

WOAH Reference Laboratory for Lumpy skin disease







Funded by the European Union

for Capripox viruses

EU Reference Laboratory



Food and Agriculture Organization of the United Nations

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EURL FOR CAPRIPOX VIRUSES

LATEST ACTIVITIES ON LUMPY SKIN DISEASE AND UPDATE ON DIAGNOSIS

Nick De Regge

Online meeting – GF-TAD SGE LSD Europe

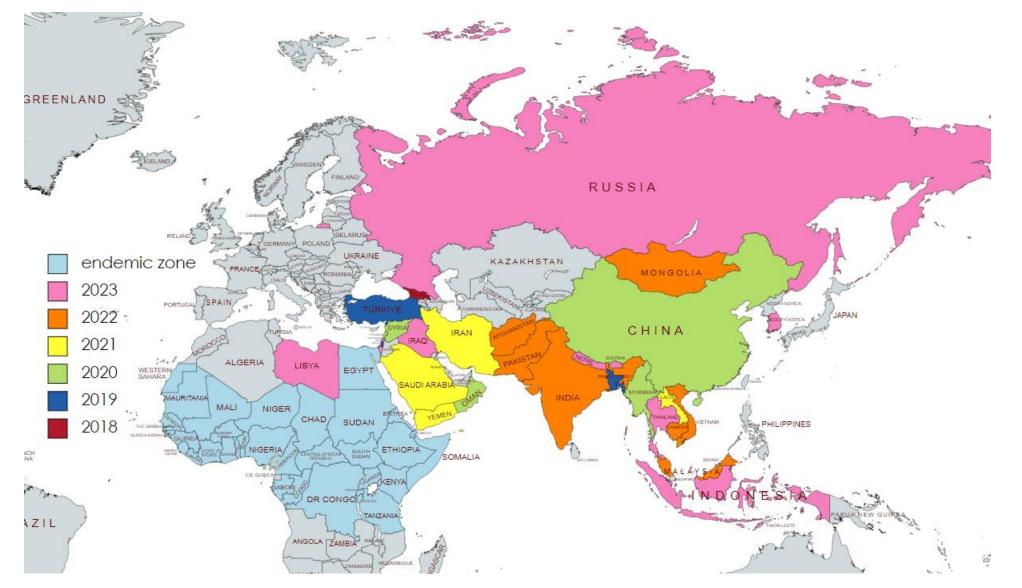
21 February 2024



- Current epidemiological situation LSDV
- LSDV diagnosis: serology
- LSDV diagnosis: virology
- LSDV vaccines: protection against recombinant strain
- LSDV transmission: non-vector transmission of the recombinant strain
- Training and support

Most recent reported LSDV outbreaks (2018 – 12/2023)

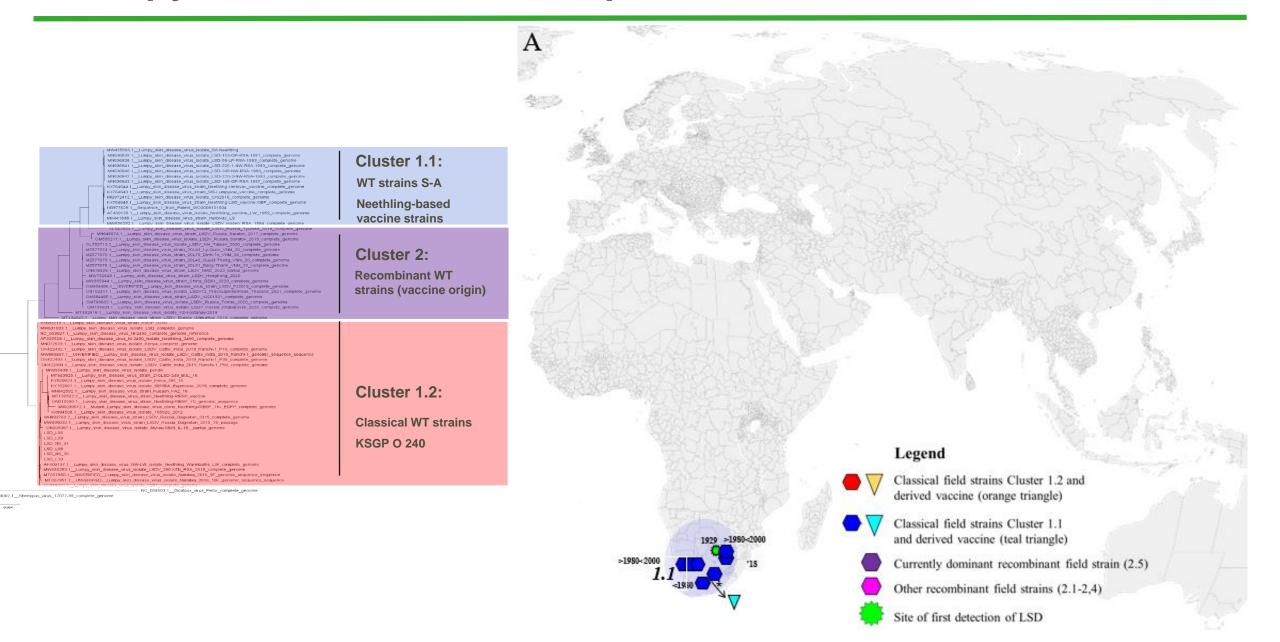
Data extracted from WOAH-WAHIS database

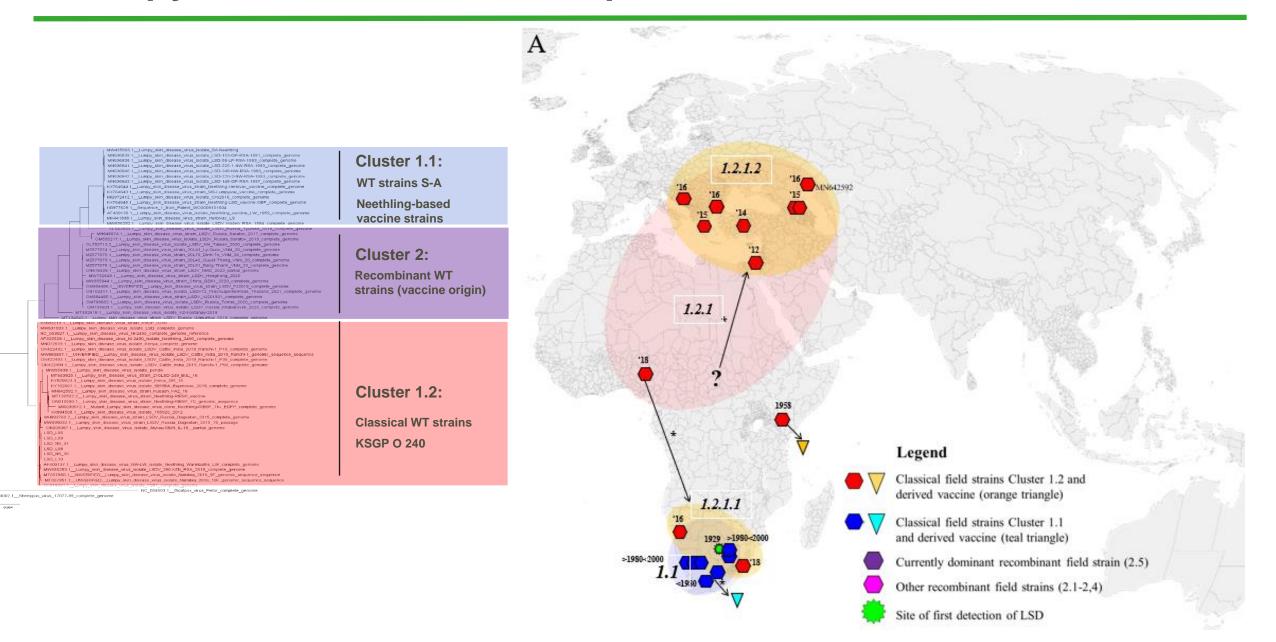


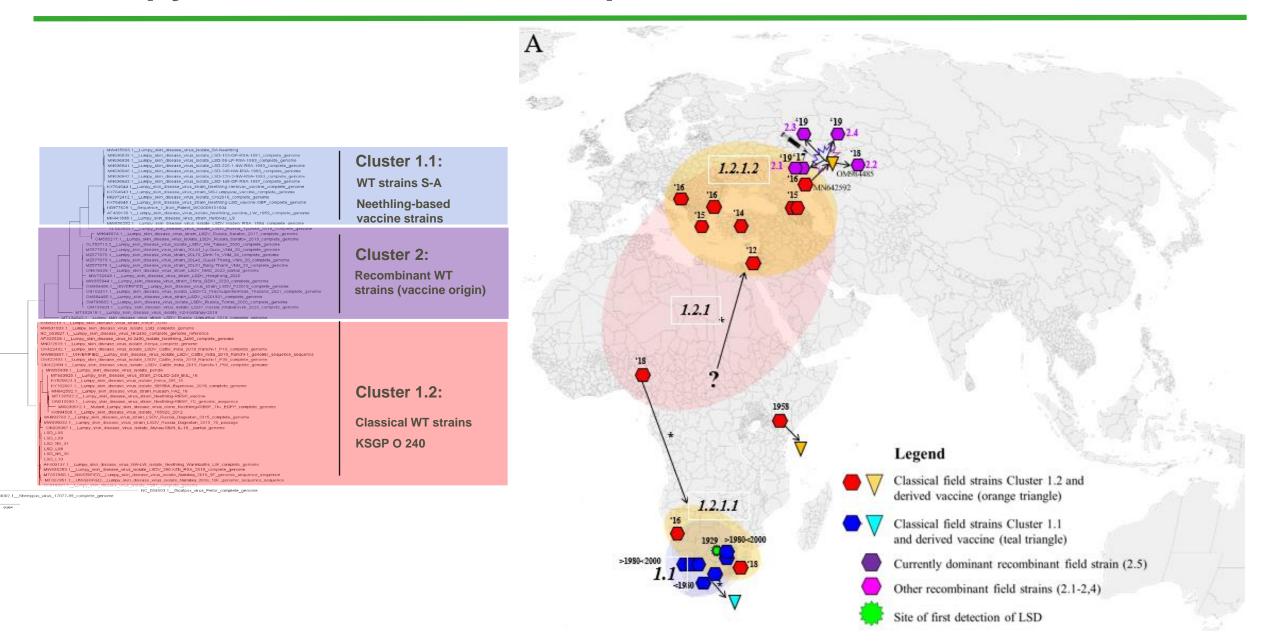
Lumpy skin disease virus: phylogeny

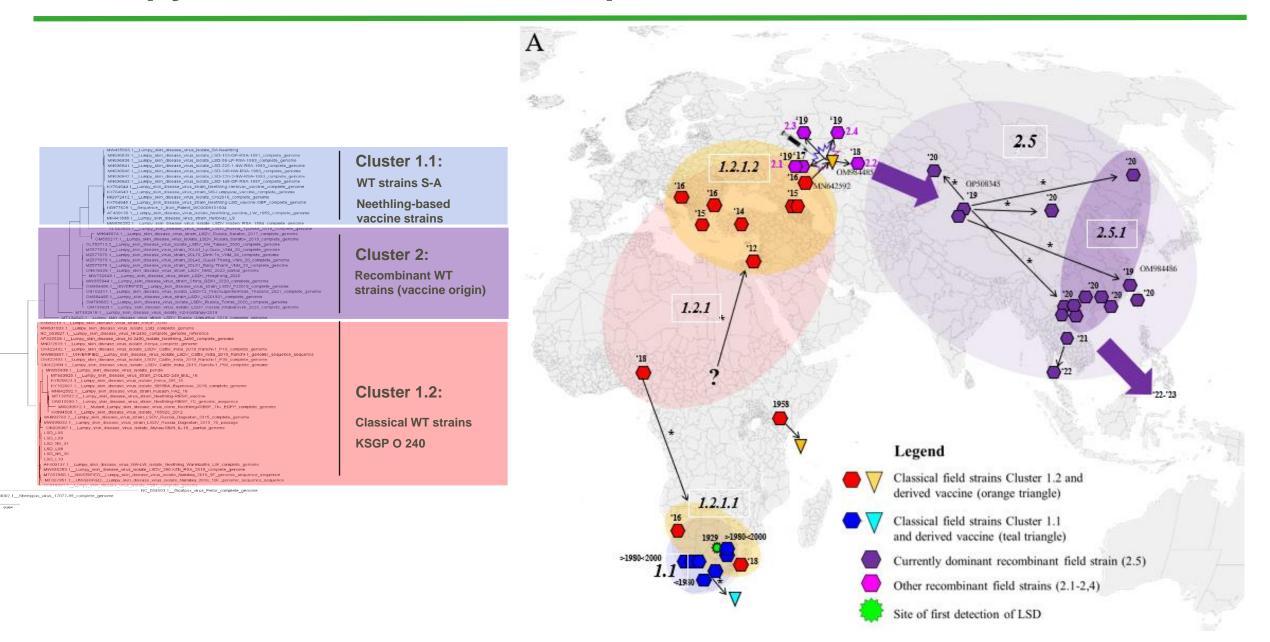
Article Lumpy Skin Disease Virus Genome Sequence Analysis: Putative Spatio-Temporal Epidemiology, Single Gene versus Whole Genome Phylogeny and Genomic Evolution Floris C. Breman *, Andy Haegeman, Nina Krešić, Wannes Philips and Nick De Regge	MW435866.1_Lumpy_skin_disease_virus_isolate_SA-Neethling MN636839.1_Lumpy_skin_disease_virus_isolate_LSD-D3-GP-RSA-1991_complete_genome MN636838.1_Lumpy_skin_disease_virus_isolate_LSD-220-1-NW-RSA-1993_complete_genome MN636840.1_Lumpy_skin_disease_virus_isolate_LSD-248-NW-RSA-1993_complete_genome MN636840.1_Lumpy_skin_disease_virus_isolate_LSD-248-NW-RSA-1993_complete_genome MN636840.1_Lumpy_skin_disease_virus_isolate_LSD-248-NW-RSA-1993_complete_genome MN636843.1_Lumpy_skin_disease_virus_isolate_LSD-248-NW-RSA-1993_complete_genome MN636843.1_Lumpy_skin_disease_virus_strain_Neethling-Herbixac_vaccine_complete_genome Kx764644.1_Lumpy_skin_disease_virus_strain_Neethling-Herbixac_vaccine_complete_genome Kx764644.1_Lumpy_skin_disease_virus_strain_Neethling-LSD-vaccine_complete_genome MK636252.1_Lumpy_skin_disease_virus_strain_Neethling_LSD_vaccine_complete_genome MK636252.1_Lumpy_skin_disease_virus_strain_Neethling_LSD_vaccine_complete_genome MK636252.1_Lumpy_skin_disease_virus_strain_Herbixac_LSD MK636252.1_Lumpy_skin_disease_virus_strain_Herbixac_LSD	Cluster 1.1: WT strains S-A Neethling-based vaccine strains	
	 OLS42833 1_Lumpy_skin_disease_virus_isolate_LSUV_Russia_lyumen_2019_complete_genome MH646674 1, Lumpy_skin_disease_virus_isolate_LSDV_Russia_Saratov_2017_complete_genome OK530217.1_Lumpy_skin_disease_virus_isolate_LSDV_RW_Tawan_2020_complete_genome OL752713.2_Lumpy_skin_disease_virus_isolate_LSDV_KM_Tawan_2020_complete_genome MZ577075.1_Lumpy_skin_disease_virus_isolate_LSDV_KM_Tawan_2020_complete_genome MZ577075.1_Lumpy_skin_disease_virus_isolate_LSDV_KM_Tawan_2020_complete_genome MZ577075.1_Lumpy_skin_disease_virus_isolate_DSV_KM_20_complete_genome MZ577075.1_Lumpy_skin_disease_virus_isolate_DSV_KMG_2020_complete_genome MZ577075.1_Lumpy_skin_disease_virus_isolate_DSV_KMG_2020_partial_genome ONI516408.1_Lumpy_skin_disease_virus_isolate_DSV_KMG_2020_complete_genome OMI93644.1_Lumpy_skin_disease_virus_isolate_DSV_KMG_2020_complete_genome OMI93648.1_UMPY_skin_disease_virus_isolate_DSV_KJ2019_Complete_genome OMI93648.1_LUMPY_skin_disease_virus_isolate_DSV_KJ20190_complete_genome OMI93648.1_LUMPY_skin_disease_virus_isolate_LSDV_ZP_rachuapKhirikhan_Thalland_2021_complete_genome OMI93663.1_Lumpy_skin_disease_virus_isolate_LSDV_Russia_Tomsk_2020_complete_genome OMI93663.1_Lumpy_skin_disease_virus_isolate_LSDV_Russia_Tomsk_2020_complete_genome OMI93663.1_LUMPY_skin_disease_virus_isolate_LSDV_Russia_Tomsk_2020_complete_genome 	Cluster 2: Recombinant WT strains (vaccine origin)	Origin: badly produced LSDV vaccine containing neethling strain, KSGP strain, and recombinants between both
	M1992618 1_Lumpy_skin_disease_virus_tsials_EK2K-kostanay-2018 MT134042.1_Lumpy_skin_disease_virus_USDV_Russia_Udmurtya_2019_complete_genome MX6931933.1_Lumpy_skin_disease_virus_Strain_KSOM_U240 MX6931933.1_Lumpy_skin_disease_virus_ISolate_LSD_complete_genome AF325528.1_Lumpy_skin_disease_virus_ISolate_KSDV_Cattle_India_2019_Ranchi-1_P10_complete_genome MX072619.1_Lumpy_skin_disease_virus_ISolate_KSDV_Cattle_India_2019_Ranchi-1_P10_complete_genome OK422492.1_Lumpy_skin_disease_virus_ISolate_LSDV_Cattle_India_2019_Ranchi-1_P10_complete_genome OK422493.1_Lumpy_skin_disease_virus_ISolate_LSDV_Cattle_India_2019_Ranchi-1_P30_complete_genome OK422493.1_Lumpy_skin_disease_virus_Isolate_LSDV_Cattle_India_2019_Ranchi-1_P50_complete_genome OK422493.1_Lumpy_skin_disease_virus_Isolate_LSDV_Cattle_India_2019_Ranchi-1_P50_complete_genome OK422493.1_Lumpy_skin_disease_virus_Isolate_ESREN_Cattle_India_2019_Ranchi-1_P50_complete_genome OK422493.1_Lumpy_skin_disease_virus_Isolate_ESREN_Cattle_India_2019_Ranchi-1_P50_complete_genome OK422493.1_Lumpy_skin_disease_virus_Isolate_ESREN_2015 OK42251_Lumpy_skin_disease_virus_Isolate_ESREN_2016 MT1030502_Lumpy_skin_disease_virus_Isolate_ESREN_2016 MT1030502_Lumpy_skin_disease_virus_strain_Neethling-RIBSP_TKGenomic_sequence MV0030512.1_Mutant_Lumpy_skin_disease_virus_Isolate_ISDSP_C129000000000000000000000000000000000000	Cluster 1.2: Classical WT strains	
	MH993760.2_LLImpy_skin_disease_virus_strain_LSUV_Russia_Dagestan_2016_76_passage - ON005067.1_Lumpy_skin_disease_virus_strain_LSUV_Russia_Dagestan_2016_76_passage - ON005067.1_Lumpy_skin_disease_virus_isolate_Atyrau-SBJN_IL-18_partial_genome I LSD_L06 LSD_NS_30 LSD_L08 LSD_L10 - AF409137.1_Lumpy_skin_disease_virus_NW-LW_isolate_Neething_Warmbaths_LW_complete_genome MW656253.1_Lumpy_skin_disease_virus_Solate_LSDV_280-K2N_RSA_2018_complete_genome MW0565253.1_LUMPy_skin_disease_virus_isolate_LSDV_280-K2N_RSA_2018_complete_genome MW0565253.1_LUMPy_skin_disease_virus_isolate_LSDV_280-K2N_RSA_2018_complete_genome MW0565253.1_LUMPy_skin_disease_virus_isolate_LSDV_280-K2N_RSA_2018_complete_genome - MT007351.1_UNVERIFIED_Lumpy_skin_disease_virus_isolate_Namibia_2016_10F_genomic_sequence_sequence - OK318001.1_1_Lumpy_skin_disease_virus_isolate_V381_complete_genome	KSGP O 240	

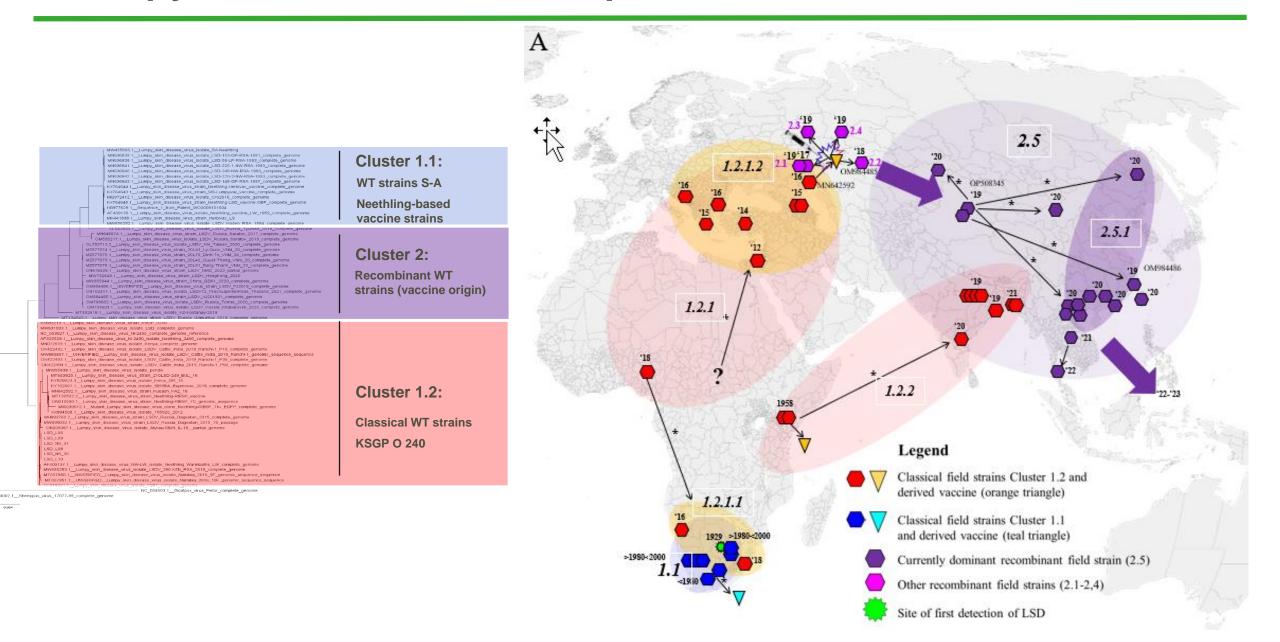
NC_004002.1__Sheeppox_virus_17077-99_complete_genome

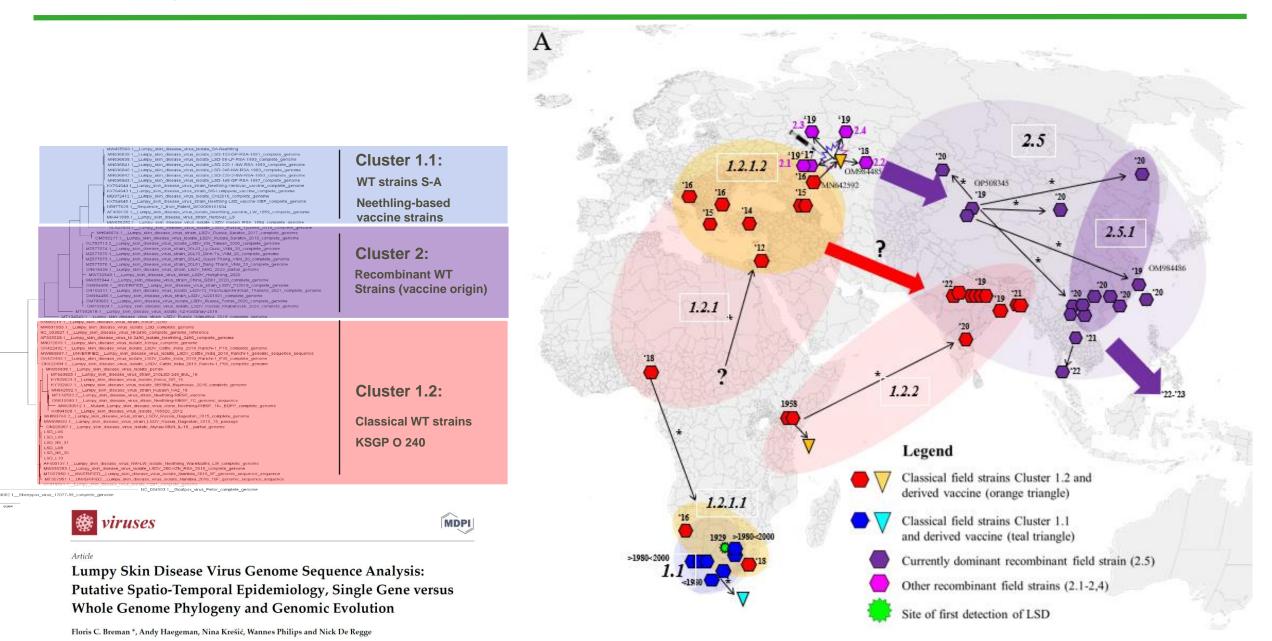






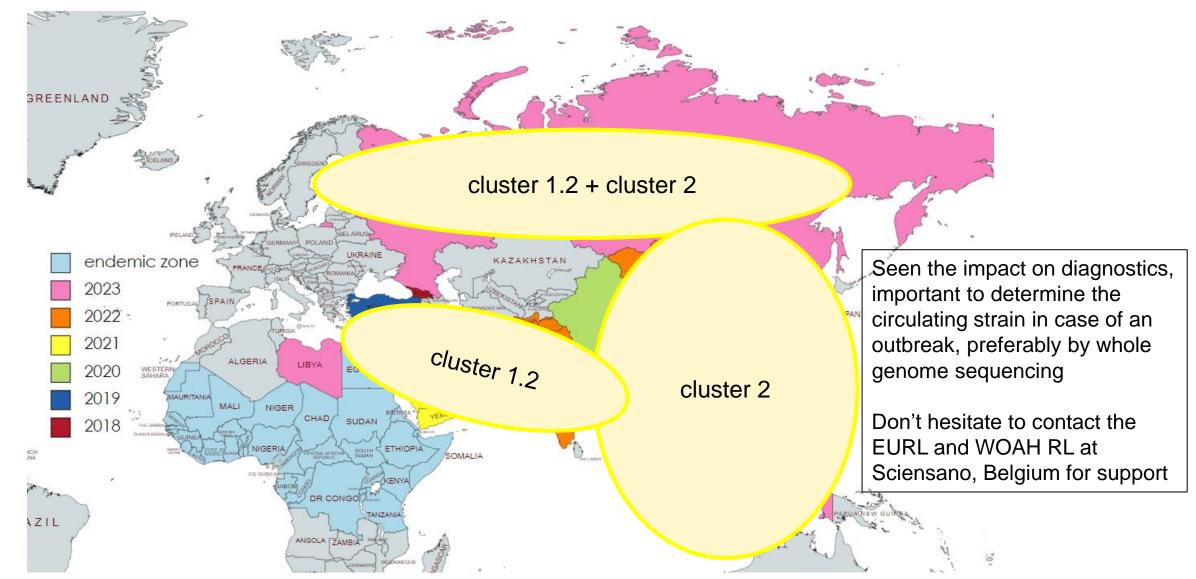






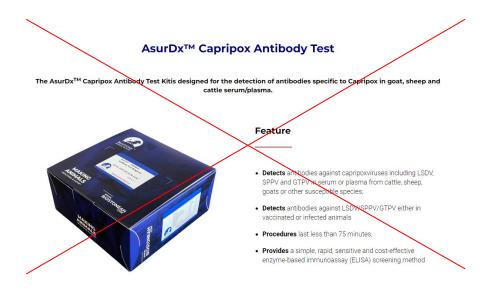
Most recent reported LSDV outbreak (2018 – 12/2023)





LSDV diagnosis - serology

- VNT IPMA commercial ELISA (ID-Vet)
- Unsatisfactory ELISA:



• Experimental DIVA ELISA:





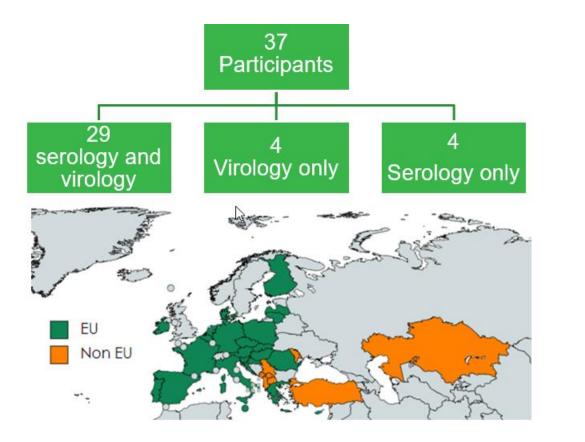
Article

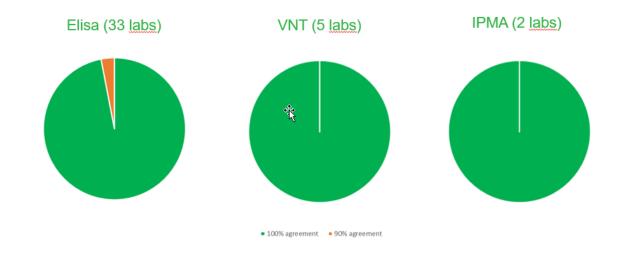
Harnessing Attenuation-Related Mutations of Viral Genomes: Development of a Serological Assay to Differentiate between Capripoxvirus-Infected and -Vaccinated Animals

Francisco J. Berguido ^{1,2,*}, Tesfaye Rufael Chibssa ³, Angelika Loitsch ⁴, Yang Liu ⁵, Kiril Krstevski ⁶, Igor Djadjovski ⁶, Eeva Tuppurainen ⁷, Tamaš Petrović ⁸, Dejan Vidanović ⁹, Philippe Caufour ¹⁰, Tirumala Bharani K. Settypalli ¹⁰, Clemens Grünwald-Gruber ¹¹, Reingard Grabherr ²⁰, Adama Diallo ¹², Giovanni Cattoli ¹ and Charles Euloge Lamien ¹⁰

LSDV diagnosis - serology

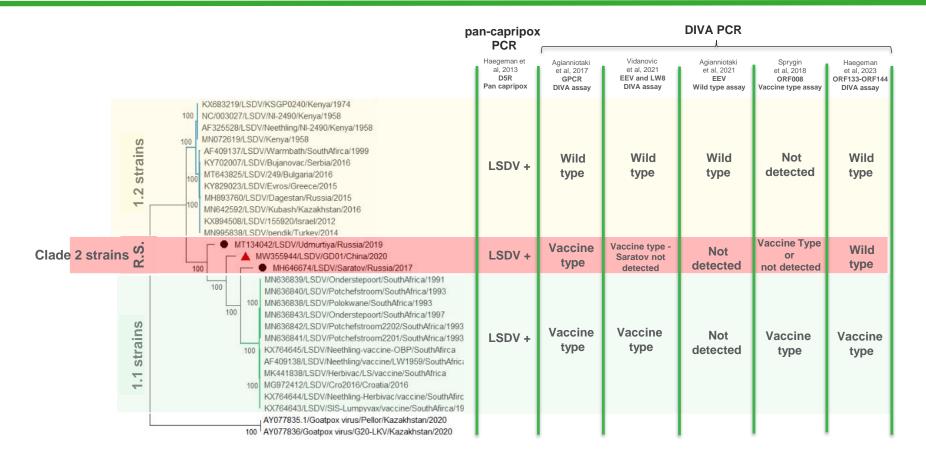
• Proficiency test 2023





For the detection of <u>specific antibodies to capripox</u> virus in bovine and ovine sera, 33 out of 33 participating laboratories performed satisfactory for all performed tests.

LSDV diagnosis - virology

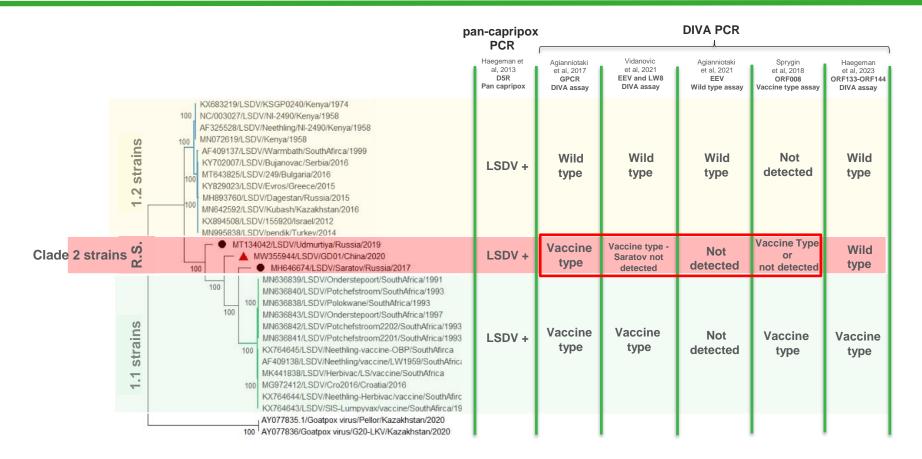


DIVA PCRs are important to differentiate adverse reactions after vaccination from clinical disease induced by virulent field

- strains: Multiple DIVA PCRs exist
 - · All have specific set-up, fit for purpose in specific epidemiological context
 - DIVA test selection depends on knowledge of locally circulating strains
 - EURL/WOAH RL available to provide help with whole genome sequencing

🐡 viruses
Article Development and Validation of a New DIVA Real-Time PCR Allowing to Differentiate Wild-Type Lumpy Skin Disease Virus Strains, Including the Asian Recombinant Strains, from Neethling-Based Vaccine Strains
Andy Haegeman ^{1,*} , Ilse De Leeuw ¹ , Wannes Philips ² and Nick De Regge ¹

LSDV diagnosis - virology



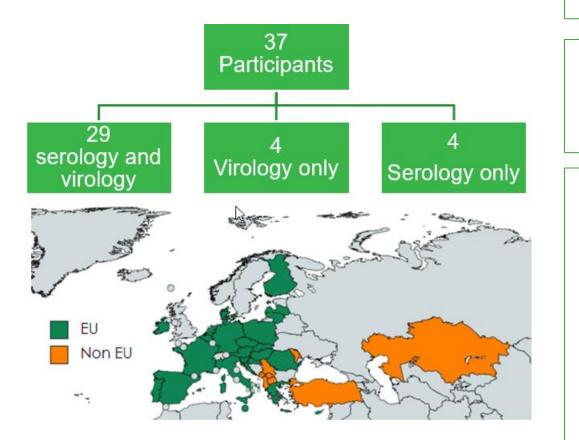
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🟶 viruses	MDPI
Allowing to Differenti	dation of a New DIVA Real-Time PCR ate Wild-Type Lumpy Skin Disease Virus Asian Recombinant Strains, Vaccine Strains
Andy Haegeman ^{1,*} , Ilse De Leeuw ¹ , V	Vannes Philips ² and Nick De Regge ¹

LSDV diagnosis - virology

• Proficiency test 2023



Pan-capripox: For the detection of capripox virus nucleic acid detection, the performance of 32 out of 33 laboratories was satisfactory (≥ 90% agreement) for all performed PCRs

Species differentiation: For the differentiation of capripox virus species, the performance of 23 out of 23 participating laboratories performing the test on all samples was satisfactory (≥ 90% agreement)

DIVA PCR: For the differentiation of capripox field from vaccine strains, the performance of 13/23 laboratories was satisfactory (≥ 90% agreement)

9/23 laboratories used an LSDV specific DIVA and did not classify the SPPV samples. All LSDV samples were correctly classified.

1/23 laboratories used an assay that could make the differentiation for all Capripox viruses. The lab misclassified 4 aliquots (TP2, TP4, TP5 and BP1) and reached a level of agreement of 60% and thus an unsatisfactory result.

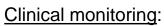
Vaccine efficacy against recombinant strain

- Homologous LAV provide good protection against the classical wild type strains (clade 1.2)
- Do they also provide protection against recombinant strains (clade 2)?

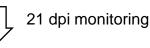
Challenge model in BSL3 animal facilities:

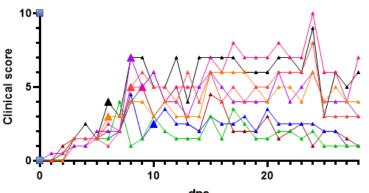


- Vietnam field isolated (cluster 2.5)
- 5ml intravenous
- 4x0,25ml intradermal



- Fever
- Swelling inoculation side
- Lnn swelling
- General health status
- · Feed intake
- # noduli
- 6/8 animals developed nodules



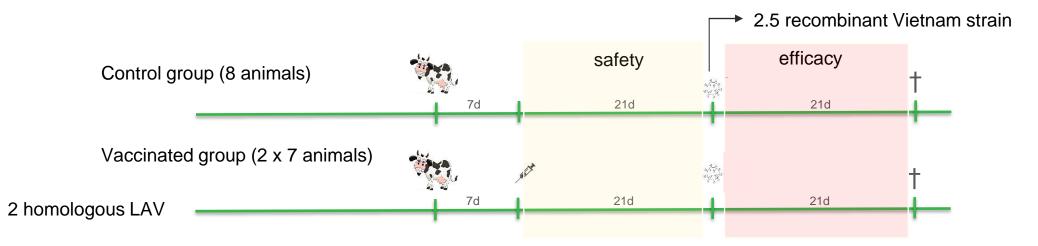






# Animals	Vaccine	Purpose
7	MSD (Lumpyvax)	Vaccine evaluation
7	OBP	Vaccine evaluation
8	N/A	Control Vaccine and infection model





Vaccine efficacy against recombinant strain

Post vaccination			Post challenge		
Clinical sign	Vaccinated animals	Clinical sign	Control animals	Vaccinated	
Fever	5-7 dpv	Fever	Prolonged	7-8 dpv	
Local reaction	Limited	Local reaction	Strong (75%)	Limited	
Nodules	No	Nodules	- 6 skin - 1 lung	No	
Other	No vaccine viremia	Other	Wide variety	No	

• Homologous live attenuated neethling-based strains provide protection against recombinant (clade 2.5) LSDV strains

Direct transmission of the recombinant strain

- Classical wild type LSDV strains (clade 1.2) are mainly spread by vectors
- Reports indicating non-vector transmission of recombinant strains (clade 2)

Non-vector-borne transmission of lumpy skin disease virus

Kononov Aleksandr¹, Byadovskaya Olga¹, Wallace B. David^{2,3}, Prutnikov Pavel¹, Pestova Yana¹, Kononova Svetlana¹, Nesterov Alexander¹, Rusaleev Vladimir¹, Lozovoy Dmitriy¹ & Sprygin Alexander¹⊠



Article

A Recombinant Vaccine-like Strain of Lumpy Skin Disease Virus Causes Low-Level Infection of Cattle through Virus-Inoculated Feed

MDPI

Irina Shumilova ¹, Alexander Nesterov ¹, Olga Byadovskaya ¹, Pavel Prutnikov ¹, David B. Wallace ^{2,3}, Maria Mokeeva ¹, Valeriy Pronin ¹, Aleksandr Kononov ¹, Ilya Chvala ¹ and Alexander Sprygin ^{1,*}

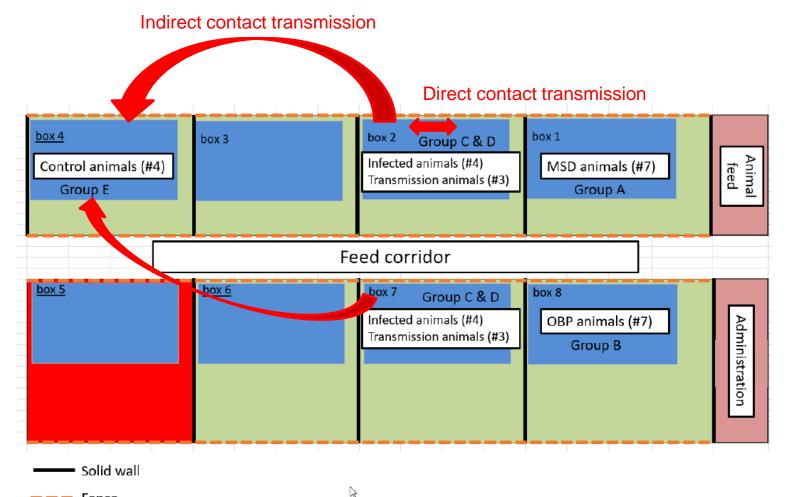
> Front Vet Sci. 2022 Oct 20;9:1001426. doi: 10.3389/fvets.2022.1001426. eCollection 2022.

Experimentally controlled study indicates that the naturally occurring recombinant vaccine-like lumpy skin disease strain Udmurtiya/2019, detected during freezing winter in northern latitudes, is transmitted *via* indirect contact

Alexander Nesterov ¹, Ali Mazloum ¹, Olga Byadovskaya ¹, Irina Shumilova ¹, Antoinette Van Schalkwyk ² ³, Alena Krotova ¹, Vladimir Kirpichenko ⁴, Irina Donnik ⁵, Ilya Chvala ¹, Alexander Sprygin ¹

Direct transmission of the recombinant strain

- Classical wild type LSDV strains (clade1.2) are mainly spread by vectors
- Reports indicating non-vector transmission of recombinant strains (clade 2)





Fence

Direct contact animals

- 6/6 developed nodules
- In general, milder disease compared to needle infected group, except 1
- Viremia detected in 5/6
- 5/6 seroconverted (other animal euthanised before seroconversion)

Indirect contact animals

- 1/4 developed nodules
- Milder disease compared to needle infected group
- Viremia detected in 1/4
- 1/4 seroconverted

- Non-vector borne transmission capacity of recombinant LSDV strains exist and is higher than for classical strains
- Impact on the LSDV epidemiology: spread during winter, more efficient spread within infected herds, even higher importance for biosecurity

Training activities

• LSDV:

- ✓ Training 2 laboratory technicians Algeria (IAEA)
- ✓ LSDV symposium Rome (EuFMD-FAO)
- ✓ LSDV online training course (EuFMD-FAO)
- ✓ LSDV-PPR-FMD meeting Bhutan (GF-TAD)
- ✓ SEE Thrace meeting on TADs (EuFMD)
- ✓ LSDV control strategy ASEAN (WOAH-FAO)
- ✓ TAD Thrace meeting (EuFMD)
- ✓ LSDV central Asia (WOAH)
- ✓ Training 2 laboratory technicians North-Macedonia (EC)

• SPPV/GTPV:

- ✓ EUVET missions (EC)
- ✓ SPPV online training course (EuFMD-FAO)
- ✓ SPPV open access online training (EuFMD)
- ✓ BTSF training SPPV/GTPV (EC)



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Contact

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