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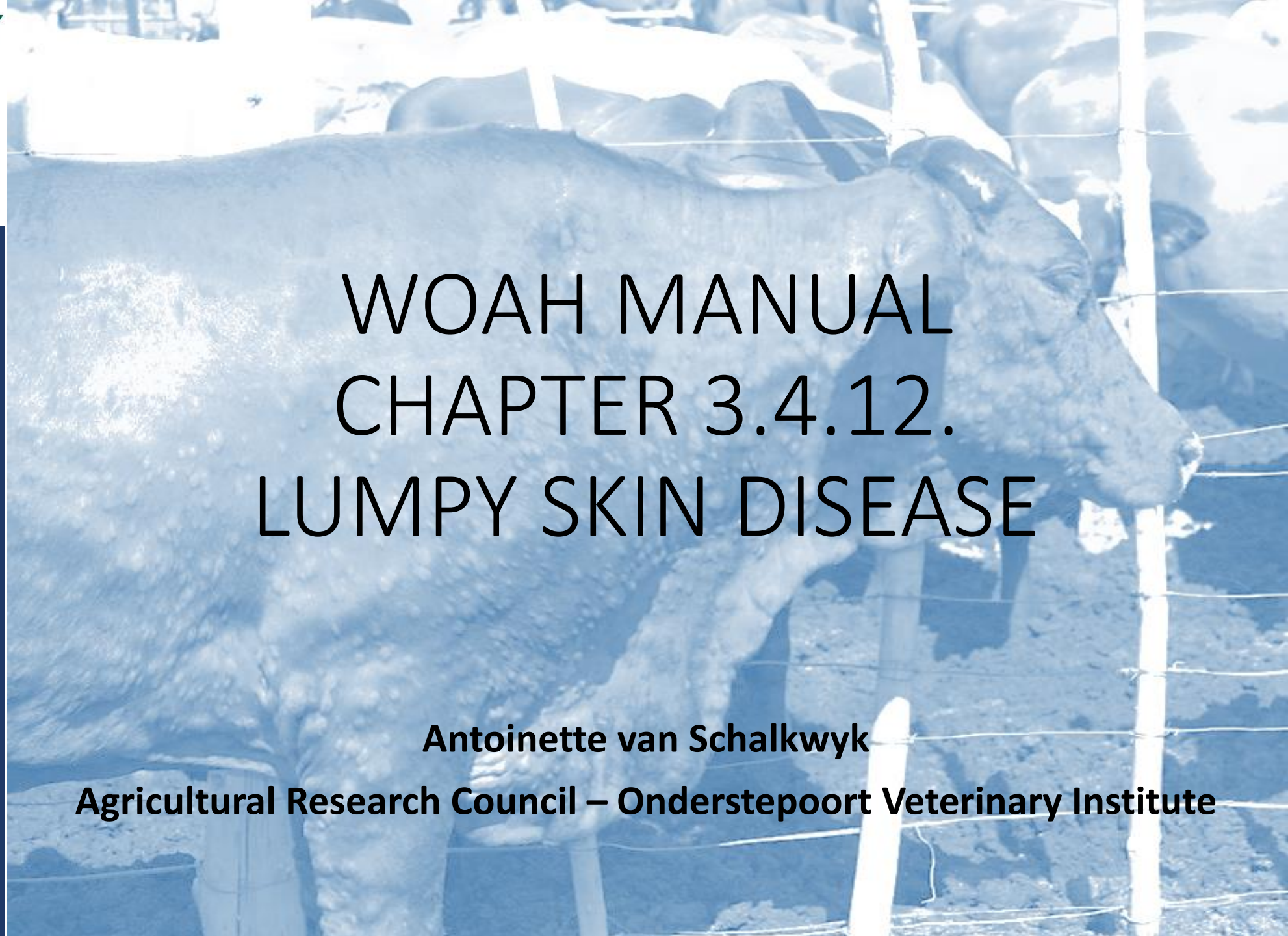

WOAH MANUAL CHAPTER 3.4.12. LUMPY SKIN DISEASE

Antoinette van Schalkwyk

Agricultural Research Council – Onderstepoort Veterinary Institute

Lumpy skin disease: Global spread

Zambia: 1929

South Africa: 1944

Kenya: 1958

Middle East: 1988 and again in 2006

Europe, Caucus and Russia: 2015

China and India: 2019

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Lumpy skin disease: Phylogenetics

Phylogenetic analysis shows the majority of LSDV strains group into two monophyletic clusters (cluster 1.1 and 1.2) (Biswas *et al.,* 2020; Van Schalkwyk *et al.,* 2021).

Cluster 1.1: Neethling Prototype strain and vaccine

Cluster 1.1 consists of LSDV Neethling vaccine strains that are based on the LSDV/Neethling/WC-1957 type-strain (Kara *et al.,* 2003; Van Rooyen *et al.,* 1959; van Schalkwyk *et al.,* 2020) and historic wild-type strains from South Africa.

Cluster 1.2: KSGPO and "wild type"

Cluster 2.1 -2.5: Five unique recombinant strains

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Lumpy skin disease: Phylogenetics (Cluster 1.1)

Cluster 1.1: Neethling Prototype strain (Alexander et al., 1957)

Oldest isolate: Haden / 1954 (van Schalkwyk et al., 2021)

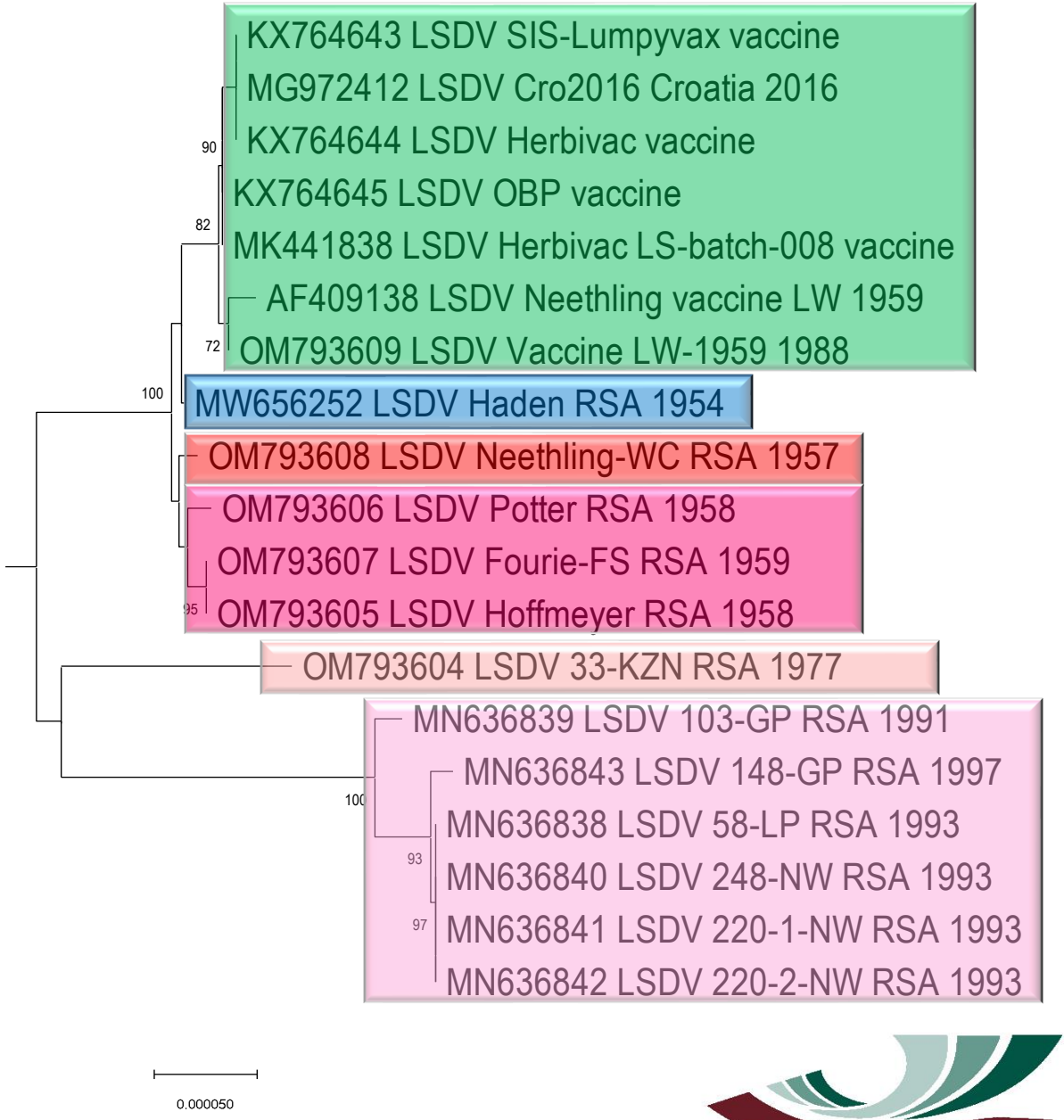
Prototype: Neethling-WC / 1957 (van Schalkwyk et al., 2022)

Cluster 1.1: Neethling vaccine 1960 (van Rooyen et al., 1959)

- Vaccine: Neethling-LW1959 (Kara et al., 2003)
- Vaccine: OBP, Herbivac, SIS-Lumpyvax (Mathijs et al., 2016; Douglass et al., 2019)

Cluster 1.1: Field isolates from South Africa (1954 – 1997)

Wild type field isolates: South Africa 1950's, 1970's and 1990's (van Schalkwyk et al., 2020 and 2022)



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Lumpy skin disease: Phylogenetics (Cluster 1.1)

Targets for molecular assays to differentiate between vaccine and wild type virus.

Current DIVA assays differentiate between Cluster 1.1 and 1.2.

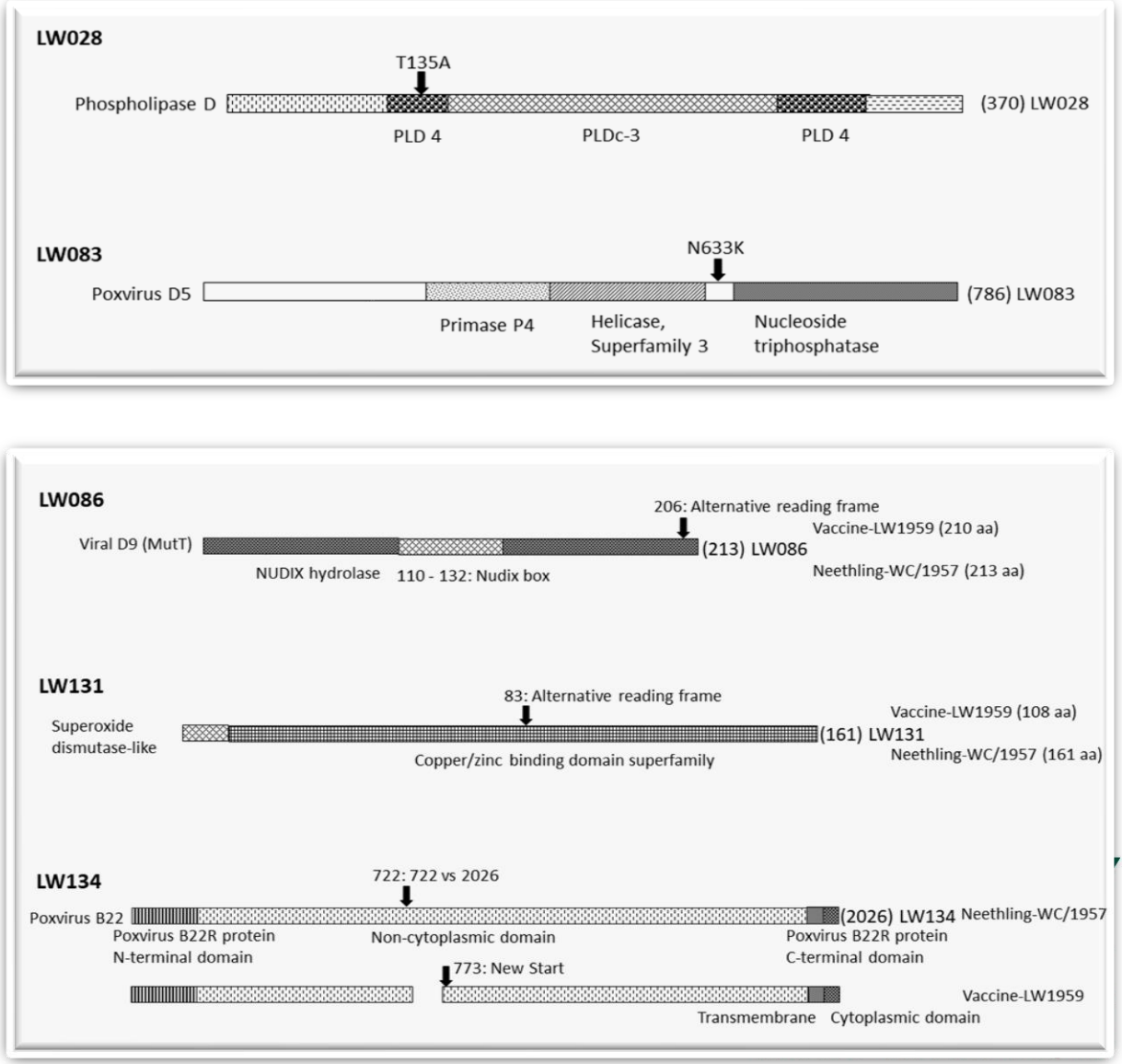
Possible genetic influences on attenuated phenotype.

Cluster 1.1 - **Attenuation**

Seven SNPs between Neethling-WC/1957 and Neethling-LW1959 vaccine
(van Schalkwyk et al., 2022)

- Non-synonymous:
  - LW028 T135A
  - LW083: K663N
  - LW098: G553S
  - LW098: I625T

- Reading frame:
  - LW086: Termination (210 aa)
  - LW131: Termination (108aa)
  - LW134: Termination (721aa)



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Cluster 1.2: KSGPO and "wild type"

Cluster 1.2 consists of wild-type strains from southern Africa, Kenya, the northern hemisphere, and the Kenyan KSGP O-240 commercial vaccine.

Cluster 2.1 -2.5: Five unique recombinant strains

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Lumpy skin disease: Phylogenetics (Cluster 1.2)

Kenya prepared a heterologous vaccine: Kenyan Sheep and Goat Pox virus (KSGPO-240 and KSGPO-180), which became KS1.

Kenya vaccine stain (KS1) detected in outbreaks in Bangladesh, India, Nepal and Pakistan.

Possible new introduction LSDV into South Africa?

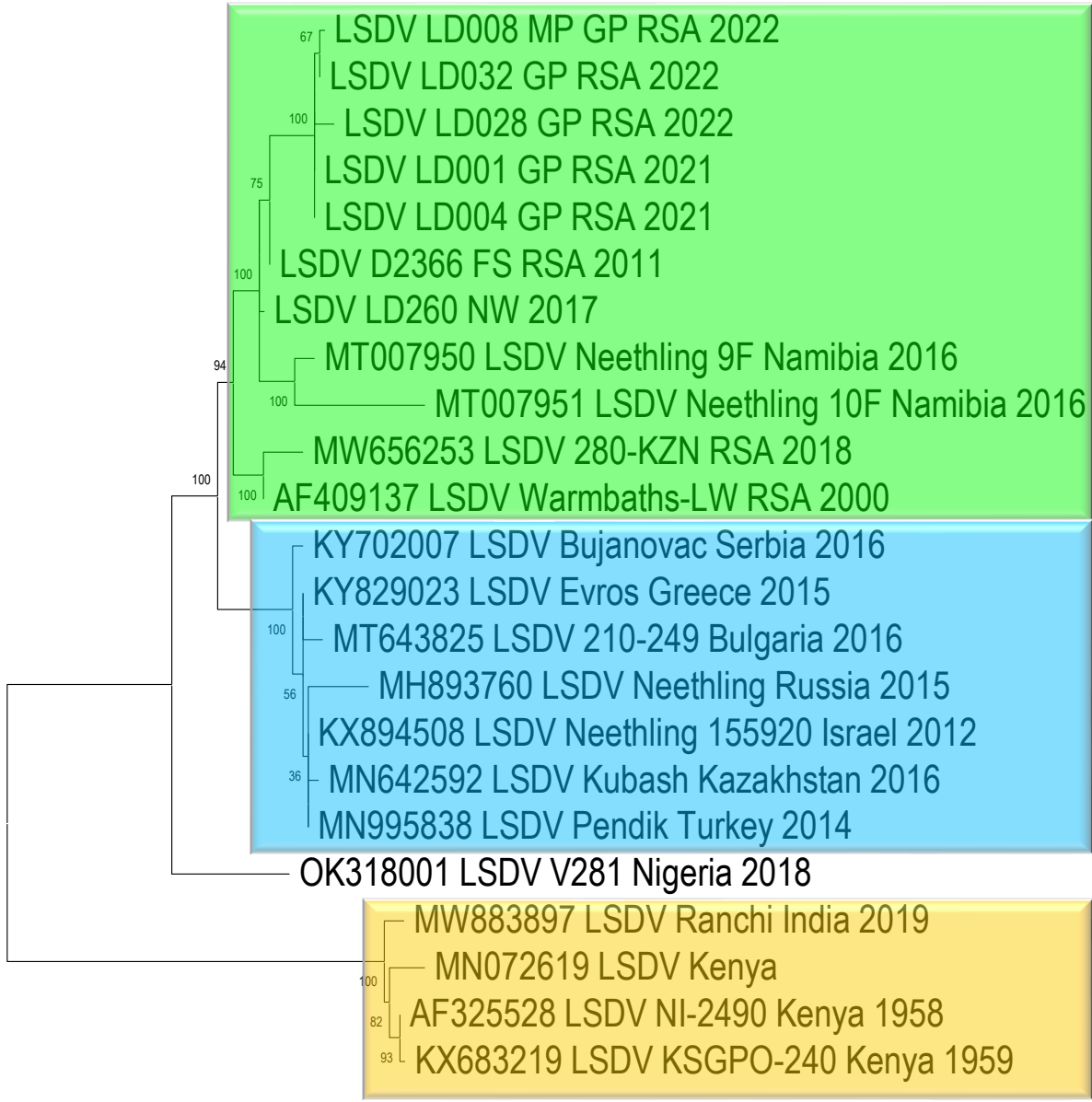
Isolate: 2490/Kenya/1958
(Tulman et al., 2000)

Vaccine: KSGPO-240/1959
(Vandenbussche et al., 2016)

Vaccine: KSGPO-240/1959.
Outbreak in Bangladesh, India, Nepal and Pakistan

Isolates from southern Africa 2000 – 2022
(Kara et al., 2003)

Isolates from Middle East, Europe and Asia 2012 – 2016



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Lumpy skin disease: Phylogenetics

Clusters 1.1 and 1.2

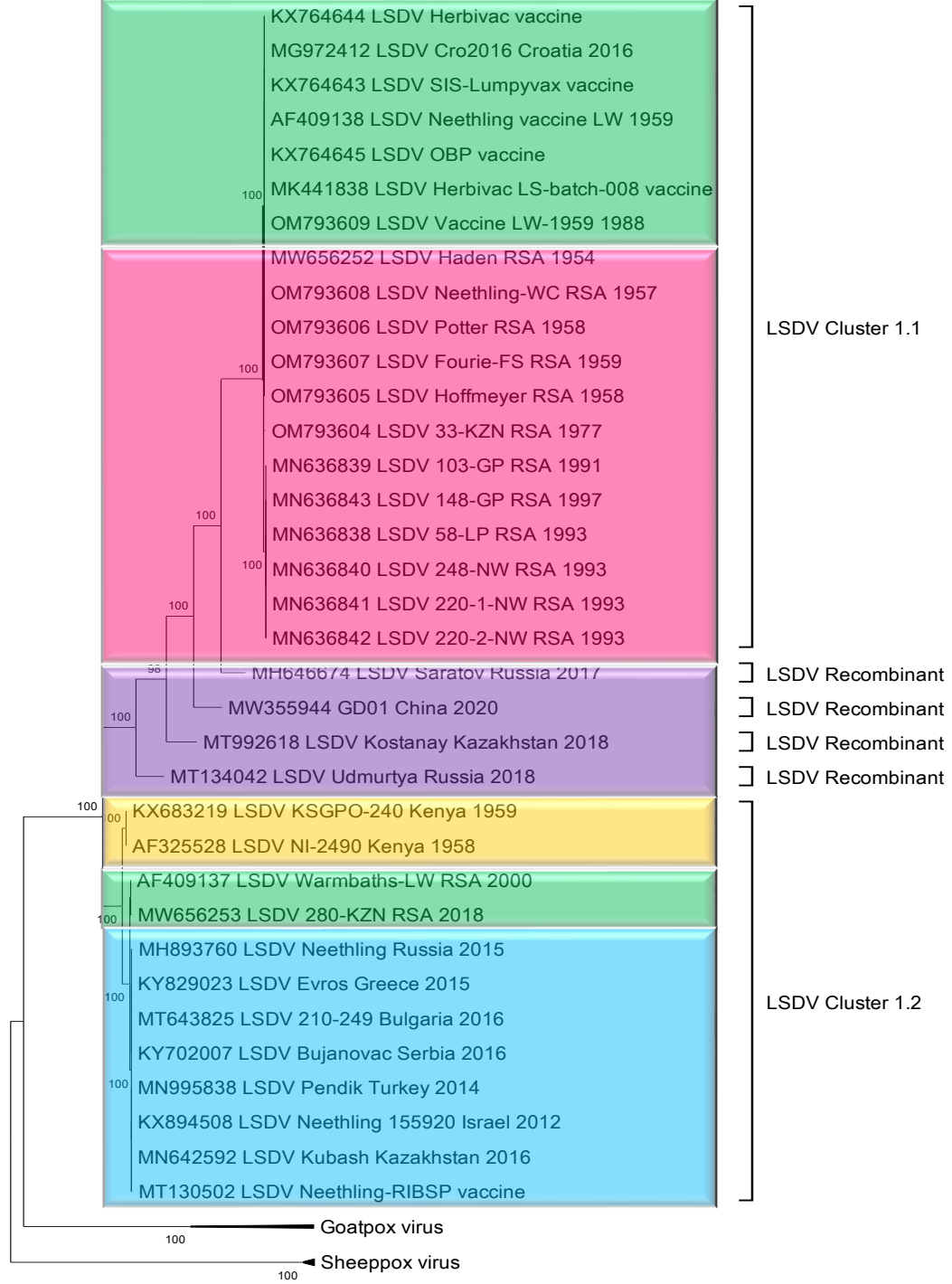
LSDVs representing sequences from both clusters were circulating in Africa in the 1950's.

± 2,200 SNPs between cluster 1.1 and 1.2
(Kara et al., 2003; van Schalkwyk et al., 2021)

- ± 1860 SNPs in 114 ORFs
  - 57% Synonymous
  - 26% Non-Synonymous
- ± 330 (15%) IGR

Majority of the DIVA assays are based on differentiation between cluster 1.1 and 1.2. Thus not suitable to detect the field isolates of cluster 1.1

TMRCA: ± 500 years



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Cluster 1.2 consists of wild-type strains from southern Africa, Kenya, the northern hemisphere, and the Kenyan KSGP O-240 commercial vaccine.

Cluster 2.1 -2.5: Five unique recombinant strains

In addition to these two clusters, there have recently been recombinant LSDV strains isolated from clinical cases of LSD in the field in Russia and central Asia (Flannery *et al.,* 2021; Sprygin *et al.,* 2018; 2020; Wang *et al.,* 2021). These recombinant viruses show unique patterns of accessory gene alleles, consisting of sections of both wild-type and "vaccine" LSDV strains.

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Lumpy skin disease: Phylogenetics (Cluster 2.1 – 2.5)

Parental sequences are both vaccines:
- Neethling-LW1959
- KSGPO-240

Genetic recombination should be removed from genetic drift analysis

Recombinants (Cluster 2.1 – 2.5)

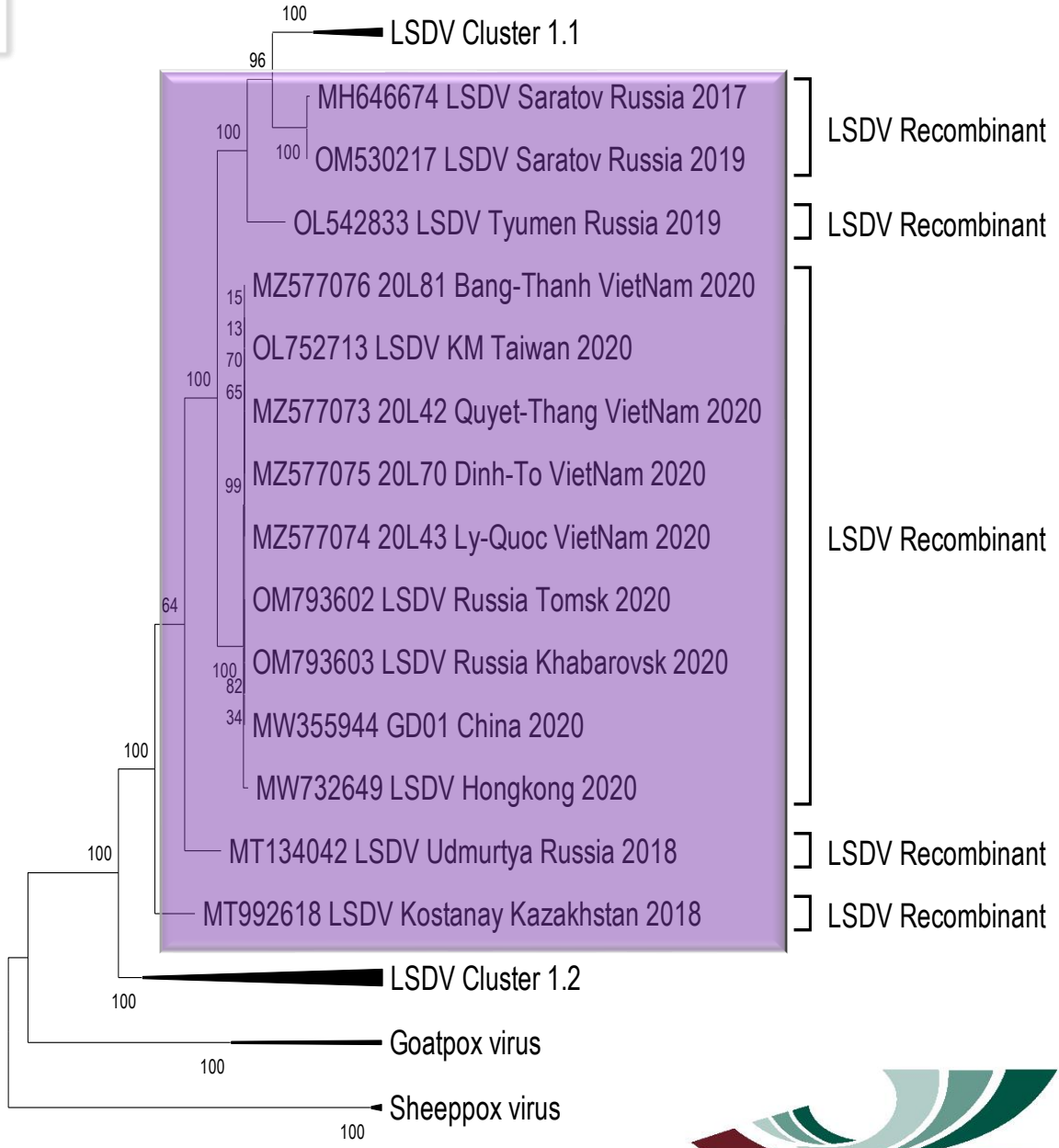
2.1: Saratov/Russia/2017
(Sprygin et al., 2018)

2.2: Udmurtya/Russia/2018
(Sprygin et al., 2018)

2.3: Kostanay/Kazakhstan/2018

2.4: Tyumen/Russia/2019
(Krotova et al., 2022)

2.5: GD01/China/2019
(Ma et al., 2021)



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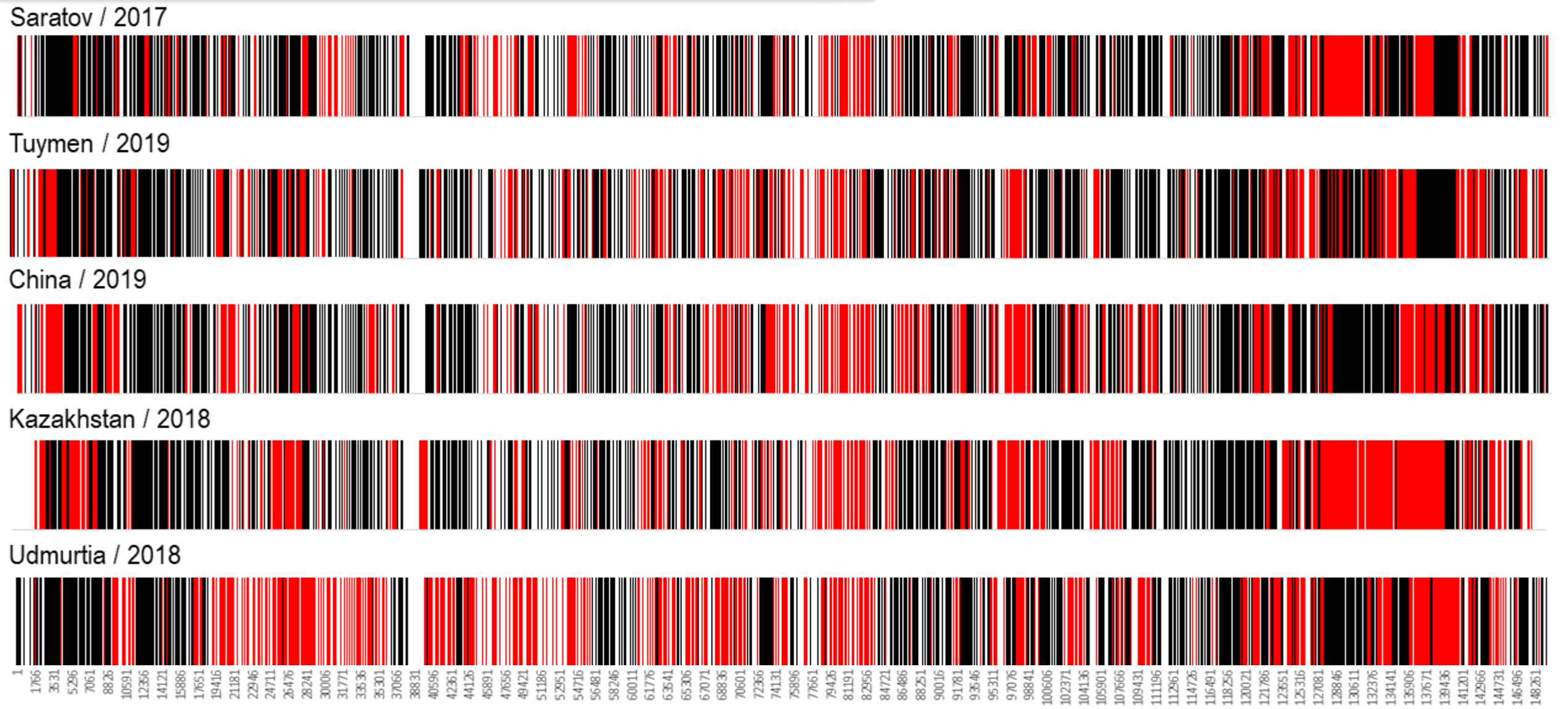
Lumpy skin disease: Phylogenetics (Cluster 2.1 – 2.5)



A: Saratov/Russia/2017; B: Tyumen/Russia/2019; C: GD01/China/2019 D: Kostanay/Kazakhstan/2018; E: Udmurtya/Russia/2018

Neethling- LW1959 KSGPO-240

Lumpy skin disease: Epidemiology

Clusters based on Markers

- 1.2
- 1.2 -KSGP
- 1.1 & 1.2
- 1.1 & 2.3
- 2.5
- 1.1 & 1.2 & 2.1 & 2.2 & 2.4 & 2.5
- No sequence data

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Lumpy skin disease: Role of wildlife species

Role of wildlife?

In 2022, isolation and characterisation of LSDV from a giraffe in a zoo was reported in Vietnam (Dao et al., 2022).

Namibia: an eland antelope (Taurotragus oryx), which was asymptomatic for LSD, but LSDV DNA isolated (Molini et al., 2021)

India: Farmed camels (Kumar et al., 2023)

India: Free living gazelle (Sundhankar et al., 2023)

There is no published evidence indicating a role for wildlife species in the maintenance and/or transmission of LSDV. Despite the easily recognisable clinical signs, disease in wildlife is exceptionally rarely reported.

This evidence is supported by extensive serosurveys of wildlife in Africa which detected antibodies in very low numbers of samples (Davies, 1982; Hedger and Hamblin, 1983), leading the authors to conclude “wildlife in Africa probably does not play a very important part in the perpetuation and spread of LSDV”.

LSDV has spread rapidly in recent years into the Middle East and Asia, and the susceptibility of wildlife species in these regions to LSDV is unknown.

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Lumpy skin disease: Role of wildlife species

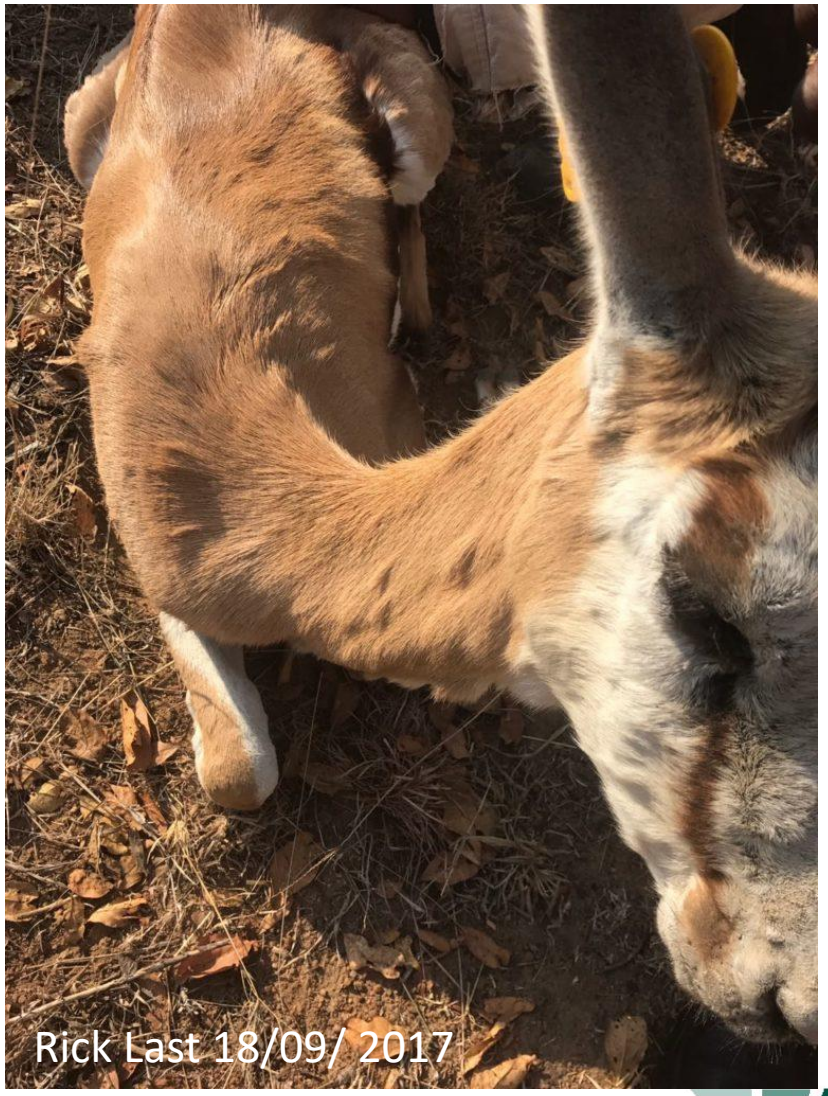
Springbuck and giraffe

National parks and game reserves

Require more investigations

In South Africa, Botswana and Namibia

- Springbuck
- Giraffe
- Oryx



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Questions?

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