



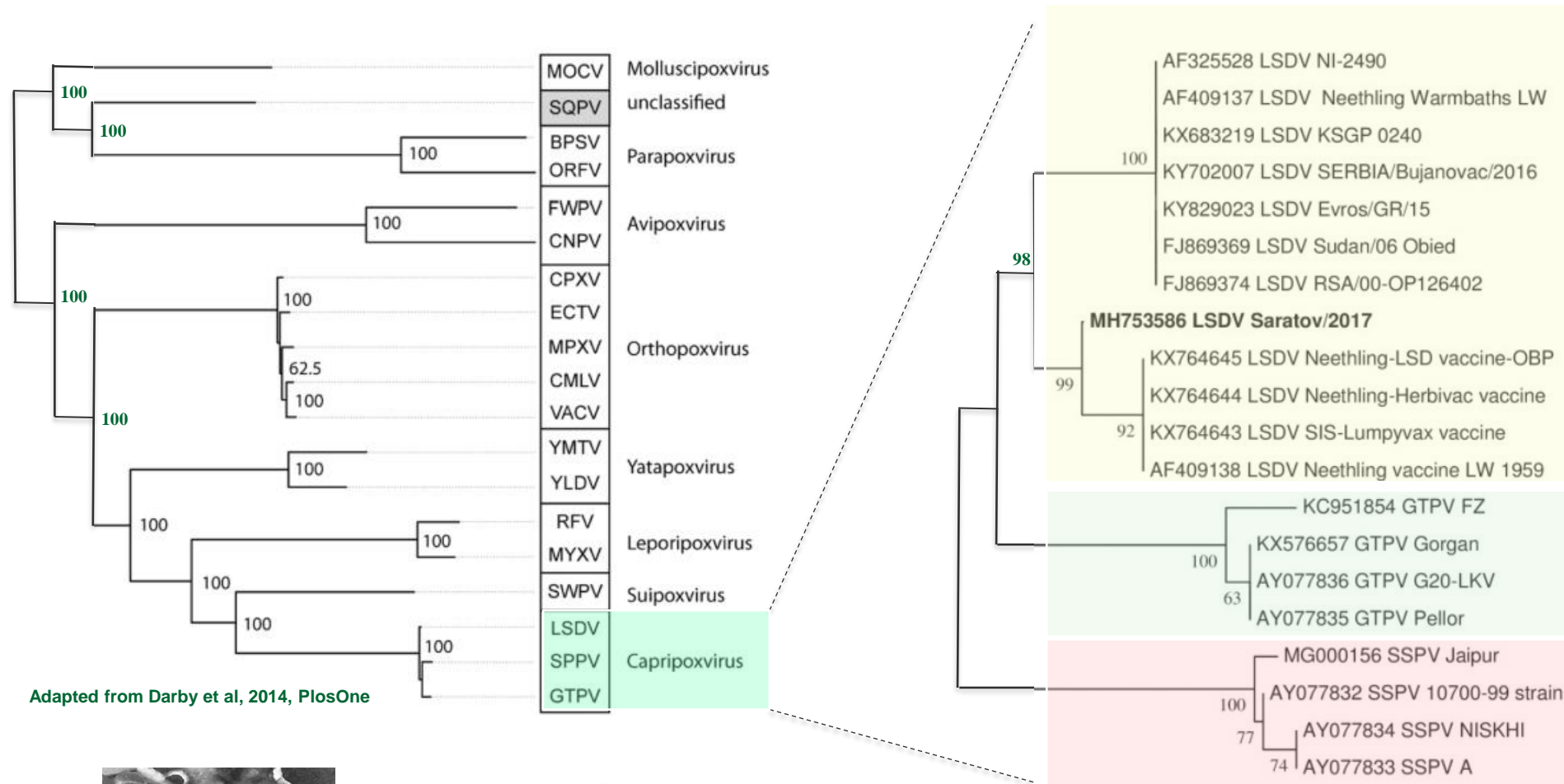
CURRENT LUMPY SKIN DISEASE VIRUS EPIDEMIOLOGY

Nick De Regge

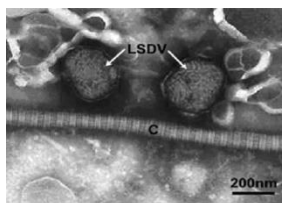
Online meeting – WOAHA central Asia

13 December 2023

Capripox viruses



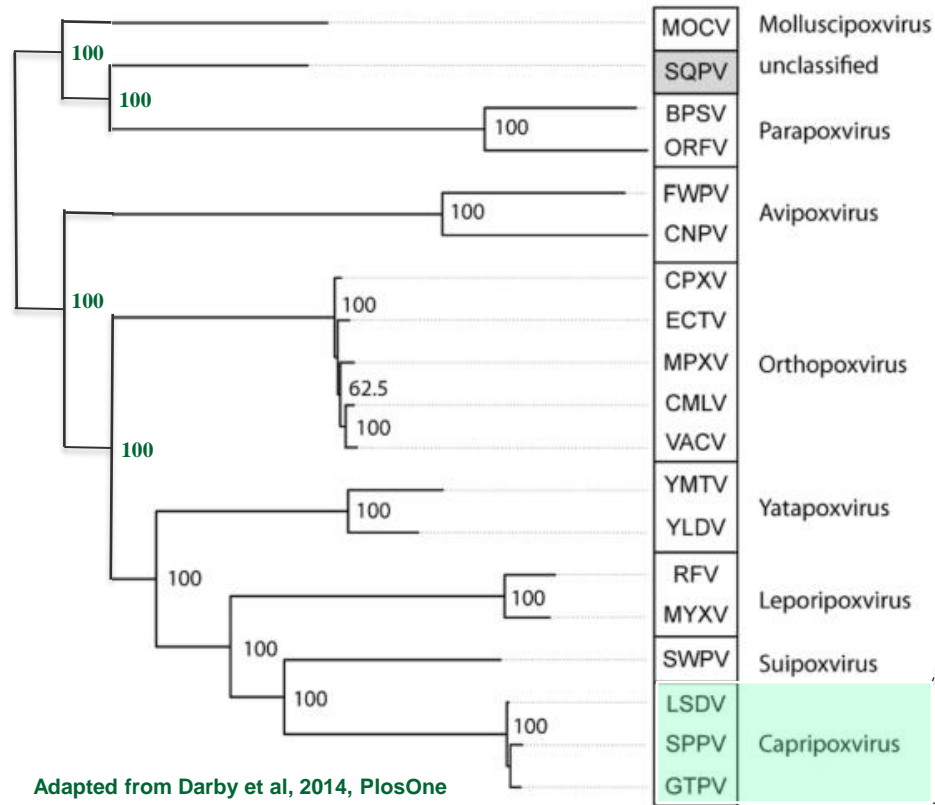
Adapted from Darby et al, 2014, PlosOne



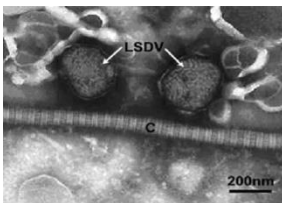
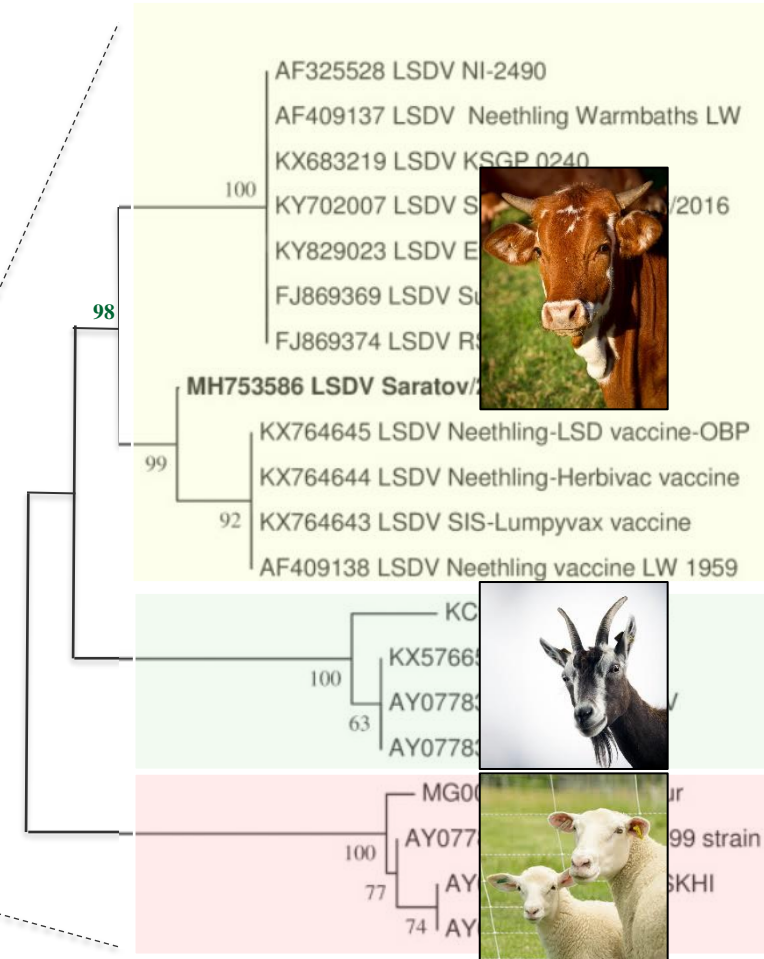
Tageldin et al 2014

- Not segmented, dsDNA
- Size: 150 to 160 kbp → +/- 147 putative genes
- High nucleotide identity between SPPV, GTPV, LSDV: +/- 96%

Capripox viruses



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Lumpy skin disease virus

- Incubation period - aspecific clinical signs (fever, depression, drop in milk production, ...)
- Disease severity varies between animals

severe LSD cases – mild LSD cases – subclinical animals – no productive infection



- 30 to 50% diseased animals in experimental settings
- Morbidity: 10 to 45%; Mortality: 1-5%
- Self limiting disease
- No-carrier status, no latency

Outline

- **Current epidemiological situation LSDV**
- **LSDV diagnostics: virology**
- **LSDV diagnostics: serology**
- **LSDV vaccines: requirements for vaccine production – quality control**
- **LSDV vaccines: recommendations from safety/efficacy studies**

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

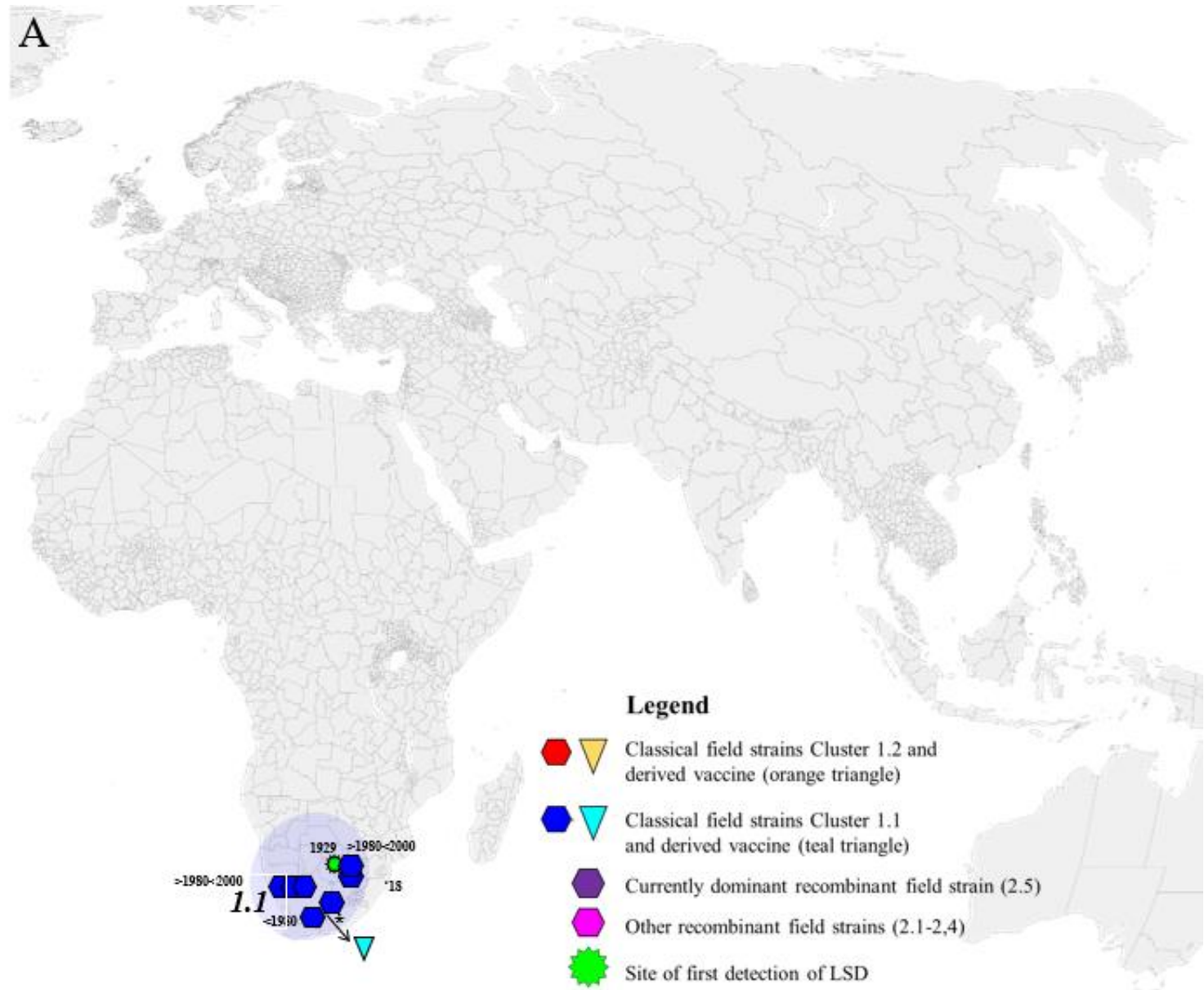
Data extracted from WOAH-WAHIS database



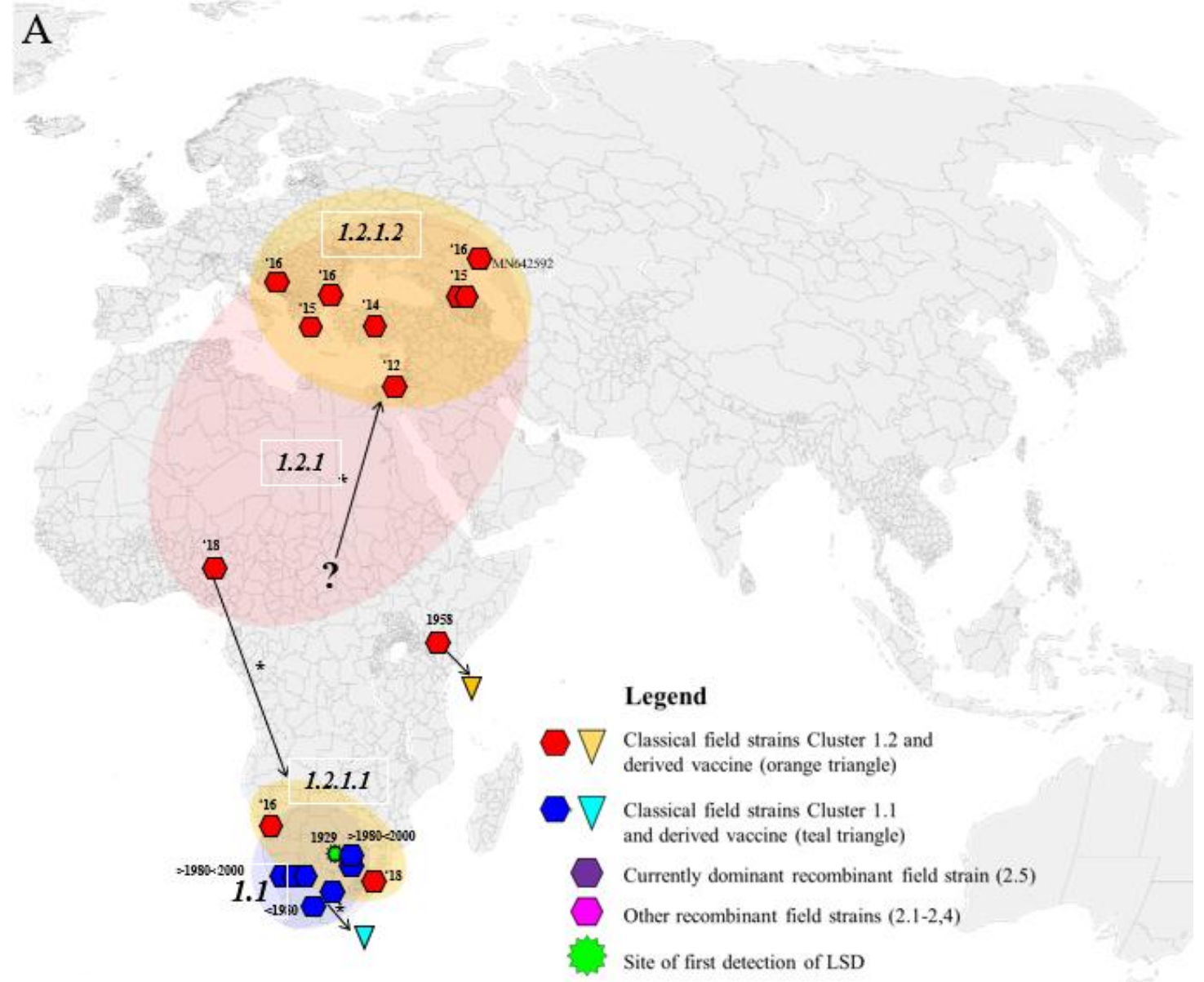
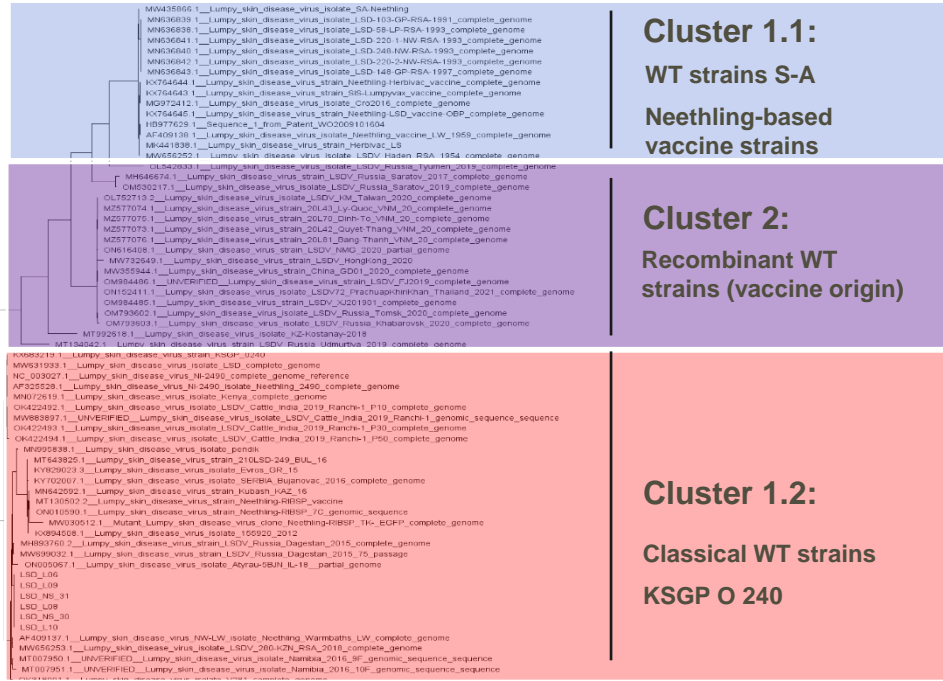
Lumpy skin disease virus: phylogeny



Lumpy skin disease virus spread

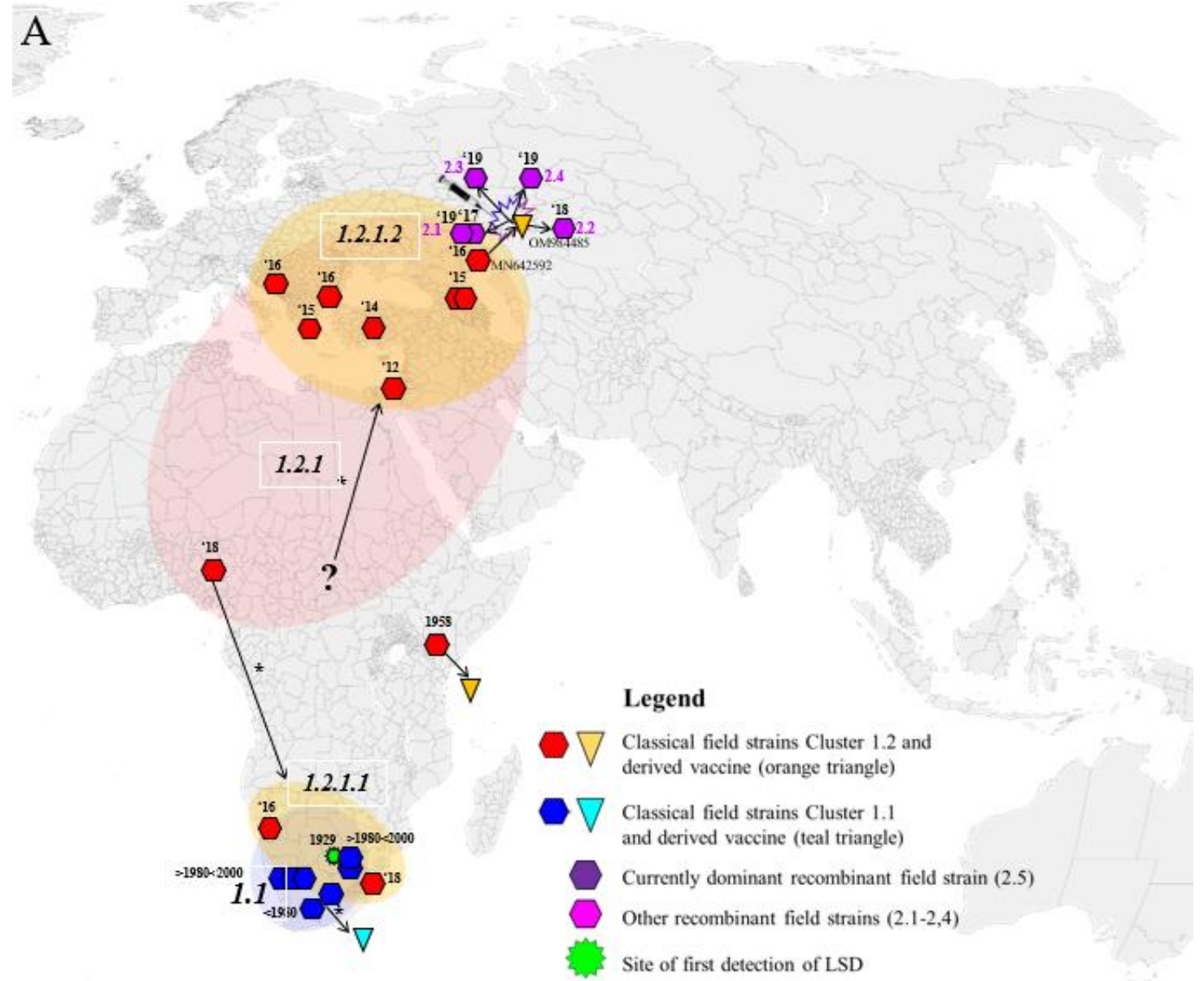


Lumpy skin disease virus spread

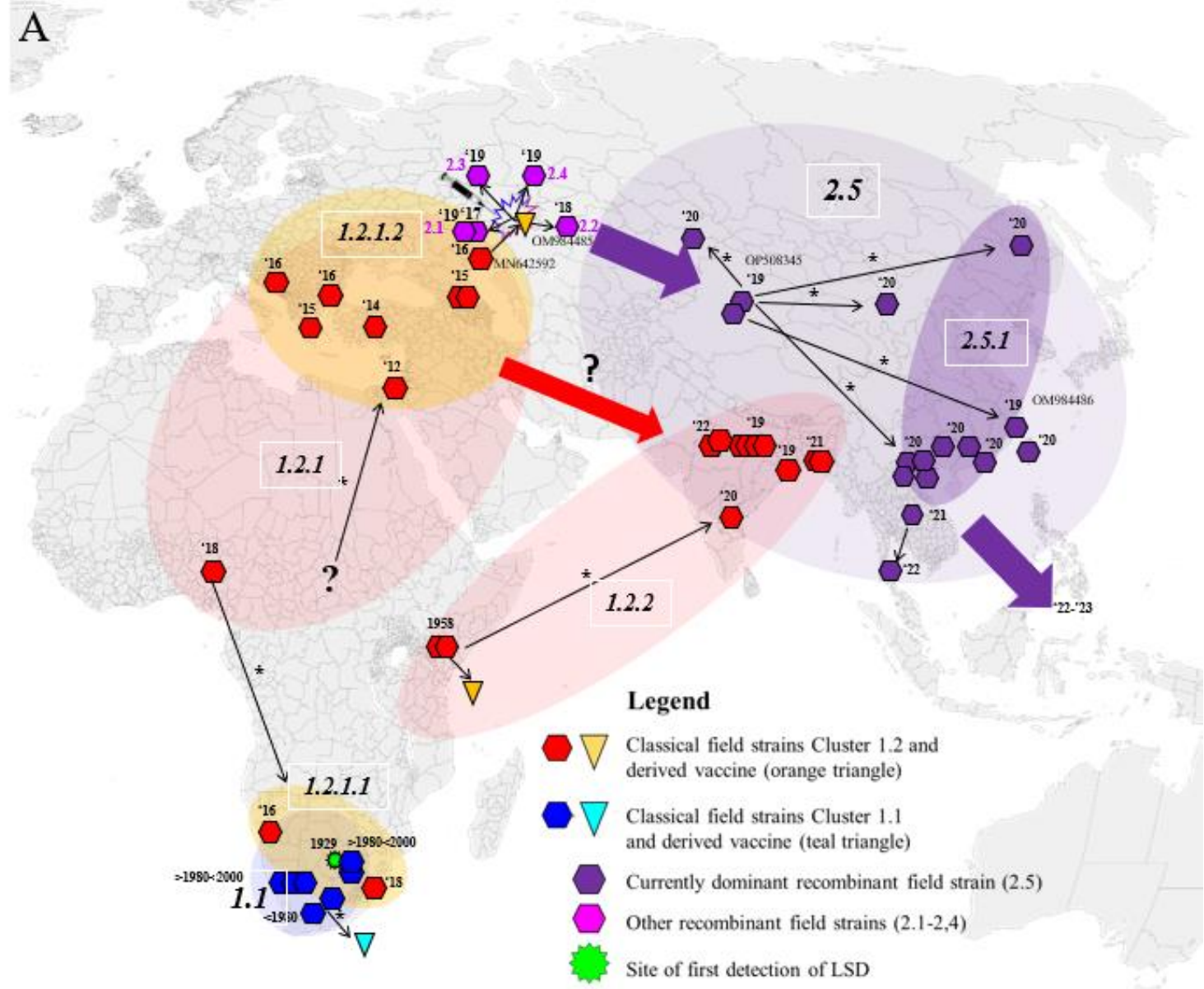
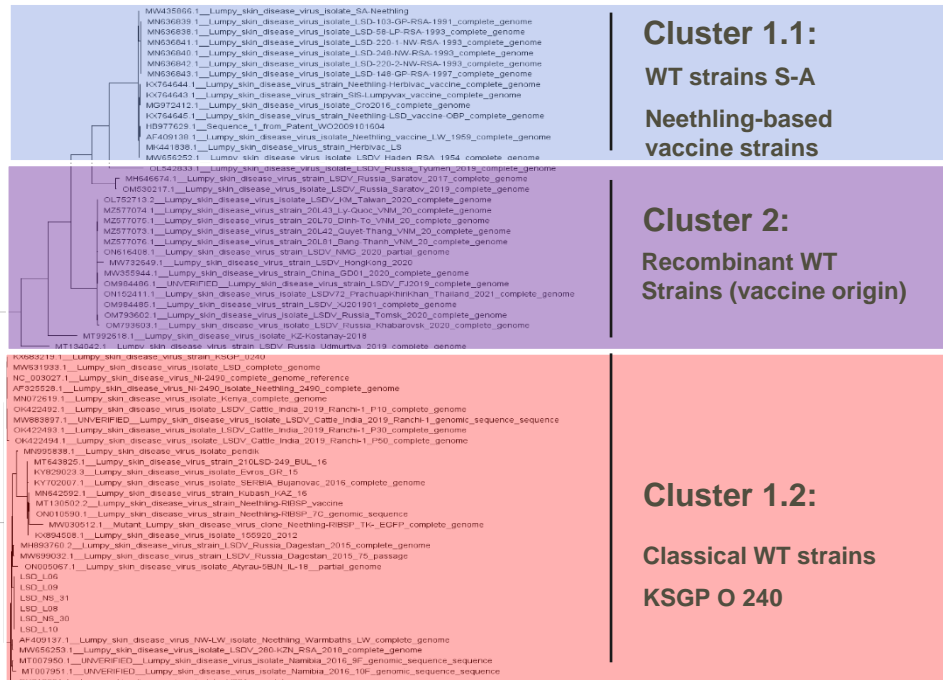


10002_1_Sheepox_virus_17077-99_complete_genome
NC_004043_1_Guillipox_virus_Pelot_complete_genome

Lumpy skin disease virus spread



Lumpy skin disease virus spread

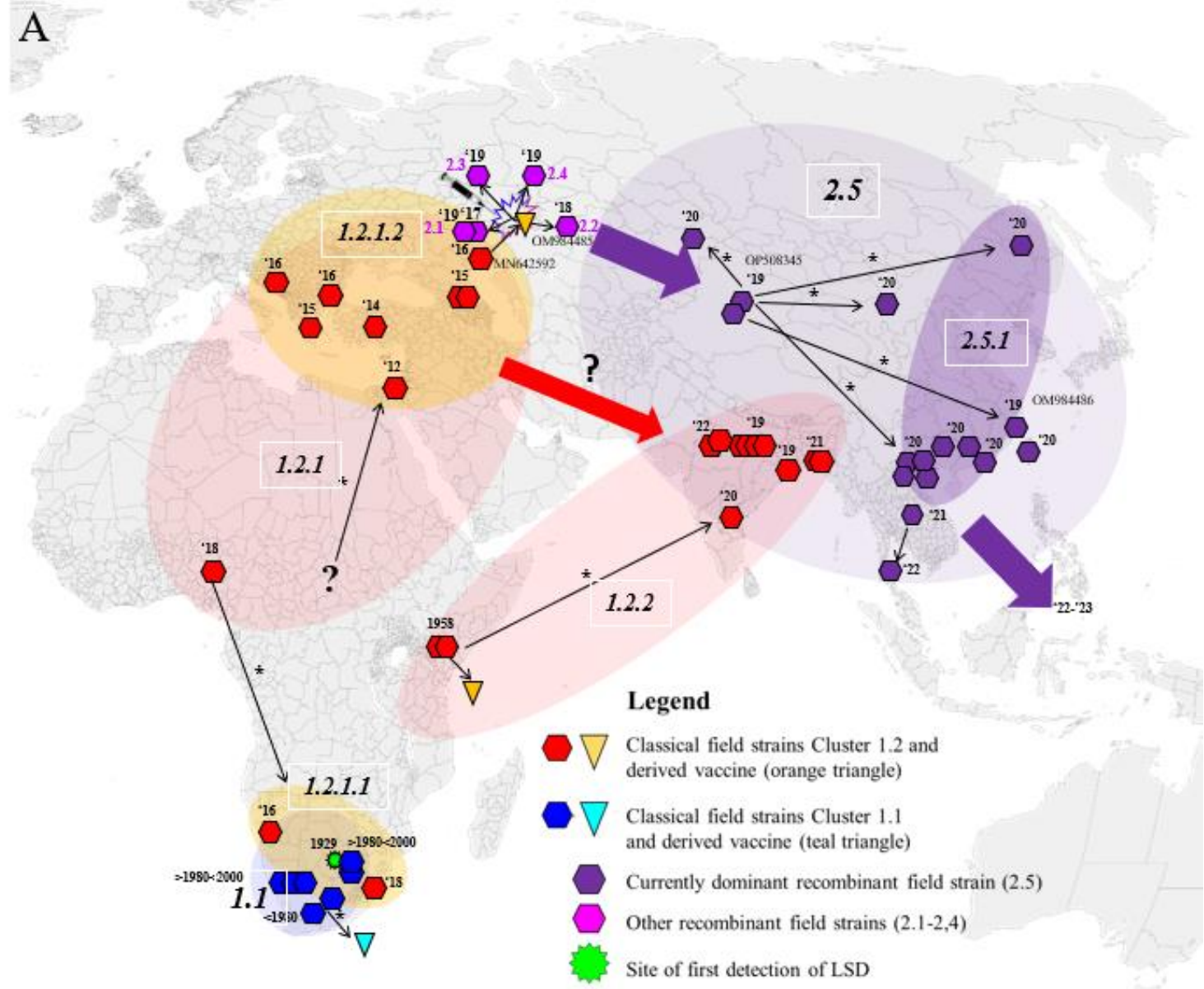
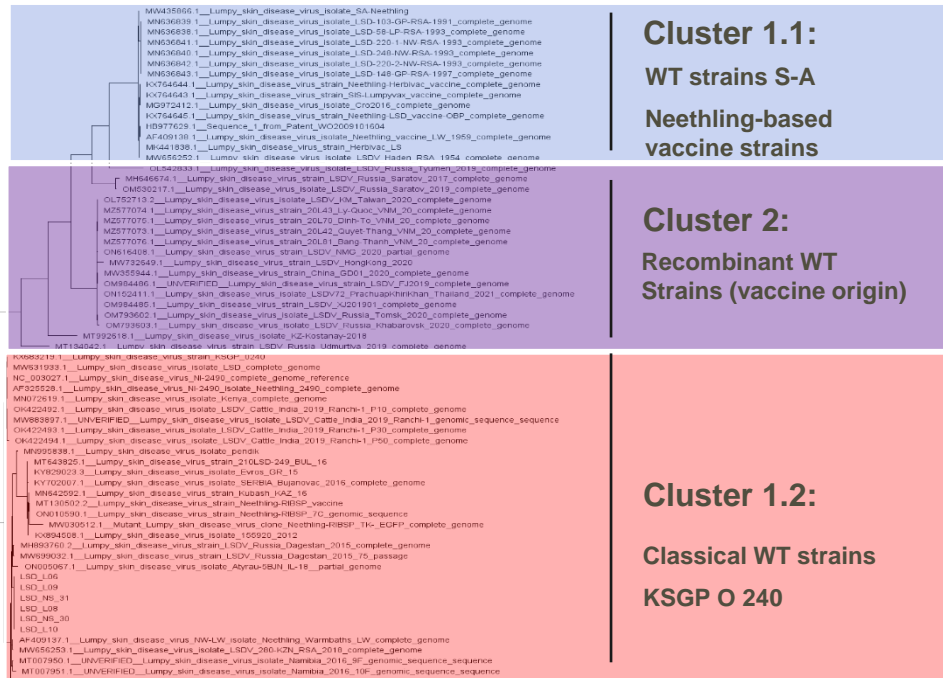


Article

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, Wannas Philips and Nick De Regge

Lumpy skin disease virus spread – recombinant strains



0002_1_Sheepox_virus_12077-99_complete_genome NC_064003.1_Gaolpo_virus_Pelot_complete_genome



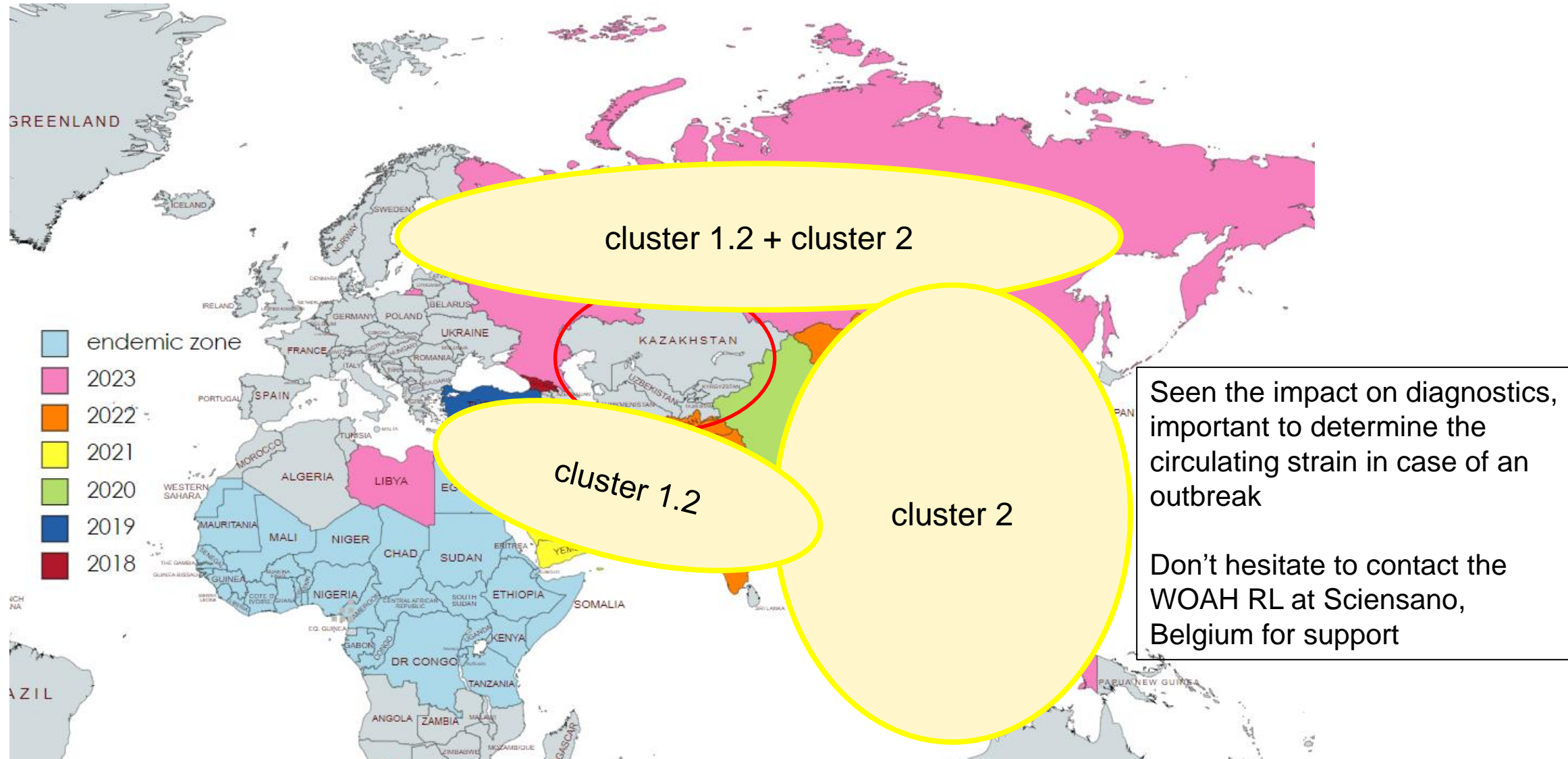
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Contact

Nick De Regge • nick.deregge@sciensano.be • +32 2 379 06 27