



Review of regional FMD situation and vaccine recommendations

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Biotechnology and
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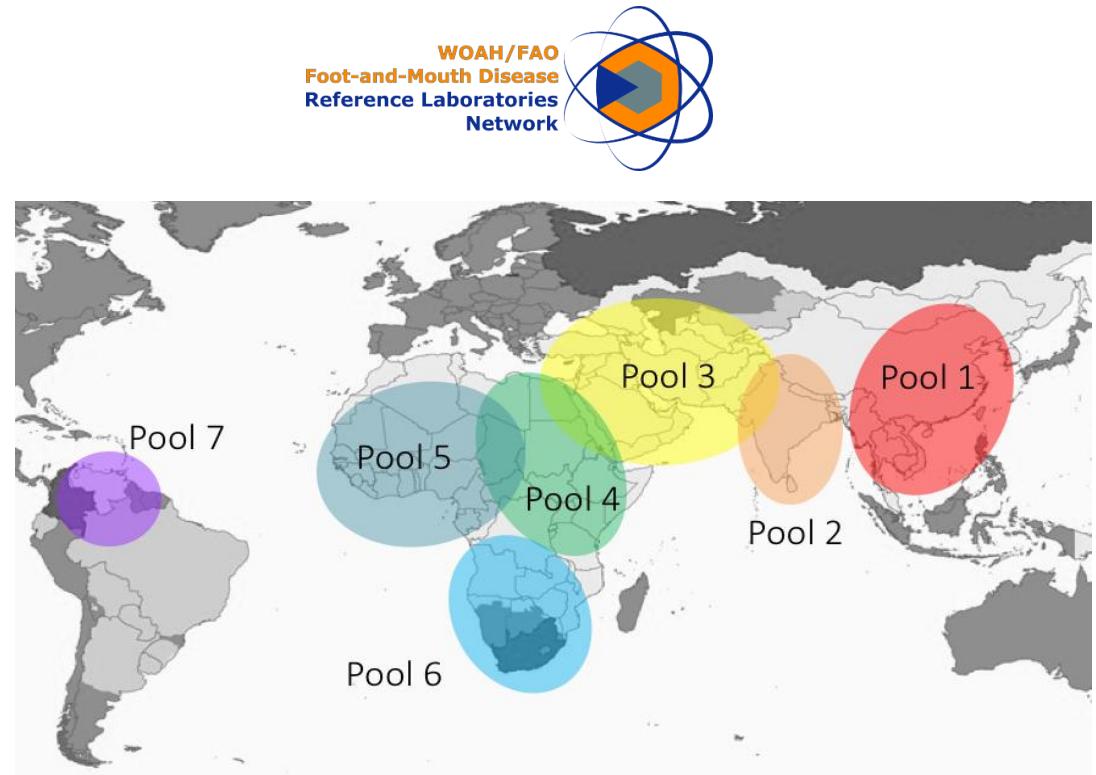
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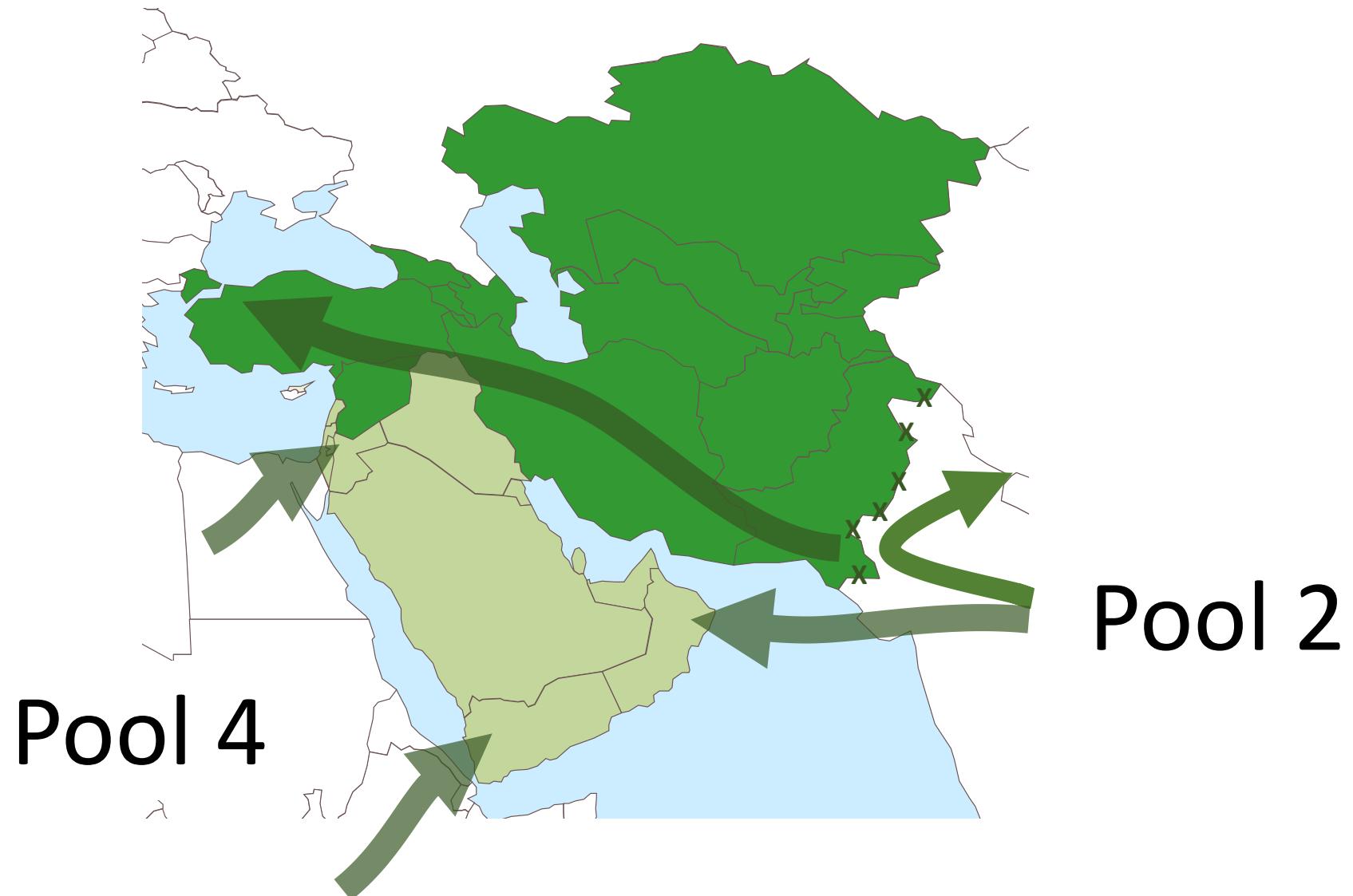
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FMD epidemiology

- The epidemiology of FMD is dynamic; defined by:
 - Seven virus ecosystems (Pools) that maintain specific FMDV strains requiring tailored diagnostics and vaccines
 - Six circulating FMDV serotypes with an unequal distribution (NB: Serotype C has not been detected globally since 2004)
 - Long-distance “trans-pool” movements of FMDV lineages which are often unpredictable
- **International partnerships are essential to collate, share and analyse data**



Pathways for virus movements within and into Pool 3

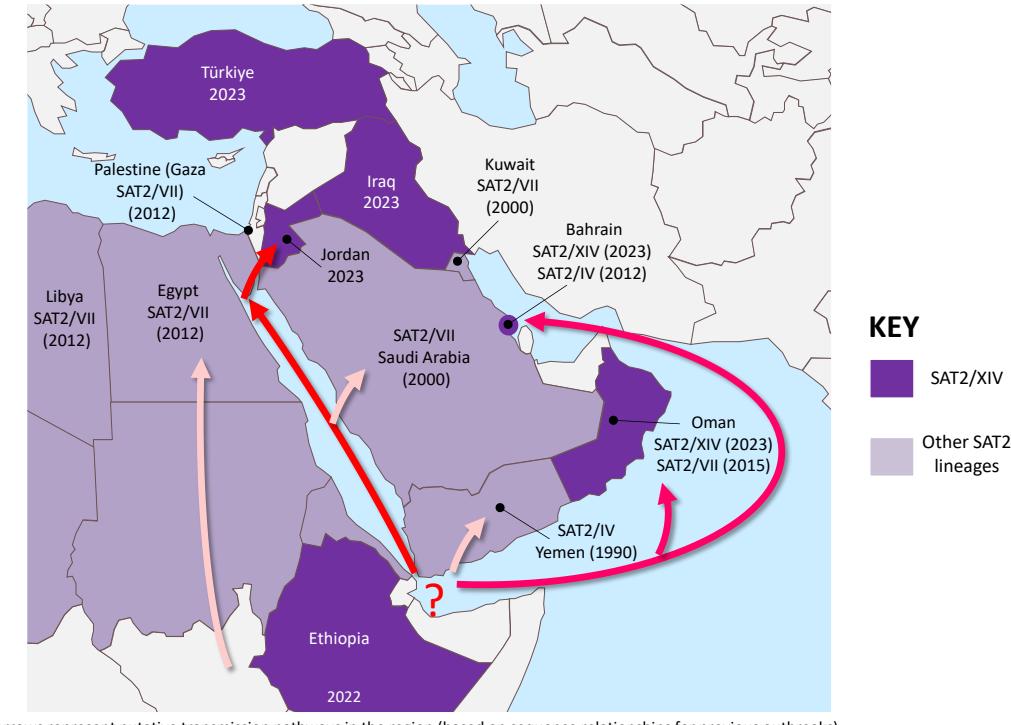


2023: New FMD outbreaks due to the SAT2/XIV topotype

- 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



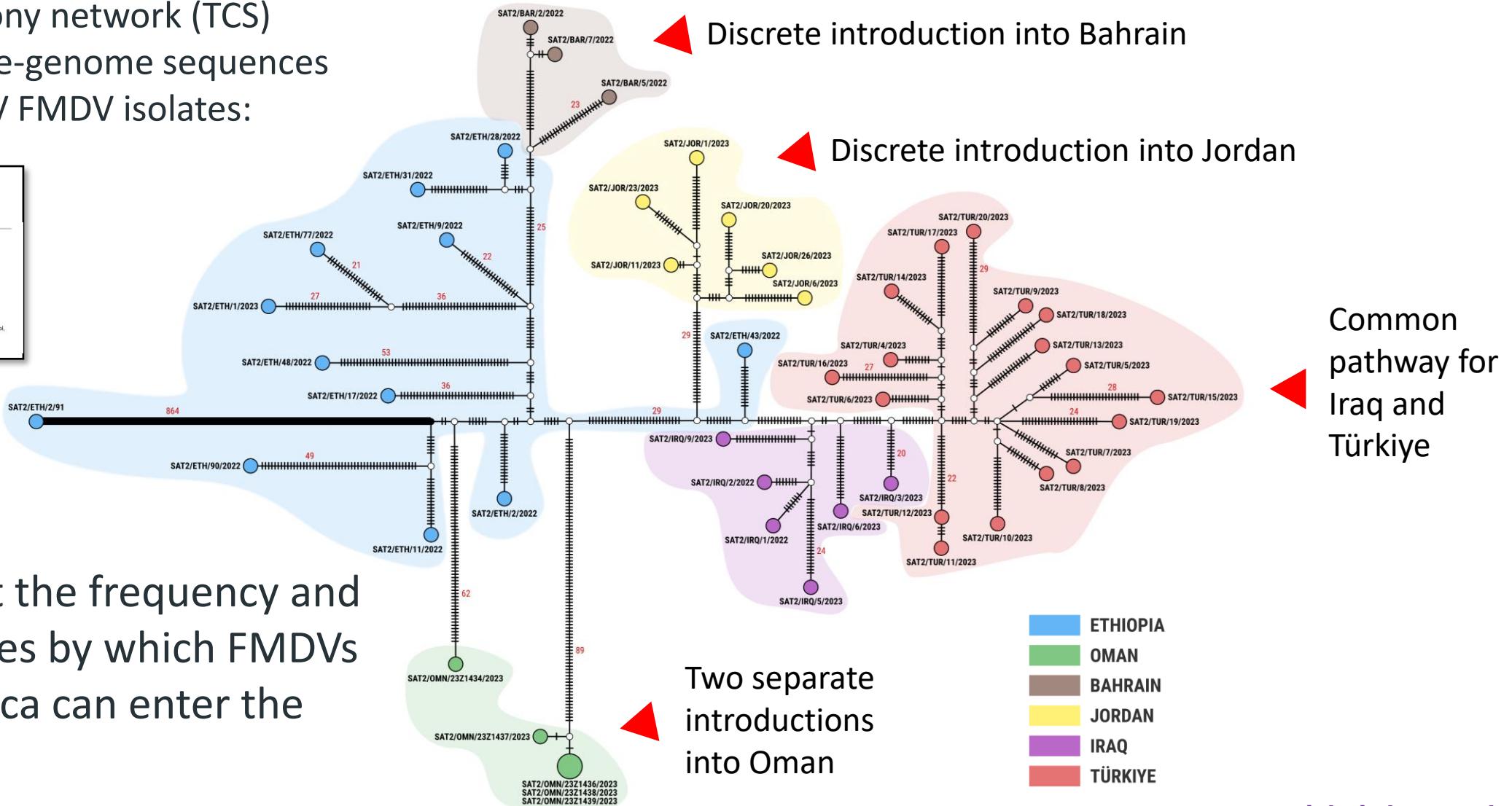
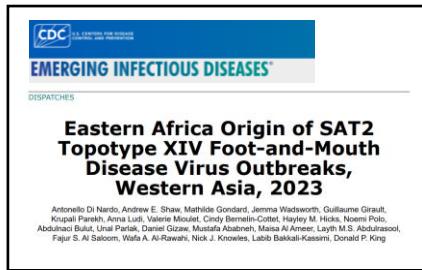
Arrows represent putative transmission pathways in the region (based on sequence relationships for previous outbreaks)

Recent detection of other East African FMDVs in the Gulf States (since 2020):
A/AFRICA/G-I Bahrain (2021)
O/EA-3 Bahrain (2021)
SAT 1 – Qatar (2023)

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:



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

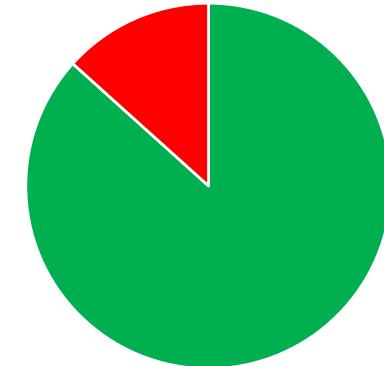
Two separate introductions into Oman

SAT2/XIV: control via vaccination?

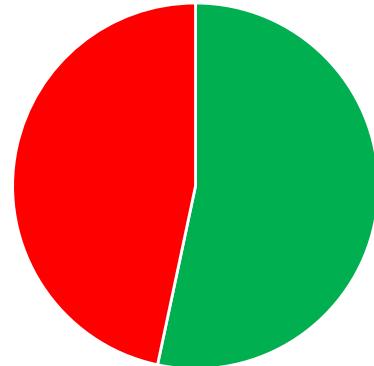
- SAT2 vaccines are not widely used to control FMD outbreaks in the region
- Vaccine matching results from Pirbright (n=15):

	SAT2 Eritrea 98 - BI		SAT2 Zim 83 - BI	
	r1-value	titre	r1-value	titre
ETH/2/2022	0.81	1.62	0.54	2.17
ETH/3/2022	0.49	1.66	0.15	1.7
IRQ/2/2022	0.73	1.75	0.38	2.04
IRQ/5/2023	0.53	1.61	0.74	2.33
IRQ/9/2023	0.42	1.51	0.31	1.95
JOR/11/2023	0.58	1.69	0.2	1.74
JOR/20/2023	0.83	1.85	0.24	1.81
JOR/26/2023	0.86	1.86	0.32	1.94
BAR/2/2022	0.4	1.5	0.39	1.85
BAR/7/2022	0.53	1.62	0.53	1.99
TUR/4/2023	1	1.68	0.31	1.95
TUR/17/2023	0.72	1.52	0.25	1.86
ETH/11/2022	0.33	1.58	0.18	1.88
ETH/105/2022	0.26	1.49	0.17	1.87
ETH/1/2023	0.27	1.49	0.1	1.64

SAT2-Eritrea-98 (BI)



SAT2-Zim 7/83 (BI)



Matched
 Not matched

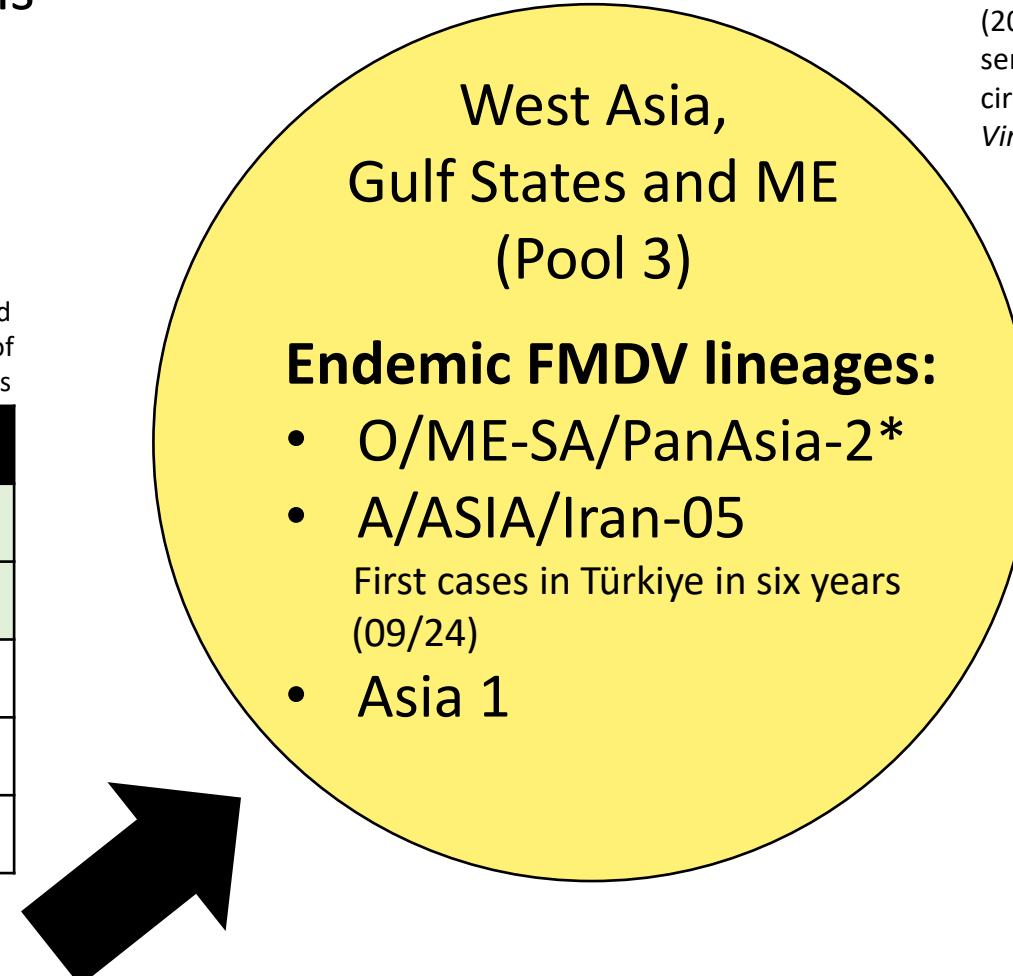
New SAT 2 vaccine from Biogenesis Bago (SAT2 Oman/2015) also tested for six isolates with encouraging results

Updated FMD risks for Pool 3 (since 2020)

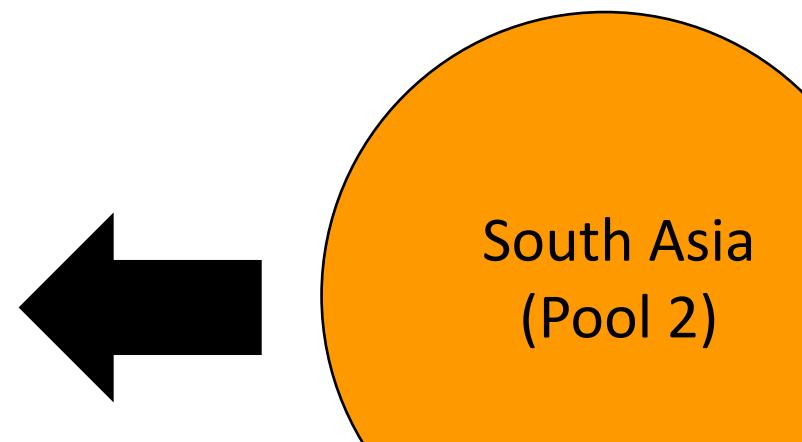
New virus introductions
from South Asia and
East Africa:

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)



*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

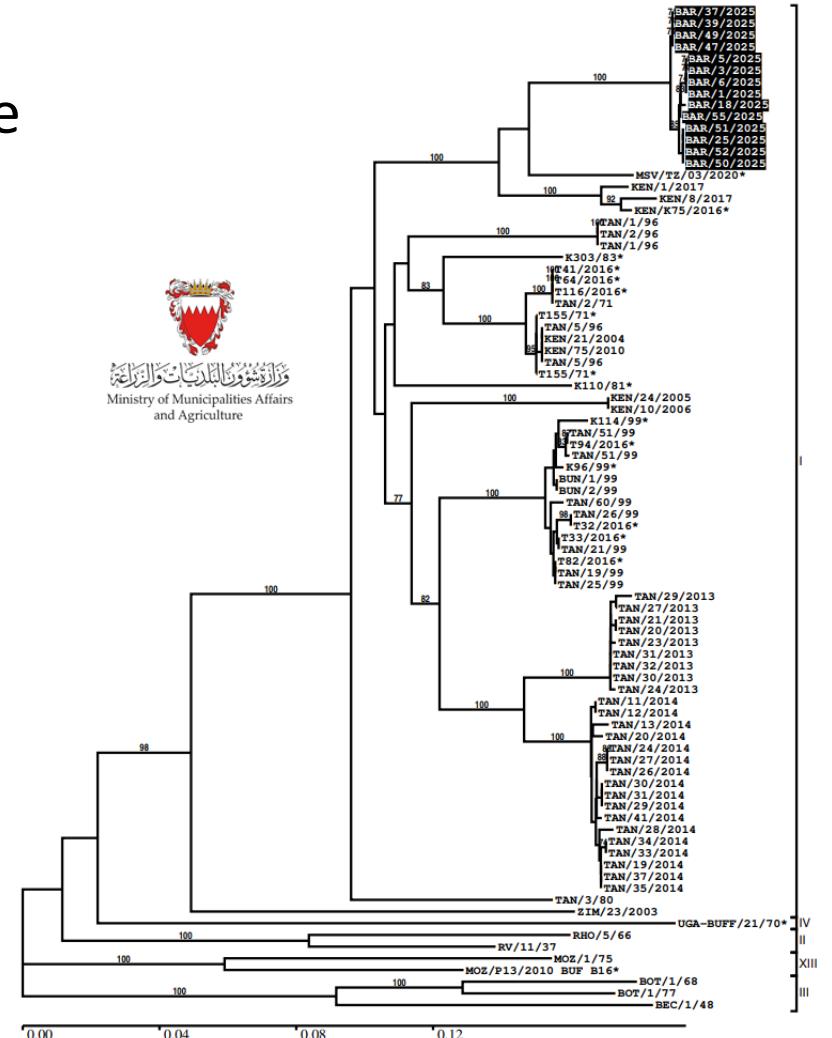


Lineage	x
O/ME-SA/SA-2018	~5
O/ME-SA/Ind-2001e	
A/ASIA/G-VII†	

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

Emergence of serotype SAT1/I in the Middle East (Bahrain)

- SAT1/I previously detected in Qatar (in 2023)
 - EuFMD supported a SSIS in Bahrain to test the performance of a SAT 2 FMD vaccine - discussion led to samples (collected during 2025) submitted to the WRLFMD
 - **SAT1/I detected**
 - Closest genetic relative from Tanzania 2020
 - Evidence for co-infection with **O/EA-2** in one sample – this topotype also originates from East Africa
 - 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 discriminate viruses from this topotype



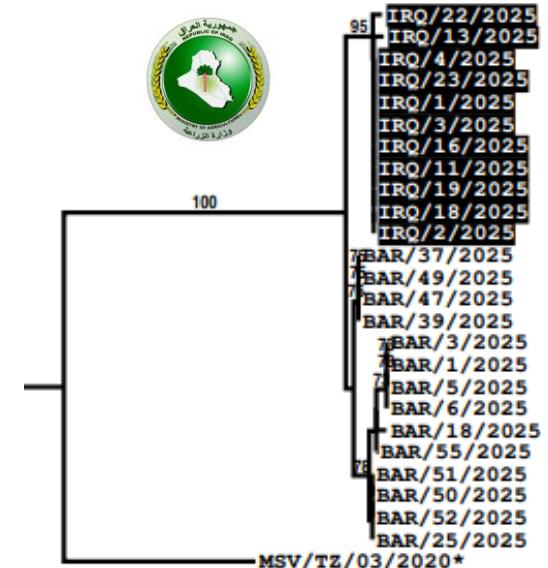
*Bachanek-Bankowska et al., (2016) Development and evaluation of tailored specific real-time RT-PCR assays for detection of foot-and-mouth disease virus serotypes circulating in East Africa. J Virol Methods 237:114-120. <https://www.foot-and-mouth.org/science/lineage-specific-fmdv-real-time-rt-pcr-assays>

Emergence of serotype SAT1/I in the Middle East (Bahrain and Iraq)

- Reports of an upsurge of FMD outbreaks in Iraq where local testing (agELISA) identified serotype SAT1 and O viruses
- **SAT1/I detected in samples sent to WRLFMD**
- Same genetic clade as the sequences from Bahrain (but, not identical!) – do these viruses represent different introductions?
- >15% nt difference to the sequences from the cases in Qatar supporting the idea that these are separate introductions into the region
- SAT1 also reported (WAHIS) for outbreaks in Kuwait – April 2025
- Limited vaccines are available for this serotype (e.g., SAT1/Rho78^{BI})
- Preliminary vaccine matching results:

Analysis will be repeated using BVS for aqueous-formulated vaccine

and for serotype O.....



Isolate	r1 value	titre
QTR/5/2023	0.39	1.85
QTR/6/2023	0.41	1.86
QTR/7/2023	0.35	1.80
BAR/37/2025	0.17	1.52
BAR/50/2025	0.11	1.33
IRQ/11/2025	0.09	1.21
IRQ/1/2025	0.10	1.25
IRQ/23/2025	0.13	1.37

Emergence of O/ME-SA/SA-2018 in Pool 3

- History tells us that pandemic serotype O lineages emerge from Pool 2
- O/ME-SA/SA-2018 lineage originates in Pool 2 (India, Nepal, Bangladesh and Sri Lanka)
- Lineage estimated to represent ~ 40% of serotype O cases in India
- Previous incursions into Pool 3 (UAE and Oman) in 2021 in small ruminants
- 2023/4: further evidence for infection in Iran, Palestinian AT and Türkiye
- **2025: cases due to this lineage detected in Iraq and Israel**
- Sequences from Palestine/Israel are distinct to those from Türkiye, Iraq and Iran (~4% nt dif.)
- **Data support multiple recent introductions of this lineage from Pool 2**

Vaccine Matching data
is available for 7 field
isolates from the O/ME-
SA/SA-2018 lineage

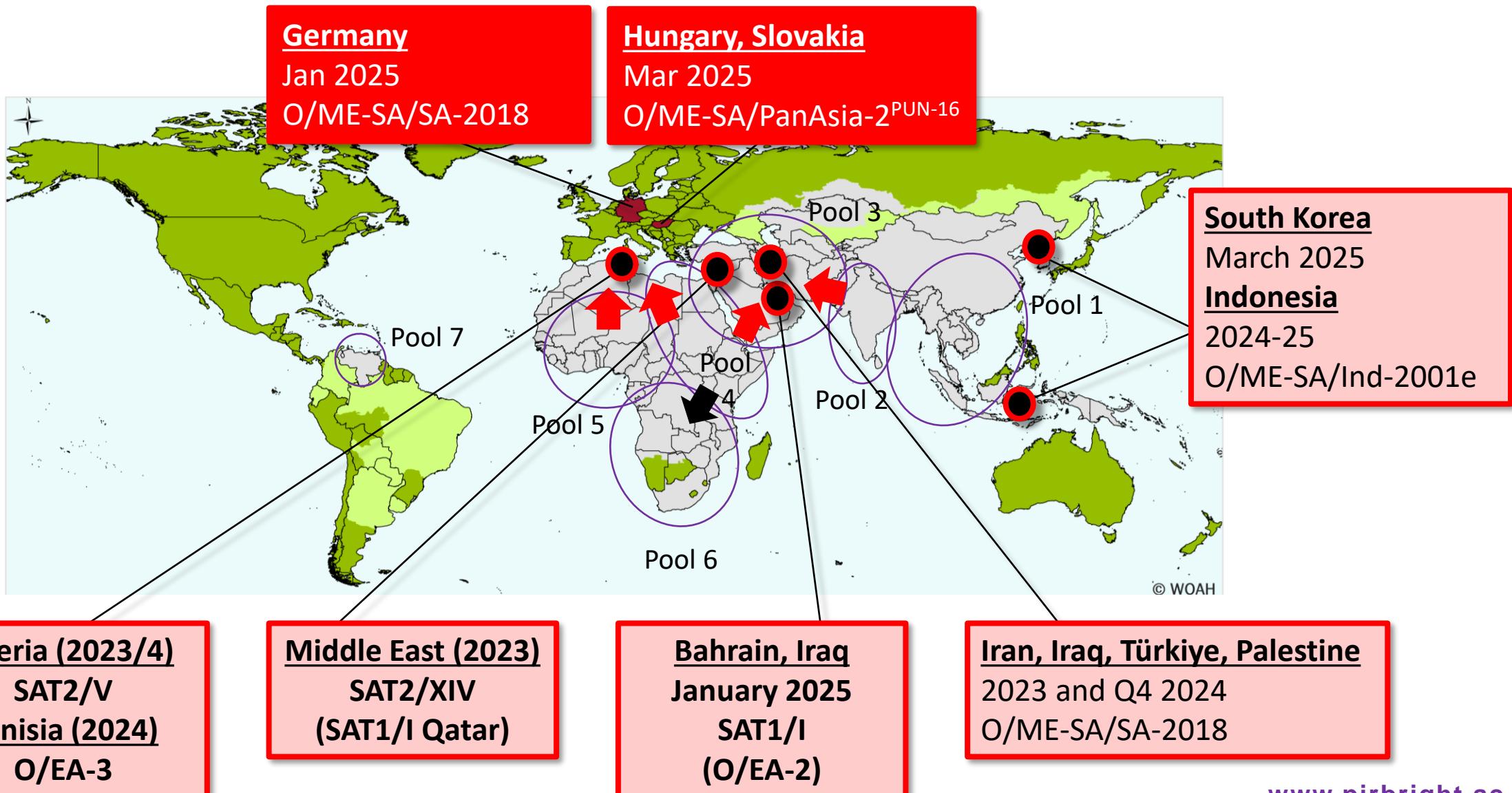
Isolate	O-Manisa BI		O-TUR/5/09 MSD		O-3039 BI		O-Campos BI		O-PanAsia-2 BI		O-Campos BB	
	r ₁ value	titre										
UAE/15/2021	0.56	2.15	0.69	2.32	0.75	1.94	0.28	2.19	0.47	2.3	0.51	2.63
UAE/9/2021	0.44	2.04	0.68	2.32	0.59	1.83	0.23	2.10	0.32	2.13	0.60	2.70
NEP/13/2022	0.63	2.33	1.00	2.32	1.00	2.02	0.40	2.28	0.57	2.35	0.51	2.65
NEP/26/2022	0.32	2.04	0.68	2.15	0.66	1.82	0.23	2.03	0.32	2.10	0.20	2.29
NEP/38/2022	0.98	2.45	0.89	2.29	0.84	2.00	0.45	2.17	0.50	2.31	0.66	2.71
NEP/13/2024	0.88	2.40	0.78	2.23	0.82	1.99	0.74	2.27	0.99	2.49	0.68	2.72
GER/1/2025	1.00	2.41	0.97	2.37	0.84	1.96	0.48	2.06	0.56	2.15	0.58	2.44



State of Palestine
Ministry of Agriculture



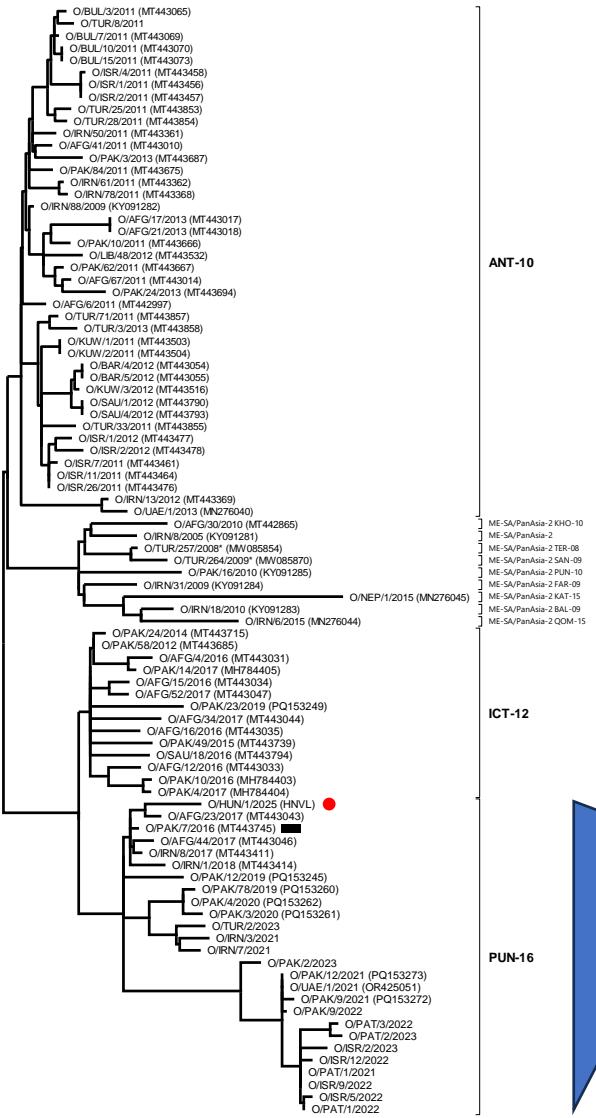
Headline global status for FMD (new events: March 25)



Talk summary

- Epidemiology of FMD is very dynamic in Pool 3
- New patterns due to virus incursions from East Africa and southern Asia
- Circulation of different FMD virus lineages impact the selection of appropriate vaccines to control outbreaks
- **Sampling of field outbreaks is critical.....**
- **WRLFMD and the WOAH/FAO Lab Network welcome sample submissions**
 - Testing is free of charge
 - Contact: donald.king@pirbright.ac.uk
- Testing/evaluation of FMD vaccines is important
 - Vaccine matching
 - Heterologous testing
 - Small scale immunogenicity studies and evaluation of FMD vaccines in the field

Proposed reclassification of O/ME-SA/PanAsia-2^{ANT-10} viruses

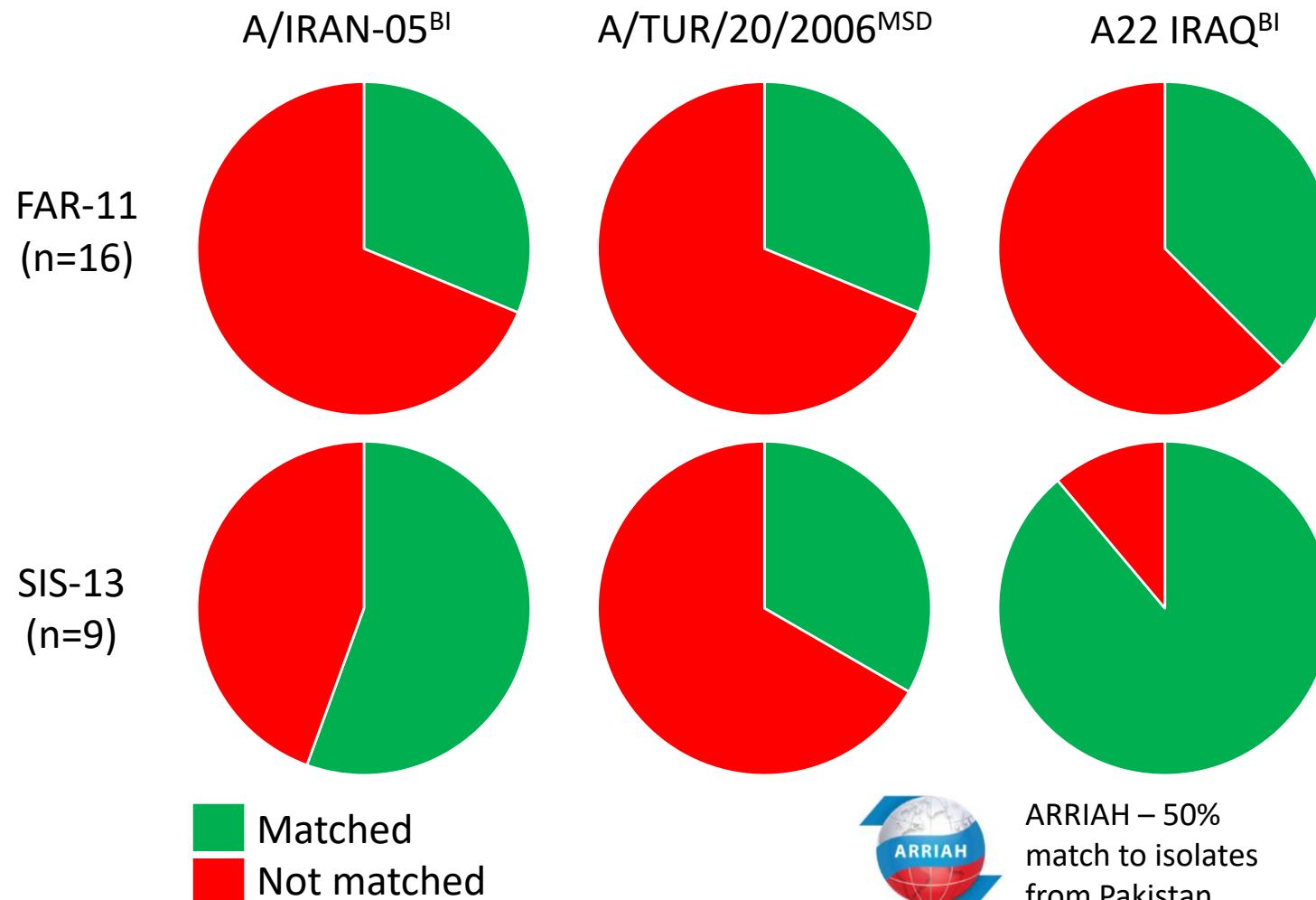


Vaccine Matching data is available for 78 isolates from the ANT-10 lineage
Data in table is for clade most closely related to HUN/1/2025 (O/ME-SA/PanAsia-2^{PUN-16})

Isolate	O-Manisa BI		O-TUR/5/09 MSD		O-3039 BI		O-Campos BI		O-PanAsia-2 BI		O-Campos BB	
	r ₁ value	titre										
AFG/23/2017	0.72		0.74		0.46							
AFG/44/2017	0.36		0.65		0.44							
IRN/8/2017	0.29	1.87	0.52	1.71	0.43	1.57						
IRN/1/2018	0.37	1.95	0.34	1.83	0.58	1.66						
PAK/12/2019	0.50	2.20	0.76	2.11	0.66	1.79						
PAK/78/2019	0.32	2.03	0.49	1.99	0.33	1.56	0.36	1.97	0.32	2.00		
PAK/3/2020	0.40	1.94	0.98	2.1	0.55	1.71			0.41	2.14	0.40	2.42
PAK/4/2020	0.07	1.41	0.59	2.07	0.11	1.10	0.26	1.83	0.36	2.05	0.56	2.19
TUR/2/2023	0.34	1.86	0.67	2.05	0.33	1.60	0.25	1.88	0.34	2.06	0.56	2.56
IRN/3/2021	0.22	1.95	0.63	2.12	0.58	1.84			0.26	2.02	0.59	
IRN/7/2021	0.31	1.94			0.50	1.78			0.22	1.95	0.48	2.46
PAK/2/2023	0.35	1.98	0.90	2.22	0.41	1.80	0.36	2.00	0.36	2.01	0.35	2.48
PAK/12/2021	0.25	2.06	0.78	2.34	0.81	1.87	0.25	1.95	0.32	2.19	0.42	2.53
UAE/1/2021	0.48	2.08	0.44	2.13	0.38	1.64	0.19	2.02	0.32	2.14	0.43	2.56
PAK/9/2021	0.19	1.94	0.30	1.92	0.45	1.61	0.15	1.72	0.32	2.19	0.47	2.58
PAK/9/2022	0.28	1.91	0.26	1.88	0.41	1.79	0.16	1.66	0.27	1.88	0.13	2.04
PAT/3/2022	0.52	1.90	0.59	2.02	0.65	1.82	0.29	1.79	0.27	1.93	0.51	2.43
PAT/2/2023	0.37	1.76	0.58	2.01	0.52	1.62	0.30	1.76	0.15	1.68	0.34	2.26
ISR/2/2023	0.32	1.85	0.47	1.84	0.38	1.74	0.26	1.75	0.28	1.80	0.45	2.40
ISR/12/2022	0.38	1.89	0.43	1.81	0.32	1.66	0.24	1.72	0.34	1.90	0.59	2.52
PAT/1/2021	0.40	2.01	0.72	2.31	0.53	1.78	0.29	2.01	0.53	2.15	0.36	2.46
ISR/9/2022	0.33	1.97	0.54	2.16	0.57	1.76	0.25	1.92	0.39	2.18	0.58	2.51
ISR/5/2022	0.33	1.97	0.57	2.18	0.48	1.69	0.18	1.78	0.32	2.09	0.42	2.37
PAT/1/2022	0.50	2.10	0.60	2.23	0.56	1.79	0.26	1.95	0.64	2.23	0.51	2.61

Note: New O/ME-SA/PanAsia-2 designations are shown 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

A/ASIA/Iran-05: vaccine matching



Poor match of
Turkish vaccines
for FAR-11
viruses from Iran

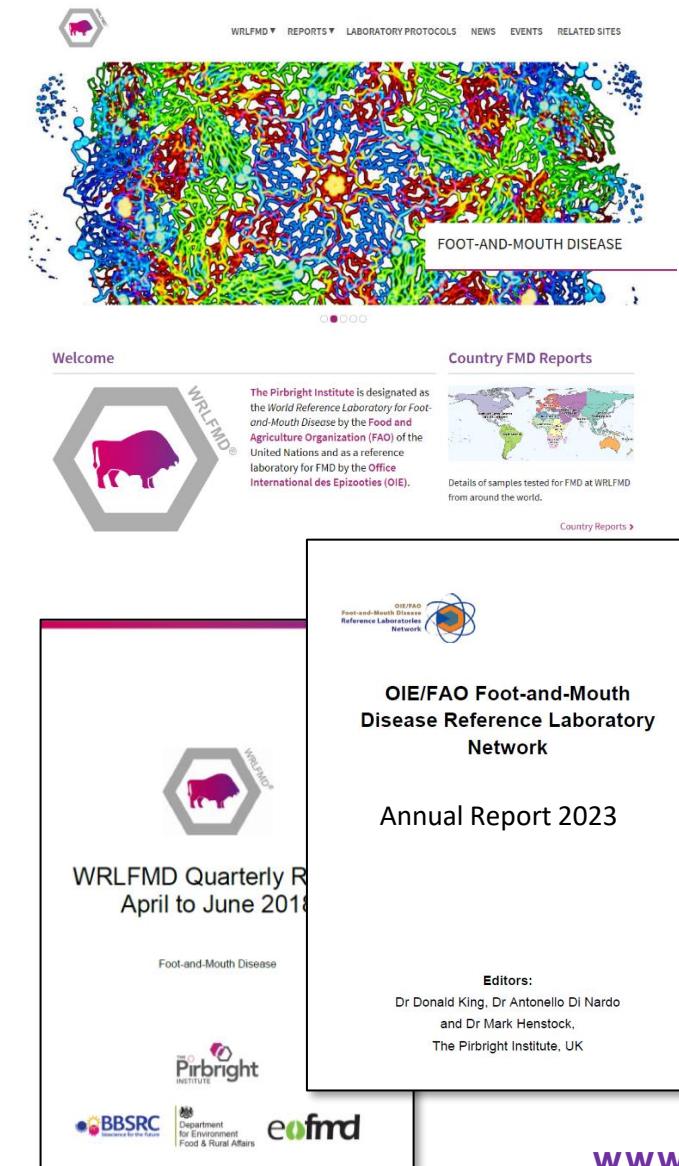


ARRIAH – 50%
match to isolates
from Pakistan

- Reinforces the importance of good quality vaccines, booster regime with good coverage in target host populations

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



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Thanks:



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

