

2023-09-15

# The role of modeling in the epidemiology and control of lumpy skin disease: a systematic review

Renald, Edwiga

Springer Berlin Heidelberg

---

<https://link.springer.com/article/10.1186/s42269-023-01111-z>

*Provided with love from The Nelson Mandela African Institution of Science and Technology*

REVIEW

Open Access



# The role of modeling in the epidemiology and control of lumpy skin disease: a systematic review

Edwiga Renald<sup>1\*</sup> , Joram Buza<sup>2</sup> , Jean M. Tchuenche<sup>1</sup>  and Verdiana G. Masanja<sup>1</sup> 

## Abstract

**Background** Lumpy skin disease (LSD) is an economically important viral disease of cattle caused by lumpy disease virus (LSDV) and transmitted by blood-feeding insects, such as certain species of flies and mosquitoes, or ticks. Direct transmission can occur but at low rate and efficiency. Vaccination has been used as the major disease control method in cooperation with other methods, yet outbreaks recur and the disease still persists and is subsequently spreading into new territories. LSD has of late been spreading at an alarming rate to many countries in the world including Africa where it originated, Middle East, Asia and some member countries of the European Union except the Western Hemisphere, New Zealand and Australia. In order to take control of the disease, various research endeavors are going on different fronts including epidemiology, virology, social economics and modeling, just to mention a few. This systematic review aims at exploring models that have been formulated and/or adopted to study the disease, estimate the advancement in knowledge accrued from these studies and highlight more areas that can be further advanced using this important tool.

**Main body of the abstract** Electronic databases of PubMed, Scopus and EMBASE were searched for published records on modeling of LSD in a period of ten (10) years from 2013 to 2022 written in English language only. Extracted information was the title, objectives of the study, type of formulated or adopted models and study findings. A total of 31 publications met the inclusion criteria in the systematic review. Most studies were conducted in Europe reflecting the concern for LSD outbreaks in Eastern Europe and also availability of research funding. Majority of modeling publications were focused on LSD transmission behavior, and the kernel-based modeling was more popular. The role of modeling was organized into four categories, namely risk factors, transmission behaviors, diagnosis and forecasting, and intervention strategies. The results on modeling outbreaks data identified various factors including breed type, weather, vegetation, topography, animal density, herd size, proximity to infected farms or countries and importation of animals and animal products. Using these modeling techniques, it should be possible to come up with LSD risk maps in many regions or countries particularly in Africa to advise cattle herders to avoid high risk areas. Indirect transmission by insect vectors was the major transmission route with *Stomoxys calcitrans* being more effective, indicating need to include insect control mechanisms in reducing the spread of LSD. However, as the disease spread further into cold climates of Russia, data show new emerging trends; in that transmission was still occurring at temperatures that preclude insect activities, probably by direct contact, and furthermore, some outbreaks were not caused by field viruses, instead, by vaccine-like viruses due to recombination of vaccine strains with field viruses. Machine learning methods have become a useful tool for diagnosing LSD, especially in resource limited countries such as in Africa.

\*Correspondence:

Edwiga Renald  
edwiga1991@gmail.com

Full list of author information is available at the end of the article



© The Author(s) 2023. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>.

Modeling has also forecasted LSD outbreaks and trends in the foreseeable future indicating more outbreaks in Africa and stability in Europe and Asia. This brings African countries into attention to develop long-term plans to deal with LSD. Intervention methods represented by culling and vaccination are showing promising results in limiting the spread of LSD. However, culling was more successful when close to 100% of infected animals are removed. But this is complicated, firstly because the cost of its implementation is massive and secondly it needed application of diagnostic techniques in order to be able to rapidly identify the infected and/or asymptomatic animals. Vaccination was more successful when an effective vaccine, such as the homologous LSD vaccine, was used and complemented by a high coverage of above 90%. This is hard to achieve in resource-poor countries due to the high costs involved.

**Short conclusion** Modeling has made a significant contribution in addressing challenges associated with the epidemiology and control of LSD, especially in the areas of risk factors, disease transmission, diagnosis and forecasting as well as intervention strategies. However, more studies are needed in all these areas to address the existing gaps in knowledge.

**Keywords** Lumpy skin disease, Cattle, Modeling, Epidemiology, Control

## Background

Lumpy skin disease (LSD) is a highly contagious and economically important viral disease of cattle caused by lumpy skin disease virus (LSDV), a member of the *Capripoxvirus* genus in the *Poxviridae* family (Gelaye and Lamien 2019; Afshari Safavi 2022; Jiang et al. 2022; Milovanović et al. 2020; Mathijs et al. 2020; Jalali et al. 2017; Limon et al. 2020; Elhaig et al. 2017; Ince et al. 2016; Manić et al. 2019; Annandale et al. 2014). The disease has been recognized by the World Organization for Animal Health (formerly the Office International des Epizooties—OIE) as a notifiable livestock trans-boundary disease (Issimov et al. 2020). The disease symptoms include fever, skin nodules, pox lesions in the mucous membranes of the digestive and respiratory tracts, emaciation, enlarged lymph nodes, edema in the skin, lachrymation, nasal discharge and excessive salivation (Gomo et al. 2017).

The economic consequences of LSD include a temporary decline in the production of milk, permanent or temporary sterility in bulls and reduced fertility of cows (Gerilovych and Stegny 2016). Sometimes, the disease results in the death of infected animals (Gerilovych and Stegny 2016). Mortality is reported to range from 1 to 3%, but depending on the presence of insect vectors and hosts susceptibility, mortality can be as high as 20–85% (MLF 2019; Ochwo et al. 2019). Prevalence of LSD is estimated to be 10% by average which ranges in the 95% confidence interval (CI): 9.4–11% (Hasib et al. 2021).

Various disease transmission routes have been proposed, which include blood-feeding insects which act as mechanical vectors (Molla et al. 2017; Agianniotaki et al. 2018), biological transmission by some tick species (Sprygin et al. 2019) and direct contact with saliva from infected animals (Namazi and Khodakaram Tafti 2021). However, other mechanisms probably exist in view of the tendency for LSD to occur in areas far away from areas of

initial outbreaks and under conditions where insects can be completely excluded.

Lumpy skin disease has recently been expanding its territories at an alarming rate to numerous countries around the world, including Africa, where it first appeared, the Middle East, Asia and some European Union (EU) member countries (Gale et al. 2016; Tuppurainen et al. 2020). The Western Hemisphere, New Zealand and Australia are the only places where LSD has not been reported (Grace and McDermott 2012). The disease was first detected in Zambia in the year 1929 (Tran et al. 2020; Casal et al. 2018; Sudhakar et al. 2021; LK 2021; Sprygin et al. 2018), was identified in East Africa the first time in Kenya in 1957 (Gerilovych and Stegny 2016) and in Tanzania in 1986 (Abdulqa et al. 2016). However, it later extended to the sub-Saharan West African countries in the 1970s. As of year 2000, the disease started spreading to the Middle Eastern countries and by 2013 the disease extended into Turkey and the Balkan countries. Recent spread has seen outbreaks occur in Georgia, Russia, Bangladesh and China which has caused considerable international concern. There is a growing fear of the introduction of the LSD in countries near the Balkans such as France (Sae-german et al. 2019).

Vaccination using attenuated virus is the most effective disease control measure (Klement et al. 2020; Rouby et al. 2021) and was particularly effective in controlling the disease in the Balkans (Klement et al. 2020). The common LSD attenuated vaccines include the homologous vaccines made from LSD virus, represented by the Neethling strain from South Africa or heterologous vaccines made from goat or sheep pox viruses (Bhanuprakash et al. 2012). While the attenuated LSD vaccines are the most effective tool against the disease, compared to other control measures, they are still considered risky in the sense that secondary mutations can cause reversion to virulence leading to disease causation (Lee et al.

2012; Sprygin et al. 2018; Krotova et al. 2022). Therefore, it is not recommended to be used in non-endemic areas. There are also reports that the Neethling LSD vaccine induces some adverse effects in vaccinated animals or causes the Neethling disease (Yeruham et al. 1994). Furthermore, there are reported failure of the Neethling LSD vaccine to protect vaccinated cattle against challenge with virulent LSD virus (Gari et al. 2015). As a result, research endeavors are going on in search for more effective and safer vaccines. Newer vaccine types, which are, however, not yet available in the market, include inactivated vaccines, recombinant vaccines, combined vaccines, genetic engineering vaccines both of which have advantages and disadvantages (Francis 2018; Wang et al. 2020). In addition to vaccines, other control measures include killing of all infected animals in a herd (though culling could be controversial (Tchuenche and Bauch 2012)), restricting animal movements, vector control through disinfection and sterilization (Al-Salihi and Hassan 2015) and strict quarantine (Gupta et al. 2020). However, application of the latter measures in the absence of vaccination has not always produced successful results (Tuppurainen and Oura 2012). To expedite healing of wounds, application of antibiotics may be used to control secondary bacterial infection (Khan et al. 2021).

LSD has been considered as a neglected disease, but since its spread to high-temperature countries, research interest has increased commensurate with the increase in the funding and publications. Some of the challenges on the epidemiology of LSD include mechanism of virus spread from one place to the other, risk factors, diagnostics, LSD control methods and other challenges. One of the epidemiological methods used to study disease is modeling. In the epidemiology of infectious diseases, modeling is a highly versatile tool that enables the detection of epidemic patterns (Alkhamis and VanderWaal 2016), extrapolation of epidemic behaviors and evaluation of the impact of interventions (Siettos and Russo 2013). Although there have been quite a number of researches where modeling was applied, the overall impact of the LSD studies using modeling tools is not yet established. It is therefore the goal of this study to systematically review the literature on LSD modeling and estimate the advancement in knowledge accrued from these studies and highlight potential areas that could be further advanced using this important tool.

## Materials and methods

### PRISMA statement

This review has been reported following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) statement (Moher et al. 2009).

### Search strategy

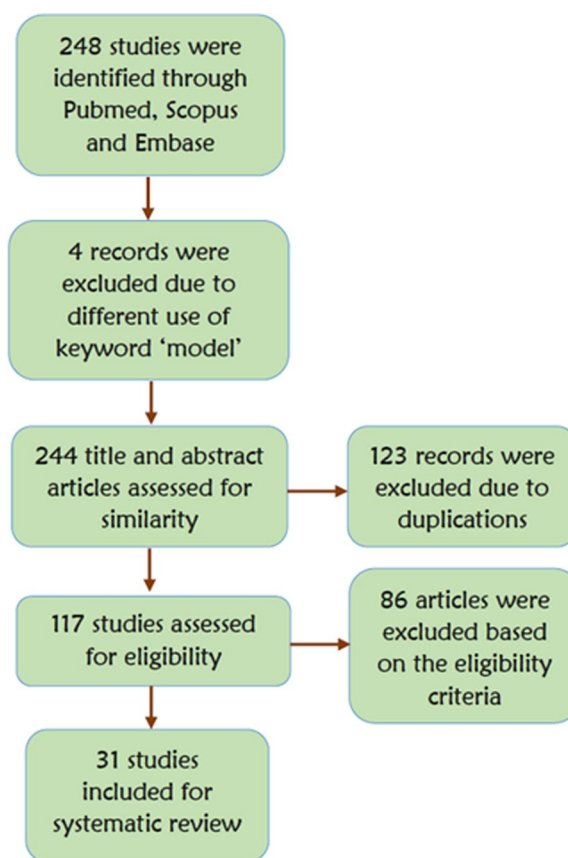
Electronic databases of PubMed, Scopus and EMBASE were searched for published literature on modeling of the lumpy skin disease. The search strategy “Lumpy Skin Disease” AND “model\*” was designed and used in searching published materials on modeling of LSD.

### Selection criteria

The eligibility and inclusion criteria for this search were based on studies on modeling for the transmission dynamics of lumpy skin disease (LSD) in a period of ten (10) years from 2013 to 2022 written in English language. Figure 1 is a PRISMA flow diagram showing the filtering process.

### Data extraction

In this process, extracted information was the title of the study, objectives, type of model used and study findings. To ensure quality of the extracted data, every article was wholly reviewed one by one and took note of the mentioned required information.



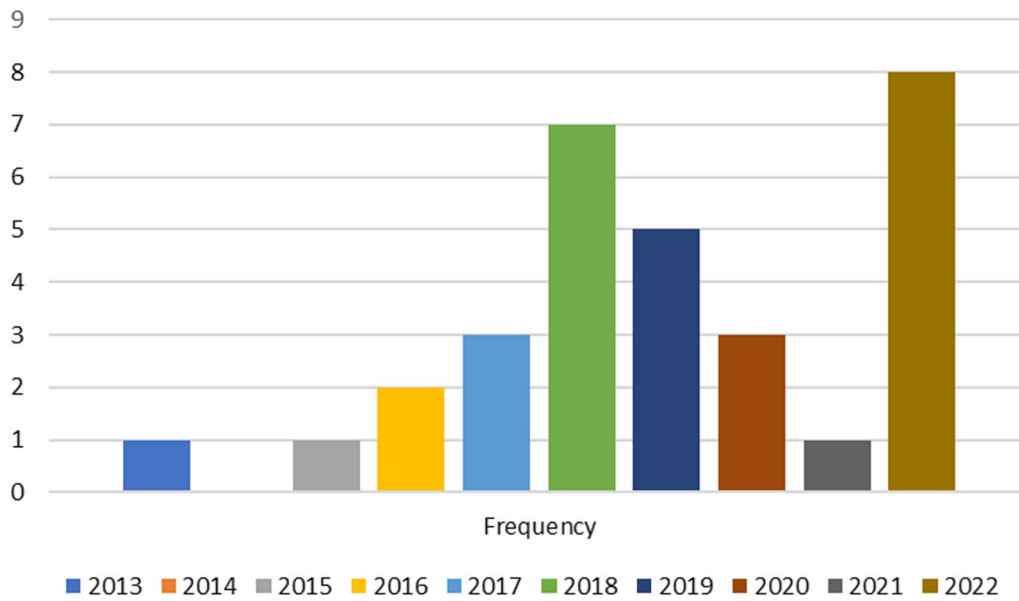
**Fig. 1** PRISMA flowchart

## Results and discussion

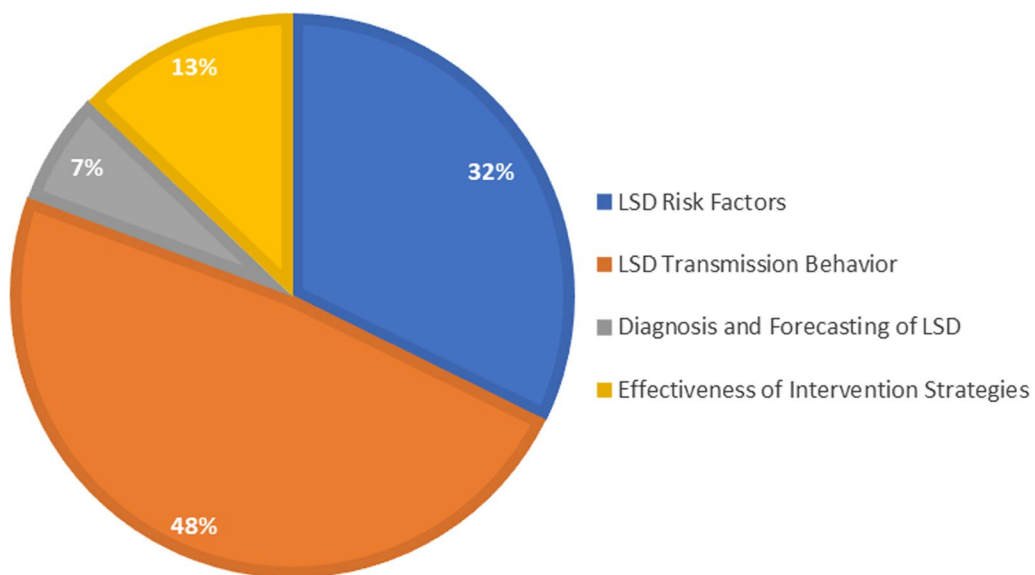
### Retrieved publications

A total of 248 publications were retrieved from PubMed, Scopus and EMBASE (49, 102 and 97, respectively) databases. Two hundred and seventeen (217) publications in total were excluded from the systematic review due to various reasons such as ineligibility (Abdalhamed et al. 2022; Chapman et al. 2021; Rouby

et al. 2021), different use of keyword “model” (Douglass et al. 2020) and appearance of keyword just in the references (Nesterov et al. 2022). Other studies such as El-Ansary et al. (2022) and Fay et al. (2022) might have been met the inclusion criteria since there were models addressing LSD matters, but the models left behind the studying of the transmission dynamics of LSD.



**Fig. 2** Distribution of number of included studies to the year of publication



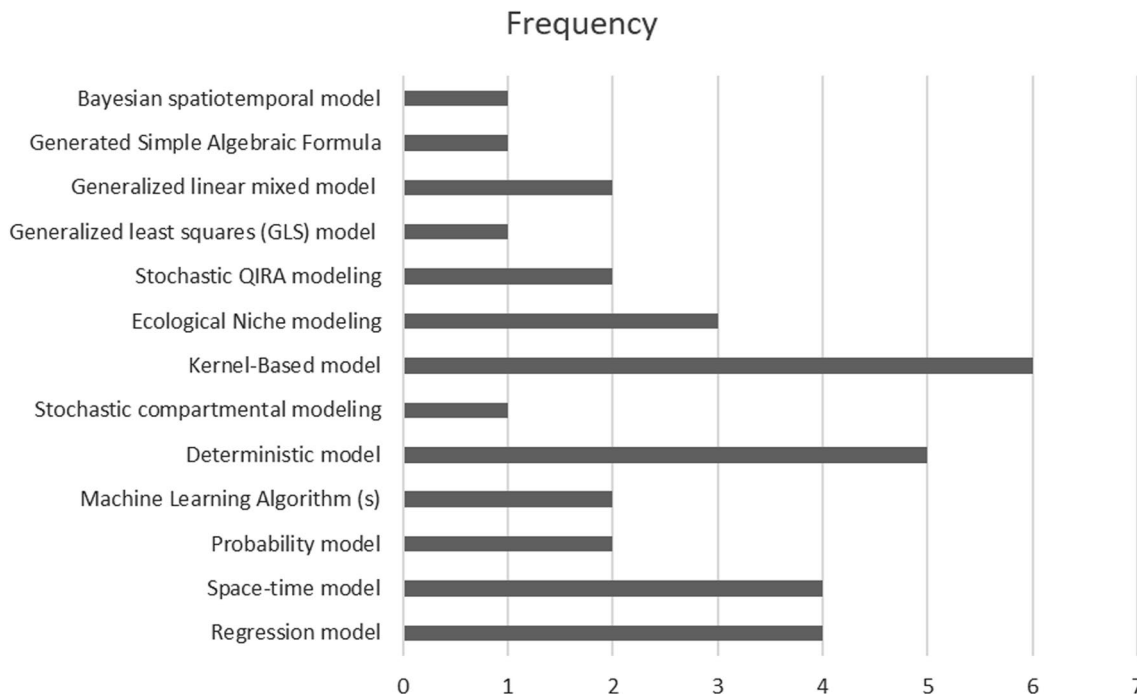
**Fig. 3** Model categories

Most studies were published in the year 2022 followed by year 2018 (Fig. 2).

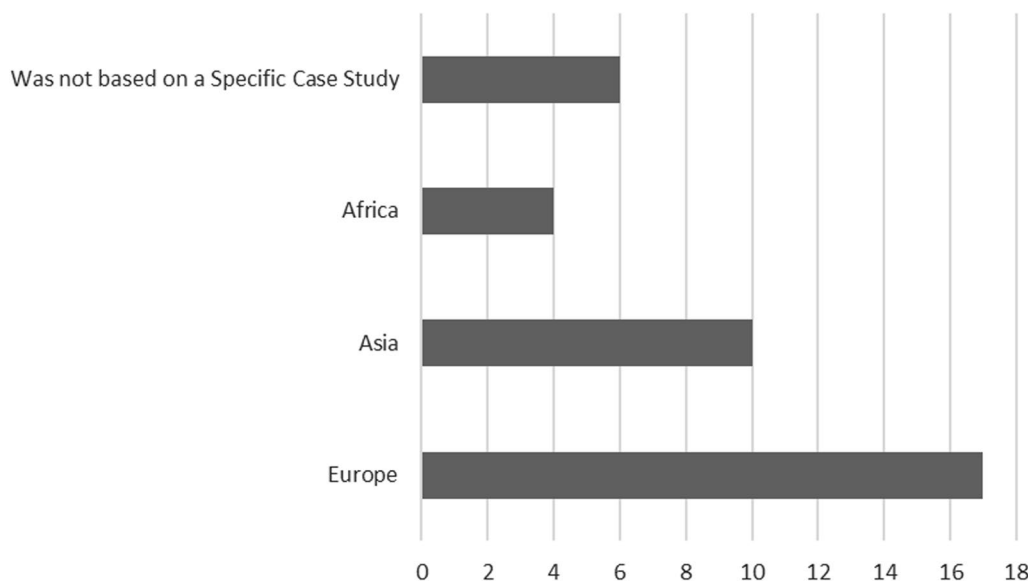
Models in the published studies are categorized into four groups, namely LSD risk factors, LSD transmission behavior, diagnosis and forecasting of LSD, and effectiveness of intervention strategies. Most studies tried to formulate various models to study the behavior of LSD

followed by models which looked at determining LSD risk factors for transmission and prevalence. For more information, see Fig. 3.

Various modeling techniques were identified from the reviewed studies with kernel-based modeling technique highly implemented (see Fig. 4).



**Fig. 4** The distribution of different modeling techniques applied in the reviewed studies



**Fig. 5** The geographical distribution (by continents) of the reviewed studies

Also, most studies were done in Europe, while very few were done in Africa (see Fig. 5). This calls for more effort on LSD modeling research to be done in Africa, where the first case of LSD occurred and still most cases of LSD occur.

### LSD risk factors

Modeling was used to predict LSD outbreak in unaffected areas in Europe and Asia. Following the spread of LSD in Asia and Eastern Europe, an increased number of studies were conducted to get to grips with the LSD outbreaks and spread, both in affected and at risk countries. Risk factors associated with positive cases were determined using various methods including modeling. This was done with the goal of envisaging intervention methods in affected and at risk areas. Şevik and Doğan (2017) used the generalized mixed linear model to evaluate risk factors associated with LSDV infection following the outbreaks of the disease in the Aegean, Central Anatolian and Mediterranean regions of Turkey between July 2014 and June 2015. The results showed positive association between LSDV infection and European breeds, small-sized family-type farms and nearness of farm to a lake. This agrees with other studies (Ayelet et al. 2013; Tageldin et al. 2014; Stojmanovski 2018; Kiplagat et al. 2020). Susceptibility of European breeds is suggested to be due to stress owing to high milk production. Small farms are more susceptible due to increased chances of insect bite, and nearness to the lake is associated with increased insect vector activity. Data from affected LSD locations between July 2012 and September 2018 in the Balkans, Caucasus and Middle East were analyzed by fitting it to a spatial regression model (Allepuz et al. 2019). Areas with great odds of being positive for LSD were mostly covered with croplands, grassland or shrubland, with higher cattle density, as well as areas with higher annual mean temperature and higher temperature diurnal range. The resulting model was utilized to predict the LSD risk in neighboring unaffected areas in Europe, the Caucasus and Central Asia. The results from this study provide useful information for the design of surveillance and awareness systems, and preventive measures, e.g., vaccination programs. Ardestani and Mokhtari (2020) used LSD outbreak data from veterinary organizations between 2012 and 2016 and analyzed the potential for an outbreak of LSD in Chaharmahal and Bakhtiari provinces in Iran based on the grid maps with the resolution of 1 km. In this study, 22 environmental variables (19 bioclimatic and 3 topography variables) were used to explore the environmental influences on LSD outbreak by maximum entropy ecological niche modeling (MaxEnt). The study found that areas that were at high risk of LSD are those areas with warm temperatures, humid (rainy) all of

which support abundance of insect vectors. Uddin et al. (2022) used multivariable Poisson's regression model to identify herd-level (herd size, management system and house type) risk factors for LSD during the outbreak in nine districts of Bangladesh between December 2019 and December 2020. The results showed that herd size (LSD higher small farms than large farms), housing type (LSD higher in hut, temporary, tin shed than semi-building houses) and management (LSD higher in semi-intensive than intensive) were all due to ability to protect against or allow biting insects. The proximity of France to Turkey and other Balkan countries where LSD outbreaks have been reported since 2015 (Saegerman et al. 2019) has stimulated concern on possible introduction of the disease in the country in view of importation of cattle and their products into France. Saegerman et al. (2019) estimated the risks of introduction of LSD in France through importation of live cattle using a quantitative import risk analysis (QIRA) model. The results estimated the yearly probability of a first outbreak of LSD in France following the import of batches of infected live cattle for breeding or fattening to be  $5.4 \times 10^{-4}$  (95% PI:  $0.4 \times 10^{-4}$ ;  $28.7 \times 10^{-4}$ ) in summer months (high vector activity) and  $1.8 \times 10^{-4}$  (95% PI:  $0.14 \times 10^{-4}$ ;  $15 \times 10^{-4}$ ) in winter months. This is very possible because cattle which are subclinically infected with LSD may be allowed for transportation by trucks into naive countries. Transportation of cattle by trucks from infected countries may also inadvertently transport insect vectors which will be able to initiate infection in a naive country. Legal and illegal movement or transportation of cattle may help explain outbreaks of LSD far away from infection foci, where movement of insect vectors can be completely excluded. Modeling of risk factors in countries or localities where LSD occurred or at risk countries has made great contribution in the control of LSD. The results from these studies provide useful information for veterinary authorities to design surveillance and awareness systems, and preventive measures such as vaccination programs.

### LSD transmission behavior

Transmission mechanisms of LSD are still not well understood and are still subject to intensive research. The disease has spread from sub-Saharan Africa (SSA) where it is endemic and has spread and caused outbreaks in Northern African, Middle East, Asia and some European countries through transmission mechanisms that are not well understood. Both direct contact and indirect contact via vectors have been proposed, with more evidence supporting higher efficiency to vector transmission than direct contact. To help unravel the transmission mechanisms of LSD, modeling has been used to compare the direct and indirect mechanisms using data

from outbreaks in different countries. Magori-Cohen et al. (2012) analyzed a dataset collected during the LSD outbreak in 2006 in a large dairy herd in Israel, which included ten separated cattle groups. Transmission by three contact modes was modeled using dynamic transmission probability model, indirect contact between the groups within a herd, direct contact or contact via common drinking water within the groups and transmission by contact during milking procedure. The results show that indirect transmission was the only parameter that could solely explain the entire outbreak dynamics and was estimated to have an overall effect that was over five times larger than all other possible routes of transmission, combined.

The thin-plate spline regression method was used to model the pattern of LSD spread from the first entry in Turkey and eight Balkan countries: Greece, Bulgaria, the Former Yugoslav Republic of Macedonia, Serbia, Kosovo and Albania between 2015 and 2016 (Mercier et al. 2018). The results showed the median spread rate of 7.3km/week; it was further observed that the spread was seasonal, peaking during summer and ceasing completely in winter which is consistent with vector transmission, although there were some aspects of long distance spread which could be accounted for by cattle trade movements. Similar conclusions for vector transmission were drawn when data from the same area were modeled using the kernel-based spread model by the European Food Safety Authority (EFSA) (2018) (EFSA 2018) covering the period between 2016 and 2017 and by Gubbins et al. (2020) who modeled the data from the 2016 LSD outbreak in Albania. However, entry of LSD in the Russia Federation (RF) in 2015 (Sprygin et al. 2018) and further outbreaks up to year 2000 has produced transmission patterns that differ slightly from other regions.

Despite the fact that most LSD outbreaks in RF between 2015 and 2020 occurred mainly during the warm months, with the majority of outbreak peaks occurring in mid-summer which support insect transmission, in 2018, LSD cases continued until November where freezing temperatures prevailed during the day and night. This precludes insects since they are unable to fly at temperatures below zero and strongly indicate alternative route of transmission. Furthermore, the outbreaks of LSD viruses were not field viruses as observed in the 2015–2016 outbreaks; instead, outbreaks were caused by vaccine-like LSD viruses caused by recombination between vaccine and field viruses. To support this, contact transmission of recombinant Saratov/2017 has recently been demonstrated in an experimental setting (Sprygin et al. 2020) indicating oronasal transmission. Another occurrence of possible contact transmission was observed when an outbreak caused by the recombinant

vaccine-like LSDV Udmurtiya/2019 occurred under freezing air temperatures (Sprygin et al. 2019).

While the role of arthropod vectors in transmission of LSD is unquestioned, there is still some research interest to identify which arthropod species are major LSD transmitters. Sanz-Bernardo et al. (2022) quantified the acquisition of the virus and its retention in different anatomical locations of four vector species *S. calcitrans*, *Ae. aegypti*, *Culex quinquefasciatus* and *Culicoides nubeculosus*. Mathematical models of the data revealed that LSD virus was mainly retained by insects when feeding from the skin lesions rather than other body parts or blood from the infected animal and that of all insect parts it is the proboscis which was efficient at retaining the virus. However, the study did not find differences between the insect species tested. Gubbins (2019) assessed the risk of transmission by calculating the basic reproduction number ( $R_0$ ) for transmission of LSDV by five species of biting insect: the stable fly, *Stomoxys calcitrans*, the biting midge, *Culicoides nubeculosus*, and three mosquito species, namely *Aedes aegypti*, *Anopheles stephensi* and *Culex quinquefasciatus*. The results suggest that *S. calcitrans* is likely to be the most efficient at transmitting LSDV, with *Ae. aegypti* also being an efficient vector. By contrast, *C. nubeculosus*, *An. stephensi* and *Cx. quinquefasciatus* are likely to be inefficient vectors of LSDV.

## Diagnosis and forecasting of LSD

### Diagnosis of LSD

Various models have been developed and/or adopted to diagnose the presence of LSD. In a study by Afshari Safavi (2022), some machine learning techniques were determined with high accuracy in predicting the LSDV occurrence in test data (up to 97%) based on some geospatial and meteorological features. In terms of area under curve (AUC) and F1 performance metric scores, the artificial neural network (ANN) algorithm outperformed other machine learning methods in predicting the occurrence of LSDV infection in unseen data with the corresponding values of 0.97 and 0.94, respectively (Afshari Safavi 2022). But random forest classifier and light gradient boosted machine classifier outperformed the other models with the F1 score of 98% (Dofadar et al. 2022) in diagnosing LSD in an animal. These results entail the essential role of artificial intelligence in LSD diagnosis. When preparing control policies, it is crucial to consider extending these tools and make them available for stakeholders. This will enhance early detection and forecast and thus will facilitate proper surveillance.

### Forecast of LSD

On the other hand, in a study by Anwar et al. (2022), a likelihood-based change point detection approach was



applied to know at what times significant changes of LSD occur. The results indicated that between 2005 and 2020, Africa had more outbreaks with Zimbabwe bearing the burden with the highest number of outbreaks. Moreover, the auto-regressive moving average (ARIMA) and neural network auto-regressive (NNAR) models using R statistical software and the available data on LSD outbreaks were used to study and forecast the trend of LSD. Here, the findings indicated an increase in outbreaks in Africa, while they predicted stabilization in Europe and in Asia. ARIMA predicted stabilization, while NNAR predicted fluctuation. The change points that had higher LSD outbreaks appeared in the periods where inefficient control measures were adopted, or when there were no control measures adopted in some areas.

#### **Effectiveness of intervention strategies**

Following the spread of LSD worldwide, various control methods were adopted to contain the disease. Some were proven to be inefficient, and the amount to administer the few which were proven to be efficient was not properly known. Interest on this was brought up by researchers, and it followed that few studies were conducted to determine the effectiveness of various intervention strategies with the help of modeling techniques.

#### **Effectiveness of culling strategy**

For instance, findings of a study by EFSA (2015) that employed the use of a kernel-based approach revealed that when control measures entail the removal of animals which were showing generalized clinical signs (as was applied in Israel during the 2012–2013 epidemic), approximately 90% of epidemics remain confined to the region around the original site of spread. However, the remaining 10% of simulated epidemics are more extensive, with the virus spreading up to approximately 300 to 400 km from the site of introduction in six months after the incursion. Moreover, prompt culling of rapidly detected herds is the one recommended since in rapid detections there will be few animals to cull. Otherwise, in late detections (detection 28 days after the LSD epidemics onset), infected farms would increase and the outbreak will not stop which implies an increase in the seroprevalence of the disease. This will require more time to implement culling. This further implies LSD prevalence is influenced by an increase in seroprevalence which will need more animals to cull to be able to eradicate it.

#### **Effectiveness of vaccination strategy**

Another report by EP, Welfare (2016) indicated that if only 40% vaccination is implemented, then the total

stamping out will help to eradicate the disease, but 75–95% vaccination brings similar results of disease eradication as stamping out. However, the duration of the vaccination campaign sufficient to eliminate LSD mainly depends on the vaccination effectiveness and coverage achieved. By using a spread epidemiological model, assuming a vaccination effectiveness of 65%, with 50% and 90% coverage, 4- and 3-year campaigns, respectively, are needed to eliminate LSD (EP, Welfare 2016). On the other hand, the protective effect of vaccination is supported by the results obtained which showed median vaccination effectiveness values of 62%, 96% and 84% in Albania, Bulgaria and Greece, respectively, with live homologous vaccine. Thus, mass vaccination with an already identified quality and efficient vaccine is the most effective way of combating LSD transmissions (EFSA 2018). On the other hand, between herds (kernel-based) taking seasonality into account and within-herd (deterministic susceptible infectious recovered vaccinated) modeling approaches were used to study dynamics of LSD in vaccinated population to achieve freedom from LSD. The results on the dynamics of the vaccinated population showed that with the absence of control measures, LSD was predicted to prevail. Three years of high vaccination coverage of 90% is sufficient to eliminate the disease if there are no new infections in the country (EFSA et al. 2018).

#### **Effectiveness of control strategy(ies) based on coverage and time**

EFSA et al. (2019) suggest that the disease threshold also known as the basic reproduction number  $R_0$  helps to show the trend of infection after incorporating controls and thus it helps to deduce the extent of applying control measures. Intervention strategies (e.g., vaccination) should be applied until when  $R_0$  decreases to below 1 (Molla et al. 2017). This corroborates other research findings. Moreover, another study by Saegerman et al. Casal et al. (2019) conducted in France deduced that assuming a 7-week period to vaccinate all the animals and a spread of the disease of 7.3 km/week, the vaccination of 740716 cattle would be enough to control an epidemic of LSD in France. These findings are in line with previous research findings which imply that applying control measures, to a larger extent, will bring the basic reproduction number below 1. This is an indication of containment of the disease in the population. Besides, effectiveness of a control method depends on the time it is conducted. According to Mat et al. (2021), mortality was higher in unvaccinated animals than in vaccinated animals, and this supports other studies' findings that it is essential to administer various control programs, especially in various ideal

times, e.g., administering vaccination after controlling vector abundance during warm months.

### Strengths and limitations of this study

The strengths of this review include compliance with accepted rigorous standards for conducting systematic reviews and the use of thorough literature searches to find pertinent information. Limitations to this systematic review include the inclusion of studies written in English language only. There is a possibility that our article misses interesting and important information from studies written in other languages. Also, in this review, we were limited to considering studies published until when the search was conducted. There might be a piece of important information published after the literature search.

### Conclusions

In the present study, various modeling techniques for lumpy skin disease were systematically reviewed looking at four factors: LSD risk factors, LSD transmission behavior, diagnosis and forecasting of LSD, and effectiveness of the implemented intervention strategies.

The results of the systematic review of studies on the modeling of the above-mentioned factors have unveiled challenges associated with the epidemiology and control of LSD. For instance, weather (humidity and temperature) which increases vector abundance has been identified as an important risk factor for LSD transmission. In addition to that, poor management of livestock keeping in general is identified as another significant risk factor in this systematic review since it increases the likelihood of vector bites, which makes herds more vulnerable to new LSD outbreaks and prevalence.

Future models may address the epidemiological features depicted in the four factors portrayed in this study in order to be able to design the most appropriate combination of intervention strategies. Moreover, based on findings of this study, the advancement of artificial intelligence tools for application in LSD diagnosis that can easily be used by stakeholders is strongly recommended to enhance early detection at the grassroots level. This will help to foster immediate implementation of control measures.

### Abbreviations

ANN	Artificial neural network
ARIMA	Auto-regressive moving average
AUC	Area under curve
CI	Confidence interval
EFSA	European Food Safety Authority
EU	European Union
LSD	Lumpy skin disease

LSDV	Lumpy skin disease virus
MaxEnt	Maximum entropy
NNAR	Neural network auto-regressive
OIE	Office International des Epizooties
PRISMA	Preferred Reporting Items for Systematic Reviews and Meta-Analyses
QIRA	Quantitative import risk analysis
RF	Russia Federation
SSA	Sub-Saharan Africa

### Acknowledgements

ER acknowledges with thanks the financial support of the International Mathematics Union (IMU) and Higher Education for Economic Transformation (HEET) project toward her PhD studies.

### Author contributions

The idea was generated by ER, who also conducted the literature review, outlined the findings and wrote the manuscript. JB, VGM and JMT participated as supervisors by assessing the work multiple times and providing feedback and suggestions for further improvement.

### Funding

Not applicable.

### Availability of data and materials

Not applicable.

### Declarations

#### Ethics approval and consent to participate

This manuscript does not contain clinical studies or patient data.

#### Consent for publication

Not applicable.

#### Competing interests

The authors declare no competing interests.

#### Author details

<sup>1</sup>School of Computational and Communication Science and Engineering, The Nelson Mandela African Institution of Science and Technology (NM-AIST), P. O. Box 447, Arusha, Tanzania. <sup>2</sup>School of Life Sciences and Biomedical Engineering, The Nelson Mandela African Institution of Science and Technology (NM-AIST), P. O. Box 447, Arusha, Tanzania.

Received: 25 July 2023 Accepted: 4 September 2023

Published online: 15 September 2023

### References

- Abdalhamed AM, Naser SM, Mohamed AH, Zeedan GSG (2022) Development of gold nanoparticles-lateral flow test as a novel field diagnostic assay for detecting foot-and-mouth disease and lumpy skin disease viruses. *Iran J Microbiol* 14(4):574. <https://doi.org/10.18502/ijm.v14i4.10245>
- Abdulqa H, Rahman H, Dyary H, Othman H (2016) Lumpy skin disease. *Reprod Immunol Open Access* 1(25):1974–2476
- Afshari Safavi E (2022) Assessing machine learning techniques in forecasting lumpy skin disease occurrence based on meteorological and geospatial features. *Trop Anim Health Prod* 54(1):1–11. <https://doi.org/10.1007/978-3-030-25385-1>
- Agianiotaki EI, Babiuk S, Katsoulou P-D, Chaintoutis SC, Praxitelous A, Quizon K, Boscos C, Polizopoulou ZS, Chondrokouki ED, Dovas CI (2018) Colostrum transfer of neutralizing antibodies against lumpy skin disease virus from vaccinated cows to their calves. *Transbound Emerg Dis* 65(6):2043–2048. <https://doi.org/10.1111/tbed.12983>
- Alkhamis MA, VanderWaal K (2016) Spatial and temporal epidemiology of lumpy skin disease in the Middle East, 2012–2015. *Front Vet Sci* 3:19. <https://doi.org/10.3389/fvets.2016.00019>

- Allepuz A, Casal J, Beltrán-Alcrudo D (2019) Spatial analysis of lumpy skin disease in Eurasia—predicting areas at risk for further spread within the region. *Transbound Emerg Dis* 66(2):813–822. <https://doi.org/10.1111/tbed.13090>
- Al-Salihi K, Hassan I (2015) Lumpy skin disease in Iraq: study of the disease emergence. *Transbound Emerg Dis* 62(5):457–462. <https://doi.org/10.1111/tbed.12386>
- Animal Health, EP, Welfare (2016) Urgent advice on lumpy skin disease. *EFSA J* 14(8):04573. <https://doi.org/10.2903/j.efsa.2016.4573>
- Annandale CH, Holm DE, Ebersohn K, Venter EH (2014) Seminal transmission of lumpy skin disease virus in heifers. *Transbound Emerg Dis* 61(5):443–448. <https://doi.org/10.1111/tbed.12045>
- Anwar A, Na-Lampang K, Preyavichayapugdee N, Punyapornwithaya V (2022) Lumpy skin disease outbreaks in Africa, Europe, and Asia (2005–2022): multiple change point analysis and time series forecast. *Viruses* 14(10):2203. <https://doi.org/10.3390/v14102203>
- Ardestani EG, Mokhtari A (2020) Modeling the lumpy skin disease risk probability in central Zagros mountains of Iran. *Prev Vet Med* 176:104887. <https://doi.org/10.1016/j.prevetmed.2020.104887>
- Ayelet G, Abate Y, Sisay T, Nigusie H, Gelaye E, Jemberie S, Smare K (2013) Lumpy skin disease: preliminary vaccine efficacy assessment and overview on outbreak impact in dairy cattle at Debre Zeit, central Ethiopia. *Antiviral Res* 98(2):261–265. <https://doi.org/10.1016/j.antiviral.2013.02.008>
- Bhanuprakash V, Hosamani M, Venkatesan G, Balamurugan V, Yogisharadhya R, Singh RK (2012) Animal poxvirus vaccines: a comprehensive review. *Expert Rev Vaccines* 11(11):1355–1374. <https://doi.org/10.1586/erv.12.116>
- Casal J, Allepuz A, Miteva A, Pite L, Tabakovsky B, Terzievski D, Alexandrov T, Beltrán-Alcrudo D (2018) Economic cost of lumpy skin disease outbreaks in three Balkan countries: Albania, Bulgaria and the former Yugoslav Republic of Macedonia (2016–2017). *Transbound Emerg Dis* 65(6):1680–1688. <https://doi.org/10.1111/tbed.12926>
- Casal J, Saegerman C, Bertagnoli S, Meyer G, Ganière JP, Caufour P, De Clercq K, Jacquiet P, Hautefeuille C, Ettore F et al (2019) A simple method to estimate the number of doses to include in a bank of vaccines. The case of lumpy skin disease in France. *PLoS One* 14(1):0210317. <https://doi.org/10.1371/journal.pone.0210317>
- Chapman R, Diepen M, Douglass N, Galant S, Jaffer M, Margolin E, Ximba P, Hermanus T, Moore PL, Williamson A-L (2021) Assessment of an LSDV-vectored vaccine for heterologous prime-boost immunizations against HIV. *Vaccines* 9(11):1281. <https://doi.org/10.3390/vaccines9111281>
- Dofadar DF, Abdullah HM, Khan RH, Rahman R, Ahmed MS (2022) A comparative analysis of lumpy skin disease prediction through machine learning approaches. In: 2022 IEEE international conference on artificial intelligence in engineering and technology (IICAET), pp 1–4. <https://doi.org/10.1109/IICAET55139.2022.9936742>
- Douglass N, Munyanduki H, Omar R, Gers S, Mutowembwa P, Heath L, Williamson A-L (2020) Influence of the viral superoxide dismutase (SOD) homologue on lumpy skin disease virus (LSDV) growth, histopathology and pathogenicity. *Vaccines* 8(4):664. <https://doi.org/10.3390/vaccines8040664>
- EFSA (2015) Scientific opinion on lumpy skin disease. *Eur Food Saf Authority J* 13(1):3986. <https://doi.org/10.2903/j.efsa.2015.3986>
- EFSA (2018) Lumpy skin disease II. Data collection and analysis. *Eur Food Saf Auth J*. <https://doi.org/10.2903/j.efsa.2018.5176>
- (EFSA) EFSA, Calistri P, DeClercq K, De Vleeschauwer A, Gubbins S, Klement E, Stegeman A, Cortiñas Abrahantes J, Antoniou S-E, Broglia A, et al (2018) Lumpy skin disease: scientific and technical assistance on control and surveillance activities. *EFSA J* 16(10):05452. <https://doi.org/10.2903/j.efsa.2018.5452>
- (EFSA) EFSA, Calistri P, DeClercq K, Gubbins S, Klement E, Stegeman A, Cortiñas Abrahantes J, Antoniou S-E, Broglia A, Gogin A, (2019) Lumpy skin disease: III. data collection and analysis. *EFSA J* 17(3):05638. <https://doi.org/10.2903/j.efsa.2019.5638>
- El-Ansary RE, El-Dabae WH, Bream AS, El Wakil A (2022) Isolation and molecular characterization of lumpy skin disease virus from hard ticks, *Ithipicephalus (Boophilus) annulatus* in Egypt. *BMC Vet Res* 18(1):302. <https://doi.org/10.1186/s12917-022-03398-y>
- Elhaig MM, Selim A, Mahmoud M (2017) Lumpy skin disease in cattle: frequency of occurrence in a dairy farm and a preliminary assessment of its possible impact on Egyptian buffaloes. *Onderstepoort J Vet Res* 84(1):1–6. <https://doi.org/10.4102/ojvr.v84i1.1393>
- Fay PC, Wijesiriwardana N, Munyanduki H, Sanz-Bernardo B, Lewis I, Haga IR, Moffat K, Vliet AH, Hope J, Graham SP et al (2022) The immune response to lumpy skin disease virus in cattle is influenced by inoculation route. *Front Immunol* 13:6947. <https://doi.org/10.3389/fimmu.2022.1051008>
- Francis MJ (2018) Recent advances in vaccine technologies. *Vet Clin Small Anim Pract* 48(2):231–241. <https://doi.org/10.1016/j.cvsm.2017.10.002>
- Gale P, Kelly L, Snary E (2016) Qualitative assessment of the entry of capripoxviruses into Great Britain from the European Union through importation of ruminant hides, skins and wool. *Microbial Risk Anal* 1:13–18. <https://doi.org/10.1016/j.mran.2015.07.001>
- Gari G, Abie G, Gizaw D, Wubete A, Kidane M, Asgedom H, Bayissa B, Ayelet G, Oura CA, Roger F et al (2015) Evaluation of the safety, immunogenicity and efficacy of three capripoxvirus vaccine strains against lumpy skin disease virus. *Vaccine* 33(28):3256–3261. <https://doi.org/10.1016/j.vaccine.2015.01.035>
- Gelaye E, Lamien CE (2019) Lumpy skin disease and vectors of LSDV. In: *Transboundary Animal Diseases in Sahelian Africa and Connected Regions*. Springer, pp 267–288. <https://doi.org/10.1007/978-3-030-25385-1>
- Gerilovych A, Stegny B (2016) Lumpy skin disease: characterization and possible risks for Central and Eastern Europe. *J Vet Med Biotechnol Biosaf* 2(Iss. 3):33–38
- Gomo C, Kanonhuwa K, Godobo F, Tada O, Makuza S (2017) Temporal and spatial distribution of lumpy skin disease (LSD) outbreaks in Mashonaland West Province of Zimbabwe from 2000 to 2013. *Trop Anim Health Prod* 49(3):509–514. <https://doi.org/10.1007/s11250-017-1222-y>
- Grace D, McDermott J (2012) *Livestock epidemic*. In: *The Routledge Handbook of Hazards and Disaster Risk Reduction*, pp 372–383. Routledge. <https://doi.org/10.4324/9780203844236>
- Gubbins S (2019) Using the basic reproduction number to assess the risk of transmission of lumpy skin disease virus by biting insects. *Transbound Emerg Dis* 66(5):1873–1883. <https://doi.org/10.1111/tbed.13216>
- Gubbins S, Stegeman A, Klement E, Pite L, Broglia A, Abrahantes JC (2020) Inferences about the transmission of lumpy skin disease virus between herds from outbreaks in Albania in 2016. *Prev Vet Med* 181:104602. <https://doi.org/10.1016/j.prevetmed.2018.12.008>
- Gupta T, Patil V, Bali D, Angaria S, Sharma M, Chahota R (2020) A review: lumpy skin disease and its emergence in India. *Vet Res Commun*. <https://doi.org/10.1007/s11259-020-09780-1>
- Hasib FMY, Islam MS, Das T, Rana EA, Uddin MH, Bayzid M, Nath C, Hossain MA, Masuduzzaman M, Das S et al (2021) Lumpy skin disease outbreak in cattle population of Chattogram, Bangladesh. *Vet Med Sci* 7(5):1616–1624. <https://doi.org/10.1002/vms3.524>
- Ince OB, Çakir S, Dereli MA (2016) Risk analysis of lumpy skin disease in Turkey. *Indian J Anim Res* 50(6):1013–1017. <https://doi.org/10.18805/ijar.9370>
- Issimov A, Rametov N, Zhugunissof K, Kutumbetov L, Zhanabayev A, Kazhgaliyev N, Nurgaliyev B, Shalmenov M, Absatirov G Dushayeva L (2020) Emergence of the first Lumpy Skin Disease outbreak among livestock in the Republic of Kazakhstan in 2016. <https://doi.org/10.20944/preprints202011.0298.v1>
- Jalali S, Rasooli A, Seifi Abad Shapuri M, Daneshi M (2017) Clinical, hematologic, and biochemical findings in cattle infected with lumpy skin disease during an outbreak in Southwest Iran. *Arch Razi Inst* 72(4):255–265. <https://doi.org/10.22092/ARI.2017.113301>
- Jiang C, Tao D, Geng Y, Yang H, Xu B, Chen Y, Hu C, Chen H, Xie S, Guo A (2022) Sensitive and specific detection of lumpy skin disease virus in cattle by CRISPR-Cas12a fluorescent assay coupled with recombinase polymerase amplification. *Genes* 13(5):734. <https://doi.org/10.3390/genes13050734>
- Khan YR, Ali A, Hussain K, Ijaz M, Rabbani AH, Khan RL, Abbas SN, Aziz MU, Ghaffar A, Sajid HA (2021) A review: surveillance of lumpy skin disease (LSD) a growing problem in Asia. *Microb Pathog* 158:105050. <https://doi.org/10.1016/j.micpath.2021.105050>
- Kiplagat SK, Kitala PM, Onono JO, Beard PM, Lyons NA (2020) Risk factors for outbreaks of Lumpy Skin Disease and the economic impact in cattle farms of Nakuru county, Kenya. *Front Vet Sci* 7:259. <https://doi.org/10.3389/fvets.2020.00259>
- Klement E, Broglia A, Antoniou S-E, Tsiamadis V, Plevraki E, Petrović T, Polaček V, Debeljak Z, Miteva A, Alexandrov T et al (2020) Neethling vaccine proved

- highly effective in controlling lumpy skin disease epidemics in the Balkans. *Prev Vet Med* 181:104595. <https://doi.org/10.1016/j.prevetmed.2018.12.001>
- Krotova A, Byadovskaya O, Shumilova I, Zinyakov N, Schalkwyk A, Sprygin A (2022) Molecular characterization of a novel recombinant lumpy skin disease virus isolated during an outbreak in Tyumen, Russia, in 2019. *Transbound Emerg Dis*. <https://doi.org/10.1111/tbed.14574>
- Lee S-W, Markham PF, Coppo MJ, Legione AR, Markham JF, Noormohammadi AH, Browning GF, Ficorilli N, Hartley CA, Devlin JM (2012) Attenuated vaccines can recombine to form virulent field viruses. *Science* 337(6091):188–188. <https://doi.org/10.1126/science.1217134>
- Limon G, Gamawa AA, Ahmed AI, Lyons NA, Beard PM (2020) Epidemiological characteristics and economic impact of lumpy skin disease, sheeppox and goatpox among subsistence farmers in Northeast Nigeria. *Front Vet Sci* 7:8. <https://doi.org/10.3389/fvets.2020.00008>
- LK, K, et al (2021) Clinico-molecular diagnosis and characterization of bovine lumpy skin disease virus in Andhra Pradesh, India. *Trop Anim Health Prod* 53(4):424–424. <https://doi.org/10.1007/s11250-021-02872-3>
- Magori-Cohen R, Louzoun Y, Herziger Y, Oron E, Arazi A, Tuppurainen E, Shpigel NY, Klement E (2012) Mathematical modelling and evaluation of the different routes of transmission of lumpy skin disease virus. *Vet Res* 43(1):1–13. <https://doi.org/10.1186/1297-9716-43-1>
- Manić M, Stojiljković M, Petrović M, Nišavić J, Bacić D, Petrović T, Vidanović D, Obrenović S (2019) Epizootic features and control measures for lumpy skin disease in South-East Serbia in 2016. *Transbound Emerg Dis* 66(5):2087–2099. <https://doi.org/10.1111/tbed.13261>
- Mathijs E, Vandenbussche F, Sadaukassova M, Kabduldjanov T, Haegeman A, Aerts L, Kyzaiabayev T, Sultanov A, Van Borm S, De Clercq K (2020) Complete coding sequence of a lumpy skin disease virus strain isolated during the 2016 outbreak in Kazakhstan. *Microbiol Resour Announc* 9(4):19–01399. <https://doi.org/10.1128/MRA.01399-19>
- Mat B, Arikan MS, Akin AC, Çevrimli MB, Yonar H, Tekindal MA (2021) Determination of production losses related to lumpy skin disease among cattle in Turkey and analysis using SEIR epidemic model. *BMC Vet Res* 17(1):1–10. <https://doi.org/10.1186/s12917-021-02983-x>
- Mercier A, Arsevska E, Bournez L, Bronner A, Calavas D, Cauchard J, Falala S, Caufour P, Tisseuil C, Lefrançois T et al (2018) Spread rate of lumpy skin disease in the Balkans, 2015–2016. *Transbound Emerg Dis* 65(1):240–243. <https://doi.org/10.1111/tbed.12624>
- Milovanović M, Miličević V, Radojičić S, Valčić M, Hoffmann B, Dietze K (2020) Suitability of individual and bulk milk samples to investigate the humoral immune response to lumpy skin disease vaccination by elisa. *Virology* 17(1):1–7. <https://doi.org/10.1186/s12985-020-01298-x>
- MLF: (2019) DISEASE FACT SHEET FOR TRANSBOUNDARY ANIMAL DISEASES (TADs) FOR FIELD VETERINARY STAFF IN TANZANIA. unpublished
- Moher D, Liberati A, Tetzlaff J, Altman DG, Group\* P (2009) Preferred reporting items for systematic reviews and meta-analyses: the Prisma statement. *Ann Intern Med* 151(4):264–269. <https://doi.org/10.1371/journal.pmed.1000097>
- Molla W, Frankena K, De Jong M (2017) Transmission dynamics of lumpy skin disease in Ethiopia. *Epidemiol Infect* 145(13):2856–2863. <https://doi.org/10.1017/S0950268817001637>
- Molla W, Frankena K, Gari G, Jong MC (2017) Field study on the use of vaccination to control the occurrence of lumpy skin disease in Ethiopian cattle. *Prev Vet Med* 147:34–41. <https://doi.org/10.1016/j.prevetmed.2017.08.019>
- Namazi F, Khodakaram Tafti A (2021) Lumpy skin disease, an emerging transboundary viral disease: a review. *Vet Med Sci*. <https://doi.org/10.1002/vms3.434>
- Nesterov A, Mazloum A, Byadovskaya O, Shumilova I, Van Schalkwyk A, Krotova A, Kirpichenko V, Donnik I, Chvala I, Sprygin A (2022) Experimentally controlled study indicates that the naturally occurring recombinant vaccine-like lumpy skin disease strain Udumrtiya/2019, detected during freezing winter in northern latitudes, is transmitted via indirect contact. *Front Vet Sci* 9:1001426. <https://doi.org/10.3389/fvets.2022.1001426>
- Ochwo S, VanderWaal K, Munsey A, Nkamwesiga J, Ndekezi C, Auma E, Mwiine FN (2019) Seroprevalence and risk factors for lumpy skin disease virus seropositivity in cattle in Uganda. *BMC Vet Res* 15(1):1–9. <https://doi.org/10.1186/s12917-019-1983-9>
- Rouby SR, Safwat NM, Hussein KH, Abdel-Raouf AM, Madkour BS, Abdel-Moneim AS, Hoseni HI (2021) Lumpy skin disease outbreaks in Egypt during 2017–2018 among sheeppox vaccinated cattle: epidemiological, pathological, and molecular findings. *PLoS ONE* 16(10):0258755. <https://doi.org/10.1371/journal.pone.0258755>
- Saegerman C, Bertagnoli S, Meyer G, Ganière J-P, Caufour P, De Clercq K, Jacquet P, Hautefeuille C, Eto F, Casal J (2019) Risk of introduction of lumpy skin disease into France through imports of cattle. *Transbound Emerg Dis* 66(2):957–967. <https://doi.org/10.1111/tbed.13111>
- Sanz-Bernardo B, Suckoo R, Haga IR, Wijesiriwardana N, Harvey A, Basu S, Larner W, Rooney S, Sy V, Langlands Z et al (2022) The acquisition and retention of lumpy skin disease virus by blood-feeding insects is influenced by the source of virus, the insect body part, and the time since feeding. *J Virol* 96(15):00751–22. <https://doi.org/10.1128/jvi.00751-22>
- Şevik M, Doğan M (2017) Epidemiological and molecular studies on lumpy skin disease outbreaks in Turkey during 2014–2015. *Transbound Emerg Dis* 64(4):1268–1279. <https://doi.org/10.1111/tbed.12501>
- Siettos CI, Russo L (2013) Mathematical modeling of infectious disease dynamics. *Virulence* 4(4):295–306. <https://doi.org/10.4161/viru.24041>
- Sprygin A, Babin Y, Pestova Y, Kononova S, Wallace DB, Van Schalkwyk A, Byadovskaya O, Diev V, Lozovoy D, Kononov A (2018) Analysis and insights into recombination signals in lumpy skin disease virus recovered in the field. *PLoS One* 13(12):0207480. <https://doi.org/10.1371/journal.pone.0207480>
- Sprygin A, Artyuchova E, Babin Y, Prutnikov P, Kostrova E, Byadovskaya O, Kononov A (2018) Epidemiological characterization of lumpy skin disease outbreaks in Russia in 2016. *Transbound Emerg Dis* 65(6):1514–1521. <https://doi.org/10.1111/tbed.12889>
- Sprygin A, Pestova Y, Wallace D, Tuppurainen E, Kononov A (2019) Transmission of lumpy skin disease virus: a short review. *Virus Res* 269:197637. <https://doi.org/10.1016/j.virusres.2019.05.015>
- Sprygin A, Pestova Y, Bjadovskaya O, Prutnikov P, Zinyakov N, Kononova S, Ruchnova O, Lozovoy D, Chvala I, Kononov A (2020) Evidence of recombination of vaccine strains of lumpy skin disease virus with field strains, causing disease. *PLoS ONE* 15(5):0232584. <https://doi.org/10.1371/journal.pone.0232584>
- Sprygin A, Van Schalkwyk A, Shumilova I, Nesterov A, Kononova S, Prutnikov P, Byadovskaya O, Kononov A (2020) Full-length genome characterization of a novel recombinant vaccine-like lumpy skin disease virus strain detected during the climatic winter in Russia. *Adv Virol* 165(11):2675–2677. <https://doi.org/10.1007/s00705-020-04756-7>
- Stojmanovski Z (2018) Space-time permutation model applied to the past outbreak data of lumpy skin disease in the Balkan Peninsula from August 2015 to July 2017. *Vet Glas* 72(1):44–55. <https://doi.org/10.2298/VETGL.1710270035>
- Sudhakar SB, Mishra N, Kalaiyarasu S, Jhade SK, Singh VP (2021) Genetic and phylogenetic analysis of lumpy skin disease viruses (LSDV) isolated from the first and subsequent field outbreaks in India during 2019 reveals close proximity with unique signatures of historical Kenyan ni-2490/Kenya/kgsp-like field strains. *Transbound Emerg Dis*. <https://doi.org/10.1111/tbed.14322>
- Tageldin MH, Wallace DB, Gerdes GH, Putterill JF, Greyling RR, Phosiwa MN, Al Buisaidy RM, Al Ismaaily SI (2014) Lumpy skin disease of cattle: an emerging problem in the Sultanate of Oman. *Trop Anim Health Prod* 46(11):241–246. <https://doi.org/10.1007/s11250-013-0483-3>
- Tchuenche JM, Bauch CT (2012) Can culling to prevent monkeypox infection be counter-productive? scenarios from a theoretical model. *J Biol Syst* 20(03):259–283. <https://doi.org/10.1142/S0218339012500106>
- Tran HTT, Truong AD, Dang AK, Ly DV, Nguyen CT, Chu NT, Hoang TV, Nguyen HT, Nguyen VT, Dang HV (2021) Lumpy skin disease outbreaks in Vietnam. *Transbound Emerg Dis* 68(3):977–980. <https://doi.org/10.1111/tbed.14022>
- Tuppurainen E, Oura C (2012) Lumpy skin disease: an emerging threat to Europe, the Middle East and Asia. *Transbound Emerg Dis* 59(1):40–48. <https://doi.org/10.1111/j.1865-1682.2011.01242.x>
- Tuppurainen E, Antoniou S, Tsiamadis E, Topkaridou M, Labus T, Debeljak Z, Plavšić B, Miteva A, Alexandrov T, Pite L et al (2020) Field observations and experiences gained from the implementation of control measures against lumpy skin disease in South-East Europe between 2015 and 2017. *Prev Vet Med* 181:104600. <https://doi.org/10.1016/j.prevetmed.2018.12.006>
- Uddin MA, Islam MA, Rahman AA, Rahman MM, Khasruzzaman A, Ward MP, Hossain MT (2022) Epidemiological investigation of lumpy skin disease outbreaks in Bangladeshi cattle during 2019–2020. *Transbound Emerg Dis*. <https://doi.org/10.1111/tbed.14696>
- Wang C, Li M, Lyu X (2020) Classification and production process of human vaccine. *Zhonghua yu Fang yi xue za zhi* [Chinese Journal of Preventive

Medicine] 54(9):1017–1025. <https://doi.org/10.3760/cmaj.cn112150-20200520-00756>

Yeruham I, Perl S, Nyska A, Abraham A, Davidson M, Haymovitch M, Zamir O, Grinstein H (1994) Adverse reactions in cattle to a capripox vaccine. *Vet Rec* 135(14):330–332. <https://doi.org/10.1136/vr.135.14.330>

### **Publisher's Note**

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

**Submit your manuscript to a SpringerOpen<sup>®</sup> journal and benefit from:**

- ▶ Convenient online submission
- ▶ Rigorous peer review
- ▶ Open access: articles freely available online
- ▶ High visibility within the field
- ▶ Retaining the copyright to your article

---

Submit your next manuscript at ▶ [springeropen.com](https://www.springeropen.com)

---