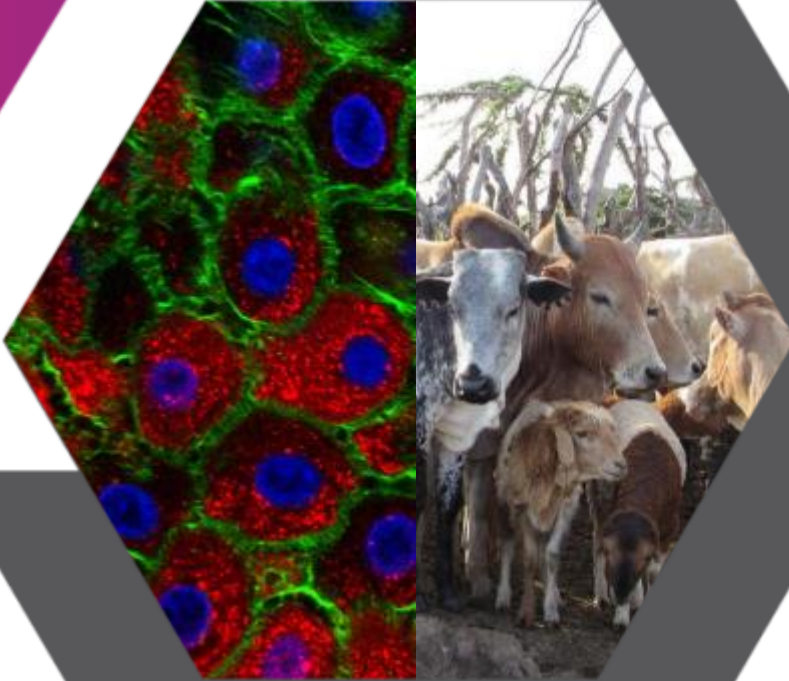


OIE/FAO
Foot-and-Mouth Disease
Reference Laboratories
Network



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FMD situation with emphasis on West Eurasia

David Paton, on behalf of Don King and colleagues

Acknowledgements: Donald King, Valerie Mioulet, Nick Knowles, Anna Ludi, Britta Wood, Ginette Wilsden, Krupali Parekh, Andrew Shaw, Antonello Di Nardo, Nuredlina Prior, Jemma Wadsworth, Clare Browning, Mark Henstock, Deyzi Santos, Hayley Hicks, Victoria Chantler, Dexter Wiseman, Ali Al-Rashed, Jozhel Baguisi, Harry Bull, Ryle Walter, Amy Sowood, Sarah Belgrave, Jessie Trussler

Dushanbe

11th November 2025



Pirbright receives strategic funding from



Department
for Environment
Food & Rural Affairs



World Organisation
for Animal Health
Founded as OIE

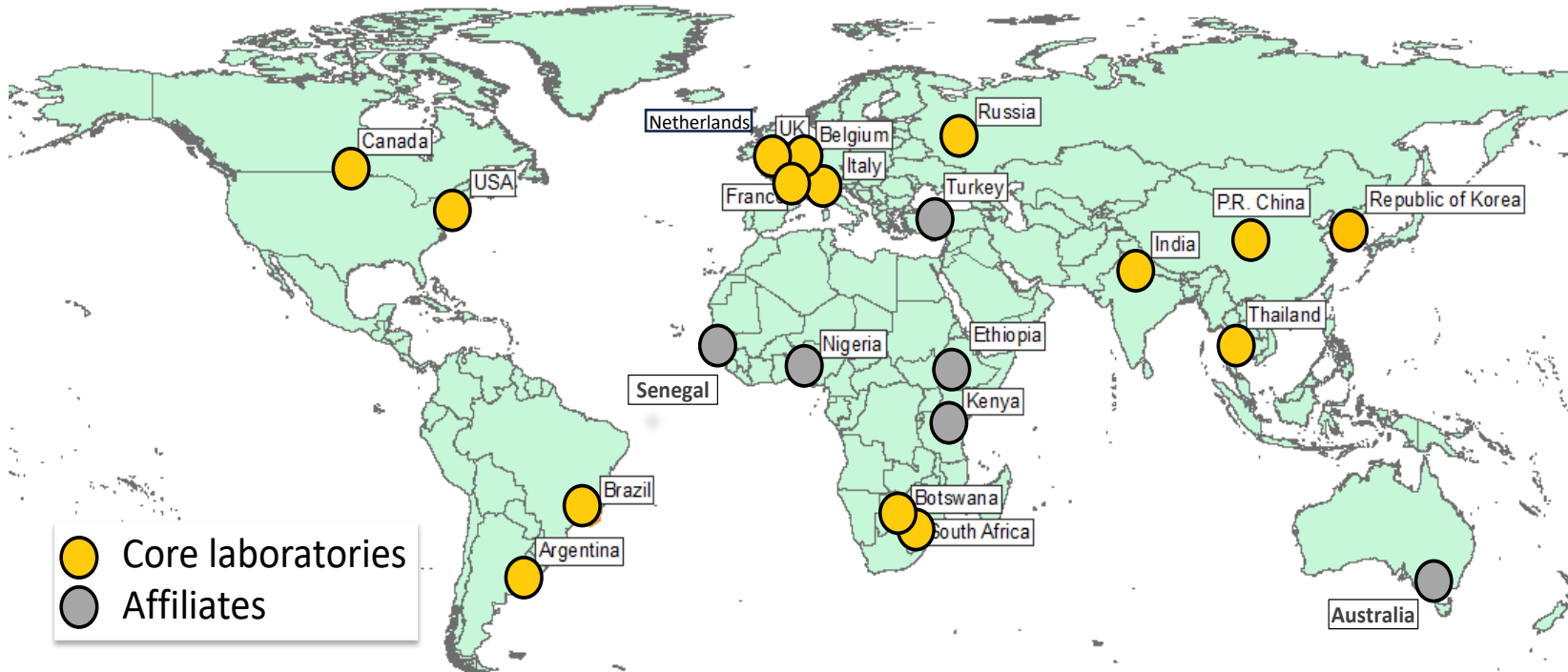
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WOAH/FAO FMD Lab Network

<https://www.foot-and-mouth.org/Ref-Lab-Network>



- Established in 2004
- 15 WOAH and FAO laboratories



This year's meeting was held on 22-24th October 2025 in Istanbul

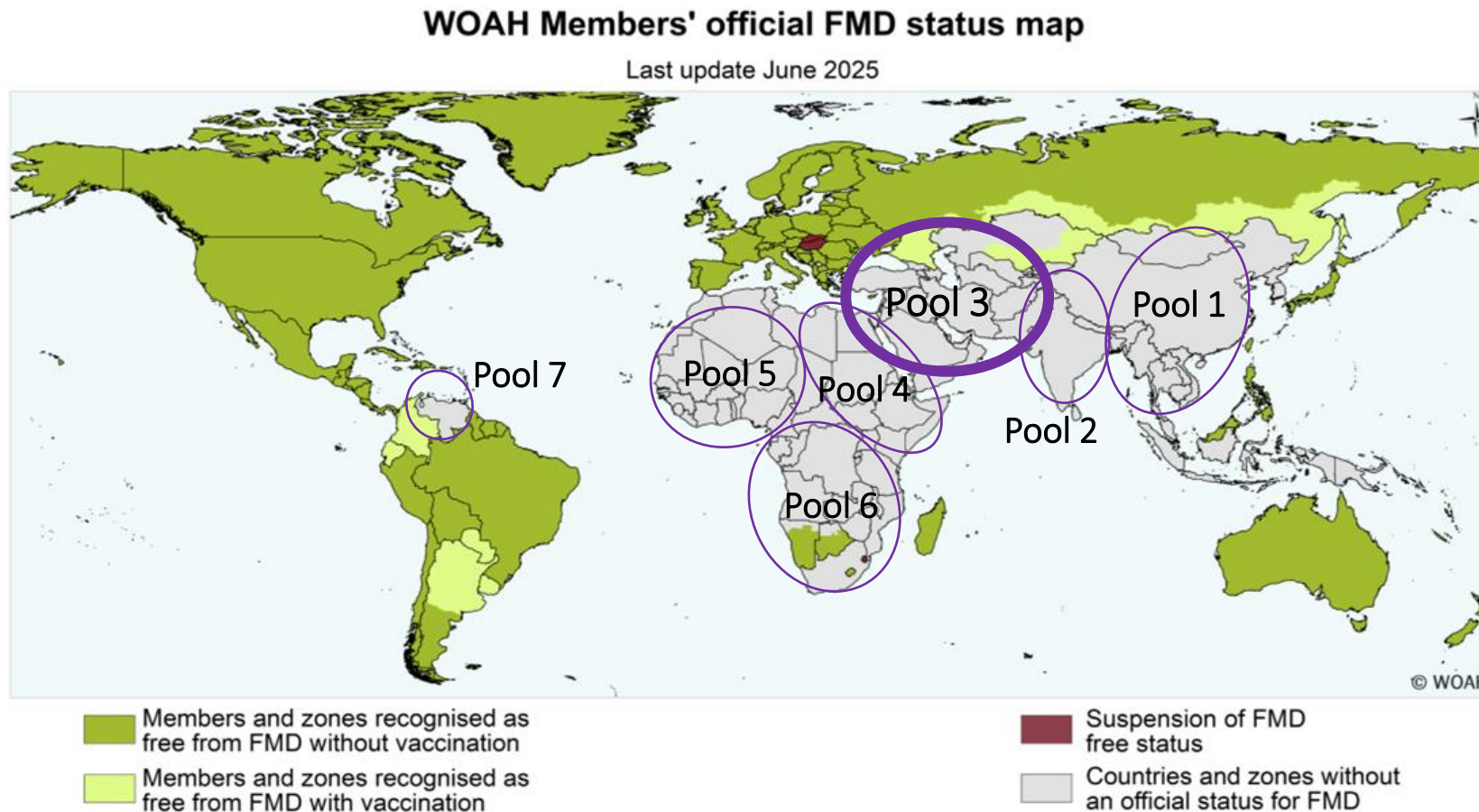
Core activities:

- FMDV confirmation and characterisation
- Collation, exchange, dissemination of data
- Test development, validation, harmonization
- Vaccine seeds, selection and performance
- Review of FMD risks
- Support to international, regional and national control efforts

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Global Overview

- FMD is Endemic in Asia and Africa (and Venezuela)



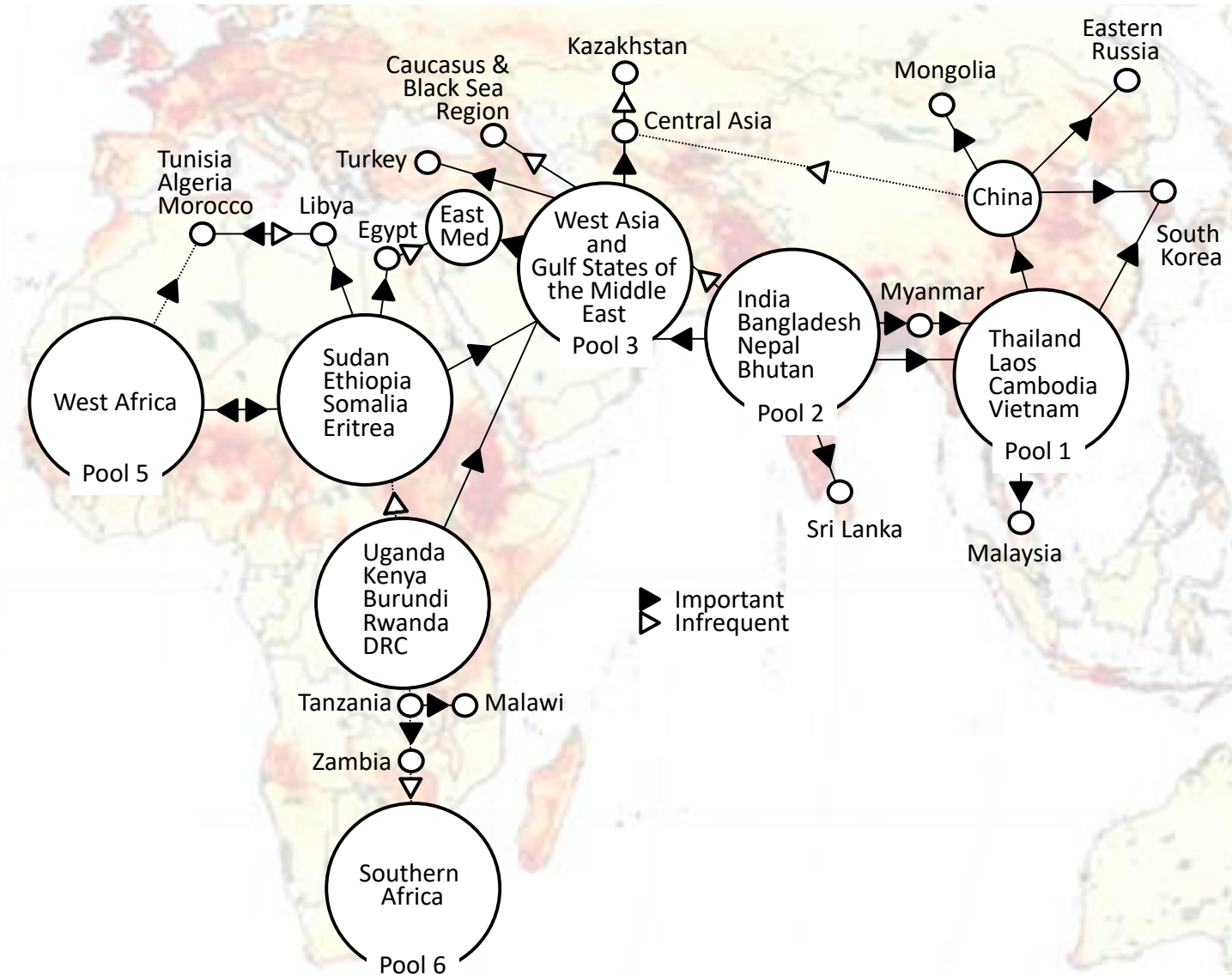
7 endemic pools of specific viral lineages

6 circulating serotypes with unequal / dynamic distributions

Serotypes O and then A most prevalent; in Africa, SAT 1 & 2 more common than SAT 3

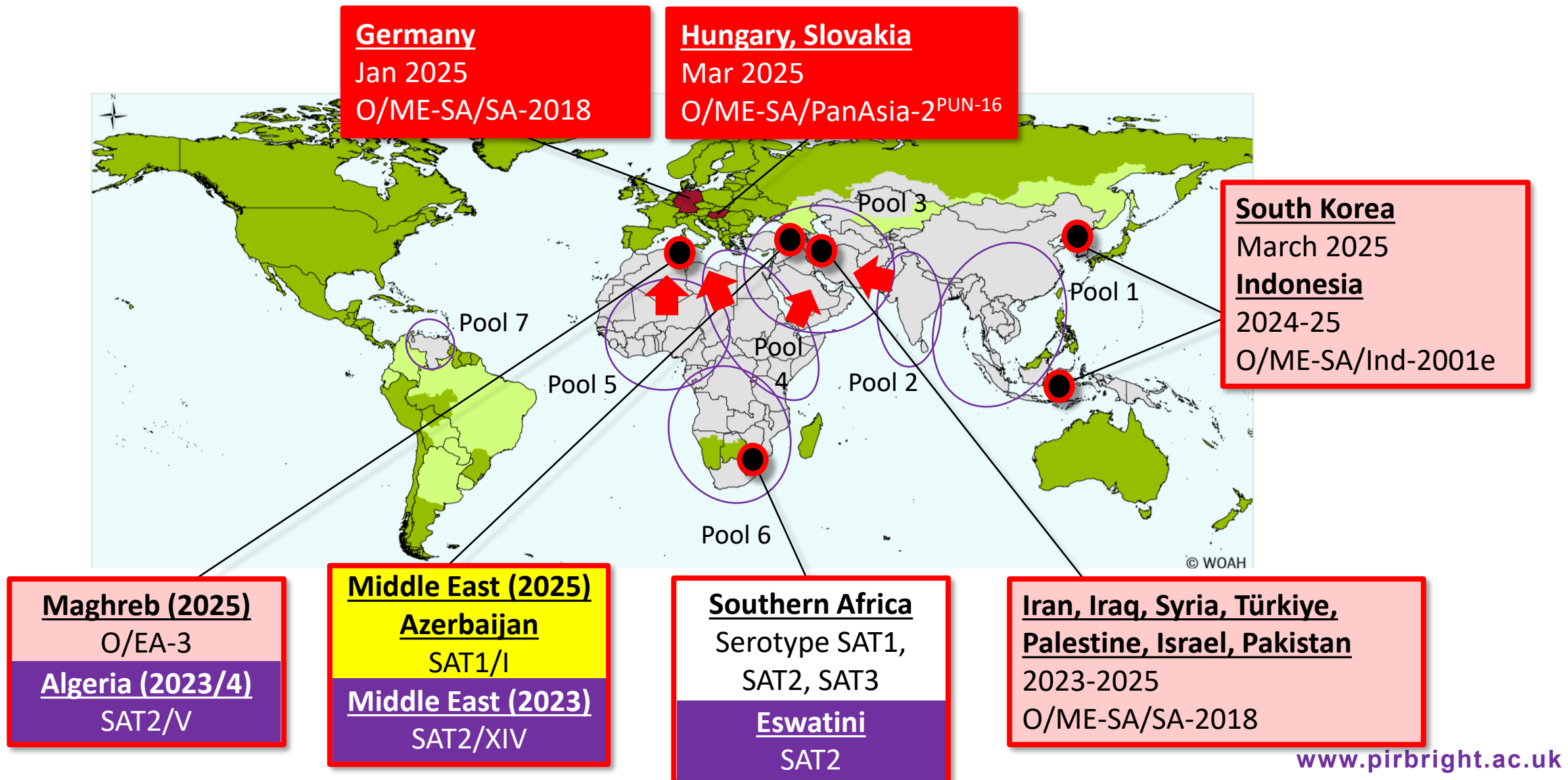
Serotype C undetected since 2004

FMDV global network (based on sequences)



- Phylogenies reveal connections between pools with directionality and frequency
- Long-distance “trans-pool” movements of FMDV lineages are incompletely predictable

Headline global status for FMD (October 2025)



Updated FMD risks for Pool 3 (since 2020)

New virus introductions from South Asia and East Africa:

Prevalence proportions estimated, Istanbul Nov 2025:

- SAT 1 to 21%
 - O/ME-SA/SA-2018 to 13%
 - Asia 1 down to 5%
 - A Iran-05 – down to 20%
 - O PanAsia 2 – down to 25%
 - SAT 2 – down to 12%
 - Remove A G-VII (0)
- Estimated number of incursions

!

Lineage	x
SAT2/XIV	5
SAT1/I	2-3
O/EA-2	1
O/EA-3	2
A/AFRICA/G-I	2

East Africa (Pool 4)

West Asia, Gulf States and ME (Pool 3)

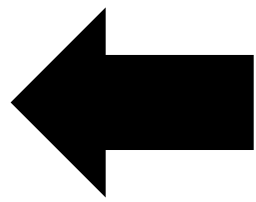
Endemic FMDV lineages:

- O/ME-SA/PanAsia-2*
- A/ASIA/Iran-05
First cases in Türkiye in six years (09/24)
- Asia 1

Due for return?

*Note: New O/ME-SA/PanAsia-2 designations are proposed by Jamal et al., (2025) Emergence of new sublineages of serotype O foot-and-mouth disease viruses circulating in Pakistan during 2012-2021. *Virology* **605**: 110455

Hungary/Slovakia 2025



South Asia (Pool 2)

Estimated number of incursions

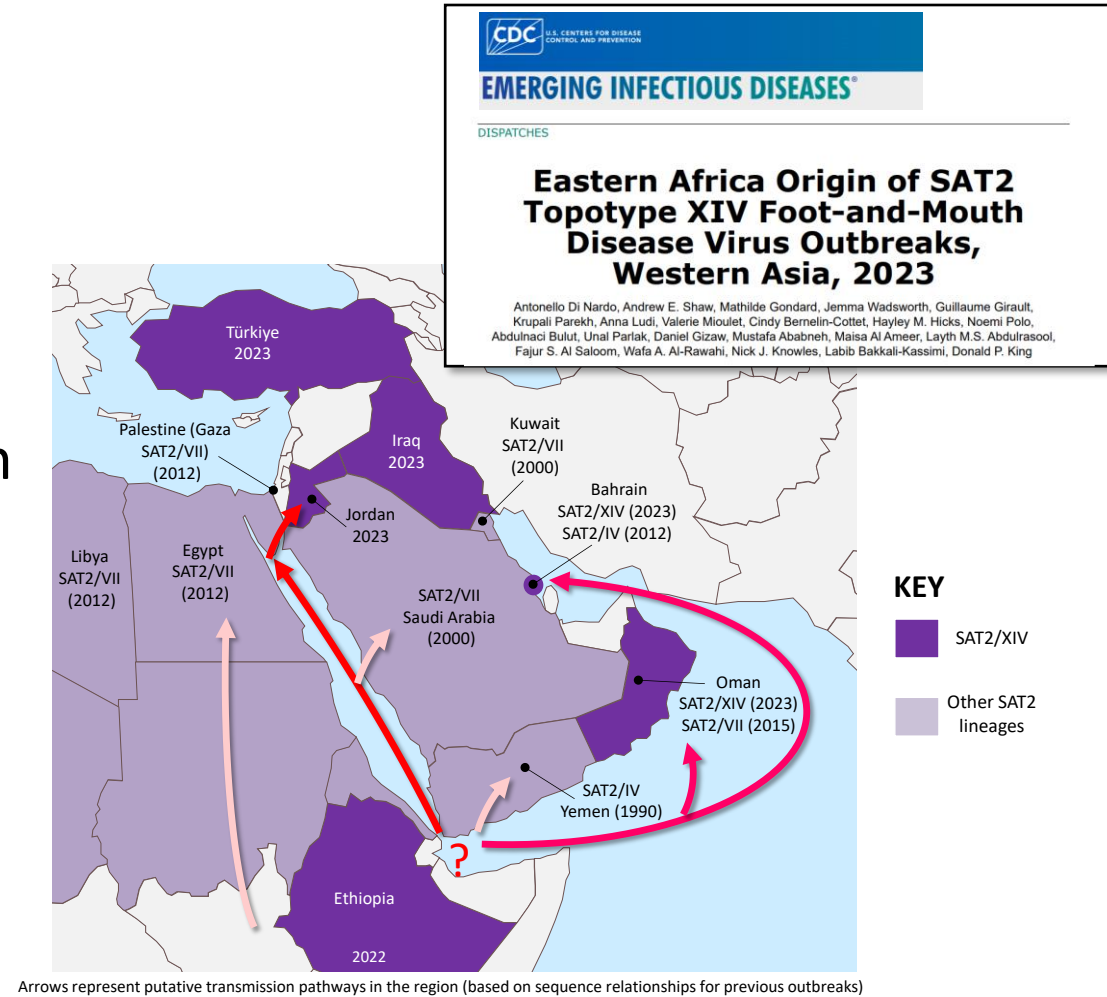
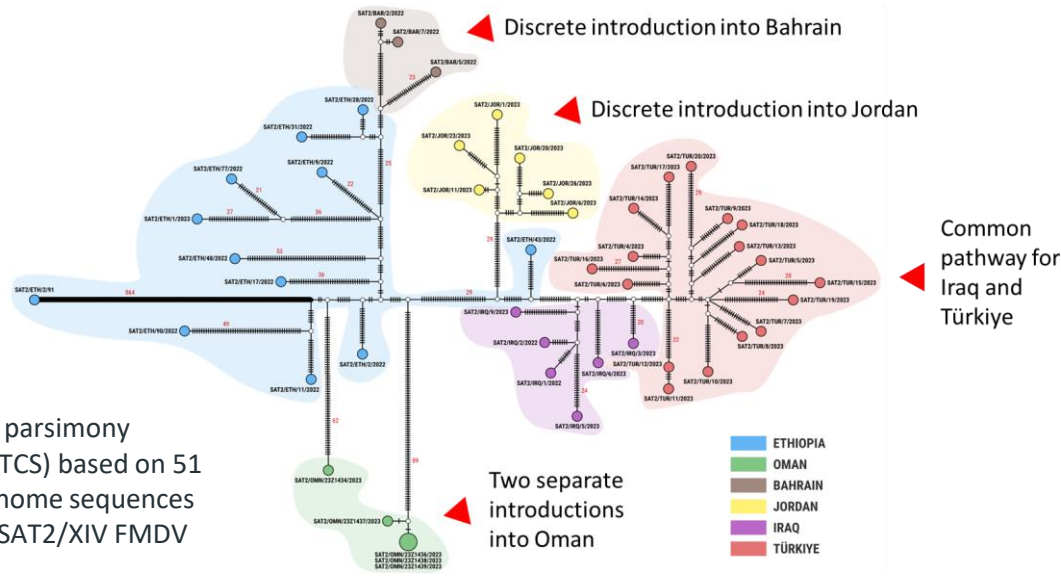
Germany 2025

Lineage	x
O/ME-SA/SA-2018	~4
O/ME-SA/Ind-2001e	
A/ASIA/G-VII†	

†Last reports cases in Pool 3 were in 2018 (Iran)

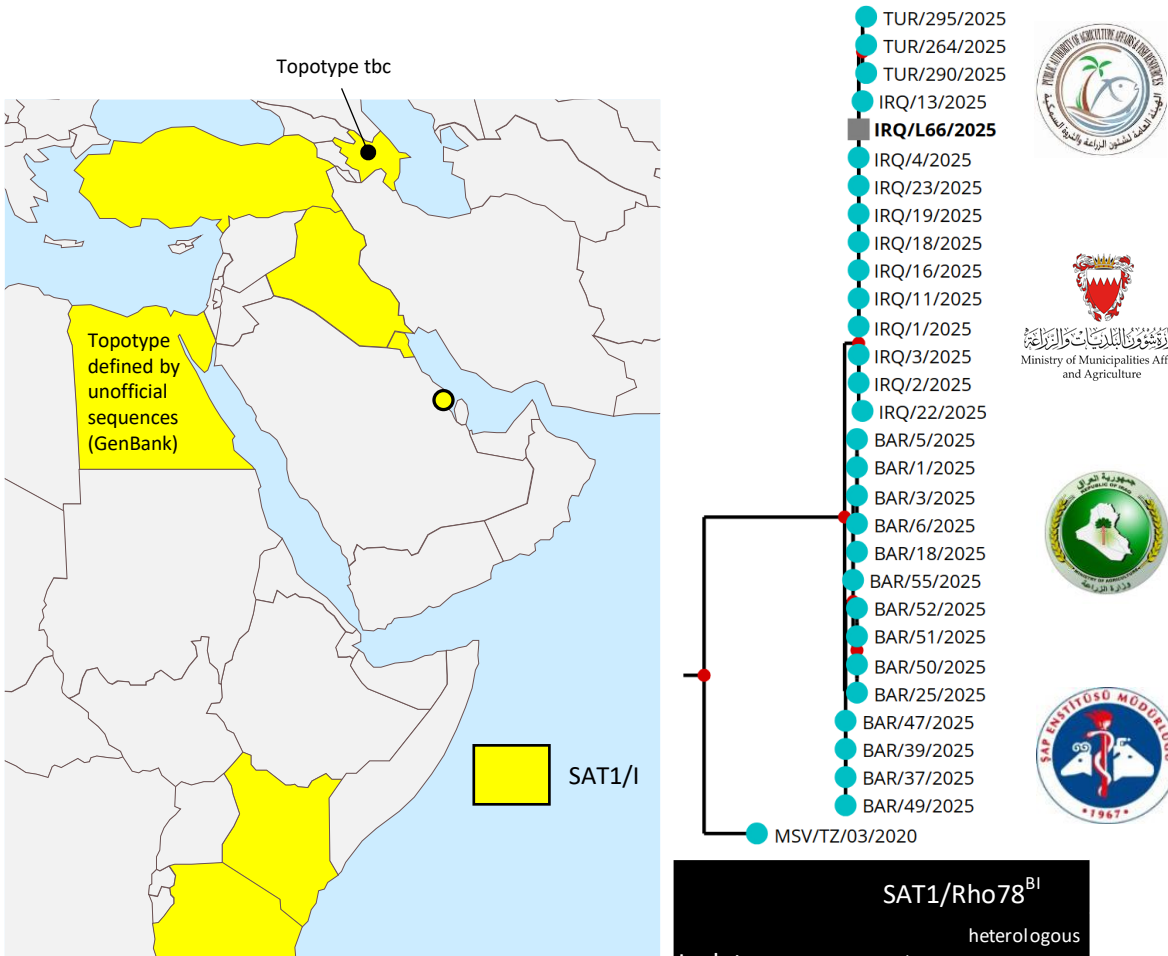
2022-23: FMD outbreaks due to the SAT2/XIV topotype

- Most closely related to sequences recovered from samples collected in SW Ethiopia in 2022
- Topotype XIV has been detected on only one other previous occasion – in 1991
- To our knowledge, this is the first time that serotype SAT 2 has been detected in Iraq, Jordan or Türkiye



2025: Emergence of serotype SAT1/I in the Middle East

- SAT1/I detected in **Qatar** quarantine station (2023)
- Then in **Bahrain** (2025) and subsequently **Kuwait** (Apr 2025), **Türkiye** (May 2025), **Egypt** (Aug 2025) and **Azerbaijan** (Oct 2025)
- Sequence differences to Qatar (2023) - separate introductions
- Closest genetic relative from **Tanzania 2020**
- **SAT 1 specific tests available** and validated for this strain:
 - SAT1/I **lineage-specific real-time RT-PCRs** have been tested (see: Bachanek-Bankowska et al., 2016*)
 - **Ag-ELISA** (from IZSLER) is able to detect and serotype viruses from this toposotype
- Animals are naïve to this serotype - **potential for rapid spread**
- **Limited vaccines available**



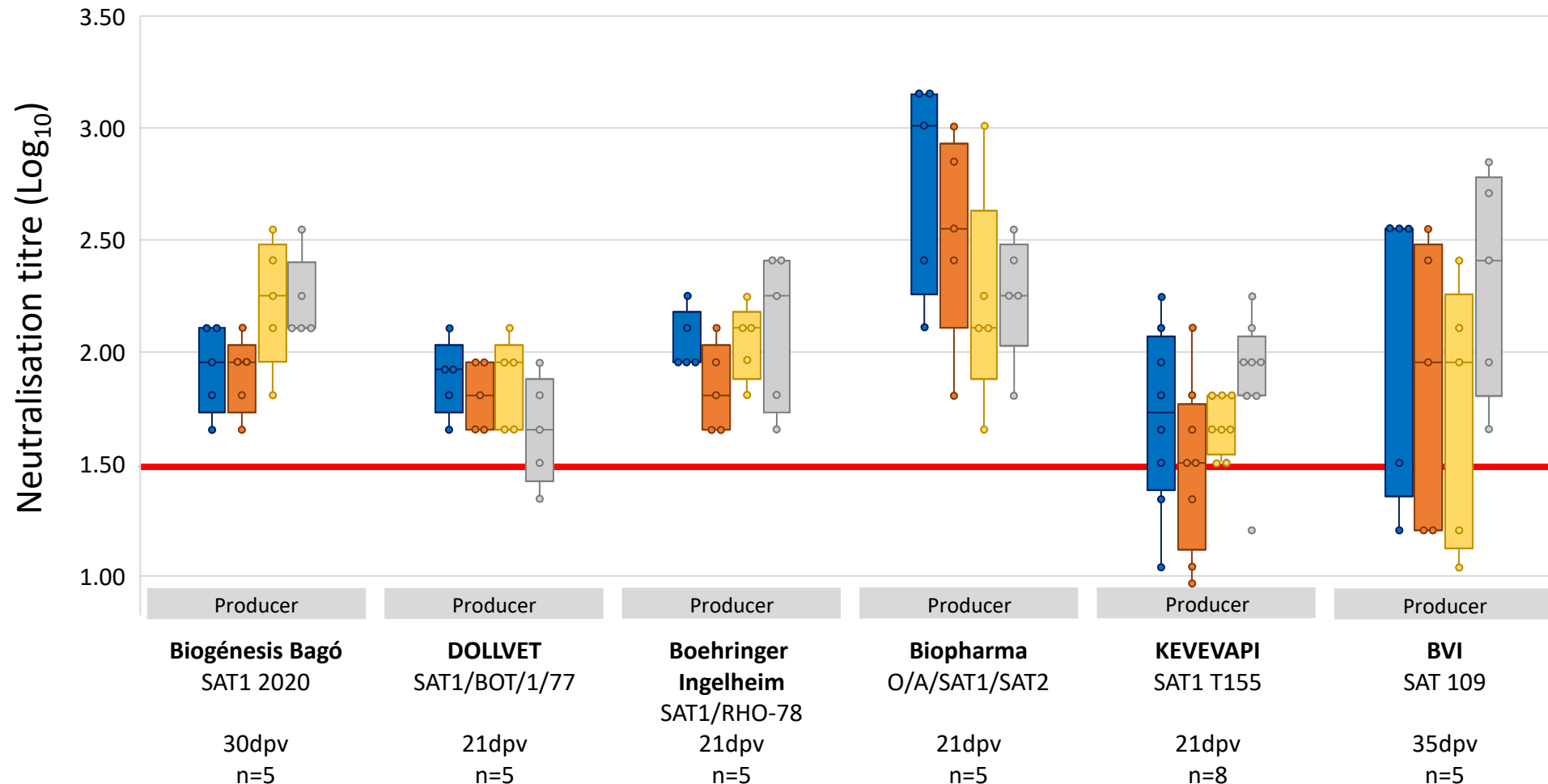
*Bachanek-Bankowska et al., (2016) Development and evaluation of tailored specific real-time RT-PCR assays for detection of foot-and-mouth disease virus serotypes circulating in East Africa. J Virol Methods **237**:114-120.
<https://www.foot-and-mouth.org/science/lineage-specific-fmdv-real-time-rt-pcr-assays>

SAT1/Rho78 ^{BI}		
Isolate	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

Heterologous responses of SAT1 vaccines against SAT1/I field isolates

Sera generated by manufacturers from trial-blends of vaccines

- shows that these vaccines have potential to elicit neutralizing antibodies against relevant field isolates
- but customers should test in-country with formulated products to confirm that responses are sufficient (RL help)



Viral antigens

- BAR/50/2025
- IRQ/11/2025
- QTR/7/2023
- TAN/22/2014*

*East Africa reference antigen (Paton et al., 2025)

Source of sera

Sera collected Day post-vaccination
www.pirbright.ac.uk



- FMDbase - sequences
- FMDtype – genotyping reports
- FMDwatch – surveillance data
- PRAGMATIST – vaccine selection

FMD Analytics

These tools makes use of both genetic sequence and epidemiological data, along with associated geographical as well as species-specific data, to help researchers understand how FMD viruses evolve and spread, and facilitate data interaction and exploration through customizable filters, sophisticated queries and intuitive visualisation further enabling download of data.

FMDwatch

PHD epidemiological intelligence for digital surveillance, exchange and communication of new disease threat

Take home messages

- Pool 3 FMD epidemiology is dynamic: virus incursions from E. Africa and S. Asia (even S. America)
- Circulation of different FMD virus lineages allows FMDV to circumvent natural immunity and impacts the selection of appropriate vaccines
- Virus characterization contributes to better FMD control
 - Identifies active serotypes and strains, reveals threats and risk pathways and provides vaccine seed viruses
 - Allows for independent vaccine evaluation
 - Vaccine matching to define antigenic similarity of putative vaccine strains
 - Heterologous testing to see if the combined effect of vaccine potency, regime and match have resulted in sufficient strain-specific immunogenicity
- **Sampling of field outbreaks, data sharing and transparency are critical.....**
- **WRLFMD and the WOAHA/FAO Lab Network welcome sample submissions**
 - This testing is free of charge
 - Contact: donald.king@pirbright.ac.uk
 - RLs can also help with serosurvey design and interpretation

Breaking news

- New information from Turkiye this week

New data from this week.....

- VP1 sequence provided from the SAP Institute, Türkiye (November 2025)
- **Characterised as SAT1/III**
- Closely related (99.5% identity) to BOT/1/77 that is used as a vaccine strain by some companies

