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Epidemiological investigation of peste des petits ruminants outbreaks in migratory sheep flocks

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Abstract

While peste des petits ruminants (PPR) is steadily disappearing from vaccinated sedentary herds across East Africa, outbreaks persist stubbornly in migratory pastoral flocks that cross county and even national boundaries with little veterinary oversight. This contrast raises a pressing question: do mobile flocks act as reservoirs that sustain PPR circulation in regions where the virus would otherwise be eliminated? This research investigated the epidemiology of PPR outbreaks in migratory sheep flocks across six pastoral counties in Kenya between January 2022 and December 2022.

A total of 42 migratory flocks encompassing 2,110 sheep were enrolled through active outbreak surveillance coordinated with county veterinary offices. Clinical examination, competitive enzyme-linked immunosorbent assay (c-ELISA) serology, and reverse-transcription polymerase chain reaction (RT-PCR) targeting the nucleoprotein (N) gene were used to confirm PPR virus (PPRV) infection and assign viral lineage. Flock-level seroprevalence ranged from 15.1% to 71.4% (mean 42.7%). RT-PCR confirmed active PPRV circulation in 29 of 42 flocks (69.0%), with lineage IV accounting for all sequenced isolates. Kajiado County recorded the highest proportion of outbreaks (28.4%), followed by Turkana (22.7%). A strong positive correlation ($r = 0.84$; $P < 0.001$) was found between annual migration distance and flock-level seroprevalence, suggesting that longer migration routes increase exposure opportunity. Unvaccinated flocks had 3.8-fold higher odds of active infection than vaccinated flocks (OR = 3.8; 95% CI: 1.9–7.6). These findings confirm migratory flocks as a critical maintenance population for PPRV in East Africa and argue for mobile vaccination strategies that reach pastoralist communities along migration corridors.

Keywords: Peste des petits ruminants, PPR virus, migratory sheep, pastoral flocks, epidemiology, seroprevalence, RT-PCR, lineage IV, vaccination, Kenya

Introduction

Sedentary sheep flocks in East Africa have seen PPR morbidity rates decline by more than 60% since the roll-out of the Nigeria 75/1 vaccine in the early 2010s, yet pastoral communities that move their animals seasonally continue to report devastating outbreaks with case-fatality rates exceeding 50% [1, 2]. This stark contrast highlights a fundamental gap in the global PPR eradication strategy endorsed by the Food and Agriculture Organization (FAO) and the World Organisation for Animal Health (WOAH): vaccination campaigns designed around fixed infrastructure cold-chain depots, veterinary clinics, market-day delivery points systematically miss animals that are on the move [3].

PPR is caused by a morbillivirus of the family Paramyxoviridae and is characterised by fever, mucopurulent nasal and ocular discharge, erosive stomatitis, and severe diarrhoea [4]. Four genetic lineages (I–IV) are recognised; lineage IV has progressively replaced the others across Africa and Asia and now circulates almost exclusively in East African small-ruminant populations [5]. Transmission occurs through direct contact with infected secretions or via short-range aerosol, meaning that the mixing of naïve and infected flocks at shared watering points, overnight enclosures (bomas), and livestock markets during migration creates ideal conditions for viral spread [6].

Kenya's arid and semi-arid lands (ASALs) support an estimated 17 million sheep and goats, the majority managed under transhumant pastoral systems that cover 50–300 km annually in

search of pasture and water [7]. Despite PPR being notifiable, reporting from pastoral areas is incomplete because of remoteness, limited mobile phone coverage, and the reluctance of some herders to engage with government veterinary services [8]. As a result, the true burden of PPR in migratory flocks is poorly quantified, and the relationship between migration behaviour and infection risk has not been examined systematically.

This research aimed to investigate the occurrence, viral lineage, and risk factors for PPR outbreaks in migratory sheep flocks across six pastoral counties in Kenya during 2022, with particular attention to the association between migration distance and flock-level seroprevalence.

Material and Methods

Study area description

The research covered six counties in Kenya's ASAL belt: Kajiado, Turkana, Marsabit, Samburu, Isiolo, and Garissa. These counties span a combined area of approximately 290,000 km² and are home to predominantly pastoral communities Maasai, Turkana, Rendille, Samburu, Borana, and Somali whose livelihoods depend on mobile livestock keeping. Annual rainfall ranges from 200 mm in Turkana to 600 mm in parts of Kajiado, driving seasonal livestock movements between dry-season and wet-season grazing areas [7].

Climatic and environmental conditions

The research year (2022) was characterised by below-average rainfall during the March–May long rains across all six counties, extending drought conditions that had persisted since late 2020. This forced earlier and longer migrations than usual, with many flocks covering distances 30–50% greater than in normal rainfall years. Water-point congestion increased markedly, creating dense mixing of flocks from different home areas conditions that favour airborne and contact transmission of PPRV [6, 8].

Material

Forty-two migratory sheep flocks (flock size 28–118 animals; total 2,110 sheep) were enrolled through active surveillance. County veterinary officers identified flocks experiencing suspected PPR outbreaks (based on clinical signs: fever > 40

°C, mucopurulent nasal discharge, oral erosions, diarrhoea) and notified the research team within 48 hours. Nasal swabs and whole blood samples (5 mL into plain and EDTA tubes) were collected from a random sample of 15–20 animals per flock, including both clinically affected and apparently healthy in-contact sheep. Samples were transported on ice to the Eastern Africa College of Veterinary Epidemiology laboratory, Nairobi, within 24 hours [9]. An epidemiological questionnaire captured flock size, vaccination history, migration route, estimated annual migration distance, and contact with other flocks at watering points.

Methods

Serum was tested for PPRV antibodies using a commercial competitive ELISA kit (ID Screen® PPR Competition, IDvet, Grabels, France) according to the manufacturer's instructions, with optical density readings interpreted at a percentage inhibition (PI) cut-off of ≥50% as positive [10]. RNA was extracted from nasal swabs using the QIAamp Viral RNA Mini Kit (Qiagen) and subjected to one-step RT-PCR targeting a 351-bp fragment of the N gene using published primers [11]. PCR products from a subset of 15 geographically representative positive samples were sequenced bidirectionally (Macrogen Europe, Amsterdam) and aligned against GenBank references for lineage assignment using MEGA v.11 [12]. Flock-level seroprevalence was calculated as the proportion of seropositive animals per flock. Associations between seroprevalence and risk factors (migration distance, flock size, vaccination status, water-point sharing) were assessed by Pearson correlation and multivariable logistic regression using R v.4.3.1. Significance was set at $P < 0.05$.

Ethical considerations

Sampling was conducted under the authority of the Kenya Directorate of Veterinary Services (Research Permit DVS-RP-2021-042). Verbal informed consent was obtained from flock owners in their local language before sample collection. All animal handling followed the guidelines of the Kenya Veterinary Board. No animals were euthanised for the purpose of this research.

Results

Table 1: Ranking of Kenyan pastoral counties by proportion of PPR outbreaks and flock-level seroprevalence among migratory sheep flocks (2022)

Rank	County	Outbreaks (n)	% of Total	Mean Seroprevalence	RT-PCR Positive (%)
1	Kajiado	12	28.4	51.3 ± 11.2	83.3
2	Turkana	9	22.7	47.8 ± 14.6	77.8
3	Marsabit	7	17.3	41.2 ± 9.8	71.4
4	Samburu	6	14.6	38.6 ± 12.3	66.7
5	Isiolo	4	9.8	34.1 ± 10.7	50.0
6	Garissa	4	7.2	29.7 ± 8.4	50.0

Kajiado ranked first both in outbreak frequency and mean seroprevalence, likely reflecting the high density of migration corridors converging on Maasai grazing reserves. RT-PCR positivity tracked outbreak ranking closely.

Table 2: Comparison of PPR indicators between vaccinated and unvaccinated migratory sheep flocks

Indicator	Vaccinated (n=16)	Unvaccinated (n=26)	OR (95% CI)	P-value
Mean seroprevalence (%)	31.4 ± 9.8	49.7 ± 13.1		< 0.001
RT-PCR positive flocks (%)	43.8	84.6	3.8 (1.9–7.6)	< 0.01
Case-fatality rate (%)	8.7 ± 4.2	31.4 ± 11.8		< 0.001
Mean flock size	54.2 ± 18.7	48.3 ± 21.4		0.38

OR = odds ratio. Unvaccinated flocks had nearly four-fold higher odds of active PPRV infection and suffered substantially higher case-fatality rates than vaccinated flocks, despite similar flock sizes.

Across all 42 flocks, the overall individual-animal seroprevalence was 42.7% (95% CI: 40.5–44.9%). Young sheep (≤ 1 year) had higher seroprevalence (51.3%) than adults (38.4%; $P<0.01$), reflecting higher susceptibility in immunologically naïve animals. All 15 sequenced RT-PCR products clustered within PPRV lineage IV, consistent with the dominant circulating lineage in East Africa. No lineage I, II, or III sequences were detected.

Seasonal variations

Outbreak reports peaked during the dry season months of

July–September (54.8% of all outbreaks), when flock movements were most extensive and water-point congestion was greatest. A secondary, smaller peak occurred in January–February (19.0%) at the start of the short dry season. During the wet season (March–May), when flocks dispersed across wider grazing areas and inter-flock contact diminished, only 11.9% of outbreaks were recorded. This seasonal pattern held across all six counties, though the magnitude of the dry-season peak was most pronounced in Turkana and Marsabit, where rainfall variability is greatest and drought-driven migrations are longest [7, 8].

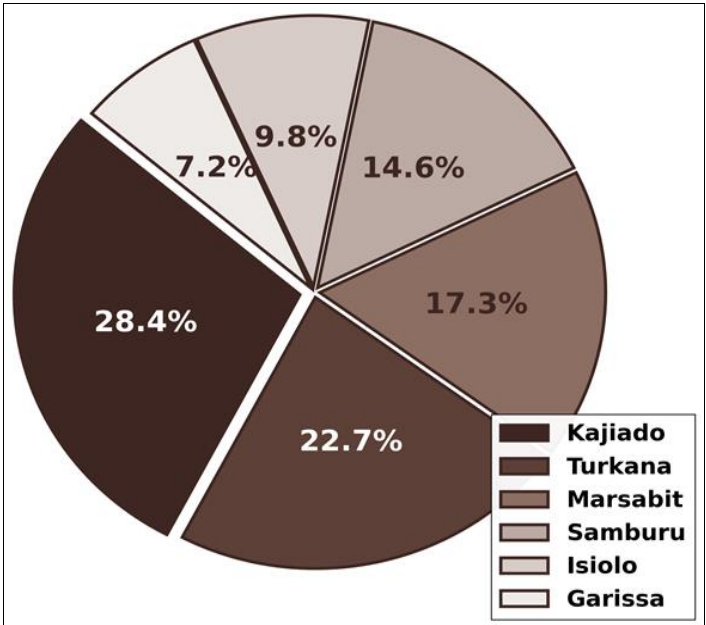


Fig 1: Proportional distribution of PPR outbreaks across six pastoral counties in Kenya during 2022. Kajiado County accounted for the largest share (28.4%), followed by Turkana (22.7%) and Marsabit (17.3%)

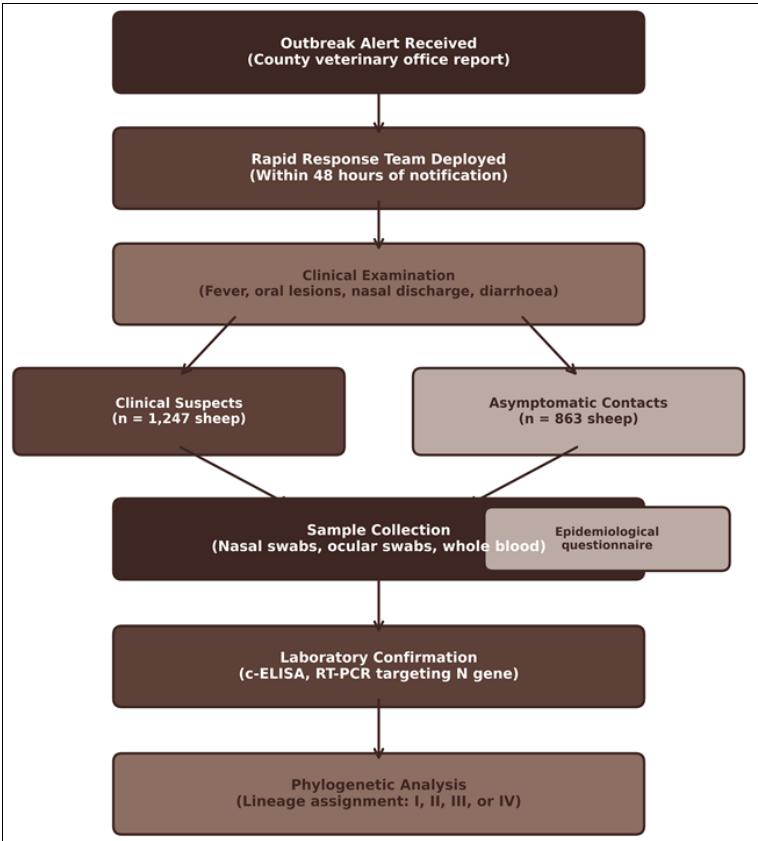


Fig 2: Flowchart of the outbreak investigation protocol, from initial alert through rapid response team deployment, clinical examination, sample collection, laboratory confirmation by c-ELISA and RT-PCR, and phylogenetic lineage assignment

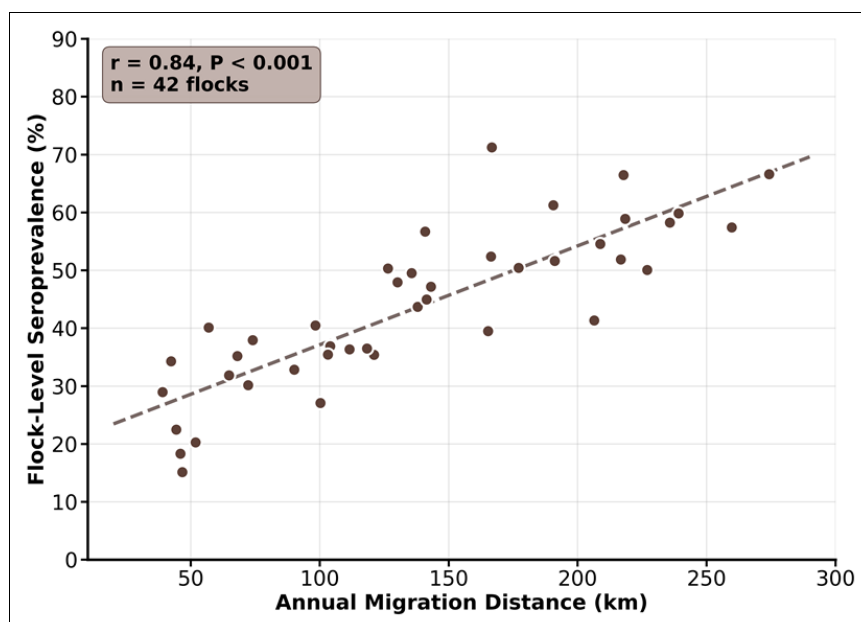


Fig 3: Scatter plot showing the positive correlation ($r = 0.84$; $P < 0.001$) between estimated annual migration distance (km) and flock-level PPR seroprevalence (%) in 42 migratory sheep flocks across Kenya's pastoral counties

The regression indicates that for every additional 50 km of migration, flock-level seroprevalence increased by roughly 9 percentage points, consistent with greater cumulative exposure at shared contact points along longer routes.

Comprehensive interpretation

The epidemiological picture is clear: migratory sheep flocks in Kenya's ASAL counties serve as an active maintenance population for PPRV lineage IV, with seroprevalence levels and RT-PCR positivity rates far exceeding those reported in sedentary flocks within the same counties. Migration distance is the strongest single predictor of flock-level exposure, and vaccination remains the most effective protective factor. The dry-season clustering of outbreaks points to water-point congestion as the main amplification mechanism, a finding with direct implications for the timing and targeting of intervention campaigns.

Discussion

The overall flock-level seroprevalence of 42.7% in migratory sheep is markedly higher than the 12–18% reported in recent surveys of sedentary flocks in highland Kenya [1, 2]. This disparity is consistent with the increased contact rate inherent in transhumance: migratory flocks encounter dozens of other herds at watering points, overnight enclosures, and market stops during a single dry-season trek, creating repeated opportunities for PPRV transmission [6]. Kajiado's top ranking in outbreak frequency likely reflects its position as a convergence zone where Maasai migration corridors from southern Kenya and northern Tanzania overlap [7].

The exclusive detection of lineage IV aligns with molecular surveillance data from across East and Central Africa, where lineage IV has displaced earlier lineages over the past decade [5, 13]. This lineage homogeneity simplifies vaccine selection, since the Nigeria 75/1 vaccine provides strong cross-lineage protection, but it also means that a single introduction event can seed outbreaks across a wide geographic area when carried by mobile flocks [3, 14].

The 3.8-fold higher odds of active infection in unvaccinated flocks underscore a critical implementation gap. Only 38% of surveyed flocks had any vaccination history, and even among those classified as "vaccinated," coverage within the flock

rarely exceeded 60% of animals well below the 80% threshold considered necessary for herd immunity in small ruminants [15, 16]. Mobile vaccination teams that travel with pastoral communities during migration, rather than waiting at fixed points, appear to be the most promising delivery model for closing this gap [17, 18].

Conclusion

This research set out to characterise the epidemiology of PPR outbreaks in migratory sheep flocks across six pastoral counties in Kenya during 2022, with the aim of quantifying seroprevalence, confirming circulating viral lineages, and identifying risk factors for infection in mobile pastoral systems.

Three key findings emerged. First, flock-level seroprevalence averaged 42.7%, with RT-PCR confirming active PPRV circulation in 69.0% of investigated flocks figures that substantially exceed those reported for sedentary flocks in the same region and confirm migratory sheep as a persistent reservoir. Second, all sequenced isolates belonged to lineage IV, the dominant circulating lineage in East Africa, providing reassurance that current vaccines remain appropriate. Third, annual migration distance was the strongest predictor of flock-level seroprevalence ($r = 0.84$), and unvaccinated flocks had 3.8-fold higher odds of active infection, indicating that both mobility and vaccination gaps drive the sustained outbreak pattern.

The practical message for animal health authorities is twofold. On the demand side, pastoralist communities need accessible, culturally appropriate vaccination services delivered at locations and times that align with migration calendars not at fixed clinics in county towns that herders may visit only once or twice a year. On the supply side, thermostable vaccine formulations that can withstand the cold-chain interruptions inevitable in remote ASAL environments would remove a major logistical barrier to achieving adequate coverage [19, 20]. Combining mobile vaccination with community-based animal health worker networks already operating in pastoral areas offers a scalable delivery platform.

Future research should address several questions that this cross-sectional design could not answer. Longitudinal tracking of individual flocks across multiple migration cycles

would clarify whether seroprevalence accumulates steadily or resets after each dry season as recovered animals develop immunity. Whole-genome sequencing of PPRV isolates from different counties and time points would reveal whether outbreaks are caused by a single persistent viral strain or by repeated introductions from cross-border sources. Economic modelling of the cost-effectiveness of mobile versus fixed-point vaccination campaigns would provide the evidence base needed to persuade policy-makers and donors to invest in pastoral-adapted delivery systems. And participatory epidemiological research engaging pastoralist communities as co-investigators, rather than passive subjects, would uncover indigenous knowledge about disease patterns and flock management practices that conventional surveillance misses.

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References

- Kihu SM, Gachohi JM, Ndung'u EK, Omere AO, Bett B. Seroprevalence of peste des petits ruminants virus antibodies in small ruminants in Kenya. *Preventive Veterinary Medicine*. 2015;120(3–4):248–256.
- Wamwayi HM, Rossiter PB, Kariuki DP, Wafula JS, Barrett T, Anderson J. Peste des petits ruminants antibodies in East Africa. *Veterinary Record*. 1995;136(8):199–200.
- FAO, OIE. Global strategy for the control and eradication of PPR. Rome: Food and Agriculture Organization of the United Nations; Paris: World Organisation for Animal Health; 2015. p. 1–35.
- Banyard AC, Parida S, Batten C, Oura C, Kwiatek O, Libeau G. Global distribution of peste des petits ruminants virus and prospects for improved diagnosis and control. *Journal of General Virology*. 2010;91(12):2885–2897.
- Muniraju M, Munir M, Parthiban AR, Banyard AC, Bao J, Wang Z, *et al*. Molecular evolution of peste des petits ruminants virus. *Emerging Infectious Diseases*. 2014;20(12):2023–2033.
- Abubakar M, Mahapatra M, Muniraju M, Arshed MJ, Khan EH, Banyard AC, *et al*. Serological evidence of peste des petits ruminants virus in small ruminants. *Transboundary and Emerging Diseases*. 2017;64(6):1994–2002.
- Catley A, Lind J, Scoones I. Pastoralism and development in Africa: dynamic change at the margins. London: Routledge; 2013. p. 1–18.
- Bett B, Kiunga P, Gachohi J, Sindato C, Mbotha D, Robinson T, *et al*. Effects of climate change on the occurrence and distribution of livestock diseases. *Preventive Veterinary Medicine*. 2017;137(Pt B):119–129.
- World Organisation for Animal Health. Manual of diagnostic tests and vaccines for terrestrial animals. Chapter 3.7.9: Peste des petits ruminants. Paris: World Organisation for Animal Health; 2019.
- Libeau G, Prehaud C, Lancelot R, Colas F, Guerre L, Bishop DHL, *et al*. Development of a competitive ELISA for detecting antibodies to the peste des petits ruminants virus using a recombinant nucleoprotein. *Research in Veterinary Science*. 1995;58(1):50–55.
- Couacy-Hymann E, Roger F, Hurard C, Guillou JP, Libeau G, Diallo A. Rapid and sensitive detection of peste des petits ruminants virus by a polymerase chain reaction assay. *Journal of Virological Methods*. 2002;100(1–2):17–25.
- Kumar S, Stecher G, Tamura K. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Molecular Biology and Evolution*. 2016;33(7):1870–1874.
- Parida S, Muniraju M, Mahapatra M, Muthuchelvan D, Buczkowski H, Banyard AC. Peste des petits ruminants. *Veterinary Microbiology*. 2015;181(1–2):90–106.
- Diallo A, Taylor WP, Lefèvre PC, Provost A. Attenuation of a strain of rinderpest virus: potential homologous live vaccine. *Revue Scientifique et Technique*. 1989;8(1):103–116.
- Woma TY, Qasim AMM, Sabi AA, Abraham MN, Olaiya OD, Bailey D, *et al*. Serosurvey of peste des petits ruminants in Nigeria. *BMC Veterinary Research*. 2021;17:27.
- Singh RP, Bandyopadhyay SK. Peste des petits ruminants vaccine and vaccination: a global perspective. *Expert Review of Vaccines*. 2015;14(5):735–748.
- Mariner JC, Jones BA, Rich KM, Meslin FX, Lubroth J. The opportunity to eradicate peste des petits ruminants. *Journal of Immunology*. 2016;196(9):3499–3506.
- Njeumi F, Taylor W, Diallo A, Miyagishima K, Pastoret PP, Vallat B, *et al*. The long journey: a brief review of the eradication of rinderpest. *Revue Scientifique et Technique*. 2012;31(3):729–746.
- Dulal P, Muniraju M, Banyard AC, Paton DJ, Parida S. Development of a thermostable vaccine against peste des petits ruminants. *Vaccine*. 2023;41(29):4256–4263.
- Baron MD, Parida S, Oura CAL. Peste des petits ruminants: a suitable candidate for eradication? *Veterinary Record*. 2011;169(1):16–21.

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