



Food and Agriculture
Organization of the
United Nations



Regional epidemiological situation on TADs of ruminants

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What are TADs?

- Infectious/Contagious diseases
- Have tendency to become **epidemics**
- Can easily **cross borders** (have many means of transmission)
- Have a **high economical impact**
 - Affect trade
 - High costs to control
 - Affect food security
- Need **regional efforts** to control
- Examples of TADs:
 - Foot and Mouth Disease (FMD)
 - Peste des petits ruminants (PPR)
 - Lumpy Skin Disease (LSD)



GF-TADs
GLOBAL FRAMEWORK FOR THE
PROGRESSIVE CONTROL OF
TRANSBOUNDARY ANIMAL DISEASES



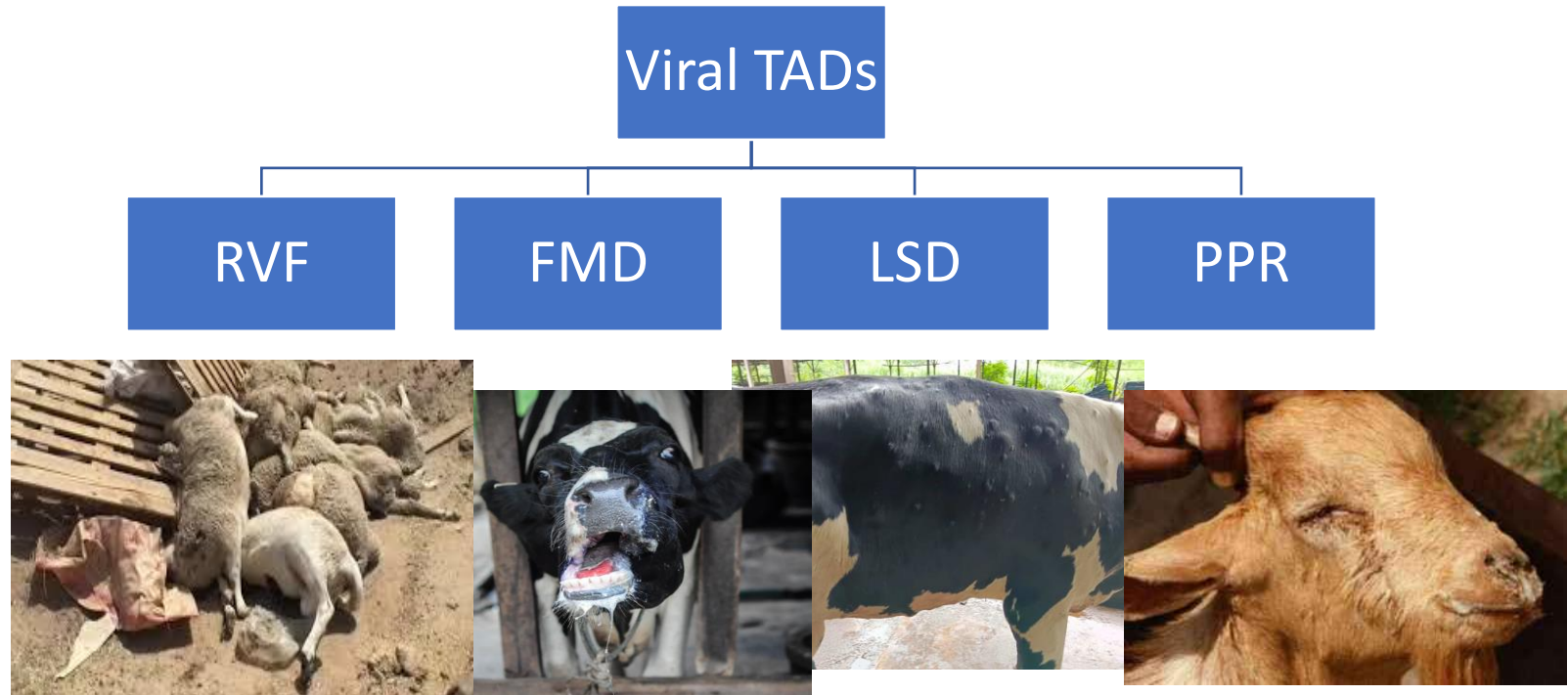
Food and Agriculture
Organization of the
United Nations



World Organisation
for Animal Health
Founded as OIE

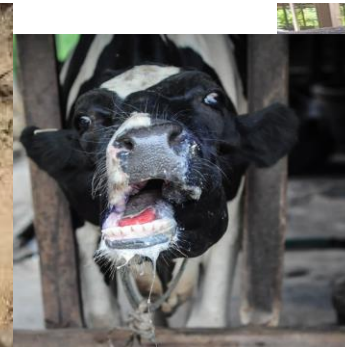
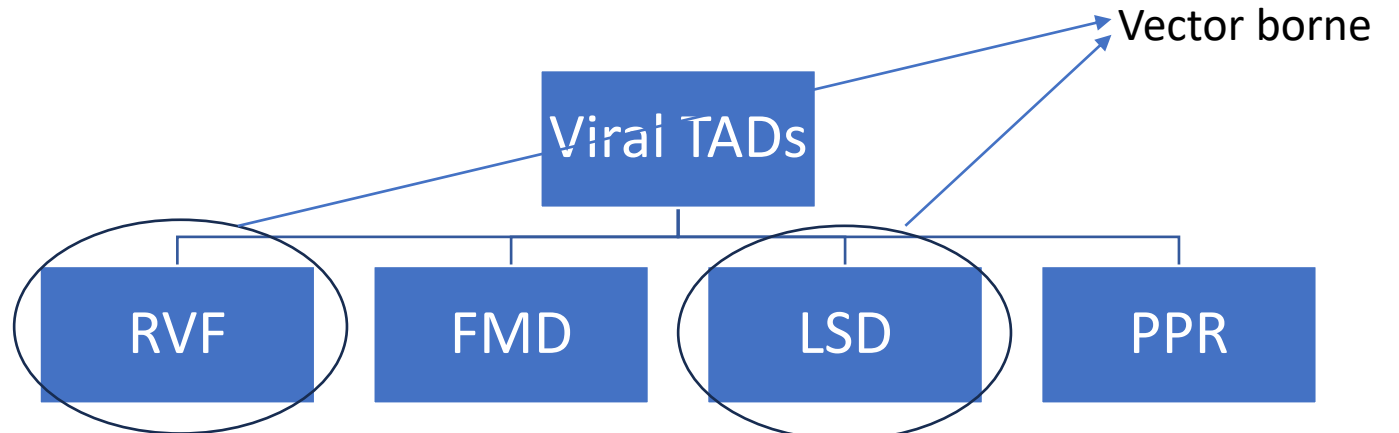
Which diseases?

- Viral
- According to the most recent prioritization



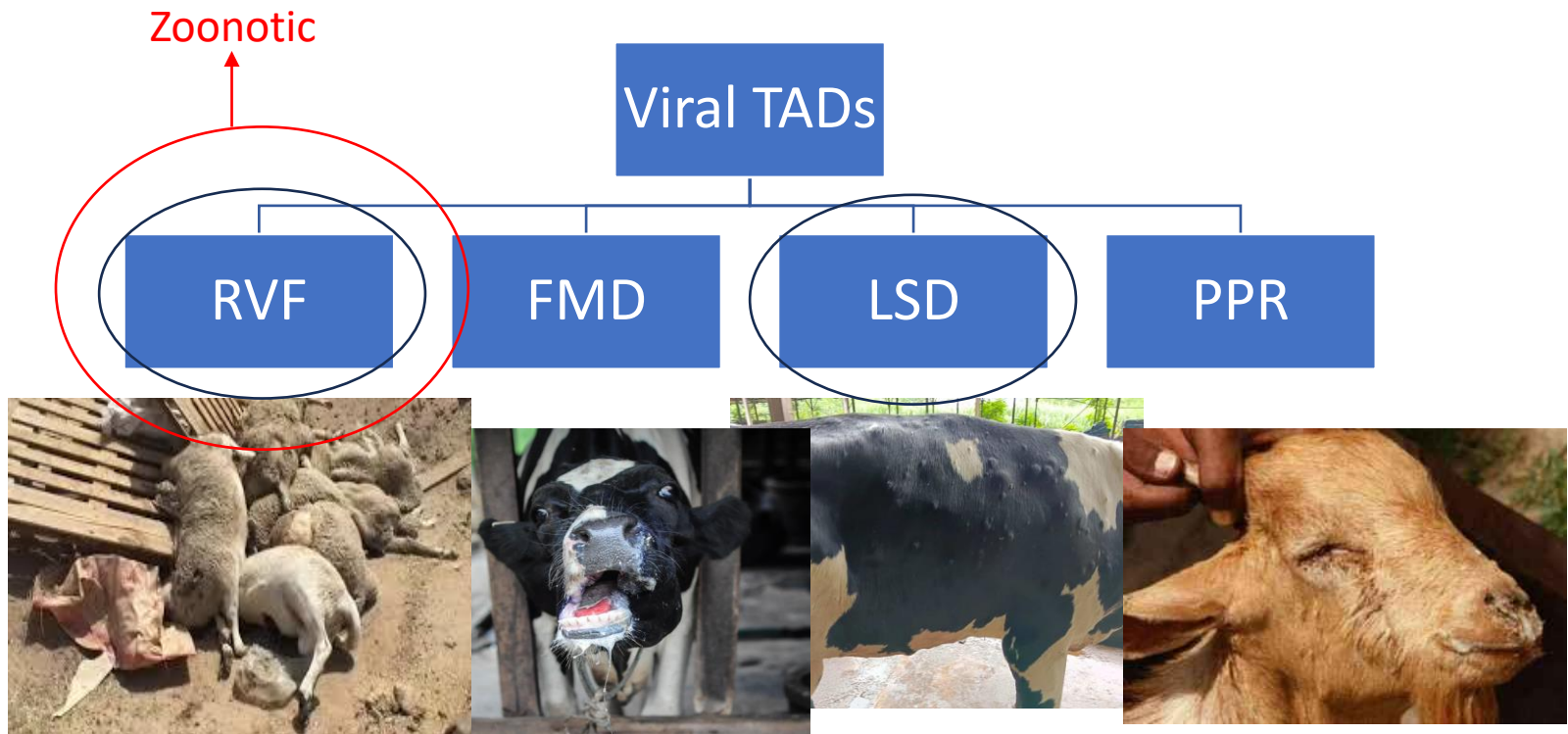
Which diseases?

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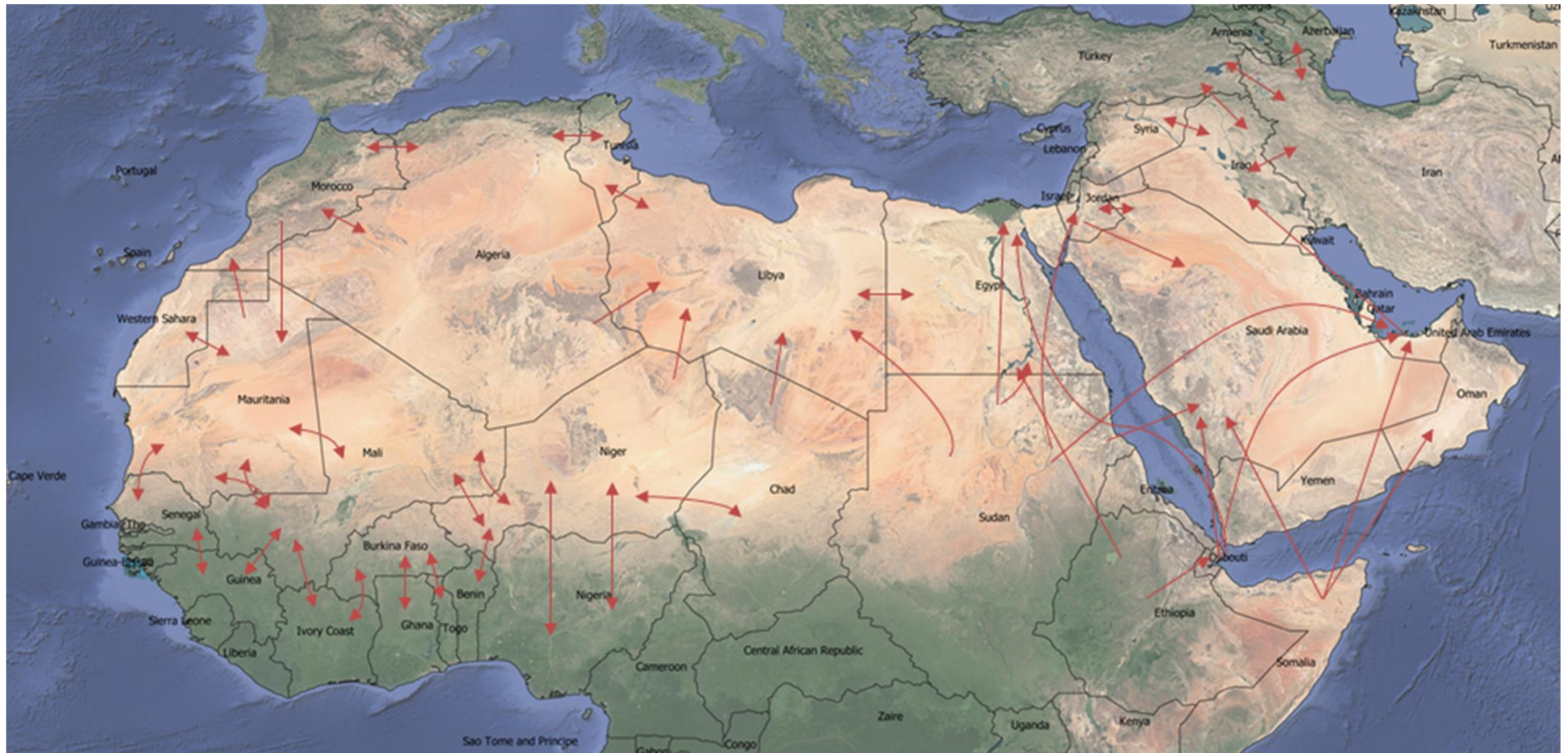


Which diseases?

- Viral
- According to the most recent prioritization



Livestock movement

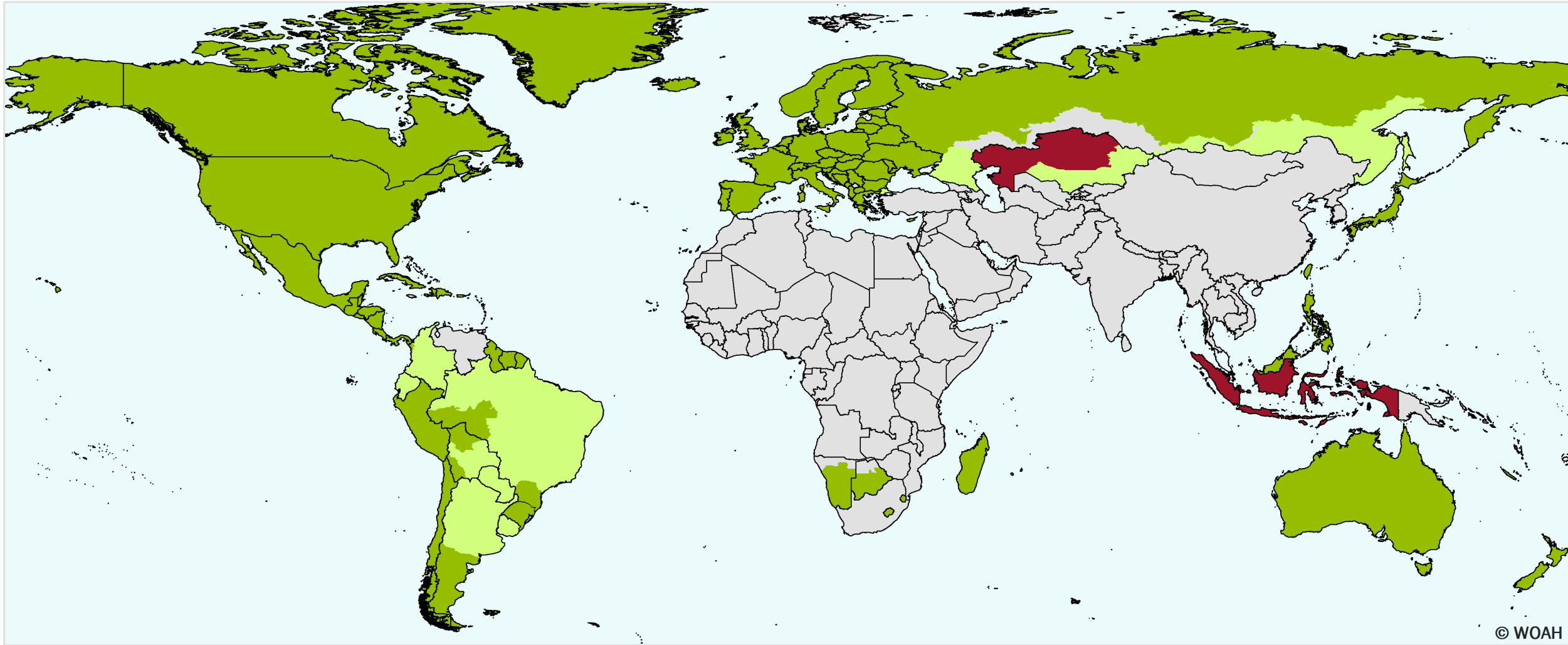


FMD

- Foot and mouth disease (FMD) is an **extremely contagious** and severe viral disease. It can cause incredible losses in cloven-hoofed livestock and wildlife species, including cattle, pigs, wild boar, sheep, bison, elk, deer and llamas.
- FMD is found in **all excretions and secretions** from infected animals.
- FMDv is an aphthovirus of the family Picornaviridae. There are seven strains (A, O, C, SAT1, SAT2, SAT3, and Asia1).
- Immunity to one FMDV serotype **does not protect** an animal from other serotypes. Protection from other strains within a serotype **varies** with their antigenic similarity.
- Various **disinfectants** including sodium hydroxide, sodium carbonate, citric acid and Virkon-S® are effective against FMDV.

WOAH Members' official FMD status map

Last update May 2023



Members and zones recognised as free from FMD without vaccination



Suspension of FMD free status



Containment zone within a FMD free zone
(please refer to the Southern Africa regional map for visualisation)

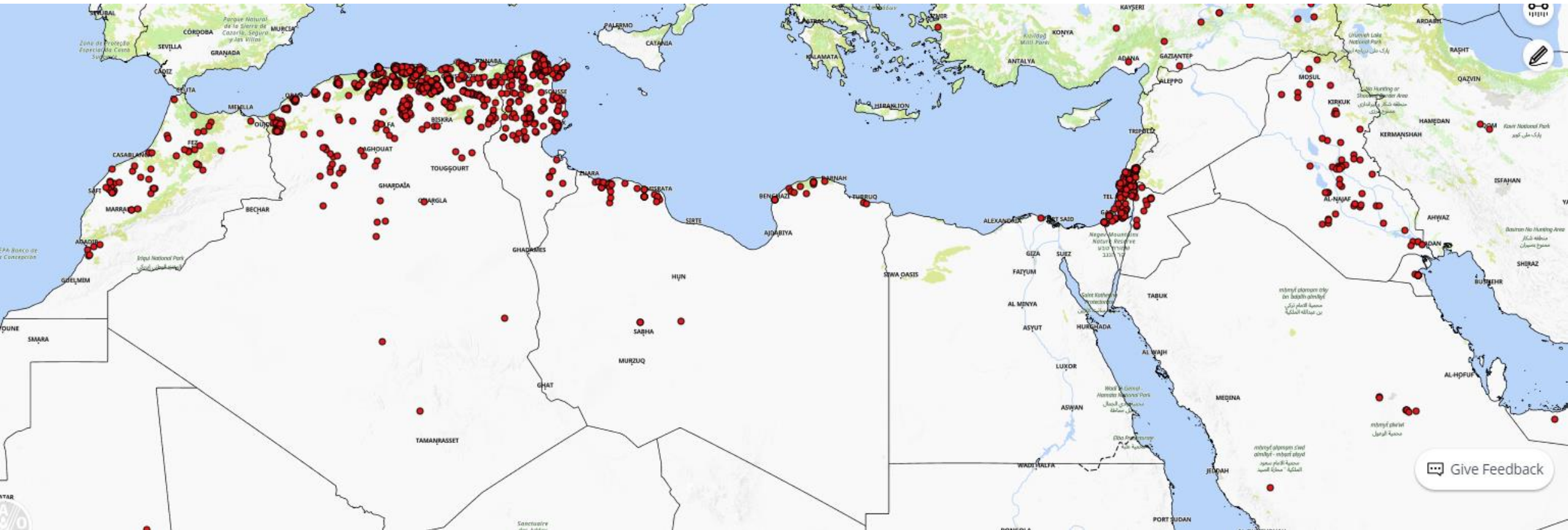


Members and zones recognised as free from FMD with vaccination



Countries and zones without an official status for FMD

Reported All serotypes (2013-2023)



Reported O serotype (2013-2023)

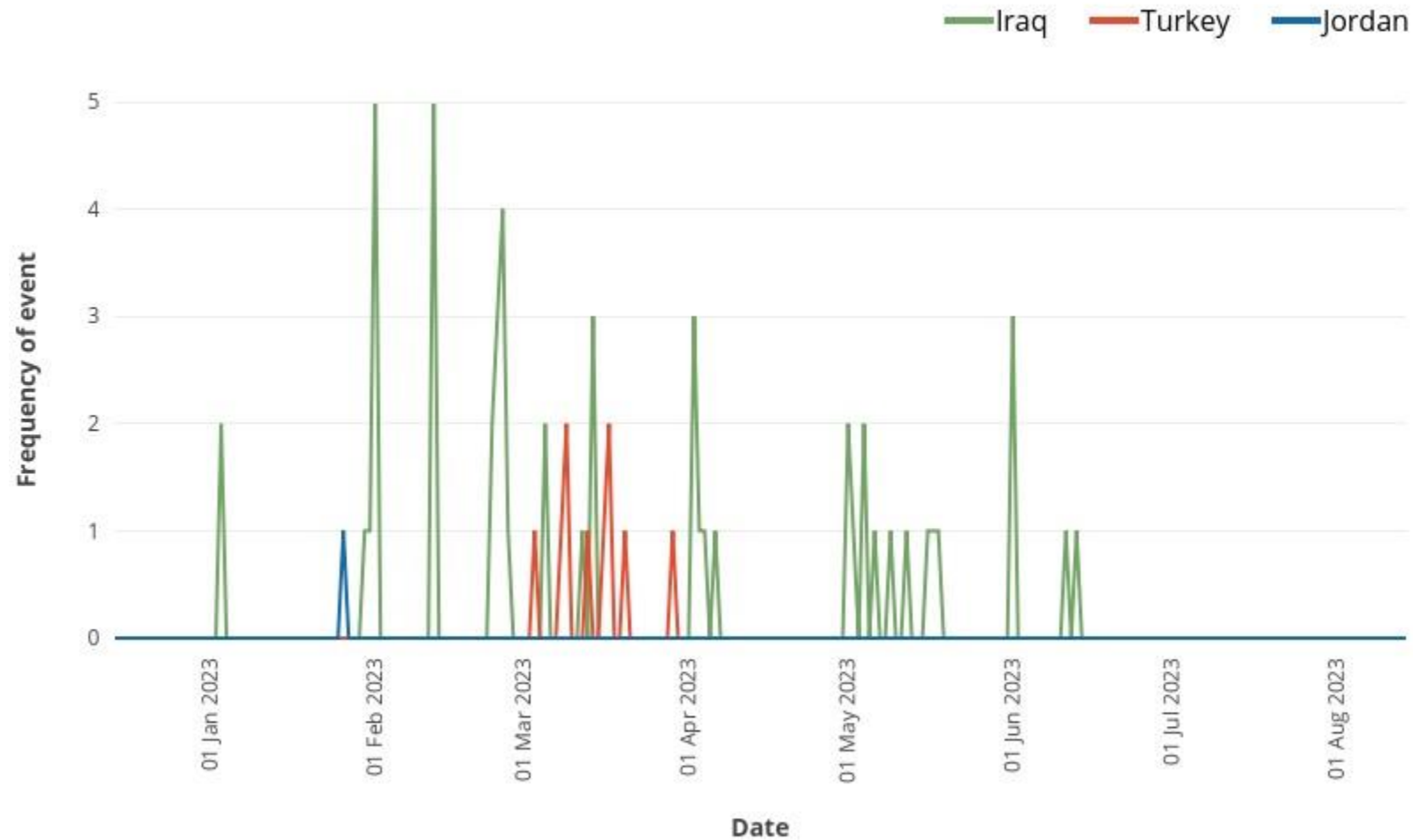


Reported SAT-2 serotype (2013-2023)



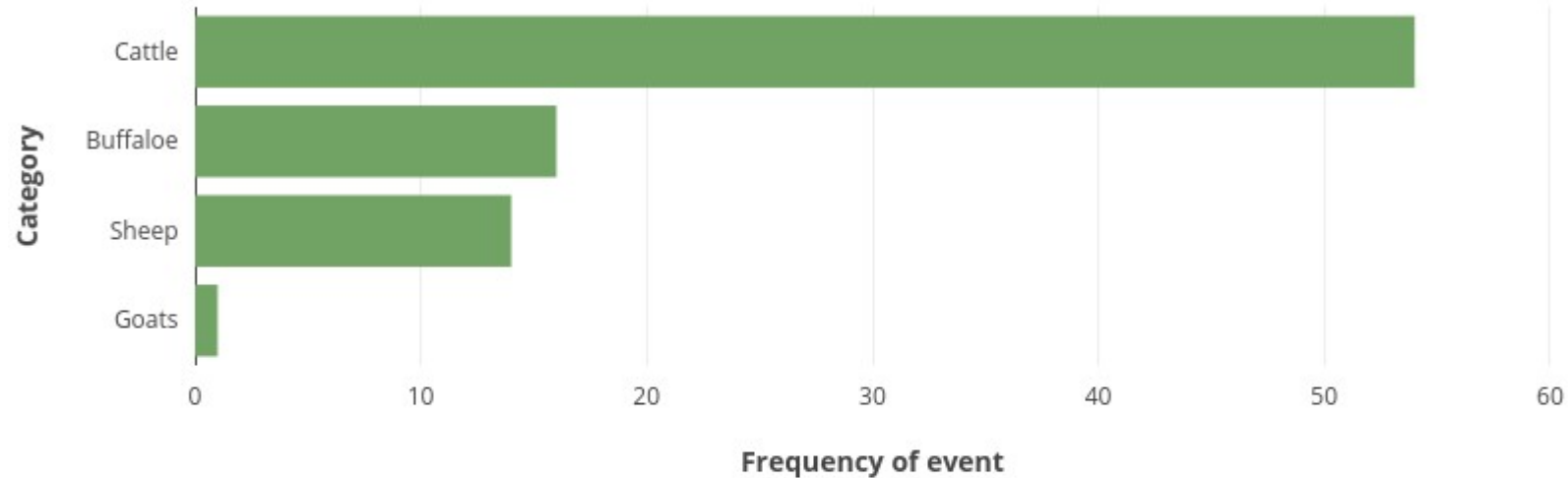
Recent SAT 2 outbreak in ME

Timeline

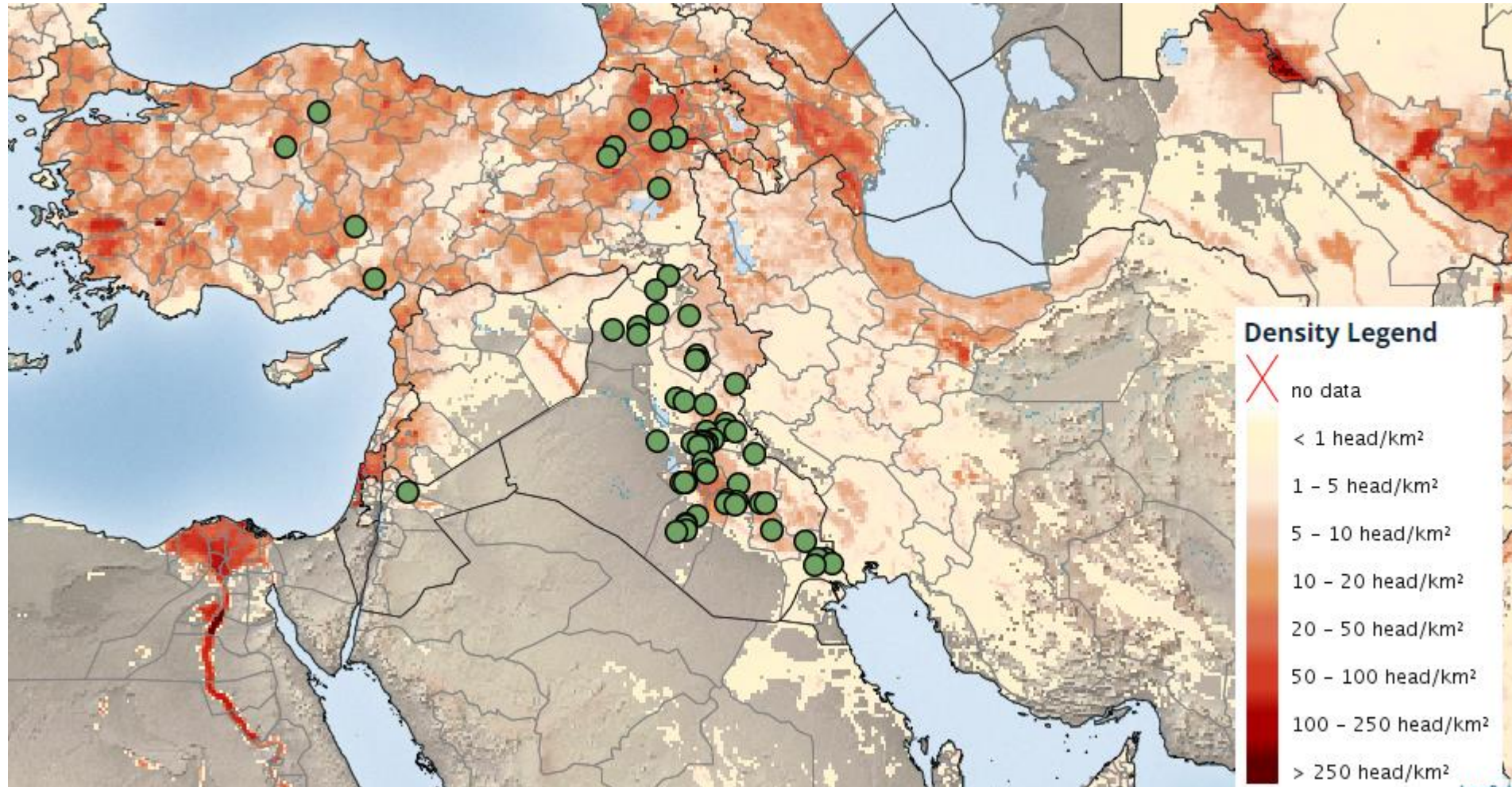


Recent SAT 2 outbreak in ME

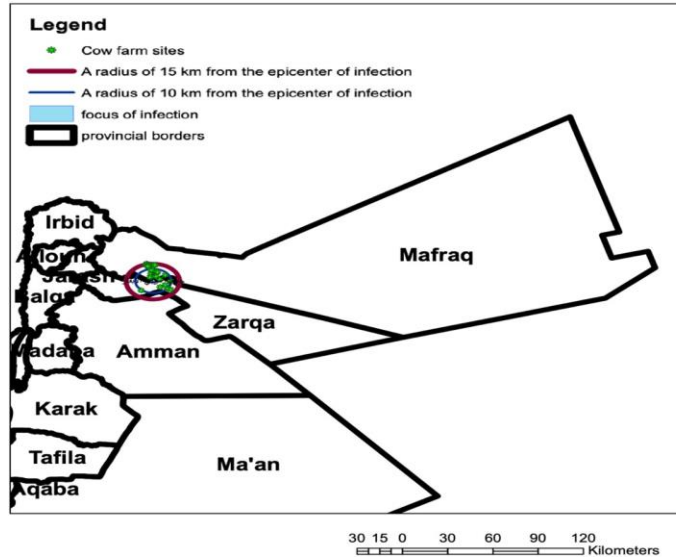
Explore epidemiology



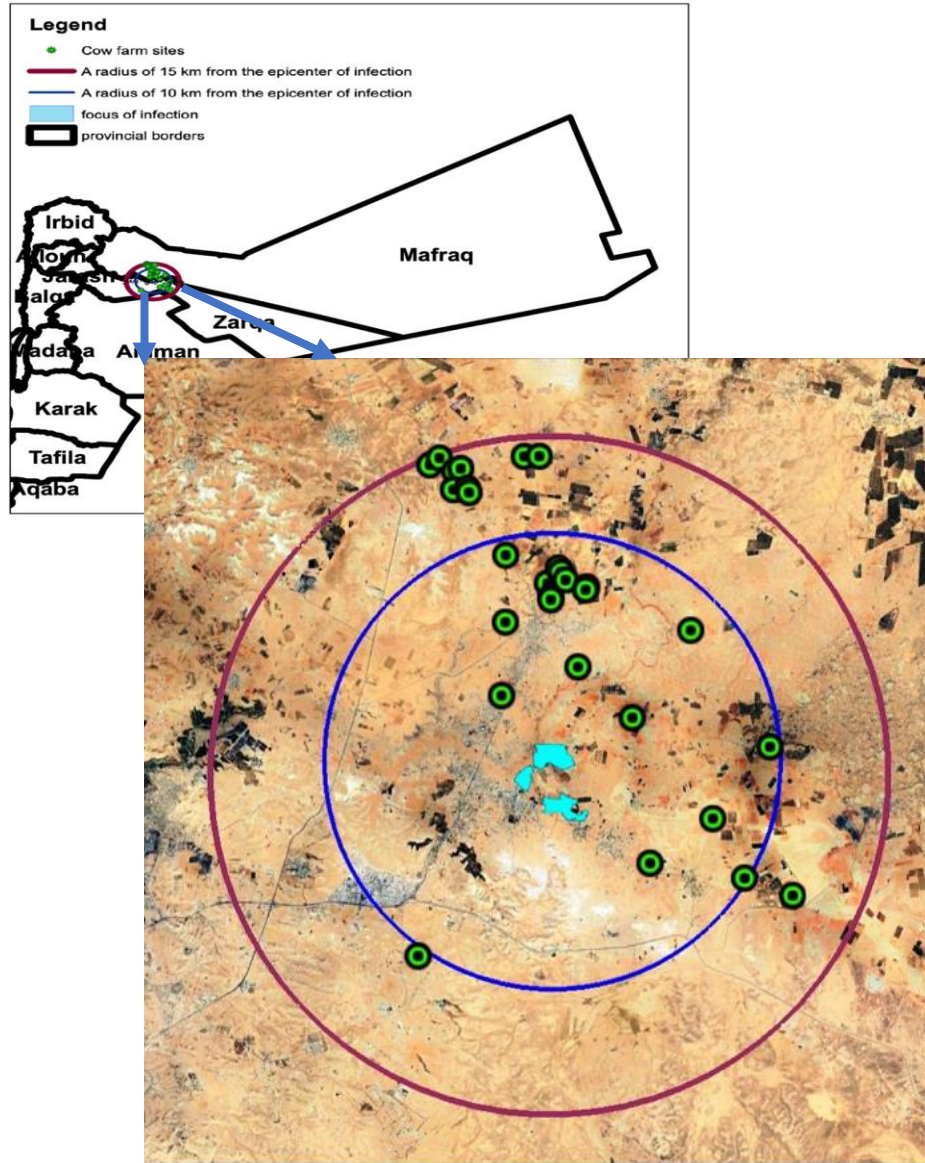
Recent SAT 2 outbreak in ME



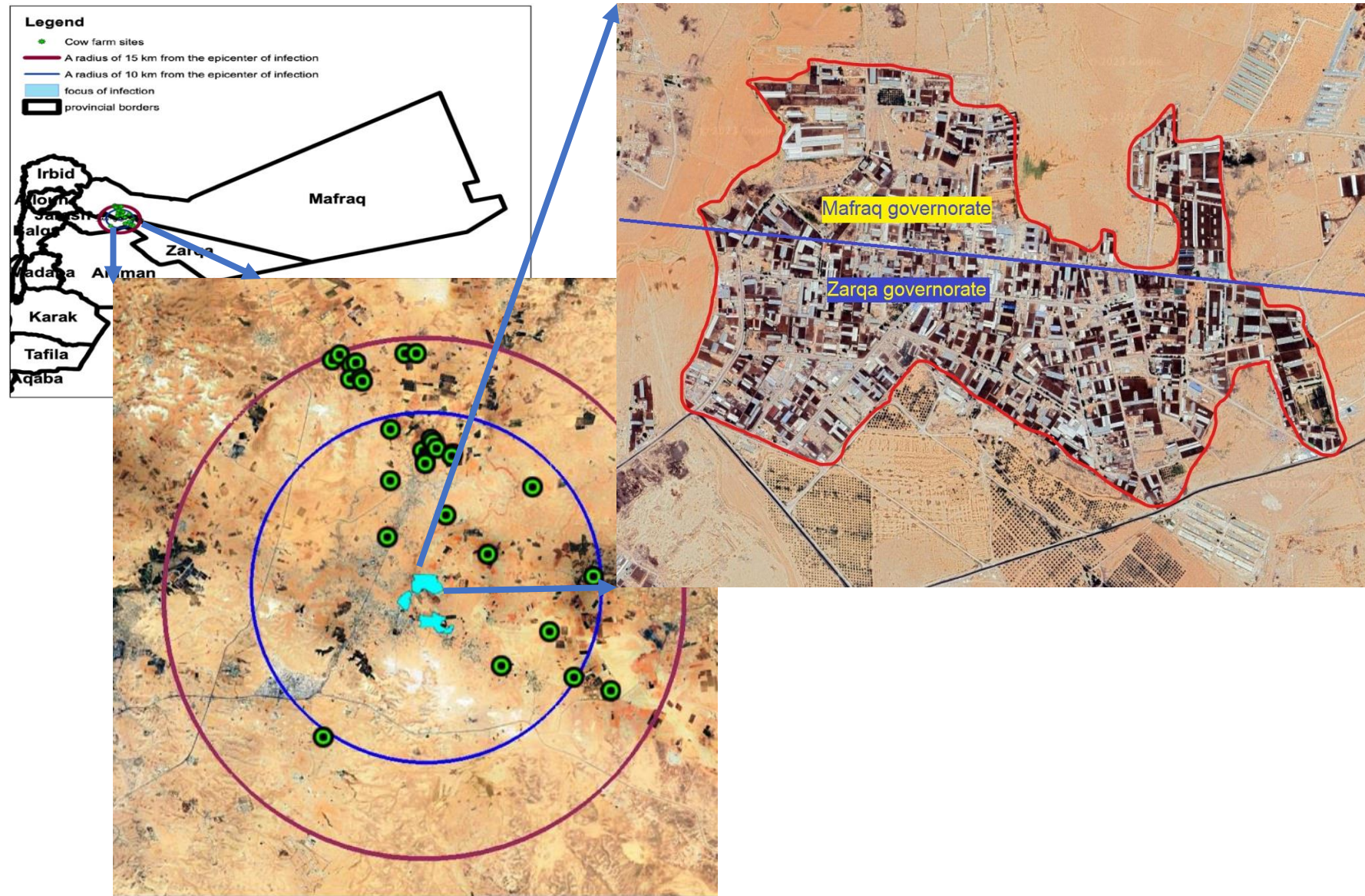
SAT2 in Jordan



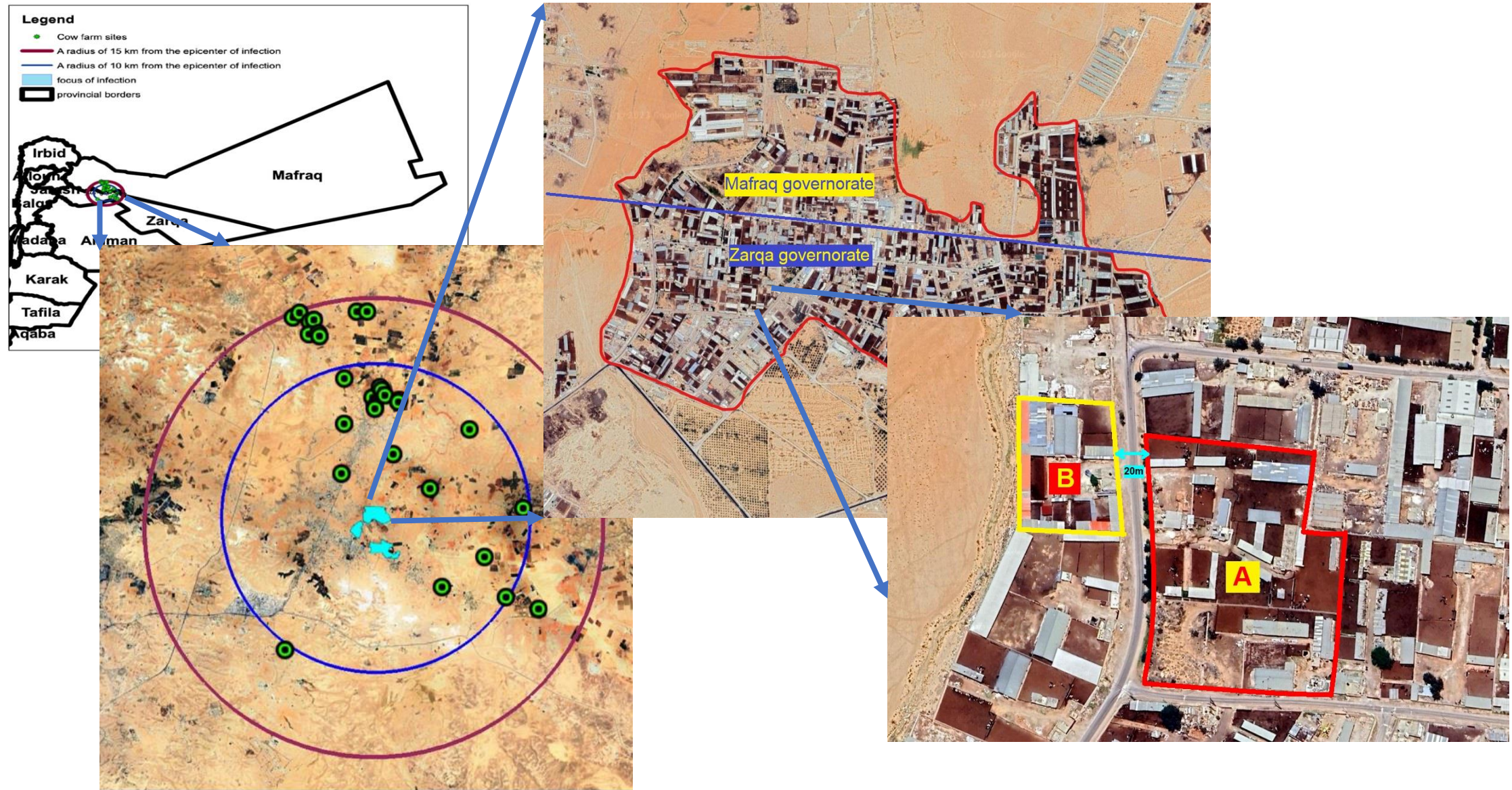
SAT2 in Jordan



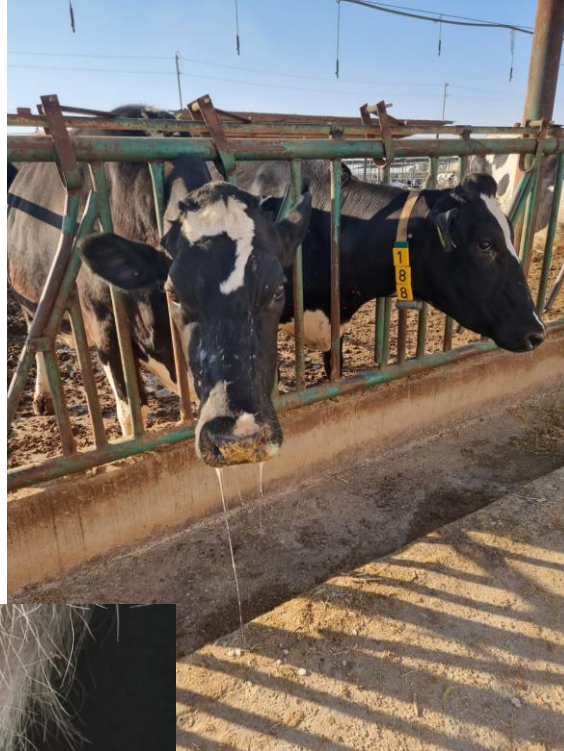
SAT2 in Jordan



SAT2 in Jordan



SAT2 in Jordan



SAT2 in Jordan

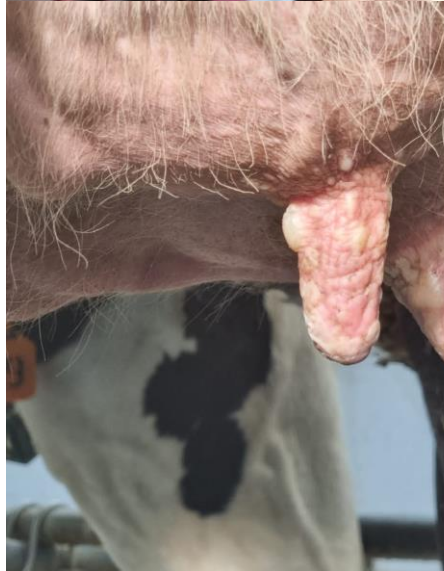
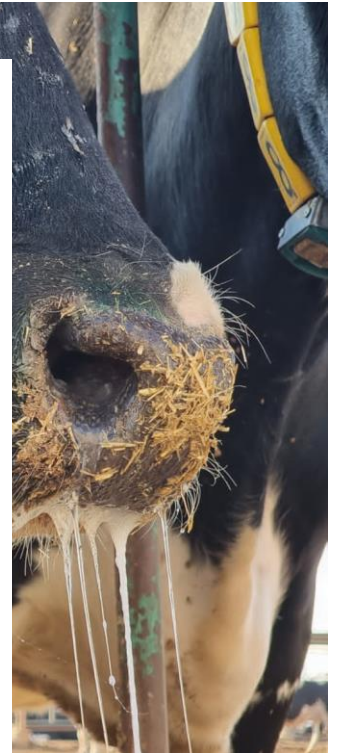
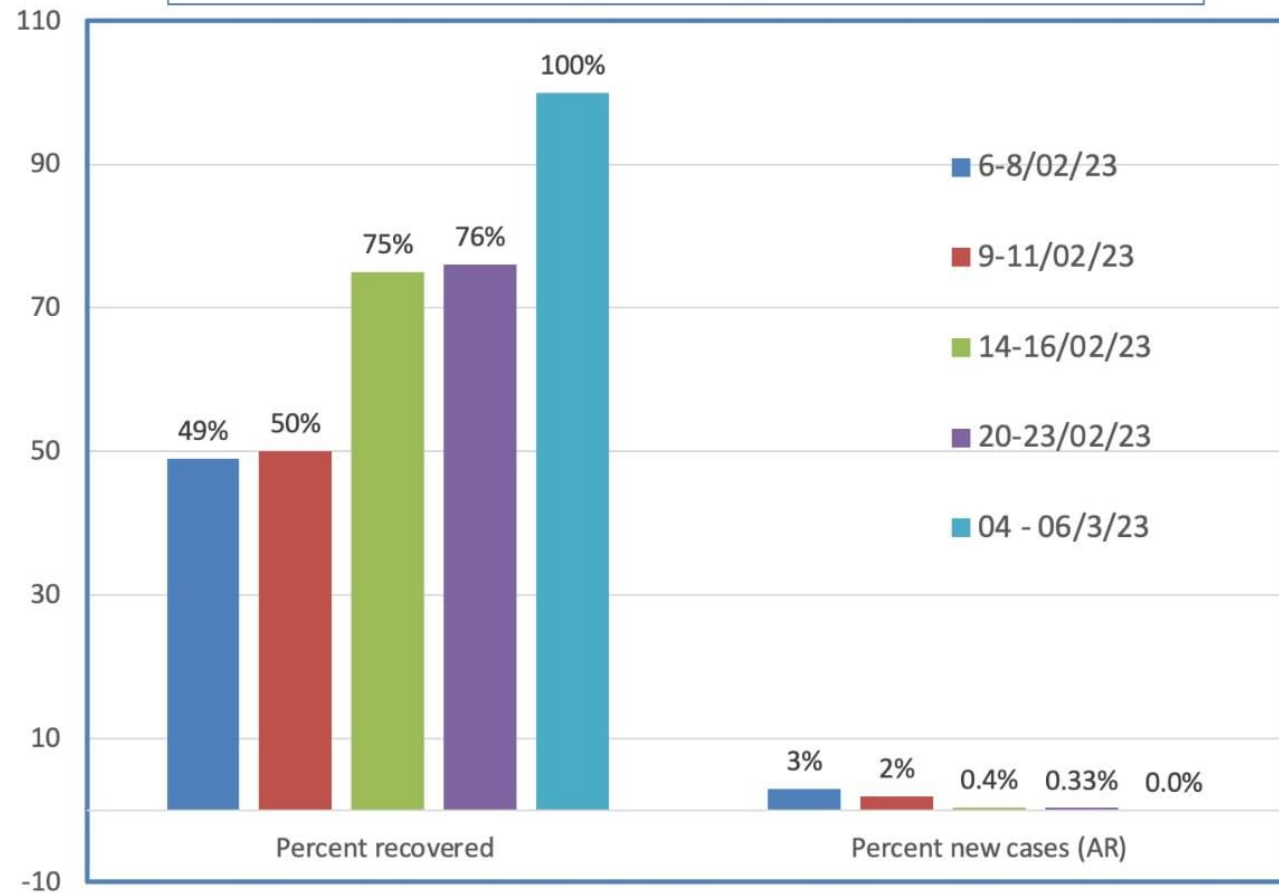
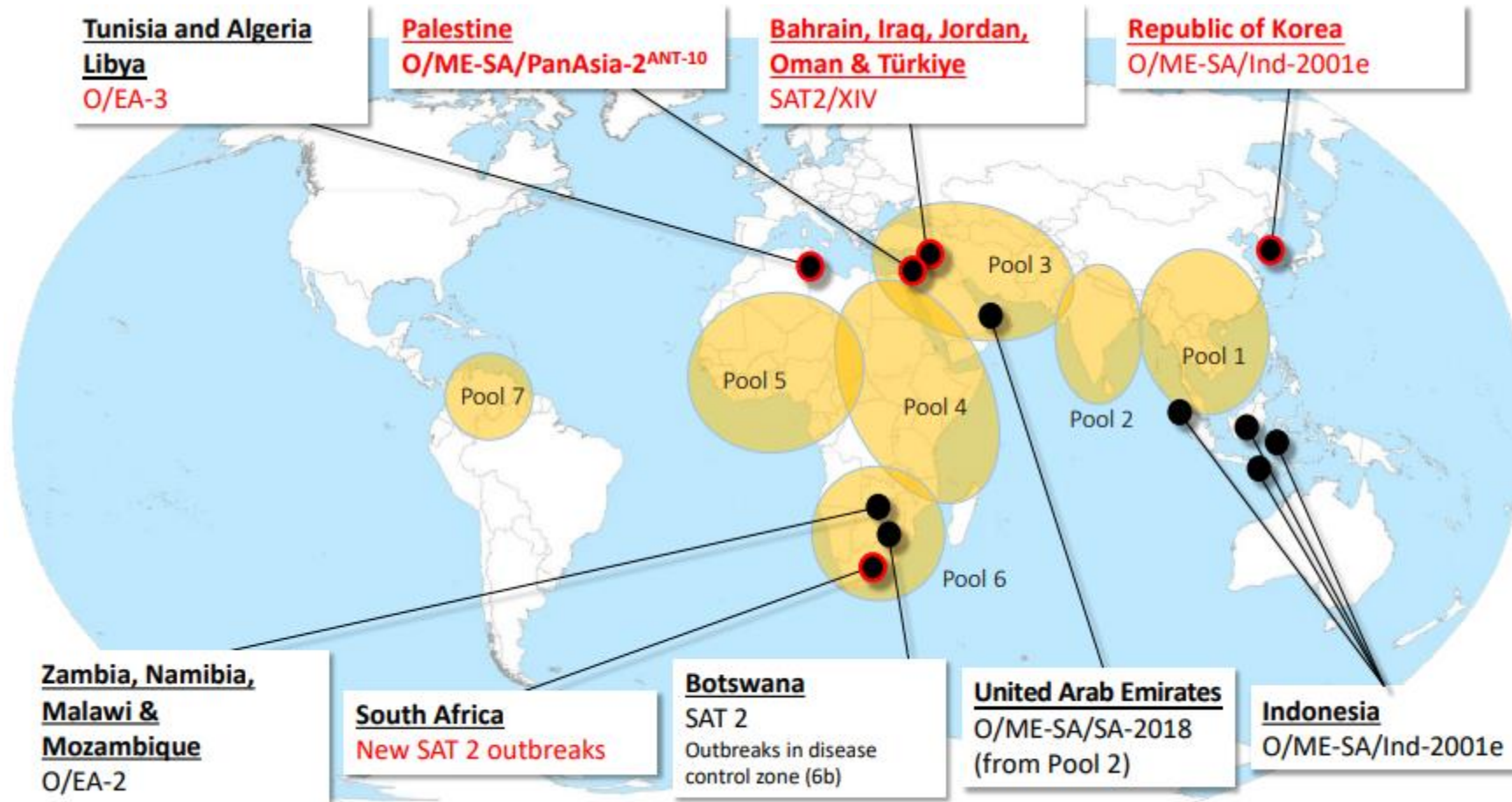


Chart Area

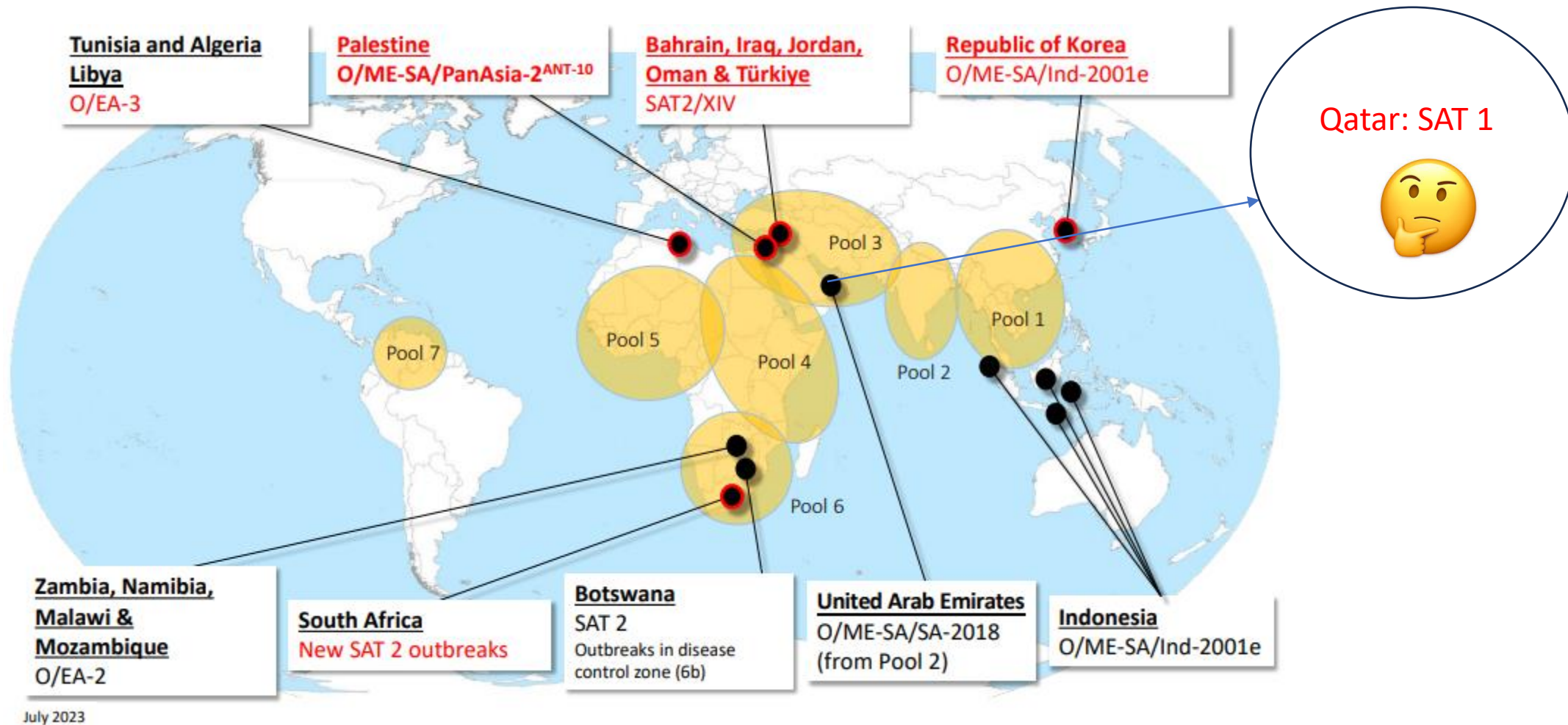
Five readings of outbreak attack rate (AR) and recovered percentage



Current circulating FMD strains



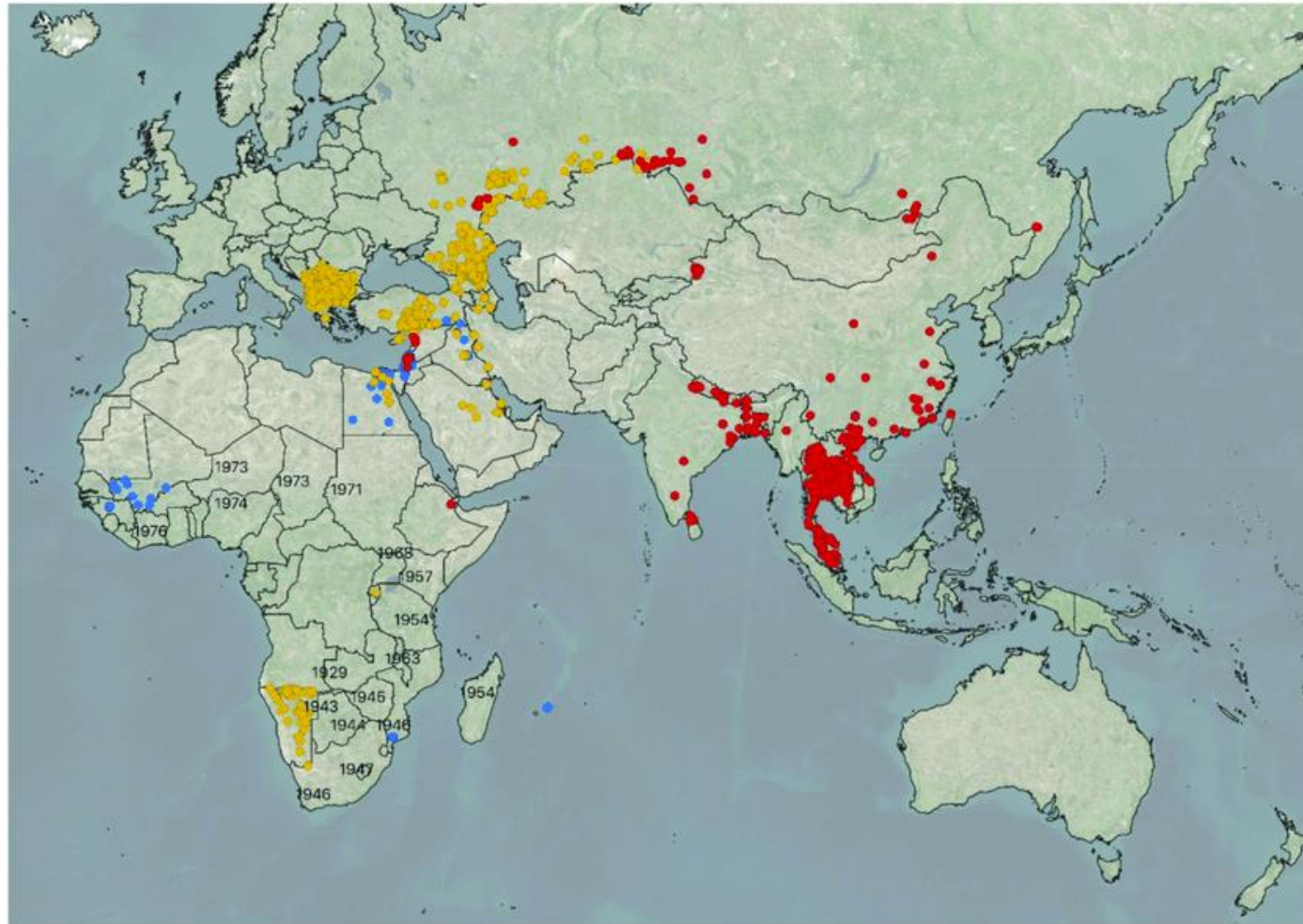
Current circulating FMD strains

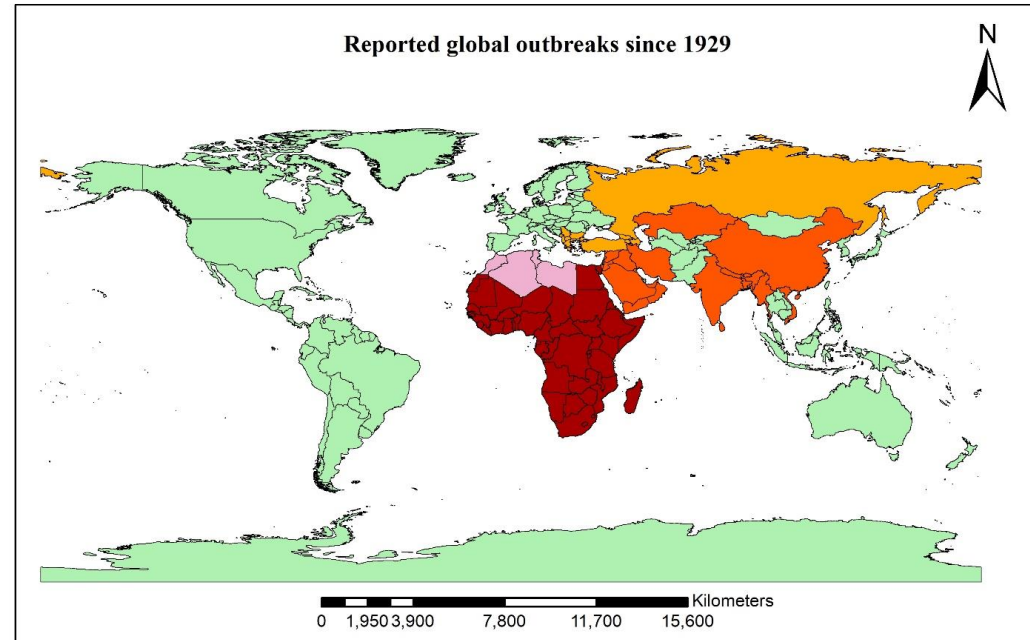
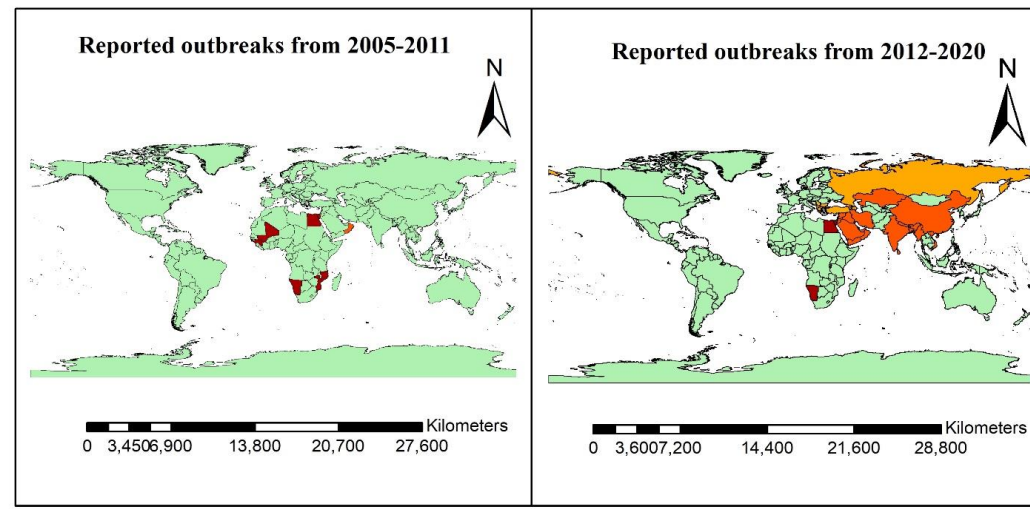


Lumpy Skin Disease

- Lumpy skin disease is a viral disease that affects cattle. It is transmitted by **blood-feeding insects**, such as certain species.
- Lumpy skin disease virus (LSDV) is a member of the genus **Capripoxvirus** and the family Poxviridae. It is closely related antigenically to sheeppox virus and goatpox virus.
- LSDV is susceptible to a number of **disinfectants** including sodium hypochlorite, iodine, quaternary ammonium disinfectants, ether, chloroform, formalin, phenol, and detergents that contain lipid solvents.

LSD outbreaks during the last 10 years





Legend

- African countries free from LSD
- African countries with recorded cases of LSD outbreaks
- Asian countries with recorded cases of LSD
- European countries with recorded cases of LSD outbreaks
- Countries free from LSD

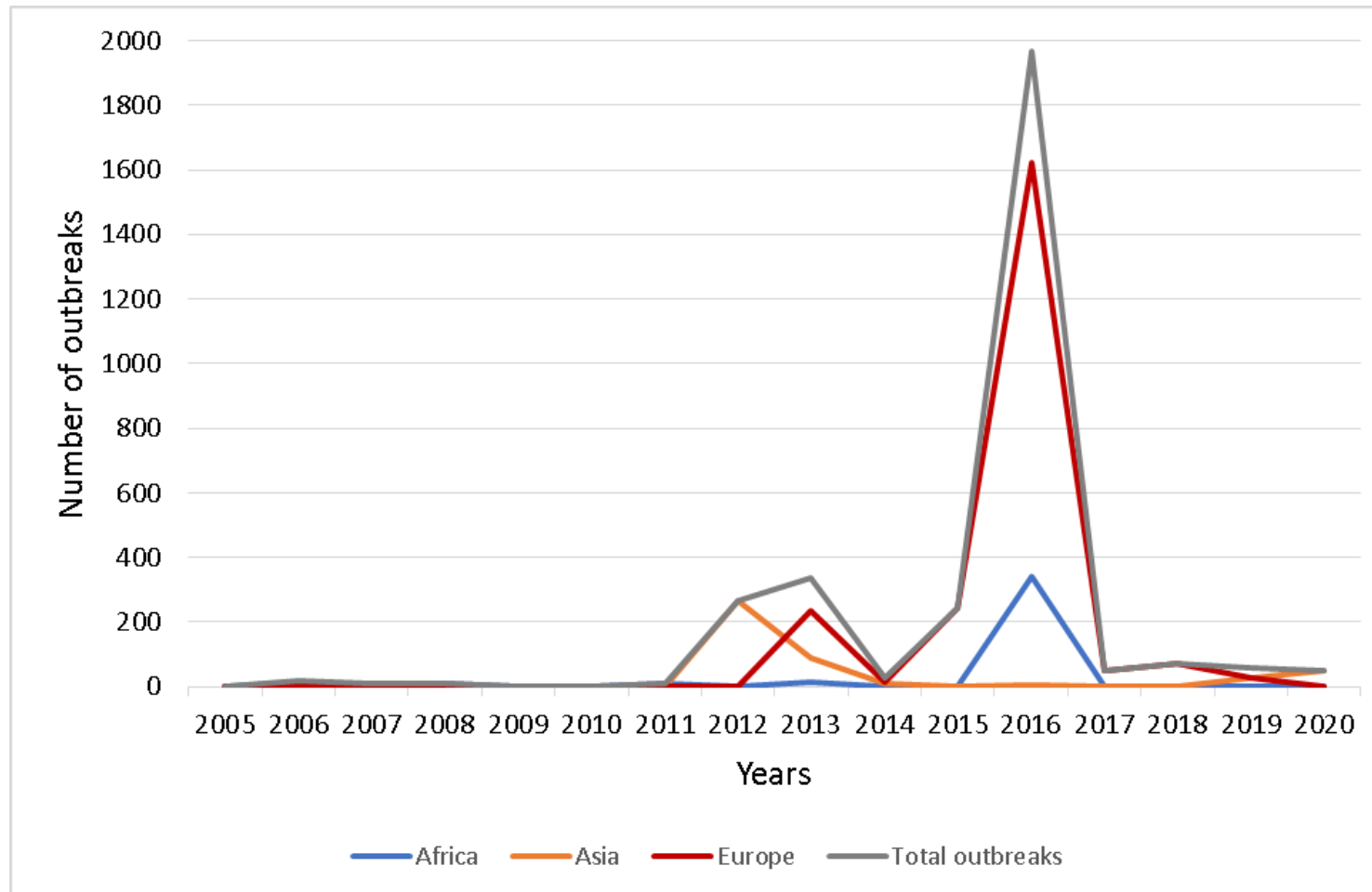
Source: Jyoti, et al, 2021

O/B during the last 15 years

Region	No. of O/B	Most affected country	The year with highest O/B
Asia	462	PA (260)	2012 (266)
Europe	2265	Russia (469)	2016 (1620)
Africa	391	Namibia (340)	2016 (341)

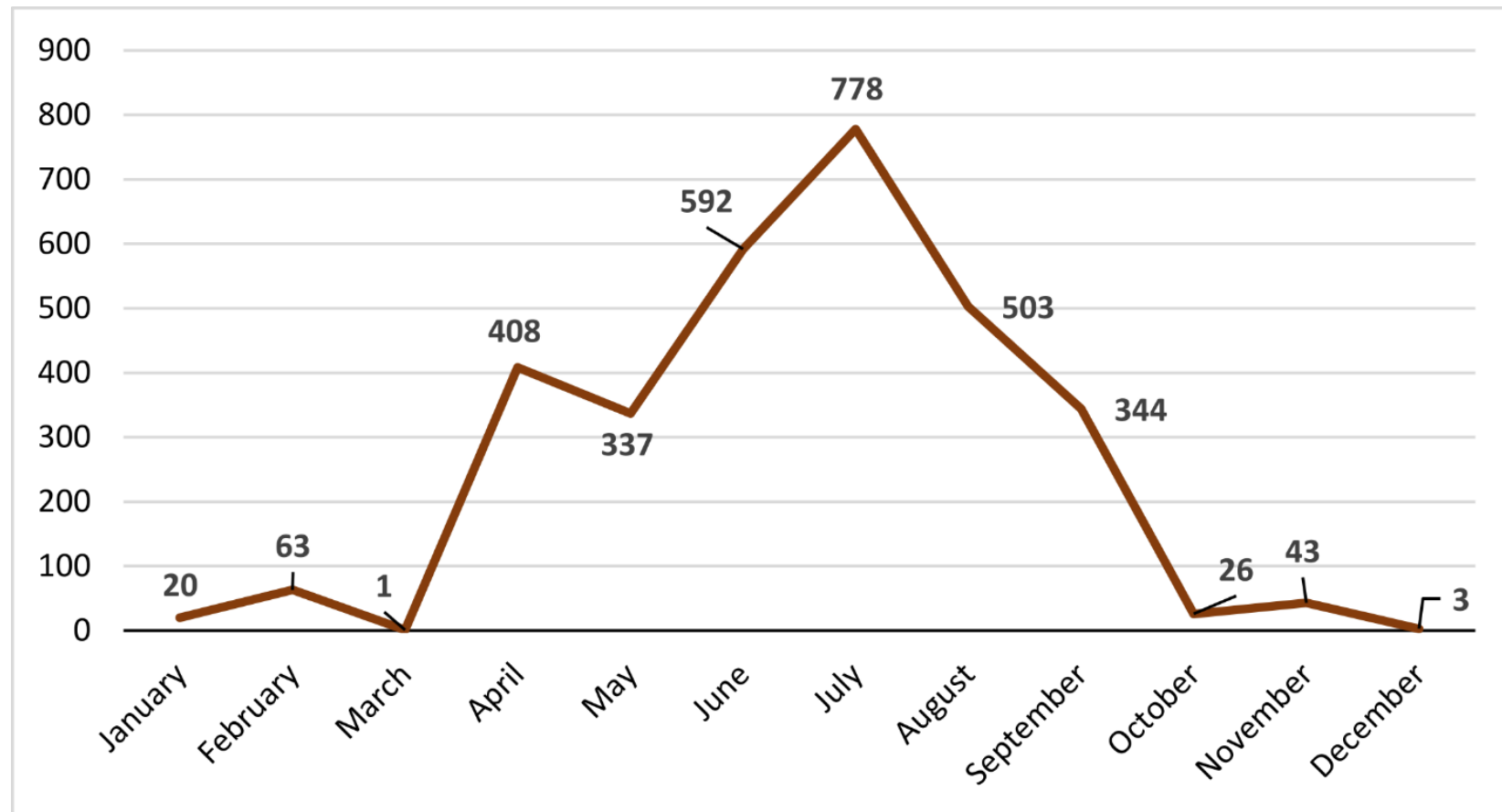
Source: Jyoti, et al, 2021

O/B by year (global)

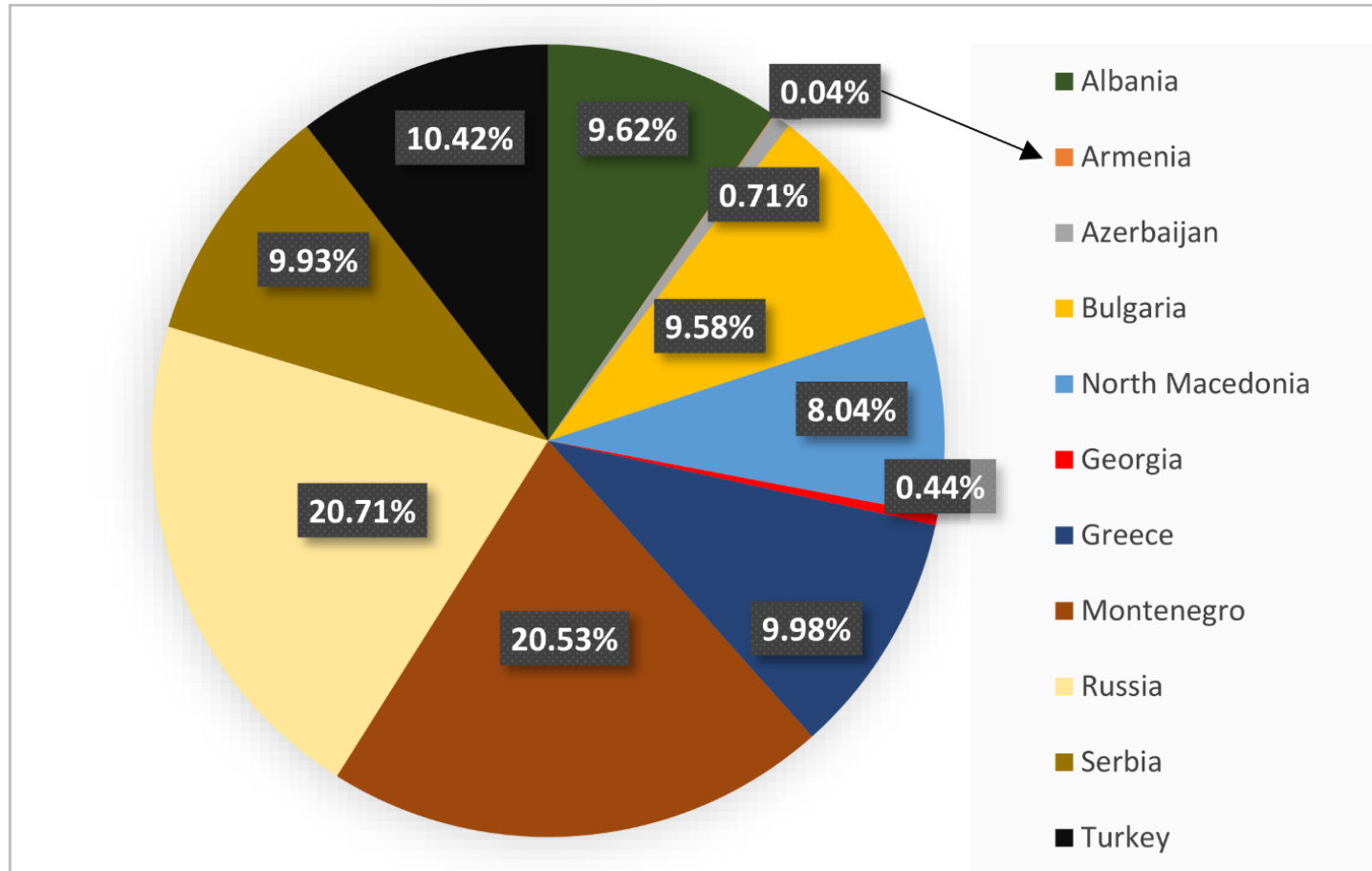


Source: Jyoti, et al, 2021

No. of outbreak/month of the year



O/B of LSD in Europe (total 1620)



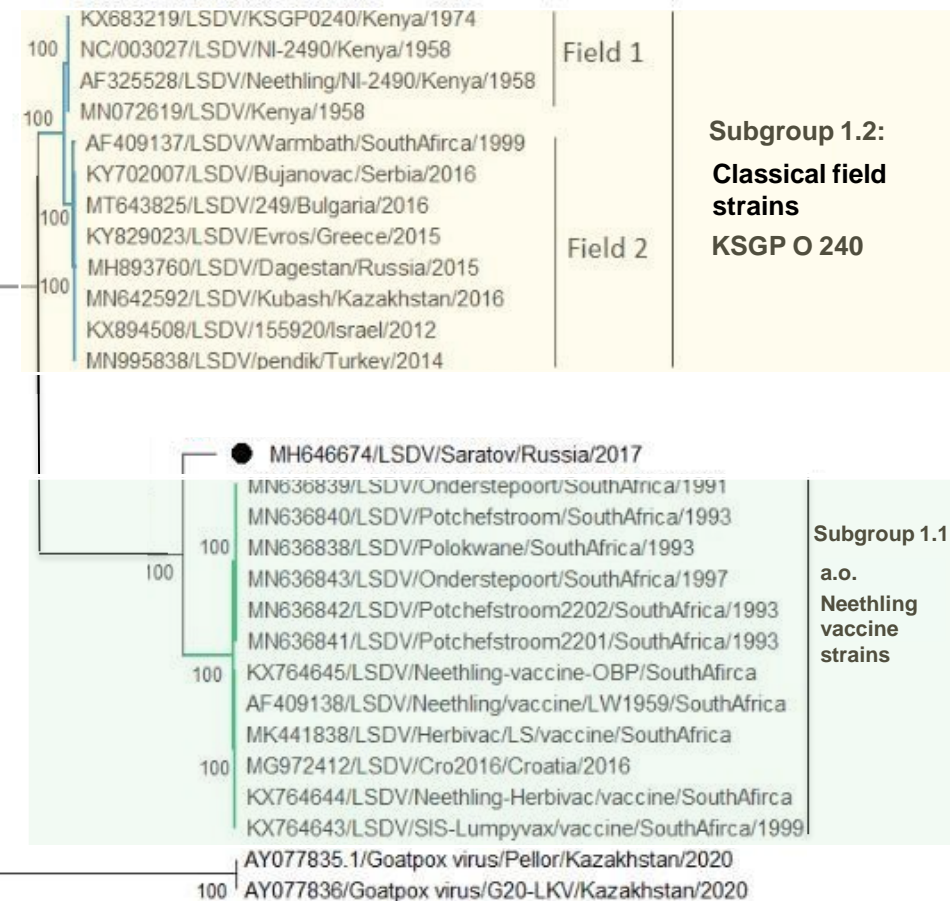
Source: Jyoti, et al, 2021

Global LSDV situation with focus on the recombinant LSDV strains

2017



Recombinant strains cluster more closely to vaccine strains, but behave as wild type field strains

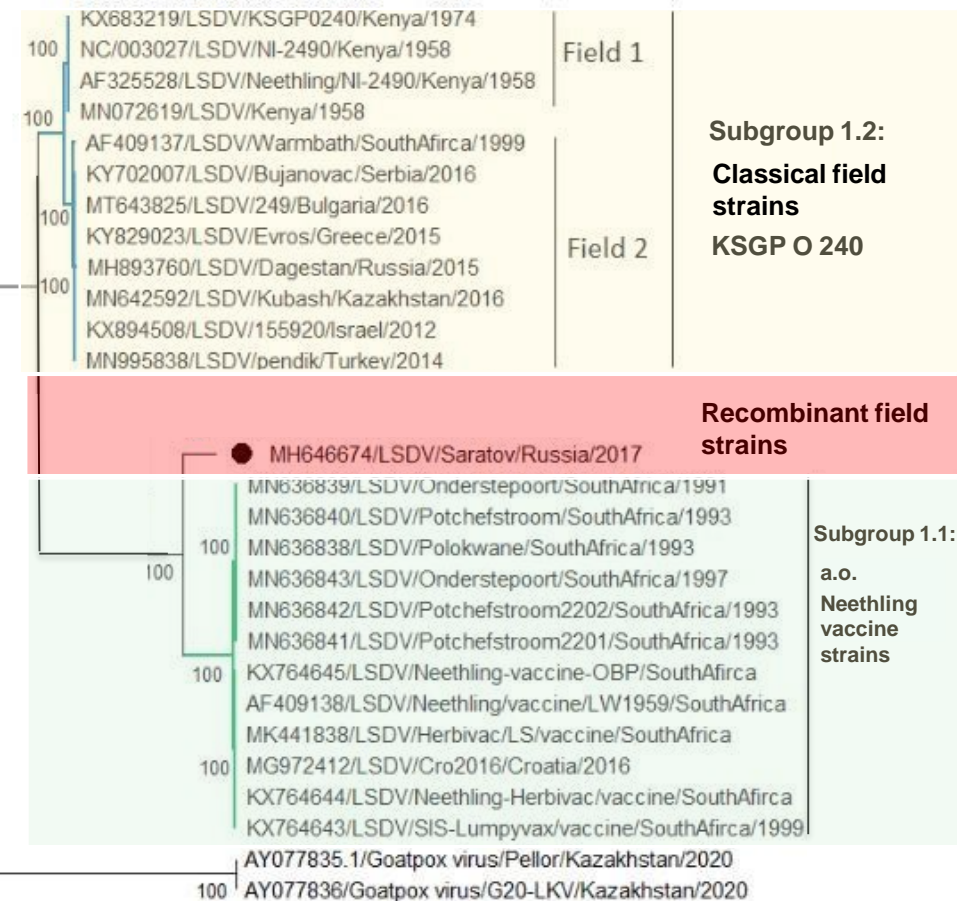


Adapted from Ma et al, 2022 – based on full genome sequences

Global LSDV situation with focus on the recombinant LSDV strains

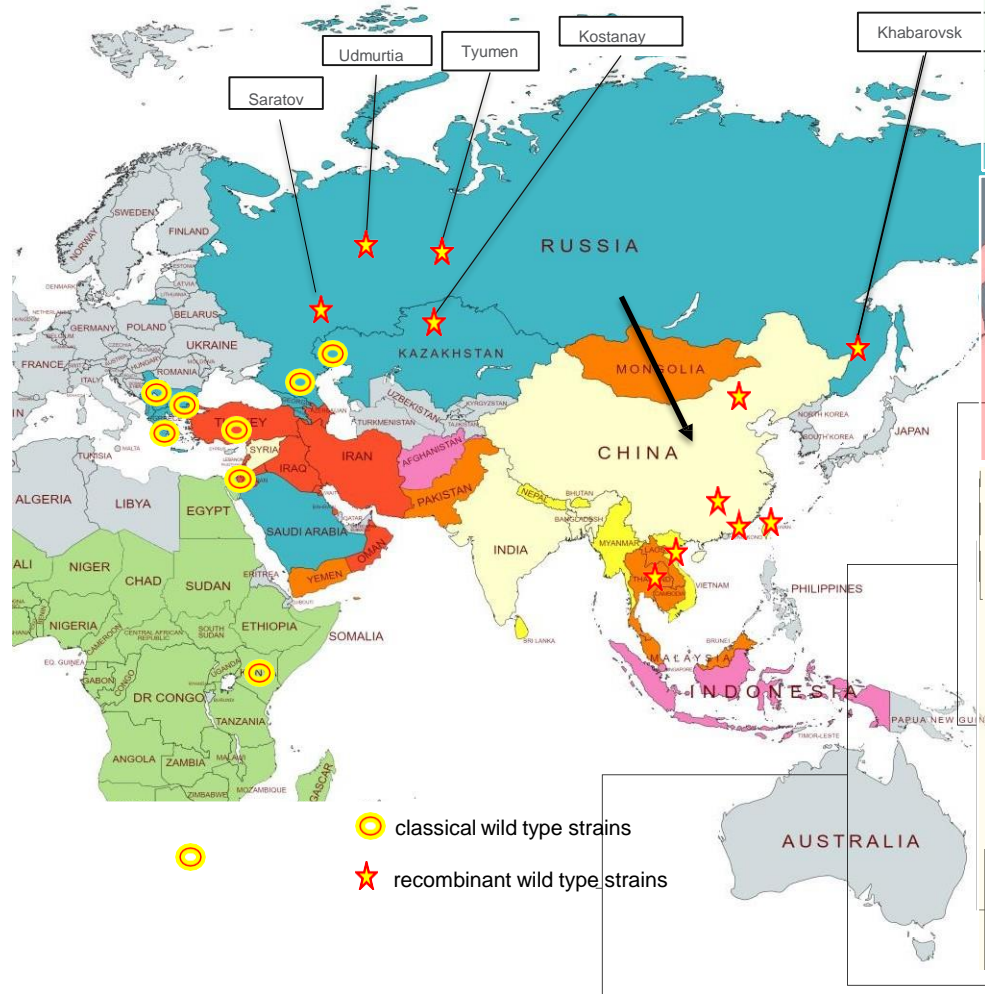


Recombinant strains cluster more closely to vaccine strains, but behave as wild type field strains



Adapted from Ma et al, 2022 – based on full genome sequences

2019-2020



MW435866.1__Lumpy_skin_disease_virus_isolate_SA-Neethling
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
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
KX764645.1__Lumpy_skin_disease_virus_strain_Neethling-LSD_vaccine-OBP_complete_genome
HB977629.1__Sequence_1_from_Patent_WO2009101604
AF409138.1__Lumpy_skin_disease_virus_isolate_Neethling_vaccine_LW_1959_complete_genome
MK441838.1__Lumpy_skin_disease_virus_strain_Herbivac_LS
MW656252.1__Lumpy_skin_disease_virus_isolate_LSDV_Haden RSA 1954 complete genome

Subgroup 1.1:

a.o.
Neethling
vaccine
strains

OL542633.1__Lumpy_skin_disease_virus_isolate_LSDV_Russia_Tyumen_2019_complete_genome
MH646674.1__Lumpy_skin_disease_virus_strain_LSDV_Russia_Saratov_2017_complete_genome
CM530217.1__Lumpy_skin_disease_virus_isolate_LSDV_Russia_Saratov_2019_complete_genome
OL762713.2__Lumpy_skin_disease_virus_isolate_LSDV_KM-Taiwan_2020_complete_genome
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
MZ577073.1__Lumpy_skin_disease_virus_strain_20L42_Quyet-Thang_VNM_20_complete_genome
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
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_Prachuapkhinkhan_Thailand_2021_complete_genome
OM984485.1__Lumpy_skin_disease_virus_strain_LSDV_KJ201901_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_Udmurtia_2019_complete_genome

Recombinant field strains

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
MW863897.1__UNVERIFIED__Lumpy_skin_disease_virus_isolate_LSDV_Cattle_India_2019_Ranchi-1_genomic_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
MN959838.1__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
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
KX894608.1__Lumpy_skin_disease_virus_isolate_155920_2012
MH893760.2__Lumpy_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_Abyrau-5BJN_IL-18_partial_genome
LSD_L08
LSD_L09
LSD_NS_31
LSD_L08
LSD_NS_30
LSD_L10
AF409137.1__Lumpy_skin_disease_virus_NW-LW_isolate_Neethling_Warmbaths_LW_complete_genome
MW699032.1__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
MT007951.1__UNVERIFIED__Lumpy_skin_disease_virus_isolate_Namibia_2016_10F_genomic_sequence
MW699032.1__Lumpy_skin_disease_virus_isolate_LSDV_280-KZN_RSA_2018_complete_genome
NC_004002.1__Sheeppox_virus_17077-99_complete_genome
NC_004003.1__Goatpox_virus_Pellor_complete_genome

Subgroup 1.2:

Classical field
strains

KSGP O 240

What led to recombination?



- Neethling like LSDV vaccine strain
- KSGP-like LSDV vaccine strain
- Sudan-like GTPV strain
- Multiple recombinant strains (almost) identical to recently described recombinant vaccine-like strains
- Most likely source of recombinant strains in the field
- Highlights importance of an independent vaccine quality control

One specific badly produced and insufficiently controlled LSDV vaccine was responsible for the release of recombinant LSDV strains in the field



Article

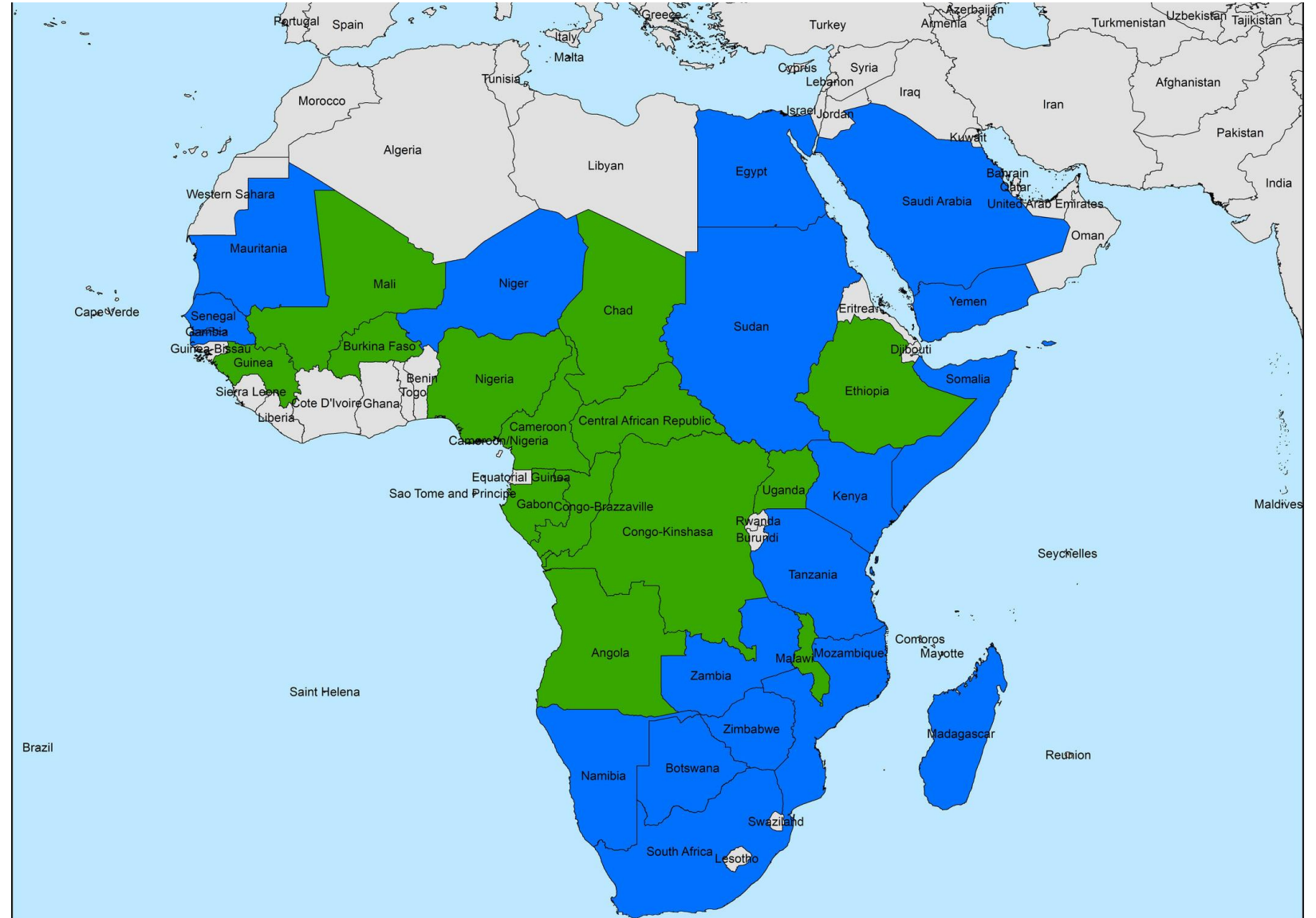
Recombinant LSDV Strains in Asia: Vaccine Spillover or Natural Emergence?

Frank Vandenbussche ^{1,*}, Elisabeth Mathijs ^{1,*}, Wannes Philips ¹, Meruyert Saduakassova ², Ilse De Leeuw ³, Akhmetzhan Sultanov ², Andy Haegeman ³ and Kris De Clercq ^{3,*}

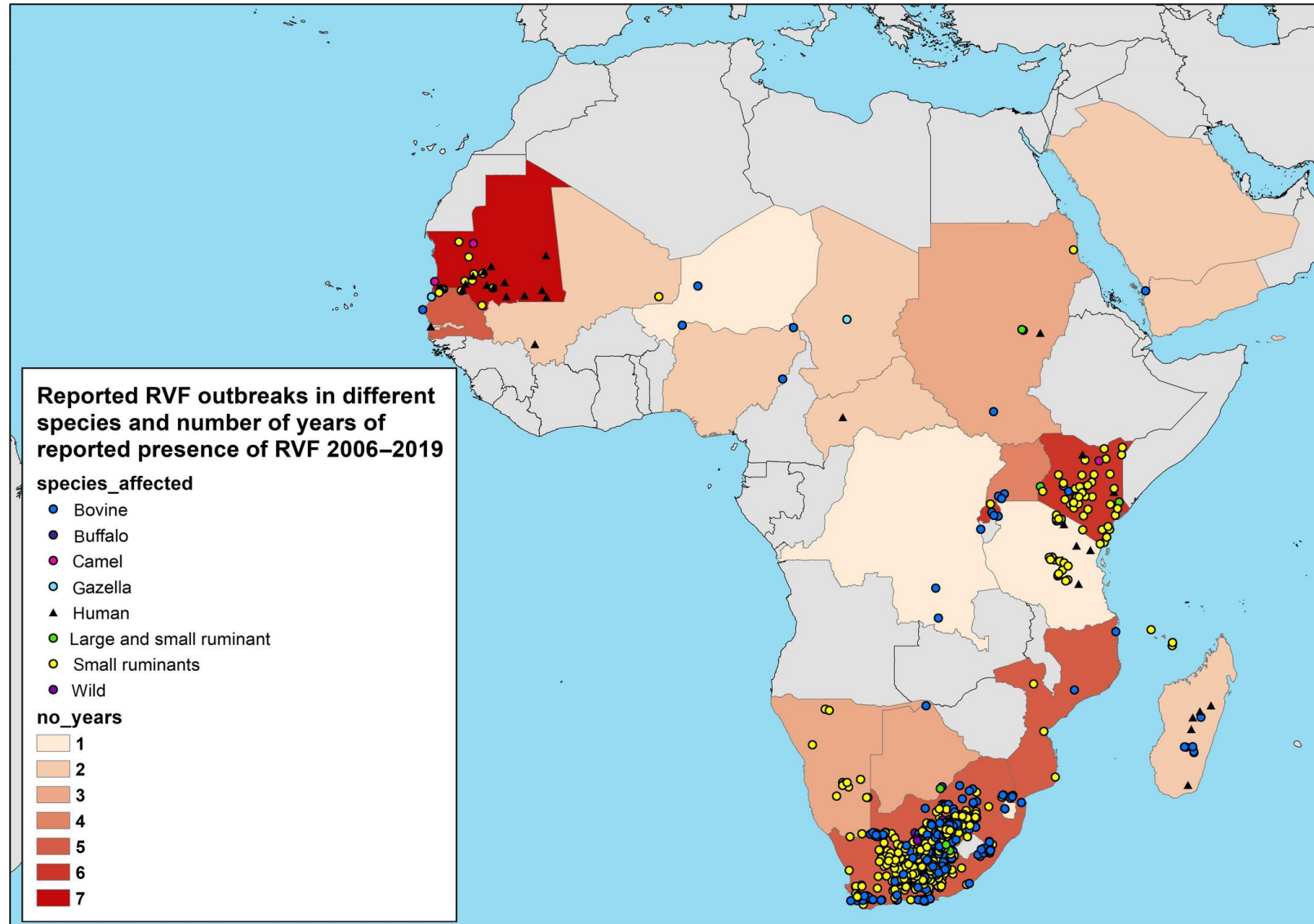
RVF

- Rift Valley fever (RVF) is a **viral zoonosis** that primarily affects animals but also has the capacity to infect humans. It is transmitted by mosquitoes and blood feeding flies.
- Rift Valley fever virus, an RNA virus in the genus **Phlebovirus** in the **family Bunyaviridae**. There are **several genetic lineages** of this virus, some of which may co-circulate, in endemic regions.
- Humans are **susceptible** to infection with Rift Valley fever virus, and can develop clinical signs. The **viremia may be sufficient** to infect mosquitoes

RVF distribution



RVF: O/B in different species and number of years reported



RVF serology reports (publications) (2022)

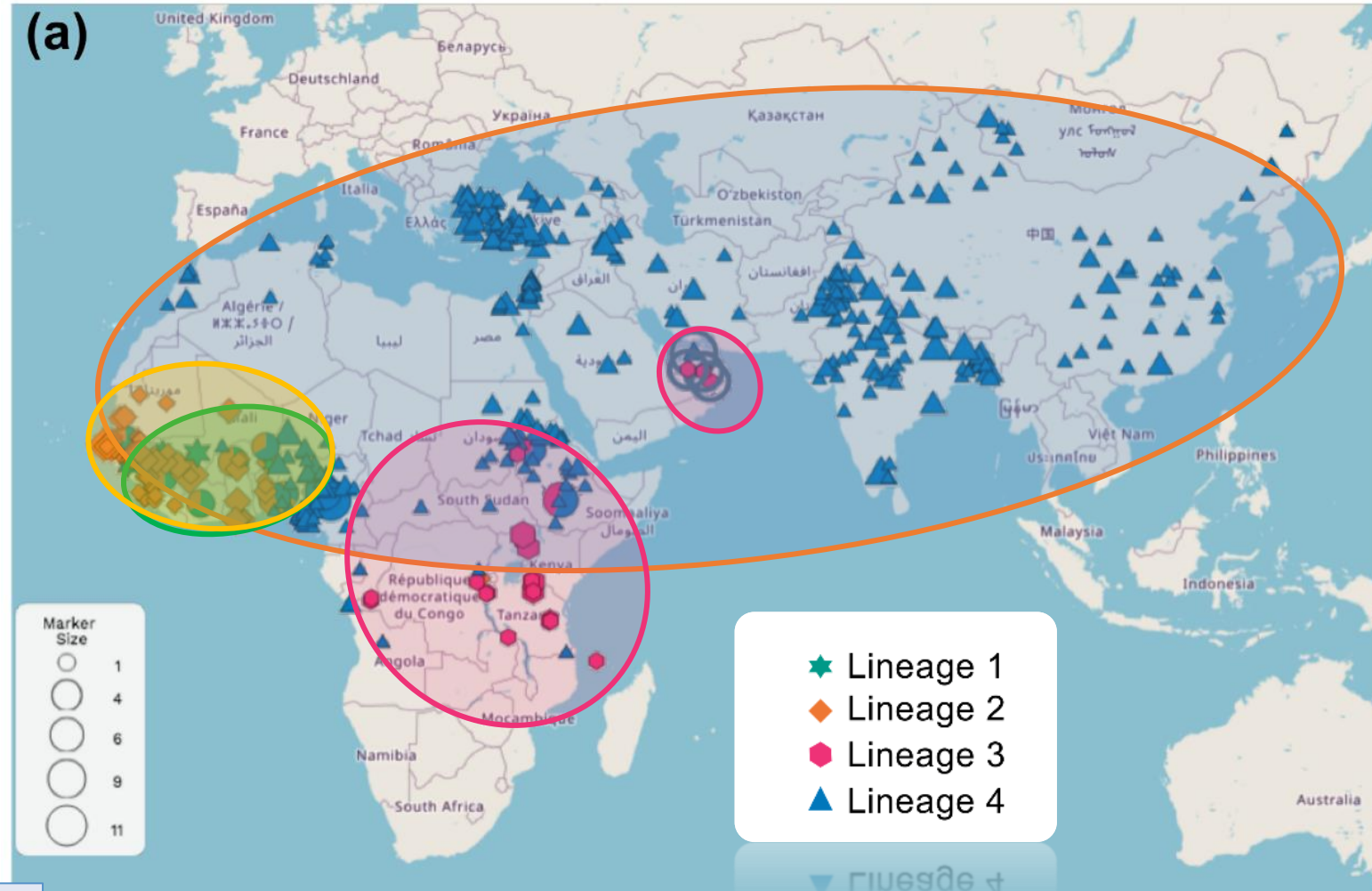
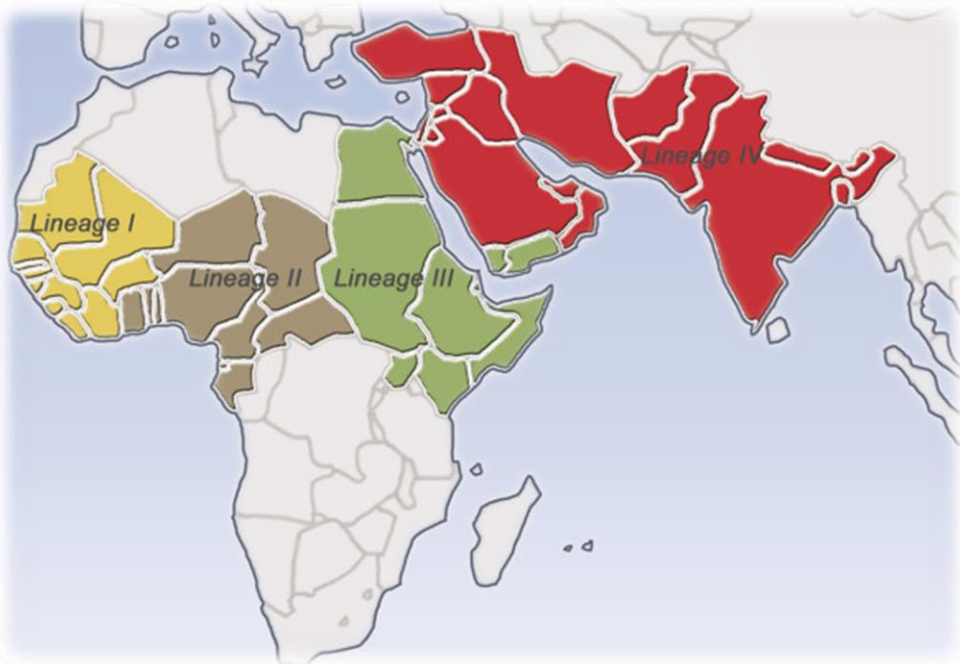


PPR

- PPR is an **acute or subacute** viral disease of goats and sheep characterized by fever, necrotic stomatitis, gastroenteritis, pneumonia, and sometimes death.
- It was reported first in Côte d'Ivoire (the Ivory Coast) in 1942, and subsequently in other parts of West Africa.
- Goats and sheep appear to be equally susceptible to the virus; however, **goats exhibit more severe clinical signs**.
- The virus also affects several wild small ruminant species.
- PPRV, a member of the ***Morbillivirus* genus** in the family Paramyxoviridae. **One serotype 4 lineages**

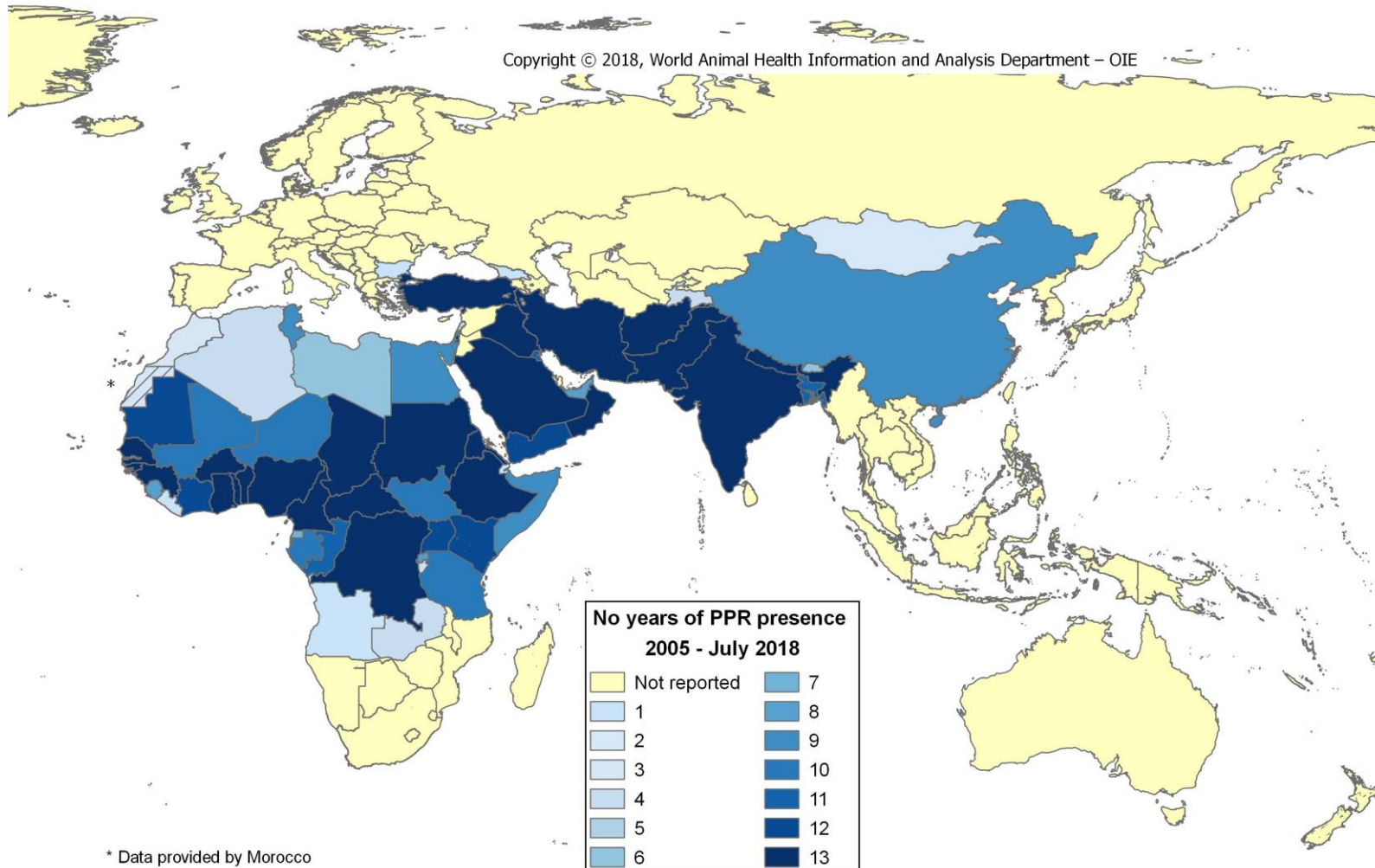
PPR Lineage

Les différentes souches du PPRV ont été classées en 4 lignées I à IV en se basant sur les études phylogénétiques des gènes N, F et H

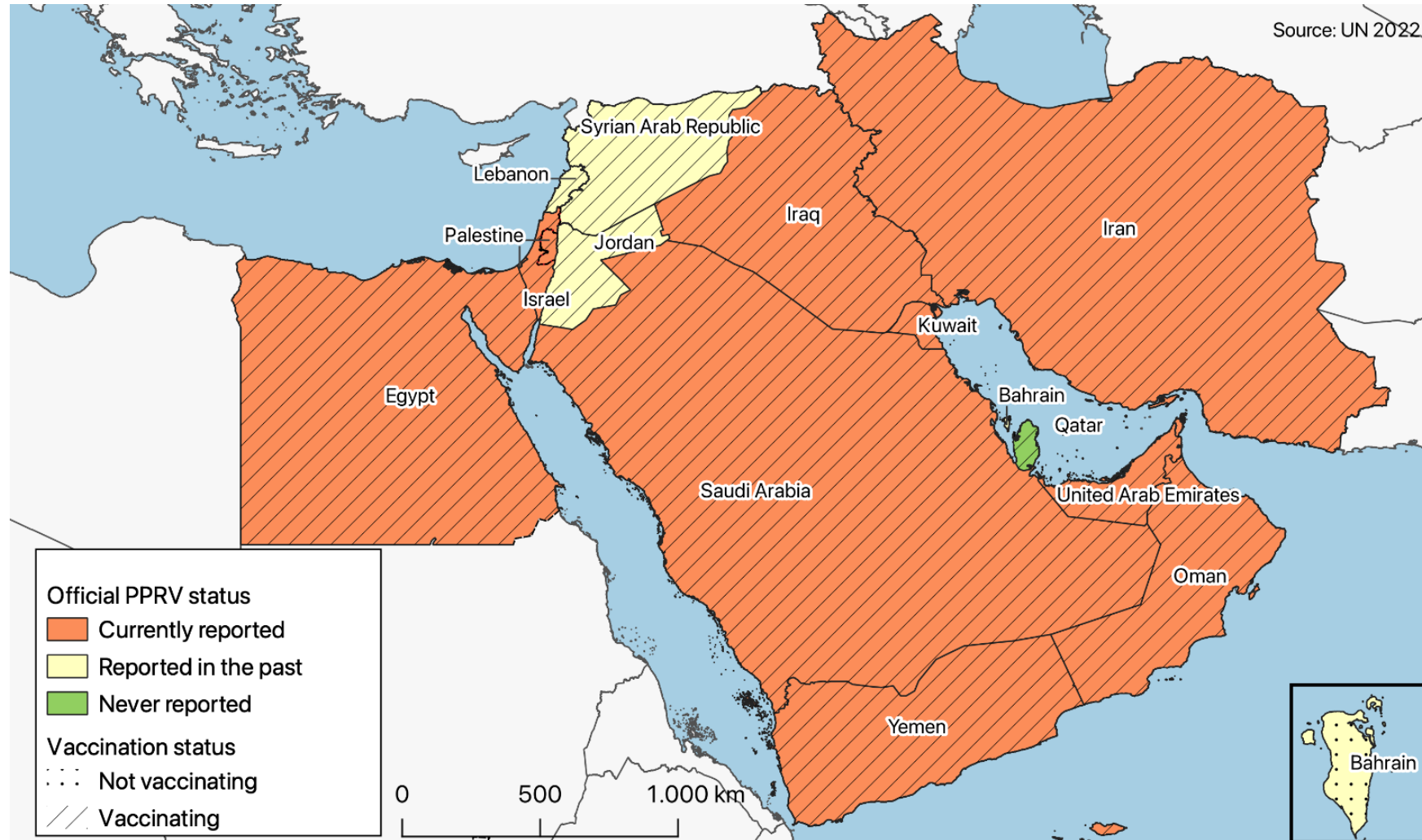


Distribution of the 4 PPRV lineages at the end of the 1990s

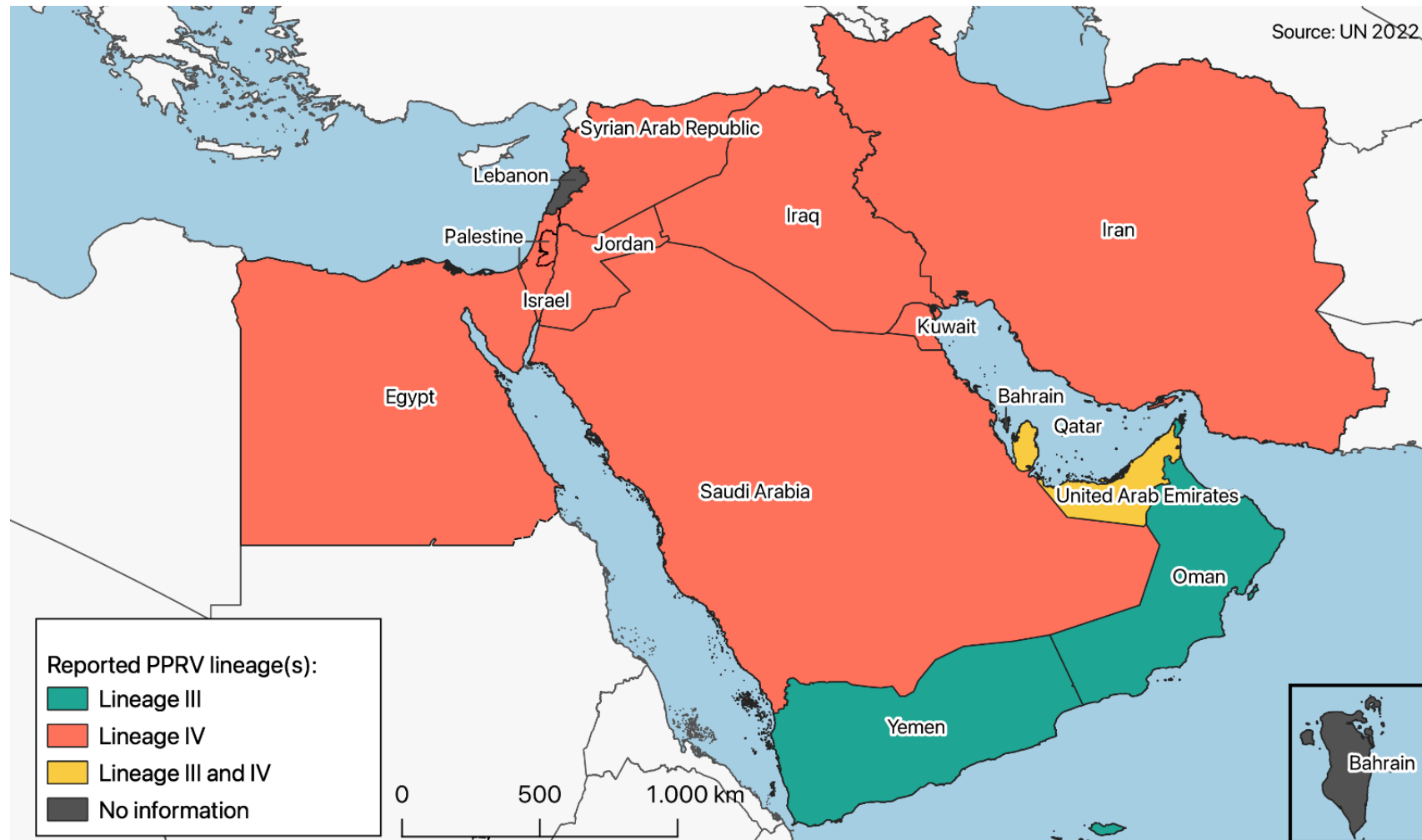
PPR distribution



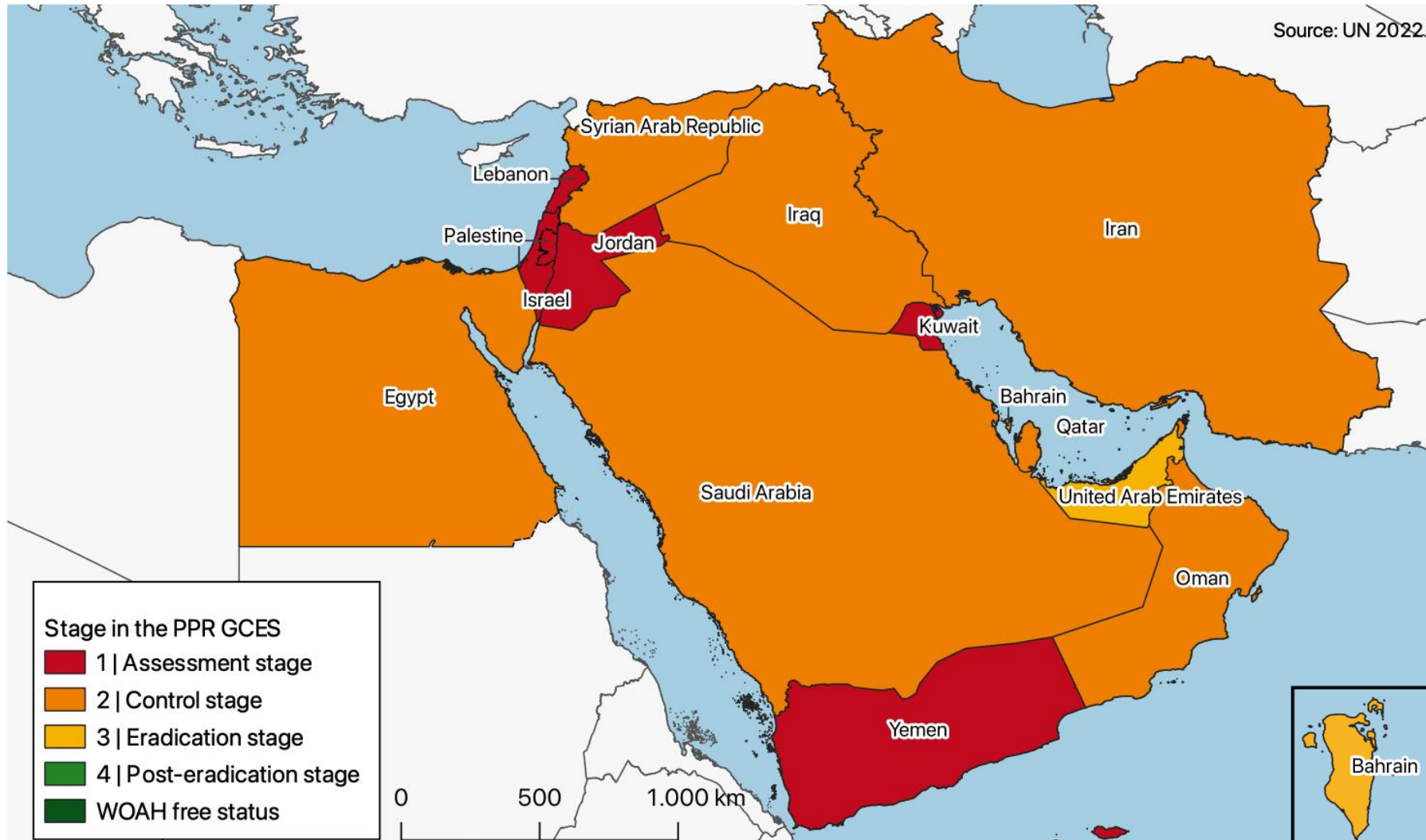
PPR distribution in ME region (2023)



PPRV lineages in the ME region (2023)

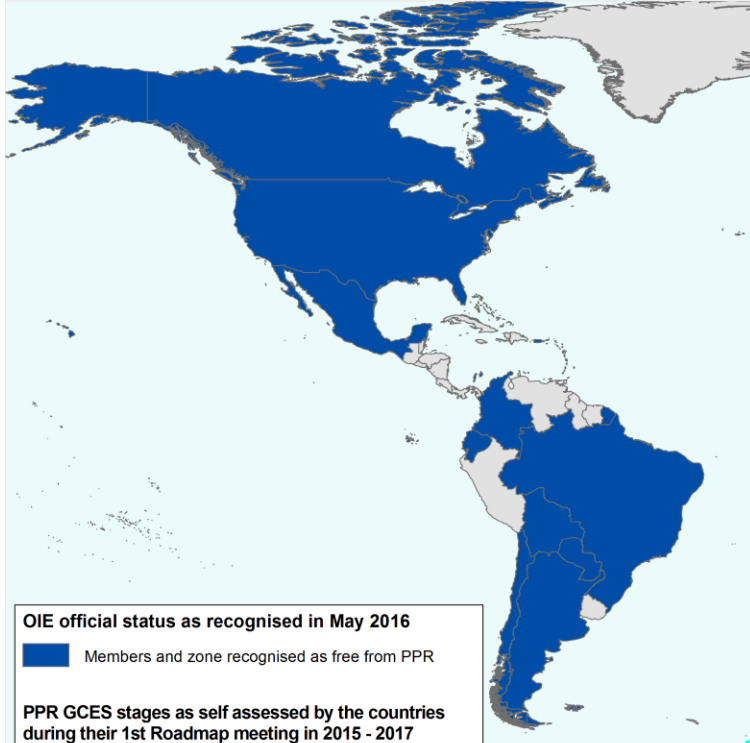


PMAT of the ME region (2023)



Peste des petits ruminants

OIE official PPR free status as of May 2016
Outcome of



OIE official status as recognised in May 2016

■ Members and zone recognised as free from PPR

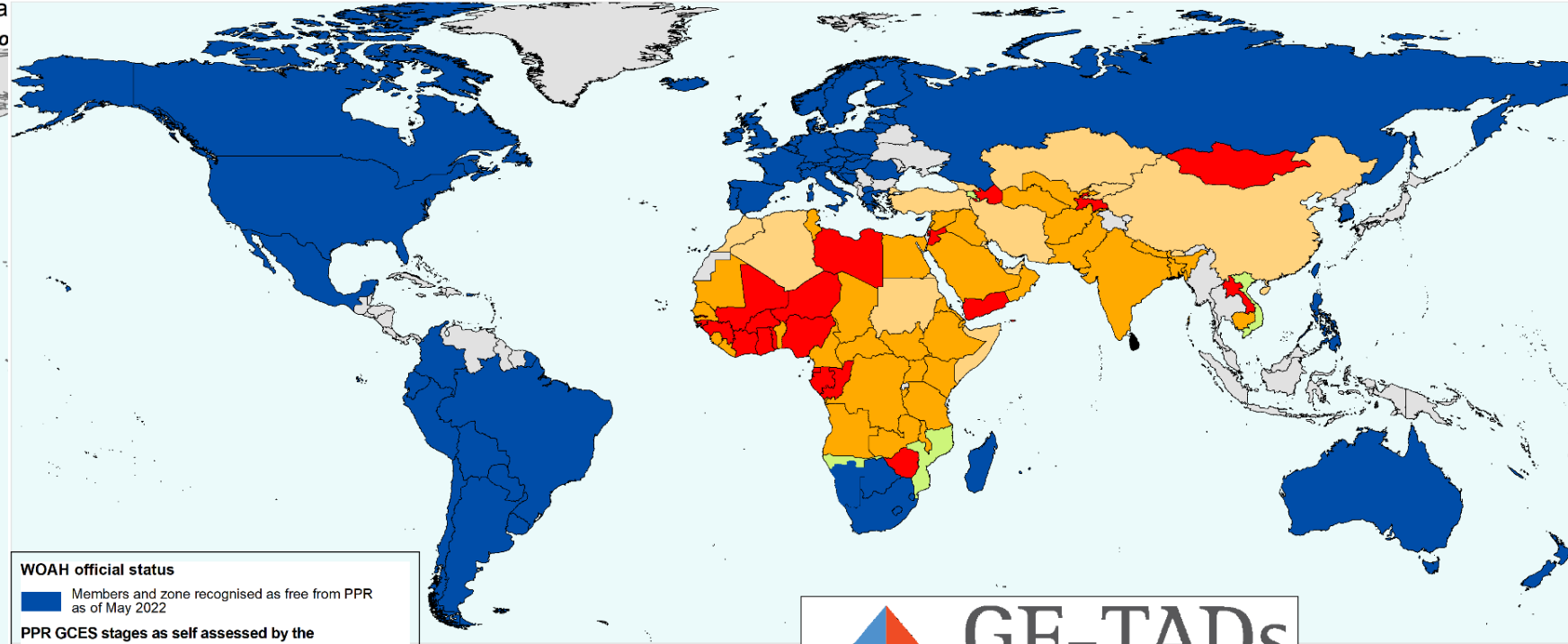
PPR GCES stages as self assessed by the countries during their 1st Roadmap meeting in 2015 - 2017

■ 4
■ 3
■ 2
■ 1
■ Below 1

■ Countries and zones without an official PPR status and which PPR-GCES stages have not been assessed

Peste des petits ruminants global situation up to June 2022

WOAH official PPR free status and PPR Global Control and Eradication Strategy (GCES)



WOAH official status

■ Members and zone recognised as free from PPR as of May 2022

PPR GCES stages as self assessed by the countries during their last PPR regional/epizone roadmap/consultation meeting (2017 - 2022)

■ 4
■ 3
■ 2
■ 1
■ Below 1

■ Countries and zones without an official PPR status and for which PPR-GCES stages have not been assessed



Challenges in diseases management in the MENA region

- The increase in **human population** and the subsequent **increase in food demand**
- Availability and prices of **animal feed**
- Farming **system** (traditional vs intensive)
- The **evolution of pathogens** and changes in the distribution of vectors as a result of **climate change**
- **Animal Health Delivery Systems**
- **Political situations**



Thanks!!!!

For contact

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