

Update on recent FMDV global events

DR GUILLAUME GIRAULT

Recent Events

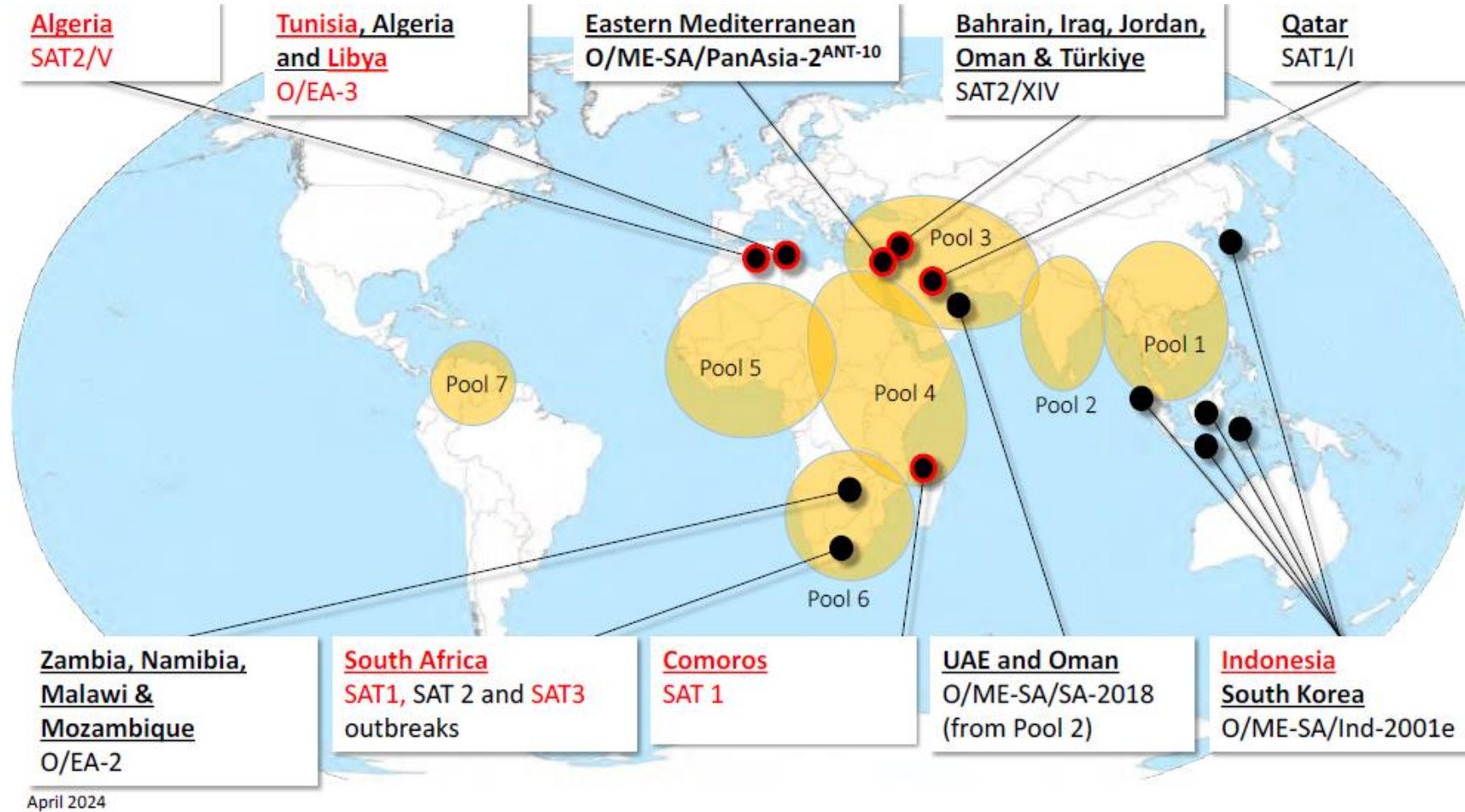


Figure 1: Recent FMD global outbreaks

Note: New headline events reported January to March 2024 are highlighted in red with FMD endemic pools highlighted in orange.

Source: WRLFMD. Map conforms to the United Nations World Map, June 2020.

(Source: FMD quarterly reports 2024 (WRL))

West EurAsia situation

West EurAsia situation

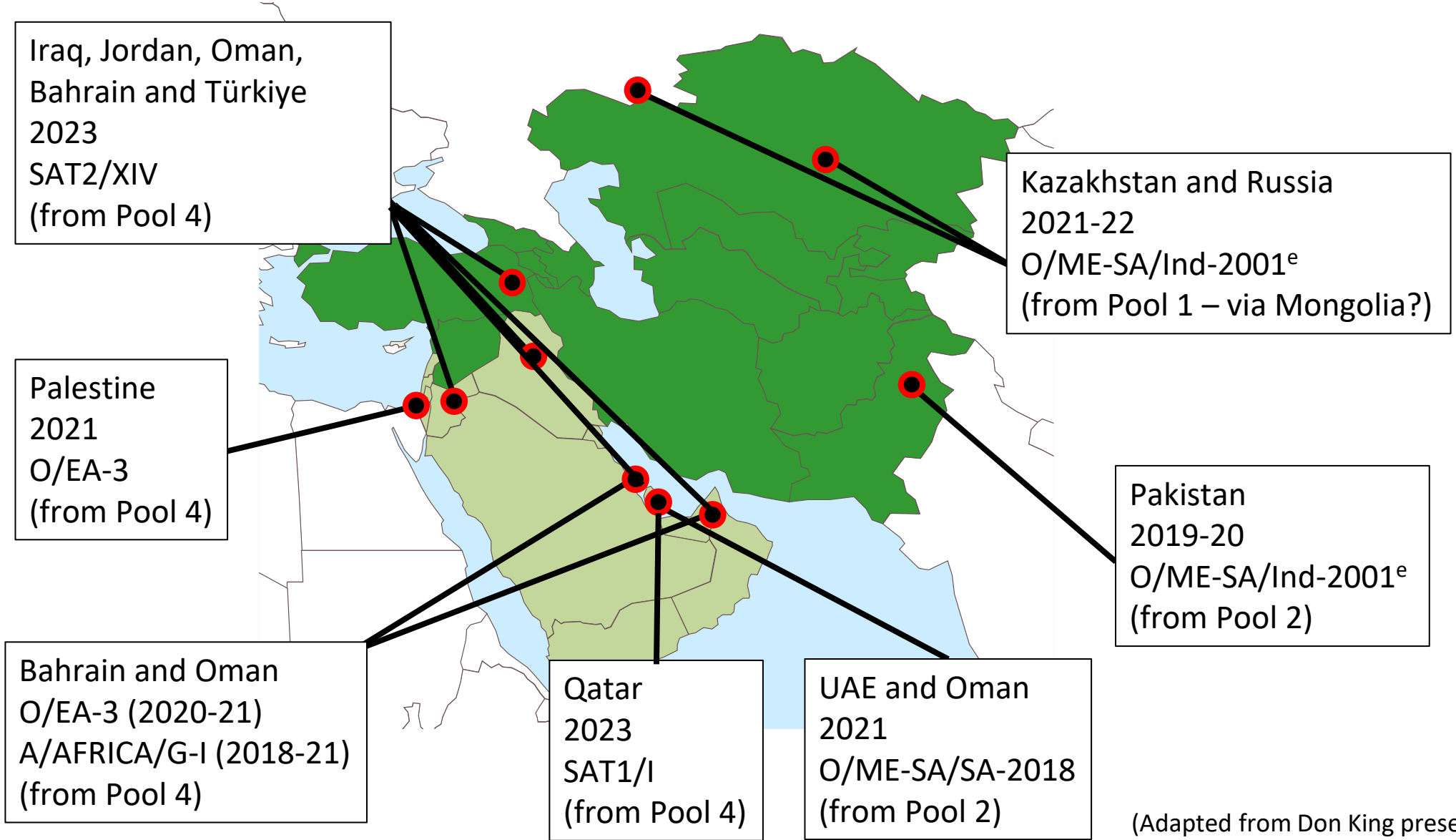
- West EurAsian countries represent an important component of FMD Endemic Pool 3 where serotypes O, A and Asia 1 circulate

Viral lineage:	West Eurasia	Gulf States
O/ME-SA/PanAsia-2 ANT-10 & QOM-15	✓	✓
A/ASIA/Iran-05 FAR-11 & SIS-13	✓	✓
Asia-1	✓	✓ 2011 (Bahrain)

- SAT2 is also present since 2023

(Adapted from Don King presentation of 2023)

Recent introductions of exotic viruses into Pool 3



(Adapted from Don King presentation of 2023)

West EurAsia situation

3.4. Pool 3 (West Eurasia and Near East)

Armenia



A spring vaccination campaign has been approved, but not yet started. The FMD vaccine will contain the following antigens: A/Iran05, A/G-VII, O/PanAsia2, Asia-1/Sindh 08 and SAT 2.

[EuFMD FAST Report](#)

The Republic of Azerbaijan



Almost 555,000 cattle and small ruminants were vaccinated in January and February 2024. Samples collected for sero-monitoring after the autumn vaccination campaign have been tested (results to be presented later).

[EuFMD FAST Report](#)

Georgia



12,000 large ruminants have been vaccinated during this quarter and a sero-surveillance campaign is being initiated.

[EuFMD FAST Report](#)

The Hashemite Kingdom of Jordan



In this quarter, over 260,000 sheep, goats and cattle have been vaccinated. A small scale sero-survey has been completed with only 11 out of 126 sheep and goats testing antibody positive.

[EuFMD FAST Report](#)

Türkiye



In this quarter, 44 new outbreaks were detected, 28 due to serotype SAT 2. To eradicate SAT 2, the vaccination strategy for large ruminants has been changed to three times a year, with emergency and pre-shipment vaccination continuing as before.

A Risk Based Surveillance Program has been initiated in the Thrace region for early detection of any outbreaks and to maintain confidence in absence of the disease, while clinical surveillance is occurring in the buffer zone along the Southeastern and Eastern borders of Anatolia.

[EuFMD FAST Report](#)

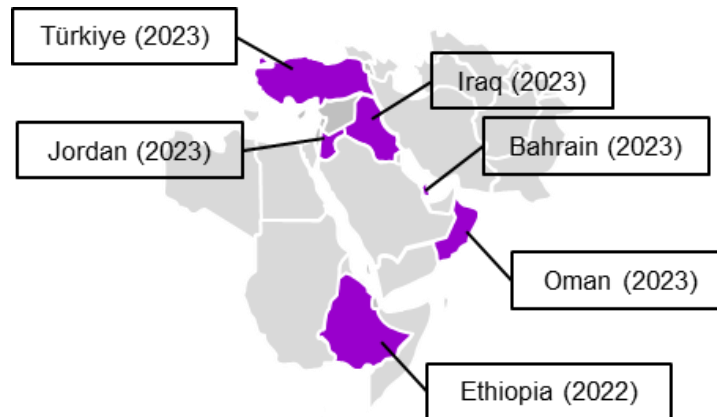
(Source: FMD quarterly reports 2024 (WRL))

SAT2/XIV : a new threat?

SAT2/XIV

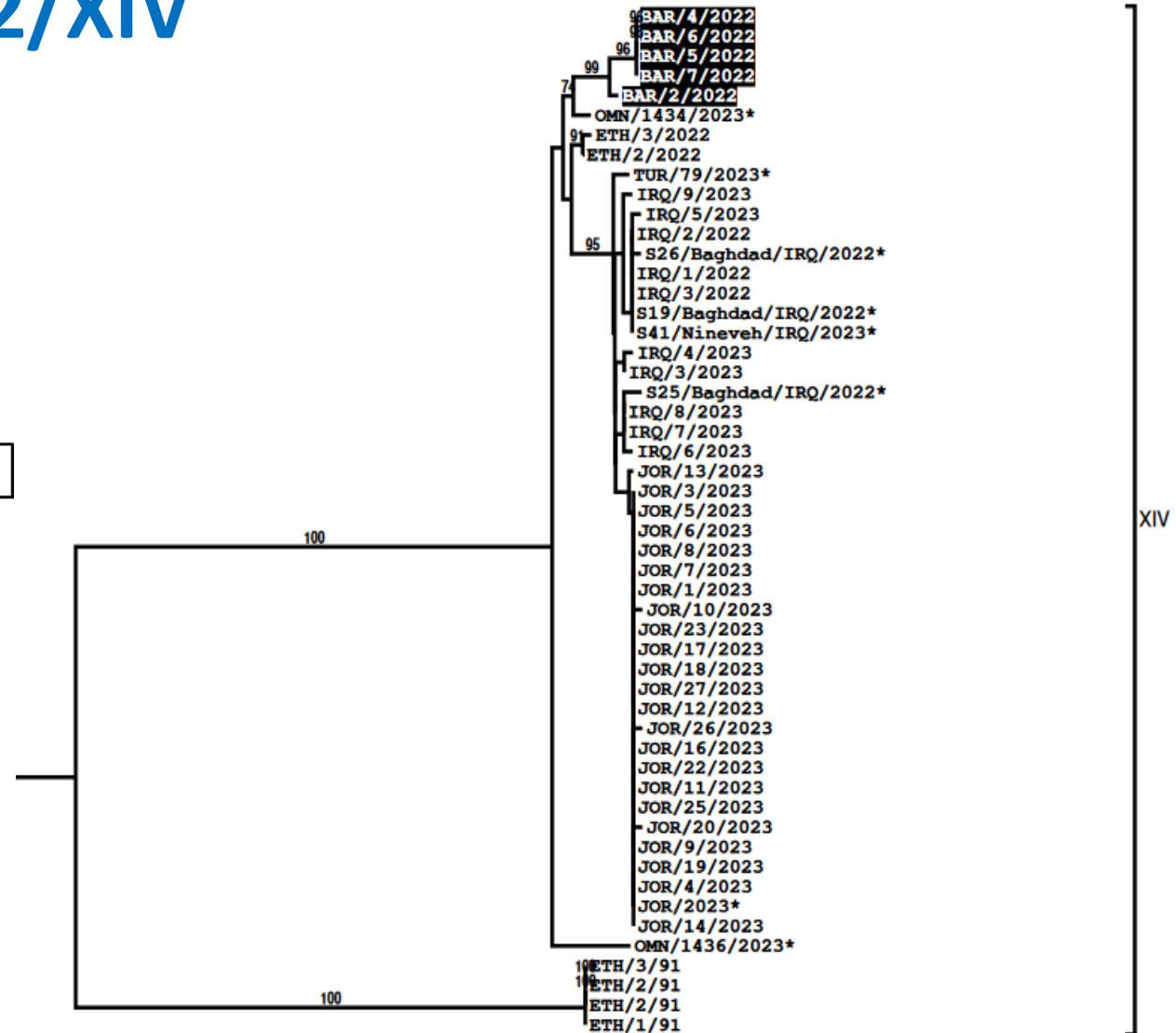
➤ At the end of 2022 and 2023, outbreaks of FMDV related to SAT2/XIV detected in several countries:

- Ethiopia
- Iraq
- Türkiye
- Jordan
- Oman
- Bahrain



➤ Most closely related to sequences recovered from samples collected in Ethiopia in 2022

➤ Topotype XIV has been detected on only one other previous occasion (in 1991)



SAT2/XIV: control via vaccination?

➤ SAT2 vaccines are not widely used to control FMD outbreaks in the region

➤ Vaccine matching results from WRL indicated good results with SAT2 Eritrea 98 (BI)

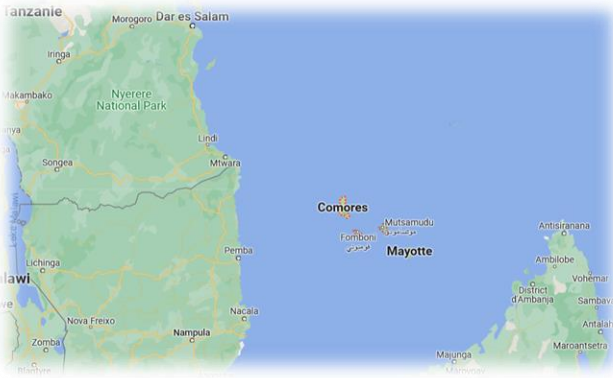
Isolate	Serotype SAT 2		Eritrea 98 <i>Boehringer Ingelheim</i>		SAT2 Zim 83 <i>Boehringer Ingelheim</i>	
	Topotype	Lineage	r ₁	titre	r ₁	titre
JOR 11/2023	XIV	-	0.58	1.69	0.20	1.74
JOR 20/2023	XIV	-	0.83	1.85	0.24	1.81
JOR 26/2023	XIV	-	0.86	1.86	0.32	1.94
ETH/2/2022	XIV	-	0.81	1.62	0.54	2.17
ETH/3/2022	XIV	-	0.49	1.66	0.15	1.70

Isolate	Serotype SAT 2		Eritrea 98 <i>Boehringer Ingelheim</i>		SAT2 Zim 83 <i>Boehringer Ingelheim</i>	
	Topotype	Lineage	r ₁	titre	r ₁	titre
ETH/3/2022	XIV	-	0.49	1.66	0.15	1.70
IRQ/9/2023	XIV	-	0.42	1.51	0.31	1.95
IRQ/2/2022	XIV	-	0.73	1.75	0.38	2.04
IRQ/5/2023	XIV	-	0.53	1.61	0.74	2.33

Source: FMD quarterly reports 2023 (WRL)

SAT1/I : spread from Africa?

SAT1/I, Comoros



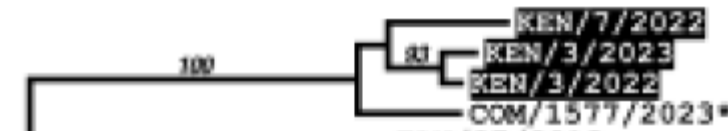
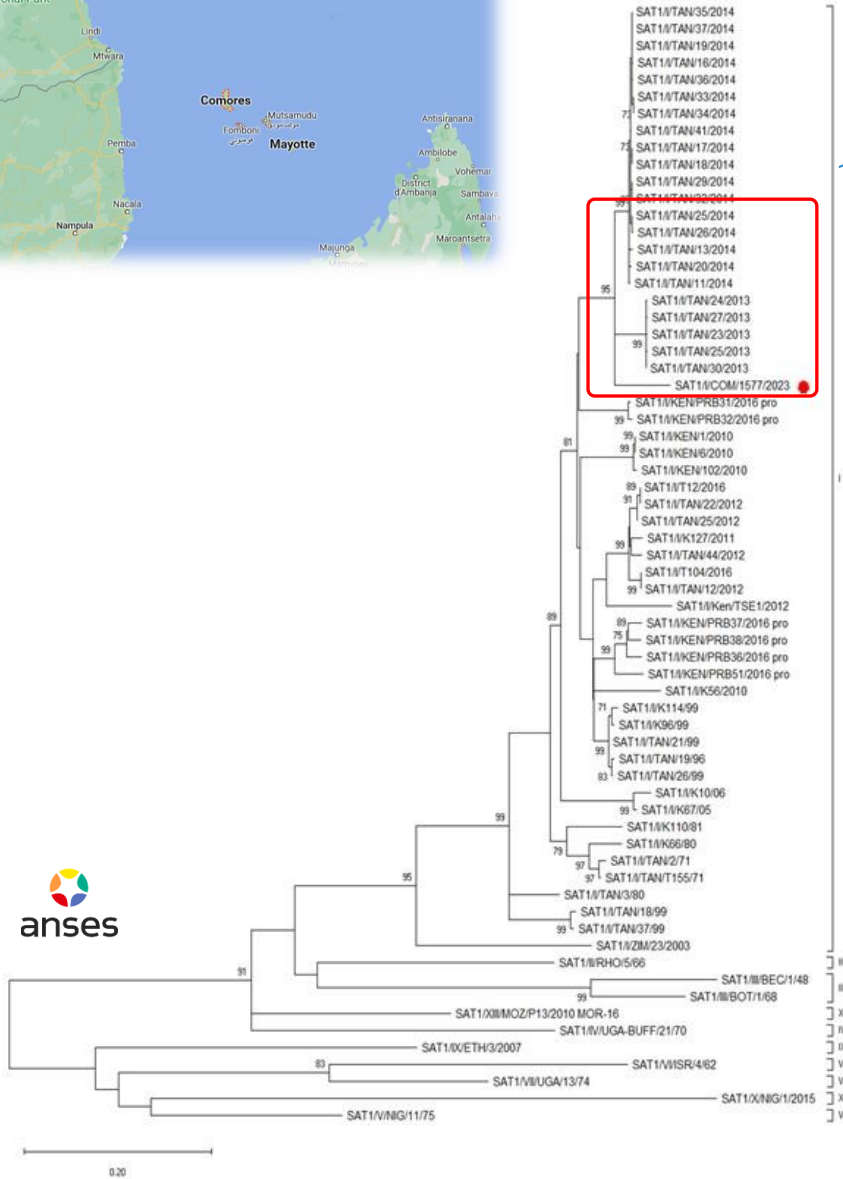
SAT1/TAN/35/2014
 SAT1/TAN/37/2014
 SAT1/TAN/19/2014
 SAT1/TAN/16/2014
 SAT1/TAN/36/2014
 SAT1/TAN/33/2014
 SAT1/TAN/34/2014
 SAT1/TAN/41/2014
 SAT1/TAN/17/2014
 SAT1/TAN/18/2014
 SAT1/TAN/28/2014
 SAT1/TAN/23/2014
 SAT1/TAN/25/2014
 SAT1/TAN/26/2014
 SAT1/TAN/13/2014
 SAT1/TAN/20/2014
 SAT1/TAN/11/2014
 SAT1/TAN/24/2013
 SAT1/TAN/27/2013
 SAT1/TAN/23/2013
 SAT1/TAN/25/2013
 SAT1/TAN/30/2013
 SAT1/COM/1577/2023

SAT1/TAN/25/2014
 SAT1/TAN/26/2014
 SAT1/TAN/13/2014
 SAT1/TAN/20/2014
 SAT1/TAN/11/2014
 SAT1/TAN/24/2013
 SAT1/TAN/27/2013
 SAT1/TAN/23/2013
 SAT1/TAN/25/2013
 SAT1/TAN/30/2013
 SAT1/COM/1577/2023

Séquences les plus proches

Virus	% Homologie	Sérotype	Topotype
TAN/36/2014	93.33	SAT I	
TAN/34/2014	93.33	SAT I	
TAN/33/2014	93.33	SAT I	
TAN/11/2014	93.33	SAT I	
TAN/41/2014	93.18	SAT I	
TAN/37/2014	93.18	SAT I	
TAN/35/2014	93.18	SAT I	
TAN/32/2014	93.18	SAT I	
TAN/29/2014	93.18	SAT I	
TAN/25/2014	93.18	SAT I	
TAN/20/2014	93.18	SAT I	
TAN/19/2014	93.18	SAT I	
TAN/18/2014	93.18	SAT I	
TAN/17/2014	93.18	SAT I	
TAN/26/2014	93.03	SAT I	
TAN/16/2014	93.03	SAT I	
TAN/13/2014	93.03	SAT I	
SEM-014-P/UGA/2016	92.88	SAT I	
ISI-046-P/UGA/2016	92.88	SAT I	

- After O/EA-2 in 2019, new introduction into Comoros, probably from animals imported from Kenya/Tanzania
- Most closely related isolate from Kenya (2022) after additional analyses from WRL



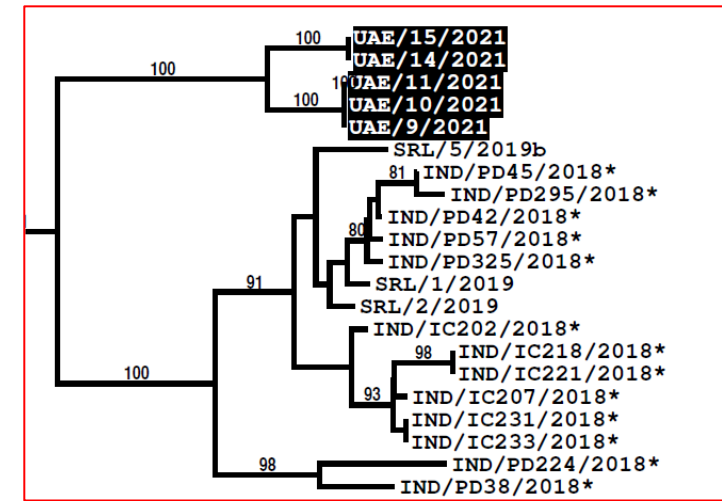
SAT1/I, Qatar

- SAT1/I detected in Qatar recently by WRL, but not directly related to the Comoros sequence
- **SAT1/I could spread from Africa?**



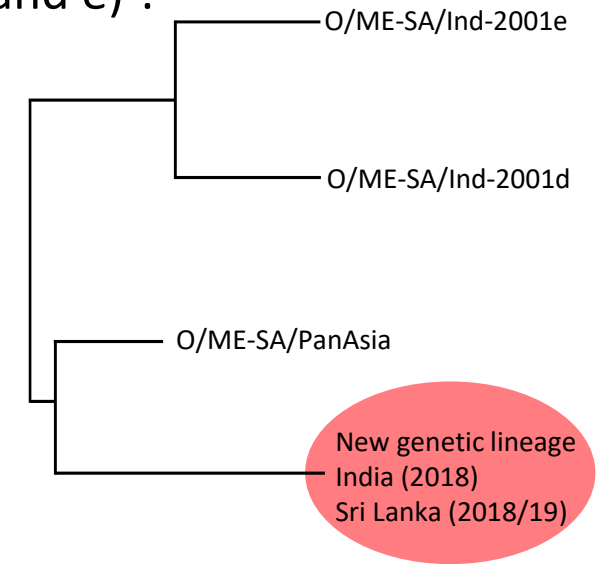
O/ME-SA/SA-2018 : the next serotype O virus lineage

O/ME-SA/SA-2018

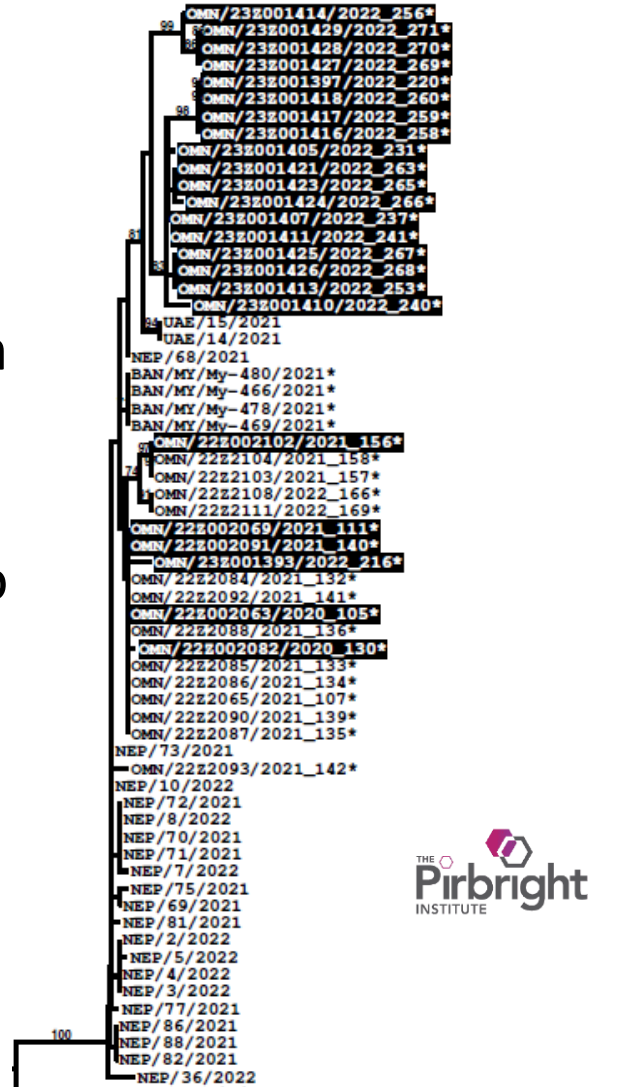


Last year, we presented O/ME-SA/SA-2018 as a potential emerging lineage

- Detected in UAE (2021) in small ruminants
- New serotype O lineage previously detected in India and Sri Lanka (2018, 2019)
- Possibility of wider dissemination following pathways for O/ME-SA/Ind-2001 (d and e) ?
- Commonly used vaccines show a good antigenic match with this virus
- About 40% of cases of serotype O in india



O/ME-SA/SA-2018, Oman

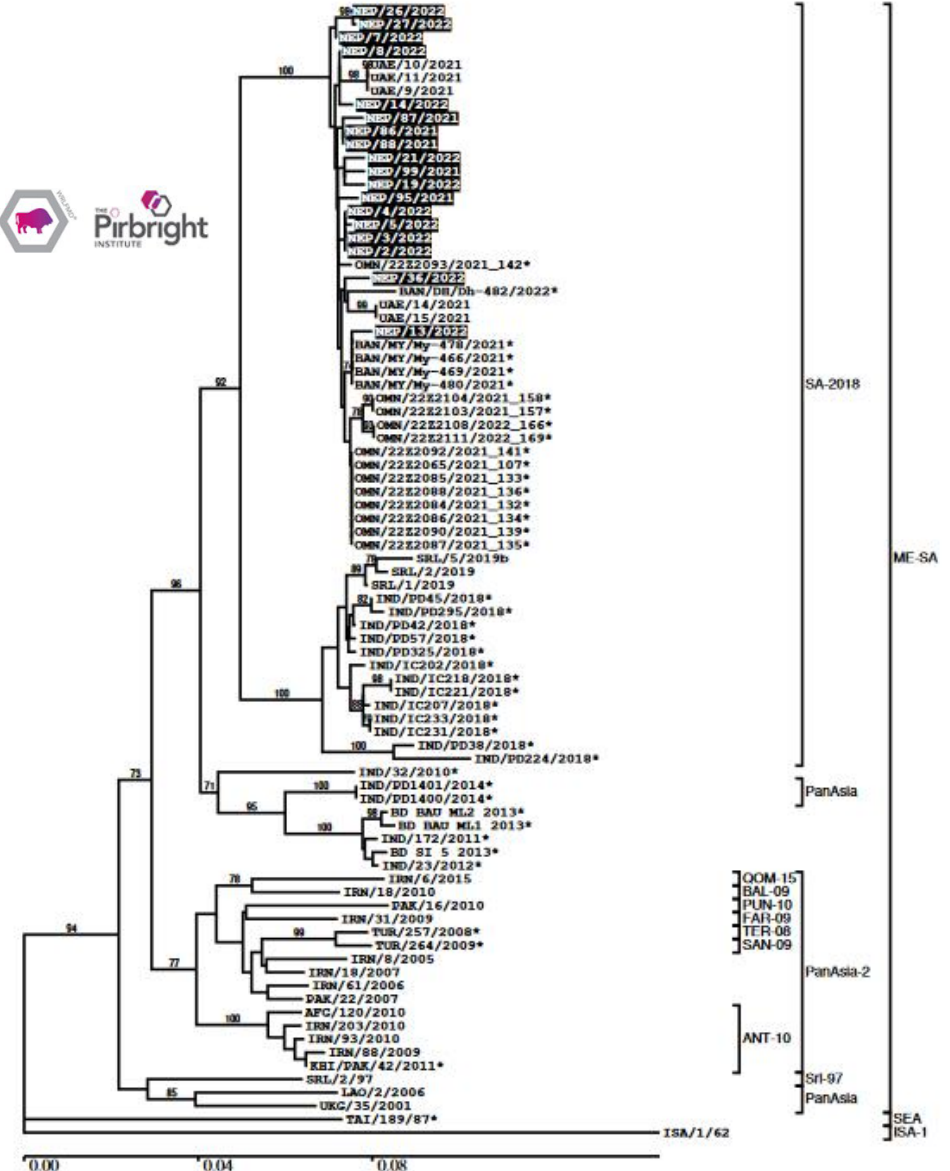


SA-2018



- ➔ Samples received from Oman between 2020 and 2022 (PhD student)
- ➔ Proximity with UAE isolates and also recent Indian isolates
- ➔ Become dominant in Oman now

O/ME-SA/SA-2018, Nepal



- Outbreaks at the beginning of 2022
- Most closely related sequences are from Oman and Bangladesh
- Spread from India?

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_51888	BAN/MY/My-469/2021	cattle	99.5	0	O	ME-SA	SA-2018	
viba_51892	BAN/MY/My-478/2021	cattle	99.5	0	O	ME-SA	SA-2018	
viba_51884	BAN/MY/My-466/2021	cattle	99.5	0	O	ME-SA	SA-2018	
viba_51896	BAN/MY/My-480/2021	cattle	99.5	0	O	ME-SA	SA-2018	
viba_51639	OMN/22Z2088/2021_136	cattle	99.2	0	O	ME-SA	SA-2018	
viba_51627	OMN/22Z2085/2021_133	sheep	99.2	0	O	ME-SA	SA-2018	
viba_51643	OMN/22Z2090/2021_139	cattle	99.2	0	O	ME-SA	SA-2018	
viba_51635	OMN/22Z2087/2021_135	sheep	99.2	0	O	ME-SA	SA-2018	
viba_51631	OMN/22Z2086/2021_134	sheep	99.2	0	O	ME-SA	SA-2018	
viba_51619	OMN/22Z2065/2021_107	cattle	99.2	0	O	ME-SA	SA-2018	

O/ME-SA/PanAsia-2^{ANT10} : still present



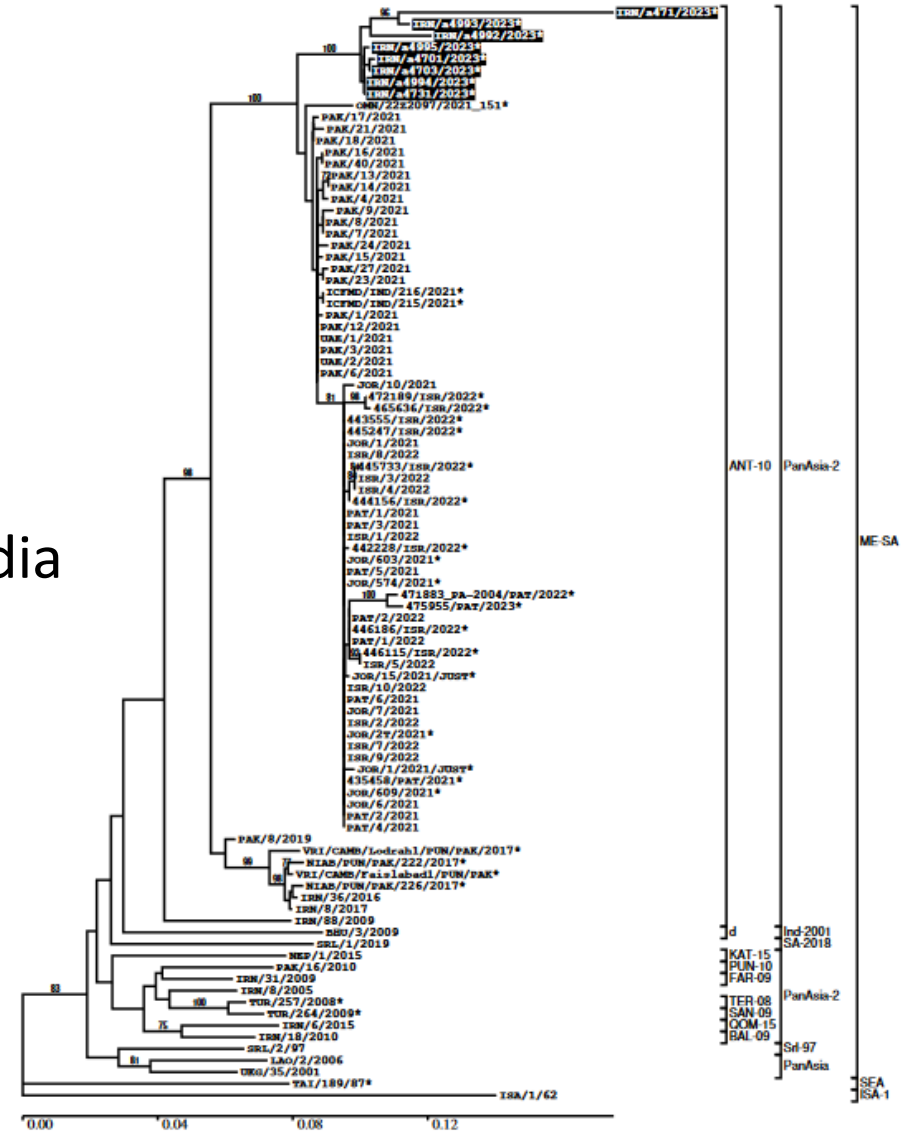
O/ME-SA/PanAsia-2^{ANT10}, Iran

➤ Outbreak at the beginning of 2022

➤ Most closely related sequences from UAE, Pakistan and India

Most Closely Related Sequences

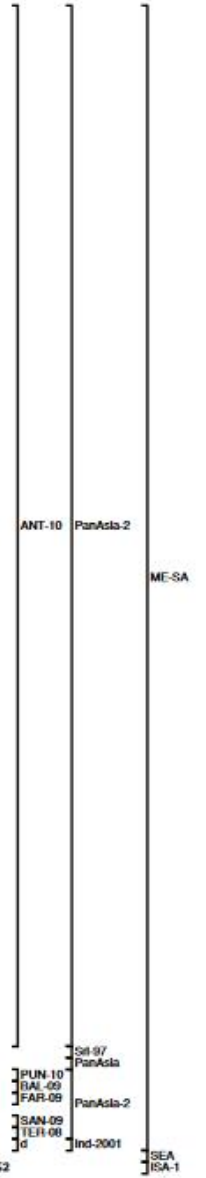
sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_50341	PAK/12/2021	water buffalo	97.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_50954	UAE/2/2021	Arabian oryx	97.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_50325	PAK/6/2021	cattle	97.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_50381	PAK/27/2021	cattle	97.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_50950	UAE/1/2021	Arabian oryx	97.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_50317	PAK/3/2021	cattle	97.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_52157	ICFMD/IND/216/2021		97.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_50369	PAK/21/2021	cattle	97.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_50333	PAK/8/2021	cattle	97.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_50313	PAK/1/2021	cattle	97.3	0	O	ME-SA	PanAsia-2	ANT-10



O/ME-SA/PanAsia-2^{ANT10}, Israel



444136/ISR/2022*
 MESSR/4/2022
 444573/ISR/2022*
 ISR/3/2022
 444156/ISR/2022*
 ISR/10/2022
 ISR/9/2022
 445247/ISR/2022*
 ISR/7/2022
 JOR/1/2021
 JOR/1/2021
 - 44228/ISR/2022*
 PAT/6/2021
 443555/ISR/2022*
 JOR/603/2021*
 PAT/4/2021
 ISR/9/2022
 - JOR/1/2021/JUST*
 JOR/574/2021*
 PAT/2/2021
 PAT/3/2021
 ISR/1/2022
 435458/PAT/2021*
 PAT/1/2021
 JOR/2/2021*
 JOR/7/2021
 ISR/2/2022
 JOR/6/2021
 JOR/603/2021*
 - JOR/10/2021
 - 471881_PA-2004/PAT/2022*
 446185/ISR/2022*
 PAT/2/2022
 PAT/1/2022
 ISR/5/2022
 446115/ISR/2022*
 - JOR/15/2021/JUST*
 - JOR/15/2021/JUST*
 PAT/4/2021
 PAK/14/2021
 PAK/13/2021
 PAK/9/2021
 PAK/8/2021
 PAK/7/2021
 - PAK/24/2021
 PAK/15/2021
 - PAK/27/2021
 PAK/23/2021
 ICSPND/IND/215/2021*
 ICSPND/IND/216/2021*
 PAK/1/2021
 PAK/16/2021
 PAK/40/2021
 PAK/2/2021
 PAK/6/2021
 PAK/12/2021
 PAK/1/2021
 PAK/3/2021
 - OMN/22x2007/2021_151*
 - PAK/21/2021
 - PAK/17/2021
 PAK/18/2021
 PAK/8/2019
 VRI/CAMB/Bhakhaz5/PUN/PAK/2017*
 VRI/CAMB/Bhakhaz4/PUN/PAK/2018*
 VRI/CAMB/Lodrah1/PUN/PAK/2017*
 VRI/CAMB/Gu jcat/PUN/PAK/2017*
 AFG/16/2017
 AFG/54/2017
 AFG/35/2017
 NIAR/PUN/PAK/223/2017*
 NIAR/PUN/PAK/222/2017*
 IRN/31/2016
 IRN/11/2017
 IRN/37/2016
 IRN/5/2017
 IRN/36/2016
 IRN/5/2017
 IRN/35/2016
 IRN/8/2017
 NIAR/PUN/PAK/226/2017*
 - AFG/44/2017
 VRI/CAMB/Fahsiwal1/PUN/PAK*
 NIAR/PUN/PAK/218/2017*
 VRI/CAMB/Fahsiwal2/PUN/PAK*
 NIAR/PUN/PAK/201/2017*
 VRI/CAMB/Bhakhaz3/PUN/PAK/2018*
 PAK/7/2016
 IRN/88/2009
 - VRI/2/97
 ORO/35/2001
 - PAK/16/2010
 IRN/18/2010
 IRN/31/2009
 IRN/8/2005
 - TUR/264/2009*
 - TUR/257/2009*
 - SHD/3/2000
 - PAK/189/87*
 ISA/1/62



➤ Outbreak at the end of 2022

➤ Most closely related sequences from Jordan and Palestine

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_51827	465636/ISR/2022	cattle	99.8	0	O	ME-SA	PanAsia-2	ANT-10
viba_50010	JOR/6/2021	cattle	99.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_49955	JOR/603/2021	cattle	99.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_50006	JOR/1/2021	cattle	99.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_50707	PAT/4/2021	sheep	99.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_50412	445247/ISR/2022	cattle	99.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_49951	JOR/574/2021	cattle	99.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_50678	ISR/7/2022	cattle	99.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_50662	ISR/2/2022	cattle	99.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_50699	PAT/2/2021	cattle	99.4	0	O	ME-SA	PanAsia-2	ANT-10



O/ME-SA/PanAsia-2^{ANT10}, Palestine

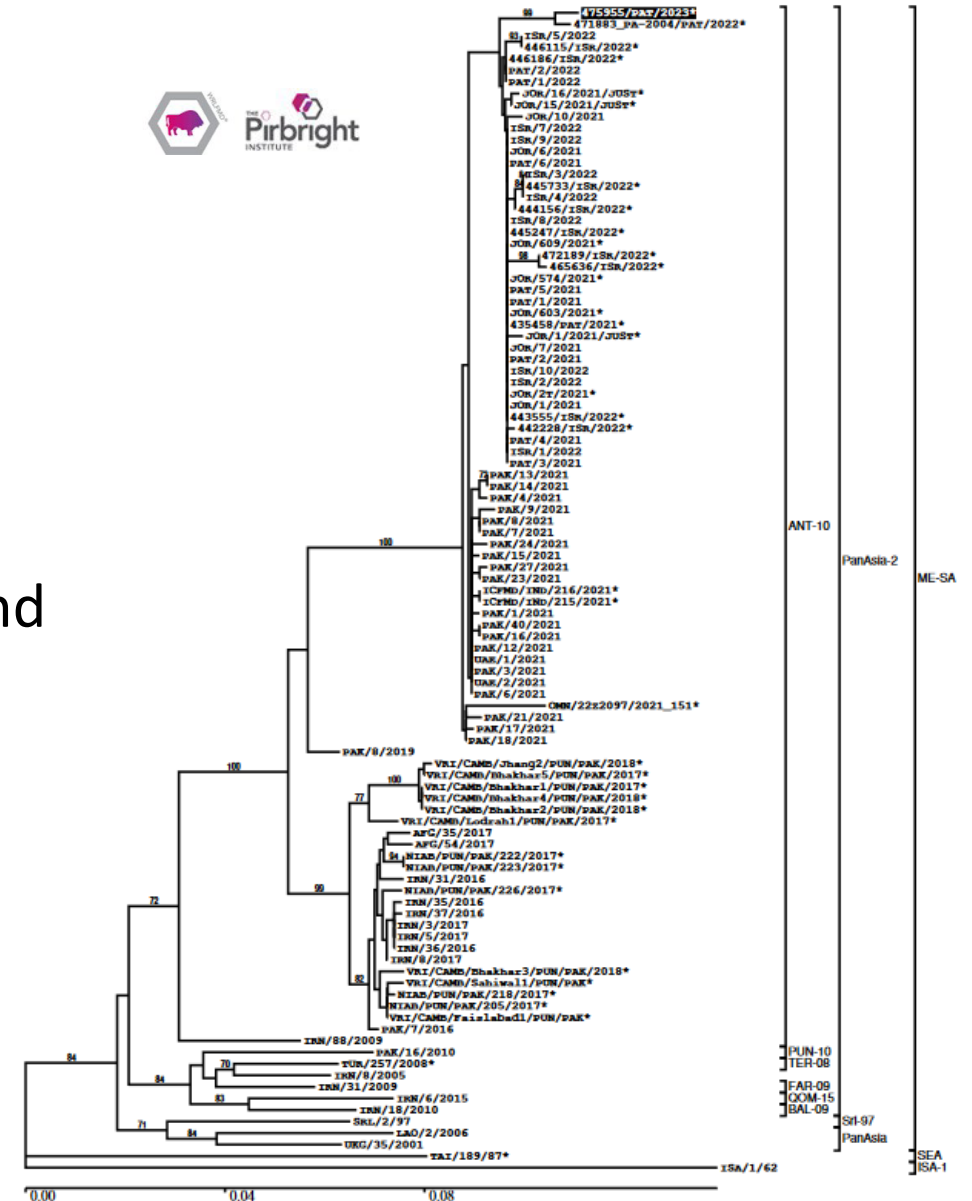


➤ Outbreak in 2022

➤ Most closely related sequences from Jordan, Israel and Palestine

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_50735	PAT/1/2022	sheep	98.6	0	O	ME-SA	PanAsia-2	ANT-10
viba_50424	446186/ISR/2022	cattle	98.6	0	O	ME-SA	PanAsia-2	ANT-10
viba_50739	PAT/2/2022	sheep	98.6	0	O	ME-SA	PanAsia-2	ANT-10
viba_50695	PAT/1/2021	cattle	98.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_50715	PAT/6/2021	goat	98.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_50010	JOR/6/2021	cattle	98.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_49955	JOR/603/2021	cattle	98.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_50662	ISR/2/2022	cattle	98.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_50690	ISR/10/2022	cattle	98.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_50711	PAT/5/2021	goat	98.4	0	O	ME-SA	PanAsia-2	ANT-10

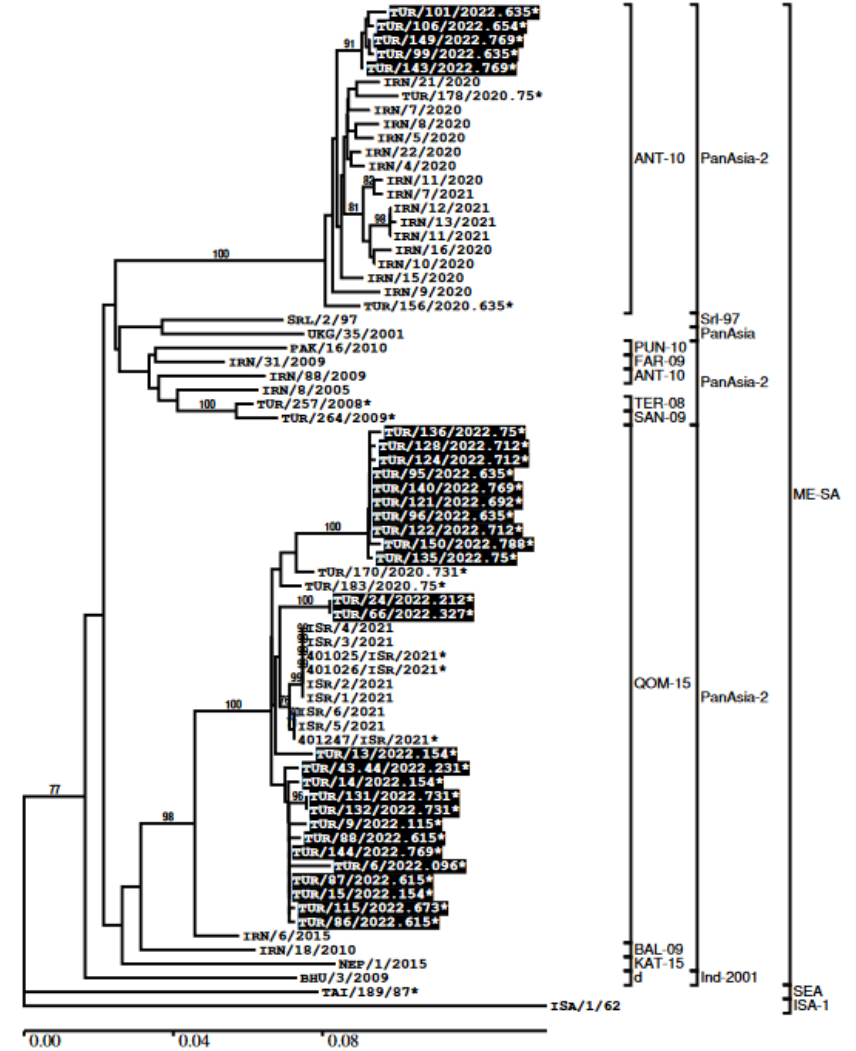




O/ME-SA/PanAsia-2^{ANT10}, Türkiye

➤ Outbreak in 2022

➤ Most closely related sequences from Iran



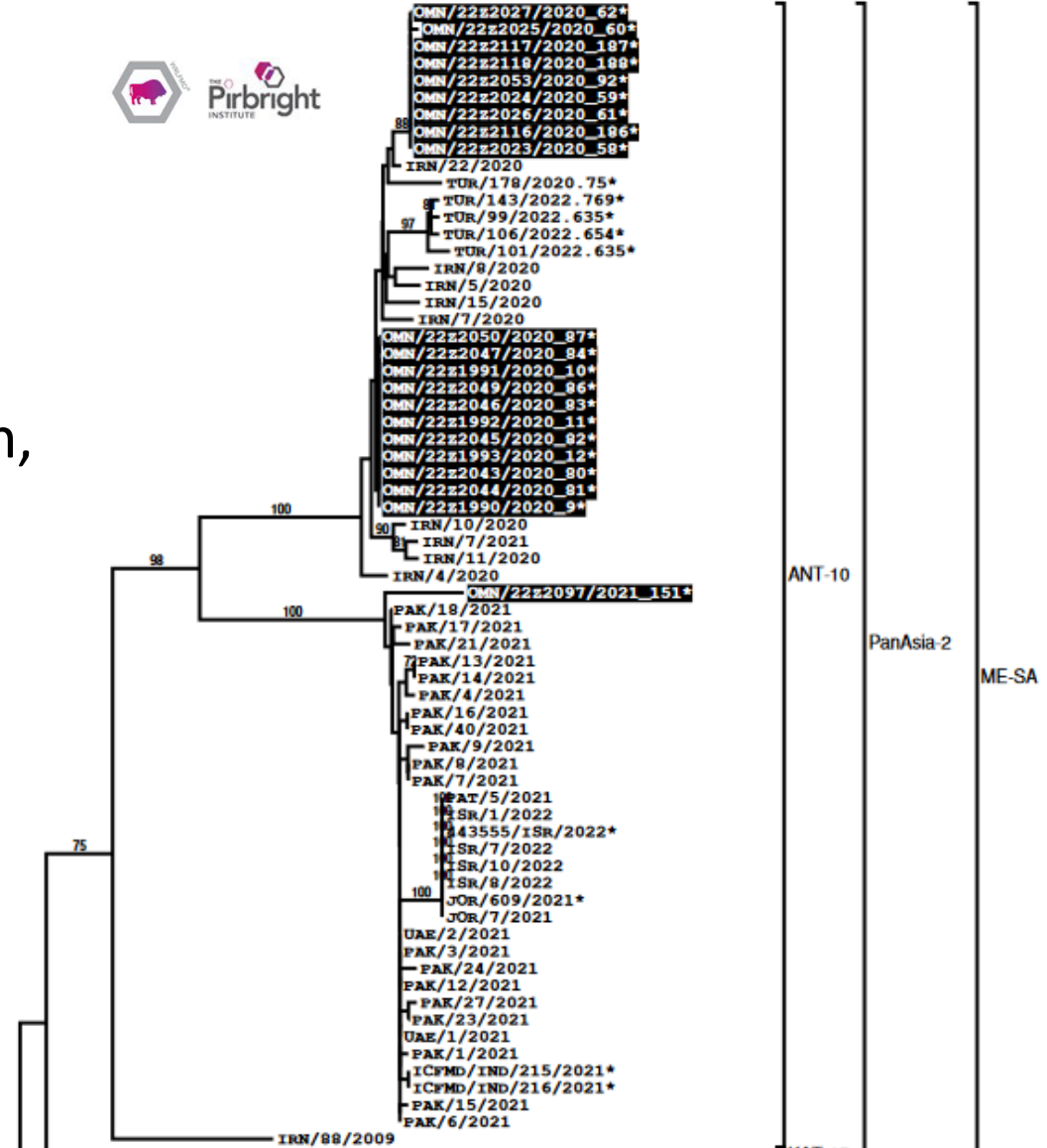
Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_52140	TUR/149/2022.769	sheep	99.8	0	O	ME-SA	PanAsia-2	ANT-10
viba_52087	TUR/106/2022.654	sheep	99.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_52132	TUR/143/2022.769	sheep	99.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_52082	TUR/101/2022.635	sheep	99.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_48434	IRN/22/2020	bovine	98.7	0	O	ME-SA	PanAsia-2	ANT-10
viba_48394	IRN/5/2020	bovine	98.6	0	O	ME-SA	PanAsia-2	ANT-10
viba_48418	IRN/15/2020	sheep	98.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_48398	IRN/7/2020	bovine	98.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_48390	IRN/4/2020	bovine	98.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_48402	IRN/8/2020	bovine	98.3	0	O	ME-SA	PanAsia-2	ANT-10





O/ME-SA/PanAsia-2^{ANT10}, Oman



Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_52311	OMN/22Z/2116/2020_186	cattle	100.0	0	O	ME-SA	PanAsia-2	ANT-10
viba_52359	OMN/22Z/2053/2020_92	cattle	100.0	0	O	ME-SA	PanAsia-2	ANT-10
viba_52295	OMN/22Z/2024/2020_59	cattle	100.0	0	O	ME-SA	PanAsia-2	ANT-10
viba_52307	OMN/22Z/2027/2020_62	cattle	100.0	0	O	ME-SA	PanAsia-2	ANT-10
viba_52291	OMN/22Z/2023/2020_58	cattle	100.0	0	O	ME-SA	PanAsia-2	ANT-10
viba_52315	OMN/22Z/2117/2020_187	cattle	100.0	0	O	ME-SA	PanAsia-2	ANT-10
viba_52303	OMN/22Z/2026/2020_61	cattle	100.0	0	O	ME-SA	PanAsia-2	ANT-10
viba_52299	OMN/22Z/2025/2020_60	cattle	99.8	0	O	ME-SA	PanAsia-2	ANT-10
viba_48434	IRN/22/2020	bovine	99.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_52242	OMN/22Z/1992/2020_11	cattle	99.4	0	O	ME-SA	PanAsia-2	ANT-10

Most Closely Related Sequences

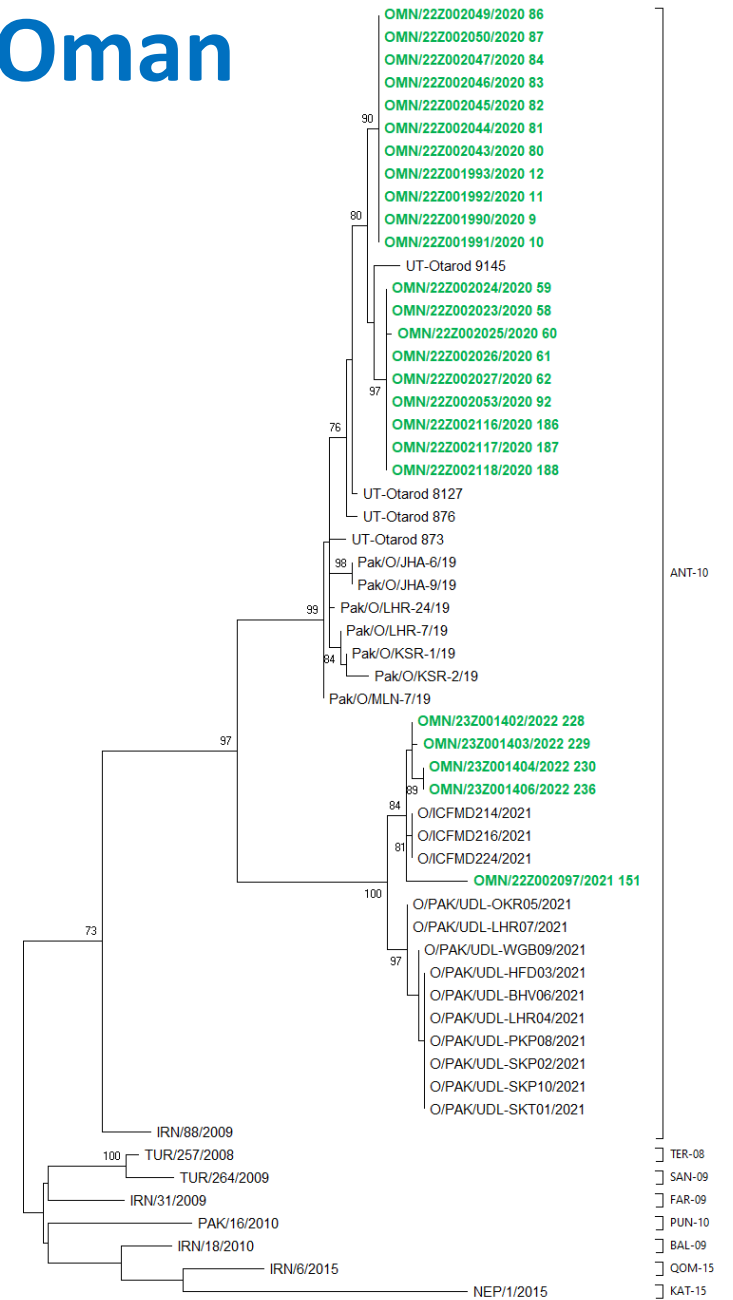
sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_50317	PAK/3/2021	cattle	98.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_50954	UAE/2/2021	Arabian oryx	98.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_50325	PAK/6/2021	cattle	98.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_50341	PAK/12/2021	water buffalo	98.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_50950	UAE/1/2021	Arabian oryx	98.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_50313	PAK/1/2021	cattle	98.1	0	O	ME-SA	PanAsia-2	ANT-10
viba_52157	ICFMD/IND/216/2021		98.1	0	O	ME-SA	PanAsia-2	ANT-10
viba_50357	PAK/16/2021	cattle	98.1	0	O	ME-SA	PanAsia-2	ANT-10
viba_52153	ICFMD/IND/215/2021		98.1	0	O	ME-SA	PanAsia-2	ANT-10
viba_50385	PAK/40/2021	cattle	98.1	0	O	ME-SA	PanAsia-2	ANT-10



O/ME-SA/PanAsia-2^{ANT10}, Oman



➤ Most closely related sequences from India and Iran



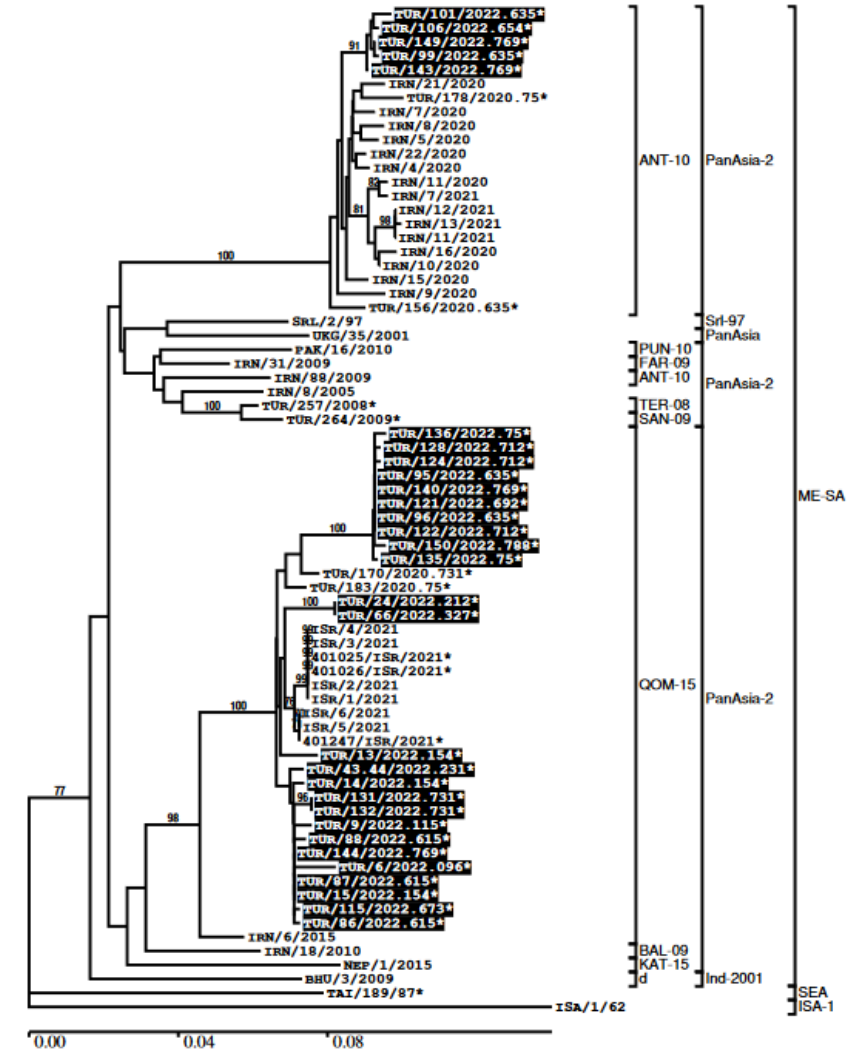
O/ME-SA/PanAsia-2^{QOM15} : still present



O/ME-SA/PanAsia-2^{QOM15}, Türkiye

- Outbreak in 2022
- Most closely related sequences from Israel
- Becoming dominant in Türkiye?

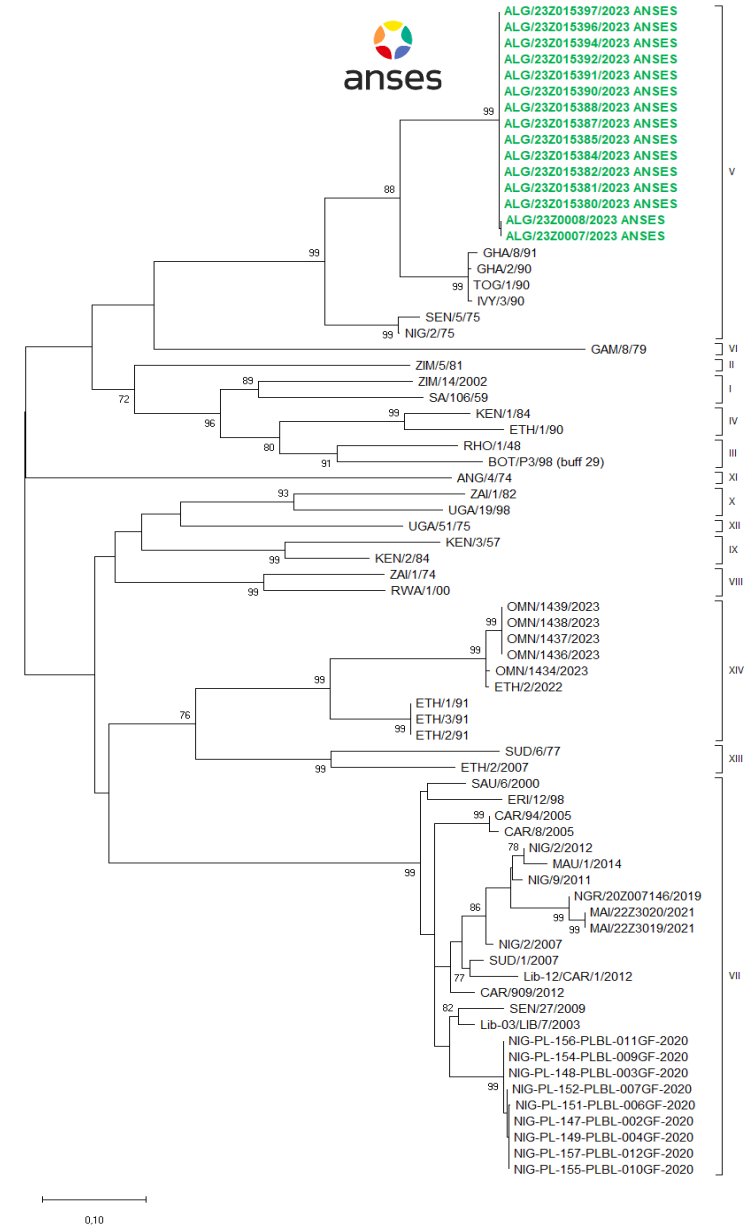
Most Closely Related Sequences								
sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_47559	ISR/5/2021	cattle	98.6	0	O	ME-SA	PanAsia-2	QOM-15
viba_47237	401247/ISR/2021	cattle	98.6	0	O	ME-SA	PanAsia-2	QOM-15
viba_47563	ISR/6/2021	cattle	98.6	0	O	ME-SA	PanAsia-2	QOM-15
viba_52041	TUR/15/2022.154	cattle	98.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_52136	TUR/144/2022.769	sheep	98.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_52037	TUR/14/2022.154	cattle	98.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_52061	TUR/87/2022.615	cattle	98.4	0	O	ME-SA	PanAsia-2	QOM-15
viba_52057	TUR/86/2022.615	cattle	98.3	0	O	ME-SA	PanAsia-2	QOM-15
viba_52029	TUR/9/2022.115	sheep	98.3	0	O	ME-SA	PanAsia-2	QOM-15
viba_52091	TUR/115/2022.673	sheep	98.3	0	O	ME-SA	PanAsia-2	QOM-15



SAT2/V : a new threat?

SAT2/V

- ❑ FMDV outbreak in Algeria in December 2023 (2 locations)
- ❑ Samples received at EURL at the end of December 2023
- ❑ Positive results in rtRT-PCR, viral isolation and Ag ELISA (serotype SAT2)
- ❑ **SAT2/V identified**
- ❑ **Unexpected result (last report of this serotype was in West Africa in 1991)**
- ❑ **Specific SAT2/V rtRT-PCR has been developed and shared with Algeria and Tunisia**
- ❑ Origin still unknown



SAT2/V

- ❑ Vaccine matching results indicate a good match with several vaccines

FMD Vaccine Matching Strain Differentiation Report

Lab Reference Batch Number: WRLFMD/2024/000002 **Report Date:** 16/02/2024
Report Number: 3473
Date Tests Completed: 08/02/2024 **Country of Origin*:** Algeria

2dm VNT r1 RESULTS

	SAT2 ALG/4/2023	SAT2 ALG/6/2023
SAT2 Eritrea 98, Boehringer Ingelheim	0.70, 1.58	0.72, 1.59
SAT2 OMN 2015 Biogénesis Bagó	0.42, 2.52	0.59, 2.67
SAT2 Zim 83, Boehringer Ingelheim	0.40, 2.07	0.40, 2.07

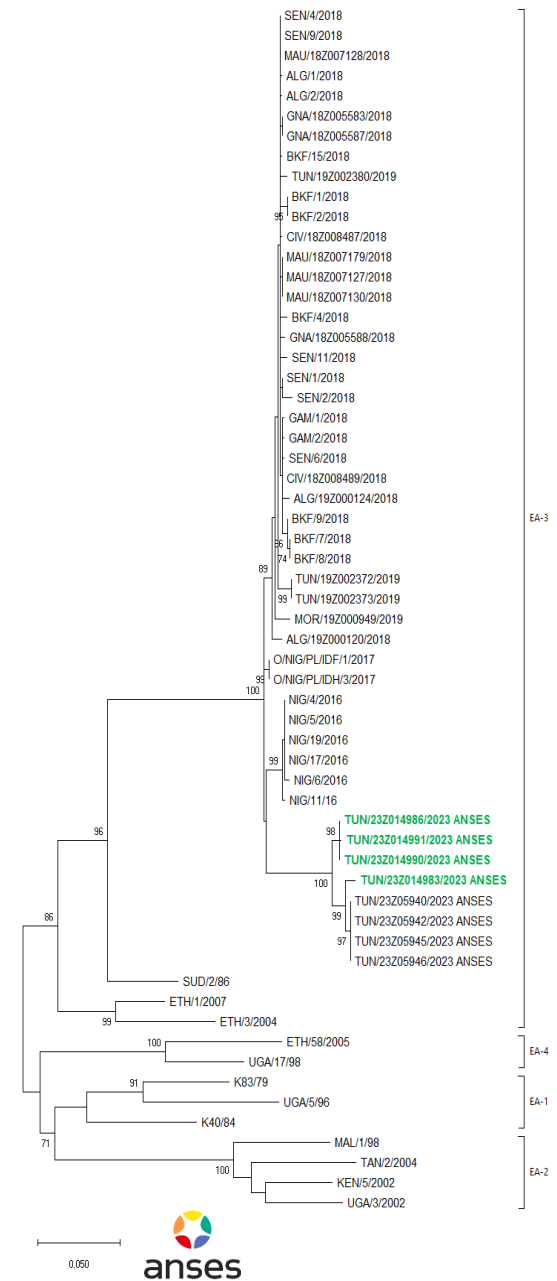


O/EA-3 : still a threat to North Africa



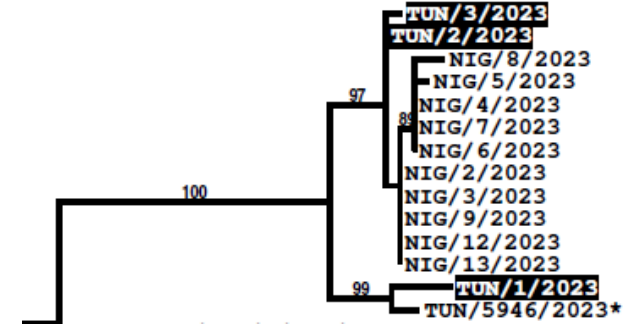
O/EA-3, Tunisia

- ❑ FMDV outbreaks in Tunisia from November to December 2023 (3 locations)
- ❑ Samples received at EURL at the end of December 2023
- ❑ Positive results in rtRT-PCR, viral isolation and Ag ELISA (serotype O)
- ❑ **O/EA-3 identified (topotype previously identified few months ago in the country)**





O/EA-3, Tunisia



Genotyping results from WRL indicate a proximity with isolates from Nigeria

Vaccine matching results indicate a good match with several vaccines

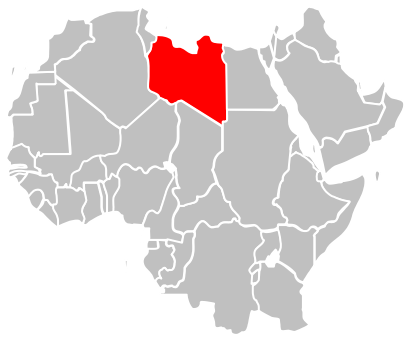
FMD Vaccine Matching Strain Differentiation Report - Final

Lab Reference Batch Number: WRLFMD/2024/000003 Report Date: 04/03/2024
 Report Number: 3677
 Date Tests Completed: 29/02/2024 Country of Origin*: Tunisia

2dm VNT r1 RESULTS

	O TUN/1/2023	O TUN/2/2023	O TUN/3/2023
O1 Campos, Biogénesis Bagó	0.98, 2.76	0.66, 2.59	0.78, 2.66
O-3039, Boehringer Ingelheim	0.90, 1.86	0.63, 1.71	0.77, 1.79
O Campos, Boehringer Ingelheim	0.47, 2.11	0.32, 1.93	0.32, 1.93
O Manisa, Boehringer Ingelheim	0.93, 2.22	0.45, 1.91	0.54, 1.98
O Panasia 2, Boehringer Ingelheim	0.42, 2.11	0.31, 1.98	0.32, 1.99
O/TUR/5/09, MSD Animal Health	0.62, 2.24	0.39, 2.03	0.46, 2.11



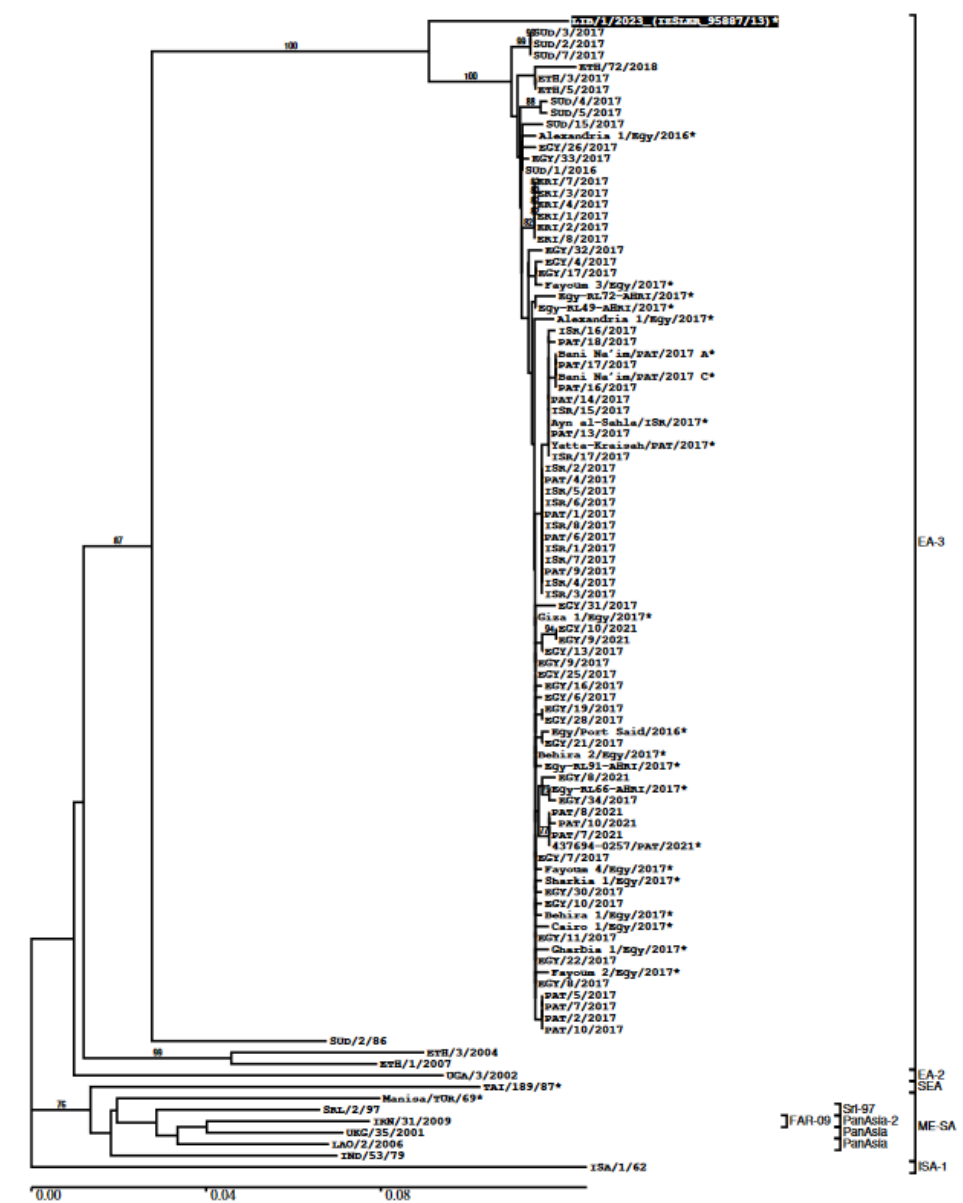


O/EA-3, Libya

- On March 2023, FMD outbreak in Libya
- Most closely related sequences : Egypt from 2017
- New introduction in Libya?

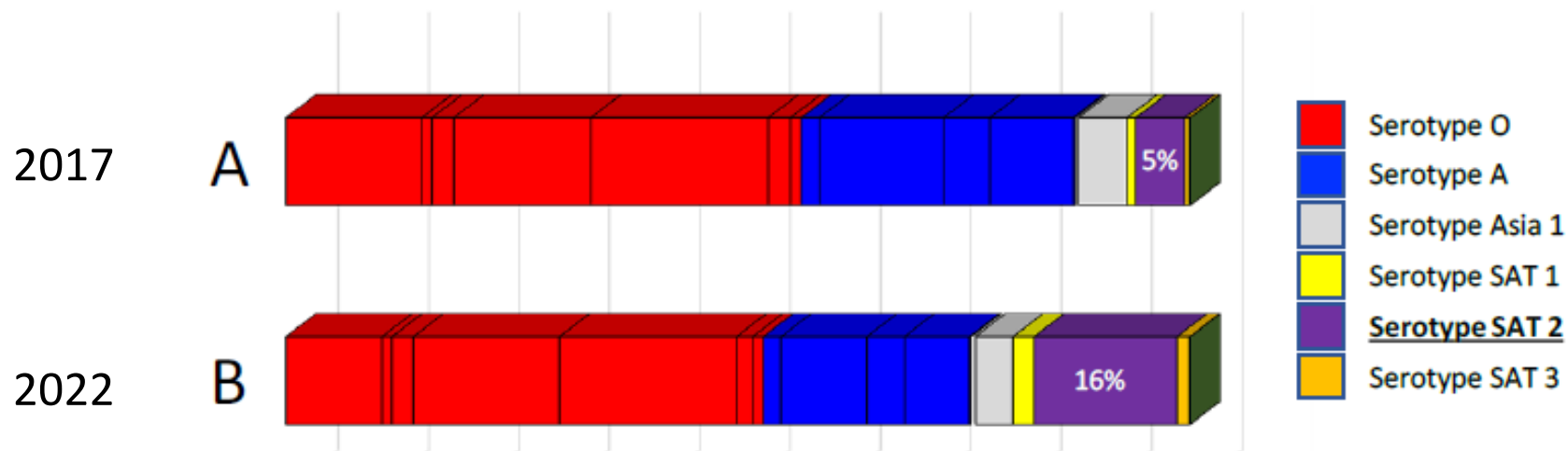
Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_34187	EGY/13/2017	cattle	94.8	0	O	EA-3		
viba_34203	EGY/21/2017	cattle	94.8	0	O	EA-3		
viba_37049	SUD/7/2017	cattle	94.6	0	O	EA-3		
viba_37033	SUD/2/2017	cattle	94.6	0	O	EA-3		
viba_35505	Giza 1/Egy/2017		94.6	0	O	EA-3		
viba_39472	Egy/Port Said/2016	cattle	94.6	0	O	EA-3		
viba_37029	SUD/1/2016	cattle	94.6	0	O	EA-3		
viba_34207	EGY/22/2017	water buffalo	94.6	0	O	EA-3		
viba_34211	EGY/25/2017	cattle	94.6	0	O	EA-3		
viba_35525	Behira 2/Egy/2017		94.6	0	O	EA-3		



Estimated risks to mainland Europe

- No direct measures of entry routes
- Source of FMD influences risk of different serotypes / strains
- Direct impact on FMD vaccine antigen prioritization
- Since SAT2/XIV outbreaks, the risks have changed

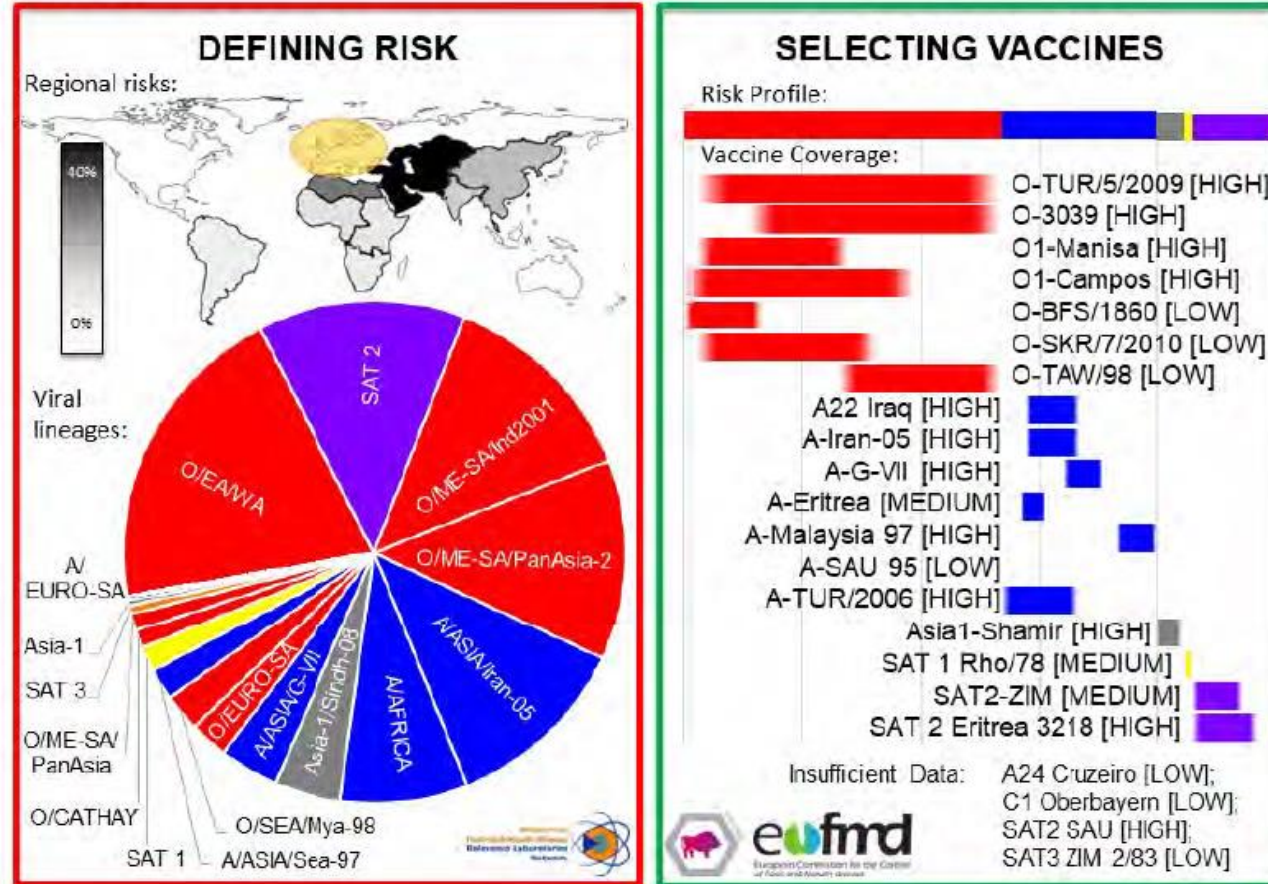


Source: FMD quarterly report April-June 2023 (WRL)

Vaccine recommendations

Vaccine Antigen Prioritisation: Europe

April 2024



NB: Analyses uses best available data, however there are gaps in surveillance and vaccine coverage data

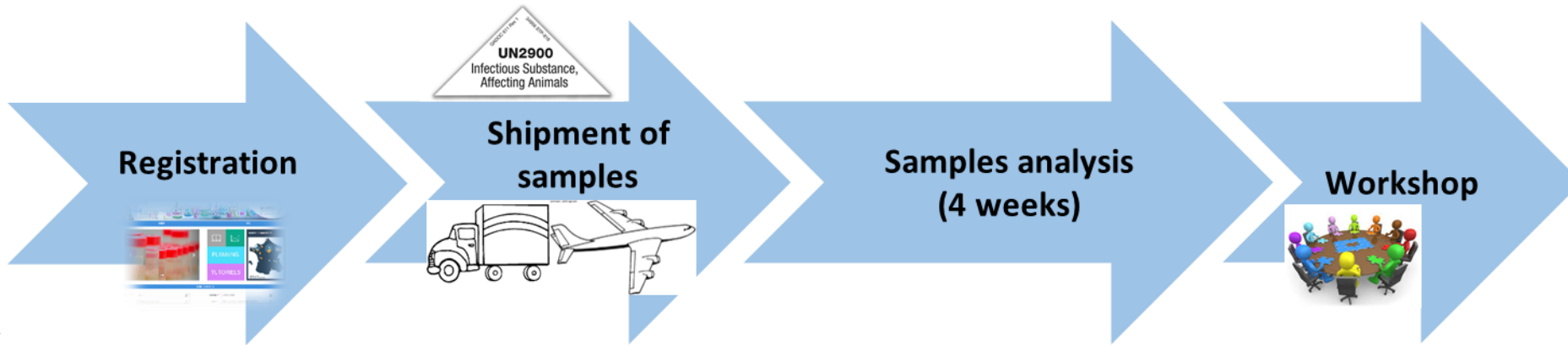
www.pirbright.ac.uk

Source: FMD quarterly report Jan-Apr 2024 (WRL)

How EURL contributes to the global effort against FMD?

Proficiency test organization

Each year, a proficiency test is organized through the European Union (including Member states, candidate countries and neighboring countries)



Panel 1: Live virus
 Panel 2: Inactivated virus
 Panel 3: Sera (FMDV/SVDV antibodies)

	2020	2021	2022	2023
Invited laboratories	40	44	52	46
Participants	38	42	46	46



Improvement of laboratory diagnostic capacity and emergency response

05-16/03/2018 (LDV, Madagascar)
13-30/04/2018 (LNERV, Senegal)



17th-21st June 2019
AQPA South Korea



July 18th – 22nd 2022
Montenegro, Slovenia, Kosovo,
Moldova, Albania



12-16/06/2023
North Africa countries



26-30/06/2023
Middle East countries



03-07/07/2023
SEEN countries



06-17/11/2023
EU countries (EuFMD)



27/11-08/12/2023
Serbia (EURL)



11/03-22/03/2024
EURL



Improvement of laboratory diagnostic capacity and emergency response

Regional training on FMD epidemiology and diagnostics



Mauritania, 03-09/10/2018

Regional training on FMD epidemiology and diagnostics



Guinea, 22-26/10/2018



Abidjan, 25-28/02/2019



WOAH Reference Laboratory for Foot-and-Mouth Disease
 Reference Centre  World Organisation for Animal Health
 Founded as OIE





World Organization for Animal Health (WOAH)



<https://wahis.woah.org/#/home>

Food and Agriculture Organization (FAO)



<http://empres-i.fao.org/>



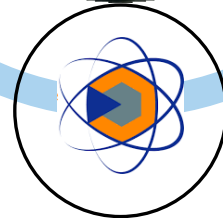
European Commission for the Control of Foot-and-Mouth Disease (EuFMD)



<https://www.eufmd.info/fastreports>

WOAH/FAO FMD Reference Laboratory Network

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



<https://www.wrlfmd.org/ref-lab-reports>



Thank you for your attention !



World Organisation
for Animal Health
Founded as OIE



Food and Agriculture
Organization of the
United Nations



WOAH/FAO FMD Reference
Laboratory Network



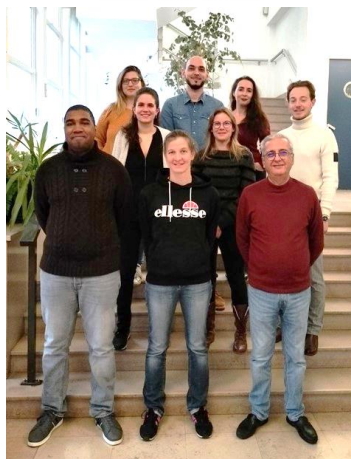
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Biology of Picornaviruses Team



Exotic Viruses and Particular Diseases Team