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Short Communication

Whole genome sequencing and phylogenetic analysis of a sheeppox virus isolate obtained during the 2023 outbreak in Aktobe, Kazakhstan

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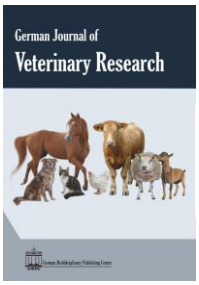

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Abstract

Sheeppox (SPPV) is a contagious viral disease affecting sheep and characterized by fever and skin lesions. SPPV re-emerged in Kazakhstan in 2023, with outbreaks recorded in the East Kazakhstan and Aktobe regions, including the first case in Katon-Karagay in 50 years. Affected sheep exhibited typical clinical signs of sheeppox, prompting laboratory confirmation and genomic investigation. This study aimed to characterize the circulating virus genome while assessing its relationship to global strains. Viral DNA extracted from skin lesions was sequenced on the Illumina MiSeq Platform, and the genome was assembled and analyzed using standard bioinformatics tools. Phylogenetic comparisons were performed against 27 complete sheeppox virus genomes from GenBank. The resulting genome, deposited under accession number PQ014465, measured 149,830 bp with 147 predicted ORFs and 25% GC content. Phylogenetic analysis showed that the Kazakhstan isolate (PQ014465) was closely related to strains circulating in Kazakhstan and European Russia, with an identity of 99,89%. A total of 24 nucleotide substitutions in several genes, and a major deletion (134 bp) in gene 117 were identified in the isolate PQ014465. Additionally, this isolate exhibited five unique amino acid substitutions in genes 8 (I74→L; S233→T), 118 (K73→R), and 134 (L608→F; N844→D). These findings provide the first genomic characterization of the 2023 outbreaks, reveal the unique molecular profile of the regional lineage, and underscore the need for sustained genomic surveillance to guide effective control strategies. The data obtained will be of significant interest to national and regional veterinary authorities.

Keywords: Deduced amino acids, Evolutionary relationships, Genomic sequence, Nucleotide substitutions, Phylogenetic tree, *Poxviridae, Variola ovina*

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Introduction

Sheeppox virus (SPPV) is one of the most significant pathogens of small ruminants and a key representative of the genus Capripoxvirus of the family *Poxviridae* (Tulman et al., 2002; Hamdi et al., 2021). Along with goatpox virus (GTPV) and lumpy skin disease virus (LSDV), SPPV forms a phylogenetically closely related group of capripoxviruses characterized by high genetic homology, pronounced species specificity, and significant epizootic potential (Babiuk et al., 2008; Clemmons et al., 2021). Sheeppox is a particularly dangerous transboundary disease that must be reported to the World Organization for Animal Health (WOAH). The infection is highly contagious and can cause significant morbidity and mortality, reaching 10–50% in susceptible populations, especially among young and non-immune animals (Beard et al., 2022). The economic damage caused by this disease stems from direct livestock losses, reduced

productivity, deterioration in wool and skin quality, reproductive disorders, costs of vaccination and sanitary measures, and trade restrictions (Tuppurainen et al., 2017; Darwish et al., 2025).

The SPPV genome is represented by linear double-stranded DNA approximately 148–150 thousand base pairs long. It contains more than 140 open reading frames (ORFs) encoding structural proteins, replication enzymes, and numerous virulence and immunomodulation factors (Tulman et al., 2002; Gari et al., 2011). The central part of the genome is highly conserved, while the terminal regions contain variable genes associated with host adaptation and immune evasion (Bukar et al., 2021). Despite the reputation of capripoxviruses as genetically stable, accumulated data indicate the presence of point mutations, deletions, and insertions that can affect the pathogenicity, transmissibility, and antigenic properties of the virus (Sprygin et al., 2022; Germán et al., 2024). SPPV is widespread in Africa, the Middle East, Asia, and Eastern Europe, covering both endemic regions and areas with periodic outbreaks of infection (Breman et al., 2024; Odoom et al., 2025). The virus is transmitted primarily through direct contact between animals, via aerosols, and via contaminated care items and mechanical vectors, contributing to the rapid spread of the disease in intensive livestock farming conditions (Tuppurainen et al., 2017). The virus's long-term survival in the external environment and resistance to adverse factors further increase the risk of recurrent outbreaks.

Despite its global distribution and significant epizootic importance, there remains a marked shortage of complete SPPV genome sequences in international nucleotide databases (GenBank, ENA, DDBJ). As of 2024, the number of available complete sheep poxvirus genomes is significantly lower than the number of sequenced LSDV genomes, which limits the possibilities for full-scale comparative and evolutionary studies (Clemmons et al., 2021; Ferdoos et al., 2025). The lack of genomic data hinders the reconstruction of phylogeographic relationships, the identification of interregional transmission routes, and the assessment of the role of anthropogenic factors, such as animal trade and vaccination, in shaping the virus's genetic diversity. Between 2020 and 2022, there was a marked increase in the number of sheep pox outbreaks, indicating that this pathogen continues to pose a threat. In Europe, a total of 67 outbreaks of the disease were recorded in four countries: the Russian Federation (18 reports), Spain (18 reports), Greece (15 reports), and Bulgaria (16 reports). These outbreaks required the introduction of strict veterinary and sanitary measures and restrictions on animal movement. (Breman et al., 2024; Bianchini et al., 2025). The African continent remained the region with the highest endemic burden, with at least 465 outbreaks documented, mainly in Eastern and Northern Africa (Hurisa et al., 2018; Zewdie et al., 2021; Bianchini et al., 2025). The most unfavourable epizootic situation was observed in Asia, where 569 outbreaks of sheep and goat pox were reported in thirteen countries. A significant proportion of cases occurred in South and East Asia, including India, Pakistan, Bangladesh, and China (Reddy et al., 2024; Suresh et al., 2022). China became the epicenter of regional virus activity, registering 263 outbreaks, highlighting the potential for rapid spread of SPPV under high livestock density and intensive animal movement (Clemmons et al., 2021; Breman et al., 2024). During the same period, at least one epizootic case was confirmed in the Republic of Kazakhstan, indicating the virus's circulation in Central Asia (Bianchini et al., 2025).

The Republic of Kazakhstan is considered endemic for sheep pox, which is attributed to its geographical location, active transboundary animal movement, and well-developed sheep farming sector (Tulman et al., 2002; Azanbekova et al., 2025). Despite this, the number of published complete SPPV genomes derived from Kazakhstani isolates remains extremely limited. The lack of representative genomic data substantially hampers the analysis of local viral evolution, the reconstruction of epidemiological links between outbreaks, and the assessment of genetic differences between field and vaccine strains. This issue is particularly relevant given the widespread use of live attenuated vaccines against capripoxvirus infections. It has previously been shown that vaccine strains can demonstrate genetic similarity to field isolates and, in some cases, participate in recombination and recirculation processes in animal populations (Sprygin et al., 2020). In this regard, whole-genome sequencing (WGS) of circulating SPPV strains is a key tool for differentiating between vaccine and field variants, assessing vaccine biosafety, and improving disease control strategies. In light of the above, the present study

aimed to perform whole-genome sequencing and molecular genetic characterization of a sheeppox virus strain isolated in the Republic of Kazakhstan during a 2023 outbreak, followed by comparative and phylogenetic analyses in the context of the global diversity of SPPV.

Material and methods

In 2023, several outbreaks of sheeppox were recorded in Kazakhstan. On February 17, a case of the disease was registered among 200 sheep in the Katon-Karagay district of the East Kazakhstan region; on March 13, the villages of Akkainar, Zhana-Ulga, and Shyngystau were quarantined. This outbreak was the first in 50 years, indicating an unfavourable epizootic situation. In Koptaqay, Oyyl district of the Aktobe region, a case of smallpox was registered among small cattle on the Sayat farm. The farm was quarantined from July 17 to August 21, 2023. A provisional diagnosis of sheeppox was established based on physical examination (Figure 1) and clinical history. The ages of the affected sheep ranged from 3 months to 4 years, encompassing domestic crossbreeds. The clinical manifestations observed included dyspnea, hyperthermia, oculonasal discharges, lethargy, cutaneous ulcerations, and pox-like lesions at various developmental stages. Following disinfection, genetic research was conducted on the skin's papular-pustular lesions.

Total DNA was isolated from the obtained samples using the PureLink Genomic DNA MiniKit (Thermo Fisher Scientific, Cat. No. K182002, Waltham, MA, USA) according to the manufacturer's protocol. Electrophoretic analysis of nucleic acids was performed on a 1% agarose gel, followed by staining with ethidium bromide. Quantitative measurements of DNA were performed using the Qubit™ dsDNA HS (High Sensitivity) Assay Kits (Waltham, MA, USA) for the Qubit 3.0 fluorometer according to the instructions. Following the directions, 1 ng of the double-stranded DNA of interest was used to create DNA libraries using the Nextera XT DNA Sample 16 Preparation Kit (Illumina, San Diego, USA). Purification of genomic libraries and selection of fractions of the required length were performed using the Agencourt AMPure XP paramagnetic bead system (Beckman Coulter, California, USA). Excess primers, nucleotides, salts, and enzymes were removed by washing with freshly prepared 80% C2H5OH. Quality analysis of genomic libraries was performed on a 2100 Bioanalyzer system (Agilent, Santa Clara, USA).

For the gene library generation and sequencing, the MiSeq Kit v3, which generates 300 bp paired-end reads, was used to sequence gene libraries on the Illumina MiSeq platform (San Diego, CA, USA). Fast QC (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) was used to perform read quality control. Trimmomatic v. 0.36 was then used to process the generated data (Bolger et al., 2014). Adapters were eliminated, and sequences with fewer than 50 nucleotides were not included in the analysis. The Geneious software was used to analyze the sequences after removing low-quality reads and trimming adapters (Kearse et al., 2012). The Geneious software program was used with default settings to assemble the entire genome of the sheeppox virus. All reads from the raw data were included in the assembly. A first-draft consensus sequence was generated using Geneious software. Read depth and coverage were also evaluated using Geneious software. A threshold of 10% read variation per base position was used to call ambiguous, non-indel sites (i.e., if >10% of the mapped reads show a consistent variant, the base was called as being ambiguous). The consensus sequences were assessed manually and curated to verify polymorphisms and indel sites. The resulting sequence has been submitted to GenBank under accession number PQ014465.

For phylogenetic analysis, 27 whole genomes from field and vaccine samples were downloaded from GenBank in August 2025. These sequences were selected based on their completeness (at least 140 kb and <1% N's). These sequences were analyzed together with the sequence generated in this study. The resulting dataset included 28 sequences, which were aligned using MAFFT in Geneious with default settings. After alignment, data curation was performed by Gblocks 0.91b (Capella-Gutiérrez et al., 2009). The Geneious was used to construct dendrograms and process partial statistical data. Building a phylogenetic tree using the K2P + G4 model involves applying the Kimura 2-Parameter (K2P) model to analyze nucleotide substitutions. This model is combined with a Gamma distribution, referred to as G4 (which includes four rate categories), to account for variability in substitution rates at different sites. The maximum likelihood method (Yang et al., 2013) was used to create a genetic similarity dendrogram based on the number of differences.

Figure 1: Clinical picture of sheeppox. A) Appearance of exfoliated epidermis and inflamed, hyperemic skin underneath. B) Papular lesions of the axillae.

Results

Characterization of the sheeppox virus genome

About 4×106 reads with a length of 301 nucleotides were obtained through sequencing. A draft genome was created by mapping these reads to the reference genome of the sheep pox virus. The complete viral genome was reconstructed using a reference-guided assembly approach. All generated reads were mapped to the sheep pox virus reference sequence, ensuring a minimum coverage depth of 100× at every nucleotide position to guarantee high assembly accuracy. It was submitted to the GenBank, had 25% GC, and was 149,830 nucleotides long (Figure 2). The genome contains 147 reading frames, 76 of which are in the reverse direction. After alignment, data curation was performed by Gblocks. Of the 150,719 alignment columns in the original file, Gblocks retained 132,653, representing approximately 88% of the alignment. The program identified 123 blocks containing conserved regions and created a new alignment file based on these blocks. This new file was then used to construct the phylogenetic tree. Twenty-eight sheep pox virus strains were compared (Figure 3), and the results showed that the viruses are distributed across three geographic groups.

Nucleotide substitutions and deduced amino acids

To further analyze the strain under study, we examined polymorphisms in viruses from Kazakhstan and Russia (Table 1). It was found that of the 146 nucleotide substitutions, 24 were characteristic of the gene sequences of this group of viruses, forming a single evolutionary group, as shown in the phylogenetic tree and table. The main distinguishing feature of this group of viruses is a large deletion of gene 117, which is characteristic of all members of the group (Limon et al., 2020).

The substitution of nucleotides for amino acid replacement is highly significant. Generally, changing the third nucleotide in a triplet does not result in an amino acid change and is mainly relevant for bioinformatics purposes. Consequently, studies were conducted on amino acid polymorphism at the same positions within the polypeptide chain (Table 2). Among all type-specific nucleotide substitutions, amino acid substitutions were identified only in three genes: 8 (I74→L; S233→T), 118 (K73→R), and 134 (L608→F; N844→D. It has been shown that almost all of the identified substitutions are critical for the structure and function of the protein, which has enormous significance in the evolution of the sheeppox virus group.

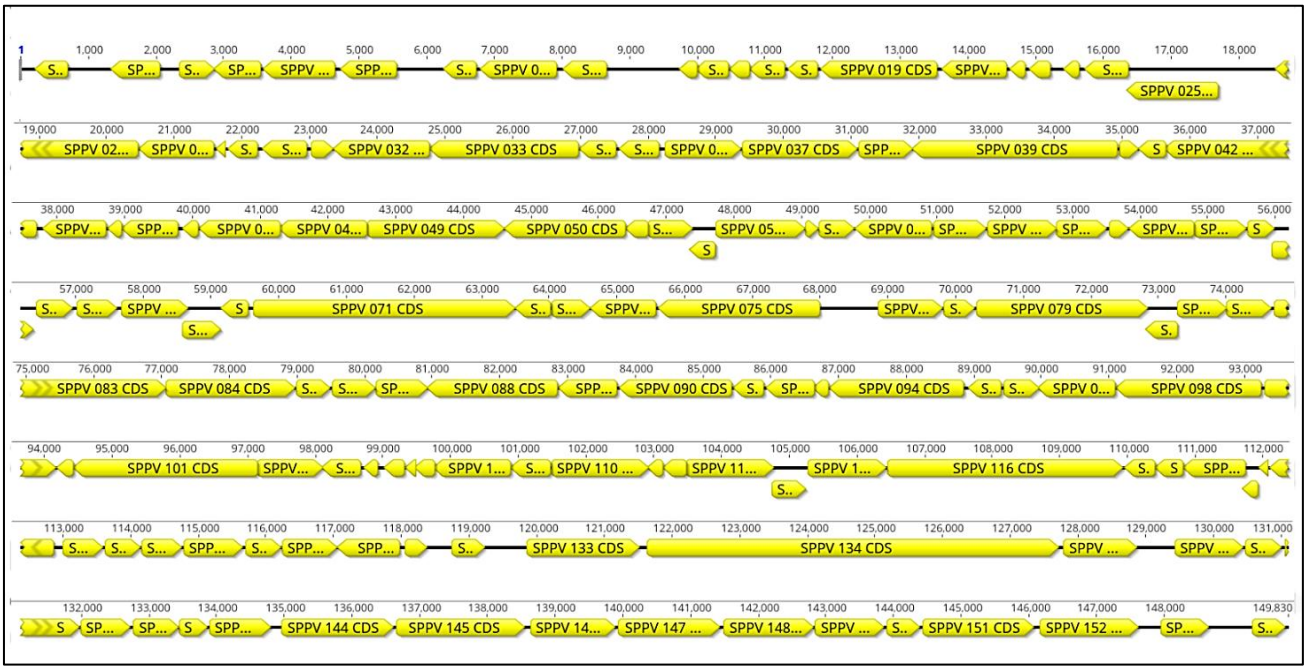

Figure 2: The complete genome map of the sheep pox virus identified during an outbreak in the Ak-Tobe region of the Republic of Kazakhstan on July 14, 2023, showing the organization of predicted open reading frames (ORFs) along the viral genome.

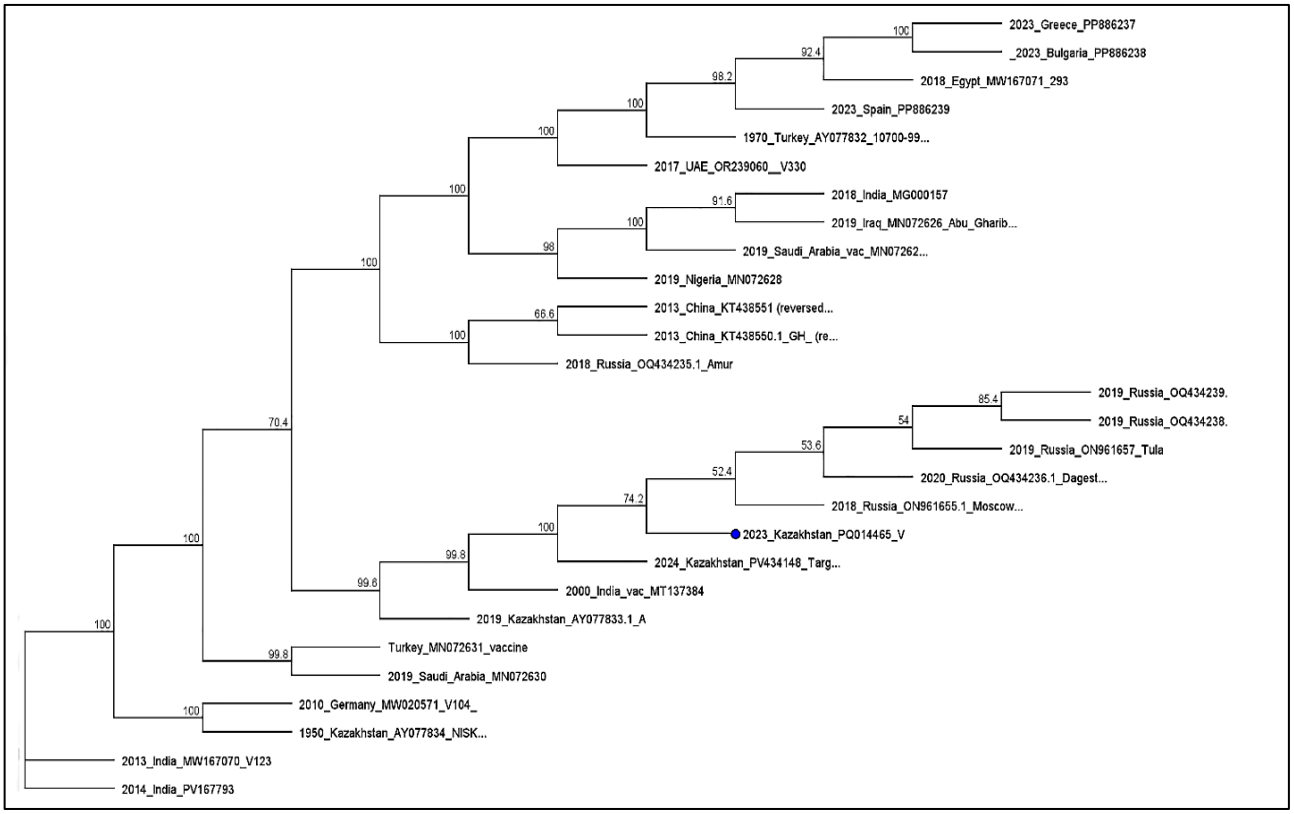

Figure 3: Whole genome sequence-based sheep pox viruses' phylogeny, including both field and vaccine strains. The Geneious was used to construct dendrograms and process partial statistical data. Building a phylogenetic tree using the K2P + G4 model involves applying the Kimura 2-Parameter (K2P) model to analyze nucleotide substitutions. The bootstrap value is 1000. The first group showcases virus variants isolated in Kazakhstan and European Russia, highlighting their regional significance (Sprygin et al., 2021; Kumar et al., 2022; Sumana et al., 2020). The second group presents vaccine strains sourced from a range of isolation sites, emphasizing the diversity of these vital immunological tools. Meanwhile, the third group features isolates from China, the Russian Far East, Egypt, and Europe, demonstrating the global impact and distribution of these pathogens (Shimizu et al., 2020; Breman et al., 2024; Kimeli et al., 2025).

Table 1: Polymorphism of the group of viruses to which the studied genome of the sheeppox virus belongs.

gene	Nucleotides substitutions	Sequence position
5	A (G)	2752
7	C (T)	4771
8	A (C)	4903
8	G (C)	5027
15	C (A)	10582
21	A (C)	15058
27	G (A)	20387
49	G (A)	43359
54	A (C)	48552
82	T (G)	74504
83	T (G)	75197
113	T (C)	104826
118	A (G)	111075
117	Deletion	109758 – 109891
122	A (C)	113479
123	A (C)	114353
131	C (T)	119454
134	T (G)	123936
134	C (T)	127354
142	T (C)	134017
143	G (A)	134442
144	C (T)	136426
145	A (C)	138240
152	A (C)	147575

Table 2: Unique amino acid substitutions in the protein-coding sequences of the sheeppox virus (isolate PQ014465).

Gene	Protein product	Nucleotide position	Nucleotide change	AA position	Substitution (Ref → Query)
8	Interferon-gamma receptor	4903	A → C	74	**I → L**
8	Interferon-gamma receptor	5027	G → C	233	**S → T**
118	Virion core protein	11075	A → G	73	**K → R**
134	VARV B22R homologue	123936	T → G	608	**L → F**
134	VARV B22R homologue	127354	C → T	844	**N → D**

Discussion

Sheeppox has a disproportionate impact on people involved in livestock production (Kimeli et al., 2025; Limon al., 2020; Oreiby et al., 2022). Outbreaks in endemic geographic regions depend on the vaccination rate of the flock and typically occur when immunity levels fall below 50% (Breman et al., 2024; Bianchini et al., 2025). Disease eradication measures typically include surveillance, animal tracking and identification, education and public awareness, as mortality and morbidity rates correlate with the presence of antibodies to the virus acquired through infection (Bianchini et al., 2025). The virus's low variability enables tracking of evolutionary processes during outbreaks and pathogen sequencing (Sprygin et al., 2022; Kumar et al., 2022). Sheeppox and goatpox viruses usually infect one animal species, but cross-contamination has been reported (Bianchini et al., 2025; Breman et al., 2024). Over the past 30 years, the epizootic situation in terms of morbidity has tended to worsen. Outbreaks of diseases have been reported in 70 countries, including those in Southern Europe, Africa, Central Asia, and the Middle East. According to the WOAH in 2021, outbreaks of SSPP were reported in countries such as Turkey, Israel, China, the Maldives, Mongolia, Thailand, Russia, Algeria, Kenya, Comoros, Tunisia, and Uganda

(Bianchini et al., 2025; Breman et al., 2024). The territory of Kazakhstan is an endemic area for outbreaks of sheep pox, and 16 outbreaks were reported to the WOAH for the period 2005-2022 (Bianchini et al., 2025). Since animals are usually vaccinated with live vaccines, a thorough study of the genetic characteristics of the virus that caused the outbreak is necessary. Our research included sequencing the complete genome of the circulating virus during the outbreak in Kazakhstan in 2023. It has been shown that the virus belongs to a group of strains causing disease in Kazakhstan and the European part of Russia (Azanbekova et al., 2025; Tulman et al., 2002; Sprygin et al., 2022).

Most nucleotide substitutions in the virus occur in intergenic regions, making it difficult to study their impact on viral virulence. However, our studies have shown that the virus has at least 24 substitutions in various regions of the genome, the main one being a deletion in gene 117, comprising approximately 200 nucleotides (Shimizu et al., 2020). Among all type-specific nucleotide substitutions, amino acid substitutions were identified only in proteins of genes 8, 118, and 134. However, if the substitutions in protein 118 are intended to compensate for the presence of a deletion in gene 117. The protein 134 is found to be the best phylogenetic marker gene for this virus group. Then the substitutions in protein 8 allow the virus to evade the cell's interferon defense system, thereby facilitating its further evolution (Shimizu et al., 2020).

Phylogenetic analysis of viruses shows that, despite more than 90% similarity between vaccine strains and viruses causing outbreaks, they form distinct phylogenetic groups, which may be associated with the presence of genes containing repeating motifs. Studies of sheep pox virus virulence determinants in the natural host may help more precisely define the mechanisms underlying smallpox virus pathogenesis and inform the development of new vaccines with improved safety, efficacy, and utility. Furthermore, viral virulence may depend on non-coding regions of the viral genome that vary in length from 4 to 282 nucleotides. (Azanbekova et al., 2025; Tulman et al., 2002; Sprygin et al., 2022). Since most infected sheep recover within approximately three weeks without systemic treatment due to the development of robust immunity, vaccination with live attenuated vaccines remains a key control measure. It is important to emphasize that the vaccines used in Kazakhstan and other countries in the region are not licensed in the EU, necessitating further evaluation of their safety, immunogenicity, and potential for recombination with circulating field strains (Sprygin et al., 2020; Kumar et al., 2022). Thus, the molecular-genetic characterization of the circulating SPPV strain in Kazakhstan provides valuable data for monitoring viral evolution, predicting outbreaks, and developing safer and more effective vaccination strategies. These findings also underscore the need for regional coordination of veterinary services to ensure timely detection and containment of infection foci, as well as for comprehensive studies on virulence factors underlying the pathogenesis of sheep pox virus.

Conclusion

Sheeppox virus is of significant economic importance in countries where the virus is endemic, and vaccination is a key control strategy. Attenuated live vaccines produced by serial passage of the sheep pox virus in tissue culture, while highly effective, do not always provide 100% protection. Problems associated with these vaccines include varying degrees and durations of protection, the lack of characterization of the vaccine virus, and safety issues. Therefore, whole-genome sequencing of the virus to study its evolutionary history is crucial for successful disease surveillance.

Article Information

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Authors' contribution: Conceptualization, AB. and U.O.; methodology, M.A.; software, M.A.; validation, U.O., M.N., A.M.; formal analysis, M.A.; investigation, U.O., M.N., A.B., Y.M., M.A., A.M. resources, U.O.; data curation, M.A.; writing—original draft preparation, A.B.; writing—review and editing, A.B., U.O.; visualization, E.M.; supervision, U.O.; project administration, M.N.; funding acquisition, U.O. All authors have read and agreed to the published version of the manuscript.

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