Update from WRLFMD

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on behalf of Don King and colleagues of the
WOAH/FAO FMD Ref lab Network (www.foot-and-mouth.org)

United Kingdom National Reference Laboratory for Vesicular Diseases
WOAH Reference Laboratory for FMD and SVD
FAO World Reference Laboratory for FMD (WRLFMD)

Work funded by:

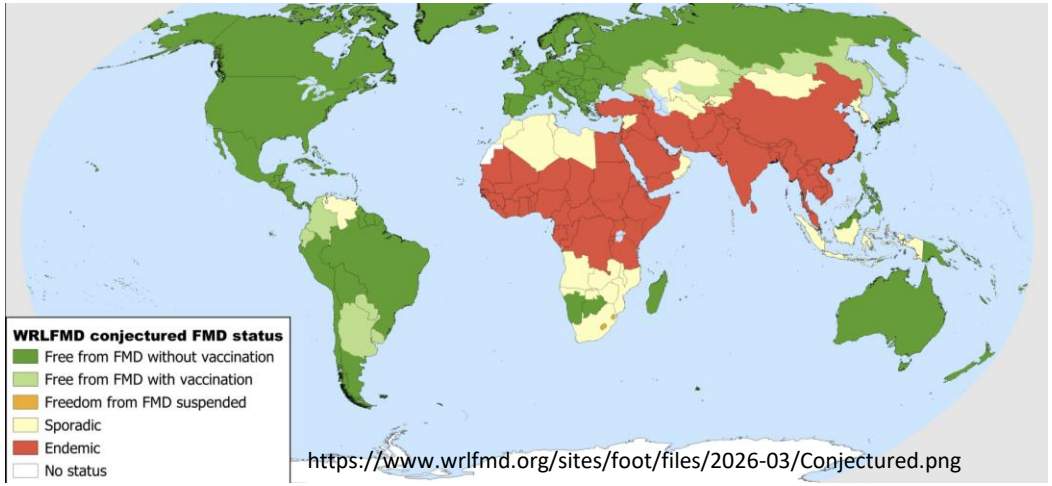
Department for Environment Food & Rural Affairs

eufmd

World Organisation for Animal Health
Founded as OIE

Foot-and-Mouth disease: difficult to control

- Affects multiple cloven-hoofed livestock and some wildlife
- Subclinical forms in small ruminants and after vaccination
- Rapid spread by direct and indirect mechanisms
- Mutable RNA virus aetiology – different serotypes and strains
- Transient immunity after vaccination
- Endemic in >100 countries in Africa and Asia
- Significant economic impact (~$21 billion annually*)



*estimated by Knight-Jones and Rushton 2013

Pictures of FMD in cattle (Pirbright Institute)

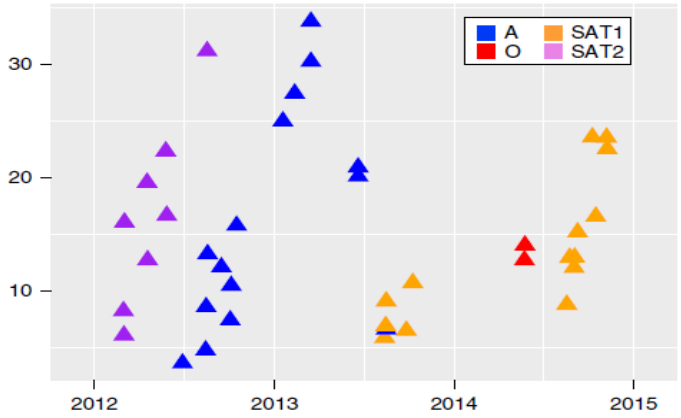
tongue lesion

interdigital foot lesion

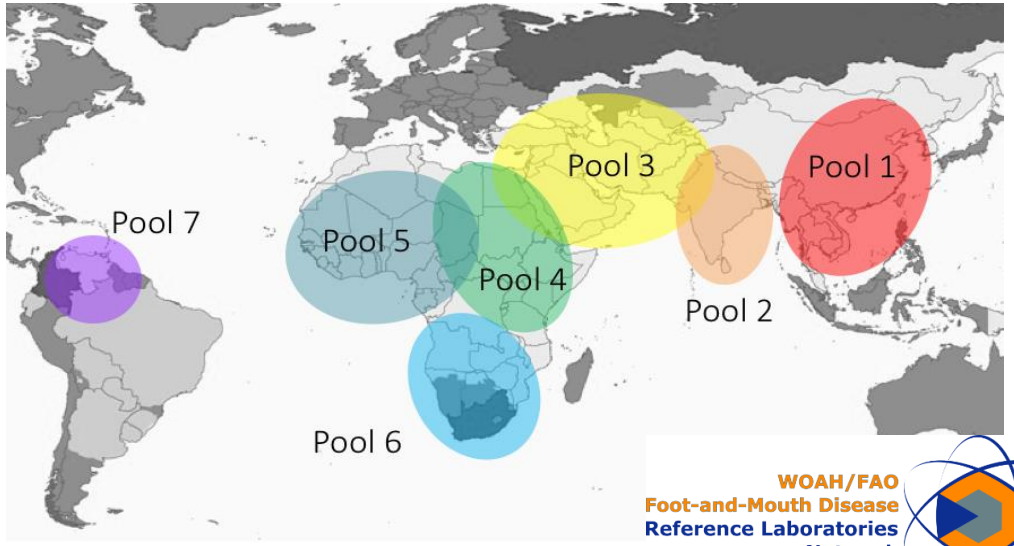
FMD epidemiology: global summary

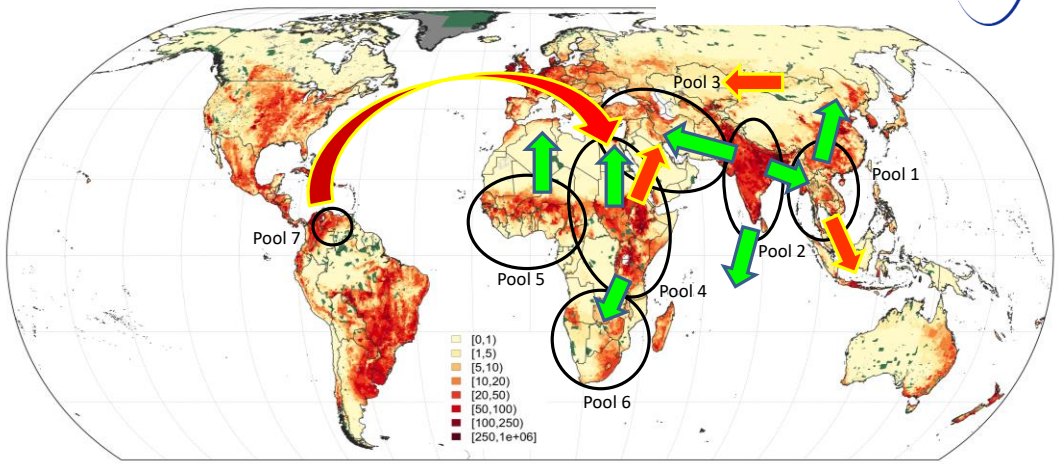
The epidemiology of FMD is dynamic

- Strains from six circulating serotypes in seven virus ecosystems (Pools)
- Cycles of changing FMDV serotype in primary endemic areas



FMDV serotype frequency over time in eastern African cattle
Casey-Bryers et al 2018.





Cattle density map — Robinson et al., 2007

- Long-distance “trans-pool” movements of FMDV are often unpredictable but linked to endemic disease upsurges, trade, porous borders, seasonal grazing and resource constrained surveillance and control

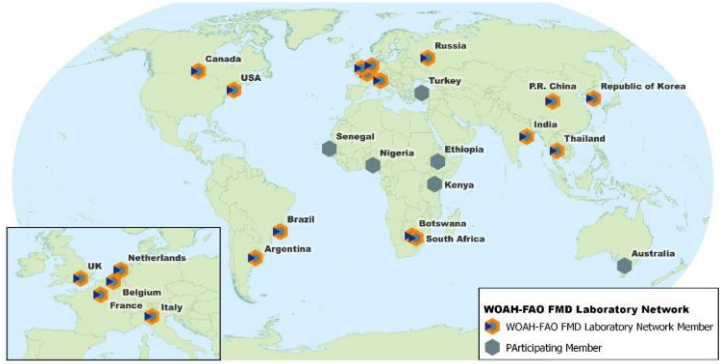
International partnerships and transparency needed to collate, share, analyse and respond to events

WOAH/FAO FMD Laboratory Network for FMD

www.foot-and-mouth.org

- Core Network activities:
  - **Data sharing** to understand **global epidemiology** of FMDV and use these data to inform **vaccine selection**
  - Improving the **quality of laboratory testing**
- Annual meeting: last one held in Istanbul during October 2025
- New member: NIAH, Japan (WOAH CC on *Diagnosis and Control of Animal Diseases and Related Veterinary Product Assessment in Asia*)

WOAH/FAO
Foot-and-Mouth Disease
Reference Laboratories
Network



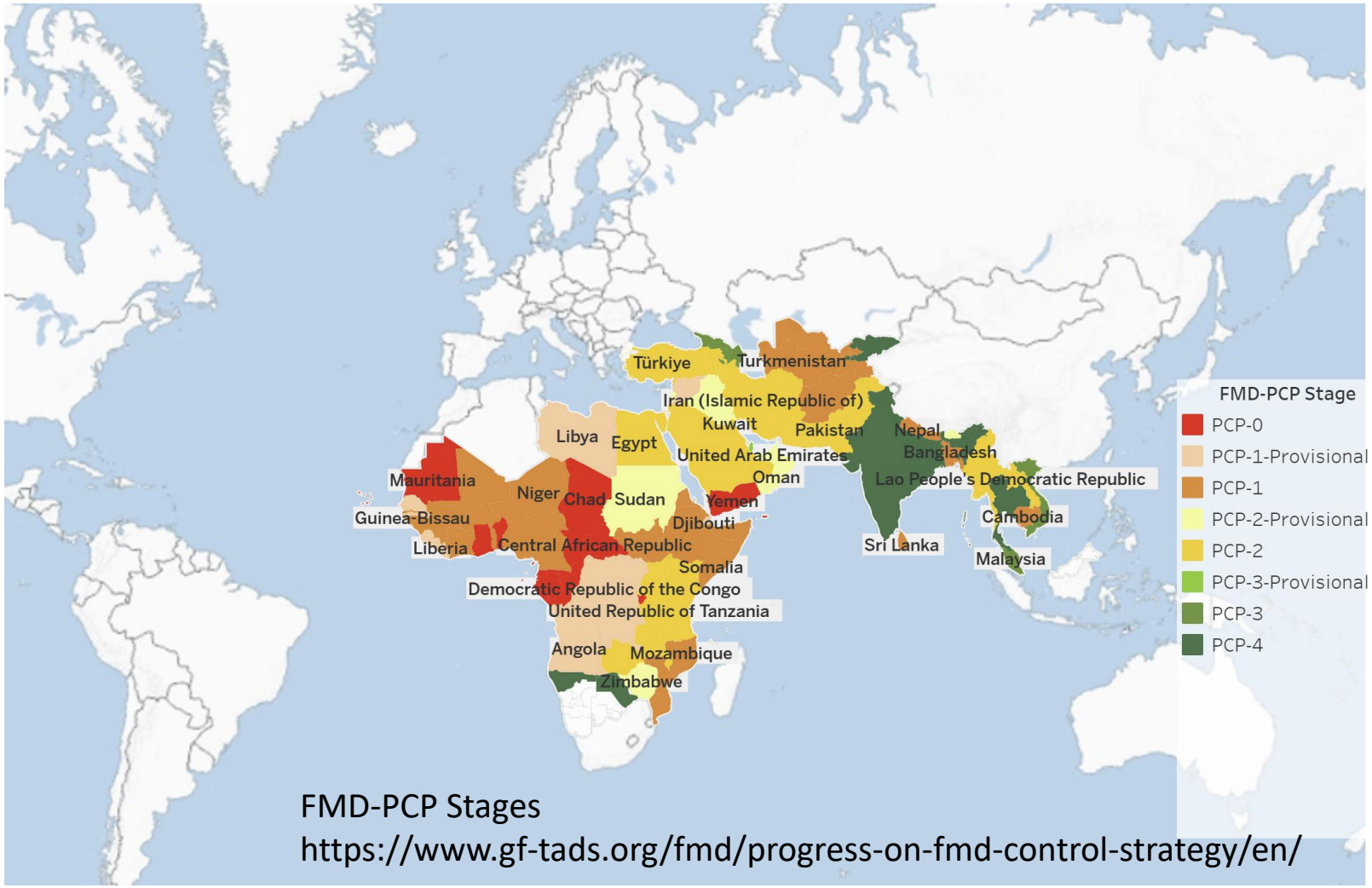
Network Meeting, Istanbul, October 2025

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

- Some successes
- Challenges of progressing to eradication
- New strategy in preparation



FMD-PCP Stages
https://www.gf-tads.org/fmd/progress-on-fmd-control-strategy/en/

Headline changes in global FMD distribution

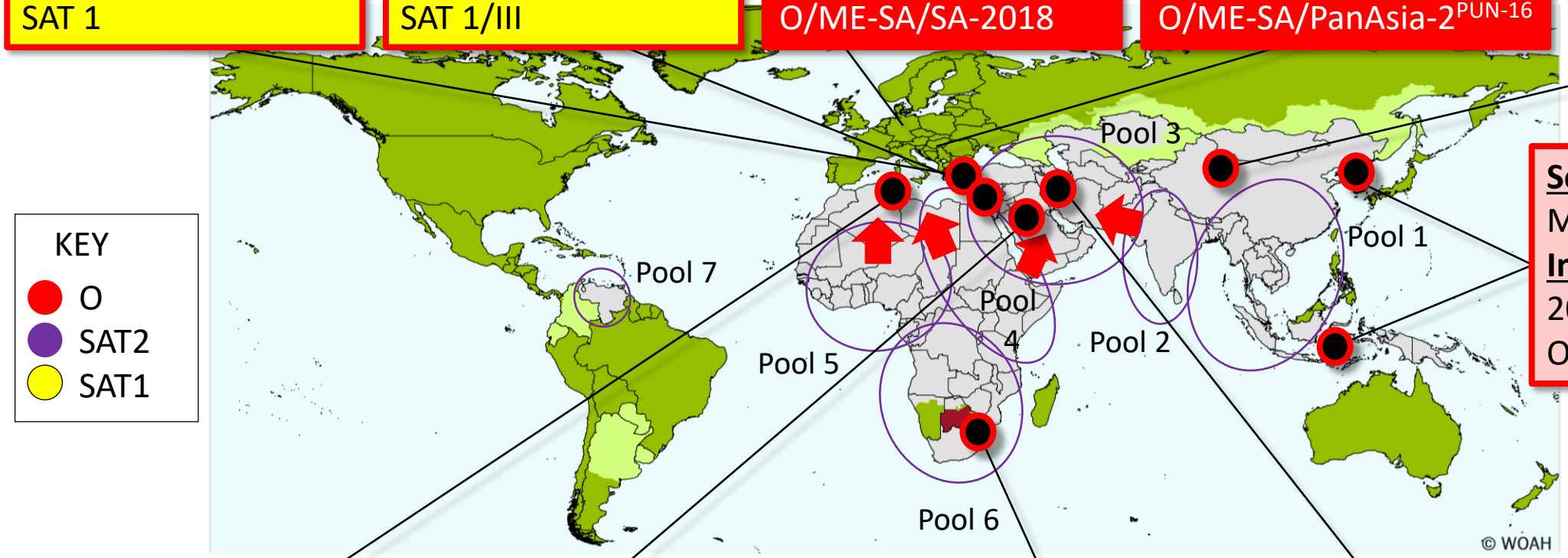
Greece
Mar 2026
SAT 1

Cyprus
Dec 2025
SAT 1/III

Germany
Jan 2025
O/ME-SA/SA-2018

Hungary, Slovakia
Mar 2025
O/ME-SA/PanAsia-2^{PUN-16}

China and Mongolia
March/May 2026
SAT 1



South Korea
Mar 2025, Mar 2026
Indonesia
2024-25
O/ME-SA/Ind-2001e

Maghreb (2025)
O/EA-3
Algeria (2023/4)
SAT2/V

Middle East (2025)
SAT1/I and SAT1/III
Middle East (23-5)
SAT2/XIV

Southern Africa
Serotypes SAT1, SAT2 and SAT3)
Eswatini
Botswana, Lesotho

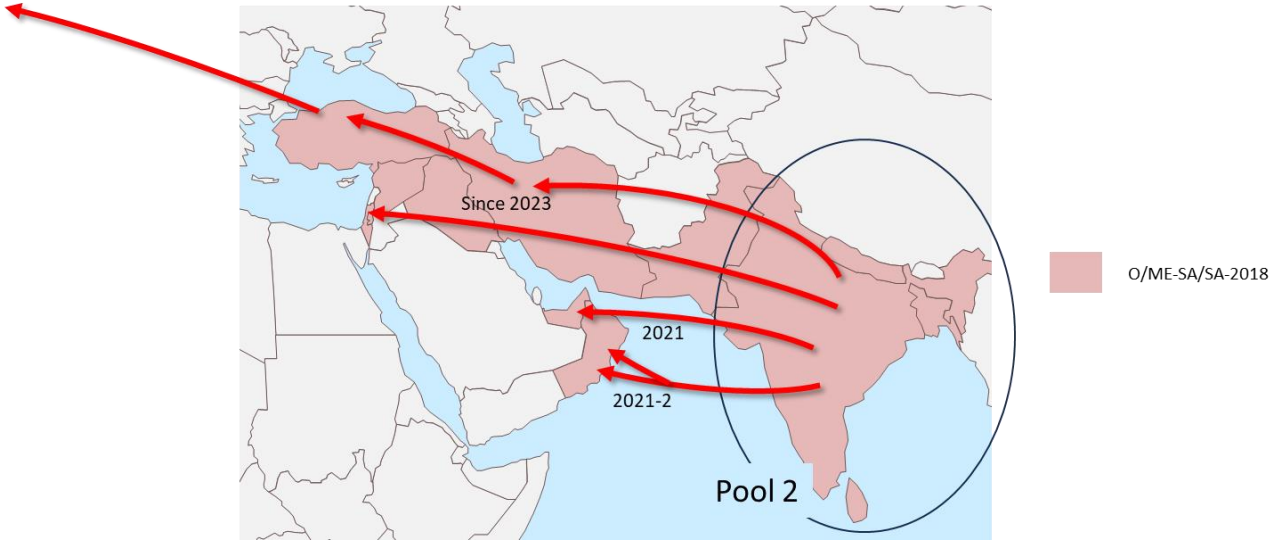
Iran, Iraq, Syria, Türkiye, Palestine, Pakistan, Israel
2023-2025
O/ME-SA/SA-2018

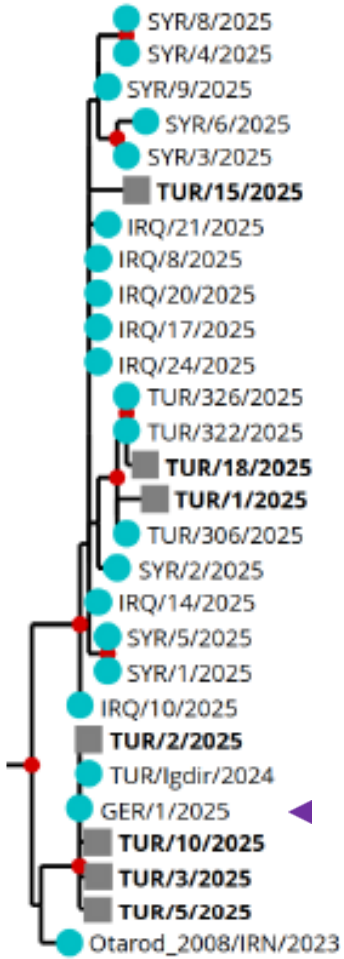
FMD headline events – 2026: incursions from South Asian countries

History tells us that pandemic serotype O lineages can emerge from South Asia (Pool 2)

The **O/ME-SA/SA-2018** lineage is frequently detected in India, Nepal, Bangladesh and Sri Lanka

Since 2021: increasingly detected in the Gulf States and West Asian countries via multiple incursions



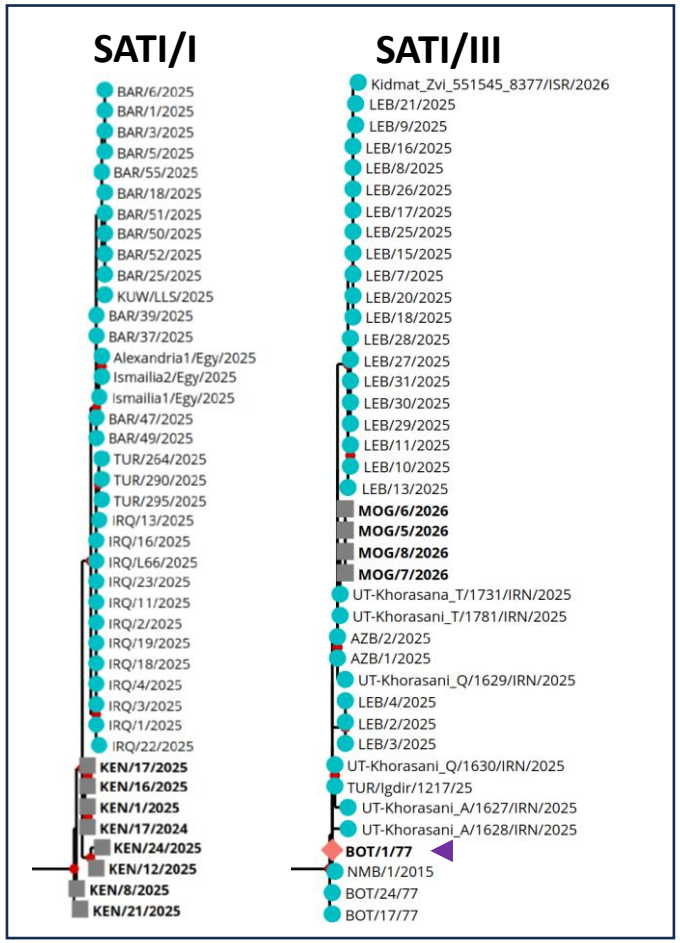


Caused outbreak in Germany in 2025 (other serotype O viruses “O/ME-SA/PanAsia-2PUN-16” from W Eurasia caused outbreaks in Hungary and Slovakia)

Scope to spread more widely – into Southeast Asia following similar pathways for O/ME-SA/Ind-2001

FMD headline events – 2026: exotic serotypes from East Africa

- **2022** — **SAT2/XIV** in Iraq, Jordan, Türkiye, Oman and Bahrain
- **Early 2025** — **SAT1/I** in Iraq and Bahrain - spread to Kuwait, Türkiye, Egypt
- **Late 2025** — Detection of **SAT1/III** in Iran and Türkiye closely related to a vaccine strain (>99% identity)
- **2025-2026** — **SAT1/III** outbreaks in Europe
- **2026** — **SAT1/III** cases reported in China (two provinces) and Mongolia



SAT1 virus origins

SAT1/I – Similar viruses in East Africa

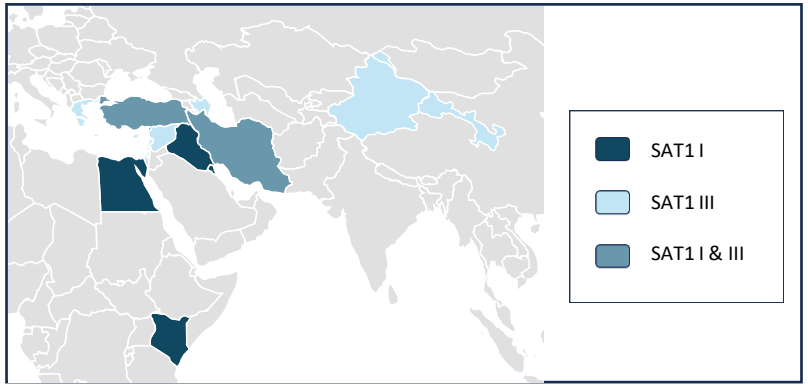
SAT1/III – Same as BOT/1/77 vaccine strain

- FMD vaccine incorrectly inactivated?
- Breach of biocontainment at vaccine plant?

Earliest SAT1 reports by country and topotype

Country	SAT 1/I	SAT 1/III
Bahrain	January 2025	
Iraq	February 2025	
Kuwait	April 2025	
Türkiye	May 2025	November 2025
Iran	*	*
Egypt	July 2025	
Azerbaijan		October 2025
Lebanon		November 2025
Israel		January 2026
Cyprus		Dec 2025/Feb 2026
Syria		January 2026*
China		March 2026
Greece (Lesvos)		March 2026
Mongolia		May 2026
Palestine	April 2026: topotype - not yet reported	

* Outbreaks not confirmed by national authority

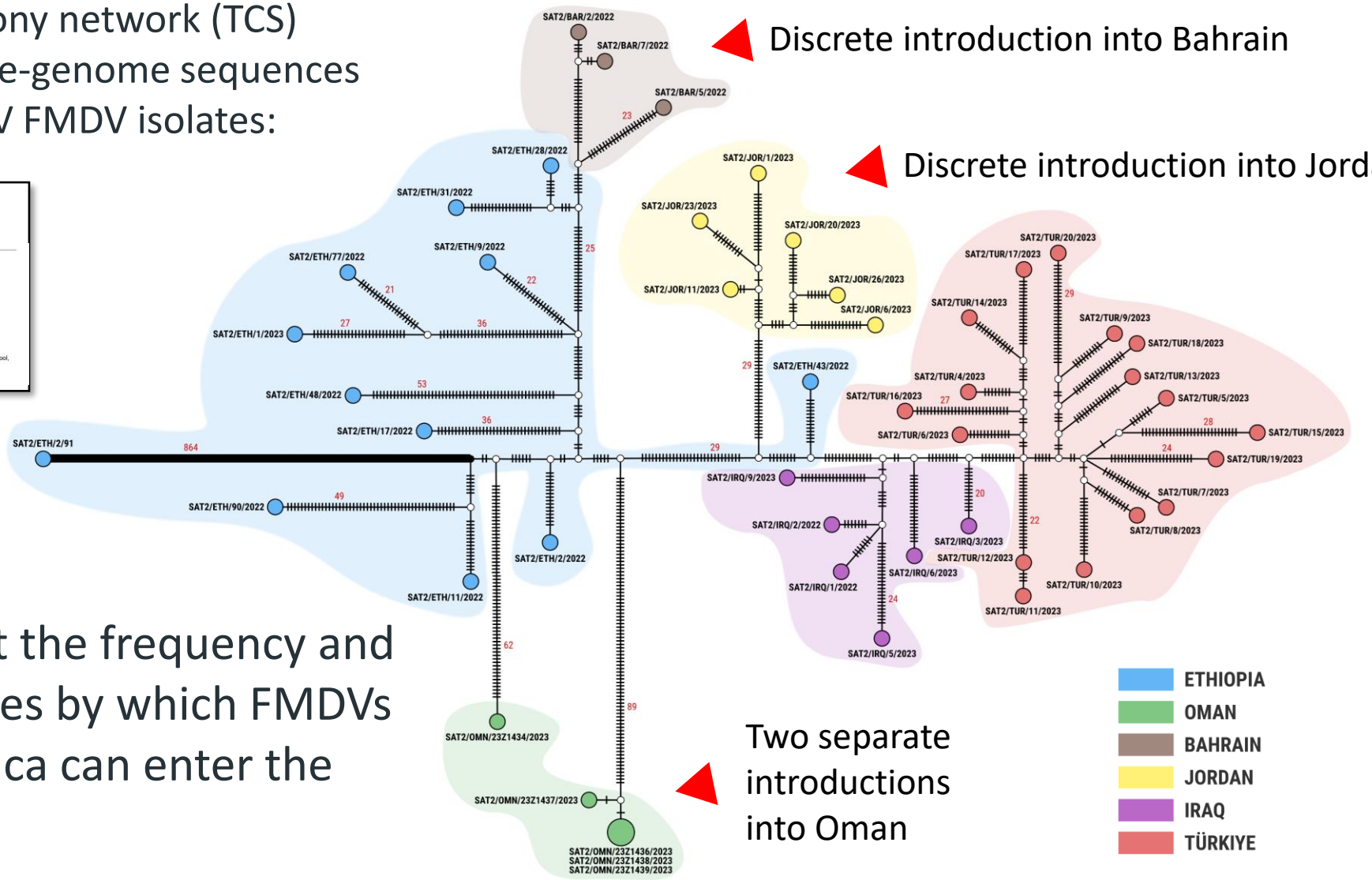


Network of Genetic Diversity

evidence for 5 introductions of the SAT2/XIV topotype

Statistical parsimony network (TCS) based on 51 whole-genome sequences (WGS) of SAT2/XIV FMDV isolates:

Published:
Di Nardo et al., (2025) *Emerging Infectious Diseases* **31** (2)



Discrete introduction into Bahrain

Discrete introduction into Jordan

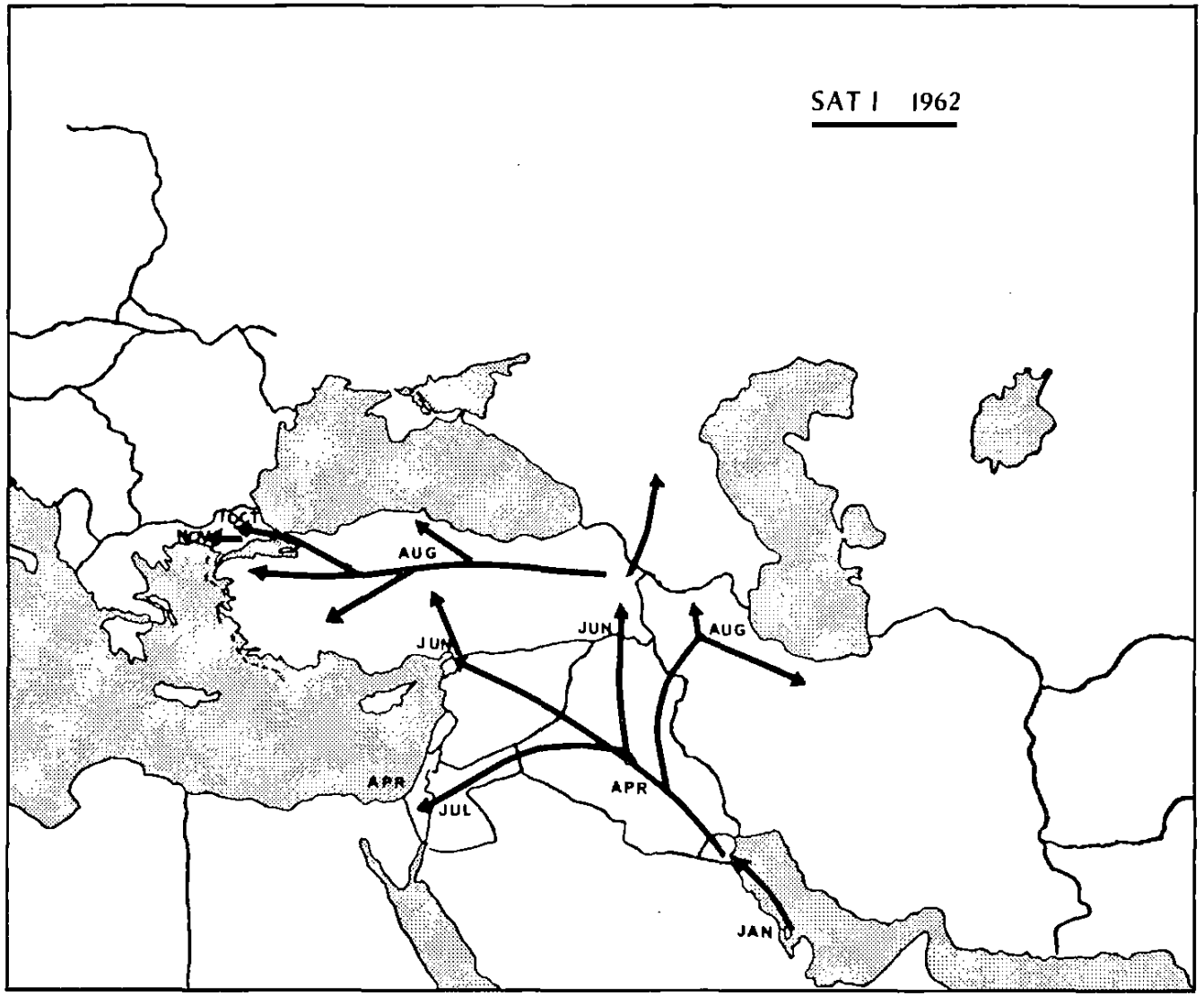
Common pathway for Iraq and Türkiye

Two separate introductions into Oman

Data highlight the frequency and different routes by which FMDVs from East Africa can enter the Middle East

J.B. BROOKSBY (1986) Foot-and-mouth disease: an introduction

Rev. sei. tech. Off. int. Epiz., 1986, 5 (2), 257-263.



Vaccine matching for SAT1 field isolates

- High genetic diversity of SAT 1 – how translates into antigenicity?
- r1 = < 0.3 - suggests that the field isolate is antigenically different to the vaccine strain.
- Vaccine efficacy also influenced by vaccine potency and vaccination regime, so if use a weakly matching vaccine, consider:
  - vaccine potency (check vaccinated animals for heterologous responses – VN titre of at least 1.5 log)
  - additional booster doses

Vaccine topotype **II**

SAT1/I isolates	SAT1/Rho78[BI]	
	r1value	heterologous titre (log_{10})
BAR/37/2025	0.31	2.20
BAR/50/2025	0.39	2.30
IRQ/1/2025	0.26	2.13
IRQ/11/2025	0.19	2.00
QTR/6/2023	0.42	2.34
QTR/7/2023	0.61	2.50
EGY/3/2025	0.33	2.14

II

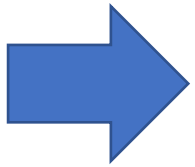
SAT1/III isolates	SAT1/Rho78[BI]	
	r1value	heterologous titre (log_{10})
BOT/1/77	0.50	2.25
AZB/1/2025	0.60	2.34
AZB/2/2025	0.51	2.27
LEB/8/2025	0.64	2.37
LEB/9/2025	0.40	2.16
LEB/10/2025	0.40	2.16
SAR/6/2025	0.38	2.24
SAR/8/2025	0.38	2.24

	II		**I**		**III**	
SAT1/III isolates	SAT1/Rho78[BI]		SAT1/IRQ2025[Dollvet]		SAT1/BOT1/1977[Dollvet]	
	$r_1$value	heterologous titre (log_{10})	$r_1$value	heterologous titre (log_{10})	$r_1$value	heterologous titre (log_{10})
MOG/5/2026	0.57	2.39	0.63	2.5	0.75	2.48
MOG/7/2026	0.97	2.62	0.74	2.58	1	2.64

Potency testing of vaccines and field isolates for SAT1/III is underway

SAT 1 potential impacts and preparedness

- Most livestock outside Africa are immunologically naïve
- Risk pathways in the region and to China are not fully understood
- **Potential spread to other countries in the Middle East, Central Asia and East/Southeast Asia**
- Rapid detection and response essential to minimise losses
- High demand for vaccines for a previously neglected serotype
- Uncertain persistence potential



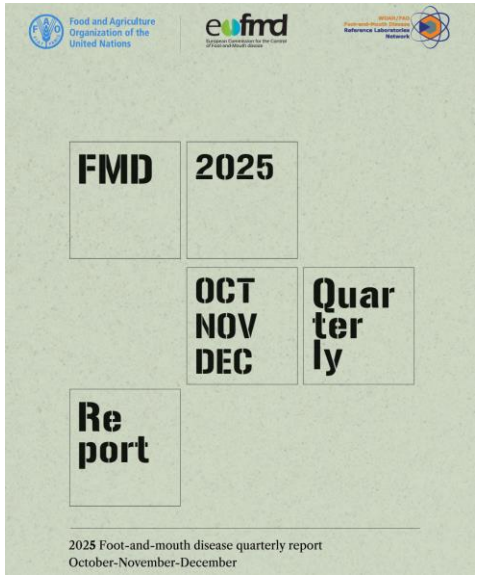
- Need to raise local and global awareness of these new risks
- Recent GF-TADs seminars on epidemiology and vaccines
- Transparency required for regional preparedness
- How to safeguard vaccine supplies?
- Importance of laboratory preparedness
  - WOAH and FAO reference laboratories support
  - Ag-ELISA (from IZSLER) and SAT1/I and SAT1/III lineage-specific real-time RT-PCRs developed (by ANSES and WRLFMD) for detection and discrimination of these viruses
  - Sequencing approaches (primers) are also available
  - Post-vaccination immunity and exit testing for status recovery

Summary of global events

- Emergence and spread of a new serotype O lineage (O/ME-SA/SA-2018) in the Middle East region
- **SAT1 in the Middle East** (Pool 3) – two co-circulating topotypes
  - SAT1/I sequences from Kenya – reinforce epidemiological connection between East Africa and the Middle East
  - SAT1/III sequences share close genetic identity to a vaccine strain (BOT/1/77)
  - Onward spread of SAT 1/III into Europe (Cyprus and Greece) and Central Asia (China and Mongolia, via poorly understood risk pathways)
- Detection of **O/EA-2** in Ethiopia for the first time
  - representing >80% of submitted samples
- A new incursion of **O/EA-3** in Algeria (December 2025)
- Upsurge of **SAT1** cases across Southern Africa – leading to the loss of FMD-free status in Botswana (two separate incursions) and Lesotho
- New incursion of **O/ME-SA/Ind-2001e** into South Korea

Further information……

- FMD reports and lab testing (https://www.wrlfmd.org/ref-lab-reports)
    - *Genotyping reports*, *Vaccine matching* and *Serotyping reports*
- Other data sources:
    - Quarterly WRLFMD/EuFMD report (https://www.wrlfmd.org/ref-lab-reports)
    - Annual report of the WOAH/FAO FMD Laboratory Network (http://foot-and-mouth.org/)
    - OpenFMD (www.openfmd.org) – sequences, genotyping, vaccine selection and surveillance



Thanks to:

- Collaborating FMD Reference Laboratories and field teams
- Partners within the WOAH/FAO FMD Lab Network
- Support for the WRLFMD and research projects

Vaccine selection for endemic settings (gaps and challenges)

1. Vaccine-matching (r_1-values) considers strain suitability but NOT the quantity/quality/combinations of antigens in a final product (and is limited due to access to vaccine strains and BVS)
2. Homologous/monovalent QA/QC (WOAH Terrestrial Manual) vs heterologous vaccine performance **in the field** with multivalent products

Proposed testing:

- Increased focus on measurement of **heterologous responses**
- Using **final formulated product supplied to customers**
- Use common/standardized FMDV viruses (**Antigen Panels**) representative of the antigenic threats in a region – proposal for reference antigens for East Africa (https://www.wrlfmd.org/node/2096/)