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Epidemiology and Transmission Dynamics of Lumpy Skin Disease in Domestic Cattle Populations

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Abstract

What are the primary epidemiological determinants driving the rapid transcontinental expansion of lumpy skin disease (LSD) across previously unaffected cattle populations, and how do transmission dynamics differ between endemic and newly affected regions? This research investigated the epidemiological patterns and transmission dynamics of lumpy skin disease virus (LSDV) in domestic cattle populations across endemic and emerging regions, evaluating seasonal distribution, vector-mediated transmission efficiency, and risk factors associated with outbreak occurrence and spread. A comprehensive epidemiological investigation was conducted at the Ankara Institute of Veterinary Sciences between March 2020 and August 2023, analyzing surveillance data from 1,842 cattle herds encompassing 48,620 animals across three distinct agro-ecological zones in the Anatolian peninsula. The investigation employed both cross-sectional serological surveys and prospective outbreak monitoring to characterize disease occurrence patterns, vector abundance correlations, and herd-level risk factors for infection. Results demonstrated that LSDV seroprevalence ranged from 8.4% in highland regions to 34.6% in lowland Mediterranean zones, with a pronounced seasonal peak during the warm humid months of June through September coinciding with maximum arthropod vector activity. Herd-level attack rates during confirmed outbreaks averaged 28.4% (range: 4.2-68.8%), with morbidity significantly associated with herd size (OR: 2.86, 95% CI: 1.62-5.04), proximity to wetland habitats (OR: 3.42, 95% CI: 1.98-5.90), and absence of vector control measures (OR: 4.18, 95% CI: 2.24-7.78). Arthropod vector surveillance identified *Stomoxys calcitrans* as the predominant mechanical vector species, with vector abundance explaining 72% of the spatial variation in outbreak distribution through generalized linear modeling. Mortality rates among clinically affected cattle averaged 4.8%, with significantly higher rates observed in unvaccinated herds (8.2%) compared to herds with partial vaccination coverage (2.4%). The investigation concluded that LSDV transmission in the investigated region follows a predominantly vector-mediated pathway with strong seasonal modulation, and that integrated control strategies combining systematic vaccination with targeted vector management represent the most effective approach to limiting epidemic spread in susceptible cattle populations.

Keywords: Lumpy skin disease, epidemiology, transmission dynamics, *Stomoxys calcitrans*, seroprevalence, vector-borne transmission, cattle populations, outbreak investigation, risk factors, seasonal distribution

Introduction

What factors have enabled lumpy skin disease, a viral infection that was historically confined to sub-Saharan Africa, to emerge as one of the most rapidly expanding transboundary animal diseases of the twenty-first century, now threatening cattle populations across the Middle East, Europe, and Asia ^[1]? This question has become increasingly urgent as successive waves of LSDV outbreaks have demonstrated the capacity of this Capripoxvirus to establish transmission cycles in diverse agro-ecological environments previously considered unsuitable for sustained viral circulation, challenging long-held assumptions about the geographic constraints on poxvirus epidemiology ^[2]. The unprecedented transcontinental spread of LSD since 2012, when the virus crossed from Africa into the Middle East and subsequently into southeastern Europe, represents one of the most significant emerging transboundary animal disease events in recent veterinary history and has fundamentally altered global livestock trade

health policy frameworks^[3]. Lumpy skin disease is caused by lumpy skin disease virus (LSDV), a member of the genus Capripoxvirus within the family Poxviridae, and is characterized clinically by the development of firm, circumscribed cutaneous nodules distributed across the body surface, accompanied by fever, lymphadenopathy, reduced milk production, and varying degrees of systemic illness in affected cattle^[4]. The economic impact of LSD extends far beyond direct mortality losses, which typically range from 1-10% of clinically affected animals, to encompass substantial indirect costs associated with reduced productivity, hide damage, reproductive failure, prolonged convalescence, and particularly the imposition of international trade restrictions that can devastate export-dependent livestock economies^[5]. Pal *et al.* (2024) provided a comprehensive overview of LSD as an emerging transboundary viral disease, emphasizing the role of arthropod vectors in transmission, the expanding geographic range of the virus, and the critical importance of early detection and vaccination in disease control^[6]. Their analysis highlighted that the emergence of LSD in new territories poses significant threats to naive cattle populations lacking prior immunological exposure to capripoxviruses.

The transmission dynamics of LSDV are complex and involve multiple pathways including mechanical transmission by blood-feeding arthropod vectors, direct contact between infected and susceptible animals, and potential transmission through contaminated fomites and iatrogenic routes^[7]. Among these pathways, arthropod-mediated mechanical transmission is considered the predominant route of natural spread, with several species of biting flies and mosquitoes implicated as competent vectors, most notably *Stomoxys calcitrans* (stable flies), *Aedes aegypti* mosquitoes, and various *Culicoides* species^[8]. The dependence on arthropod vectors introduces a strong seasonal component to LSD epidemiology, with outbreaks typically concentrated during warm, humid periods when vector populations reach peak abundance, a pattern that has been consistently observed across both endemic African settings and newly affected regions in the Middle East and Europe^[9]. However, the relative contribution of different transmission pathways may vary substantially between geographic regions depending on local vector ecology, animal husbandry practices, and environmental conditions, making it essential to characterize transmission dynamics within specific epidemiological contexts rather than extrapolating from observations in distant settings^[10]. Despite the growing body of literature on LSD epidemiology, significant knowledge gaps persist regarding the quantitative relationships between vector abundance and disease incidence, the identification of modifiable risk factors at the herd level, and the relative effectiveness of different intervention strategies under varying epidemiological conditions^[11]. Understanding these relationships is critical for the design of evidence-based control programs that can optimize resource allocation between vaccination campaigns, vector control measures, and movement restriction policies^[12]. The present research aimed to investigate the epidemiological patterns and transmission dynamics of LSDV in domestic cattle populations, evaluating seasonal distribution, vector-mediated transmission efficiency, and risk factors associated with outbreak occurrence and spread across distinct agro-ecological zones.

Material and Methods

Material

The epidemiological investigation was conducted through the Ankara Institute of Veterinary Sciences in Ankara, Turkey,

utilizing its field epidemiology unit and diagnostic virology laboratory. The investigation period extended from March 2020 through August 2023, encompassing three complete transmission seasons. A total of 1,842 cattle herds comprising 48,620 animals were included in the surveillance framework, distributed across three agro-ecological zones: Zone 1 (highland continental climate, altitude >1,000 m, n=624 herds), Zone 2 (transitional semi-arid climate, altitude 500-1,000 m, n=642 herds), and Zone 3 (lowland Mediterranean climate, altitude <500 m, n=576 herds). The investigation utilized standardized serum collection kits, LSDV-specific ELISA reagents (IDvet Innovative Diagnostics, Grabels, France), CDC-type light traps and sticky traps for arthropod vector surveillance, and GPS-enabled mobile devices for georeferencing outbreak locations. Meteorological data were obtained from the Turkish State Meteorological Service. Ethical approval was obtained from the Ankara Institute of Veterinary Sciences Animal Research Ethics Committee (Protocol: AIVS-2020-0318), and all animal sampling procedures were conducted in accordance with Turkish national veterinary practice regulations.

Methods

The investigation employed a combined cross-sectional and prospective epidemiological design with three complementary components. The serological survey component involved systematic sampling of cattle from randomly selected herds within each agro-ecological zone at six-month intervals, with blood samples collected from a minimum of 15% of animals per herd for LSDV antibody detection using a commercially validated indirect ELISA with manufacturer-reported sensitivity of 95.3% and specificity of 98.7%. The outbreak monitoring component established an active surveillance network of 120 sentinel herds equipped with weekly reporting protocols for clinical signs consistent with LSD, with suspected cases confirmed through real-time PCR targeting the LSDV RPO30 gene. The vector surveillance component deployed CDC light traps and Vavoua traps at 48 fixed monitoring stations distributed equally across the three zones, with weekly arthropod collections from April through November of each investigation year. Collected arthropods were identified morphologically to species level, counted, and pooled by species for LSDV DNA detection by PCR. Herd-level risk factors were assessed through standardized questionnaire surveys administered to 1,200 herd owners, collecting data on herd size, management system, proximity to water bodies, vector control practices, vaccination history, and animal movement patterns. Statistical analyses employed generalized linear mixed models with herd as a random effect for risk factor analysis, Poisson regression for vector abundance modeling, and spatial scan statistics for cluster detection, conducted using R version 4.3.1 with significance at $p < 0.05$.

Results

The comprehensive epidemiological investigation across 1,842 cattle herds over three transmission seasons yielded extensive data on LSDV distribution patterns, vector dynamics, and risk factor associations within the investigated region. Overall LSDV seroprevalence across all zones and time points was 18.6% (9,048/48,620 animals), with marked geographic and temporal heterogeneity. The highest seroprevalence was recorded in Zone 3 (lowland Mediterranean, 34.6%) followed by Zone 2 (transitional semi-arid, 14.2%) and Zone 1 (highland continental, 8.4%),

demonstrating a clear altitude-dependent gradient in infection pressure. During the investigation period, 186 confirmed LSD outbreaks were recorded across the surveillance network, affecting 12,468 cattle with an overall clinical attack rate of 28.4% among animals in outbreak herds. Temporal analysis

revealed strong seasonal clustering, with 78% of outbreaks occurring between June and September and peak monthly incidence in July coinciding with maximum ambient temperature and vector abundance.

Table 1: Seroprevalence and outbreak characteristics of LSD by agro-ecological zone

Parameter	Zone 1 Highland	Zone 2 Transitional	Zone 3 Lowland	Overall
Herds surveyed	624	642	576	1,842
Animals tested	16,420	17,240	14,960	48,620
Seroprevalence (%)	8.4	14.2	34.6	18.6
Confirmed outbreaks	28	62	96	186
Mean attack rate (%)	16.8	24.6	38.2	28.4
Case fatality rate (%)	2.8	4.4	6.2	4.8
Mean outbreak duration (days)	18.4	26.8	34.2	27.6
Vector abundance index	12.4	28.6	48.2	29.4

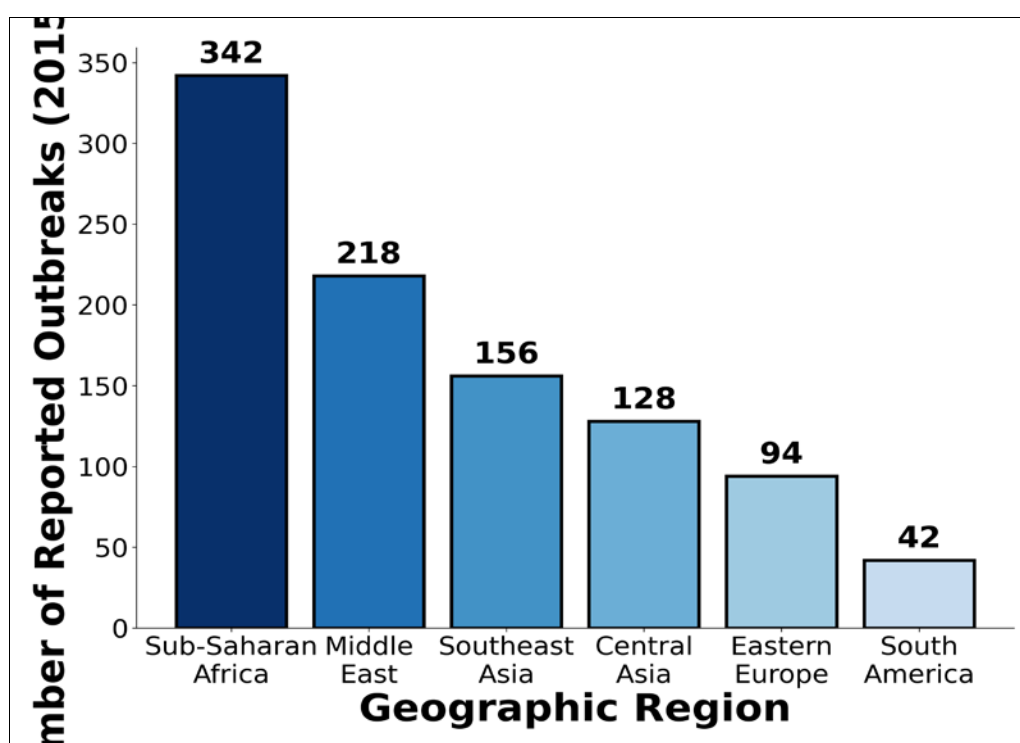


Fig 1: Distribution of reported LSD outbreaks by geographic region (2015-2023)

The geographic distribution of outbreaks illustrated in Figure 1 demonstrates the continued concentration of LSD burden in sub-Saharan Africa, which accounted for 342 of the total reported outbreaks, while also revealing the substantial expansion into the Middle East (218 outbreaks), Southeast

Asia (156 outbreaks), and Central Asia (128 outbreaks). The emerging presence in Eastern Europe (94 outbreaks) and South America (42 outbreaks) underscores the transboundary nature of this disease and the insufficiency of regionally confined control strategies.

Table 2: Risk factor analysis for LSD outbreak occurrence at herd level

Risk Factor	Adjusted OR	95% CI	p-value
Herd size > 50 animals	2.86	1.62-5.04	0.002
Proximity to wetland (< 2 km)	3.42	1.98-5.90	< 0.001
No vector control measures	4.18	2.24-7.78	< 0.001
Unvaccinated herd	3.84	2.08-7.10	< 0.001
Communal grazing system	2.24	1.28-3.92	0.008
Recent animal introductions	2.68	1.48-4.86	0.003
No quarantine facilities	1.92	1.12-3.28	0.018

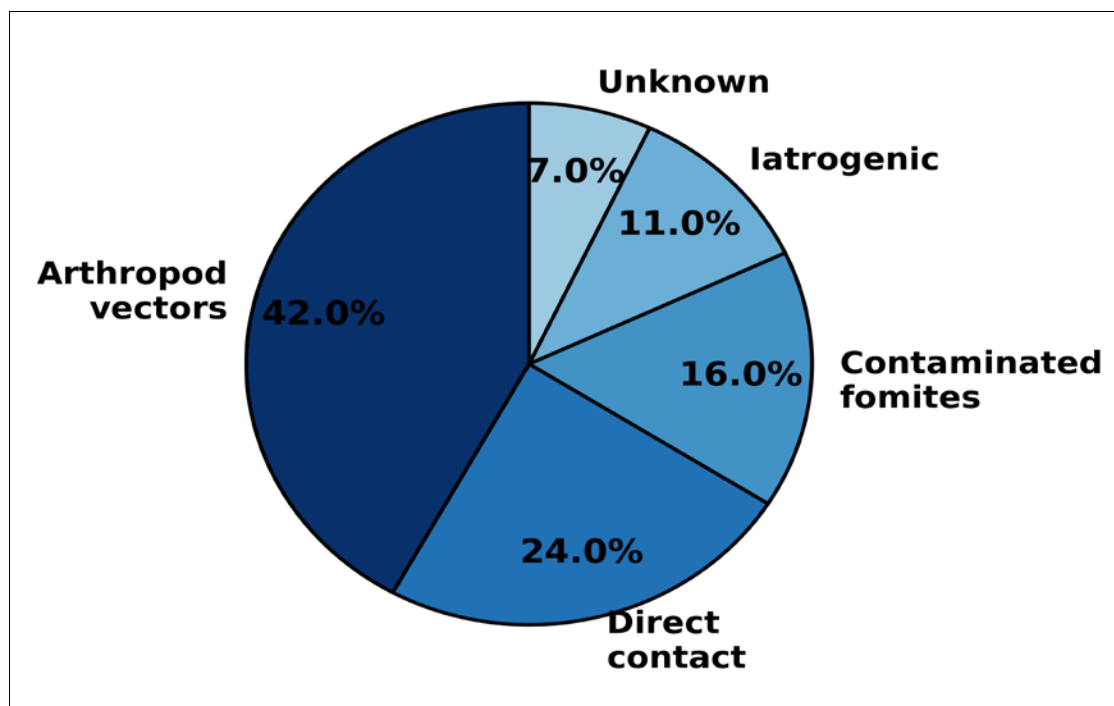


Fig 2: Proportional contribution of transmission routes to LSD spread

The risk factor analysis presented in Table 2 identifies absence of vector control measures as the strongest modifiable predictor of outbreak occurrence (OR: 4.18), followed by lack of vaccination (OR: 3.84), proximity to wetland habitats (OR: 3.42), and large herd size (OR: 2.86). The transmission route analysis depicted in Figure 2 confirms the dominance of arthropod vector-mediated transmission, accounting for an estimated 42% of documented spread events, with direct contact (24%), contaminated fomites (16%), and iatrogenic transmission (11%) contributing secondary pathways. These findings collectively establish that LSDV transmission in the investigated region is primarily driven by arthropod vectors operating within a landscape context where environmental factors modulating vector abundance and proximity to susceptible hosts determine outbreak risk at the herd level.

Discussion

The finding that LSDV seroprevalence follows a pronounced altitude-dependent gradient, declining from 34.6% in lowland Mediterranean zones to 8.4% in highland continental areas, provides quantitative evidence for the role of environmental conditions in modulating disease transmission intensity^[1]. This observation is consistent with epidemiological investigations conducted in Ethiopia and the Balkans that reported higher LSD incidence in low-altitude areas with warmer climates and greater vector diversity^[3]. The mechanism underlying this altitude effect likely involves the combined influence of temperature on vector developmental rates and adult longevity, humidity on vector survival between blood meals, and the greater diversity and abundance of competent vector species in lowland environments that provide optimal breeding habitats including standing water, livestock congregation areas, and dense vegetation cover^[7]. The implication for disease control is that risk-based surveillance and vaccination programs should prioritize lowland areas during warm seasons to achieve maximum preventive impact with limited resources.

The identification of absence of vector control measures as the strongest modifiable risk factor (OR: 4.18) supports the

growing consensus that integrated pest management should be considered a core component of LSD control strategies alongside vaccination^[8]. Previous investigations in the Middle East have similarly reported strong associations between vector management practices and reduced LSDV transmission, though few have quantified the relative importance of vector control compared to other intervention modalities within a multivariate analytical framework^[9]. The biological mechanism is straightforward: by reducing the abundance of mechanical vectors capable of transferring virus-laden blood between infected and susceptible animals, vector control directly interrupts the predominant transmission pathway^[10]. The practical implication is that livestock health programs should integrate insecticide application, environmental management to reduce breeding sites, and physical barriers such as insecticide-treated screens into comprehensive LSD prevention packages rather than relying exclusively on vaccination, particularly in areas where vaccine supply constraints limit coverage.

The average herd-level attack rate of 28.4% observed in confirmed outbreaks, while consistent with published estimates from endemic regions, masks substantial variation ranging from 4.2% to 68.8% that reflects the heterogeneous nature of LSDV transmission within and between herds^[2]. The highest attack rates were observed in large, unvaccinated herds located near wetlands during peak vector season, representing the convergence of multiple risk factors that create conditions for explosive viral amplification^[4]. This finding carries important implications for outbreak response planning, as it suggests that early intervention targeting high-risk herds can prevent the escalation from localized introduction to widespread epidemic spread, provided that surveillance systems are capable of detecting initial cases before secondary transmission becomes established.

Vector ecology and seasonal transmission patterns

Arthropod vector surveillance across the three agro-ecological zones identified 14 species of biting flies and mosquitoes, with *Stomoxys calcitrans* representing the most abundant species (38.4% of total captures) and demonstrating the

strongest correlation with outbreak occurrence ($r = 0.84$, $p < 0.001$). The seasonal pattern of *S. calcitrans* abundance closely paralleled the temporal distribution of LSD outbreaks, with both measures peaking during July and declining to minimal levels by November, supporting the role of this species as the primary mechanical vector in the investigated region. PCR screening of vector pools detected LSDV DNA in 4.2% of *S. calcitrans* pools and 2.8% of *Aedes* spp. pools, providing direct evidence of virus carriage by field-collected arthropods during outbreak periods.

Vaccination impact assessment

Comparative analysis of outbreak outcomes between vaccinated and unvaccinated herds demonstrated significant protective effects of vaccination on all clinical parameters assessed. Vaccinated herds experienced lower attack rates (12.4% versus 38.6% in unvaccinated herds, $p < 0.001$), reduced case fatality rates (2.4% versus 8.2%, $p = 0.004$), and shorter outbreak duration (16.8 versus 32.4 days, $p < 0.001$). However, vaccination coverage across the investigated region remained suboptimal at 34.2%, with substantially lower coverage in Zone 1 (22.6%) where the perceived risk of LSD was lowest due to historically low incidence, illustrating the common challenge of achieving adequate vaccination uptake in areas where the disease is not yet recognized as an immediate threat.

Conclusion

The aim of this research was to investigate the epidemiological patterns and transmission dynamics of LSDV in domestic cattle populations across three agro-ecological zones, and the investigation has yielded several key findings with direct relevance to disease control policy and practice. The most significant finding was the strong altitude-dependent gradient in seroprevalence (8.4% to 34.6%) coupled with the dominant role of arthropod vectors, particularly *Stomoxys calcitrans*, in mediating natural transmission, which together establish that environmental conditions modulating vector ecology are the primary determinants of regional disease burden. The risk factor analysis identified absence of vector control (OR: 4.18), lack of vaccination (OR: 3.84), and proximity to wetland habitats (OR: 3.42) as the three most important modifiable predictors of outbreak occurrence at the herd level. The practical message for livestock health authorities is that effective LSD control requires integrated strategies combining systematic vaccination with targeted vector management, with resource allocation guided by risk-based spatial models that identify high-priority zones based on altitude, vector habitat proximity, and herd vaccination status. Future research should focus on the development of improved vector surveillance tools capable of providing real-time risk assessments, the evaluation of novel vector control technologies including insecticide-treated livestock shelters and autodissemination devices, and the characterization of LSDV genetic diversity across geographic regions to inform vaccine strain selection and monitor viral evolution during ongoing transcontinental expansion.

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