.4%) and SAT 1 and Asia 1 (13.5%) seen in some of the cattle sampled. The broad serotype diversity observed in cattle further reinforces their role as key amplifiers and reservoirs of FMD, a pattern also described by Arzt et al. (2021). This reservoir potential not only increases the risk of cross-species transmission but may also drive the emergence of novel recombinant strains. Our study supports a couple of other reports on multiple co-infections of various FMD serotypes in clinically and sub clinically infected animals (Fomenky et al., 2023; Wungak et al., 2017), showing that the multivalent vaccination against different serotypes is indeed needed. The differences in serotype distribution and co-infection patterns seen across species and geographical regions indicate complex transmission patterns that need to be studied in detail. Furthermore, animals in poor body condition scores and those that were unhealthy showed similar trends of serotype co-infection patterns, with unhealthy animals and those with poor body scores showing combination of “O and Asia 1”, and “SAT 2 and Asia 1”. This suggests that compromised immunity, possibly due to malnutrition or other conditions, may increase susceptibility not just to infection, but to specific types of serotype combinations. The extension of the studies to co-infections also contributes to the understanding of the interactions between serotypes, which remains a relatively under-researched subject. In addition, the presence of serotype co-infections underscores the need for multivalent vaccines to address the dominant strains effectively. Altogether, the observed species-specific, geographic, and health-related variations in co-infection patterns indicate that a uniform, one-size-fits-all vaccination strategy is unlikely to be effective. Instead, tailored interventions that account for the dominant serotype pairings within each region and animal population are essential for efficient control.

The practical applications of our study are that it provides evidence that more specific preventive efforts should be designed for particular species and areas. There is thus the need to prioritise the high-risk regions, which include the North-Central and the South-East in terms of surveillance and vaccination. On the same note, it is also necessary to note that better nutrition and health care of livestock can also minimise vulnerability to FMD. Our study went further to highlight specific serotype co-infection dominant in different species, geographical locations and unhealthy animals. These insights also inform policy makers how to develop sound strategies, for instance, improving the coverage of the vaccines to include the circulating serotypes, or reconsidering the measures put in place for border control in light of the actual epidemiology of the region. In a theoretical sense, the study opens up a new approach to the existing models of FMD epidemiology by including species susceptibility, health status and regional variations together in one study. It goes beyond single species or single serotype evaluations and provides a broader perspective on the disease dynamics. Altogether, the outcome of the present study can provide useful information on the current situation, risk factors concerning FMD infection, affected species, geography, health effects, and serotypes. Our results therefore hold important implications for disease management and control measures, highlighting the need for context-specific approaches in the fight against FMD. Through targeting high-risk groups, enhancing animal health, and improving vaccination strategies, policymakers and stakeholders can ensure that the impact of FMD is minimised and communities' welfare, livestock farmers livelihood and national food security are protected. Although the current study provides useful information regarding the epidemiological aspects of FMD, the following limitations have to be recognised in order to avoid misinterpretation of the results. One limitation concerns the imbalance of sample size across species with cattle having the highest representation in the sample. Also, the body condition scoring was subjective, which could hinder an empirical comparability of health status. However, these limitations do not reduce the usefulness of the study for the advancement of FMD research.

In conclusion, we found that the health and nutritional state of animals influenced their susceptibility to infection because animals with poor health conditions showed more seropositivity with severity of viral infections involving multiple serotypes. Improved management practices which focus on nutrition and animal welfare are critical elements in FMD prevention. The polyvalent vaccination is required to protect livestock against the dominant serotypes. Further, improved surveillance systems and regional vaccination strategies for cattle with greater risks of exposure is needed. Since the serological profiles of other animals in this study mirrors what is observed in cattle, this could infer the possibility of transmission across several host species in shared ecosystems hence the need to enforce control measures in other species to fully control the spread of FMD in Nigeria. This study highlights several directions for future research to deepen understanding and improve control of Foot-and-Mouth Disease (FMD). A priority is expanding sample sizes and ensuring balanced species representation, particularly including underrepresented regions, to enhance cross-species and geographical comparisons. Longitudinal studies are also essential for tracking changes in FMD prevalence, serotype distribution, and co-infections over time. Further investigation into molecular and genetic factors could uncover species-specific susceptibility and resistance traits, while research on environmental, trade-related, and

management practices, especially in the light of unexpected findings like the limited role of border proximity, can help clarify complex regional dynamics. Additional research should focus on evaluating the impact of targeted health and nutrition interventions on FMD susceptibility, given the strong associations observed between poor condition and infection. Vaccine development also warrants attention, particularly the need for effective multi-serotype formulations to address the widespread presence of serotype O and frequent co-infections. Unanswered questions regarding regional variability in serotype distribution and the ecological and genetic drivers of disease patterns present valuable opportunities for hypothesis-driven studies. Collectively, these research avenues can build on current findings to inform more targeted, effective, and sustainable FMD control strategies.

Declarations

Ethics Approval and Consent to Participate

Ethical approval was obtained from the Ethical Review Committee of the National Veterinary Research Institute (NVRI), Vom, Nigeria with reference number AEC/02/148/24. All participants were provided with detailed information about the study and they gave written informed consent before participation.

Consent for Publication

All the farmers that participated in this study and allowed their animals to be recruited for this study gave written informed consent for the publication of anonymized data and findings for this study. No personally identifiable information is disclosed in this publication.

Availability of Data and Materials

The dataset generated during this study are available online in the Harvard Dataverse repository and can be accessed using this link – <https://doi.org/10.7910/DVN/NYPX2S>

Competing Interests

The authors of this paper declare that they have no competing interests.

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Authors Contribution

A.E.S. has made substantial contributions to the conception and design of the work, the acquisition, analysis, and interpretation of data, has drafted the work and approved the submitted version, and has agreed both to be personally accountable for the author's own contributions and to ensure that questions related to the accuracy or integrity of any part of the work.

A.F. has substantively revised the work, approved the submitted version and has agreed both to be personally accountable for the author's own contributions and to ensure that questions related to the accuracy or integrity of any part of the work

A.P has substantively revised the work and approved the submitted version and has agreed both to be personally accountable for the author's own contributions and to ensure that questions related to the accuracy or integrity of any part of the work.

A.B.O has substantively revised the work and approved the submitted version and has agreed both to be personally accountable for the author's own contributions and to ensure that questions related to the accuracy or integrity of any part of the work.

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Figures

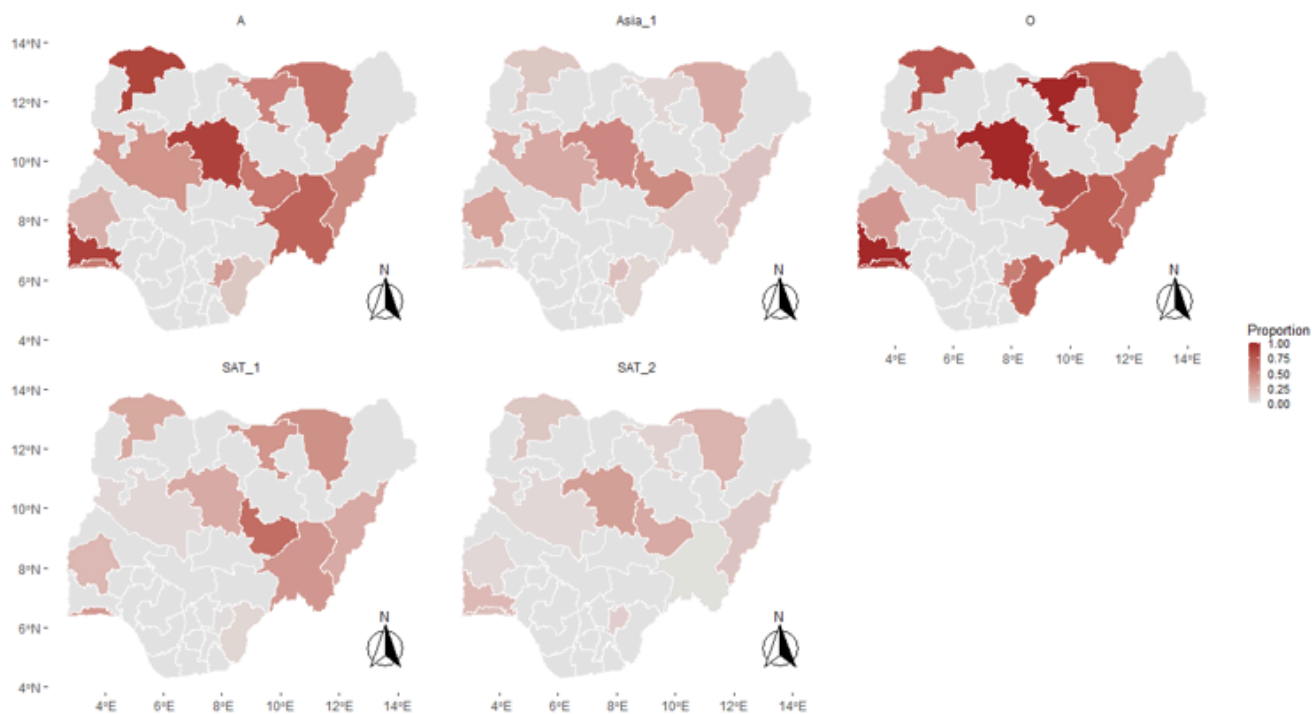


Figure 1

State-wide distribution of FMDV by serotype among infected animals among in Nigeria. The plot is facitted according to serotype, the legend shows a color scale representing prevalence rates of FMD serotypes by proportion where 1 = 100%.

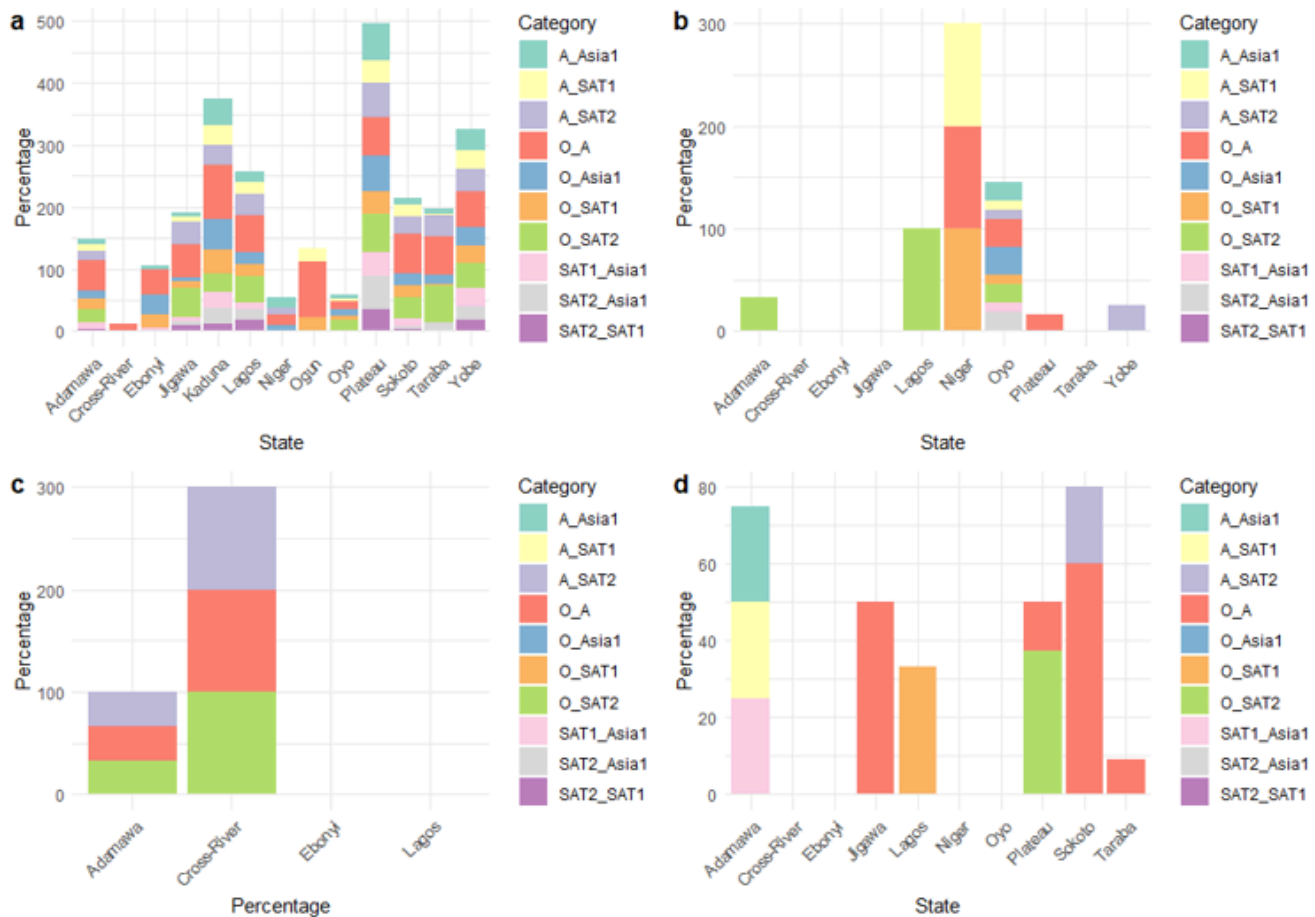


Figure 2

State-wide distribution of FMDV by serotype among infected animals among in Nigeria with a. representing cattle; b. representing goats; c. representing pig; and d. representing sheep

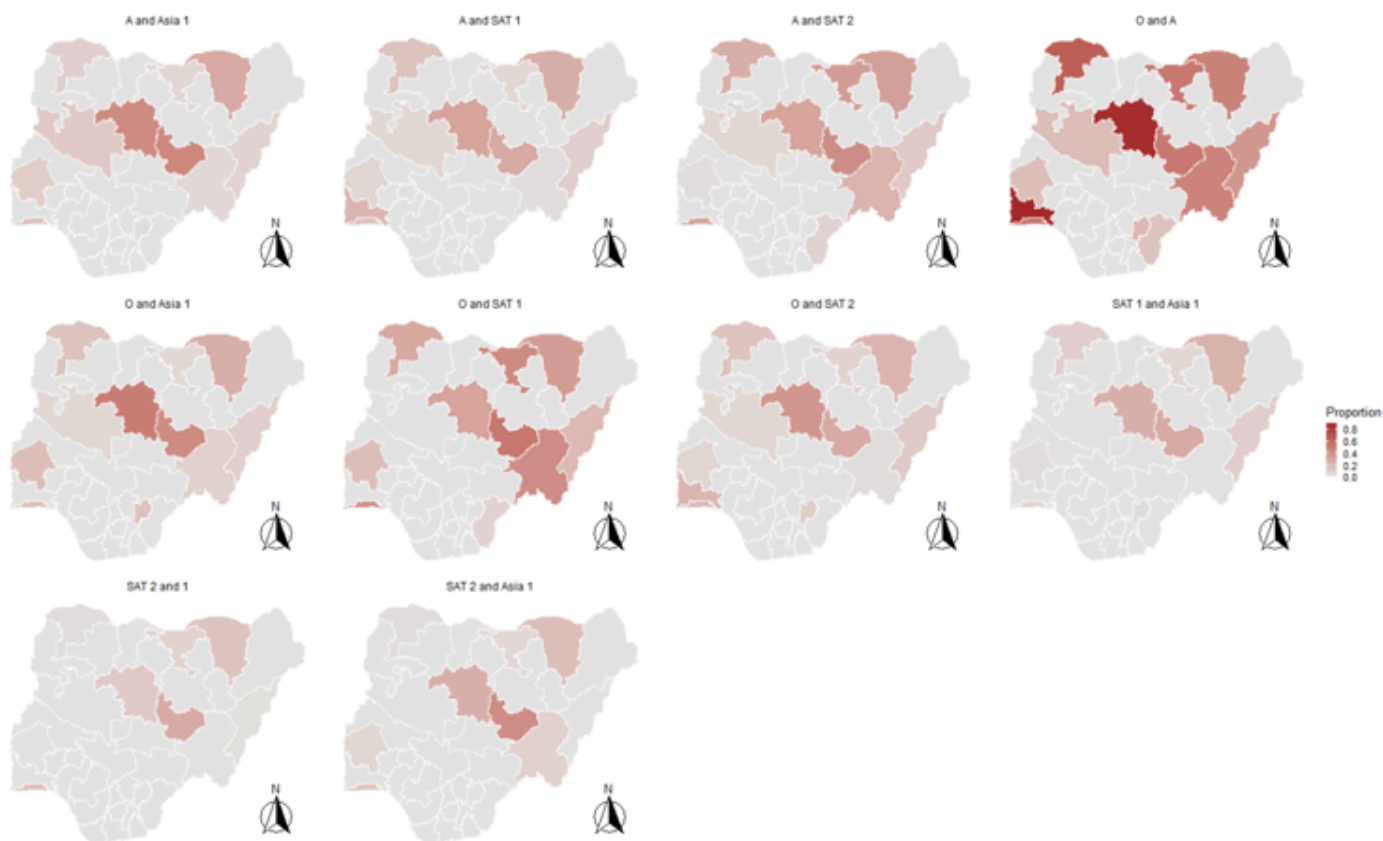


Figure 3

State-wide distribution of FMDV Serotype co-infection among animals in Nigeria. The plot is faceted according to co-infecting serotypes, the legend shows a color scale representing prevalence rates of FMD serotypes combination by proportion where 1 = 100%.