Reference Centre

World Organisation

for Animal Health





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INFORMATION ON LSDV STRAINS IN **EUROPE**

Nick De Regge

GFTAD meeting, webinar on PPR and LSDV in Europe **03 July 2025, online**



LSDV whole genome sequencing: potential usefulness

No sequences of the ongoing LSDV outbreak available yet

Can WGS be used to do molecular outbreak tracing?

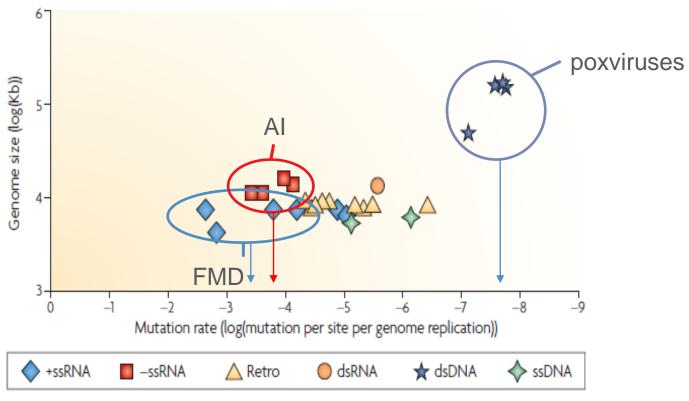
NO

 Can WGS be useful to determine the origin and route of introduction of an LSDV outbreak in a new region?

IT COULD IN THEORY, BUT PROBABLY NOT WITH THE LOW NUMBER OF ACTUALLY AVAILABLE WGS IN THE DATABASES

Molecular outbreak tracing

Poxviridae, genus capripoxvirus, dsDNA, ~150-151kb in size.

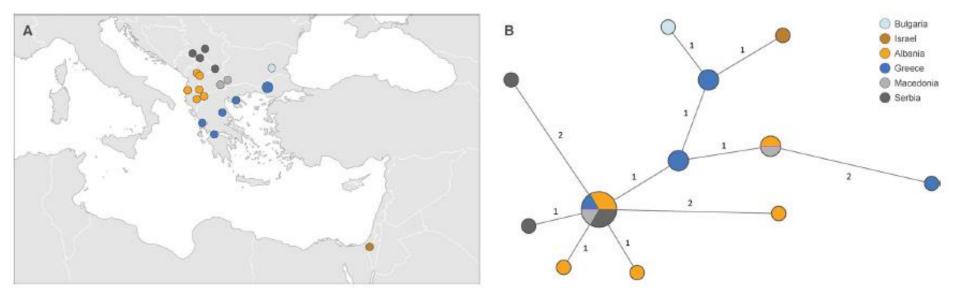


Duffy et al, 2008, Nature reviews genetics

Genetically stable → no molecular outbreak tracing

Molecular outbreak tracing

LSDV outbreak in the Balkans 2015-2017, >7000 outbreaks



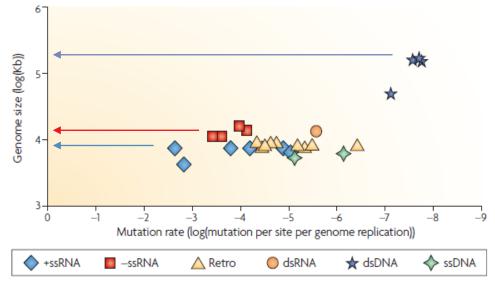
Van Borm et al, 2023, Journal of Virology

Within the southeastern European outbreak, LSDV genomes differ by a maximum of five single nucleotide substitutions, without evidence for clustering per country (Fig. 2). Eleven unique haplotype variants are present in the population of 19 wild-type samples from southeastern Europe. A single haplotype is shared by samples from four sampled

→ no molecular outbreak tracing possible

Origin and route of introduction of outbreak strains

- High number of WGS necessary, with a good geographical coverage
- In 2023: +/- 80; in 2025: +/-170



Duffy et al, 2008, Nature reviews genetics

- WGS of capripox viruses is not straightforward (long, AT-rich, inverted terminal repeats)
- Often on single or a few gene(s) using Sanger Sequencing are used insufficient genetic variation



Lumpy skin disease virus: phylogeny

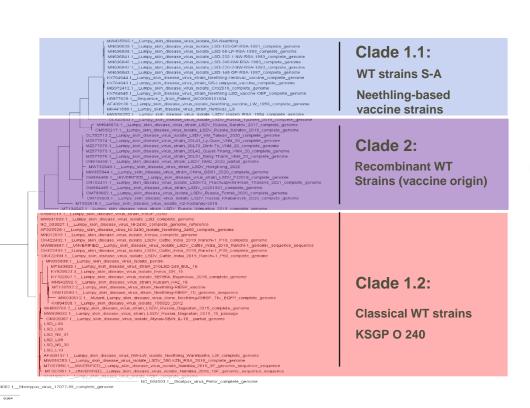
2023 MW435866.1__Lumpy_skin_disease_virus_isolate_SA-Neethling **Clade 1.1:** MN636839.1__Lumpy_skin_disease_virus_isolate_LSD-103-GP-RSA-1991_complete_genome MN636838.1__Lumpy_skin_disease_virus_isolate_LSD-58-LP-RSA-1993_complete_genome MN636841.1 Lumpy skin disease virus isolate LSD-220-1-NW-RSA-1993 complete genome MN636840.1__Lumpy_skin_disease_virus_isolate_LSD-248-NW-RSA-1993_complete_genome MN636842.1__Lumpy_skin_disease_virus_isolate_LSD-220-2-NW-RSA-1993_complete_genome **WT strains S-A** viruses MDPI MN636843.1 Lumpy skin disease virus isolate LSD-148-GP-RSA-1997 complete genome KX764644.1__Lumpy_skin_disease_virus_strain_Neethling-Herbivac_vaccine_complete_genome KX764643.1__Lumpy_skin_disease_virus_strain_SIS-Lumpyvax_vaccine_complete_genome MG972412.1__Lumpy_skin_disease_virus_isolate_Cro2016_complete_genome **Neethling-based** KX764645.1 Lumpy skin disease virus strain Neethling-LSD vaccine-OBP complete genome HB977629.1 Sequence 1 from Patent WO2009101604 vaccine strains AF409138.1__Lumpy_skin_disease_virus_isolate_Neethling_vaccine_LW_1959_complete_genome Lumpy Skin Disease Virus Genome Sequence Analysis: MK441838.1__Lumpy_skin_disease_virus_strain_Herbivac_LS MW656252.1 Lumpy skin disease virus isolate LSDV Haden RSA 1954 complete genome Putative Spatio-Temporal Epidemiology, Single Gene versus OL542833.1 Lumpy skin disease virus isolate LSDV Russia Tyumen 2019 complete ge MH646674.1__Lumpy_skin_disease_virus_strain_LSDV_Russia_Saratov_2017_complete_genome OM530217.1__Lumpy_skin_disease_virus_isolate_LSDV_Russia_Saratov_2019_complete_genome Whole Genome Phylogeny and Genomic Evolution OL752713.2__Lumpy_skin_disease_virus_isolate_LSDV_KM_Taiwan_2020_complete_genome Clade 2: MZ577074.1__Lumpy_skin_disease_virus_strain_20L43_Ly-Quoc_VNM_20_complete_genome MZ577075.1__Lumpy_skin_disease_virus_strain_20L70_Dinh-To_VNM_20_complete_genome Floris C. Breman *, Andy Haegeman, Nina Krešić, Wannes Philips and Nick De Regge MZ577073.1__Lumpy_skin_disease_virus_strain_20L42_Quyet-Thang_VNM_20_complete_genome **Recombinant WT** MZ577076.1__Lumpy_skin_disease_virus_strain_20L81_Bang-Thanh_VNM_20_complete_genome ON616408.1__Lumpy_skin_disease_virus_strain_LSDV_NMG_2020_partial_genome MW732649.1__Lumpy_skin_disease_virus_strain_LSDV_HongKong_2020 strains (vaccine origin) MW355944.1__Lumpy_skin_disease_virus_strain_China_GD01_2020_complete_genome OM984486.1__UNVERIFIED__Lumpy_skin_disease_virus_strain_LSDV_FJ2019_complete_genome ON152411.1__Lumpy_skin_disease_virus_isolate_LSDV72_PrachuapKhiriKhan_Thailand_2021_complete_genome OM984485.1__Lumpy_skin_disease_virus_strain_LSDV_XJ201901_complete_genome OM793602.1__Lumpy_skin_disease_virus_isolate_LSDV_Russia_Tomsk_2020_complete_genome OM793603.1__Lumpy_skin_disease_virus_isolate_LSDV_Russia_Khabarovsk_2020_complete_genome MT992618.1 Lumpy skin disease virus isolate KZ-Kostanay-2018 — MT134042.1 Lumpy_skin_disease_virus_strain_LSDV_Russia_Udmurtiya_2019_complete_ger KX683219.1__Lumpy_skin_disease_virus_strain_kSGP_0240 MW631933.1__Lumpy_skin_disease_virus_isolate_LSD_complete_genome NC_003027.1__Lumpy_skin_disease_virus_NI-2490_complete_genome_reference AF325528.1 Lumpy_skin_disease_virus_NI-2490_isolate_Neethling_2490_complete_genome MN072619.1__Lumpy_skin_disease_virus_isolate_Kenya_complete_genome OK422492.1__Lumpy_skin_disease_virus_isolate_LSDV_Cattle_India_2019_Ranchi-1_P10_complete_genome MW883897.1_UNVERIFIED_Lumpy_skin_disease_virus_isolate_LSDV_Cattle_India_2019_Ranchi-1_genomic_sequence_sequence OK422493.1__Lumpy_skin_disease_virus_isolate_LSDV_Cattle_india_2019_Ranchi-1_P30_complete_genome OK422494.1__Lumpy_skin_disease_virus_isolate_LSDV_Cattle_India_2019_Ranchi-1_P50_complete_genome MN995838.1__Lumpy_skin_disease_virus_isolate_pendik MT643825.1__Lumpy_skin_disease_virus_strain_210LSD-249_BUL_16 KY829023.3 Lumpy_skin_disease_virus_isolate_Evros_GR_15 **Clade 1.2:** KY702007.1__Lumpy_skin_disease_virus_isolate_SERBIA_Bujanovac_2016_complete_genome MN642592.1__Lumpy_skin_disease_virus_strain_Kubash_KAZ_16 MT130502.2 Lumpy skin disease virus strain Neethling-RIBSP vaccine ON010590.1__Lumpy_skin_disease_virus_strain_Neethling-RIBSP_7C_genomic_sequence - MW030512.1_Mutant_Lumpy_skin_disease_virus_clone_Neethling-RIBSP_TK-_EGFP_complete_genome **Classical WT strains** KX894508.1__Lumpy_skin_disease_virus_isolate_155920_2012 viiii wikiii Jumpy_skin_disease_virus_strain_LSDV_Russia_Dagestan_2015_complete_genome MW699032.1 Lumpy skin disease virus strain LSDV Russia Dagestan 2015 75 passage ON005067.1__Lumpy_skin_disease_virus_isolate_Atyrau-5BJN_IL-18__partial_genome **KSGP 0 240** LSD L09 LSD_NS_31 LSD L08 LSD NS 30 AF409137.1__Lumpy_skin_disease_virus_NW-LW_isolate_Neethling_Warmbaths_LW_complete_genome MW656253.1__Lumpy_skin_disease_virus_isolate_LSDV_280-KZN_RSA_2018_complete_genome MT007950.1__UNVERIFIED__Lumpy_skin_disease_virus_isolate_Namibia_2016_9F_genomic_sequence_sequence · MT007951.1__UNVERIFIED__Lumpy_skin_disease_virus_isolate_Namibia_2016_10F_genomic_sequence_sequence

NC_004003.1__Goatpox_virus_Pellor_complete_genome



NC 004002.1 Sheeppox virus 17077-99 complete genome

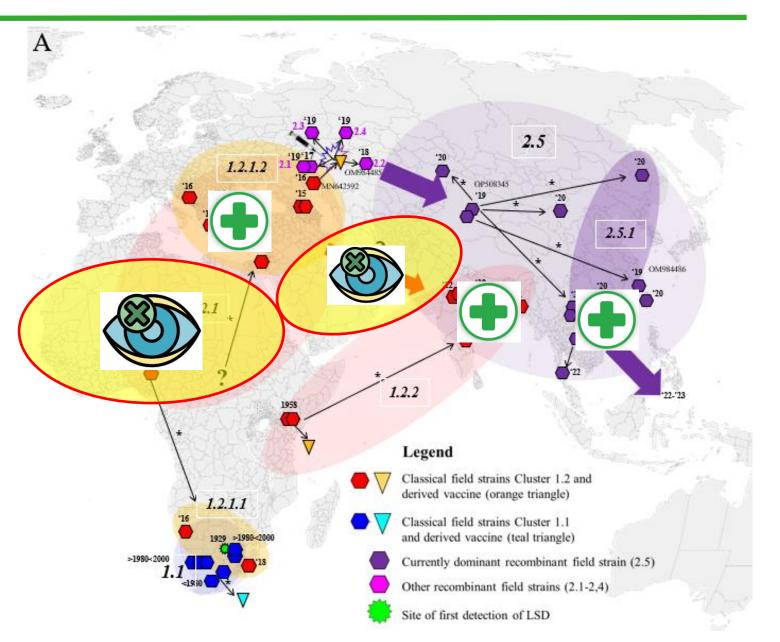
Lumpy skin disease virus spread



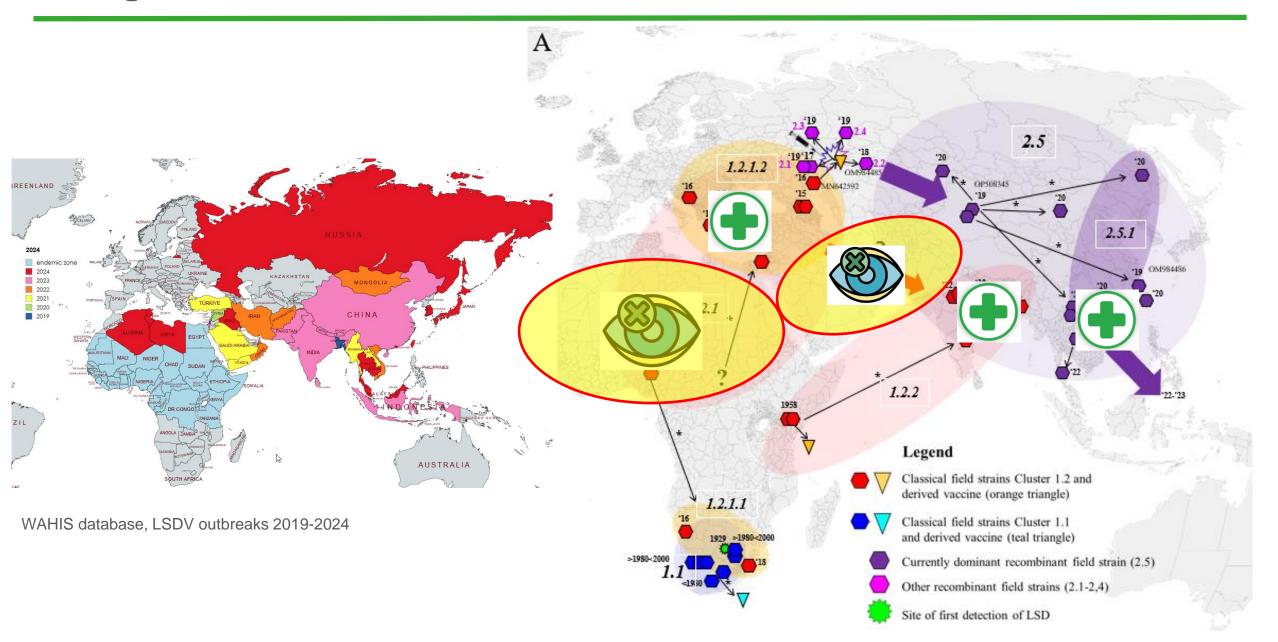
2.5 2.5.1 1.2.1 Legend Classical field strains Cluster 1.2 and derived vaccine (orange triangle) 1.2.1.1 Classical field strains Cluster 1.1 and derived vaccine (teal triangle) Currently dominant recombinant field strain (2.5) Other recombinant field strains (2.1-2,4) Site of first detection of LSD

Origin and route of introduction of outbreak strains

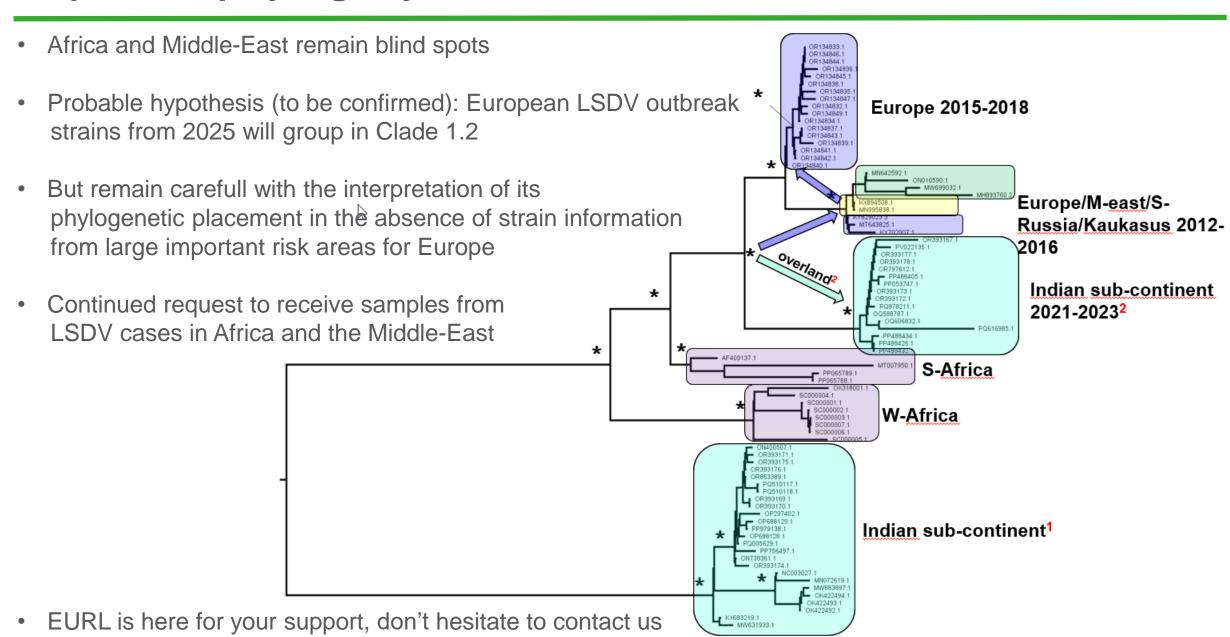
clade	2023	2025	Additional sequences
1.1	10	10	
1.2	32	88	Europe, India
2.5	22	56	SE Asia
2.x	6	6	



Origin and route of introduction of outbreak strains



Updated phylogeny 2025: clade 1.2





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