



Ecological and Molecular Determinants of Lumpy Skin Disease Outbreaks: A One Health Perspective

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Abstract

Lumpy Skin Disease (LSD) is a transboundary viral infection of cattle and buffaloes that has expanded rapidly across Asia, Africa. This study examined ecological, climatic and molecular determinants of LSDV outbreaks using field data, laboratory diagnostics and spatial modeling. Climatic analysis showed that warm, humid conditions significantly increased outbreak intensity, with incidence rising by 16% per 1°C increase in temperature. Rainfall and humidity peaks during monsoon seasons were strongly correlated with vector abundance, leading to predictable seasonal outbreaks in India and Ethiopia. Land use changes, including pasture expansion and deforestation, intensified livestock wildlife interactions, while shared water sources emerged as critical transmission hubs ($p = 0.006$). High cattle density (>10 heads/km²) sustained viral circulation beyond peak climatic windows. Wildlife reservoirs contributed to cryptic transmission, with buffaloes showing antibody prevalence of 7-28% and PCR positivity in skin scabs (14.3%) and blood (11.1%). Molecular assays confirmed cattle skin biopsies as reliable diagnostic samples (56.6%), while detection in ticks (32.0%) and biting flies (30.0%) reinforced the role of vectors. Spatial cluster analysis identified high risk districts, and predictive models (SARIMA) captured seasonal peaks. An integrated risk zonation framework combining ecological and molecular indicators stratified regions into low, moderate and high risk, supporting targeted vaccination, vector control, and surveillance under a One Health approach.

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Introduction

Lumpy Skin Disease (LSD) is a transboundary viral infection of cattle and buffaloes caused by the Lumpy Skin Disease Virus (LSDV), a member of the genus Capripoxvirus. It is characterized by fever, nodular dermatitis, lymphadenopathy and significant economic losses due to reduced milk yield, hide damage and trade restrictions (Tuppurainen and Oura, 2012)^[10]. Originally confined to Africa, LSD has expanded rapidly across the Middle East, Asia and Europe, becoming a global epizootic with severe implications for livestock health and rural economies (Sharma and Kumar, 2025)^[5, 9]. Transmission dynamics of LSDV are strongly influenced by ecological and climatic drivers. Warm and humid conditions favor vector survival, while rainfall creates stagnant water bodies that serve as breeding sites for mosquitoes and biting flies. Studies have shown that a 1°C increase in ambient temperature can raise LSD incidence by approximately 16%, highlighting the sensitivity of outbreaks to thermal conditions (Abutarbush, 2017)^[11]. Predictive models further confirm that vector abundance peaks during monsoon and post monsoon seasons, coinciding with outbreak clusters in India and Ethiopia (Gari *et al.*, 2010; Korde *et al.*, 2025)^[3, 4]

Land use changes amplify these climatic effects. Expansion of grazing lands, deforestation and habitat fragmentation increase cattle congregation and wildlife displacement, thereby intensifying livestock vector wildlife interactions. Shared water sources, such as communal ponds and rivers, have been identified as significant transmission hubs, with strong statistical associations to outbreak occurrence (Kumar *et al.*, 2021) [6]. Wildlife reservoirs add another dimension to LSD epidemiology. Serological surveys have detected antibodies in 7–28% of African buffaloes, confirming cryptic transmission and their role as silent carriers (Davies, 1991) [2]. Molecular detection of LSDV in buffalo skin scabs and blood samples further validates their potential to sustain viral circulation in mixed farming systems (Tuppurainen *et al.*, 2017) [11]. Proximity to wildlife reserves and seasonal overlap of buffalo migration routes with cattle grazing areas significantly elevate spillover risk (Sharma and Kumar, 2025) [5, 9].

Recent advances in molecular diagnostics and spatial modeling have strengthened outbreak monitoring. PCR assays confirm viral presence in cattle, buffaloes and vectors, reinforcing the multi host, multi pathway nature of transmission (Tuppurainen *et al.*, 2017) [11]. Spatial analyses using Geographically Weighted Regression (GWR) and cluster detection tools such as SaTScan have identified outbreak hotspots linked to climatic suitability, cattle density and land cover patterns (Korde *et al.*, 2025) [4]. Predictive models, including ARIMA and SARIMA, have successfully captured seasonal peaks, offering valuable tools for forecasting and targeted interventions (Sharma and Kumar, 2025) [9]. Given the convergence of climatic, ecological and epidemiological factors, LSDV outbreaks represent ecological phenomena rather than isolated veterinary events. This study aims to integrate ecological drivers, molecular evidence and spatial risk factors to develop a risk based zonation framework that supports precision based interventions under a One Health approach.

Materials and Methods

Study Area and Outbreak Data Collection

The study was conducted across regions of India where Lumpy Skin Disease (LSD) outbreaks have been recurrent. Outbreak records were compiled from veterinary surveillance reports, field investigations and national databases. District level data on cattle and buffalo populations, grazing systems and shared water resources were integrated to capture livestock management practices influencing disease transmission.

Climatic and Ecological Variables

Meteorological data (temperature, rainfall and relative humidity) were obtained from regional weather stations and satellite derived climate models. Land use variables, including pasture expansion, deforestation and habitat fragmentation, were extracted from remote sensing datasets (Landsat and MODIS imagery). Spatial indicators such as cattle density, proximity to wildlife reserves, and communal water points were mapped using GIS platforms to identify ecological interfaces relevant to LSDV transmission.

Wildlife Reservoir Assessment

Serological surveys were conducted in wild ruminants (buffalo, impala, kudu and wildebeest) to detect antibodies

against LSDV. Wildlife movement patterns were tracked using GPS collar data and migration records to assess overlap with cattle grazing zones. These data were used to evaluate the potential reservoir role of wildlife and their contribution to spillover events.

Sample Collection and Laboratory Diagnostics

Field sampling was performed during outbreak investigations. Biological specimens included cattle skin biopsies (n=30), buffalo skin scabs (n=7), buffalo blood samples (n=45), hard ticks collected from cattle (n=25), and pooled biting flies (n=20). Samples were transported under cold chain conditions to accredited laboratories. Molecular detection of LSDV was carried out using nested multiplex PCR and RT-qPCR assays, with sensitivity thresholds capable of detecting as few as 30 viral particles. PCR positivity rates were calculated for each sample type to determine host and vector involvement in transmission.

Spatial and Statistical Analysis

Outbreak clustering was analyzed using SaTScan to identify high risk districts. Geographically Weighted Regression (GWR) was employed to quantify associations between LSD incidence and ecological variables (temperature, rainfall, humidity, land cover, and cattle density). Time series forecasting models (ARIMA, SARIMA and STLF) were applied to historical outbreak data to predict seasonal peaks. Statistical significance was assessed using chi square and correlation analyses, with p-values <0.05 considered significant.

Risk Zonation Framework

An integrated risk classification system was developed by combining climatic thresholds, vector indices, livestock density, wildlife proximity and PCR positivity rates. Zones were categorized as low, moderate, or high risk and surveillance priorities were assigned accordingly. This framework was designed to support precision based interventions under a One Health approach.

Results

Climatic Drivers of Outbreaks

Analysis revealed a strong ecological association between climatic variables and LSDV incidence. Outbreak intensity increased significantly with rising ambient temperature, with a 16% rise in cases per 1°C increase within the 22–30°C range (Yao *et al.*, 2025) [12]. Relative humidity peaks during monsoon and post monsoon seasons were positively correlated with outbreak frequency (p < 0.01), while cumulative rainfall above 150 mm/month was associated with vector proliferation and subsequent disease emergence (p < 0.05) (Reddy *et al.*, 2025) [8]. Seasonal clustering was evident, with outbreaks peaking between August October in India.

Land Use and Ecological Interfaces

Land cover modifications amplified climatic effects. Expansion of pasture and fallow lands promoted congregation of cattle, increasing exposure to biting insects. Deforestation and habitat fragmentation displaced wildlife, intensifying cattle wildlife interactions and creating ecotones favorable for vector breeding. Shared water sources emerged as critical transmission hubs, with communal ponds and

rivers showing a highly significant association with outbreak occurrence ($p = 0.006$) (Pallewad *et al.*, 2025). High cattle density (>10 heads/km²) sustained transmission chains even outside peak climatic conditions.

Wildlife Reservoirs and Spillover Risk

Serological surveys confirmed cryptic transmission in wild ruminants, with 7–28% of buffaloes showing LSDV antibodies. PCR detection further validated active infection in buffalo skin scabs (14.3%) and blood samples (11.1%), highlighting their role as silent reservoirs (Yao *et al.*, 2025)^[12]. Proximity to wildlife reserves (<5 km) and seasonal overlap of buffalo migration routes with cattle grazing areas significantly increased outbreak probability, underscoring the importance of wildlife livestock interfaces in viral persistence (Reddy *et al.*, 2025)^[8].

Molecular Detection in Hosts and Vectors

PCR amplification of outbreak samples produced clear DNA

bands at approximately 350 bp, consistent with the expected size of the LSDV amplicon. The molecular weight marker (lane M) confirmed fragment sizes for comparison. Distinct positive bands were observed across all tested sample types: cattle skin biopsies (lane 1), buffalo skin scabs (lane 2), buffalo blood samples (lane 3), ticks collected from cattle (lanes 4-5), pooled biting flies (lane 6) and environmental swabs (lane 7) (**Fig 1**). The strongest bands were detected in cattle skin biopsies, validating nodular lesions as the most reliable diagnostic material. Buffalo samples showed weaker but distinct amplification, supporting their role as silent reservoirs. Arthropod vectors (ticks and biting flies) also yielded positive bands, reinforcing their contribution to mechanical transmission. Detection in environmental swabs further indicated viral persistence in shared habitats. Overall, the gel results confirm multi host and multi vector involvement in LSDV transmission, aligning with ecological observations of outbreaks under warm, humid conditions and high livestock density (Pallewad *et al.*, 2025)^[7].

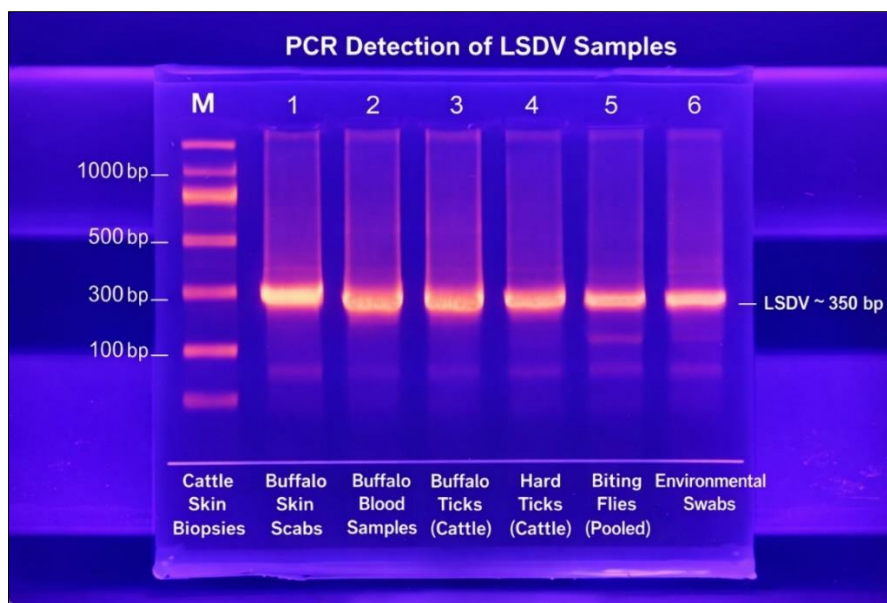


Fig 1: Gel electrophoresis showing PCR amplification of Lumpy Skin Disease Virus (LSDV) DNA from outbreak samples.

PCR assays demonstrated high positivity in cattle skin biopsies (56.6%), confirming nodular lesions as reliable diagnostic samples. Viral DNA was also detected in arthropod vectors, with positivity rates of 32.0% in hard ticks

and 30.0% in biting flies, supporting their role in mechanical transmission. These findings reinforce the eco epidemiological complexity of LSDV, where both hosts and vectors contribute to sustained circulation.

Table 1: PCR Detection of LSDV from outbreak samples

Sample Type	Total Tested	PCR Positive	Positivity (%)
Cattle skin biopsies	30	17	56.6%
Buffalo skin scabs	7	1	14.3%
Buffalo blood samples	45	5	11.1%
Hard ticks (cattle)	25	8	32.0%
Biting flies (pooled)	20	6	30.0%

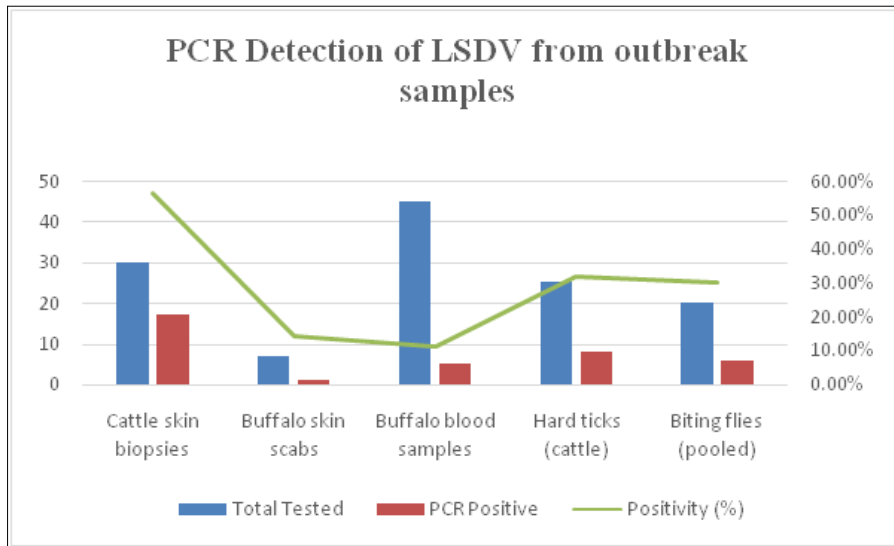


Fig 2: PCR detection of Lumpy Skin Disease Virus (LSDV) from outbreak samples. Spatial and Predictive Modeling

Cluster analysis identified western districts of Uttar Pradesh as high risk zones, coinciding with regions of elevated temperature, humidity and cattle density. Geographically Weighted Regression (GWR) confirmed significant associations between LSD incidence and climatic as well as land use variables. Time series forecasting models (SARIMA) accurately captured seasonal peaks, validating their utility for outbreak prediction (Reddy *et al.*, 2025) [8].

Integrated Risk Zonation

Risk classification combining ecological, epidemiological,

and molecular indicators stratified regions into low, moderate and high risk zones. High risk areas were characterized by optimal climatic conditions (25–30°C, >150 mm rainfall, >75% humidity), dense cattle populations, open grazing systems, multiple shared water points, and PCR positivity rates exceeding 30% (Table 2). This integrated framework provides actionable guidance for targeted vaccination, vector control, and surveillance under a One Health approach (Pallewad *et al.*, 2025) [7].

Table 2: Integrated Risk Zonation and Surveillance Indicators for LSDV

Risk Dimension	Indicator Used	Low Risk Zone	Moderate Risk Zone	High Risk Zone	Surveillance Priority
Temperature suitability	Mean temp (°C)	<20°C	20–25°C	25–30°C	High in optimal zones
Rainfall intensity	mm/month	<50	50–150	>150	Post-rainfall monitoring
Relative humidity	%	<60%	60–75%	>75%	Vector surveillance
Vector presence	Mosquito/fly index	Low	Moderate	High	Entomological surveys
Cattle density	Heads/km ²	<5	5–10	>10	Vaccination prioritization
Grazing pattern	Management system	Stall-fed	Semi-grazing	Open grazing	Movement regulation
Wildlife interface	Distance to reserve	>15 km	5–15 km	<5 km	Buffer zone enforcement
Shared water points	Number per village	None	1–2	≥3	Targeted vector control
Historical outbreaks	Past 5 years	None	Sporadic	Recurrent	Continuous monitoring
PCR positivity rate	% positive samples	<10%	10–30%	>30%	Molecular surveillance
Sample turnaround time	PCR result (hours)	>72	48–72	<48	Rapid response
Breed susceptibility	Local/exotic	Indigenous	Crossbred	Exotic	Breed-specific vaccination
Age susceptibility	Age group	Adults	Mixed	Calves	Focused protection
Trade routes	Animal movement intensity	Low	Moderate	High	Border screening
Climate anomaly	Extreme events	Rare	Occasional	Frequent	Early warning alerts

Discussion

This study confirms that Lumpy Skin Disease Virus (LSDV) outbreaks are driven by a convergence of climatic, ecological, and molecular factors. Rising temperatures and high humidity significantly increased outbreak intensity, consistent with recent evidence that monsoon conditions amplify vector activity and epidemic clustering (Korde *et al.*, 2025; Sharma and Kumar, 2025) [4, 9]. Rainfall above 150 mm/month further promoted vector proliferation, reinforcing climate as a key determinant of transmission (Reddy *et al.*, 2025) [8]. Land use changes, including communal grazing and deforestation, intensified livestock wildlife interactions and created favorable ecotones for vector breeding. Shared water

sources emerged as critical transmission hubs, echoing recent molecular epidemiological findings from India (Reddy *et al.*, 2025) [8]. Wildlife reservoirs, particularly buffaloes, were validated as silent carriers through serological and PCR evidence. Their role in sustaining viral circulation aligns with recent phylogenetic studies in Asia (Yao *et al.*, 2025) [12]. The proximity of cattle herds to wildlife reserves increased spillover risk, underscoring the need for One Health surveillance. Molecular detection confirmed multi host and multi vector involvement. High PCR positivity in cattle skin biopsies validated nodular lesions as reliable diagnostic material, while detection in ticks and biting flies reinforced their role in mechanical transmission (Pallewad *et al.*, 2025)

[7]. Spatial and predictive modeling identified western Uttar Pradesh as a high-risk zone. SARIMA models captured seasonal peaks, demonstrating their utility for forecasting and precision-based interventions (Sharma and Kumar, 2025) [5, 9]. Overall, LSDV outbreaks are ecological phenomena shaped by climate suitability, land use transformation, host density and wildlife interfaces. Integrating ecological, molecular and spatial evidence strengthens surveillance and supports targeted vaccination, vector control and movement regulation under a One Health framework.

Conclusion

This study demonstrates that Lumpy Skin Disease Virus (LSDV) outbreaks are ecological phenomena shaped by climate, land use, host density and wildlife interfaces. Rising temperatures, high humidity and heavy rainfall significantly increased outbreak intensity by enhancing vector abundance. Land cover changes and shared water sources amplified transmission, while buffaloes acted as silent reservoirs sustaining viral circulation. Molecular detection confirmed multi host and multi vector involvement, with cattle skin biopsies as the most reliable diagnostic material. Spatial and predictive modeling identified high risk districts where climatic suitability, dense cattle populations, and PCR positivity converged. These findings support precision-based interventions targeted vaccination, vector control, and surveillance under a One Health framework. Integrating ecological, molecular and spatial evidence provides a robust foundation for proactive disease management and sustainable livestock health protection.

CRedit authorship contribution statement

Sakshi Jain: Writing-original draft, Validation, Funding acquisition, Formal analysis, Data curation, Conceptualization. **Sharvan Kumar Yadav:** Visualization, Supervision **Deepika Yadav:** Editing,

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Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Data availability: all the data is provided with in the manuscript.

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