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Decoding Lumpy Skin Disease Virus: Molecular insights for diagnostics and disease management

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Abstract

Lumpy Skin Disease Virus (LSDV), a member of the *Capripoxvirus* genus within the *Poxviridae* family, is a double-stranded DNA virus responsible for severe economic losses in the cattle industry due to its high morbidity and impact on livestock productivity. The genome of LSDV, approximately 151 kbp in size, encodes a diverse array of genes involved in viral replication, host range determination, immune modulation, and virulence. Recent advancements in molecular biology and genomics have enabled the detailed characterization of the genetic architecture of LSDV, uncovering critical insights into its pathogenic mechanisms, genetic variability, and evolutionary dynamics. This review synthesizes the current knowledge on the genetic basis of LSDV, focusing on the functional roles of key genes, mechanisms of immune evasion, and genetic determinants of virulence. Additionally, it highlights the utility of genomic tools in outbreak tracing, disease diagnosis, and vaccine development. Key findings emphasize the role of genomic stability in LSDV's persistence and the emerging challenges posed by strain variation and host adaptability. The review further addresses unresolved genomic questions by outlining the gaps in current knowledge and proposing future research directions, this article aims to contribute to the development of targeted molecular interventions and enhance the global effort toward effective control and eradication of LSDV.

Keywords: Lumpy skin disease, virus, genomics, virulence, molecular diagnostics, vaccine

Introduction

Lumpy Skin Disease Virus (LSDV), a member of the *Capripoxvirus* genus within the *Poxviridae* family, is a highly pathogenic double-stranded DNA virus responsible for Lumpy Skin Disease (LSD) in cattle (Gupta *et al.,* 2020) [1]. First identified in Zambia in 1929, the disease has since spread across Africa, the Middle East, Asia, and parts of Europe, emerging as a significant transboundary animal disease (Mazloum *et al.,* 2023, Davis, 1991) [2, 9]. LSDV is characterized by its ability to cause high morbidity, reduced productivity, and economic losses in livestock industries due to weight loss, decreased milk production, and damage to hides (Akther *et al.,* 2023) [3].

LSDV is primarily transmitted through arthropod vectors, making it a vector-borne disease. This mode of transmission plays a significant role in the seasonal and geographical spread of the virus, particularly in regions with high vector populations (Sprygin *et al.,* 2019) [4]. Blood-feeding insects, including species of *Stomoxys* (stable flies), *Culicoides* (biting midges), and *Tabanidae* (horseflies), are key mechanical vectors of LSDV (Sprigin *et al.,* 2022) [5]. These insects facilitate virus spread by transferring infected blood between animals during feeding. The abundance of these vectors during warm and humid seasons aligns with higher outbreak rates, emphasizing the environmental influence on LSDV epidemiology (Bianchinj *et al.,* 2023) [6]. Although the exact role of each vector species varies, *Stomoxys calcitrans* can mechanically transmit LSDV within 48 hours of contact with infected animals (Haegeman *et al.,* 2023) [7].

Direct contact between infected and susceptible animals can lead to virus transmission, although this route is less efficient than vector-mediated spread. The virus is present in various bodily fluids, including saliva, nasal discharge, lacrimal secretions, and milk, and can be transmitted through close physical interactions or contaminated feed and water. Experimental studies have also detected LSDV in semen, raising concerns about potential transmission during artificial insemination (Annandale *et al.,* 2014) [8]. LSDV can survive in scabs and other infected tissues for extended periods, contributing to transmission through fomites. Contaminated equipment, such as needles or grooming tools, may facilitate virus spread, especially in intensive farming systems where animals share common resources.

LSDV is highly stable in the environment and can remain infectious for weeks in dried scabs, skin nodules, and other organic materials (Sprygin *et al.,* 2019) [4]. This resilience enhances its potential for indirect transmission, particularly in areas where infected animals have been housed. Figure 1 shows infected Cow with LSD virus.

While horizontal transmission through vectors and direct contact is well-documented, evidence of vertical transmission (from dam to offspring) is limited and requires further investigation. Studies suggest that infected milk could potentially serve as a transmission route to suckling calves (Bianchinj *et al.,* 2023) [6].

Fig 1: LSDV infected Cow

Understanding the genetic basis of LSDV is pivotal for effective disease control and vaccine development. The LSDV genome, approximately 151 kbp in length, encodes over 150 open reading frames (ORFs) associated with viral replication, immune evasion, and pathogenesis (Tulman *et al.,* 2001) [10]. Genomic studies have revealed that LSDV shares significant homology with other *Capripoxviruses,* such as Sheeppox Virus (SPPV) and Goatpox Virus (GTPV), while possessing unique genetic features that confer its host specificity and virulence (Tulman *et al.,* 2002) [11]. Advances in molecular tools, including whole-genome sequencing and transcriptomic analyses, have provided valuable insights into viral evolution, genetic variability, and the development of vaccine strains.

This review aims to provide a comprehensive overview of the genetic architecture and functional genomics of LSDV, with a focus on its virulence determinants, mechanisms of immune evasion, and genomic tools for diagnosis and control. It also highlights unresolved genomic questions and proposes future research directions to address the gaps in current knowledge. By integrating current findings, this work seeks to enhance the understanding of LSDV genetics, contributing to the global effort to mitigate its impact through targeted molecular interventions and effective vaccination strategies.

Classification of LSDV

LSDV is a member of the *Poxviridae* family, specifically within the *Capripoxvirus* genus, which also includes Sheeppox Virus (SPPV) and Goatpox Virus (GTPV) (Diallo *et al.,* 2007) [12]. These viruses are significant pathogens affecting livestock, leading to substantial economic losses in affected regions. LSDV, SPPV, and GTPV share a high degree of genetic similarity, with approximately 96% nucleotide identity across their genomes (Tulman *et al.,* 2001, Tulman *et al.,* 2002) [10, 11]. Despite this similarity, they exhibit distinct host specificities and pathogenic profiles. Table 1 shows Classification of Lumpy Skin Disease Virus and Related Viruses.

LSDV primarily infects cattle, causing nodular skin lesions, fever, and lymphadenopathy. Recent genomic studies have identified unique genetic variations that may contribute to its host specificity and virulence (Yadav et al., 2024) [13].

SPPV affects sheep, leading to systemic disease characterized by skin lesions and respiratory symptoms. Comparative genomic analyses have revealed specific gene mutations that differentiate SPPV from other *Capripoxviruses* (Tulman *et al.,* 2002) [11].

GTPV targets goats, causing clinical signs similar to SPPV. Genomic sequencing has identified unique genetic markers that distinguish GTPV from SPPV and LSDV (Tulman *et al.,* 2002) [11].

Understanding the genetic distinctions among these viruses is crucial for developing accurate diagnostic tools and effective vaccines. Recent advancements in whole-genome sequencing have enhanced our ability to differentiate between these closely related viruses, facilitating better disease management strategies.

Table 1: Classification of Lumpy Skin Disease Virus and Related Viruses

Virus Name	Genus	Genome Size (kb)	Host Species	Geographic Distribution
Lumpy Skin Disease Virus (LSDV)	Capripoxvirus	~150-151	Cattle (Bos species)	Africa, Middle East, Asia, Europe
Sheeppox Virus (SPPV)	Capripoxvirus	~150-151	Sheep (Ovis aries)	Africa, Asia, Middle East
Goatpox Virus (GTPV)	Capripoxvirus	~150-151	Goats (Capra hircus)	Africa, Asia, Middle East
Vaccinia Virus (VACV)	Orthopoxvirus	~200-205	Multiple species	Worldwide (laboratory and outbreaks)
Cowpox Virus (CPXV)	Orthopoxvirus	~200-220	Cattle, rodents, humans	Europe, Asia
Smallpox Virus (Variola)	Orthopoxvirus	~186	Humans	Historically global (eradicated)

While LSDV shares significant genetic homology with SPPV and GTPV, specific genomic variations underpin its unique host range and pathogenicity. Ongoing research continues to elucidate these differences, contributing to improved control measures against *Capripoxvirus* infections.

Genomic Structure of LSDV

LSDV is a large, double-stranded DNA virus and approximately 151 kilobase pairs (kbp) in size, circularly permuted, and encodes for over 150 open reading frames (ORFs), including essential genes for viral replication, immune modulation, and pathogenesis (Tulman *et al.,* 2001) [10]. The LSDV genome shares significant similarity with other *Capripoxviruses*, such as Sheeppox Virus (SPPV) and Goatpox Virus (GTPV), while retaining unique genetic features that define its host specificity and virulence (Tulman *et al.,* 2001, Tulman *et al.,* 2002) [10, 11]. The LSDV genome consists of coding and non-coding regions, arranged in a highly conserved organization characteristic of poxviruses (Sendow *et al.,* 2024) [14].

Coding Regions: The central part of the genome, spanning approximately 100 kbp, is densely packed with conserved ORFs involved in core viral functions such as DNA replication, transcription, and virion assembly. These genes are highly conserved across the Poxviridae family (Tulman *et al.,* 2001) [10].

Non-Coding Regions: Flanking the coding regions are variable sequences that contain regulatory elements, including promoters and enhancers, which control the temporal expression of viral genes. Non-coding regions also contribute to genome organization and may play a role in host adaptation (Yadav *et al.,* 2024) [13].

Terminal Inverted Repeats (TIRs): LSDV contains terminal inverted repeats at both ends of the genome, each approximately 2.5-3 kbp in size. These sequences are complementary and inverted, playing a critical role in genome stability, replication, and packaging (Tulman *et al.,* 2001) [10].

Immune Modulatory Genes: LSDV encodes a range of genes that modulate host immune responses, such as poxviral ankyrin repeat proteins (ARPs) and inhibitors of apoptosis (IAPs). These genes are located in the flanking regions of the genome and are less conserved than core genes, reflecting their role in host-virus interactions (Herbert *et al.,* 2015) [15].

Host-Range Genes: Genes facilitating replication in cattle, such as K3L and E3L homologs, are scattered throughout the genome. These genes contribute to the virus's ability to adapt to its host and evade immune defences (Bratke *et al.,* 2013) [16].

GC Content and Structural Stability: The LSDV genome exhibits a relatively high GC content (~45%), which is thought to enhance structural stability and facilitate specific protein coding regions (Bhat *et al.,* 2023) [17].

The central coding region of the genome encodes conserved enzymes and structural proteins necessary for the virus's lifecycle, while the terminal regions harbor genes that influence virulence, immune evasion, and host specificity. This genetic organization underscores LSDV's adaptability and its capacity to evade host immune responses.

The elucidation of LSDV's genomic structure has paved the way for advancements in diagnostics, vaccine development, and the understanding of viral evolution. Ongoing research focusing on the functional genomics of coding and non-coding regions will further enhance the ability to combat LSDV outbreaks effectively.

Functional Genomics of LSDV

LSDV exhibits a complex genomic structure that encodes over 150 open reading frames (ORFs), governing key functions such as replication, immune evasion, and host interaction (Xie *et al.,* 2024) [18]. Structural proteins, including the major envelope protein P37, facilitate virion assembly and release, enabling efficient virus spread (Perlmutter *et al.,* 2015) [19]. Virulence factors like poxviral ankyrin repeat proteins (ARPs) and inhibitors of apoptosis (IAPs) modulate host immune responses and prevent premature cell death, ensuring prolonged viral replication (Herbert *et al.,* 2015) [15].

Table 2: Overview of LSDV Genome Features

Genomic Feature	Description	Size (bp)	Function
Terminal Inverted Repeats (TIRs)	Overview of LSDV Genome Features	~2,400	Essential for replication, packaging, and genome stability.
Open Reading Frames (ORFs)	Coding sequences within the genome, annotated to encode proteins.	156 ORFs	Encode structural proteins, enzymes, and factors for immune evasion and replication.
Core Genes	Highly conserved genes shared across Poxviridae.	~90 ORFs	Critical for basic replication machinery and virion assembly.
Host-Range Genes	Genes facilitating infection and replication in specific hosts.	Variable	Modulate host specificity and immune evasion.
Regulatory Elements	Non-coding sequences upstream of genes.	Variable	Regulate transcription and gene expression.
Intergenic Regions	Non-coding sequences between genes.	~5,000-10,000	Potentially involved in regulation and genome organization.
Virulence Genes	Genes associated with pathogenicity and host immune response modulation.	Variable	Contribute to disease severity and immune suppression.
GC-Rich Regions	Segments with high GC content dispersed in the genome.	Variable	May play roles in structural stability and specific protein coding.

Immune evasion is further supported by genes encoding Vaccinia Virus Complement Control Proteins (VCPs) and E3 ubiquitin ligases, which inhibit host antiviral responses. While approximately 90 ORFs are conserved across *Capripoxviruses* (Cui et al., 2021) [20], LSDV possesses unique genes, particularly in its terminal genomic regions, which enhance its adaptation and specificity to cattle (Tulman *et al.,* 2001, Tulman *et al.,* 2002) [10, 11]. These genes differentiate LSDV from related viruses such as Sheeppox Virus (SPPV) and Goatpox Virus (GTPV), highlighting its evolutionary specialization (Wolff et al., 2020) [21].

Table 2 shows overview of LSDV Genome Features. Host-pathogen interactions play a pivotal role in disease progression, with LSDV leveraging its immune-modulatory and host-specific genes to evade defenses and establish infection. Understanding these genomic features and their functional roles is crucial for designing targeted interventions and vaccines to combat this economically significant virus.

Genetic Variability and Evolution of LSDV

LSDV exhibits remarkable genomic stability compared to RNA viruses, yet genetic variability is observed among strains, driven by mechanisms such as mutations and recombination (Sprygin *et al.,* 2022) [22]. As a double-stranded DNA virus, LSDV has a relatively low mutation rate due to the proofreading capability of its DNA polymerase. However, single nucleotide polymorphisms (SNPs) and small insertions or deletions (indels) have been identified in genes encoding virulence factors, immune evasion proteins, and host-range determinants, contributing to its adaptability and pathogenic diversity (Tulman *et al.,* 2001, Tulman *et al.,* 2002) [10, 11].

Recombination plays a significant role in the genetic evolution of LSDV, particularly in regions of high genomic plasticity, such as the terminal regions. These events can result in the exchange of genetic material between LSDV strains or with related *Capripoxviruses*, such as Sheeppox Virus (SPPV) and Goatpox Virus (GTPV). Recombination contributes to the emergence of novel genetic variants, potentially influencing virulence, host range, and vaccine efficacy (Sprygin *et al.,* 2022, Perez-Losada *et al.,* 2015) [22, 23].

Genetic diversity across geographical isolates of LSDV is evident from whole-genome sequencing studies. Isolates from different regions, such as Africa, the Middle East, Asia, and Europe, show subtle genomic differences, particularly in genes associated with host-pathogen interactions and immune modulation (Sendow *et al.,* 2024, Haga *et al.,* 2024) [14, 24]. For instance, isolates from recent outbreaks in Asia and Europe have demonstrated unique SNPs and indels that may reflect local adaptation to cattle populations or differences in selective pressures (Anwar *et al.,* 2022) [25]. These variations highlight the importance of continuous genomic surveillance to monitor the evolution of LSDV and its potential impact on disease control measures.

Phylogenetic analyses of LSDV have consistently grouped isolates within the *Capripoxvirus* clade, confirming their close genetic relationship with SPPV and GTPV (Zhou *et al.*, 2012) [26]. Evolutionary studies suggest that LSDV diverged from a common ancestor shared with other *Capripoxviruses*, with host specificity likely driven by selective pressures and gene adaptation events. The clustering of isolates based on geographical origin further indicates the role of localized evolutionary forces in shaping LSDV diversity (Ochwo *et al.*, 2018) [27].

Understanding the genetic variability and evolutionary dynamics of LSDV is crucial for developing effective diagnostic tools, vaccines, and control strategies. Insights into the mechanisms driving variability and adaptation can help predict potential outbreaks and assess the risks associated with strain emergence or vaccine escape. Future research focusing on recombination hotspots, SNP dynamics, and adaptive evolution will enhance our ability to mitigate the impact of LSDV on global cattle populations.

Genetic Determinants of Virulence in LSDV

The virulence of LSDV is governed by a set of genes that facilitate replication, immune evasion, and host adaptation, contributing to its pathogenicity in cattle. Key virulence genes, such as poxviral ankyrin repeat proteins (ARPs) and inhibitors of apoptosis (IAPs), play critical roles in modulating host immune responses and preventing premature cell death, thereby prolonging viral replication. Vaccinia Virus Complement Control Proteins (VCPs) and E3 ubiquitin ligases further enhance immune evasion by inhibiting the complement cascade and degrading host antiviral proteins (Girgis *et al.*, 2011) [28]. Host specificity is influenced by genetic factors such as host-range genes, including homologs of K3L and E3L, which adapt LSDV to bovine hosts by counteracting antiviral defences (Haller *et al.*, 2014) [29]. Geographic isolates of LSDV exhibit single nucleotide polymorphisms (SNPs) and variations in regulatory regions, reflecting adaptation to local cattle populations and environmental pressures. The virus employs diverse immune evasion strategies, including complement inhibition, apoptosis suppression, cytokine modulation, and the production of antigenic decoy proteins, to evade host defences and establish infection (Alcami *et al.*, 2016) [30]. These genetic determinants not only drive the virulence and adaptability of LSDV but also provide critical targets for vaccine development and therapeutic interventions. Understanding these mechanisms is essential for developing effective control measures against this economically significant pathogen.

Genomics in Disease Diagnosis of LSDV

The application of genomic tools has significantly enhanced the early and accurate diagnosis of LSDV, enabling rapid detection and effective management of outbreaks. These tools leverage the genetic makeup of LSDV to provide highly specific and sensitive diagnostic methods.

Genomic approaches, such as polymerase chain reaction (PCR) and real-time quantitative PCR (qPCR), are widely used for the detection of LSDV (Table 3.). These assays target conserved genetic regions, including the P32 and RPO30 genes, which are unique to LSDV and critical for its identification (Agianniotaki *et al.*, 2017) [31]. PCR-based diagnostics offer high specificity and sensitivity, making them the gold standard for confirming LSDV infections, even in early stages of disease or in asymptomatic animals. Loop-mediated isothermal amplification (LAMP) is another genomic tool that has gained attention for its simplicity and speed, allowing on-site detection of LSDV in resource-limited settings (Avaz *et al.*, 2023) [32].

Table 3: Genomic Tools for LSDV Diagnosis

Tool/Assay	Genetic Target	Sensitivity	Specificity
PCR for LSDV-Specific Genes	LSDV-specific genes such as P32 or RPO30	High	High
Real-Time PCR (qPCR)	Quantification of LSDV genome copies	Very High	Very High
Loop-Mediated Isothermal Amplification (LAMP)	LSDV-specific conserved regions	High	Moderate
Whole-Genome Sequencing (WGS)	Complete LSDV genome	Very High	Very High
Restriction Fragment Length Polymorphism (RFLP)	LSDV genomic variations	Moderate	Moderate
High-Resolution Melt Analysis (HRMA)	SNP detection in LSDV genome	High	High
Next-Generation Sequencing (NGS)	Identification of novel mutations or outbreaks	Very High	Very High

Whole-genome sequencing (WGS) has become an indispensable tool for understanding LSDV outbreaks. By providing comprehensive insights into the viral genome, WGS facilitates the identification of genetic variations, including single nucleotide polymorphisms (SNPs) and recombination events, that may influence virulence, host adaptation, and transmission dynamics (Gilchrist *et al.*, 2015) [33]. Phylogenetic analyses using WGS data enable the tracking of outbreak origins and the differentiation of field strains from vaccine-derived strains. Such information is crucial for monitoring the spread of the virus and implementing targeted control measures.

Molecular diagnostics have been refined to enhance the detection and monitoring of LSDV. PCR-based methods, including qPCR, have been developed to quantify viral DNA in clinical samples, providing insights into the viral load and disease progression (Zeedan *et al.*, 2024) [34]. High-resolution melt (HRM) analysis and next-generation sequencing (NGS) techniques further aid in detecting genetic variations and emerging strains (Twist *et al.*, 2013) [35].

These assays are complemented by advancements in rapid point-of-care tests, which integrate genomic tools for field diagnosis, bridging the gap between laboratory capabilities and on-site outbreak management. Table 3 shows some of the Genomic Tools for LSDV Diagnosis.

The integration of genomic tools into the diagnostic workflow for LSDV has revolutionized disease detection and outbreak investigation. From early detection through PCR to comprehensive genomic analyses using WGS, these methods provide unparalleled accuracy and depth of information. Continued development of molecular assays will enhance our ability to control and prevent LSDV outbreaks, ultimately safeguarding livestock health and mitigating economic losses.

Implications for Vaccine Development

Genomic insights into LSDV have been pivotal in advancing the development and refinement of vaccines, which are critical for controlling the spread of this economically significant pathogen. Genomic tools provide a detailed understanding of the virus's genetic architecture, enabling the design of safer, more effective, and distinguishable vaccines.

Genomic analyses have identified key virulence and host-range genes that can be selectively attenuated to create live-attenuated vaccines. For instance, the Neethling strain, widely used as a live-attenuated vaccine, has been genomically characterized to ensure the deletion or mutation of virulence-associated genes, such as those encoding poxviral ankyrin repeat proteins (ARPs) and immune-modulatory factors (Shumilova *et al.*, 2024) [36]. Advances in whole-genome sequencing (WGS) have further facilitated the identification of genetic modifications in vaccine strains, ensuring their safety and efficacy. Moreover, genomics has enabled the exploration of recombinant vaccine strategies that incorporate immunogenic proteins from LSDV into other viral backbones, broadening the scope of protective immunity.

The development of Differentiating Infected from Vaccinated Animals (DIVA) vaccines has been a key focus in LSDV control programs (Capua et al., 2003) [37]. Genomics has been instrumental in identifying genetic markers that distinguish vaccine strains from wild-type viruses. Deletions or insertions in non-essential genes, such as the thymidine kinase (TK) gene, serve as reliable markers for DIVA diagnostics (Schnitzlein *et al.,* 1995) [38]. These markers allow for the simultaneous vaccination and monitoring of disease outbreaks, enabling more efficient disease control and eradication efforts.

The genomic stability of LSDV vaccine strains is a critical factor in ensuring their long-term safety and effectiveness. Genomic studies have shown that live-attenuated vaccine strains, such as the Neethling strain, exhibit minimal genetic drift under laboratory and field conditions, reducing the risk of reversion to virulence (Twist *et al.,* 2013) [35]. This stability is attributed to the low mutation rate of the LSDV genome and careful selection of attenuation strategies that target non-essential or host-specific genes. Continuous genomic surveillance of vaccine strains in endemic regions is essential to monitor for any potential recombination or mutation events that could compromise vaccine safety.

Genomics has revolutionized the design, differentiation, and evaluation of LSDV vaccines, offering a robust framework for developing next-generation immunization strategies. By leveraging genomic data to identify key genetic markers and ensure the stability of vaccine strains, researchers can create safer and more effective vaccines. The integration of DIVA-compatible vaccines with genomic surveillance will further strengthen control efforts, aiding in the global campaign to mitigate the impact of LSDV.

Challenges and Future Directions

While substantial progress has been made in understanding the genomic architecture of LSDV, several gaps in knowledge persist. Addressing these gaps is essential for advancing disease control, vaccine development, and precision livestock management.

Despite the availability of complete genome sequences for multiple LSDV strains, significant gaps remain in the functional annotation of genes, particularly in the terminal regions of the genome where many virulence and host-specificity factors reside. The regulatory roles of non-coding regions and their influence on gene expression and pathogenesis are poorly understood. Additionally, the mechanisms underlying genomic stability and the limited genetic variability of LSDV compared to other viruses require further investigation. Understanding how LSDV interacts with diverse cattle breeds and environmental factors is another area requiring in-depth study, particularly as the virus expands into new geographic regions.

Advancements in genomic technologies are opening new avenues for LSDV research. CRISPR-Cas9-based gene editing offers the potential to functionally validate key virulence genes and unravel their roles in host-pathogen interactions. Similarly, transcriptomics can provide insights into the temporal expression of viral genes during different stages of infection, shedding light on the regulatory networks that drive virulence and immune evasion. Metagenomics and single-cell RNA sequencing could also be employed to study the interaction of LSDV with host microbiomes and individual immune cells, respectively. High-throughput sequencing technologies, coupled with bioinformatics tools, can facilitate the identification of novel genetic markers and targets for diagnostics, vaccines, and antiviral therapeutics.

Genomic insights into LSDV have significant implications for precision livestock management. Whole-genome sequencing and phylogenetic analyses can support real-time tracking of outbreaks, enabling targeted interventions to minimize economic losses. By integrating genomic data with host susceptibility profiles, precision breeding programs could be developed to enhance the genetic resistance of cattle to LSDV. Furthermore, genomic surveillance can monitor vaccine performance, detect emerging strains, and ensure that control strategies remain effective. Combining genomic data with geographic information systems (GIS) and machine learning algorithms could enhance predictive modeling of outbreaks, guiding resource allocation and disease prevention efforts.

Addressing the gaps in LSDV genomic knowledge through emerging technologies like CRISPR and transcriptomics will provide deeper insights into the molecular mechanisms of the virus. These advances, coupled with precision livestock management strategies, have the potential to transform the control and prevention of LSDV. By leveraging genomics, researchers and policymakers can develop innovative, data-driven approaches to mitigate the impact of this economically significant disease on global cattle populations.

Conclusion

LSDV is a genetically complex pathogen whose genomic analysis has provided critical insights into its biology, evolution, and virulence. Key findings in LSDV genetics highlight the importance of conserved core genes for replication and virion assembly, as well as the role of terminal region genes in host specificity, immune evasion, and virulence. Genomic studies have also uncovered subtle variations among strains, driven by single nucleotide polymorphisms (SNPs), recombination, and local adaptation, which impact the virus's pathogenicity and spread. Advances in genomic tools, including whole-genome sequencing, transcriptomics, and CRISPR-based approaches, have been instrumental in refining diagnostic techniques, improving vaccine development, and understanding the molecular mechanisms of LSDV.

The broader implications of these findings extend to the field of molecular biology and livestock disease management. Genomic insights have enabled the design of targeted vaccines, such as DIVA-compatible strains, and the development of highly specific molecular diagnostics. These advancements facilitate better outbreak control, enhance disease surveillance, and provide a foundation for precision livestock management strategies. Moreover, the integration of genomic data with predictive modeling and real-time outbreak tracking has transformed the ability to respond proactively to emerging threats.

Genomics holds immense potential in the ongoing battle against LSDV. As research continues to bridge the gaps in our understanding of the virus's genetics and host-pathogen interactions, it opens new avenues for developing innovative control measures. The application of cutting-edge genomic technologies will not only advance the field of LSDV research but also contribute to broader efforts in combating transboundary livestock diseases. By harnessing the power of genomics, the global livestock industry can move closer to mitigating the economic and animal health impacts of LSDV, paving the way for more sustainable and resilient disease management practices.

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Conflict of interest: Author declares that they do not carry any conflict of interest.

References

1. Gupta T, Patial V, Bali D, Angaria S, Sharma M, Chahota R. et al A review: Lumpy skin disease and its emergence in India. Veterinary Research Communications,2020:44(4):111–118.
2. Mazloum A, Van Schalkwyk A, Babiuk S, Venter E, Wallace DB, Sprygin A. Lumpy skin disease: history, current understanding and research gaps in the context of recent geographic expansion. Frontiers in Microbiology,2023:14:1266759.
3. Akther M, Akter SH, Sarker S, Aleri JW, Annandale H, Abraham S, Uddin JM. Global burden of lumpy skin disease, outbreaks, and future challenges. Viruses,2023:15(9):1861.
4. Sprygin A, Pestova Y, Wallace DB, Tuppurainen E, Kononov AV. Transmission of lumpy skin disease virus: A short review. Virus Research,2019:269:197637.
5. Sprygin A, Nesterov A, Shumilova I, Prutnikov P, Vaskovic N, Byadovskaya O. Evidence of Lumpy Skin Virus DNA in Blood-Feeding Flies During Outbreaks in Russia in 2018-2019. Acta Veterinaria,2022:72(4):485–492.
6. Bianchini J, Simons X, Humblet MF, Saegerman C. Lumpy skin disease: a systematic review of mode of transmission, risk of emergence and risk entry pathway. Viruses,2023:15(8):1622.
7. Haegeman A, Sohier C, Mostin L, De Leeuw I, Van Campe W, Philips W, et al. Evidence of lumpy skin disease virus transmission from subclinically infected cattle by *Stomoxys calcitrans*. Viruses,2023:15(6):1285.
8. Annandale CH, Holm DE, Ebersohn K, Venter EH. Seminal transmission of lumpy skin disease virus in heifers. Transboundary and Emerging Diseases,2014:61(5):443–448.
9. Davies FG. Lumpy skin disease of cattle: a growing problem in Africa and the Near East. World Animal Review,1991:68(3):37–42.
10. Tulman ER, Afonso CL, Lu Z, Zsak L, Kutish GF, Rock DL. Genome of lumpy skin disease virus. Journal of Virology,2001:75(15):7122–7130.
11. Tulman ER, Afonso CL, Lu Z, Zsak L, Sur JH, Sandybaev NT, et al. The genomes of sheeppox and goatpox viruses. Journal of Virology,2002:76(12):6054–6061.
12. Diallo A, Viljoen GJ. Genus capripoxvirus. InPoxviruses,2007:167–181.
13. Yadav P, Kumar A, Nath SS, Devasurmutt Y, Shashidhar G, Joshi M, et al. Unravelling the genomic origins of lumpy skin disease virus in recent outbreaks. BMC Genomics,2024:25(1):196.
14. Sendow I, Meki IK, Dharmayanti NL, Hoerudin H, Ratnawati A, Settypalli TB, et al. Molecular characterization of recombinant LSDV isolates from 2022 outbreak in Indonesia through phylogenetic networks and whole-genome SNP-based analysis. BMC Genomics,2024:25(1):240.
15. Herbert MH, Squire CJ, Mercer AA. Poxviral ankyrin proteins. Viruses,2015:7(2):709–738.
16. Bratke KA, McLysaght A, Rothenburg S. A survey of host range genes in poxvirus genomes. Infection, Genetics and Evolution,2013:14:406–425.
17. Bhat S, Chaudry W, Mittal P, Ahmad B, Haroon Z, Shaheen S, et al. Complete genome sequence of the lumpy skin disease virus reported from Jammu and Kashmir, India, during 2022 outbreak. Microbiology Resource Announcements,2023:12(11):00317–23.
18. Xie S, Cui L, Liao Z, Zhu J, Ren S, Niu K, et al. Genomic analysis of lumpy skin disease virus asian variants and evaluation of its cellular tropism. NPJ Vaccines,2024:9(1):65.
19. Perlmutter JD, Hagan MF. Mechanisms of virus assembly. Annual Review of Physical Chemistry,2015:66(1):217–239.
20. Cui H, Zhang Y, Zhang L. Progress on poxvirus E3 ubiquitin ligases and adaptor proteins. Frontiers in Immunology,2021:12:740223.
21. Wolff J, King J, Moritz T, Pohlmann A, Hoffmann D, Beer M, et al. Experimental infection and genetic characterization of two different capripox virus isolates in small ruminants. Viruses,2020:12(10):1098.
22. Sprygin A, Mazloum A, Van Schalkwyk A, Babiuk S. Capripoxviruses, leporipoxviruses, and orthopoxviruses: Occurrences of recombination. Frontiers in Microbiology,2022:13:978829.
23. Pérez-Losada M, Arenas M, Galán JC, Palero F, González-Candelas F. Recombination in viruses: mechanisms, methods of study, and evolutionary consequences. Infection, Genetics and Evolution,2015:30:296–307.
24. Haga IR, Shih BB, Tore G, Polo N, Ribeca P, Gombo-Ochir D, et al. Sequencing and Analysis of Lumpy Skin Disease Virus Whole Genomes Reveals a New Viral

Subgroup in West and Central Africa. Viruses,2024:16(4):557.

25. Anwar A, Na-Lampang K, Preyavichyapugdee N, Punyapornwithaya V. Lumpy skin disease outbreaks in Africa, Europe, and Asia (2005–2022): multiple change point analysis and time series forecast. Viruses,2022:14(10):2203.
26. Zhou T, Jia H, Chen G, He X, Fang Y, Wang X, et al. Phylogenetic analysis of Chinese sheeppox and goatpox virus isolates. Virology Journal,2012:9(1):1–8.
27. Ochwo S, VanderWaal K, Ndekezi C, Nkamwesiga J, Munsey A, Witto SG, et al. Molecular detection and phylogenetic analysis of lumpy skin disease virus from outbreaks in Uganda 2017–2018. BMC Veterinary Research,2020:16(1):1–10.
28. Girgis NM, DeHaven BC, Xiao Y, Alexander E, Viner KM, Isaacs SN. The vaccinia virus complement control protein modulates adaptive immune responses during infection. Journal of Virology,2011:85(6):2547–2556.
29. Haller SL, Peng C, McFadden G, Rothenburg S. Poxviruses and the evolution of host range and virulence. Infection, Genetics and Evolution,2014:21:15–40.
30. Alcami A. Viral anticytokine strategies. Encyclopedia of Immunobiology,2016:597.
31. Agianniotaki EI, Chaintoutis SC, Haegeman A, Tasioudi KE, De Leeuw I, Katsoulos PD, et al. Development and validation of a TaqMan probe-based real-time PCR method for the differentiation of wild type lumpy skin disease virus from vaccine virus strains. Journal of Virological Methods,2017:249:48–57.
32. Ayaz Kök S, Üstün S, Taşkent Sezgin H. Diagnosis of ruminant viral diseases with loop-mediated isothermal amplification. Molecular Biotechnology,2023:65(8):1228–1241.
33. Gilchrist CA, Turner SD, Riley MF, Petri Jr WA, Hewlett EL. Whole-genome sequencing in outbreak analysis. Clinical Microbiology Reviews,2015:28(3):541–563.
34. Zeedan GS, Abdalhamed AM, Allam AM, Abdel-Shafy S. Molecular detection of lumpy skin disease virus in naturally infected cattle and buffaloes: unveiling the role of tick vectors in disease spread. Veterinary Research Communications,2024:48(6):3921–3939.
35. Twist GP, Gaedigk R, Leeder JS, Gaedigk A. High-resolution melt analysis to detect sequence variations in highly homologous gene regions: application to CYP2B6. Pharmacogenomics,2013:14(8):913–922.
36. Shumilova I, Shalina K, Abed Alhussen M, Prutnikov P, Krotova A, Byadovskaya O, et al. An Attenuated Vaccine Virus of the Neethling Lineage Protects Cattle against the Virulent Recombinant Vaccine-like Isolate of the Lumpy Skin Disease Virus Belonging to the Currently Established Cluster 2.5. Vaccines,2024:12(6):598.
37. Capua I, Terregino C, Cattoli G, Mutinelli F, Rodriguez JF. Development of a DIVA (Differentiating Infected from Vaccinated Animals) strategy using a vaccine containing a heterologous neuraminidase for the control of avian influenza. Avian Pathology,2003:32(1):47–55.
38. Schnitzlein WM, Winans R, Ellsworth S, Tripathy DN. Generation of thymidine kinase-deficient mutants of infectious laryngotracheitis virus. Virology,1995:209(2):304–314.