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WOAH Reference Laboratory
for **Lumpy skin disease**

Reference Centre
World Organisation
for Animal Health
Founded as OIE

**EU Reference Laboratory
for Capripox viruses**

Funded by the
European Union

Food and Agriculture
Organization of the
United Nations

healthy all life long

INFORMATION ON LSDV STRAINS IN EUROPE

Nick De Regge

GFTAD meeting, webinar on PPR and LSDV in Europe

03 July 2025, online

.be

LSDV whole genome sequencing: potential usefulness

- No sequences of the ongoing LSDV outbreak available yet

- Can WGS be used to do molecular outbreak tracing?

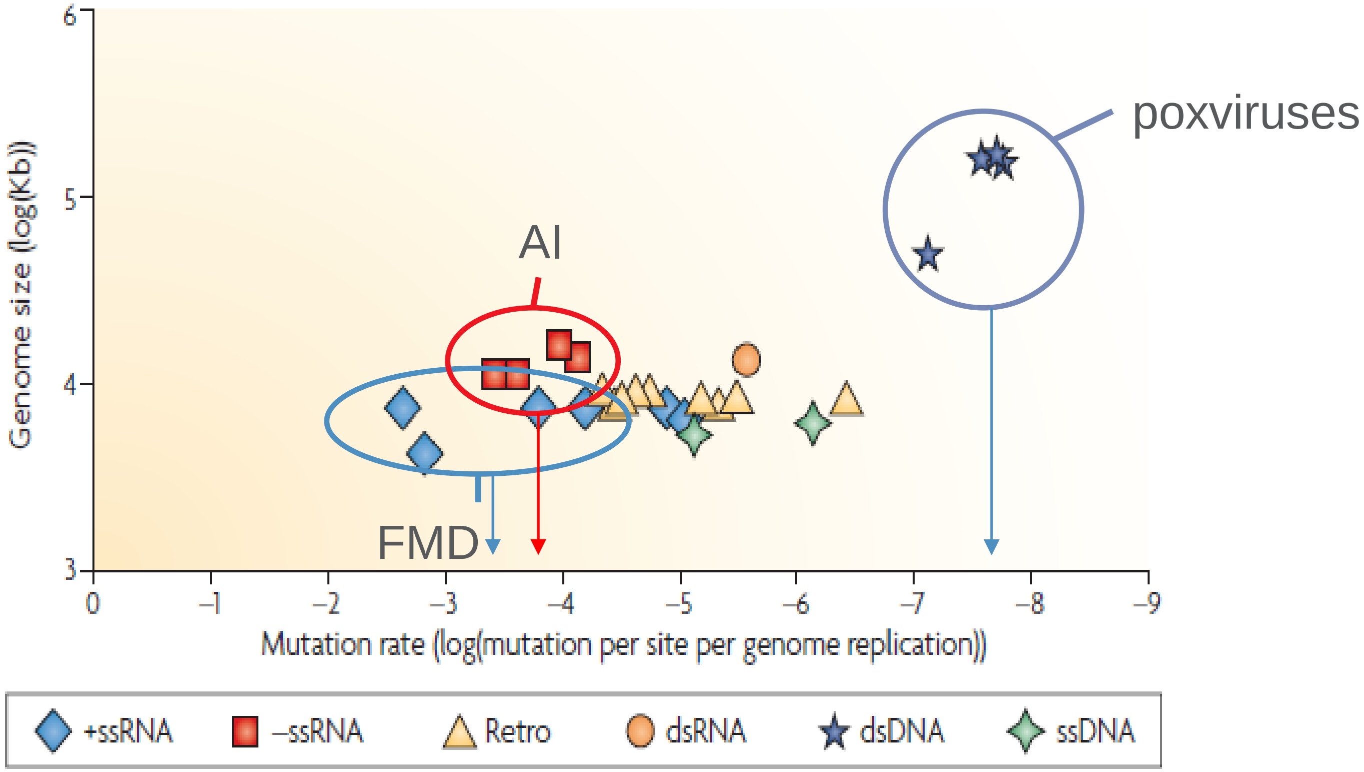
  NO

- 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.

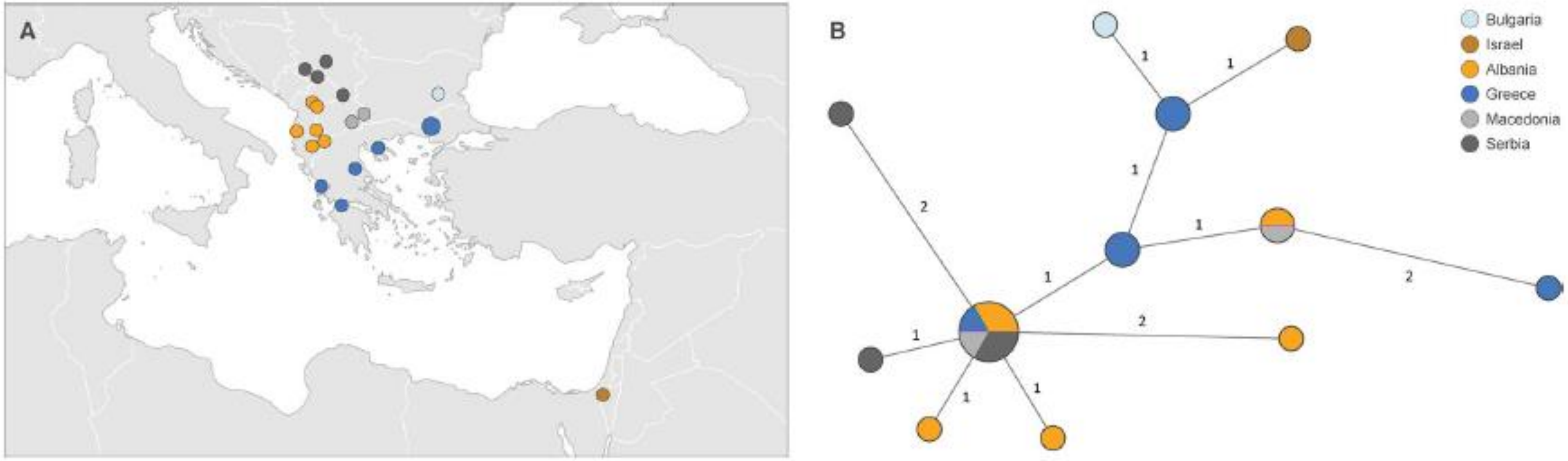


Duffy et al, 2008, Nature reviews genetics

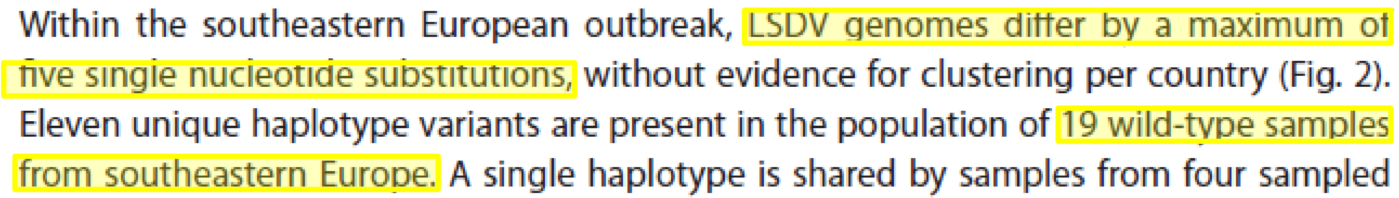
- Genetically stable → no molecular outbreak tracing

Molecular outbreak tracing

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



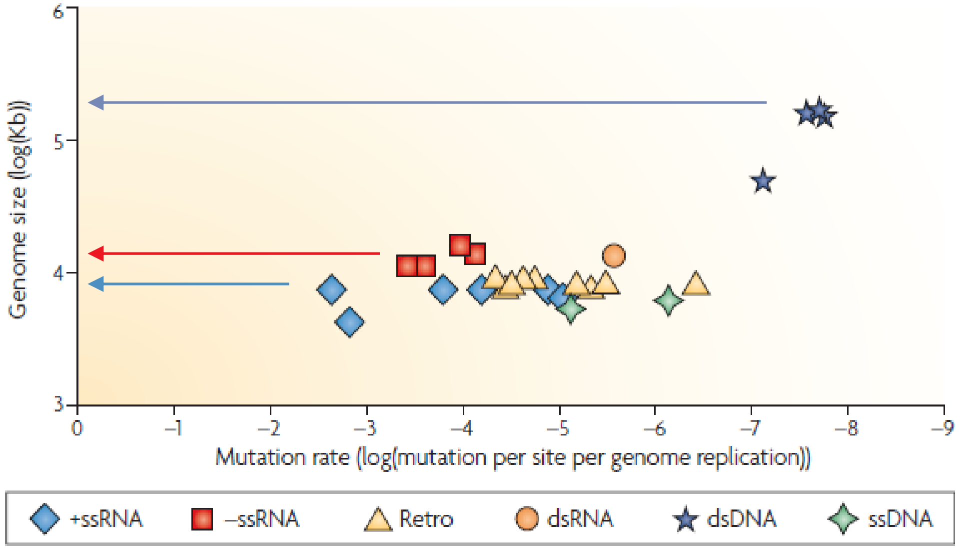
Van Borm et al, 2023, Journal of Virology


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

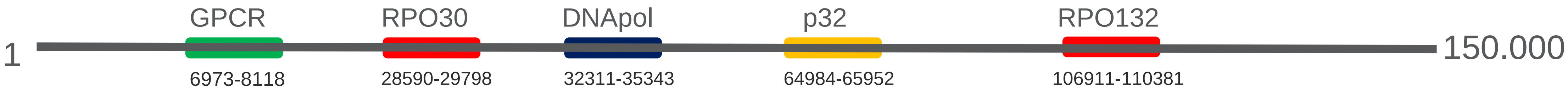
Origin and route of introduction of outbreak strains

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



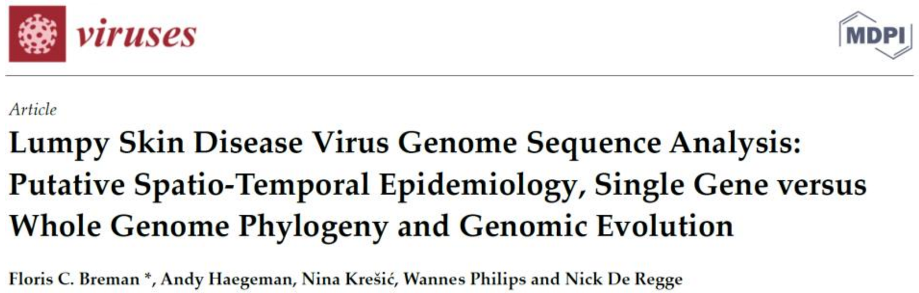
Duffy et al, 2008, Nature reviews genetics

- 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



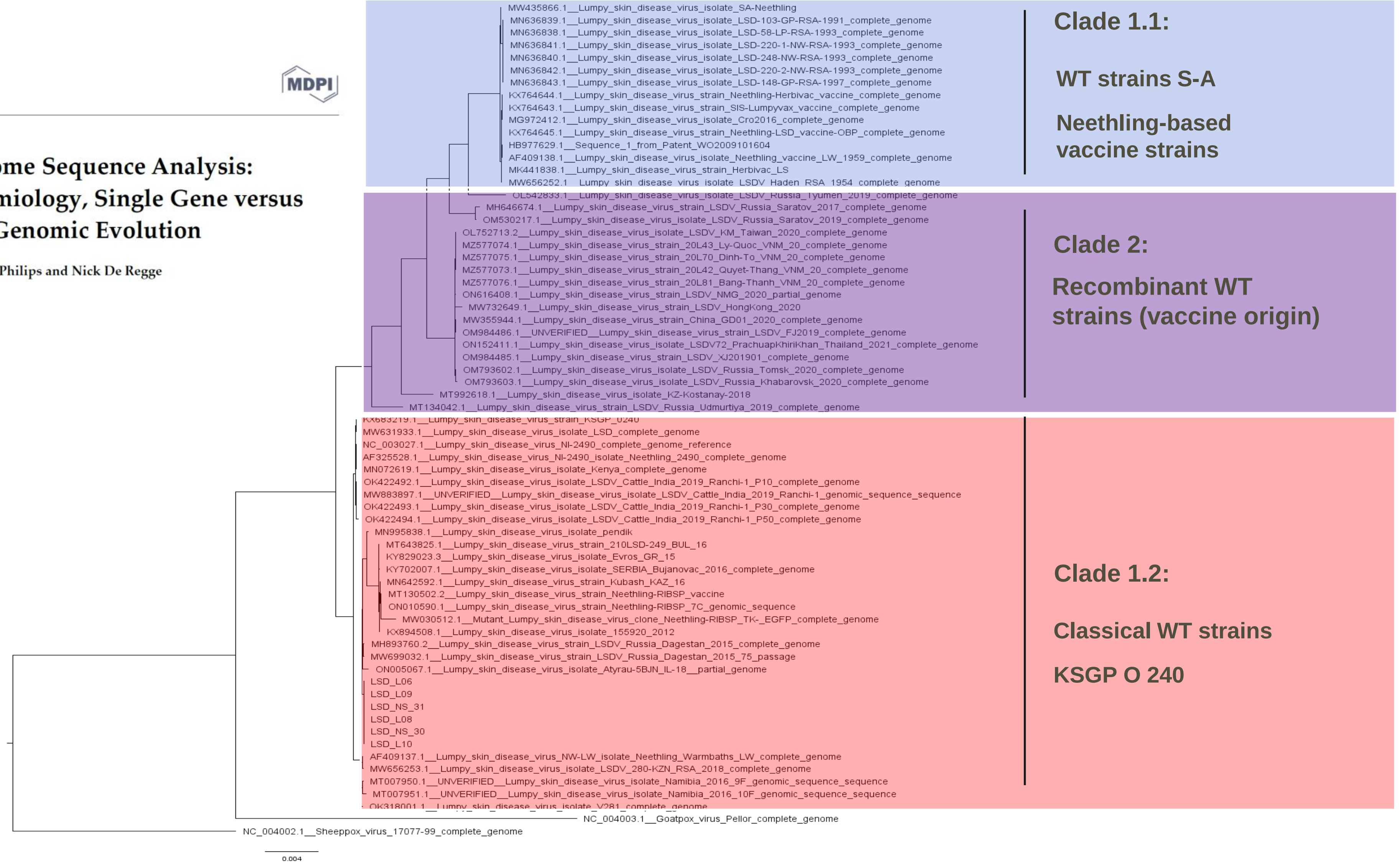
viruses

MDPI

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



Clade 1.1:

WT strains S-A

Neethling-based vaccine strains

Clade 2:

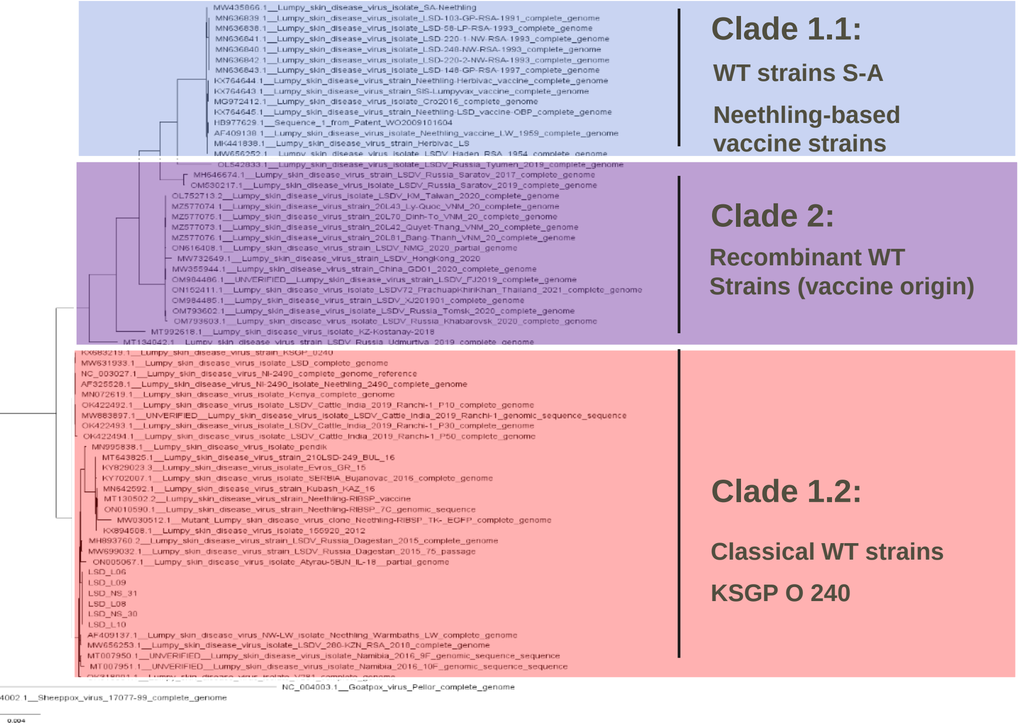
Recombinant WT strains (vaccine origin)

Clade 1.2:

Classical WT strains

KSGP O 240

Lumpy skin disease virus spread



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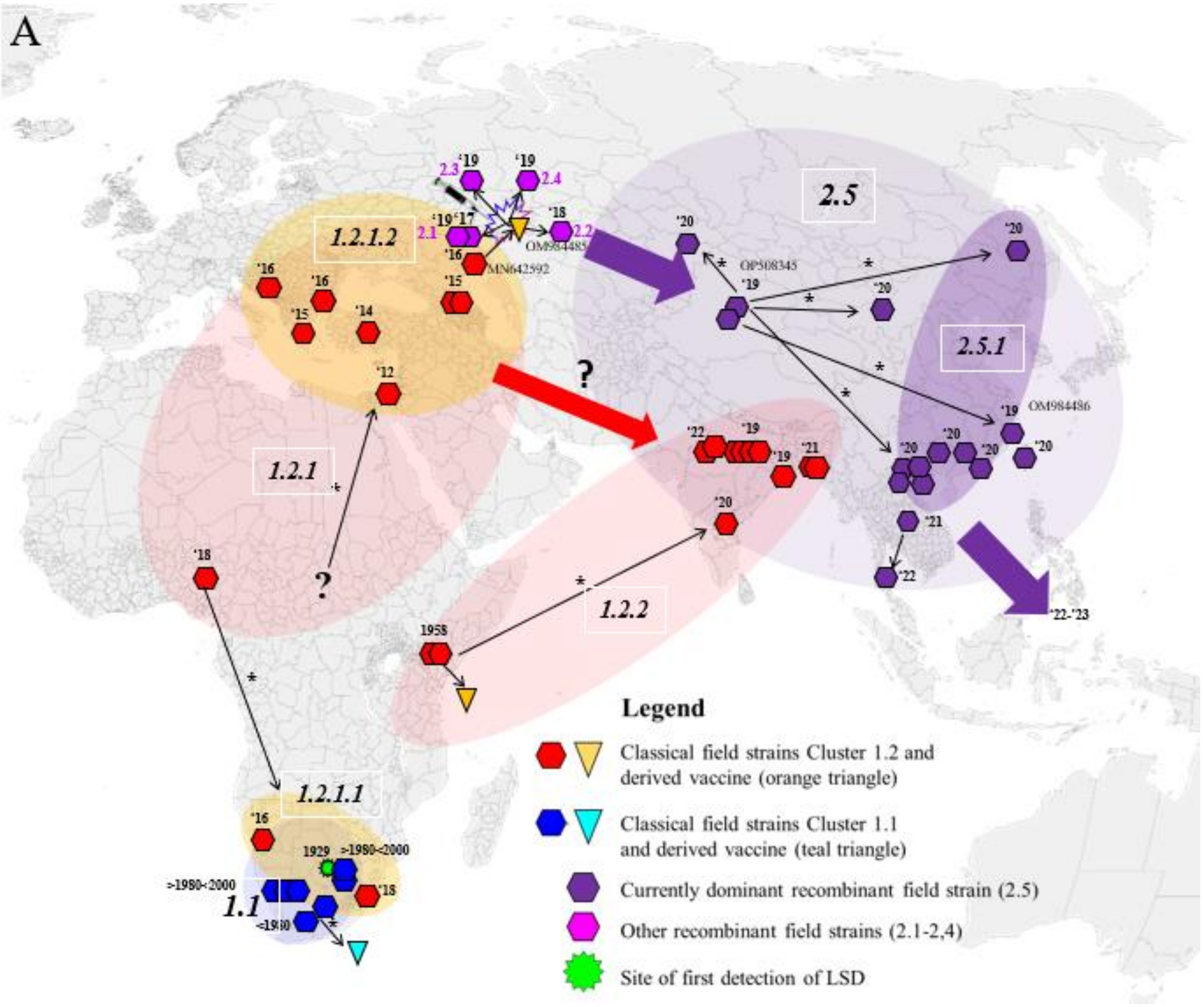
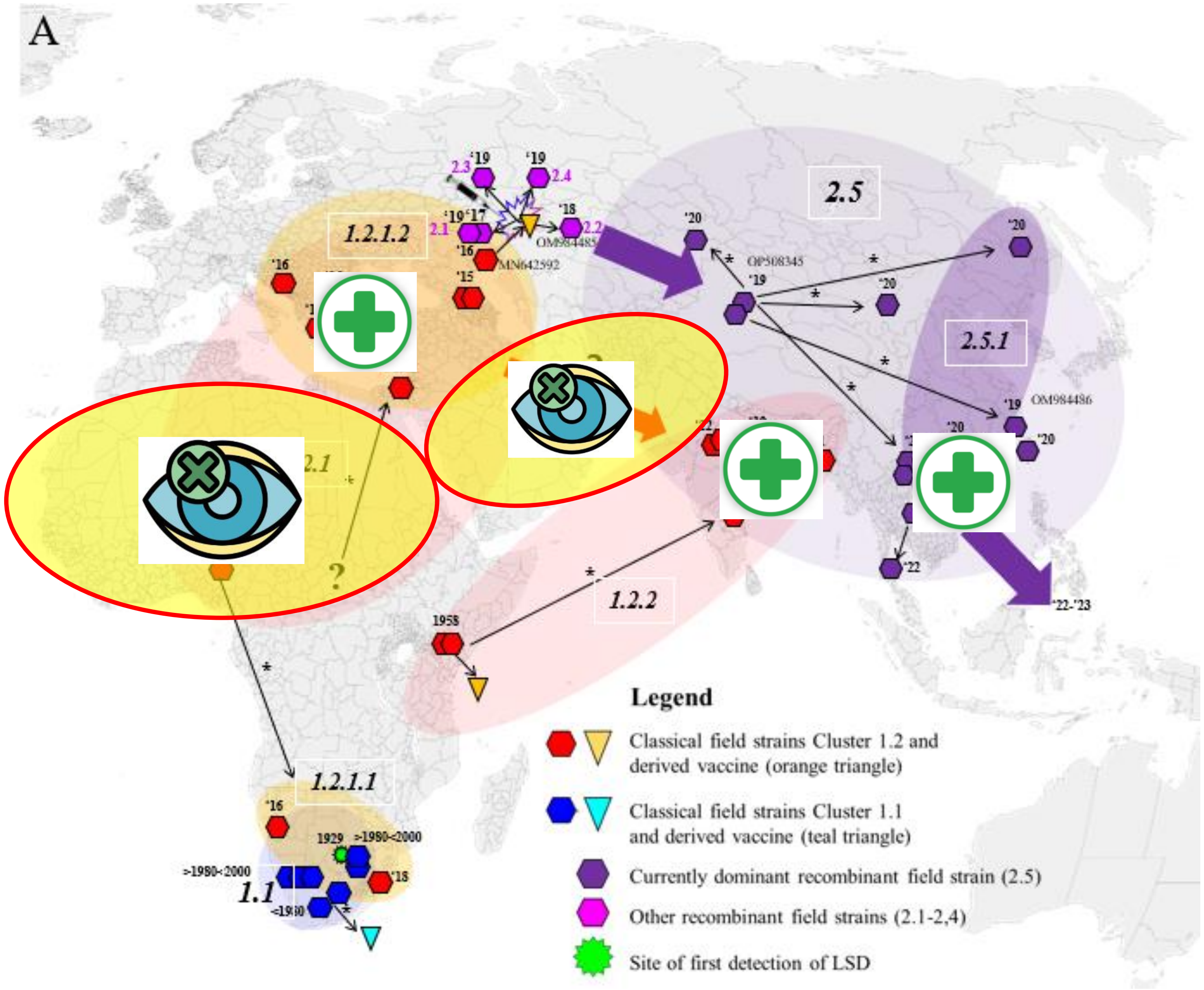
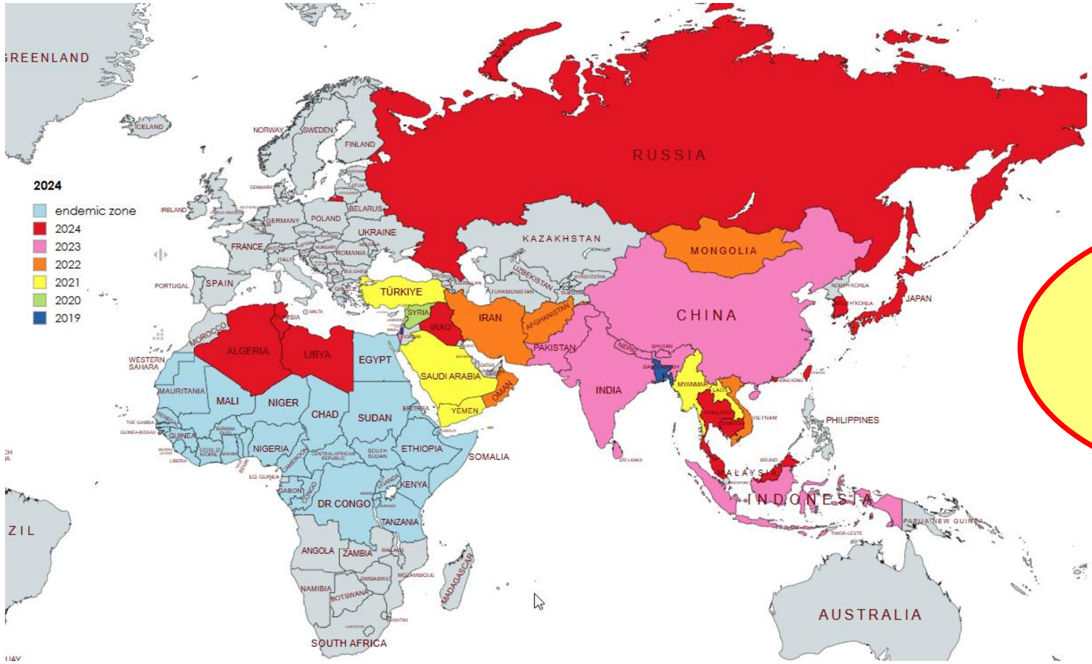


Origin and route of introduction of outbreak strains

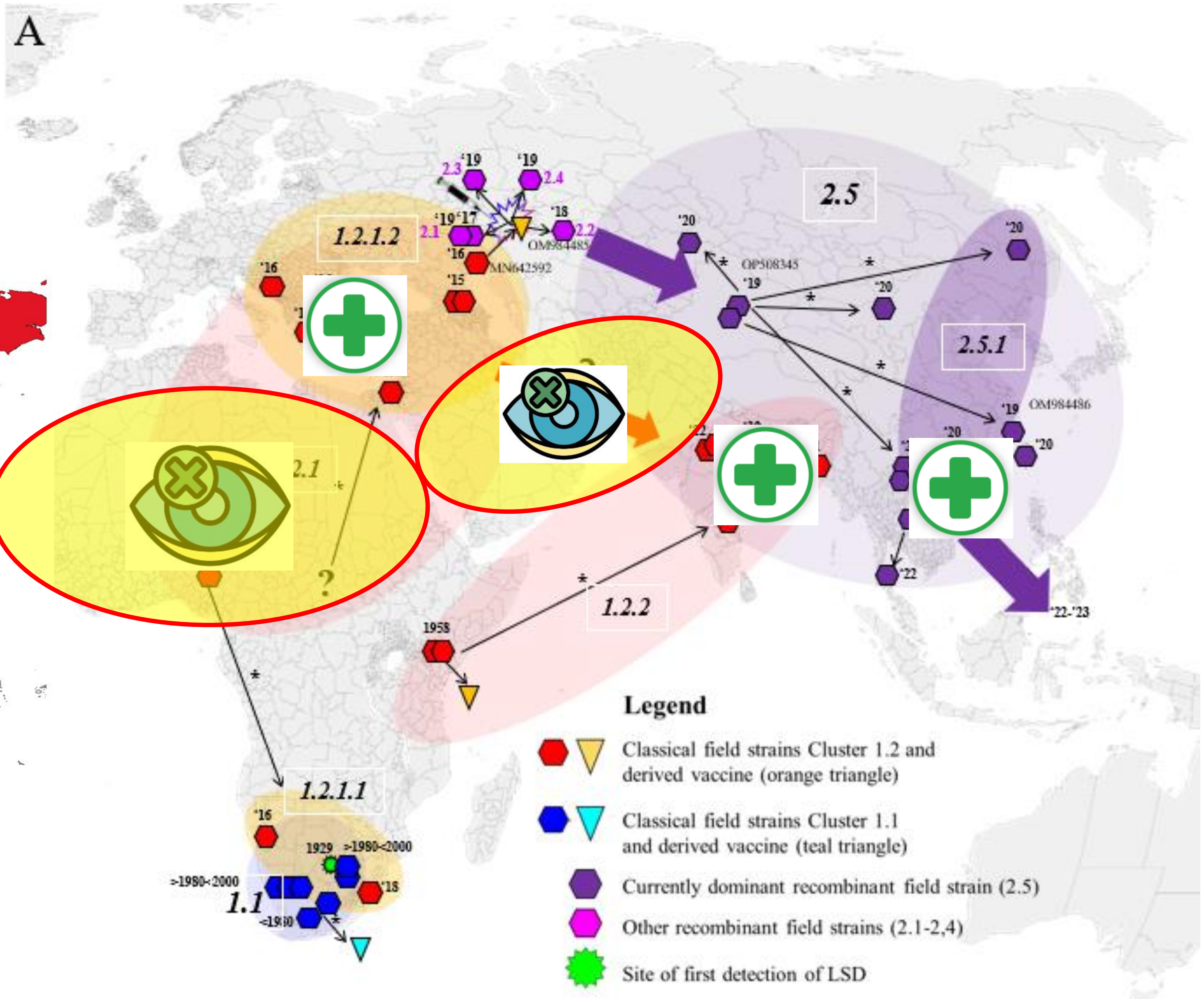
clade	2023	2025	Additional sequences
1.1	10	10	
1.2	32	88	Europe, India
2.5	22	56	SE Asia
2.x	6	6	



Origin and route of introduction of outbreak strains

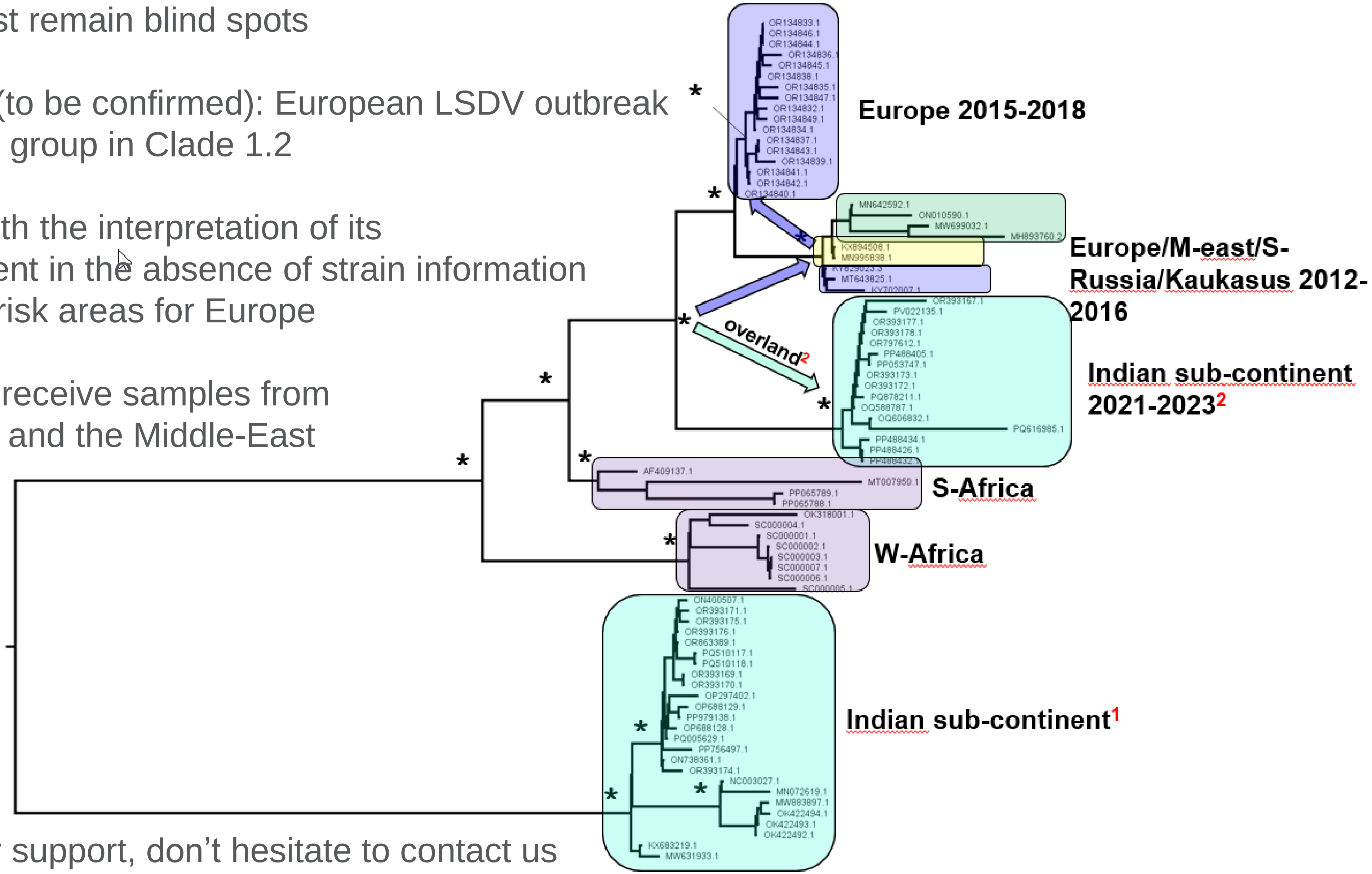


WAHIS database, LSDV outbreaks 2019-2024



Updated phylogeny 2025: clade 1.2

- Africa and Middle-East remain blind spots
- Probable hypothesis (to be confirmed): European LSDV outbreak strains from 2025 will group in Clade 1.2
- But remain carefull with the interpretation of its phylogenetic placement in the absence of strain information from large important risk areas for Europe
- Continued request to receive samples from LSDV cases in Africa and the Middle-East



- EURL is here for your support, don’t hesitate to contact us

Contact

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