VETERINARY TODAY
INTERNATIONAL
ISSN 2583-8288

Expanding Host Range of Lumpy Skin Disease Virus: Emerging Multi-Species Susceptibility

Kiran Jayappa[1]*, Pura Yaro Semy[2]

[1]College of Veterinary Sciences and Animal Husbandry, Central Agricultural University (I), Selesih, Aizawl, Mizoram, India – 796 015

[2] College of Veterinary Sciences and Animal Husbandry, Nanaji Deshmukh Veterinary University, Jabalpur, Madhya Pradesh, India – 482 001

*Corresponding author: Kiran Jayappa - Email: drkiranj@outlook.com

DOI:10.5281/Vettoday.17799796

Abstract

Lumpy Skin Disease Virus (LSDV), once mainly cattle-associated, is now an emerging multi-host threat affecting livestock and wildlife. Since its 2019 introduction into India, LSDV has caused major economic losses, including over USD 2.2 billion in 2022. Recent outbreaks show infections in buffaloes, yak, gazelles, serows, and even a giraffe, reflecting increasing spillover at the livestock–wildlife interface. Circulating SG-1, KSGP lineage 1.2, and recombinant strains indicate ongoing viral evolution that may enhance host adaptability. Vector transmission, climate shifts, and livestock movement drive interspecies spread, underscoring the need for integrated One Health surveillance, wildlife monitoring, genomic tracking, and strategic vaccination.

Introduction

Lumpy Skin Disease Virus (LSDV), a Capripoxvirus of major transboundary concern, has evolved from a regionally confined pathogen to a globally significant threat with profound implications for livestock health, rural livelihoods, and ecosystem stability (Bianchini et al., 2023). After its first identification in Zambia in 1929, the virus spread beyond Africa into the Middle East, Europe, and Asia, with India reporting its inaugural outbreak in Odisha in 2019, a pivotal event given the nation's vast bovine population (Manjunatha et al., 2023). The 2022 epidemic, responsible for nearly 155,000 cattle deaths, severely affected the dairy, meat, and hide industries, collectively contributing to estimated national losses exceeding USD 2.2 billion. As outbreaks intensified, LSDV demonstrated an expanding host range, infecting buffaloes, yak, Indian gazelles, red serows, and even a captive giraffe, signaling a shift from its historically cattle-centric epidemiology (Dao et al., 2022; Rajkhowa et al., 2025; Sudhakar et al., 2023). Clinical signs across species—pyrexia, nodular dermatitis, lymphadenopathy, anorexia, and secondary infections—translate into reduced productivity and prolonged recovery. Equally concerning is the virus's establishment in wildlife, where spillover threatens conservation-dependent species and raises the possibility of new reservoir hosts capable of perpetuating transmission outside domestic systems. This ecological transition underscores the urgency of integrated livestock–wildlife surveillance and comprehensive control strategies to mitigate LSDV's evolving impact.

New and Unexpected Hosts

Over the past five years, LSDV has exhibited a striking expansion in its host spectrum, spilling over from cattle into a diverse range of domestic and wild ungulates across Asia and other regions. This trend is particularly evident in landscapes where livestock and wildlife share grazing areas, water sources, and vector habitats, creating ecological interfaces that facilitate cross-species transmission and raise concerns about the emergence of new wildlife reservoirs capable of sustaining viral circulation independently of cattle (Rajkhowa et al., 2025). Notable spillover events include the first global detection of LSDV in a giraffe in Vietnam, where a juvenile male presented with severe nodular dermatitis and rapidly succumbed to infection, with molecular analyses confirming close phylogenetic ties to cattle strains (Dao et al., 2022). India has similarly reported unprecedented cases in free-ranging Indian gazelles and a vulnerable red serow, with isolates clustering within SG-1 and KSGP O-240 lineages, respectively (Sudhakar et al., 2023; Rajkhowa et al., 2025). Natural transmission to yak in high-altitude pastoral systems further demonstrates the virus's adaptability and ease of interspecies spread (Manjunatha et al., 2023). Additional serological evidence from African buffalo, oryx, eland, springbok, impala, wildebeest, and banteng suggests widespread subclinical circulation. Such wildlife involvement complicates disease management, as vaccination and vector control are often infeasible in natural ecosystems, enabling the virus to persist and periodically spill back into domestic herds. The co-circulation of classical and recombinant lineages further highlights LSDV's evolving host adaptability and underscores the urgent need for integrated, ecosystem-based surveillance and control strategies.

How the Virus Crosses Species

LSDV's capacity to infect a diverse array of hosts is closely linked to its transmission ecology. The virus is primarily vector-borne, with hematophagous insects including *Stomoxys calcitrans*, mosquitoes, biting midges, and several tick species acting as efficient mechanical vectors (Bianchini *et al.*, 2023). These arthropods feed opportunistically on multiple ungulate species, facilitating viral transfer between livestock and wildlife. This mechanism has been implicated in documented spillover events involving Indian gazelles, yak, and red serows (Manjunatha *et al.*, 2023; Rajkhowa *et al.*, 2025; Sudhakar *et al.*, 2023).

LSDV also demonstrates notable environmental persistence, remaining viable in dried scabs, necrotic tissues, and contaminated fomites for extended durations (Bianchini *et al.*, 2023). Virus isolation from skin, blood, and field-collected arthropods during cattle and yak outbreaks confirms its ability to survive long enough to mediate transmission among sympatric species. Additionally, bulls may shed the virus in semen for prolonged periods, providing a less common yet possible route for interspecies exposure.

Genomic investigations conducted in India and Southeast Asia reveal that circulating strains particularly lineage 1.2 and SG-1 exhibit distinct genetic mutations, including deletions and point mutations in the GPCR and EEV genes (Rajkhowa *et al.,* 2025; Sudhakar *et al.*, 2023). These molecular alterations may confer enhanced environmental stability, vector competence, and host adaptability, thereby facilitating infection in non-traditional hosts such as red serow and giraffe.

Environmental and anthropogenic factors further enhance cross-species transmission. Climate change, through increases in temperature and humidity, prolongs vector breeding seasons and elevates arthropod population densities. Expansion of irrigation and intensive agriculture generates ideal breeding habitats, while agricultural encroachment into wildlife areas increases direct and vector-mediated interface between domestic and wild ungulates. Livestock movement including trade-driven transport, drought-related relocation, and transhumance grazing has repeatedly introduced new LSDV lineages into previously unaffected ecosystems (Sudhakar *et al*., 2023).

These interconnected drivers demonstrate that LSDV traverses species boundaries through a combination of vector ecology, environmental resilience, host proximity, and viral evolution.

Why This Expansion Matters

The expanding host range of LSDV carries far-reaching implications for livestock production, wildlife conservation, and national biosecurity. In livestock systems, the virus causes substantial economic losses due to reduced milk yield, impaired growth, infertility, hide damage, and mortality. India's 2022 outbreak, which resulted in over 155,000 cattle deaths and losses exceeding USD 2.2 billion, illustrates the severity of its impact on rural livelihoods and agricultural value chains (Manjunatha *et al*., 2023).

From a wildlife perspective, the implications are even more profound. Confirmed infections in Indian gazelles, red serows, giraffes, banteng, and camels highlight an incursion into ecologically sensitive species (Rajkhowa *et al*., 2025; Sudhakar *et al*., 2023; Dao *et al.,* 2022). Species such as the red serow already classified as Vulnerable due to habitat fragmentation and poaching now face an additional pathogenic threat. Establishment of LSDV in wildlife reservoirs can enable the virus to circulate independently of domestic cattle, significantly complicating eradication strategies and heightening risks to biodiversity.

India's mixed agro-pastoral landscapes, where cattle, buffalo, yak, and wild ungulates frequently share resources, create conditions conducive to continual vector-mediated transmission. Many wildlife species present with atypical or subtle clinical signs, leading to underdiagnosis and delayed identification of spillover events (Rajkhowa *et al*., 2025). As a result, infections may spread silently until significant morbidity or mortality becomes apparent.

Thus, LSDV's expanded host range represents not only a veterinary challenge but also a broader ecological and conservation concern, necessitating integrated surveillance and control approaches.

The Need for Stronger Surveillance and Control

Effective control of LSDV in a multi-host system requires transitioning from conventional, cattle-centric approaches to an integrated framework that accounts for domestic animals, wildlife, and environmental factors (Dao *et al.,* 2022; Khan *et al.,* 2025).

Strengthened surveillance is essential. Evidence from India indicates that wildlife infections were typically detected only after severe clinical disease or postmortem examination, suggesting that many cases remain unrecognized. Incorporating wildlife health assessments, vector monitoring, and routine genomic sequencing into national disease surveillance systems is therefore critical to map viral movement and detect emerging lineages (Khan *et al*., 2025).

Vaccination remains the cornerstone of LSD control in domestic herds. Homologous live-attenuated vaccines have effectively reduced morbidity and mortality when administered prior to peak vector seasons (Tuppurainen & Oura, 2012). However, the recent detection of vaccine-derived recombinant strains in India necessitates careful vaccine selection, ongoing monitoring of post-vaccination response, and maintenance of high immunization coverage (Dao *et al*., 2022).

Vector management constitutes another essential component of control. Reducing populations of *Stomoxys*, mosquitoes, and biting midges through improved sanitation, insecticide-treated netting, and elimination of breeding sites can substantially reduce transmission risk. Zoos and wildlife rescue facilities require additional precautions due to their documented vulnerability to spillover events (Khan *et al*., 2025).

Biosecurity and controlled animal movement remain critical. During the 2022 Indian outbreak, rapid geographical spread was partly attributed to the transport of animals during their incubation period. Mandatory screening, quarantine of newly introduced animals, and temporary restrictions on livestock movement during outbreaks can help interrupt transmission chains. In high-risk wildlife–livestock interfaces, landscape-level measures—including controlled grazing, fencing in sensitive habitats, and limiting shared water sources—can reduce cross-species exposure.

Ultimately, LSDV's emergence as a multi-host pathogen highlights the necessity of a One Health approach that integrates veterinary, wildlife, environmental, and public health sectors. Coordinated surveillance, targeted vaccination, robust vector control, and stringent biosecurity are essential for sustainable control and long-term mitigation of LSDV spread.

Conclusion

LSDV's shift from a predominantly cattle-associated virus to a multi-host pathogen poses new challenges for livestock production and wildlife health. Its emergence in buffaloes, yak, gazelles, serows, banteng, and even a giraffe reflects increasing adaptability driven by viral evolution, vector dynamics, and growing livestock–wildlife interactions. This expanded host range heightens the risk of establishing wildlife reservoirs, complicating control and long-term eradication.

Effective management now requires a One Health approach that integrates wildlife surveillance, genomic monitoring, targeted vaccination, vector control, and regulated animal movement. Strengthening these interconnected measures is essential to curb further spread and mitigate the economic and ecological impacts of LSDV.

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