Foot-and-mouth Disease

Global risks and vaccine selection

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Acknowledgements: 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, David Paton, Dexter Wiseman, Ali Al-Rashed, Jozhel Baguisi, Harry Bull, Ryle Walter, Amy Sowood, Sarah Belgrave, Jessie Trussler

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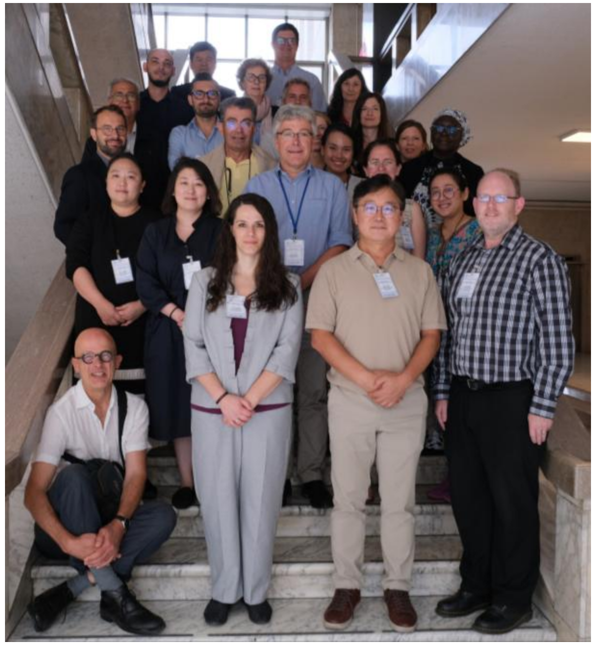
FMD Reference Laboratory

www.pirbright.ac.uk

WOAH/FAO FMD Laboratory Network for FMD

www.foot-and-mouth.org

- Established in 2004
- 15 WOAH and FAO laboratories
- Important contribution of “affiliates” -leading regional laboratories in Africa and Asia where the disease is endemic
- Core activities of the Network:
  - **Using data shared between partners**........ to understand global epidemiology of FMDV and use these data to inform vaccine recommendations
  - To harmonise and improve the quality of laboratory testing



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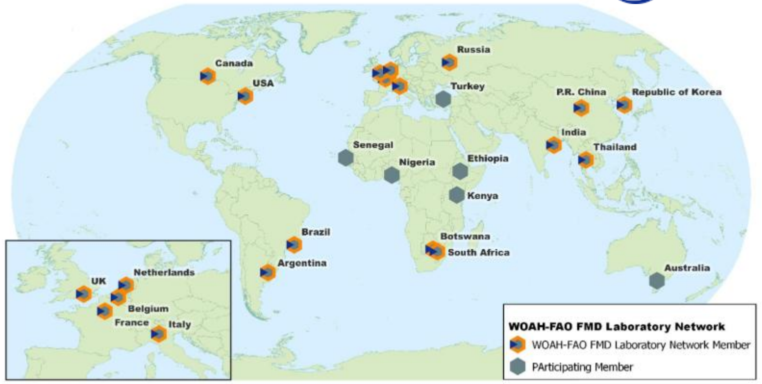
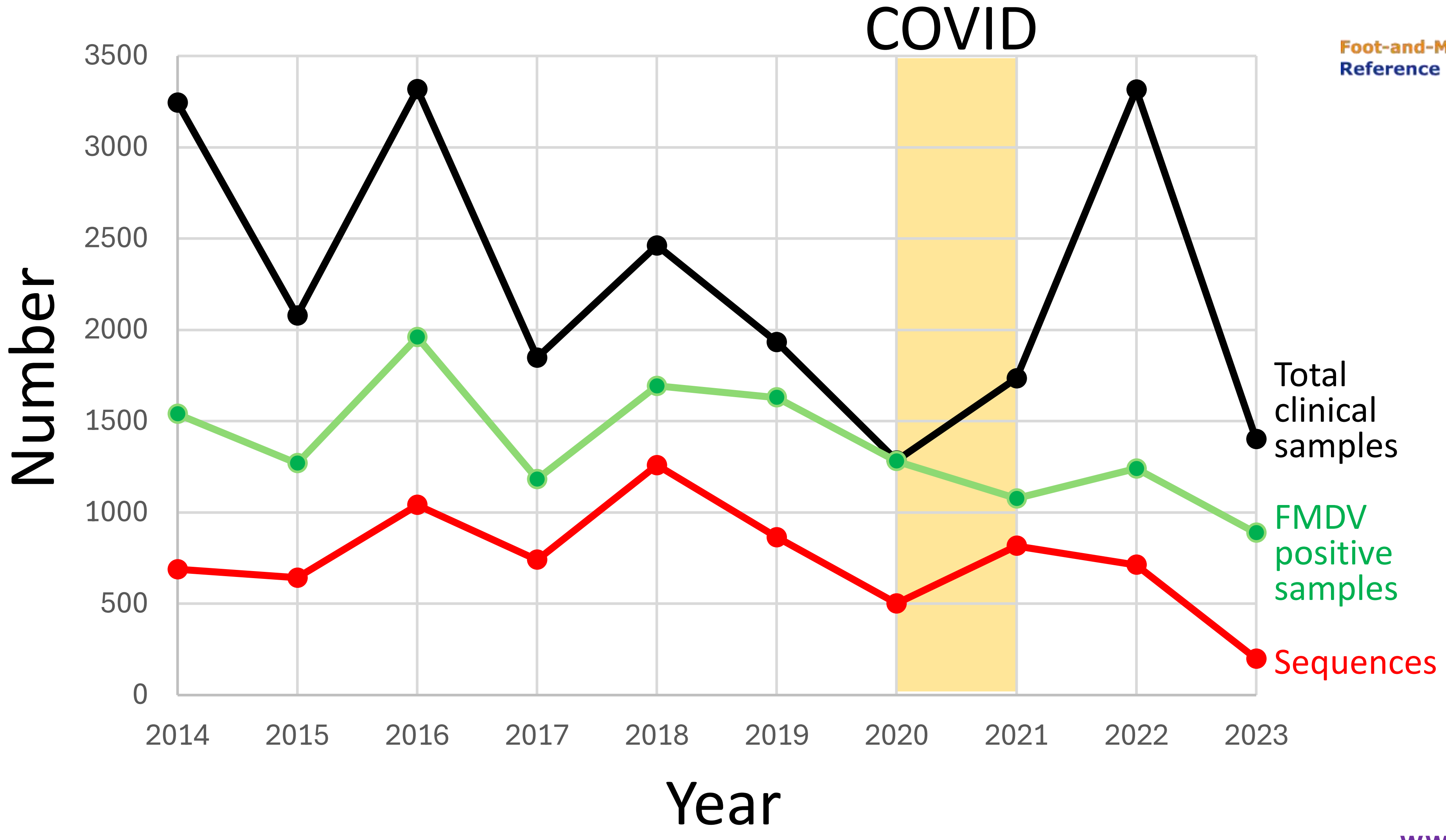


Network Meeting, Rome, September 2024

Reported samples across the global Network

From clinical cases/outbreaks…….



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FMD epidemiology: global summary

- 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**

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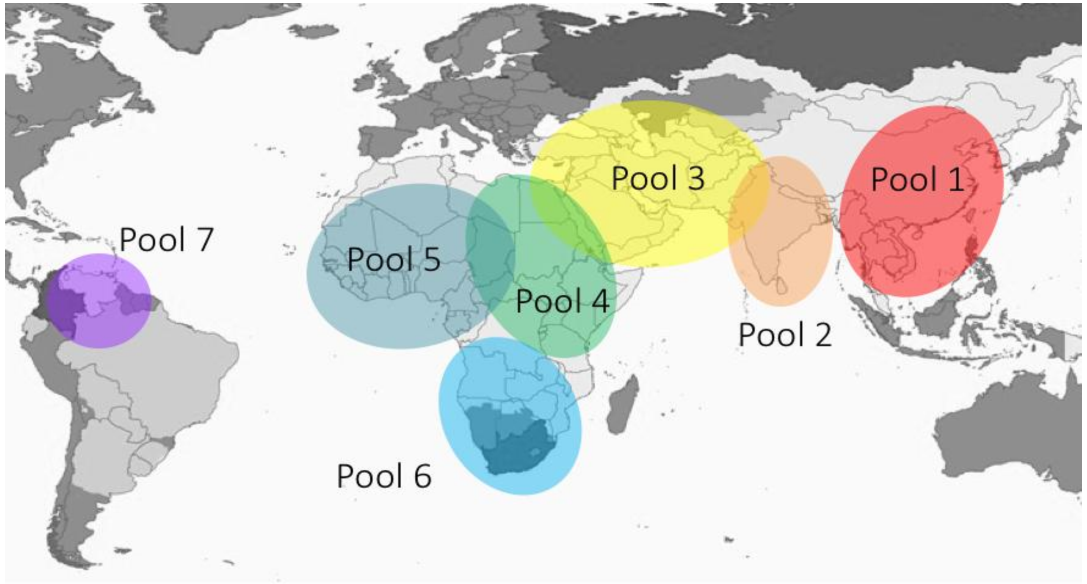
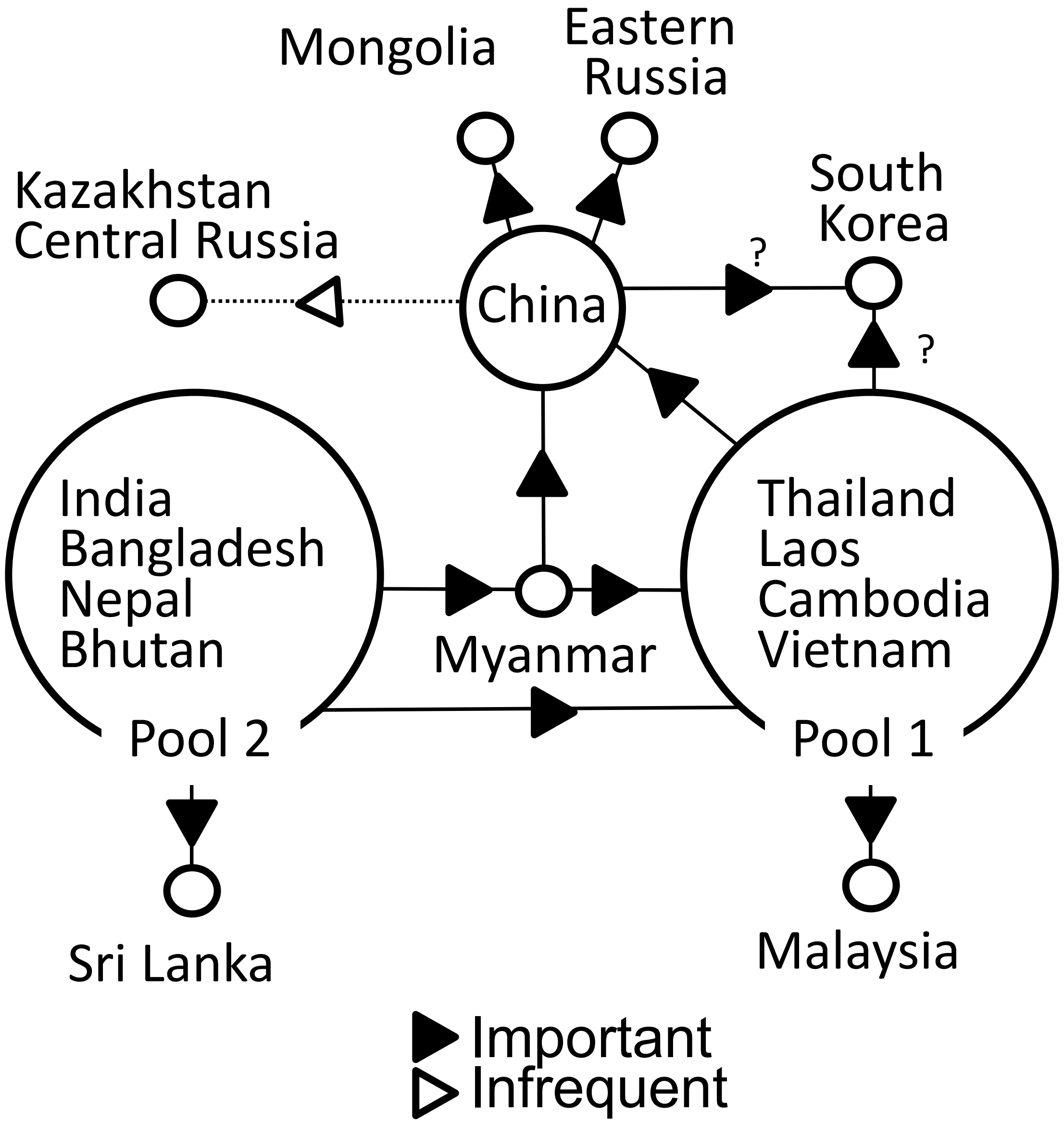


Conjectured FMDV connections: South Asia, Southeast/East Asia



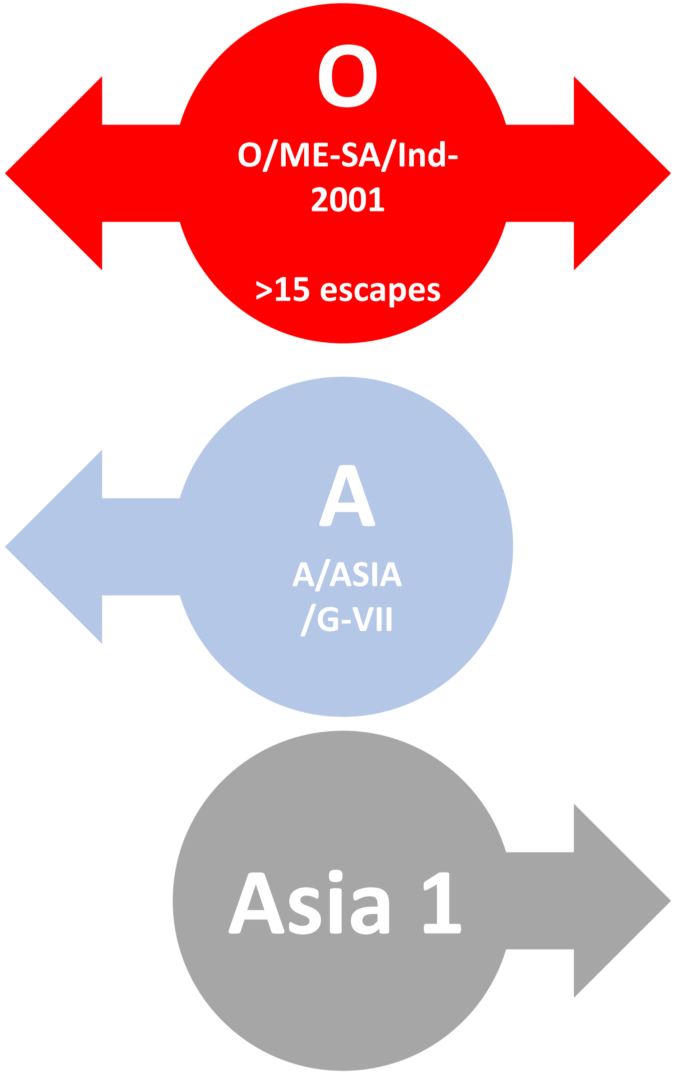
Viral sequences highlight most frequent connections between countries (reflect trade and animal movements)

Potential risk pathways:

- Illegal imports
- Import of fodder
- Overseas workers
- Returning travellers
- Wildlife

Spread beyond Pool 2 – 10-year historical context

POOL 2



2013+
North Africa
Gulf States
Mauritius (2016 & 2022)

O
O/ME-SA/Ind-2001
>15 escapes

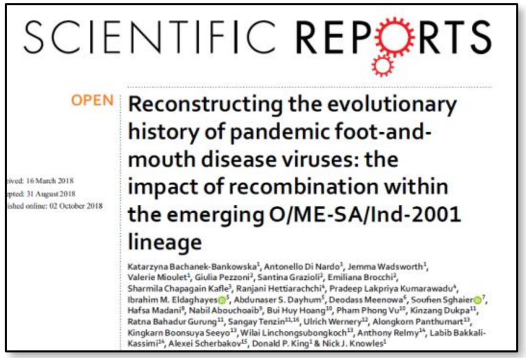
2015+
Mainland SEA

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

A
A/ASIA
/G-VII

Asia 1

2017
Myanmar
(Bo et al., 2019 – TBED)



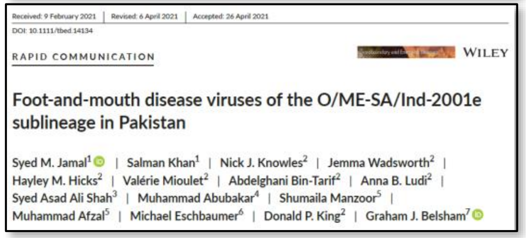
SCIENTIFIC REPORTS

OPEN

ived: 16 March 2018
pted: 31 August 2018
ished online: 02 October 2018

Reconstructing the evolutionary history of pandemic foot-and-mouth disease viruses: the impact of recombination within the emerging O/ME-SA/Ind-2001 lineage

Katarzyna Bachanek-Bankowska[1], Antonello Di Nardo[1], Jemma Wadsworth[1], Valerie Mioulet[1], Giulia Pezzoni[2], Santina Grazioli[2], Emiliana Brocchi[2], Sharmila Chapagain Kafle[3], Ranjani Hettiarachchi[4], Pradeep Lakpriya Kumarawadu[4], Ibrahim M. Eldaghayes[5], Abdunaser S. Dayhum[5], Deodass Meenowa[6], Soufien Sghaier[7], Hafsa Madani[8], Nabil Abouchoaib[9], Bui Huy Hoang[10], Pham Phong Vu[10], Kinzang Dukpa[11], Ratna Bahadur Gurung[11], Sangay Tenzin[11,16], Ulrich Wernery[12], Alongkorn Panthumart[13], Kingkarn Boonsuya Seeyo[13], Wilai Linchongsubongkoch[13], Anthony Relmy[14], Labib Bakkali-Kassimi[14], Alexei Scherbakov[15], Donald P. King[1] & Nick J. Knowles[1]



Received: 9 February 2021 | Revised: 6 April 2021 | Accepted: 26 April 2021
DOI: 10.1111/tbed.14134

RAPID COMMUNICATION

WILEY

Foot-and-mouth disease viruses of the O/ME-SA/Ind-2001e sublineage in Pakistan

Syed M. Jamal[1] | Salman Khan[1] | Nick J. Knowles[2] | Jemma Wadsworth[2] | Hayley M. Hicks[2] | Valérie Mioulet[2] | Abdelghani Bin-Tarif[2] | Anna B. Ludi[2] | Syed Asad Ali Shah[3] | Muhammad Abubakar[4] | Shumaila Manzoor[5] | Muhammad Afzal[5] | Michael Eschbaumer[6] | Donald P. King[2] | Graham J. Belsham[7]

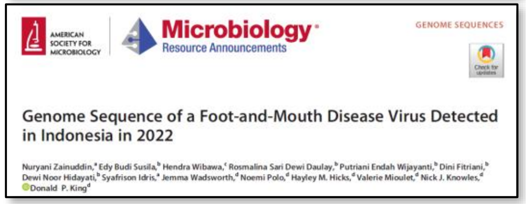
Received: 30 May 2022 | Revised: 6 June 2022 | Accepted: 6 June 2022
DOI: 10.1111/tbed.14607

RESEARCH NEWS

Transboundary and Emerging Diseases WILEY

Foot-and-mouth disease in Kazakhstan

SB Tyulegenov[1] | A Zhakupbayev[2] | M Berdikulov[3] | T Karibayev[3] | GN Yessembekova[1] | AA Sultanov[4] | AM Perez[5] | SK Abdrakhmanov[1]

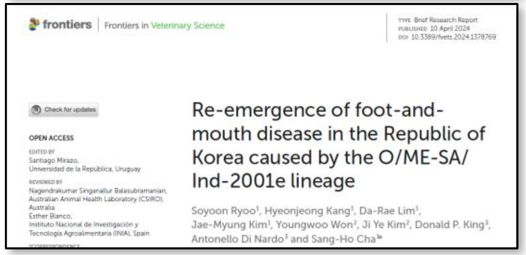


AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

GENOME SEQUENCES

Genome Sequence of a Foot-and-Mouth Disease Virus Detected in Indonesia in 2022

Nuryani Zainuddin,[a] Edy Budi Susila,[b] Hendra Wibawa,[c] Rosmalina Sari Dewi Daulay,[b] Putriani Endah Wijayanti,[b] Dini Fitriani,[b] Dewi Noor Hidayati,[b] Syafrison Idris,[a] Jemma Wadsworth,[d] Noemi Polo,[d] Hayley M. Hicks,[d] Valerie Mioulet,[d] Nick J. Knowles,[d] Donald P. King[d]



frontiers | Frontiers in Veterinary Science

TYPE Brief Research Report
PUBLISHED 10 April 2024
DOI 10.3389/fvets.2024.1378769

Check for updates

OPEN ACCESS

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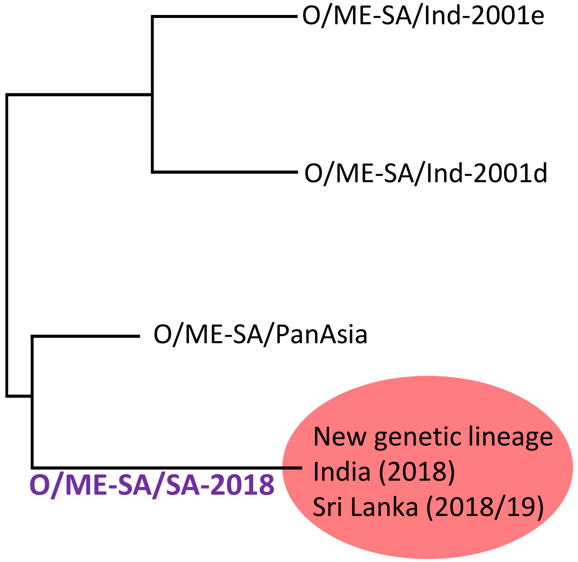
Tecnología Agroalimentaria (INIA), Spain

Re-emergence of foot-and-mouth disease in the Republic of Korea caused by the O/ME-SA/Ind-2001e lineage

Soyoon Ryoo[1], Hyeonjeong Kang[1], Da-Rae Lim[1], Jae-Myung Kim[1], Youngwoo Won[2], Ji Ye Kim[2], Donald P. King[3], Antonello Di Nardo[3] and Sang-Ho Cha[1*]

Brewing up the next serotype O virus lineage from Pool 2

- History tells us that pandemic serotype O lineages emerge from **Pool 2**
- O/ME-SA/SA-2018 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 (and perhaps also in Iran?)
- 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



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

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

- 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**
- **This lineage poses a risk for countries in Southeast Asia**

State of Palestine
Ministry of Agriculture

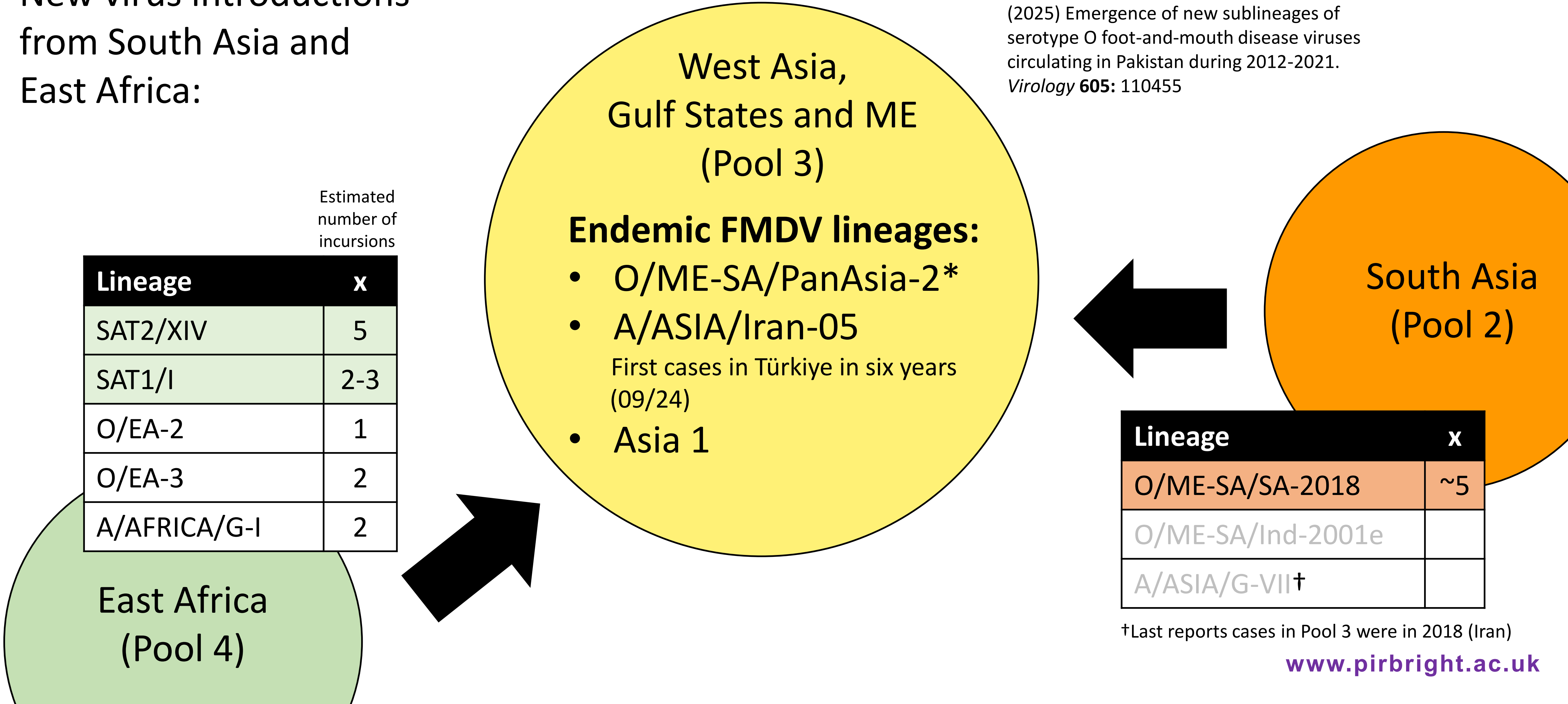
Vaccine Matching data is available for 9 field isolates from the O/ME-SA/SA-2018 lineage

	O1-Manisa ^{BI}		O-TUR/5/09 ^{MSD}		O-3039 ^{BI}		O-Campos ^{BI}		O-PanAsia-2 ^{BI}		O-Campos ^{BB}	
Isolate	r1value	heterologous titre (log$_{10}$)	r1value	heterologous titre (log$_{10}$)	r1value	heterologous titre (log$_{10}$)	r1value	heterologous titre (log$_{10}$)	r1value	heterologous titre (log$_{10}$)	r1value	heterologous titre (log$_{10}$)
UAE/15/2021	0.56	2.15	0.69	2.32	0.75	1.94	0.28	2.19	0.47	2.30	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
IRQ/10/2025	0.73	2.23	0.62	2.23	0.46	1.87	0.38	2.22	0.50	2.21	0.59	2.64
IRQ/21/2025	0.70	2.22	0.71	2.29	0.64	2.01	0.39	2.23	0.54	2.24	0.50	2.56
► 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

Updated FMD risks for Pool 3 (since 2020)

New virus introductions from South Asia and East Africa:

*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



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

South Asia (Pool 2)

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)

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

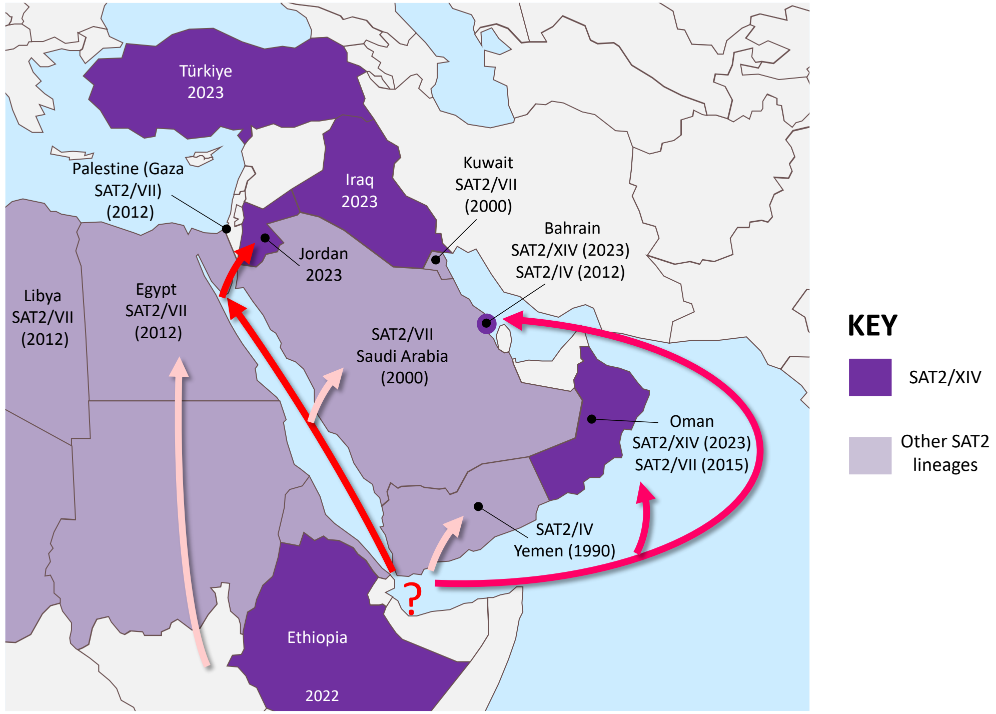
- VP1 sequence data and samples:

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

Ministry of Municipalities Affairs and Agriculture

anses

- 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:

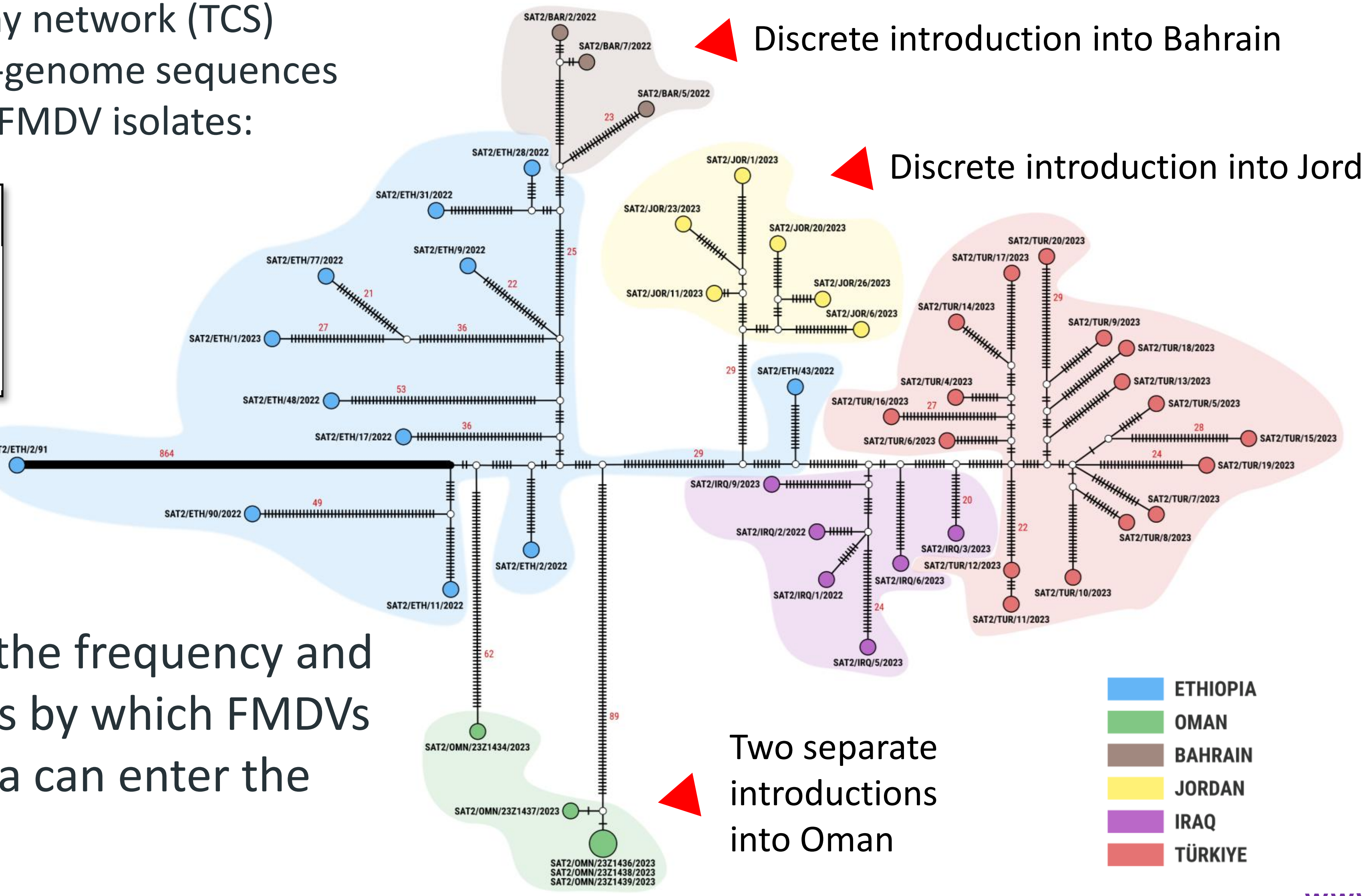
EMERGING INFECTIOUS DISEASES®

DISPATCHES

Eastern Africa Origin of SAT2 Topotype XIV Foot-and-Mouth Disease Virus Outbreaks, Western Asia, 2023

Antonello Di Nardo, Andrew E. Shaw, Mathilde Gondard, Jemma Wadsworth, Guillaume Girault, Krupali Parekh, Anna Ludi, Valerie Mioulet, Cindy Bernelin-Cottet, Hayley M. Hicks, Noemi Polo, Abdulnaci Bulut, Unal Parlak, Daniel Gizaw, Mustafa Ababneh, Maisa Al Ameer, Layth M.S. Abdulrasool, Fajur S. Al Saloom, Wafa A. Al-Rawahi, Nick J. Knowles, Labib Bakkali-Kassimi, Donald P. King

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

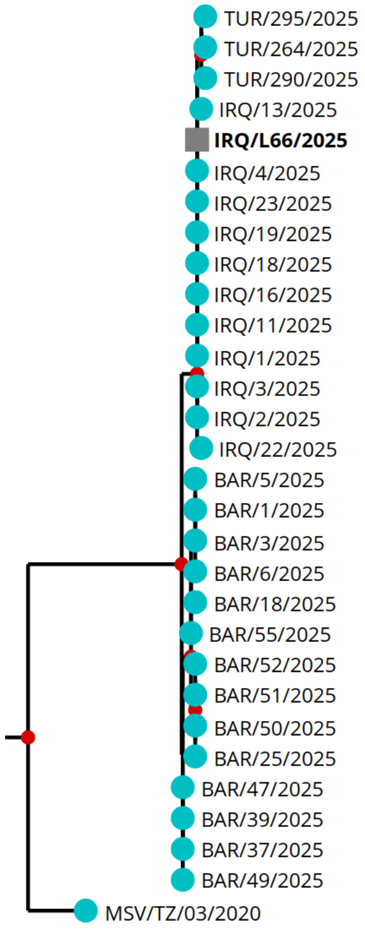
Two separate introductions into Oman

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

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

Bahrain, Kuwait, Iraq and Türkiye

- Reports of an upsurge of FMD outbreaks in Iraq where local testing (by agELISA) identified serotype SAT1 and O viruses
- **SAT1/I detected in samples sent to WRLFMD**
- Closest genetic relative from Tanzania 2020
- >15% nt difference to the sequences from Qatar (2023)
- Animals are naïve to this serotype - potential for rapid spread
- **ALERT FROM FAO** (https://doi.org/10.4060/cd5055en)
- **Monitoring the spread of this exotic virus – data sharing is critical**
- SAT1 also reported (WAHIS) for outbreaks in Kuwait (April 2025) and Türkiye (May 2025)
- SAT1/I lineage-specific real-time RT-PCRs and Ag-ELISA are able to detect and discriminate viruses from this topotype

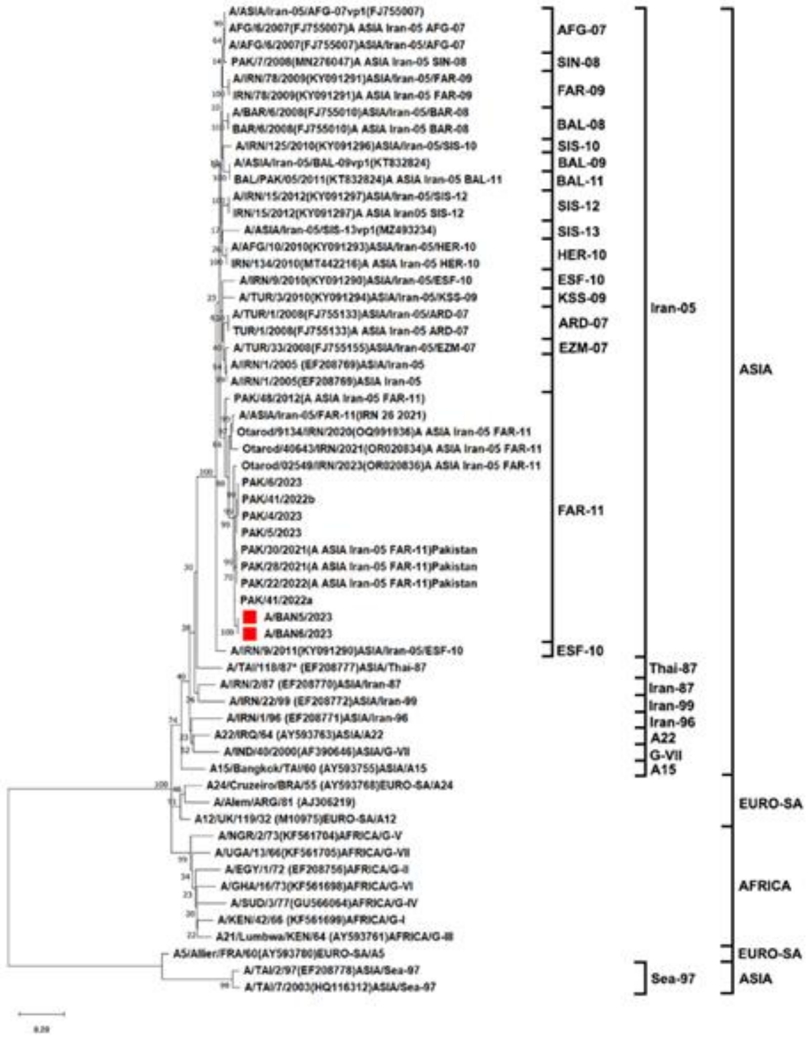


Detection of A/ASIA/Iran-05 in Bangladesh

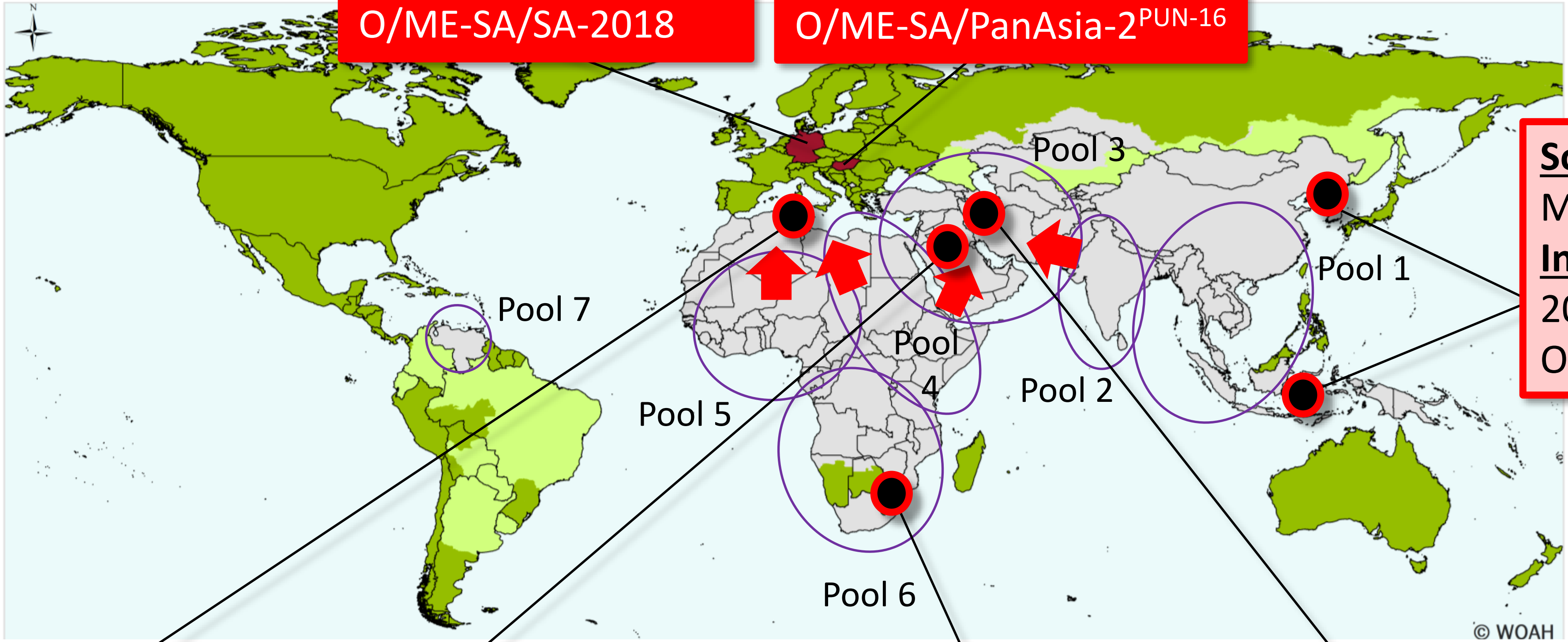
Animal and Plant Quarantine Agency

- Viruses that originate from Pool 3 are not normally detected in Pool 2
- A/ASIA/Iran-05 has been historically confined to Pool 3, particularly within Iran, Pakistan, and the Western Asia region
- 2023 – two samples of A/ASIA/Iran-05$^{\text{FAR-11}}$ detected in Bangladesh
- Most closely related to viruses from Pakistan (2021-2023)

- **Provides evidence for connectivity between Pool 3 and Pool 2**



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



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

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

South Korea
March 2025
Indonesia
2024-25
O/ME-SA/Ind-2001e

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

Middle East (2025)
SAT1/I
Middle East (2023)
SAT2/XIV

Southern Africa
Serotype SAT2
(and SAT1 & SAT3)
Eswatini
SAT2

Iran, Iraq, Türkiye, Palestine, Israel
2023/2024
O/ME-SA/SA-2018

Pool 1: Status in 2025 – what is missing?

Characterisation of different FMD virus lineages

Based on data from WRLFMD, RRLSEA, the WOAH/FAO Lab Network, publications* 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	2024	2016		2024		2016		
Laos	2020	2017		2023		2018		
Malaysia	2022	2016	2005	2023	2009	2022		
Myanmar	2021	2021				2021	2010	2017
Thailand	2024	2018	2012	2019		2022		
Vietnam	2023	2023	2018	2023		2017		2007
PR China	2023	2020	2022	2019		2019		2009
Indonesia	2025							
Mongolia	2022	2018		2017		2016		

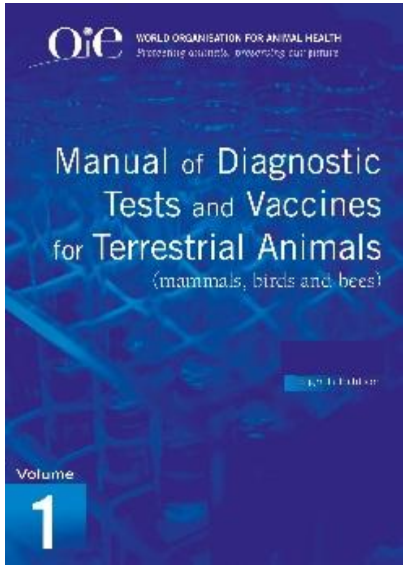
*Recent papers: Khanh et al., (2025)

Vaccine selection for endemic settings (gaps and challenges)

1. Homologous/monovalent QA/QC (WOAH Terrestrial Manual) vs heterologous vaccine performance **in the field** with multivalent products
2. 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)

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/)

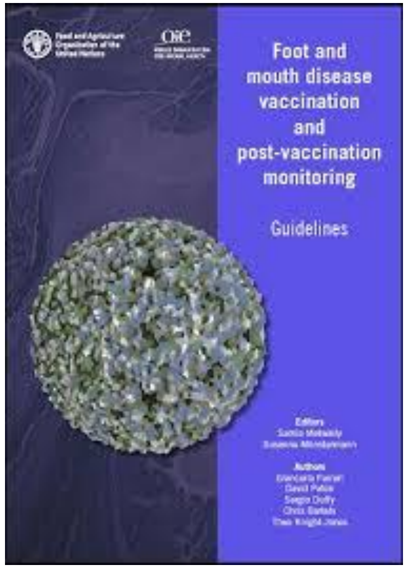


OIE WORLD ORGANISATION FOR ANIMAL HEALTH

Manual of Diagnostic Tests and Vaccines for Terrestrial Animals

(mammals, birds and bees)

Volume 1



Foot and mouth disease vaccination and post-vaccination monitoring

Guidelines

The important question about vaccine quality…….

- Paper published in May 2025:

npj | vaccines **Article**

Published in partnership with the Sealy Institute for Vaccine Sciences

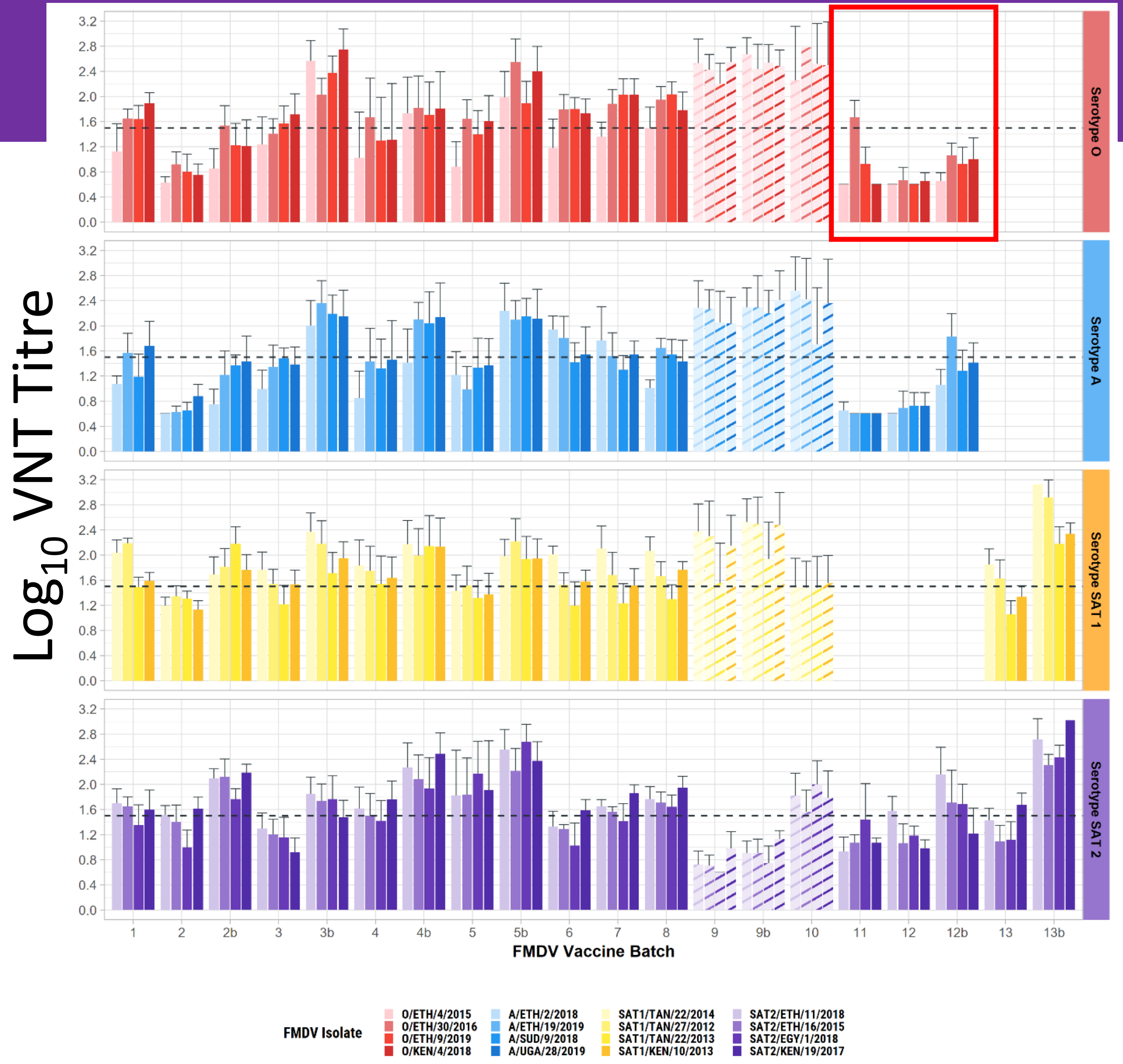
https://doi.org/10.1038/s41541-025-01128-7

An antigen panel to assess the regional relevance of foot and mouth disease vaccines

Check for updates

David J. Paton[1] ✉, Ginette Wilsden[1], Clare FJ Browning[1], Efrem A. Foglia[2], Antonello Di Nardo[1], Nick J. Knowles[1], Jemma Wadsworth[1], Simon Gubbins[1], Ethel Chitsungo[3], Cisse Rahamatou Moustapha Boukary[3], Gelagay Ayelet[3], Charles S. Bodjo[3], Nick Nwankpa[3], Emiliana Brocchi[2], Santina Grazioli[2], Anna Ludi[1] & Donald P. King[1]

Independent testing



- Data for commercial FMD vaccines used in East Africa
- Data for 5 suppliers (13 batches)
- Cattle sera (minimum of 5 animals) primary course (+/- booster)
- VNT 1.5 $\log_{10}$ cut-off for four antigens/serotype

- Important to recruit seronegative animal
- Identifies vaccines with poor responses, and reinforces the benefits of booster vaccination

Advantages of "heterologous" testing pipeline

1. Serological performance is assessed using the **formulated vaccine** which may contain multiple FMD vaccine antigens
2. Data can be used to compare responses for different vaccines
   - But need to adopt standardized protocols for sera (numbers of animals and sampling time points [including booster doses])
3. Testing can be designed to assess animal-to-animal variability of responses in target host populations (incl. different species)
4. Once generated, the reference sera can be used to assess the suitability of the vaccines in other regions or against emerging virus lineages

5. Reference antigen panels can be developed in partnership with regional networks
   - **Proposal for Pool 1 shortly**

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Network

Talk summary

- Epidemiology of FMD is very dynamic
- 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
- **New risks for countries in Southeast Asia**
- 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

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

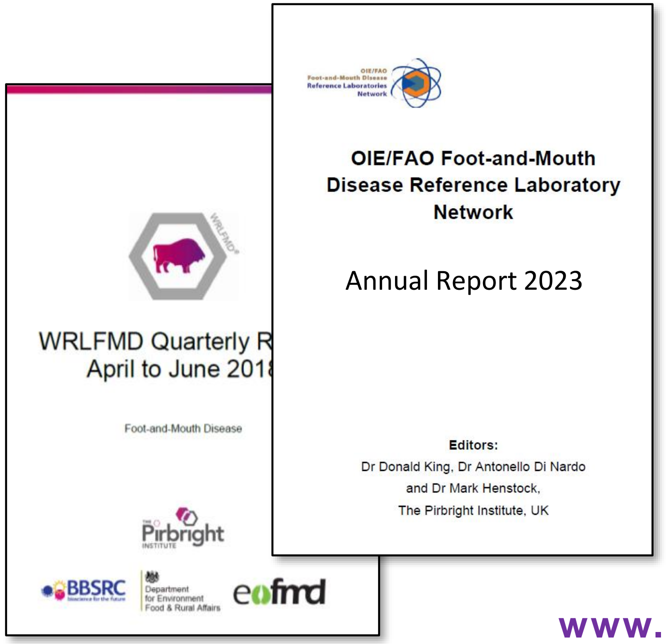
Welcome

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).

Country FMD Reports

Details of samples tested for FMD at WRLFMD from around the world.

Country Reports ›



WRLFMD Quarterly R
April to June 201

Foot-and-Mouth Disease

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

Annual Report 2023

Editors:
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