Bibliografi Lumpy Skin Disease Virus

PERPUSTAKAAN BALAI BESAR PENGUJIAN STANDAR INSTRUMEN VETERINER

BADAN STANDARISASI INSTRUMEN PERTANIAN

KEMENTERIAN PERTANIAN

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Puji syukur kami panjatkan ke hadirat Tuhan Yang Maha Esa atas tersusunnya Bibliografi Lumpy Skin Disease Virus ini. Bibliografi ini disusun sebagai referensi bagi pemustaka yang membutuhkan informasi ilmiah terkait Lumpy Skin Disease Virus (LSDV), mencakup aspek epidemiologi, diagnostik, vaksinasi, serta berbagai penelitian terbaru mengenai penyakit ini.

Penyakit Lumpy Skin Disease merupakan salah satu penyakit infeksius yang berdampak signifikan terhadap kesehatan dan produktivitas ternak sapi. Oleh karena itu, pemahaman yang komprehensif mengenai virus ini menjadi sangat penting bagi para peneliti, praktisi veteriner, dan pembuat kebijakan dalam upaya pengendalian dan pencegahannya.

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Perpustakaan Balai Besar Pengujian Standar Instrumen Veteriner

DAFTAR ISI

1. **Inferences about the transmission of lumpy skin disease virus between herds from outbreaks in Albania in 2016,** Simon Gubbins, Arjan Stegeman, Eyal Klement, Ledi Pite, Alessandro Broglia, José Cortiñas Abrahantes, **Preventive Veterinary Medicine**, Volume 181, 2020, 104602, https://doi.org/10.1016/j.prevetmed.2018.12.008.

Abstract:

Lumpy skin disease has recently emerged as a major threat to cattle populations outside of Africa, where it is endemic. In 2015 the first ever European outbreaks occurred in Greece, which were followed by spread across much of the Balkans in 2016. Here we use a simple mathematical model for the transmission of lumpy skin disease virus (LSDV) between herds to explore factors influencing its spread by fitting it to data on outbreaks in Albania in 2016. We show that most transmission occurs over short distances (<5 km), but with an appreciable probability of transmission at longer distances. We also show that there is evidence for seasonal variation in the force of infection associated with temperature, possibly through its influence on the relative abundance of the stable fly, Stomoxys calcitrans. These two results together are consistent with LSDV being transmitted by the bites of blood-feeding insects, though further work is required to incriminate specific species as vectors. Finally, we show that vaccination has a significant impact on spread and estimate the vaccine effectiveness to be 76%.

Keywords: Epidemiology; Cattle; Mathematical modelling; Vaccination; LSDV

2. **Complete Coding Sequences of Lumpy Skin Disease Virus Strains Isolated from Cutaneous Lesions in Namibian Cattle during 2016 Outbreaks,** Elisabetta Di Felice, Chiara Pinoni, Siegfried Khaiseb, Cesare Camma, Andrea Capobianco Dondona, Andrea Polci, Umberto Molini, Federica Monaco, Simon Roux, **Microbiology Resource Announcements**, Volume 9, Issue 28, 2020, https://doi.org/10.1128/mra.00124-20.

Abstract:

Between September and October 2016, an outbreak of lumpy skin disease (LSD) was monitored in the Okakarara veterinary district of Namibia. The complete coding sequences were obtained for LSD virus isolates from skin nodules from two symptomatic animals.

3. **Improved safety profile of inactivated Neethling strain of the Lumpy Skin Disease Vaccine,** Matome Selina Matsiela, Leeann Naicker, Vusi Saul Dibakwane, Nomfundo Ntombela, Thandeka Khoza, Nobalanda Mokoena, **Vaccine: X**, Volume 12,2022,100209, https://doi.org/10.1016/j.jvacx.2022.100209.

Abstract:

The Lumpy Skin Disease Virus (LSDV) Neethling vaccine strains have been used for decades for prophylactic immunization of domestic ruminants against the disease. Commercial products against Lumpy skin disease are supplied as live attenuated vaccines and often are associated with adverse reactions warranting studies towards development of safe and efficacious vaccine alternatives. The present study was designed to investigate the ability of Montanide™ Gel 01 PR adjuvanted inactivated Neethling vaccine strain of the lumpy skin disease to induce immune response in rabbits. Complete virus inactivation was achieved following treatment of live vaccine strain with binary ethyleneimine (BEI) at 2 mM final concentration. Inactivated virus antigen, formulated with Montanide™ Gel 01 was injected at 1,00E + 05 and 1,00E + 06 TCID50 per dose in rabbits. The second injection with same vaccine dosages was administered 21 days after the primary vaccination. Rabbits that received a 1,00E + 05 TCID50/dose of inactivated LSDV vaccine formulation induced maximum neutralizing antibody titres on day 13 post second vaccinations. Rabbits vaccinated and prime boosted with the 1,00E + 06 TCID50/dose of inactivated LSDV vaccine formulation, induced neutralizing antibody titres on day 14 after first vaccination. The maximum antibody titres for the 1,00E + 06 TCID50/dose of the inactivated LSDV vaccine formulation was obtained on day 35 post vaccination. The 1,00E + 06 TCID50 dose of the inactivated LSDV vaccine Montanide™ Gel-01 PR formulation induced higher neutralizing antibodies. The MontanideTM Gel-01 PR offers safer profile to oil adjuvants and can be developed further to protect target animals against LSDV in non-endemic areas.

Keywords: Lumpy skin disease; Virus Inactivation; Montanide™ Gel 01 adjuvant; Immunogenicity

4. **Complete Coding Sequence of a Lumpy Skin Disease Virus Strain Isolated during the 2016 Outbreak in Kazakhstan,** Elisabeth Mathijs, Frank Vandenbussche, Meruyert Saduakassova, Tursyn Kabduldanov, Andy Haegeman, Laetitia Aerts, Taskyn Kyzaibayev, Akhmetzhan Sultanov, Steven Van Borm, Kris De Clercq, Kenneth M. Stedman, **Microbiology Resource Announcements**, Volume 9, Issue 4, 2020, https://doi.org/10.1128/mra.01399-19.

Abstract:

Lumpy skin disease virus (LSDV) causes an economically important disease in cattle. Here, we report the complete coding sequence of the LSDV isolate Kubash/KAZ/16, detected in a clinical sample from an infected cow from the outbreak reported on 7 July 2016 in Kazakhstan (Atyrau Region).

5. **Dynamical analysis of a novel discrete fractional lumpy skin disease model,** Amr Elsonbaty, Mohammed Alharbi, A. El-Mesady, Waleed Adel, **Partial Differential Equations in Applied Mathematics**, Volume 9, 2024, 100604, https://doi.org/10.1016/j.padiff.2023.100604.

Abstract:

Lumpy skin disease is a viral disease that affects cattle and is caused by the lumpy skin disease virus. This work is devoted to presenting and analyzing the nonlinear dynamics of a novel discrete fractional model for lumpy skin disease. The equilibrium points of the proposed discrete fractional model are found. The stability analysis of equilibrium points is carried out. The influences of key parameters in the model are investigated, and then the stability regions of a disease-free steady state in the space of parameters are obtained. A proposed efficient control scheme is implemented to stabilize the disease-free equilibrium point when it is unstable. The influences of fractional-order parameters on the applied control scheme are explored. Finally, numerical simulations are performed to verify the theoretical findings obtained and confirm the effectiveness of the employed control scheme.

Keywords: Lumpy skin disease; Epidemics; Equilibrium points; Stability; Fractional Caputo differences; Linear control

6. **Development of in-house ELISA for detection of antibodies against lumpy skin disease virus in cattle and assessment of its performance using a bayesian approach,Nattawooti Sthitmatee,** Pallop Tankaew, Wittawat Modethed, Amarin Rittipornlertrak, Anucha Muenthaisong, Nisachon Apinda, Pongpisid Koonyosying, Boondarika Nambooppha, Paweena Chomjit, Kanokwan Sangkakam, Tawatchai Singhla, Paramintra Vinitchaikul, Kittikorn Boonsri, Kidsadagon Pringproa, Veerasak Punyapornwithaya, Khwanchai Kreausukon, **Heliyon**, Volume 9, Issue 2, 2023, e13499, https://doi.org/10.1016/j.heliyon.2023.e13499.

Abstract:

Lumpy skin disease (LSD) is a contagious disease among cattle and buffalo worldwide. Currently, an enzyme-linked immunosorbent assay (ELISA) has been recognized as an efficient diagnostic tool that is less time-consuming and easier than the viral neutralization test to measure the antibody levels. In the present study, an in-house method of indirect ELISA was developed to detect the bovine antibodies against Lumpy skin disease virus (LSDV) and its performance was

assessed using field samples. This in-house method has been compared with the commercial ELISA test kit for detection of bovine antibodies against LSDV. The sensitivity (Se) and the specificity (Sp) of the test were estimated using a Bayesian latent class model. Checkerboard titration was performed using the naturally LSDV-infected bovine sera and colostrum-deprived calf sera. The LSDV antigen concentrations (1 TCID50/mL), the sample serum (1:500), and goat anti-bovine immunoglobulin G (IgG) labeled with horseradish peroxidase (HRP) (1:10,000) were determined to be optimal for this assay. The calculated cut-off value was 0.067, and there were no differences in the results of tests that utilized positive and negative sera ($p < 0.05$). The characteristics of two diagnostic tests were evaluated using a conditional dependent and one-population Bayesian model. The Se value of an in-house indirect ELISA were almost similar to ELISA test kit. On the other hand, the Sp value of the in-house ELISA test was lower than that of the commercial ELISA test with the median values of 89% (95% PPI = 75.9–99.3%) and 91.4% (95% PPI = 85.3–95.5%), respectively. A posterior estimate for the prevalence was 66.9% (95% PPI = 60.8–83.3%) and higher than initially expected.

Keywords: Bayesian latent class analysis; Indirect ELISA; Lumpy skin disease; Sensitivity; Specificity

7. **Complete genome sequence of the lumpy skin disease virus reported from Jammu and Kashmir, India, during 2022 outbreak**, Shabir Bhat, Waseem Chaudry, Purnima Mittal, Bilal Ahmad, Zahoor Haroon, Shaista Shaheen, Masood Mir, Manjunath Reddy, Mohammad Wani, Kenneth M. Stedman, **Microbiology Resource Announcements**, Volume 12, Issue 11, 2023, https://doi.org/10.1128/MRA.00317-23.

Abstract:

Lumpy skin disease virus (LSDV) is the causative agent of an economically important disease of cattle and water buffaloes. Here, we announce the complete genome sequence of the LSDV from Jammu and Kashmir, India. LSDV/02/KASH/IND/2022 was detected in skin biopsy sample of an LSD-infected dairy cow on 24 October 2022.

Keywords: Complete genome sequence; Lumpy skin disease virus

8. **Production of recombinant lumpy skin disease virus A27L and L1R proteins for application in diagnostics and vaccine development,** Nomfundo Ntombela, Matome Matsiela, Sbahle Zuma, Suhavna Hiralal, Leeann Naicker, Nobalanda Mokoena,

Thandeka Khoza, **Vaccine: X**, Volume 15, 2023, 100384, https://doi.org/10.1016/j.jvacx.2023.100384.

Abstract:

Vaccination using live attenuated vaccines (LAVs) is considered the most effective method for control of lumpy skin disease (LSD). However, this method is limited by safety concerns, with reports of adverse reactions following vaccination. This study evaluates A27L and L1R which are essential proteins for virus attachment and membrane fusion as recombinant sub-unit vaccines against LSD. These proteins were recombinantly expressed in Escherichia coli and purified using affinity chromatography. Purified proteins were formulated individually (A27L or L1R) and in combination (A27L and L1R) with 10% (w/w) Montanide™ Gel 01 PR adjuvant at a final antigen dose of 20 µg per protein. The safety and immunogenicity of these formulations were evaluated in rabbits in a 42-day clinical trial. Animals were vaccinated on day 0 and boost injection administered 21 days later. No reduced morbidity, increased temperature and any other clinical signs were recorded in vaccinated animals for all three vaccine formulations. The highest neutralizing antibody response was detected on day 42 post-primary vaccination for all formulations when using serum neutralising assay. The neutralisation data correlates with antibody titres quantified using a whole cell ELISA. Evaluating the combination of A27L and L1R as potential diagnostic reagents showed highest sensitivity for detection of antibodies against LSD when compared to individual proteins. This study reports the immunogenicity of recombinant A27L and L1R combination for successful application in LSD vaccine development. Furthermore, these proteins demonstrated the potential use in LSD diagnostics.

Keywords: Lumpy skin disease virus; A27L; L1R; Subunit vaccines; Montanide™ Gel 01 PR

9. **Phylogenetic and pathogenic characterization of lumpy skin disease virus circulating in China,** Shanhui Ren, Haotai Chen, Lvfeng Yuan, Xue Yang, Tadele Berihun Afera, Zaib Ur Rehman, Huibao Wang,Xiangwei Wang, Chunling Ma, Yuguang Lin, Xusheng Qiu, Xiangping Yin, Yuefeng Sun, **Virology**, Volume 585, 2023, Pages 127-138, https://doi.org/10.1016/j.virol.2023.06.008.

Abstract:

The genomic characterization of emerging pathogens is critical for unraveling their origin and tracking their dissemination. Lumpy skin disease virus (LSDV) is a rapidly emerging pathogen in Asia including China. Although the first Lumpy skin disease (LSD) outbreak was reported in 2019, the origin, transmission, and evolutionary trajectory of LSDV in China have remained obscure. The viral genome of a circulating LSDV strain in China, abbreviated LSDV/FJ/CHA/2021, was

sequenced using the next-generation sequencing technique. The morphology and cytoplasmic viral factory of these LSDV isolates were observed using transmission electron microscopy. Subsequently, the genomic characterization of this LSDV isolate was systematically analyzed for the first time using the bioinformatics software. The current study revealed that several mutations in the genome of LSDV isolates circulating in China were identified using single nucleotide polymorphisms (SNPs) analysis, an instrument to evaluate for continuous adaptive evaluation of a virus. Furthermore, phylogenomic analysis was used to identify the lineage using the whole genome sequences of 44 LSDV isolates. The result revealed that the isolates from China were closely similar to that of the LSDV isolates from Vietnam, which are divided into a monophyletic lineage sub-group I. The SNPs and Simplot analysis indicate no significant occurrence of the recombinant event on the genome of LSDV isolates in China. Notably, the live virus challenge experiment demonstrated that the pathogenic characterization of this LSDV isolate belongs to a virulent strain. Collectively, we gain the first insight into the evolutionary trajectory, spatiotemporal transmission, and pathogenic characterization of circulating LSDV in China. This study provides a unique reference for risk assessment, guiding diagnostics, and prevention in epizootic and non-epizootic areas.

Keywords: Dissemination; Lumpy skin disease virus; Phylogenetic; Pathogenicity; Surveillance

10. **Complete Coding Sequence of Lumpy Skin Disease Virus Isolated from Kinmen Island, Taiwan, in 2020,** Chih-Wei Huang, Lu-Jen Ting, Yu-Pin Liu, Yu-Ju Lin, Fan Lee, Chwei-Jang Chiou, John J. Dennehy, **Microbiology Resource Announcements**, Volume 11, Issue 4, 2022, https://doi.org/10.1128/mra.01204-21.

Abstract:

We reported the complete coding sequence of a lumpy skin disease virus (LSDV) isolated from cattle from Kinmen, Taiwan, in 2020. The nucleotide sequence of LSDV/KM/Taiwan/2020 was most closely related to strains from an outbreak in China and Vietnam in 2020 and clustered within the vaccine or vaccine-derived clade.

11. **Potential mechanical transmission of Lumpy skin disease virus (LSDV) by the stable fly (Stomoxys calcitrans) through regurgitation and defecation,** Anca I. Paslaru, Niels O. Verhulst, Lena M. Maurer, Alexsandra Brendle, Nicole Pauli, Andrea Vögtlin, Sandra Renzullo, Yelena Ruedin, Bernd Hoffmann, Paul R. Torgerson, Alexander Mathis, Eva Veronesi, **Current Research in Insect Science**, Volume 1, 2021, 100007, https://doi.org/10.1016/j.cris.2020.100007.

Abstract:

Lumpy skin disease (LSD) is a viral disorder of cattle caused by the lumpy skin disease virus (LSDV) which can induce severe infections leading to high economic losses. Being of African origin, the first LSD outbreaks in Europe occurred in Greece and later in the Balkan region. Little is known about the mode of transmission, especially in relation to the potential role of arthropods vectors. The purpose of our study was to investigate the role of Stomoxys calcitrans in the transmission of LSDV and their presence at different farms in Switzerland. Laboratory-reared flies were exposed to LSDV spiked-blood and incubated under a realistic fluctuating temperature regime. Body parts, regurgitated blood, and faecal samples were analysed by qPCR for the presence of viral DNA and infectious virus at different time points post-feeding (p.f.). LSDV DNA was detected in heads, bodies, and regurgitated blood up to three days p.f. and up to two days p.f. in the faeces. Infectious virus was isolated from bodies and faeces up to two days and in the regurgitated blood up to 12 h p.f. There was no increase in viral load, consolidating the role of S. calcitrans as mechanical vectors for LSDV. Stomoxys flies were present at all eight farms investigated, including a farm located at 2128 m asl. The persistence of LSDV in S. calcitrans in combination with the long flight ranges of this abundant and widespread fly might have implications on LSD epidemiology and on implementing control measures during disease outbreaks.

Keywords: Artificial feeding; Biting flies; Cattle infectious disease; Sticky traps; Virus excretion

12. **Mathematical study of lumpy skin disease with optimal control analysis through vaccination,** Azhar Iqbal Kashif Butt, Hassan Aftab, Muhammad Imran, Tariq Ismaeel, **Alexandria Engineering Journal**, Volume 72, 2023, Pages 247-259, https://doi.org/10.1016/j.aej.2023.03.073.

Abstract:

In this study, we develop a new mathematical model with vaccination to properly comprehend dynamics of the Lumpy Skin Disease (LSD) ailment. We analyze the model for the existence of a unique positive and bounded solution. To assess the contagiousness of the disease and to test the proposed model for local and global stability at the disease-free and endemic equilibrium points, we determine the reproduction number R0. We also investigate the influence of model parameters on reproduction number R0 by performing sensitivity analysis. The main objective of this study is to carry out different disease control techniques to determine the optimal one. As a first strategy, we analyze the effect of different constant vaccination rates and constant exposure rates on disease control. Secondly, we construct an optimal control problem to investigate the influence of vaccination on disease control with possible elimination from society. The numerical

findings reveal that the proposed optimal control strategy for control of LSD is more effective in lowering the number of infected animals.

Keywords: LSD; Vaccination; Existence and uniqueness; Local and global stabilities; Sensitivity analysis; Optimal control; Pontryagin maximum principle

13. **A novel mathematical study to understand the Lumpy skin disease (LSD) using modified parameterized approach,** Wafa F. Alfwzan, Mahmoud H. DarAssi, F.M. Allehiany, Muhammad Altaf Khan, Mohammad Y. Alshahrani, Elsayed M. Tag-eldin, **Results in Physics**, Volume 51, 2023, 106626, https://doi.org/10.1016/j.rinp.2023.106626.

Abstract:

The LSD mainly affects the cattle population and other animals, especially buffalo and cows. Due to the significant loss of dairy products and cattle population, it is necessary to highlight this issue by means of a mathematical modeling approach. We formulate a mathematical model for understanding LSD by taking all the possible routes that cause the disease to spread in the community. We study the basic results for the model and then obtain their possible equilibria. The model's local and global asymptotical stability analysis is shown for the basic reproduction number less than unity. We further find a list of suitable parameter values for the model parameters and present the graphical results of the model. A new approach to solve fractional order system has been given, and applied to the proposed model. For the model's sensitive parameters, we give a numerical simulation and show their impact on disease transmission.

Keywords: LSD; Mathematical model; Stability; Numerical results

14. **Protocol for next-generation sequencing of the LSD virus genome using an amplicon-based approach,** Rahul C. Bhoyar, Bani Jolly, Harie Vignesh, Lenin Bhatt, Vigneshwar Senthivel, Ravi Israni, Vinod Scaria, Sridhar Sivasubbu, **STAR Protocols**, Volume 5, Issue 3, 2024, 103020, https://doi.org/10.1016/j.xpro.2024.103020.

Summary

Lumpy skin disease (LSD) is a viral disease predominantly affecting cattle caused by a poxvirus belonging to the capripoxvirus genus. Here, we present a protocol for next-generation sequencing of the LSD virus genome using an amplicon-based approach. We describe steps for DNA extraction, viral DNA enrichment, amplicon pooling and purification, and library preparation

and pooling. We then detail procedures for sequencing and computational analysis. This protocol can be adapted to any Illumina sequencing platform as an accelerated and scalable system. For complete details on the use and execution of this protocol, please refer to Bhatt et al.1,2

Keywords: bioinformatics; sequence analysis; Genomics; sequencing; high-throughput screening

15. **An extensive investigation of convolutional neural network designs for the diagnosis of lumpy skin disease in dairy cows,** Dip Kumar Saha, **Heliyon**, Volume 10, Issue 14, 2024, e34242, https://doi.org/10.1016/j.heliyon.2024.e34242.

Abstract:

Cow diseases are a major source of concern for people. Some diseases in animals that are discovered in their early stages can be treated while they are still treatable. If lumpy skin disease (LSD) is not properly treated, it can result in significant financial losses for the farm animal industry. Animals like cows that sign this disease have their skin seriously affected. A reduction in milk production, reduced fertility, growth retardation, miscarriage, and occasionally death are all detrimental effects of this disease in cows. Over the past three months, LSD has affected thousands of cattle in nearly fifty districts across Bangladesh, causing cattle farmers to worry about their livelihood. Although the virus is very contagious, after receiving the right care for a few months, the affected cattle can be cured. The goal of this study was to use various deep learning and machine learning models to determine whether or not cows had lumpy disease. To accomplish this work, a Convolution neural network (CNN) based novel architecture is proposed for detecting the illness. The lumpy disease-affected area has been identified using image preprocessing and segmentation techniques. After the extraction of numerous features, our proposed model has been evaluated to classify LSD. Four CNN models, DenseNet, MobileNetV2, Xception, and InceptionResNetV2 were used to classify the framework, and evaluation metrics were computed to determine how well the classifiers worked. MobileNetV2 has been able to achieve 96% classification accuracy and an AUC score of 98% by comparing results with recently published relevant works, which seems both good and promising.

Keywords: Computer vision; Segmentation; CNN; MobileNetV2; LSD

16. **An Immunoperoxidase Monolayer Assay (IPMA) for the detection of lumpy skin disease antibodies,** Andy Haegeman, Ilse De Leeuw, Laurent Mostin, Willem Van

Campe, Laetitia Aerts, Maria Vastag, Kris De Clercq, **Journal of Virological Methods**, Volume 277, 2020, 113800, https://doi.org/10.1016/j.jviromet.2019.113800.

Abstract:

During this study a new Immunoperoxidase Monolayer Assay (IPMA) was developed for the detection of antibodies against lumpy skin disease virus (LSDV) in an easy and low tech setting. Using two dilutions (1:50 and 1:300) in a duplicate format, the test was shown to be highly sensitive, specific and repeatable. In comparison to the VNT and a commercial ELISA, the LSDV-IPMA was able to detect the LSDV antibodies earlier in infected, vaccinated and vaccinated/infected animals. The assay is very flexible as it can be easily adapted for the detection of sheeppox or goatpox antibodies and it can be scaled-up to handle medium size sample sets by preparing the IPMA plates in advance. These plates are safe and can be handled in low biosafety level labs.

Keywords: IPMA; LSDV; Antibodies

17. **Madin-Darby bovine kidney (MDBK) cells are a suitable cell line for the propagation and study of the bovine poxvirus lumpy skin disease virus,** Petra C. Fay, Charlotte G. Cook, Najith Wijesiriwardana, Gessica Tore, Loic Comtet, Alix Carpentier, Barbara Shih, Graham Freimanis, Ismar R. Haga, Philippa M. Beard, **Journal of Virological Methods**, Volume 285, 2020, 113943, https://doi.org/10.1016/j.jviromet.2020.113943.

Abstract:

Lumpy skin disease virus (LSDV) is a poxvirus that causes systemic disease in cattle, resulting in substantial economic loss to affected communities. LSDV is a rapidly emerging pathogen of growing global concern that recently spread from Africa and the Middle East into Europe and Asia, impacting the cattle population in these regions. An increase in research efforts into LSDV is required to address key knowledge gaps, however this is hampered by lack of suitable cell lines on which to propagate and study the virus. In this work we describe the replication and spread of LSDV on Madin-Darby bovine kidney (MDBK) cells, and the formation of foci-type poxvirus plaques by LSDV on MDBK cells. Methods utilising MDBK cells to quantify neutralising antibodies to LSDV, and to purify LSDV genomic DNA suitable for short read sequencing are described. These research methods broaden the tools available for LSDV researchers and will facilitate the gathering of evidence to underpin the development of LSD control and prevention programmes.

Keywords: Lumpy skin disease virus; Poxvirus; Capripoxvirus; Neutralization; Viral genome sequencing

18. **Complete Coding Sequence of a Lumpy Skin Disease Virus from an Outbreak in Bulgaria in 2016,** Elisabeth Mathijs, Frank Vandenbussche, Emiliya Ivanova, Andy Haegeman, Laetitia Aerts, Ilse De Leeuw, Steven Van Borm, Kris De Clercq, Jelle Matthijnssens, **Microbiology Resource Announcements**, Volume 9, Issue 43, 2020, https://doi.org/10.1128/mra.00977-20.

Abstract:

Lumpy skin disease (LSD) is an emerging cattle disease with serious economic consequences. We report the complete coding sequence of LSD virus 210LSD-249/BUL/16, detected in a blood sample from a diseased cow during an outbreak in Bulgaria (Kabile Village, Yambol Region) in June 2016.

19. **In-silico characterization of LSDV132 protein divulged its BCL-2-like nature,** Muhammad Farhan Sarwar, Qurat ul Ain Waseem, Mudassar Fareed Awan, Sajed Ali, Ajaz Ahmad, Saif ul Malook, Qurban Ali, **Heliyon**, Volume 10, Issue 6, 2024, e27657, https://doi.org/10.1016/j.heliyon.2024.e27657.

Abstract:

Lumpy skin disease virus (LSDV) belongs to Poxviridae family. This virus possesses various proteins which impart potential functions to it including assembly of newly synthesized viruses in the replication cycle and forming their structure. LSDV132 protein is also one of such proteins. Its key characteristics were unknown because, no any relevant study was reported about it. This study aimed to investigate its characteristic features and essential functions using several bioinformatics techniques. These analyses included physiochemical characterization and exploring the crucial functional and structural perspectives. Upon analysis of the physiochemical properties, the instability index was computed to be 30.89% which proposed LSDV132 protein to be a stable protein. Afterwards, the phosphorylation sites were explored. Several sites were found in this regard which led to the hypothesis that it might be involved in the regulation of apoptosis and cell signaling, among other cellular processes. Furthermore, the KEGG analysis and the analysis of protein family classification confirmed that the LSDV132 protein possessed Poxvirus-BCL-2-like motifs, indicating that it might be responsible in modulating the apoptosis of host cells. This crucial finding suggested that the protein under study possessed BCL-2-like features. Proceeding this very important finding, the molecular docking analysis was performed. In this context, various viral BCL-2 inhibitors were retrieved from the ChEMBL database for docking purpose. The docking results revealed that pelcitoclax exhibited best docking scores i.e.,

−9.1841 kcal/mol, among all of the other docked complexes. This fact signified that this compound might serve as an inhibitor of LSDV132 protein.

Keywords: BCL-2-like protein; In-silico analysis; Lumpy skin disease virus (LSDV); LSDV132 protein; Virtual screening

20. **Coding-Complete Genome Sequence of a Lumpy Skin Disease Virus Isolated during the 2021 Thailand Outbreak,** Weena Paungpin, Ladawan Sariya, Somjit Chaiwattanarungruengpaisan, Metawee Thongdee, Bunlue Kornmatitsuk, Akarapong Jitwongwai, Sarawut Taksinoros, Kripitch Sutummaporn, Sookruetai Boonmasawai, Chowalit Nakthong, Jelle Matthijnssens, **Microbiology Resource Announcements**, Volume 11, Issue 8, 2022, https://doi.org/10.1128/mra.00375-22.

Abstract:

Lumpy skin disease (LSD) is an economically devastating and transboundary disease in cattle. Here, we report the coding-complete genome sequence of the LSDV72/PrachuapKhiriKhan/Thailand/2021 strain, which was isolated from an affected cow during the first LSD outbreak in Thailand in 2021. The sequence will be beneficial for future genomic studies of the virus.

21. **Diagnostic utility of intranodular saline lavage in TaqMan probe-based real-time PCR diagnosis of lumpy skin disease,** Ajay Pratap Singh, Nidhi Dangi, Prachi Singh, Vinod Kumar Singh, Shyama N Prabhu, Neeraj Kumar Gangwar, Sanchay Kumar Biswas, **Emerging Animal Species**, Volume 10, 2024, 100037, https://doi.org/10.1016/j.eas.2023.100037.

Abstract:

Lumpy skin disease (LSD), caused by the poxvirus lumpy skin disease virus has entered India, causing serious economic consequences for the Indian dairy sector. To evaluate the diagnostic value of intranodular saline lavage in the identification of LSD-infected animals, skin nodule tissue biopsy, intranodular saline lavage, whole blood, and nasal swab specimens were collected simultaneously from LSD-symptomatic animals. TaqMan probe-based real-time PCR was performed targeting the EEV glycoprotein gene (LSDV126) and the results were compared. qPCR analysis could detect LSDV in all the skin nodule tissue biopsy and intranodular saline lavage. The mean cycle threshold (Cq) values of skin nodule tissue biopsy samples (23.94 ± 2.97) were also comparable with intranodular saline lavage (25.23 ± 2.41) samples. Whole blood and nasal swabs

have an extremely poor detection rate for PCR-based viral detection.Our findings demonstrate that intranodular saline lavage is an excellent alternative specimen for the detection of LSDV. Taking into consideration, the simplicity of specimen collection, intranodular saline lavage could be adopted in field conditions for accurate LSDV surveillance testing.

Keywords: Lumpy skin disease; Clinical sample; real-time PCR; EEV glycoprotein; Diagnosis

22. **Prevalence of tick-borne haemoparasites and their perceived co-occurrences with viral outbreaks of FMD and LSD and their associated factors,** Osama Abas, Amir Abd-Elrahman, Asmaa Saleh, Mohamed Bessat, **Heliyon**, Volume 7, Issue 3, 2021, e06479, https://doi.org/10.1016/j.heliyon.2021.e06479.

Abstract:

Species of Theileria, Babesia, and Anaplasma are Tick-borne pathogens (TBPs) that are prevalent throughout the world, particularly in the tropical and subtropical regions. Associated diseases of Theileriosis, Babesiosis, and Anaplasmosis, respectively, represents a major threat to livestock production in many countries. TBPs have a high prevalence in different geographical locations in Egypt. Foot and mouth disease (FMD) and Lumpy skin disease (LSD) are considered endemic bovine viral diseases in Egypt. Our clinical observations during the epidemics of LSD and FMD viruses showed higher prevalence rates for the TBPs. To investigate this correlation, a total of 670 samples from cattle and buffalo were collected during the summers of 2017 and 2018 distributed throughout ranches and smallholders in two geographical locations in Egypt. Two farms with a recent clinical outbreak of LSD with a total of 270 animals, while the other location included three farms with a recent FMD outbreak with a combined 400 cattle. Examined animals were classified mainly according to age, gender, species, breed (native versus crossbred), and the presence of ticks. Whole blood samples were collected for TBPs and viral (LSD and FMD) examinations, while tissue specimens were collected for detection of FMD and LSD viruses by real-time PCR. Our results confirmed significantly higher prevalence rates for the TBPs in LSD-positive than LSD-negative animals, while no significant difference could be detected for the prevalence rate of the TBPs in the FMD positive and negative groups. The prevalence of Babesia and Theileria was significantly ($P < 0.05$) higher in cross-breeds than native cattle. Infections with Anaplasma and co-infections with Babesia-Anaplasma and Theileria-Anaplasma were significantly higher in native than cross-breeds cattle. The intensity of parasitic infection (parasitemia) has a significant difference in the positive groups for the two viruses compared to the negative groups. These results collectively confirming the enhancing role of LSD on the prevalence rate of the haemoprotozoal infections leading to more serious outcomes to the

livestock infections, and therefore the control of haemoprotozoal infections should be implemented as a part of viral epidemics control.

Keywords: Tick-borne pathogens; Babesia; Anaplasma; Theileria; Foot and mouth disease; Lumpy skin disease; Egypt

23. **Molecular Detection of Lumpy Skin Disease Virus in Malaysia 2021,** C.K. Khoo, R. Dahlan, Z. Mat Desa, P.N.A. Syarina, S.S.H. Mohd. Salim, Z. Barker, M.H. Abu Hassan, R. Hassan, F.H. Mohd Saeid, **International Journal of Infectious Diseases**, Volume 116, Supplement, 2022, Page S64, https://doi.org/10.1016/j.ijid.2021.12.150.

Abstract:

Purpose

Lumpy skin disease (LSD) is an emerging transboundary notifiable viral disease by the World Organisation for Animal Health (OIE). A member of Capripoxvirus within the Poxviridae family, LSD virus (LSDV) caused loss of production, infertility, damage to hides and mortality, leading to significant social-economic implications. Originated from the Africa continent, LSD has never been reported in Malaysia before but recently detected in several areas in Asia including Thailand. In May 2021, reports and samples of unknown skin disease in dairy cattle were presented for laboratory diagnosis to confirm provisional LSD clinical diagnosis. This study aims to molecular detects and confirms the causative agent to enable subsequent control measures to be applied.

Methods & Materials

Three out of 11 dairy cattle from a dairy farm in Perak were showing clinical signs with nodules spotted on the skin of animals. Skin nodule (n=3) and whole blood (n=11) were sampled and tested for LSDV by PCR to confirm the presence of LSDV nucleic acids. The amplicon obtained was subsequently sequenced by Sanger sequencing.

Results

All three skin nodule samples were positive for Capripoxvirus by PCR. The nucleotide sequence homology analysis indicates high nucleotide homology to LSDV, confirming the first molecular detection of LSDV in Malaysia. Conversely, all blood samples were negative for Capripoxvirus by PCR.

Conclusion

We detected and confirmed the LSD outbreak in Malaysia. Our result indicates transboundary expansion of LSD in the region. This emphasized the importance of tighten border control and lab preparedness to prevent disease introduction and rapid detection of disease. Following this, surveillance, stamping out of the infected animals, suspended the import of animals from infected country and animal movement were carried out and imposed to contain and control the spreading of LSD.

24. **Development of a paper-based fluorescent carbon quantum dots MIPs sensor for selective detection of lumpy skin disease virus,** Dalia M. El-Husseini, Dalia M. A. Elmasry, Eman M. Abo Hatab, Samr Kassem, **RSC Advances**, Volume 14, Issue 37, 2024, Pages 27438-27448, https://doi.org/10.1039/d4ra04895d.

Abstract:

Lumpy skin disease (LSD) is a contagious viral disease caused by the Lumpy Skin Disease virus (LSDV), a member of the Capripoxviridae family. Traditional LSDV diagnostic procedures proved to have challenges in terms of cross reactivity as well as limited sensitivity and specificity. Herein, we combined molecularly imprinted polymers (MIPs) and quantum dots (QDs) technology to develop a paper-based turn on fluorescence sensor for rapid, sensitive and selective detection of LSDV. Under optimal conditions, the sensor showed linear enhancement in fluorescence intensity with the increase of LSDV concentration and exhibited a detection limit of 101 log10 TCID50 per ml. It also presented high specificity towards LSDV compared to other viruses viz sheep pox virus (SPV). Furthermore, the proposed sensor was successfully tested with spiked and real LSDV samples, proving its potential to serve as a sensitive selective sensor for LSDV diagnosis. Based on our knowledge, this is the first record of a paper-based diagnostic sensor for LSDV utilizing a CQDs-MIPs turn-on mechanism.

25. **Qualitative assessment of the probability of introduction and onward transmission of lumpy skin disease in Ukraine,**Dima Farra, Marco De Nardi, Viktoria Lets, Sergii Holopura, Oleksiy Klymenok, Roger Stephan, Oksana Boreiko**, Microbial Risk Analysis**, Volume 20, 2022, 100200, https://doi.org/10.1016/j.mran.2021.100200.

Abstract:

Lumpy skin disease (LSD) is a transboundary disease affecting bovine animals, which may result in severe economic implications. Ukraine is considered particularly vulnerable to LSD due to its proximity to regions where the virus is circulating. In addition, its ecological and environmental

parameters can sustain, in summer, the spread of the disease in case it entered the country. This qualitative risk assessment aimed to investigate the probability that LSD virus is introduced to Ukraine and, if introduced, what would be the probability of onward transmission in the country within the next year. The risk assessment followed the OIE import risk analysis for animals and animal products guidelines and was undertaken with the support of local experts via an expert elicitation workshop. A modified Delphi approach was used to gather experts inputs. The illegally traded cattle was the pathway considered to have the highest probability of LSD introduction; however the probability was estimated to be low. When assessing the probability of an animal being exposed to the virus and further onward transmission in Ukraine, the highest probability estimate was related to flying vectors (high probability). During the expert opinion workshop, the Delphi approach helped to increase the agreement between experts and to assess the uncertainty related to some of the probability estimates. Throughout the risk assessment, some data gaps were identified and highlighted. The lack of reliable data on animal movements and biosecurity in Ukraine were emphasized. Based on the elicited probability estimates, the local experts generated recommendations for risk management practices. To our knowledge, this is the first risk assessment performed on LSDV in Eastern Europe and the conceptual framework adopted can help other countries willing to do a risk assessment in a similar data scarce environment.

Keywords: Lumpy Skin Disease (LSD); Risk Assessment; IE; Ukraine

26. **Genome Sequence of Atyrau-5BJN(IL18), a Recombinant Lumpy Skin Disease Virus with Knockout of Virulence Genes,** Aisha U. Issabek, Mukhit B. Orynbayev, Kulyaisan T. Sultankulova, Asylulan Amirgazin, Kunsulu D. Zakarya, Zamira Omarova, Olga V. Chervyakova, Simon Roux, **Microbiology Resource Announcements**, Volume 11, Issue 7, 2022, https://doi.org/10.1128/mra.00380-22.

Abstract:

Here, we present the coding sequence of the genome of the recombinant lumpy skin disease virus (LSDV) Atyrau-5BJN(IL18), obtained by knocking out four genes in the genome of a virulent field LSDV isolate. Genome sequencing confirmed the deletion of genes and the insertion of a foreign sequence in the viral genome.

27. **Long-term monitoring of immune response to recombinant lumpy skin disease virus in dairy cattle from small-household farms in western Thailand,** Nutthakarn Suwankitwat, Kultyarat Bhakha, Lamul Molee, Tapanut Songkasupa, Kanokwan Puangjinda, Tapakorn

Chamchoy, Orapun Arjkumpa, Bandit Nuansrichay, Smit Srisomrun, Phitcha Pongphitcha, Porntippa Lekcharoensuk, Pipat Arunvipas, **Microbiology and Infectious Diseases**, Volume 99, 2023, 102008, https://doi.org/10.1016/j.cimid.2023.102008.

Abstract:

Lumpy skin disease (LSD) was firstly reported in Thailand in 2021 which affected the cattle industry. However, there is limited information on the immune response of LSDV infection in Thailand where recombinant vaccine strain circulated. The aim of this research was to study the duration of LSD immune response of subclinical and clinical animals after natural infection in dairy cattle. Sixty-six dairy cattle from ten farms in central and western regions of Thailand were investigated. Antibody was detected by virus neutralization test and ELISA. Cell mediated immunity (CMI)-related cytokine gene expressions were evaluated. Antibody was detected until at least 15 months after the noticeable symptom. Cattle with subclinical disease had lower antibody levels compared to animals which had clinical disease. IFN-γ and TNF-α levels were increased, while IL-10 level was decreased in the infected animals compared to the controls. This study elucidated immune responses in dairy cattle herd affected by recombinant LSDV.

Keywords: Lumpy skin disease; Antibody; Cell-mediated immunity; Thailand

28. **Genomic Sequence of the New Attenuated Vaccine Strain Neethling-RIBSP of the Lumpy Skin Disease Virus,** M. B. Orynbayev, R. K. Nissanova, T. U. Argimbayeva, K. D. Zakarya, B. S. Myrzakhmetova, A. M. Melisbek, S. M. Barmak, A. U. Issabek, A. K. Nakhanov, A. Shevtsov, N. S. Kozhabergenov, K. T. Sultankulova, Jelle Matthijnssens, **Microbiology Resource Announcements**, Volume 9, Issue 26, 2020, https://doi.org/10.1128/mra.00318-20.

Abstract:

We report here the draft genome sequence of the new attenuated strain Neethling-RIBSP of the lumpy skin disease virus, obtained by sequential and alternating passages in cell culture and developing chicken embryos. Genome sequencing allowed the identification of differentiation markers of the new strain.

29. **A deterministic mathematical model with non-linear least squares method for investigating the transmission dynamics of lumpy skin disease,** Edwiga Renald, Verdiana G. Masanja, Jean M. Tchuenche, Joram Buza, **Healthcare Analytics**, Volume 5, 2024, 100343, https://doi.org/10.1016/j.health.2024.100343.

Abstract:

Lumpy skin disease (LSD) is an economically significant viral disease of cattle caused by the lumpy disease virus (LSDV) which is primarily spread mechanically by blood feeding vectors such as particular species in flies, mosquitoes and ticks. Despite efforts to control its spread, LSD has been expanding geographically, posing challenges for effective control measures. This study develops a Susceptible–Exposed–Infectious–Recovered–Susceptible (SEIRS) model that incorporates cattle and vector populations to investigate LSD transmission dynamics. The model considers the waning rate of natural active immunity in recovered cattle, disease-induced mortality, and the biting rate. Using a standard dynamical system approach, we conducted a qualitative analysis of the model, defining the invariant region, establishing conditions for solution positivity, computing the basic reproduction number, and examining the stability of disease-free and endemic equilibria. We employ a non-linear least squares method for model calibration, fitting it to a synthetic dataset. We subsequently test it with actual infectious cases data. Results from the calibration and testing phases demonstrate the model's validity and reliability for diverse settings. Local and global sensitivity analyses were conducted to determine the model's robustness to parameter values. The biting rate emerged as the most significant parameter, followed by the probabilities of infection from either population and the recovery rate. Additionally, the waning rate of LSD infection-induced immunity gained positive significance in LSD prevalence from the beginning of the infectious period onward. Simulation results suggest reducing the biting rate as the most effective LSD control measure, which can be achieved by applying vector repellents in cattle farms/herds, thereby mitigating the disease's prevalence in both cattle and vector populations and reducing the chances of infection from either population. Furthermore, measures aiming to boost LSD infection-induced immunity upon recovery are recommended to preserve the immune systems of the cattle population.

Keywords: Deterministic mathematical model; Non-linear least squares; SEIRS model; Endemic equilibria; Invariant region; Lumpy skin disease

30. **Is it time to define vaccines to be used for lumpy skin disease?,** Krishna Prasad Acharya, Bhoj Raj Singh, **Health Sciences Review**, Volume 12, 2024, 100192, https://doi.org/10.1016/j.hsr.2024.100192.

Abstract:

Only homologous LSD vaccine should be used in absence of efficacy of experimental studies indicating the effectiveness of heterologous LSD vaccine.

Keywords: LSD; Homologous vaccines; Heterologous vaccines; Vaccine efficacy