



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



# Overview of global FMD events

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WOAH Reference Laboratory for FMD

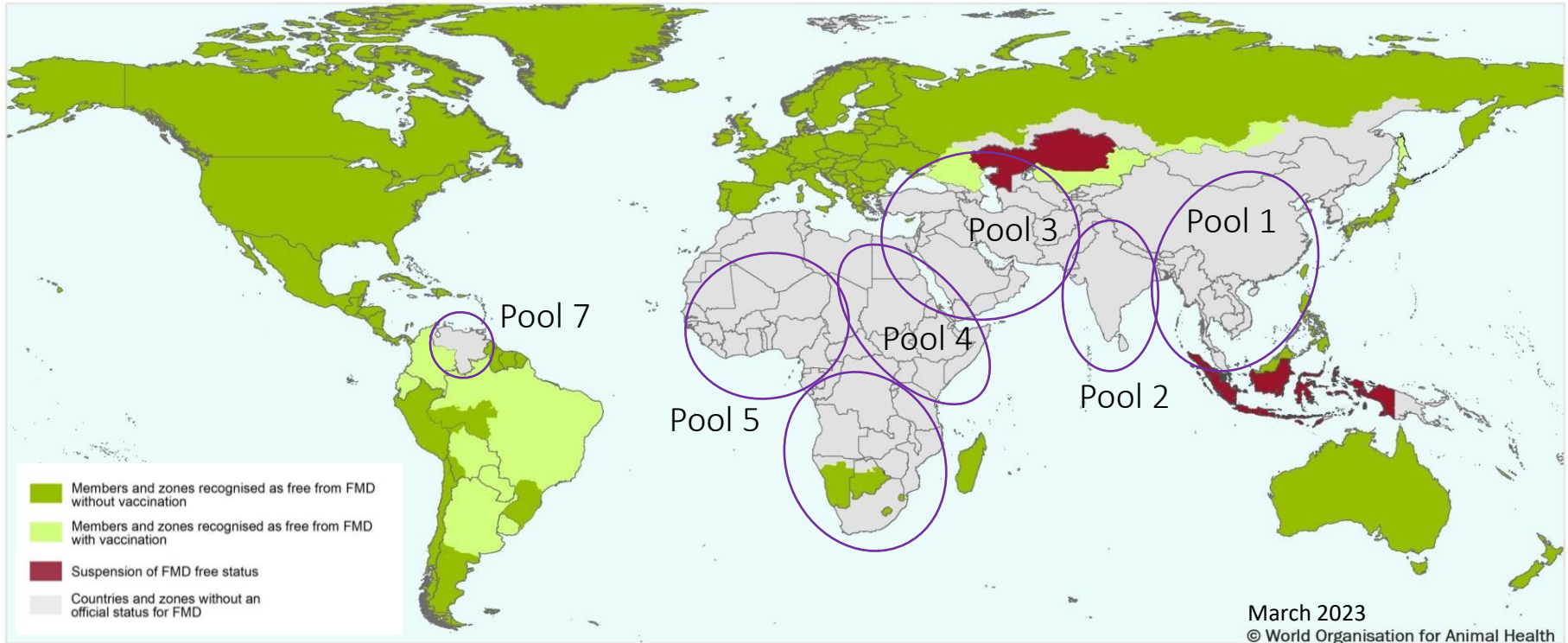
The Pirbright Institute

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# Global status of FMD

- FMD is endemic in much of Asia and Africa (and parts of South America)



- **Seven endemic pools** that maintain specific viral lineages
- Six circulating FMDV serotypes with an unequal distribution
  - Serotype C has not been detected globally since 2004

# WOAH/FAO FMD Laboratory Network

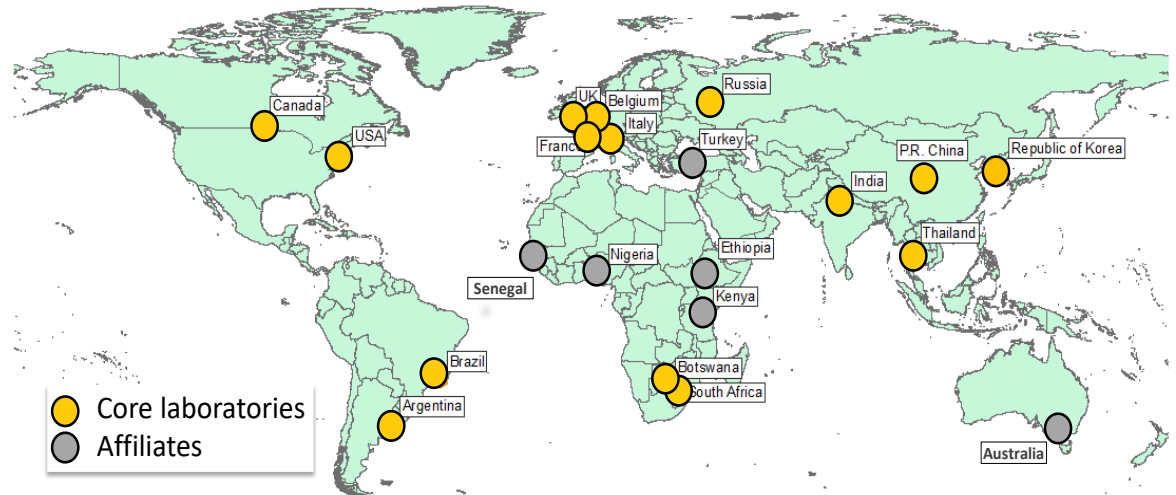
[www.foot-and-mouth.org](http://www.foot-and-mouth.org)



Network Members and affiliates:

## Core activities:

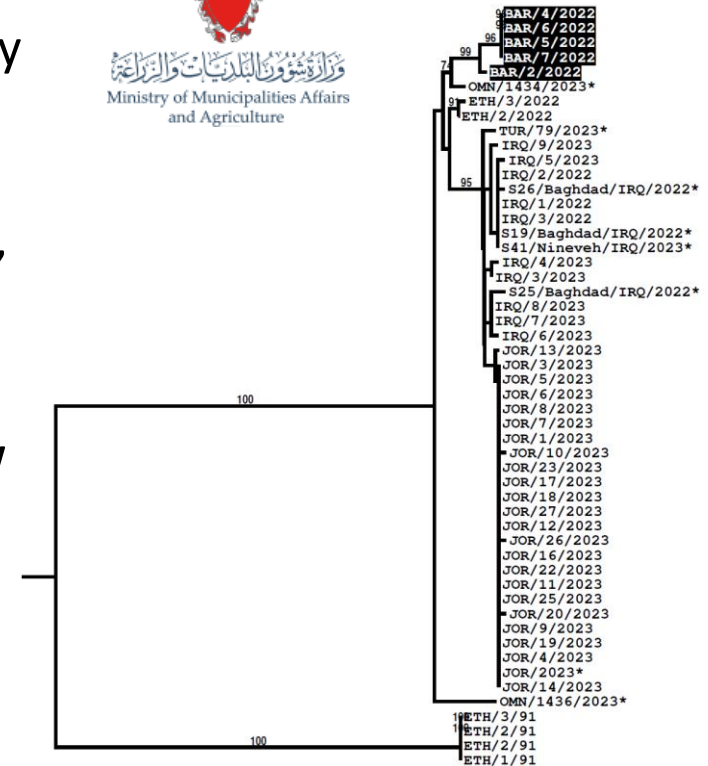
- Collation and exchange of data
- Test improvement and harmonization
- Vaccine performance
- Review of FMD risks
- Support to GF-TADs regional RoadMaps



2022 Network Meeting, Lelystad, The Netherlands

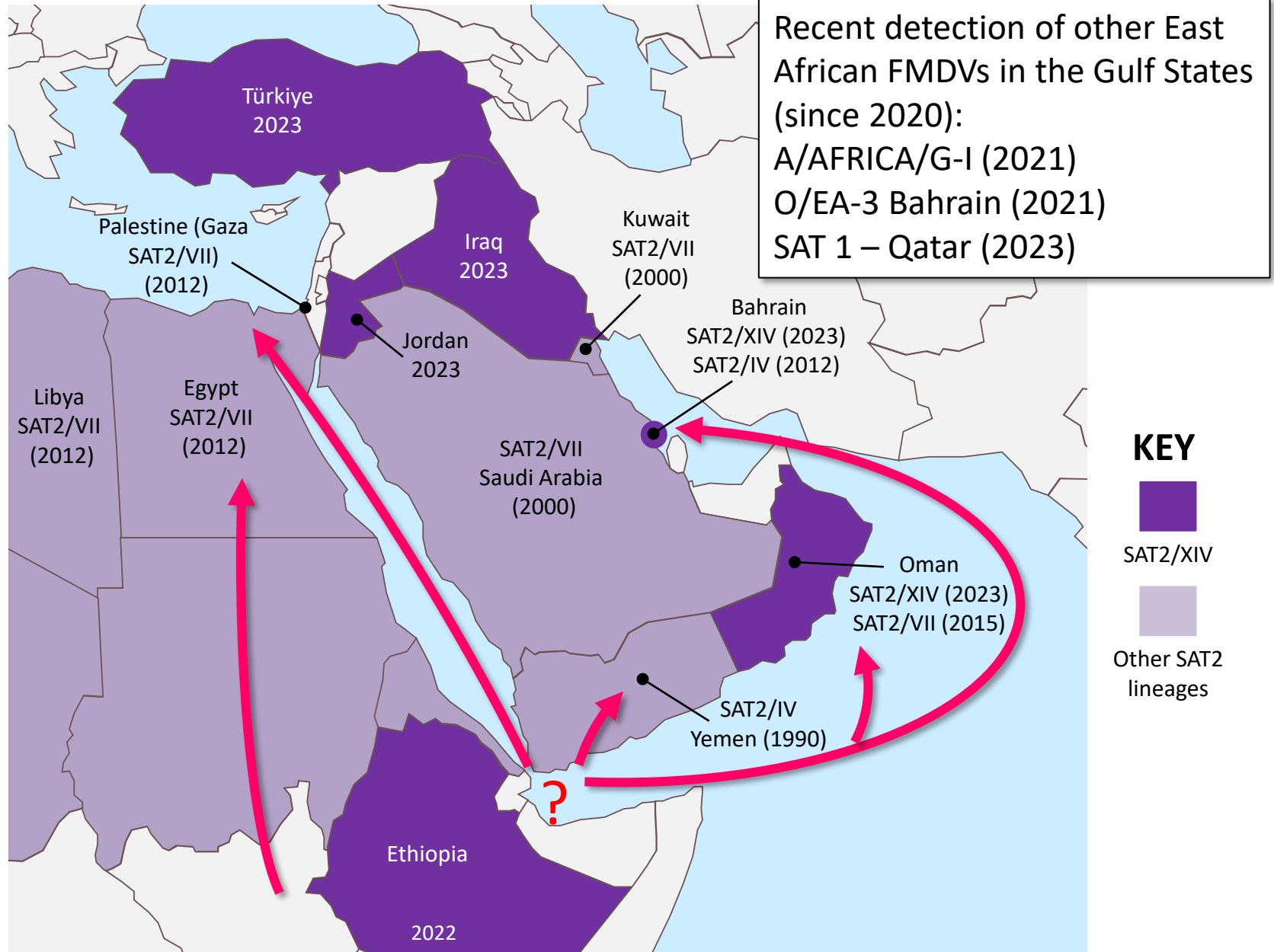
# New FMD outbreaks due to the SAT2/XIV topotype

- VP1 sequence data and samples: kindly shared by colleagues at: Central Veterinary laboratory and Researches Veterinary Dept, Iraq; FMD (ŞAP) Institute, Türkiye; JUST, Jordan, Central Laboratory of Animal Health, Oman; Sultan Qaboos University, Oman; ANSES, France and AHI, Ethiopia
- Most closely related to sequences recovered from samples collected in SW Ethiopia in 2022
- To our knowledge, this is the first time that serotype SAT 2 has been detected in Iraq, Jordan or Türkiye
- Topotype XIV has been detected on only one other previous occasion – in 1991





# SAT 2 outbreaks in North Africa/Middle East



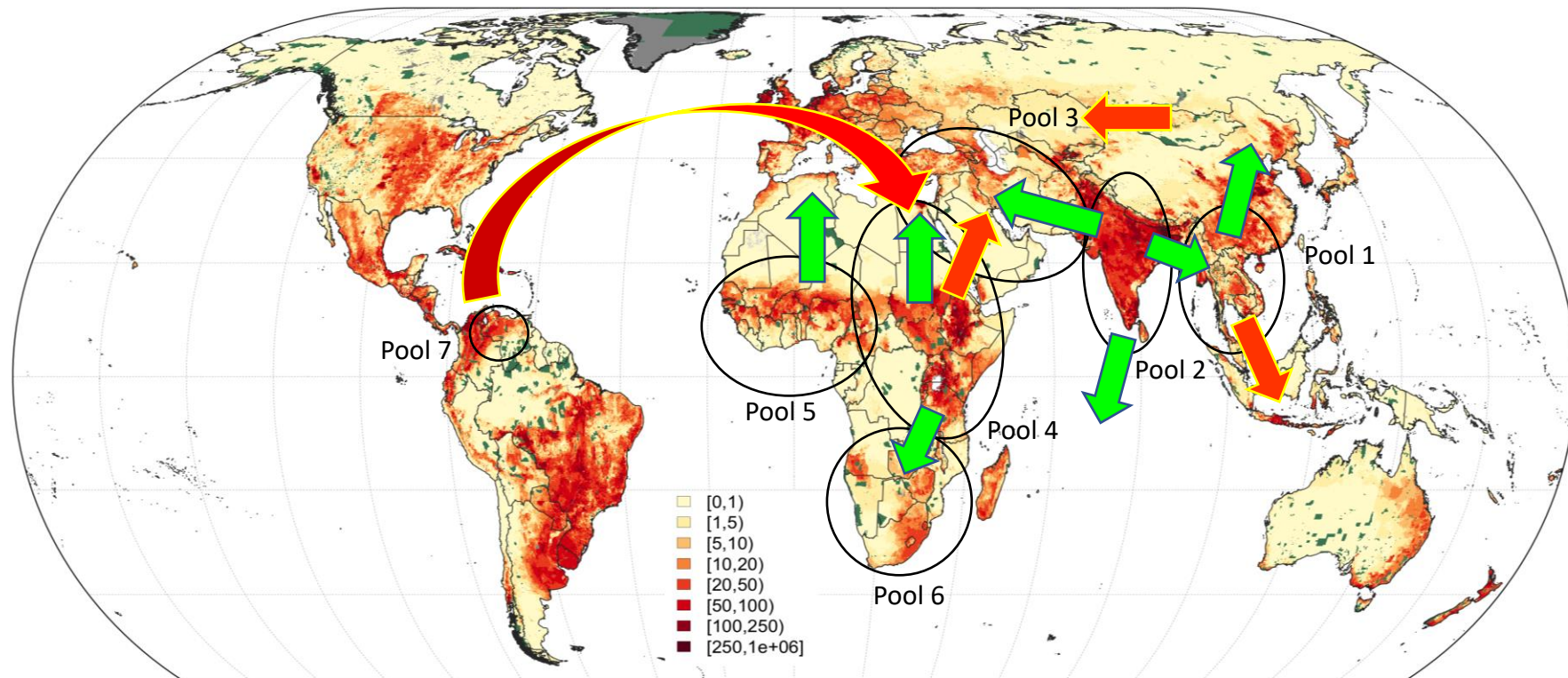
Arrows represent putative transmission pathways in the region (based on sequence relationships for previous outbreaks)

# SAT2/XIV – a quickly changing situation

## Some points to consider....

1. SAT2/XIV is spreading in naïve animals without any immunity conferred by previous infection/vaccination
2. Reports of mortality associated with SAT2/XIV infection (or secondary infection) and corresponding disease severity particularly in large ruminants (cattle/buffalo) – similar to reports in Egypt in 2012 associated with SAT2/VII outbreaks?
3. Source (and timing) of the virus in the region is currently still being investigated as well as the risk pathways by which SAT2/XIV has been introduced into the region
4. There is uncertainty about the status of neighbouring countries in the region (wrt SAT2/XIV)
5. Opportunities for rapid spread elsewhere in West EurAsia (incl. Caucasus countries, as well as into FMD free regions (such as the Balkans)).

# Trans-pool movements are important



Cattle density map

Robinson et al., 2007

 New events 2021-23

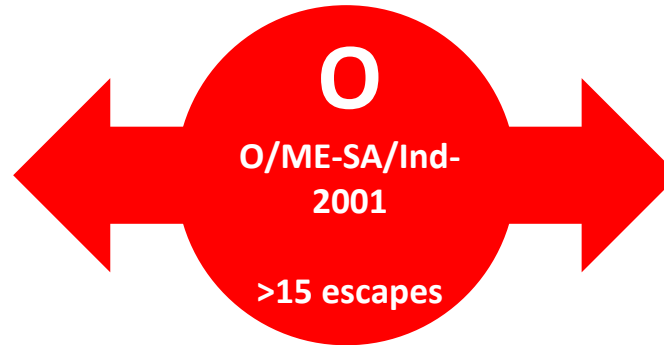
Long distance (trans-pool) FMDV movements (since 2015)

- Impact/change regional FMD risks including FMD free countries
- Selection of vaccines to control outbreaks

# Spread beyond Pool 2 – 10-year historical context

## POOL 2

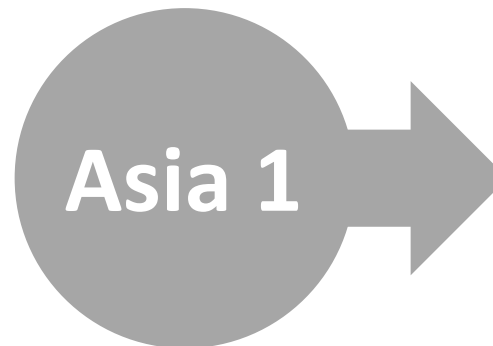
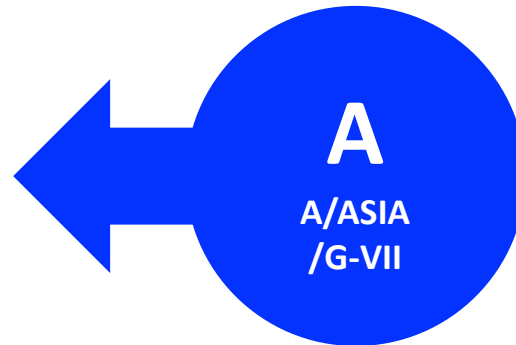
**2013-17**  
North Africa  
Gulf States  
Mauritius (2016 & 2022)



**2015-18**  
Mainland SEA

(Bachanek-Bankowska et al., 2018 – Sci. Reps.)

**2015**  
Saudi Arabia, Türkiye,  
Iran, Armenia, Israel  
(Bachanek-Bankowska et al., 2018 – EID)

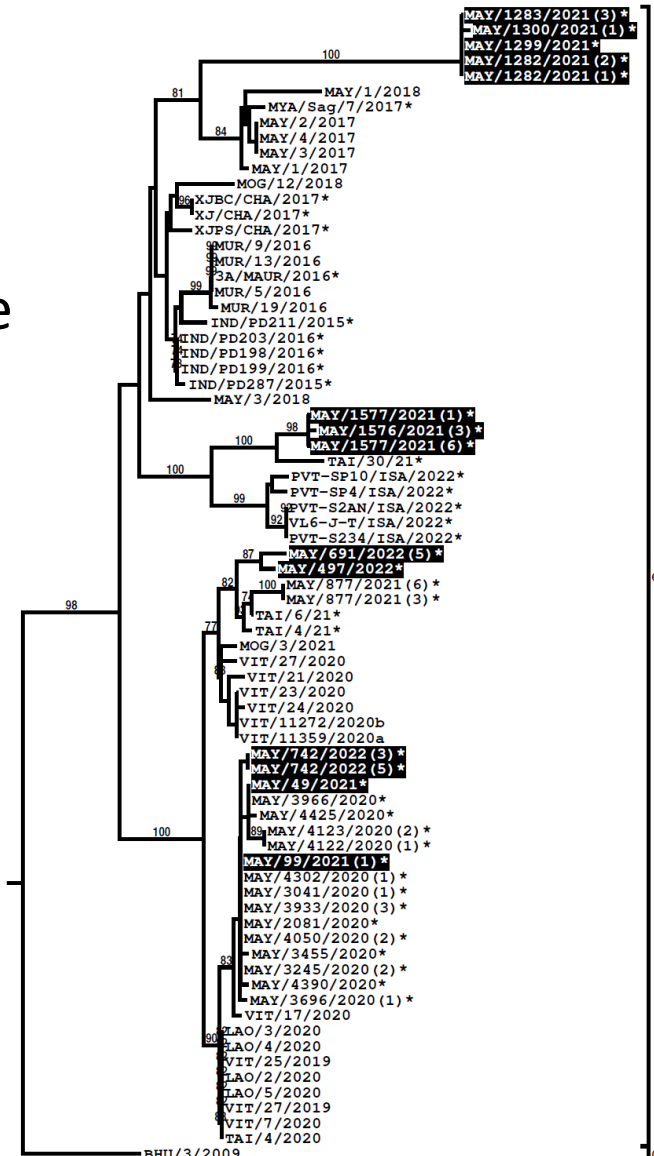
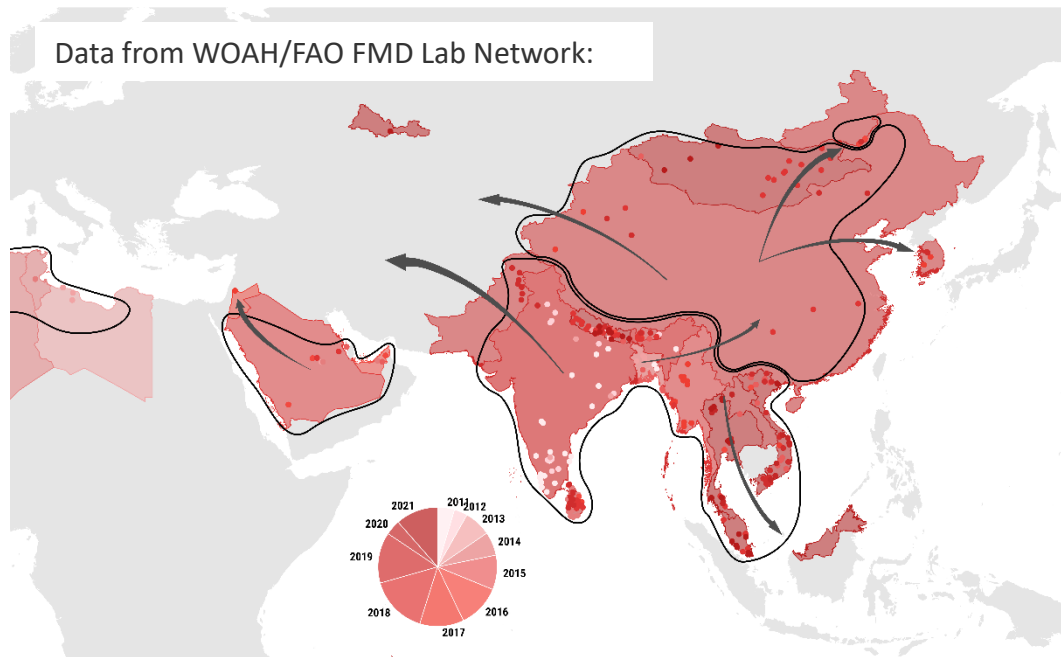


**2017**  
Myanmar  
(Bo et al., 2019 – TBED)



# Conjectured distribution of O/ME-SA/Ind2001e

- O/ME-SA/Ind-2001e is the most widely-spread FMD lineage
- Sequences are heterogenous in SEA (i.e. multiple genetic clades of this lineage are present)



Data kindly shared by the Malaysian National Foot-and-Mouth Disease Laboratory (MNFMDL)

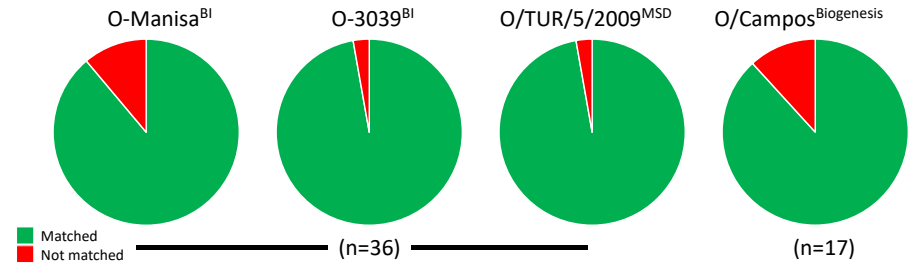


# O/ME-SA/Ind-2001e: vaccine matching (2017-2023)

- Vaccine matching data for field isolates from regions where this lineage is present
- Recent vaccine matching data from WRLFMD for an Indonesian/South Korea field isolate supports the selection of these vaccines
- Data supported by *in vivo* studies with O-3039, O-Manisa and combination (Boehringer-Ingelheim)

Fishbourne et al., (2017) Vaccine 35: 2761-2765

Singanallur et al., (2021) Vaccines 9: 1110



Samples from Pusvetma, Indonesia

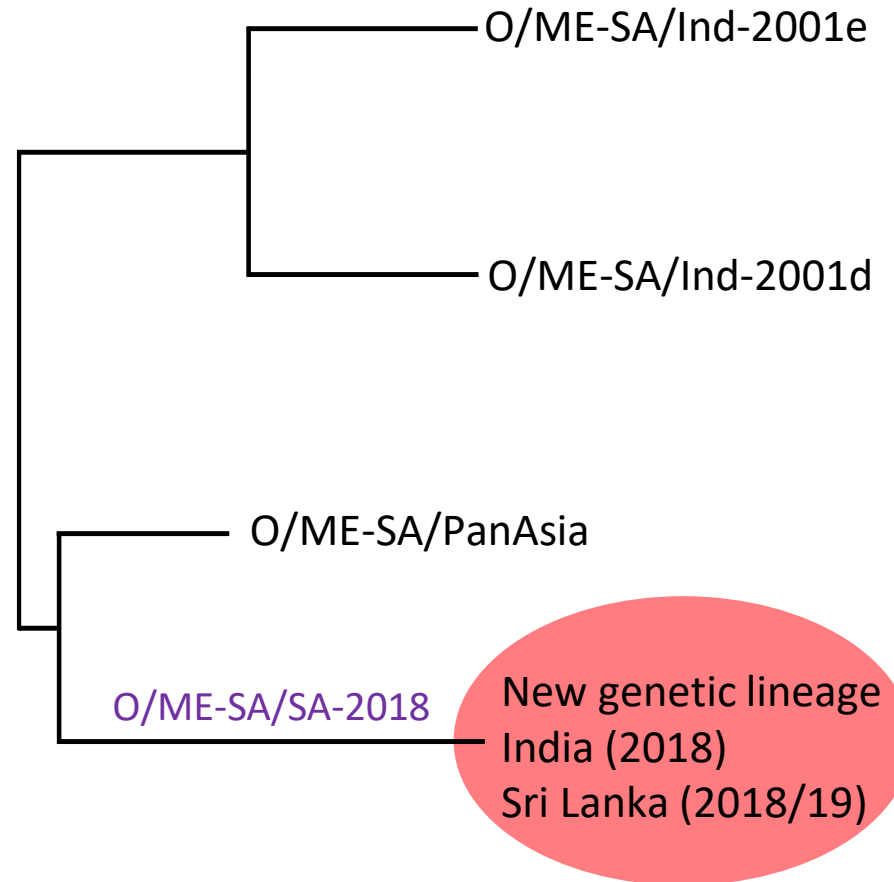
	O ISA/3/22
	r-value titre
O1 Campos, Biogénesis Bagó	0.47, 2.46
O-3039, Boehringer Ingelheim	0.69, 1.76
O Campos, Boehringer Ingelheim	0.20, 1.92
O Manisa, Boehringer Ingelheim	0.54, 2.14
O Panasia 2, Boehringer Ingelheim	0.40, 2.12
O/TUR/5/09, MSD Animal Health	0.50, 2.09

# Brewing up the next serotype O virus lineage

- History of pandemic serotype O lineages emerge from Pool 2

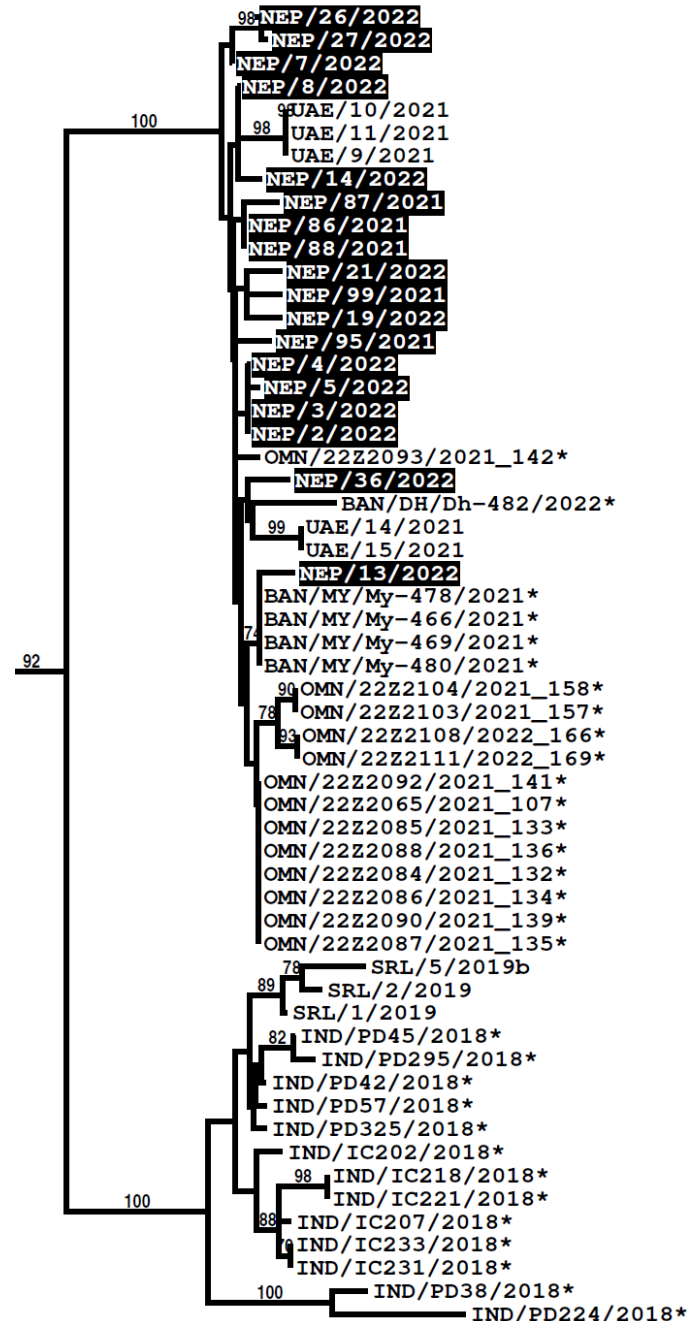


<https://www.thinglink.com/scene/451911993104793602>



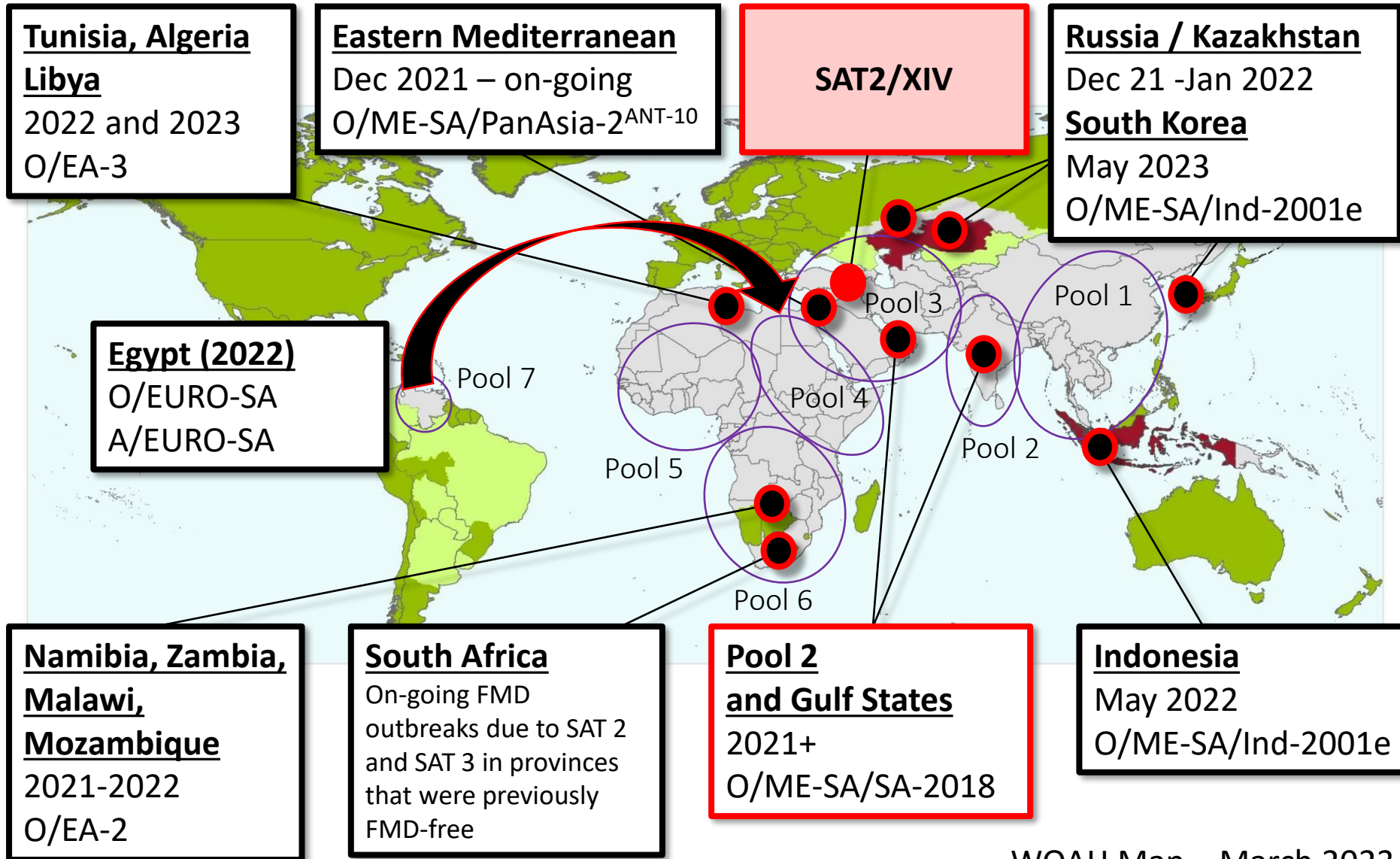
# Pool 2/3: O/ME-SA/SA-2018: an emerging lineage that threatens SEA ?

- New serotype O lineage detected in Pool 2 (India, Nepal, Bangladesh and Sri Lanka)
- Lineage estimated to represent ~ 40% of serotype O cases in India
- Detected in Pool 3 (UAE and Oman) in 2021 in small ruminants
- Scope to spread more widely – following pathways for O/ME-SA/Ind-2001 (d and e)
- Vaccine matching for this lineage appears to be similar to O/ME-SA/Ind-2001e





# Headline global events (2021/23)



WOAH Map – March 2023

# Pool 1: Status in 2023

## Characterisation of different FMD virus lineages



Based on data from WRLFMD, RRLSEA, the OIE/FAO Lab Network and reported @SEACFMD

Country	O					A		Asia-1
	ME-SA/Ind-2001e	SEA / Mya-98	CATHAY	ME-SA / PanAsia	ME-SA/ PanAsia-2	ASIA / Sea-97	ASIA/Ind	
Cambodia	2019	2016		2019		2016		
Laos	2020	2017		2018		2018		
Malaysia	2022	2016	2005	2020	2009	2014		
Myanmar	2021	2021				2021	2010	2017
Thailand	2021	2018	2012	2019		2021		
Vietnam	2022	2019	2018	2018		2017		2006
PR China	2021	2020	2022	2019		2019		2009
Indonesia	2022							
Mongolia	2022	2018		2017		2016		

Is this the true picture of FMD in SEACFMD countries?

..... or does under-sampling bias our understanding of the epidemiology?

# FMD vaccines

- Which FMD vaccine should I purchase?
  - How can I ensure that it is fit for purpose? (i.e., will it be efficacious for the specific viruses that threaten livestock in my country?)
1. Antigenic match between a field virus and a vaccine strain defined by vaccine matching
  2. Testing of the vaccine in the field can also be very important (SSIS and PVM)



# Why FMD vaccines fail?

- Poor quality vaccine (potency, 146S content)
- Poor antigenic match to the circulating strains
- Failure in the cold chain
- Low coverage in the target population
- Failure to follow recommended vaccination schedules
- Failure to employ complementary control measures





# Establishing “pragmatic” serological cut-offs

- Vaccine-induced antibody responses correlate to protection
- Testing can be focussed to measure **heterologous responses** (i.e., vaccine to field strain)
- Calibration to ELISA methods is an on-going priority

frontiers | Frontiers in Veterinary Science

TYPE Original Research  
PUBLISHED 01 December 2022  
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## Predicting cross-protection against foot-and-mouth disease virus strains by serology after vaccination

Simon Gubbins<sup>1†</sup>, David J. Paton<sup>1\*†</sup>, Aldo Dekker<sup>2</sup>,  
Anna B. Ludi<sup>1</sup>, Ginette Wilsden<sup>1</sup>, Clare F. J. Browning<sup>1</sup>,  
Michael Eschbaumer<sup>3</sup>, Jamie Barnabei<sup>4</sup>, Hernando Duque<sup>4†</sup>,  
Lisa L. Pauszek<sup>4</sup> and Donald P. King<sup>1</sup>

- Day-of-challenge sera (n = 180) from 13 previous FMD cross-protection experiments for serotypes O (n = 2), A (n = 10), and SAT 2 (n = 1)
- Sera retested at WRLFMD

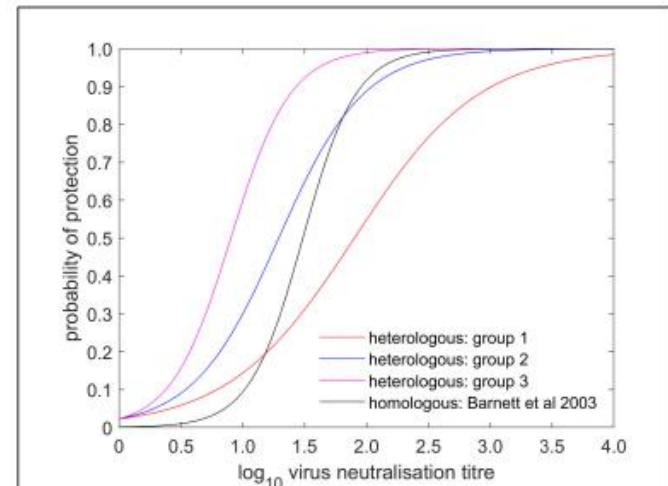


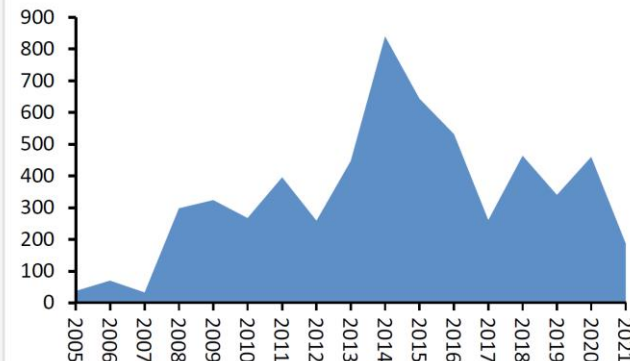
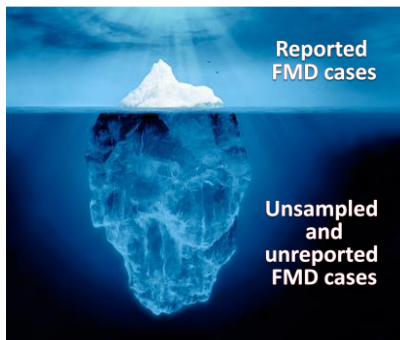
FIGURE 2

Estimated probability that a vaccinated bovine animal is protected following challenge and its dependence on log<sub>10</sub> virus neutralisation titre. The plot shows the posterior median for the probability of heterologous protection for group 1 (comprising experiments 1 & 2; red), group 2 (comprising experiments 3, 4, 5, 6, 7, 11, & 18; blue) and group 3 (comprising experiments 8, 9, 10, 12, 13, 14, 15, 16, & 17; magenta) and the probability of homologous protection as estimated by Barnett et al. (5) (black).



# Talk summary

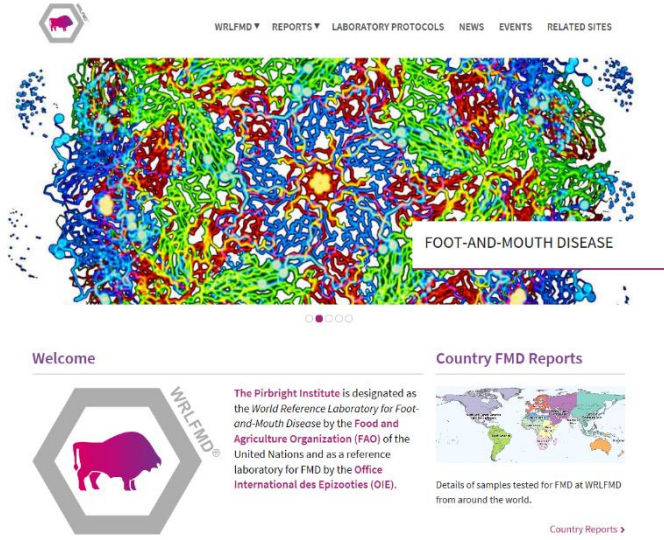
- Epidemiology of FMD is very dynamic with strong epidemiological connections between Pool 2 and Pool 1
- **Sampling of field outbreaks is critical**
  - Monitor epidemiology and assess impacts of the disease
  - Emergence of new strains
  - Inform vaccine selection and deployment of vaccines



- WRLFMD and the WOA/FAO Lab Network welcome sample submissions from member states
  - Testing of clinical samples is free of charge
  - Contact: [donald.king@pirbright.ac.uk](mailto:donald.king@pirbright.ac.uk)

# 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 WOA/FAO FMD Laboratory Network (<http://foot-and-mouth.org/>)



The screenshot shows the WRLFMD website interface. At the top, there is a navigation menu with links for WRLFMD, REPORTS, LABORATORY PROTOCOLS, NEWS, EVENTS, and RELATED SITES. Below the menu is a large, colorful world map with a text box labeled 'FOOT-AND-MOUTH DISEASE'. A 'Welcome' section features the WRLFMD logo and a paragraph stating that the Pirbright Institute is designated as the World Reference Laboratory for Foot-and-Mouth Disease by the Food and Agriculture Organization (FAO) of the United Nations and as a reference laboratory for FMD by the Office International des Epizooties (OIE). To the right, there is a 'Country FMD Reports' section with a world map and a link to 'Country Reports >'. Below the screenshot are two overlapping document covers. The left cover is the 'WRLFMD Quarterly Report April to June 2018', featuring the WRLFMD logo and logos for BBSRC, the Department for Environment, Food & Rural Affairs, and eofmd. The right cover is the 'OIE/FAO Foot-and-Mouth Disease Reference Laboratory Network Annual Report 2021', featuring the OIE/FAO logo and listing the editors: Dr Donald King, Dr Antonello Di Nardo, and Dr Mark Henstock, The Pirbright Institute, UK.

# Acknowledgements

- Collaborating FMD Reference Laboratories and field teams
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Department  
for Environment  
Food & Rural Affairs

